Multilevel and Longitudinal Modeling Using Stata

Volume I: Continuous Responses

Third Edition

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To my children Astrid and Inge
Anders Skrondal

To Simon
Sophia Rabe-Hesketh

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Preface

This book is about applied multilevel and longitudinal modeling. Other terms for multilevel models include hierarchical models, random-effects or random-coefficient models, mixed-effects models, or simply mixed models. Longitudinal data are also referred to as panel data, repeated measures, or cross-sectional time series. A popular type of multilevel model for longitudinal data is the growth-curve model.

The common theme of this book is regression modeling when data are clustered in some way. In cross-sectional settings, students may be nested in schools, people in neighborhoods, employees in firms, or twins in twin-pairs. Longitudinal data are by definition clustered because multiple observations over time are nested within units, typically subjects.

Such clustered designs often provide rich information on processes operating at different levels, for instance, people's characteristics interacting with institutional characteristics. Importantly, the standard assumption of independent observations is likely to be violated because of dependence among observations within the same cluster. The multilevel and longitudinal methods discussed in this book extend conventional regression to handle such dependence and exploit the richness of the data.

Volume 1 is on multilevel and longitudinal modeling of continuous responses using linear models. The volume consists of four parts: I. Preliminaries (a review of linear regression modeling, preparing the reader for the rest of the book), II. Two-level models, III. Models for longitudinal and panel data, and IV. Models with nested and crossed random effects. For readers who are new to multilevel and longitudinal modeling, the chapters in part II should be read sequentially and can form the basis of an introductory course on this topic. A one-semester course on multilevel and longitudinal modeling can be based on most of the chapters in volume 1 plus chapter 10 on binary or dichotomous responses from volume 2. For this purpose, we have made chapter 10 freely downloadable from http://www.stata-press.com/books/mlmus3_ch10.pdf.

Volume 2 is on multilevel and longitudinal modeling of categorical responses, counts, and survival data. This volume also consists of four parts: I. Categorical responses (binary or dichotomous responses, ordinal responses, and nominal responses or discrete choice), II. Counts, III. Survival (in both discrete and continuous time), and IV. Models with nested and crossed random effects. Chapter 10 on binary or dichotomous responses is a core chapter of this volume and should be read before embarking on the other chapters. It is also a good idea to read chapter 14 on discrete-time survival before reading chapter 15 on continuous-time survival.

Our emphasis is on explaining the models and their assumptions, applying the methods to real data, and interpreting results. Many of the issues are conceptually demanding but do not require that you understand complex mathematics. Wherever possible, we therefore introduce ideas through examples and graphical illustrations, keeping the technical descriptions as simple as possible, often confining formulas to subsections that can be skipped. Some sections that go beyond an introductory course on multilevel and longitudinal modeling are tagged with the symbol ❖ . Derivations that can be skipped by the reader are given in displays. For an advanced treatment, placing multilevel modeling within a general latent-variable framework, we refer the reader to Skrondal and Rabe-Hesketh (2004a), which uses the same notation as this book.

This book shows how all the analyses described can be performed using Stata. There are many advantages of using a general-purpose statistical package such as Stata. First, for those already familiar with Stata, it is convenient not having to learn a new standalone package. Second, conducting multilevel-analysis within a powerful package has the advantage that it allows complex data manipulation to be performed, alternative estimation methods to be used, and publication-quality graphics to be produced, all without having to switch packages. Finally, Stata is a natural choice for multilevel and longitudinal modeling because it has gradually become perhaps the most powerful general-purpose statistics package for such models.

Each chapter is based on one or more research problems and real datasets. After describing the models, we walk through the analysis using Stata, pausing when statistical issues arise that need further explanation. Stata can be used either via a graphical user interface (GUI) or through commands. We recommend using commands interactively—or preferably in do-files—for serious analysis in Stata. For this reason, and because the GUI is fairly self-explanatory, we use commands exclusively in this book. However, the GUI can be useful for learning the Stata syntax. Generally, we use the `typewriter font` to refer to Stata commands, syntax, and variables. A "dot" prompt followed by a command indicates that you can type verbatim what is displayed after the dot (in context) to replicate the results in the book. Some readers may find it useful to intersperse reading with running these commands. We encourage readers to write do-files for solving the data analysis exercises because this is standard practice for professional data analysis.

The commands used for data manipulation and graphics are explained to some extent, but the purpose of this book is not to teach Stata from scratch. For basic introductions to Stata, we refer the reader to Acock (2010), Kohler and Kreuter (2009), or Rabe-Hesketh and Everitt (2007). Other books and further resources for learning Stata are listed at the Stata website.

If you are new to Stata, we recommend running all the commands given in chapter 1 of volume 1. A list of commands that are particularly useful for manipulating, describing, and plotting multilevel and longitudinal data is given in the appendix of volume 1. Examples of the use of these and other commands can easily be found by referring to the "commands" entry in the subject index.

We have included applications from a wide range of disciplines, including medicine, economics, education, sociology, and psychology. The interdisciplinary nature of this book is also reflected in the choice of models and topics covered. If a chapter is primarily based on an application from one discipline, we try to balance this by including exercises with real data from other disciplines. The two volumes contain over 140 exercises based on over 100 different real datasets. Solutions to exercises that are available to readers are marked with Solutions and can be downloaded from http://www.stata-press.com/books/mlmus3-answers.html. Instructors can obtain solutions to all exercises from Stata Press.

All datasets used in this book are freely available for download; for details, see http://www.stata-press.com/data/mlmus3.html. These datasets can be downloaded into a local directory on your computer. Alternatively, individual datasets can be loaded directly into net-aware Stata by specifying the complete URL. For example,

```
. use http://www.stata-press.com/data/mlmus3/pefr
```

If you have stored the datasets in a local directory, omit the path and just type

```
. use pefr
```

We will generally describe all Stata commands that can be used to fit a given model, discussing their advantages and disadvantages. An exception to this rule is that we do not discuss our own `gllamm` command in volume 1 (see the `gllamm` companion, downloadable from http://www.gllamm.org, for how to fit the models of volume 1 in `gllamm`). In volume 1, we extensively use the Stata commands `xtreg` and `xtmixed`, and we introduce several more specialized commands for longitudinal modeling, such as `xthtaylor`, `xtivreg`, and `xtabond`. The new `sem` command for structural equation modeling is used for growth-curve modeling.

In volume 2, we use Stata's `xt` commands for the different response types. For example, we use `xtlogit` and `xtmelogit` for binary responses, and `xtpoisson` and `xtmepoisson` for counts. We use `stcox` and `streg` for multilevel survival modeling with shared frailties. `gllamm` is used for all response types, including ordinal and nominal responses, for which corresponding official Stata commands do not yet exist. We also discuss commands for marginal models and fixed-effects models, such as `xtgee` and `clogit`. The *Stata Longitudinal-Data/Panel-Data Reference Manual* (StataCorp 2011) provides detailed information on all the official Stata commands for multilevel and longitudinal modeling.

The `nolog` option has been used to suppress the iteration logs showing the progress of the log likelihood. This option is not shown in the command line because we do not recommend it to users; we are using it only to save space.

We assume that readers have a good knowledge of linear regression modeling, in particular, the use and interpretation of dummy variables and interactions. However, the first chapter in volume 1 reviews linear regression and can serve as a refresher.

Errata for different editions and printings of the book can be downloaded from http://www.stata-press.com/books/errata/mlmus3.html, and answers to exercises can be downloaded from http://www.stata-press.com/books/mlmus3-answers.html.

In this third edition, we have split the book into two volumes and have added five new chapters, comprehensive updates for Stata 12, 49 new exercises, and 36 new datasets. All chapters of the previous edition have been substantially revised.

Berkeley and Oslo Sophia Rabe-Hesketh
February 2012 Anders Skrondal

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Some journals, such as *Biometrics*, *Journal of Applied Econometrics*, *Journal of Business & Economic Statistics*, *Journal of the Royal Statistical Society (Series A)*, and *Statistical Modelling*, encourage authors to make their data available on the journal website. We are grateful to J. Abrevaya, P. K. Chintagunta, N. Goldman, D. C. Jain, E. Lesaffre, D. Moore, E. Ross, G. Rodríguez, B. Spiessens, F. Vella, M. Verbeek, N. J. Vilcassim, and R. Winkelmann for making their data available this way.

We also used datasets from textbooks with accompanying webpages; some of these datasets are available (together with worked examples using various software packages, including Stata) through UCLA Technology Services
(see http://www.ats.ucla.edu/stat/examples/default.htm). The books by Allison (1995, 2005); Baltagi (2008); Bollen and Curran (2006); Brown and Prescott (2006); Cameron

and Trivedi (2005); De Boeck and Wilson (2004); Davis (2002); DeMaris (2004); Dohoo, Martin, and Stryhn (2010); Fitzmaurice, Laird, and Ware (2011); Fox (1997); Frees (2004); Gelman and Hill (2007); Greene (2012); Johnson and Albert (1999); Hand et al. (1994); Hayes and Moulton (2009); Littell et al. (2006); O'Connell and McCoach (2008); Rabe-Hesketh and Everitt (2007); Singer and Willett (2003); Skrondal and Rabe-Hesketh (2004b); Therneau and Grambsch (2000); Train (2009); Vonesh and Chinchilli (1997); Weiss (2005); West, Welch, and Galecki (2007); and Wooldridge (2010) were particularly helpful in this regard.

Sometimes data are printed in papers or books, allowing patient people like us to type them. Data were provided in this form by D. Altman, W. S. Aranov, G. E. Battese, M. Bland, D. T. Burwell, D. T. Danahy, W. A. Fuller, R. M. Harter, G. Koch, A. J. Macnab, R. Mare, R. Prakash, and P. Sham.

We thank Chapman & Hall/CRC for permission to use figures and tables from our book *Generalized Latent Variable Modeling: Multilevel, Longitudinal and Structural Equation Models*.

Any omissions are purely accidental.

Multilevel and longitudinal models: When and why?

Just as in standard regression analysis, the purpose of multilevel modeling is to model the relationship between a response variable and a set of explanatory variables. The difference is that multilevel modeling involves units of observation at different "levels".

For example, when considering the salaries of professors at universities, the levels could be individual professors (level 1), departments (level 2), or universities (level 3). Explanatory variables or covariates often reside at a given level. For instance, professors are characterized by their productivity, departments by the marketability of the discipline, and universities by whether they are private or public. If university-level explanatory variables are of interest, it might appear necessary to treat university as the unit of analysis by regressing university-mean-salaries on characteristics of universities.

If professor-level explanatory variables are aggregated to the university level for a university-level analysis, the estimated relationships are generally different from those found if professor is treated as the unit of analysis. Interpreting associations at the higher level as pertaining to the lower level is known as the *ecological fallacy*, whereas the reverse is called the *atomistic fallacy*. Instead of having to make a decision regarding the unit of analysis, we can use multilevel modeling to avoid the fallacies by considering all levels simultaneously and including explanatory variables from the professor, department, and university levels.

There is a preponderance of multilevel data. Examples discussed in this book include patients in hospitals[1], children in classes or schools[2], soldiers in army companies[3], residents in neighborhoods[4] or countries[5], siblings in families[6], rat pups in litters[7], cows in herds[8], eyes on heads[9], twins in twin-pairs[10], and police stops in city precincts[11].

Level-1 units within the same level-2 unit or cluster tend to be more similar to each other than to units in other clusters. One reason for this is that units do not end up in the same cluster by chance but through some mechanism that may be related to their characteristics. For instance, which schools children go to is influenced by their family background through the place of residence or parental choice, so children within a school already have something in common from the first day of school. Perhaps more importantly, children within a school are subsequently affected by their peers, teachers, and school policies, making them even more similar. Such within-school similarity or dependence will be particularly apparent if there are large between-school differences in terms of children's backgrounds and school environment and policies. In the same vain,

siblings are similar at birth because they have the same parents and therefore share genes, and they subsequently become even more similar by being raised in the same family, where they share a common environment and experiences.

Within-cluster dependence violates the assumption of ordinary regression models that responses are conditionally independent given the covariates (the residuals are independent). Consequently, ordinary regression produces incorrect standard errors, a problem that can be overcome by using multilevel models.

More importantly, multilevel modeling allows us to disentangle processes operating at different levels, both by including explanatory variables at the different levels and by attributing unexplained variability to the different levels. One important challenge in multilevel modeling is to distinguish within- and between-cluster effects of lower-level covariates. For instance, for students nested in schools, an important student-level explanatory variable for achievement is socioeconomic status (SES). In addition to the effect of own SES, the school-average SES can be strongly associated with achievement, both through peer effects and because low-SES children tend to end up in worse schools.

Policy interventions often occur at the level of institutions, and it is important to understand how such higher-level variables affect the response variable. In the school setting, typical examples would be new curricula or different kinds of teacher professional development. The effect of such interventions on achievement is usually the primary concern, but it is also important to investigate the differential effects for different student subpopulations. For instance, a new science curriculum may be particularly beneficial for girls and hence reduce the gender gap in science achievement. If it does, then there is a cross-level interaction between the level-1 variable gender and the level-2 variable curriculum.

It will generally not be possible to explain all within-school and between-school variability in achievement. Quantifying the amount of unexplained variability at the different levels can be of interest in its own right, and sometimes multilevel models without explanatory variables are used to see how much the higher-level membership matters. For instance, achievement may vary less between schools in Scandinavia than in the U.S., and this tells us something about the societies and schooling systems.

Repeated observations on the same units are also clustered data, for instance, longitudinal or panel data on children's weight[12], mothers' postnatal depression[13], taxpayers' tax liability[14], employees' wages and union membership[15], and the investments[16] or number of patents[17] of firms. Although longitudinal data are quite different from clustered cross-sectional data, the same kinds of questions arise and the same kinds of models can be used to address them. For instance, for data on children's weight, growth is about the relationship between weight and the level-1 variable time. Level-2 explanatory variables include gender and ethnicity. Cross-level interactions between these variables and time represent differences in growth rates between groups. Clearly, not all differences in initial weight and growth rate can be explained by gender and ethnicity, and multilevel models can quantify how much variability remains within groups.

Disentangling the within- and between-effects of level-1 (or time-varying) covariates can be important for causal inference. For instance, evaluation of policies, such as bans of smoking in public places, typically rely on observational data where policies were implemented for some of the clusters, such as states, at different times during the longitudinal study. When considering the effect of the legislation on cigarette consumption, it is important to estimate the within-state effects, to control for any state-level variables that affect legislation as well as cigarette consumption. Within-state effects could of course be due to general time trends, which can be controlled by considering the mean difference in within-state differences for states that did and did not implement the policy.

Sources of multilevel and longitudinal data

Multistage surveys

In surveys, units are randomly selected according to a careful survey design to produce results that are representative of a population. The simplest design is simple random sampling, where every unit has the same probability of selection. However, such designs require a list of all eligible units, which is rarely available. Furthermore, it is often cheaper to sample units in batches, and for this reason, samples are often drawn in stages. In the first stage, primary sampling units (PSUs) such as areas or schools are sampled (often within strata). Lists of units within these PSUs are then assembled and units sampled from these lists. The resulting data are highly clustered by design. In contrast, simple random sampling will often lead to a few instances of multiple units per cluster.

In this book, we consider several multistage surveys, including the British Social Attitudes Survey (BSA)[18] and the Program for International Student Assessment (PISA)[19]. In the BSA, PSUs were postcode sectors, from which addresses were sampled in stage 2 and one respondent per household was selected in stage 3. In the PISA, a large number of countries conducted surveys by first sampling regions and then schools, or by directly sampling schools. In the final stage, students were sampled from schools.

Often the design falls short of being a proper survey in the sense that the PSUs, or clusters, are selected by convenience. Another important source of clustered data is administrative data—such as national death registries, hospital patient databases, and social security claims databases—collected by government and other institutions that cover an entire well-defined population. Administrative data are often linked with other administrative data, survey data, and census data.

Examples are the family birthweight data[20] from the Medical Birth Registry of Norway, and the neighborhood-effects data[21] from an education authority in Scotland. In the latter data, pupils' national examination test scores from the Examination Board were linked to survey data on individual characteristics, family background, and census data on the neighborhoods. Aggregate economic data[22], such as unemployment rates for regions of a country, are typically provided by the national statistical agencies, whereas

international data are provided by organizations such as the Organization for Economic Cooperation and Development (OECD)[23].

A good book on multistage surveys is Heeringa, West, and Berglund (2010).

Cluster-randomized studies

Health, educational, and other interventions are often administered to groups or clusters of individuals. For instance, sex education for teenagers typically takes place in school classes. Randomized experiments to study the effectiveness of such interventions therefore naturally rely on assigning entire clusters of subjects to interventions. Such studies are called cluster-randomized trials. Another reason for not assigning different units in the same cluster to different interventions is that there may be a risk of contamination in the sense that someone assigned to the control intervention may benefit from the treatment given to another subject. An example would be if the intervention group is given a cookbook for healthy eating and these subjects end up sharing meals and recipes with those in the control group.

Cluster-randomized studies considered in this book include Scottish schools assigned to sex education programs[24], Kenyan schools assigned to nutritional interventions[25], and U.S. schools assigned to a smoking prevention and cessation program[26].

In quasi-experiments, assignment to treatments or interventions is not random. An example considered in this book is a study by the World Health Organization (WHO) where hospitals in one region of China implemented a program of case management to discourage inappropriate prescription of antibiotics to young children with acute respiratory infection[27]. Another example is where some cities were declared as enterprise zones that provided tax credits to reduce unemployment whereas other cities served as controls[28]. Here deprived cities were more likely to be declared as enterprise zones because the intervention was more needed there.

A good book on cluster-randomized trials is Hayes and Moulton (2009).

Multisite studies and meta-analysis

Clinical trials and other randomized intervention studies are often conducted at several sites, either because individual sites do not have enough eligible patients to obtain reliable results or because data from several settings can provide evidence that the effects hold more generally (external validity). The important difference between a multisite and a cluster-randomized design is that the randomization is within clusters in a multisite study, with each site constituting its own, usually small, randomized study. Examples include a hypertension trial conducted at 29 centers[29] and a class-size experiment conducted in 79 schools[30].

Meta-analysis is used to summarize the evidence accumulated to date about a treatment from a range of published studies. The idea is similar to a multisite trial in that

each study constitutes a (typically randomized) trial in a different setting. However, the differences between studies tend to be more fundamental, often with important variations in the treatments, protocols, and outcome measures. Another distinguishing feature of a meta-analysis is that the data from the different studies are typically available only in aggregated form, in terms of estimated effect sizes and standard errors[31]. Meta-analysis is used not only to estimate treatment effects but is useful also for pooling estimates of any kind across studies.

A good book on meta-analysis is Borenstein et al. (2009).

Family studies

Data on groups of more-or-less genetically related subjects are often collected to examine similarities between the subjects[32] and possibly to disentangle the sources of similarity into nature (genetics) and nurture (environment). In twin designs[33], comparison of identical twins (who share all genes) and fraternal twins (who share half their genes) allows the proportion of variability that is due to genes (heritability) to be estimated. Data on parents and their children can also be used to estimate heritability, as we do with birthweights[34] in this book.

A good book on analysis of family data is Sham (1998).

Longitudinal studies

In longitudinal or panel data, each unit is observed at several occasions over time. This makes it possible to study individual change, either due to the passage of time or due to explanatory variables.

Clinical trials are usually longitudinal because treatments take some time to have an effect. For instance, in a clinical trial for the treatment of postnatal depression, women were randomized to receive an estrogen patch or a placebo. They were assessed for depression before randomization and then monthly for six months after beginning treatment[35].

Panel surveys, where respondents are interviewed annually (in panel "waves") or at other regular time intervals, are popular in the social sciences. For example, the antisocial-behavior data[36] consist of three biennial waves of data from the U.S. National Longitudinal Survey of Youth on children and their mothers. A major advantage of longitudinal data is that it allows comparisons to be made within subject, hence controlling for (possibly unknown) subject characteristics that are constant over time. For instance, we can estimate the effect of child poverty on antisocial behavior by considering the change in antisocial behavior for children who move into or out of poverty.

Instead of passively observing explanatory variables, such as child poverty, in an observational study, we can sometimes apply a sequence of treatments or conditions to each subject over a set of occasions to allow within-subject comparisons to be made. In this

case, time or order effects are a nuisance and are typically dealt with by counterbalancing the order of the treatments (typically by random assignment). An example considered in this book is a four-period two-treatment double-blind cross-over trial where patients are randomized to receive different sequences of artificial sweetener and placebo, each taken for a week, and the number of headaches is recorded[37]. In contrast to regular clinical trials, the treatment effect is estimated using a within-subject comparison, giving more reliable estimates. Longitudinal designs with time-varying treatments are also important in experimental psychology, where they are called repeated-measures designs. For instance, in the verbal aggression data[38], there is a within-subject factorial design consisting of four situations that may cause aggression, three aggressive behaviors, and two modes of response.

Good books on the analysis of longitudinal data include Fitzmaurice, Laird, and Ware (2011) in biostatistics and Wooldridge (2010) in econometrics.

Measurement studies

Variables are usually treated as if they represent the concept implied by their name. For instance, achievement scores are viewed as representing achievement, and peak-expiratory-flow measurements are viewed as representing peak expiratory flow (strength of breathing out). However, even if the measures are valid (measure what they are supposed to measure and not something else), they are invariably subject to measurement error (that is, they differ from the true score). The amount and sources of measurement error can be investigated by conducting a measurement study, or generalizability study, where measurements of the same truth are repeated under different conditions. For example, in the peak-expiratory-flow study, subjects were measured on two occasions (test–retest data) by two different methods[39]. In the essay-grading data, several graders graded each of 198 essays[40]. Multilevel models can be used to estimate the measurement error variance and partition the measurement error variance into components due to different sources, such as raters and methods.

Item response theory (IRT) models for binary responses to test or questionnaire items can also be viewed as multilevel models. A typical application is measurement of students' math achievement[41].

A good book on the design and analysis of measurement studies is Dunn (2004).

Spatial data

Units are often expected to be more similar if they are located close together in space. If it makes sense to partition space into regions, the data can be viewed as clustered within the regions, such as zip codes, neighborhoods, counties, states, or countries. For example, in the skin-cancer data[42], the subjects are nested in counties, the counties are nested in regions, and the regions are nested in countries.

In small-area estimation, sparse data on small areas are used to estimate area-level means, proportions, or incidence rates. Area-specific estimates tend to be imprecise because of the low numbers, and some amount of averaging or pooling of data across areas is necessary to obtain more reliable estimates. Multilevel models can be used to estimate the variability between areas, and this information can be used to determine the adequate degree of pooling (shrinkage estimation or empirical Bayes prediction). A good display of small-area estimates is a map where areas are shaded according to the magnitudes of the estimates. If the estimates are disease rates, producing the maps is called disease mapping[43].

A good book on small-area estimation and disease mapping, from a multilevel modeling perspective, is Lawson, Browne, and Vidal Rodeiro (2003).

Notes

[1]Exercises 8.4 and 16.3

[2]Exercise 8.6

[3]Exercise 4.5

[4]Exercises 2.4 and 3.1

[5]Exercise 13.7

[6]Exercise 14.5

[7]Exercise 3.4

[8]Exercises 10.5 and 8.8

[9]Exercise 14.6

[10]Exercises 2.3 and 8.10

[11]Exercise 13.3

[12]Section 7.2

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[26]Exercises 11.3 and 14.7

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[40]Exercise 2.5 and section 11.9

[41]Exercise 16.10

[42]Exercise 16.7

[43]Section 13.13

Part I

Preliminaries

1 Review of linear regression

1.1 Introduction

In this chapter, we review the statistical models underlying independent-samples t tests, analysis of variance (ANOVA), analysis of covariance (ANCOVA), simple regression, and multiple regression. We formulate all of these models as linear regression models.

We take a model-based approach in this chapter; that is, we state all aspects of the model, including a normal distribution of the residuals. However, as we will see, statistical inferences can be valid even if some model assumptions, such as normality, are violated. We focus on model specification and interpretation of regression coefficients, and we discuss in detail the use of dummy variables and interactions.

The regression models considered here are essential building blocks for multilevel models. Although linear multilevel or mixed models for continuous responses are sometimes viewed from an ANOVA perspective, the regression perspective is beneficial because it is easily generalizable to binary and other types of responses. Furthermore, the Stata commands for multilevel modeling follow a regression syntax.

This chapter is not intended as a first introduction to linear regression, but rather as a refresher for readers already familiar with most of the ideas. Even experienced regression modelers are likely to benefit from reading this chapter because it introduces our notation and terminology as well as Stata commands used in later chapters, including factor variables for specifying dummy variables and interactions within estimation commands instead of creating new variables. If you are able to answer the self-assessment exercise 1.6 at the end of this chapter, you should be well prepared for the rest of the book.

1.2 Is there gender discrimination in faculty salaries?

DeMaris (2004) analyzed data on the salaries of faculty (academic staff) at Bowling Green State University in Ohio, U.S.A., in the academic year 1993–1994. The data are provided with his book *Regression with Social Data: Modeling Continuous and Limited Response Variables* and have previously been analyzed by Balzer et al. (1996) and Boudreau et al. (1997). The primary purpose of these studies was to investigate whether evidence existed for gender inequity in faculty salaries at the university.

The data considered here are a subset of the data provided by DeMaris, comprising $n = 514$ faculty members, excluding faculty from the Fireland campus, nonprofessors

(instructors/lecturers), those not on graduate faculty, and three professors hired as Ohio Board of Regents Eminent Scholars. We will use the following variables:

- `salary`: academic year (9-month) salary in U.S. dollars
- `male`: gender (1 = male; 0 = female)
- `market`: marketability of academic discipline, defined as the ratio of the national average salary paid in the discipline to the national average across all disciplines
- `yearsdg`: time since degree (in years)
- `rank`: academic rank (1 = assistant professor; 2 = associate professor; 3 = full professor)

We start by reading the data into Stata:

```
. use http://www.stata-press.com/data/mlmus3/faculty
```

If you already have a dataset open in Stata that you do not need to save, add the `clear` option:

```
. use http://www.stata-press.com/data/mlmus3/faculty, clear
```

1.3 Independent-samples t test

If we have an interest in gender inequity, an obvious first step is to compare mean salaries between male and female professors at the university. We can use the `tabstat` command to produce a table of means, standard deviations, and sample sizes by gender:

```
. tabstat salary, by(male) statistics(mean sd n)
Summary for variables: salary
     by categories of: male
  male |      mean        sd         N
-------+--------------------------------
 Women |   42916.6   9161.61       128
   Men |  53499.24  12583.48       386
-------+--------------------------------
 Total |  50863.87  12672.77       514
-------------------------------------------
```

We see that the male faculty at the university earn, on average, over $10,000 more than the female faculty. The standard deviation is also considerably larger for the men than for the women.

Due to chance or sampling variation, the large difference between the mean salary $\overline{y}_1$ of the n_1 men and the mean salary $\overline{y}_0$ of the n_0 women in the sample does not necessarily imply that the corresponding population means or *expectations* μ_1 and μ_0 for male and female faculty differ (the Greek letter μ is pronounced "mew"). Here *population* refers either to an imagined infinite population from which the data can

be viewed as sampled or to the statistical model that is viewed as the data-generating mechanism for the observed data.

To define a statistical model, let y_i and x_i denote the salary and gender of the ith professor, respectively, where $x_i = 1$ for men and $x_i = 0$ for women. A standard model for the current problem can then be specified as

$$y_i|x_i \sim N(\mu_{x_i}, \sigma^2_{x_i})$$

Here "$y_i|x_i \sim$" means "y_i, for a given value of x_i, is distributed as", and $N(\mu_{x_i}, \sigma^2_{x_i})$ stands for a normal distribution with conditional mean parameter μ_{x_i} and conditional variance parameter $\sigma^2_{x_i}$ (the Greek letter σ is pronounced "sigma"). The term *conditional* simply means that we are considering only the subset of the population for which some condition is satisfied—in this case, that x_i takes on a particular value. In other words, we are considering the distribution of salaries for men ($x_i = 1$) separately from the distribution for women ($x_i = 0$).

When conditioning on a categorical variable like gender, the expression "conditional on gender" can be replaced by "within gender" or "separately for each gender". Because x_i takes on only two values, we can be more explicit and write the statistical model as

$$\begin{aligned} y_i|x_i = 0 &\sim N(\mu_0, \sigma^2_0) \\ y_i|x_i = 1 &\sim N(\mu_1, \sigma^2_1) \end{aligned}$$

Each conditional distribution has its own conditional expectation, or conditional population mean,

$$\mu_{x_i} \equiv E(y_i|x_i)$$

denoted μ_1 for men and μ_0 for women ($\equiv$ stands for "defined as"). Each conditional distribution also has its own conditional variance

$$\sigma^2_{x_i} \equiv \mathrm{Var}(y_i|x_i)$$

denoted σ^2_1 for men and σ^2_0 for women. A final assumption is that y_i is conditionally independent of $y_{i'}$, given the values of x_i and $x_{i'}$, for different professors i and i'. This means that knowing one professor's salary does not help us predict another professor's salary if we already know that other professor's gender and the corresponding gender-specific mean salary.

By modeling y_i conditional on x_i, we are treating y_i as a *response variable* (sometimes also called dependent variable or criterion variable) and x_i as an *explanatory variable* or *covariate* (sometimes referred to as independent variable, predictor, or regressor).

The normality assumptions stated above are usually assessed by inspecting the conditional sample distributions for the men and women, using box plots,

```
. graph box salary, over(male) ytitle(Academic salary) asyvars
```

(see left panel of figure 1.1), or histograms,

```
. histogram salary, by(male, rows(2)) xtitle(Academic salary)
```

(see left panel of figure 1.2). We see that both distributions are somewhat positively skewed.

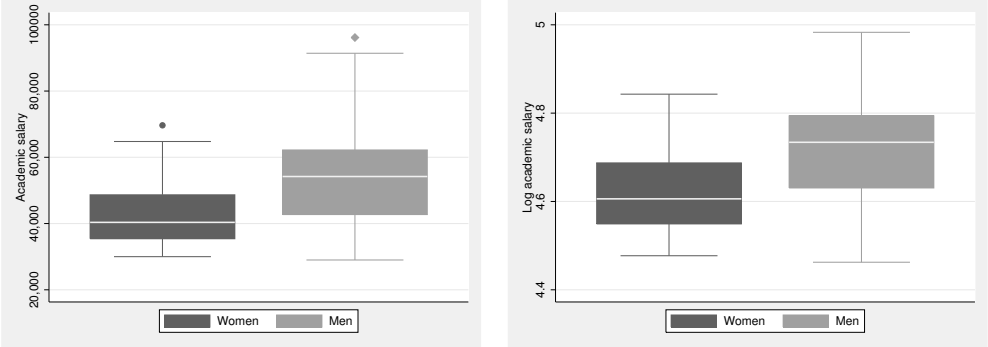


Figure 1.1: Box plots of salary and log salary by gender

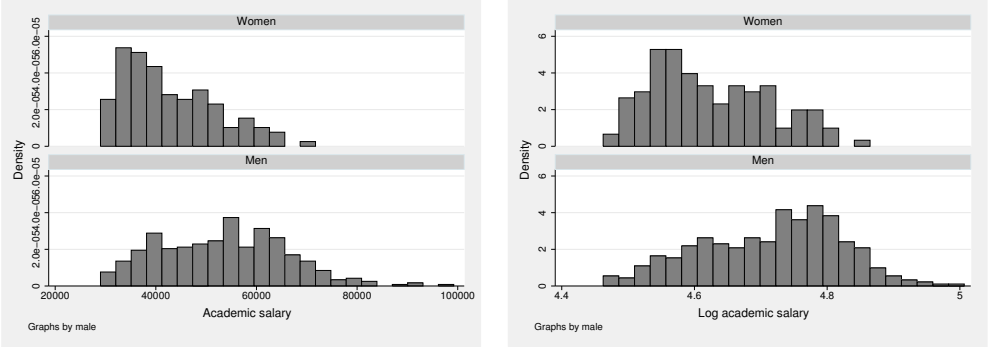


Figure 1.2: Histograms of salary and log salary by gender

A logarithmic transformation of salary makes the distributions more symmetric (like normal distributions)

```
. generate lsalary = log10(salary)
. graph box lsalary, over(male) ytitle(Log academic salary) asyvars
. histogram lsalary, by(male, rows(2)) xtitle(Log academic salary)
```

(see right panels of figures 1.1 and 1.2).

We have specified a full statistical model for the data and will now turn to making inferences about the means μ_0 and μ_1. Note that the methods of inference discussed in this chapter do not rely on the normality assumptions unless the sample is small.

We use the `ttest` command to estimate the population means, produce confidence intervals, and test the null hypothesis that the two population means are equal,

$$H_0\text{: } \mu_0 = \mu_1 \qquad \text{or} \qquad H_0\text{: } \mu_0 - \mu_1 = 0$$

against the two-sided alternative that they are different,

$$H_a\text{: } \mu_0 \neq \mu_1 \qquad \text{or} \qquad H_a\text{: } \mu_0 - \mu_1 \neq 0$$

The most popular version of the t test makes the additional assumption that the conditional variances are equal, $\sigma_0^2 = \sigma_1^2$, which we denote by dropping the subscript of $\sigma_{x_i}^2$, that is,

$$\text{Var}(y_i|x_i) \;=\; \sigma^2$$

so that the model becomes

$$y_i|x_i \;\sim\; N(\mu_{x_i}, \sigma^2)$$

The equal-variance assumption seems more reasonable for the log-transformed salaries than for the salaries on their original scale. However, salary in dollars is more interpretable than its log transformation, so for simplicity, we will work with the untransformed variable in this chapter (but see exercise 1.5).

We can perform t tests with the assumption of equal variances using

```
. ttest salary, by(male)
Two-sample t test with equal variances
```

Group	Obs	Mean	Std. Err.	Std. Dev.	[95% Conf.	Interval]
Women	128	42916.6	809.7795	9161.61	41314.2	44519.01
Men	386	53499.24	640.4822	12583.48	52239.96	54758.52
combined	514	50863.87	558.972	12672.77	49765.72	51962.03
diff		-10582.63	1206.345		-12952.63	-8212.636

```
   diff = mean(Women) - mean(Men)                                t =  -8.7725
Ho: diff = 0                                     degrees of freedom =      512

   Ha: diff < 0                 Ha: diff != 0                 Ha: diff > 0
 Pr(T < t) = 0.0000         Pr(|T| > |t|) = 0.0000          Pr(T > t) = 1.0000
```

and without the assumption of equal variances by specifying the `unequal` option:

```
. ttest salary, by(male) unequal
Two-sample t test with unequal variances
```

Group	Obs	Mean	Std. Err.	Std. Dev.	[95% Conf.	Interval]
Women	128	42916.6	809.7795	9161.61	41314.2	44519.01
Men	386	53499.24	640.4822	12583.48	52239.96	54758.52
combined	514	50863.87	558.972	12672.77	49765.72	51962.03
diff		-10582.63	1032.454		-12614.48	-8550.787

```
    diff = mean(Women) - mean(Men)                                t = -10.2500
Ho: diff = 0                     Satterthwaite's degrees of freedom =  297.227

    Ha: diff < 0                 Ha: diff != 0                 Ha: diff > 0
 Pr(T < t) = 0.0000         Pr(|T| > |t|) = 0.0000          Pr(T > t) = 1.0000
```

For both versions of the t test, the population means are estimated by the sample means,

$$\widehat{\mu}_0 = \overline{y}_0, \quad \widehat{\mu}_1 = \overline{y}_1$$

where the "hat" ($\widehat{\ }$) denotes an estimator. The t statistic is given by

$$t \;=\; \frac{\widehat{\mu}_0 - \widehat{\mu}_1}{\widehat{\mathrm{SE}}(\widehat{\mu}_0 - \widehat{\mu}_1)}$$

the estimated difference in population means (the difference in sample means) divided by the estimated standard error of the estimated difference in population means. Under the null hypothesis of equal population means, the statistic has a t distribution with df degrees of freedom, where $\mathrm{df} = n-2$ (sample size n minus 2 for two estimated means $\widehat{\mu}_0$ and $\widehat{\mu}_1$) for the test assuming equal variances.

The 95% confidence interval for the difference in population means $\mu_0 - \mu_1$ is

$$\widehat{\mu}_0 - \widehat{\mu}_1 \;\pm\; t_{0.975,\mathrm{df}}\, \widehat{\mathrm{SE}}(\widehat{\mu}_0 - \widehat{\mu}_1)$$

where $t_{0.975,\mathrm{df}}$ is the 97.5th percentile of the t distribution with df degrees of freedom.

The standard error is estimated as \$1,206.345 under the equal-variance assumption $\sigma_0^2 = \sigma_1^2$ and as \$1,032.454 without the equal-variance assumption; the degrees of freedom also differ. In both cases, the two-tailed p-value (given under `Ha: diff != 0`) is less than 0.0005 (typically reported as $p < 0.001$), leading to rejection of the null hypothesis at, say, the 5% level. For example, with the equal-variance assumption, $t = -8.77$, $\mathrm{df} = 512$, $p < 0.001$. The 95% confidence intervals for the difference in population mean salary for men and women are from $-$\$12,953 to $-$\$8,213 under the equal-variance assumption and from $-$\$12,615 to $-$\$8,551 without the equal-variance assumption. Repeating the analysis for log-salary (not shown) also gives $p < 0.001$ and a smaller relative difference between the estimated standard errors for the two versions of the t test.

It is important to note that the normality assumption is not necessary for valid estimation of the model parameters (the population means and population standard deviations) and the standard error(s) used for inference. Normality ensures that the t statistic has a t distribution under the null hypothesis, but this null distribution is also approximately correct in large samples if normality is violated. These remarks apply to the rest of this volume.

1.4 One-way analysis of variance

The model underlying the t test with equal variances is also called a one-way analysis-of-variance (ANOVA) model.

Analysis of variance involves partitioning the *total sum of squares* (TSS), the sum of squared deviations of the y_i from their overall mean,

$$\text{TSS} \;=\; \sum_{i=1}^{n}(y_i-\overline{y})^2$$

into the *model sum of squares* (MSS) and the *sum of squared errors* (SSE).

The MSS, also known as regression sum of squares, is

$$\text{MSS} \;=\; \sum_{i=1}^{n}(\widehat{y}_i-\overline{y})^2 = \sum_{i,\,x_i=0}(\overline{y}_0-\overline{y})^2 + \sum_{i,\,x_i=1}(\overline{y}_1-\overline{y})^2 = n_0(\overline{y}_0-\overline{y})^2 + n_1(\overline{y}_1-\overline{y})^2$$

the sum of squared deviations of the sample means from the overall mean, interpretable as the between-group sum of squares (here "i, x_i=0" and "i, x_i=1" mean that the sums are taken over females and males, respectively).

The SSE, also known as residual sum of squares, is

$$\text{SSE} \;=\; \sum_{i=1}^{n}(y_i-\widehat{y}_i)^2 = \sum_{i,\,x_i=0}(y_i-\overline{y}_0)^2 + \sum_{i,\,x_i=1}(y_i-\overline{y}_1)^2 = (n_0-1)s_0^2 + (n_1-1)s_1^2$$

the sum of squared deviations of responses from their respective sample means, interpretable as the within-group sum of squares (s_0 and s_1 are the within-group sample standard deviations).

The group-specific sample means can be viewed as predictions, $\widehat{y}_i = \widehat{\mu}_{x_i} = \overline{y}_{x_i}$, representing the best guess of the salary when all that is known about the professor is the gender. These predictions, $\overline{y}_0$ and $\overline{y}_1$, minimize the SSE and are therefore referred to as *ordinary least-squares* (OLS) estimates. When evaluating the quality of the predictions $\widehat{y}_i$, the SSE is interpreted as the sum of the squared prediction errors $y_i - \widehat{y}_i$.

The total sum of squares equals the model sum of squares plus the sum of squared errors

$$\text{TSS} \;=\; \text{MSS} + \text{SSE}$$

The deviations contributing to each of these sums of squares are shown in figure 1.3 for an observation y_i (shown as $\bullet$) in a hypothetical dataset. These deviations add up in the same way as the corresponding sums of squares. For example, for men, $y_i - \overline{y} = (\overline{y}_1 - \overline{y}) + (y_i - \overline{y}_1)$.

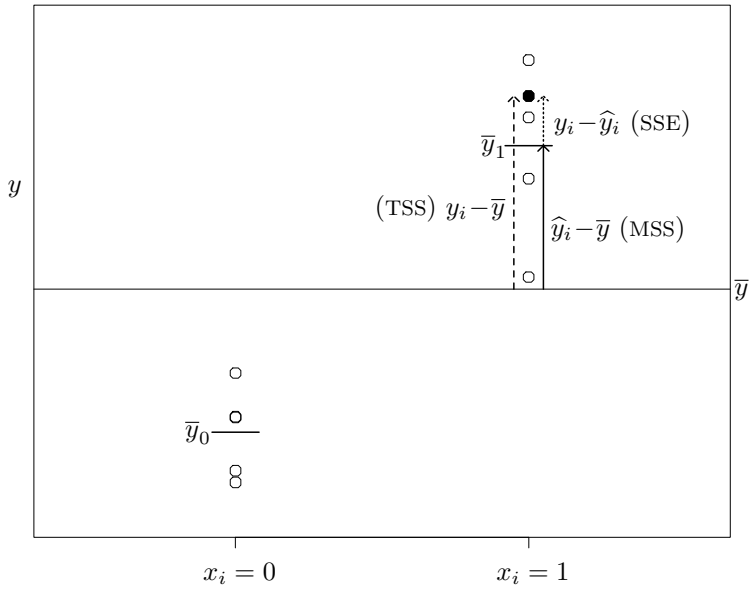


Figure 1.3: Illustration of deviations contributing to total sum of squares (TSS), model sum of squares (MSS), and sum of squared errors (SSE)

The model mean square (MMS) and mean squared error (MSE) can be obtained from the corresponding sums of squares by dividing by the appropriate degrees of freedom as shown in table 1.1 for the general case of g groups (for comparing males and females, $g = 2$).

Table 1.1: Sums of squares (SS) and mean squares (MS) for one-way ANOVA

Source	SS	df	MS $= \frac{\text{SS}}{\text{df}}$	
Model	MSS	$g-1$	MMS	Between group
Error	SSE	$n-g$	MSE	Within group
Total	TSS	$n-1$		

The MSE is the pooled within-group sample variance, which is an estimator for the population variance parameter σ^2:

$$\widehat{\sigma^2} \;=\; \text{MSE}$$

The F statistic for the null hypothesis that the population means are the same (against the two-sided alternative) then is

$$F \;=\; \frac{\text{MMS}}{\text{MSE}}$$

Under the null hypothesis, this statistic has an F distribution with $g-1$ and $n-g$ degrees of freedom. When $g=2$ as in our example, the F statistic is the square of the t statistic from the independent-samples t test under the equal-variance assumption and the p-values from both tests are identical.

We can perform a one-way ANOVA in Stata using

```
. anova salary male
```

```
                   Number of obs =     514     R-squared     =  0.1307
                   Root MSE      = 11827.4     Adj R-squared =  0.1290

          Source |  Partial SS    df       MS           F     Prob > F
-----------------+------------------------------------------------------
           Model |  1.0765e+10     1  1.0765e+10      76.96     0.0000
                 |
            male |  1.0765e+10     1  1.0765e+10      76.96     0.0000
                 |
        Residual |  7.1622e+10   512   139887048
-----------------+------------------------------------------------------
           Total |  8.2387e+10   513   160599133
```

This gives a statistically significant difference in mean salaries for men and women as before [$F(1, 512) = 76.96$, $p < 0.001$]. The estimate $\sqrt{\widehat{\sigma^2}} = \$11{,}827$ is given under `Root MSE` in the output. Estimates of μ_0 and μ_1 are not shown but can be obtained using the postestimation command `margins` (available as of Stata 11):

```
. margins male
Adjusted predictions                            Number of obs   =        514
Expression   : Linear prediction, predict()
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
male						
0	42916.6	1045.403	41.05	0.000	40867.65	44965.56
1	53499.24	601.9981	88.87	0.000	52319.34	54679.13

1.5 Simple linear regression

Salaries can vary considerably between academic departments. Some disciplines are more marketable than others, perhaps because there are highly paid jobs in those dis-

ciplines outside academia or because there is a low supply of qualified graduates. The dataset contains a variable, `market`, for the marketability of the discipline, defined as the mean U.S. faculty salary in that discipline divided by the mean salary across all disciplines.

Let us now investigate the relationship between salaries and marketability of the discipline. Marketability ranges from 0.71 to 1.33 in this sample, taking on 46 different values. A one-way ANOVA model, allowing for a different mean salary μ_{x_i} for each value of marketability x_i would have a large number of parameters and many groups containing only one individual and would hence be *overparameterized*. There are two popular ways of dealing with this problem: 1) categorize the continuous explanatory variable into intervals, thus producing fewer and larger groups or 2) assume a parametric, typically linear, relationship between μ_{x_i} and x_i.

Taking the latter approach, a *simple linear regression model* can be written as

$$y_i|x_i \sim N(\mu_{x_i}, \sigma^2)$$

where

$$\mu_{x_i} \equiv E(y_i|x_i) = \beta_1 + \beta_2 x_i$$

Alternatively, it can be written as

$$y_i = \beta_1 + \beta_2 x_i + \epsilon_i, \qquad \epsilon_i|x_i \sim N(0, \sigma^2)$$

where ϵ_i is the residual or error term for the ith professor, assumed to be independent of the residuals for other professors. Here β_1 (the Greek letter β is pronounced "beta") is called the *intercept* (often denoted β_0 or α) and represents the conditional expectation of y_i when $x_i=0$:

$$E(y_i|x_i=0) = \beta_1$$

β_2 is called the *slope*, or *regression coefficient*, of x_i and represents the increase in conditional expectations when x_i increases one unit, from some value a to $a+1$:

$$E(y_i|x_i=a+1) - E(y_i|x_i=a) = [\beta_1 + \beta_2(a+1)] - [\beta_1 + \beta_2 a] = \beta_2$$

We refer to $\beta_1 + \beta_2 x_i$ as the *fixed part* and ϵ_i as the *random part* of the model.

In addition to assuming that the conditional expectations fall on a straight line, the model assumes that the conditional variances, or residual variances, of the y_i are equal for all x_i,

$$\text{Var}(y_i|x_i) = \text{Var}(\epsilon_i|x_i) = \sigma^2$$

known as the *homoskedasticity* assumption (in contrast to *heteroskedasticity*).

A graphical illustration of the simple linear regression model is given in figure 1.4. Here the line represents the conditional expectation $E(y_i|x_i)$ as a function of x_i, and the density curves represent the conditional distributions of $y_i|x_i$ shown only for some values of x_i.

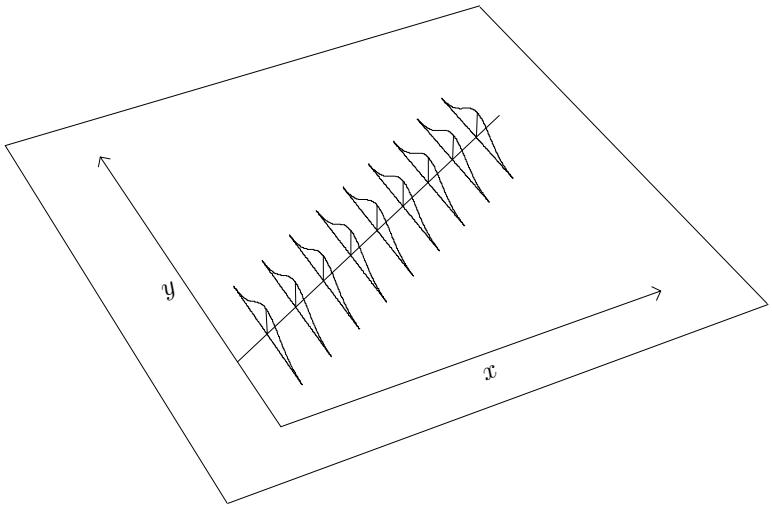


Figure 1.4: Illustration of simple linear regression model

We have described the regression coefficients as changes in conditional expectations without making any causal claims. Sometimes, especially in econometrics, regression coefficients are interpreted as causal effects; this necessitates further assumptions known as exogeneity assumptions, which are discussed in section 1.13. We will occasionally use the term *effect* in this book, but this does not necessarily mean that we are making causal claims.

For OLS estimates, we can partition the TSS into MSS and SSE exactly as in section 1.4, the only difference being the form of the predicted value of y_i:

$$\widehat{y}_i \;=\; \widehat{\beta}_1 + \widehat{\beta}_2 x_i \tag{1.1}$$

The contribution to each sum of squares is shown in figure 1.5 for an observation (shown as $\bullet$) in a hypothetical dataset. The OLS estimates of β_1 and β_2 are obtained by minimizing the SSE, and the estimate of σ^2 is again the MSE, where the error degrees of freedom are $n-2$ (number of observations n minus 2 estimated regression coefficients $\widehat{\beta}_1$ and $\widehat{\beta}_2$). Maximum likelihood estimation, used for more complex models in later chapters, gives the same estimates of the regression coefficients as OLS but a smaller estimate of the residual variance because the latter is given by the SSE divided by n instead of divided by $n-2$ as for OLS.

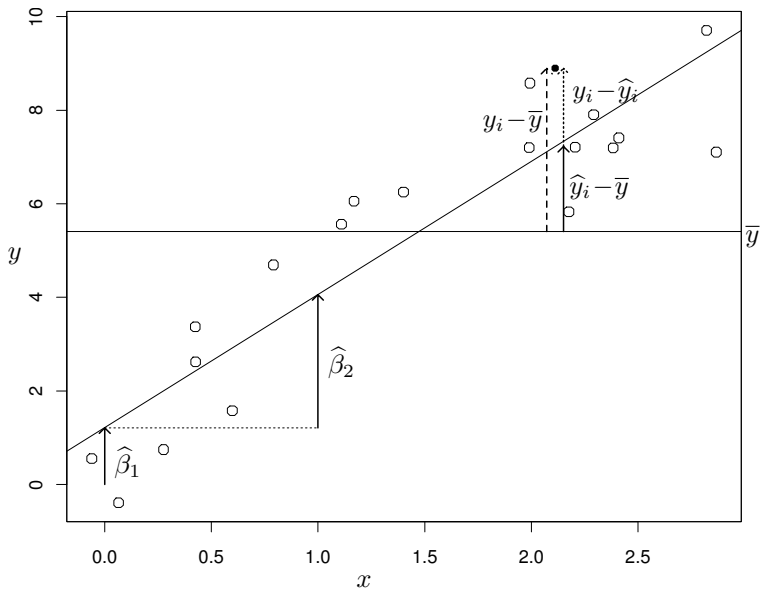


Figure 1.5: Illustration of sums of squares for simple linear regression

The *coefficient of determination* R^2 is defined as

$$R^2 \equiv \frac{\text{MSS}}{\text{TSS}} = \frac{\text{TSS} - \text{SSE}}{\text{TSS}}$$

and can be motivated as the proportion of the total variability (TSS) that is "explained" by the model that includes the covariate x_i (MSS). Alternatively, if TSS is viewed as the sum of squared prediction errors when the predictions are simply $\widehat{y}_i = \overline{y}$ (not using x_i to make predictions) whereas SSE is the sum of squared prediction errors taking into account x_i as in (1.1), then R^2 can be interpreted as the proportional reduction in prediction error variability due to knowing x_i.

R^2 is not a measure of model fit, but rather, as the name *coefficient of determination* implies, a measure of how well x_i predicts y_i. If the true model is a regression model with a large residual variance, then R^2 will tend to be small, and it would therefore be erroneous to interpret a small R^2 as indicating model misspecification. R^2 is also not a measure of the magnitude of the effect of x_i (or effect size), which is estimated by $\widehat{\beta}_2$. For a given estimated effect size $\widehat{\beta}_2$, R^2 will decrease as the estimated residual variance $\widehat{\sigma}^2$ increases (leading to a larger SSE) or the sample variance of x_i decreases (leading to a larger MSS).

The Stata command for the simple linear regression model is

```
. regress salary market
```

Source	SS	df	MS	Number of obs =	514
				F(1, 512) =	101.77
Model	1.3661e+10	1	1.3661e+10	Prob > F =	0.0000
Residual	6.8726e+10	512	134231433	R-squared =	0.1658
				Adj R-squared =	0.1642
Total	8.2387e+10	513	160599133	Root MSE =	11586

salary	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
market	34545.22	3424.333	10.09	0.000	27817.75	41272.69
_cons	18096.99	3288.009	5.50	0.000	11637.35	24556.64

The estimated coefficient of marketability is given next to `market` in the regression table, and the estimated intercept is given next to `_cons`. The reason for the label `_cons` is that the intercept can be thought of as the coefficient of a variable that is equal to 1 for each observation, referred to as a constant (because it does not vary).

The estimated regression coefficients, their estimated standard errors, and the estimated residual standard deviations are given for all models fit in this chapter in table 1.2, starting with the estimates for the model above in the first two columns under "Section 1.5".

Table 1.2: Ordinary least-squares (OLS) estimates for salary data (in U.S. dollars)

	Section 1.5				Section 1.6		Section 1.7				Section 1.8	
	Est	(SE)	Est	(SE)	Est	(SE)	Est	(SE)	Est	(SE)	Est	(SE)
[_cons]	18,097	(3,288)	50,864	(511)	42,917	(1,045)	44,324	(983)	34,834	(734)	36,774	(1,072)
[male]					10,583	(1,206)	8,708	(1,139)	2,040	(783)	−593	(1,320)
[market]	34,545	(3,424)										
[marketc]			34,545	(3,424)			29,972	(3,302)	38,402	(2,172)	38,437	(2,161)
[yearsdg]									949	(36)	763	(83)
[male×yearsdg]											227	(92)
[associate]												
[full]												
[male×associate]												
[male×full]												
[marketc×yearsdg]												
[yearsdg2]												
σ	11,586		11,586		11,827		10,986		7,148		7,112	

	Section 1.9				Section 1.10				Section 1.11	
	Est	(SE)	Est	(SE)	Est	(SE)	Est	(SE)	Est	(SE)
[_cons]	39,866	(746)	37,493	(989)	36,397	(886)	36,044	(712)	38,838	(1,027)
[male]			−1,043	(1,215)	465	(1,119)	926	(712)	−1,182	(1,252)
[market]										
[marketc]			36,987	(1,975)	36,951	(1,985)	46,906	(3,456)	46,578	(3,544)
[yearsdg]			405	(87)	552	(52)	541	(51)	39	(145)
[male×yearsdg]			184	(85)					178	(89)
[associate]	7,285	(1,026)	3,349	(872)	3,008	(1,307)	3,303	(860)	4,812	(968)
[full]	21,267	(966)	11,168	(1,168)	9,099	(1,894)	11,573	(1,166)	12,791	(1,230)
[male×associate]					284	(1,575)				
[male×full]					2539	(1,920)				
[marketc×yearsdg]							−750	(214)	−726	(222)
[yearsdg2]									10	(4)
σ	8,917		6,482		6,506		6,434		6,353	

We obtain the estimates $\widehat{\beta}_1 = \$18{,}097$, $\widehat{\beta}_2 = \$34{,}545$, and $\sqrt{\widehat{\sigma^2}} = \$11{,}586$. The estimated intercept $\widehat{\beta}_1$ is the estimated population mean salary when marketability is zero, a value that does not occur in this sample and is meaningless. Before interpreting the estimates, we therefore refit the model after mean-centering `market`:

```
. egen mn_market = mean(market)
. generate marketc = market - mn_market
. regress salary marketc
```

Source	SS	df	MS		Number of obs =	514
					F(1, 512) =	101.77
Model	1.3661e+10	1	1.3661e+10		Prob > F =	0.0000
Residual	6.8726e+10	512	134231433		R-squared =	0.1658
					Adj R-squared =	0.1642
Total	8.2387e+10	513	160599133		Root MSE =	11586

salary	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
marketc	34545.22	3424.333	10.09	0.000	27817.75	41272.69
_cons	50863.87	511.029	99.53	0.000	49859.9	51867.85

Here `mn_market`, the sample mean of `market`, was subtracted from `market` so that `marketc` equals zero when `market` is equal to its sample mean. The only estimate that is affected by the centering is the intercept that now represents the estimated population mean salary when marketability is equal to its sample mean (when `marketc` is zero). The estimated standard error of the intercept is considerably smaller after mean-centering because we are no longer extrapolating outside the range of the data.

For each unit increase in marketability, the population mean salary is estimated to increase by \$34,545 (with 95% confidence interval from \$27,818 to \$41,273). Because marketability ranges from 0.71 to 1.33, with no two people differing by as much as 1 unit, we could consider the effect of a 0.1 point increase in marketability, which is associated with an estimated increase in population mean salary of \$3,454 ($= \widehat{\beta}_2/10$). Alternatively, we could standardize marketability (giving it a standard deviation of one in addition to a mean of zero), in which case the estimated regression parameter would be interpreted as the estimated increase in population mean salary when marketability increases by one sample standard deviation.

If we standardize both the response variable `salary` and the covariate `market`, the estimated regression coefficient becomes a *standardized regression coefficient*, interpreted as the estimated number of standard deviations that salary increases, on average, when marketability increases by one standard deviation. Standardized regression coefficients can also be obtained by using the `beta` option in the `regress` command. However, they should be used with caution because they depend on sample-specific standard deviations, which invalidates comparisons across samples. See Greenland, Schlesselman, and Criqui (1986) for further discussion. A similar issue arises for mean-centering based on sample means. It might have been preferable to subtract 1 (where the mean salary for the discipline equals the mean salary across disciplines) from `marketability` instead of subtracting the sample mean 0.9485214.

To test the null hypothesis that the regression coefficient of marketability is zero, H_0: $\beta_2 = 0$, against the two-sided alternative H_a: $\beta_2 \neq 0$, we again use a t statistic, now given by

$$t \;=\; \frac{\widehat{\beta}_2}{\widehat{\mathrm{SE}}(\widehat{\beta}_2)}$$

If the null hypothesis is true, this statistic has a t distribution with degrees of freedom given by the error degrees of freedom, denoted `Residual df` in the regression output. Here $t = 10.09$, df $= 512$, and $p < 0.001$, so we can reject the null hypothesis at the 5% level of significance. The null hypothesis for the intercept H_0: $\beta_1 = 0$ is usually irrelevant, and p-values for intercepts are thus ignored.

To visualize the fitted model, we can calculate predicted values $\widehat{y}_i$ using the postestimation command `predict` with the `xb` option (were `xb` is short for "x's times betas" and stands for $\widehat{\beta}_1 + \widehat{\beta}_2 x_i$ here):

```
. predict yhat, xb
```

We can then produce a scatterplot of the data points $(y_i,\ x_i)$ together with a line connecting the predicted points $(\widehat{y}_i,\ x_i)$ with the following command:

```
. twoway (scatter salary market) (line yhat market, sort),
> ytitle(Academic salary) xtitle(Marketability)
```

The graph in figure 1.6 shows that a straight line appears to fit reasonably well and that the constant-variance assumption does not appear to be violated.

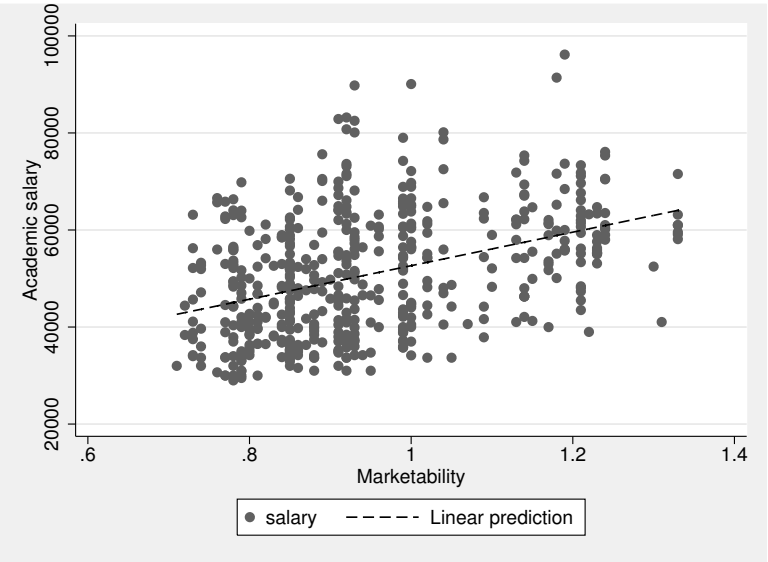


Figure 1.6: Scatterplot with predicted line from simple regression

There is considerable scatter around the regression line with only 16.6% (`R-squared` in regression output) of the variability in salaries being explained by marketability.

1.6 Dummy variables

Instead of using a t test to compare the population mean salaries between men and women, we can use simple linear regression. This becomes obvious by considering the diagram in figure 1.7, where we have simply used the variable x_i, equal to 1 for men and 0 for women, and connected the corresponding conditional expectations of y_i by a straight line.

We are not making any assumption regarding the relationship between the conditional means and x_i here because any two means can be connected by a straight line. (In contrast, assuming in the previous section that the conditional means for the 46 values of marketability lay on a straight line was a strong assumption.) We are, however, assuming equal conditional variances for the two populations because of the homoskedasticity assumption discussed earlier.

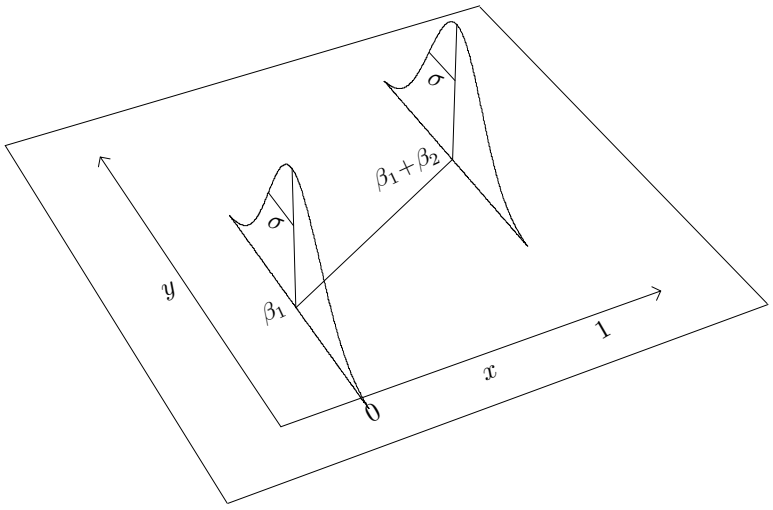


Figure 1.7: Illustration of simple linear regression with a dummy variable

The model can be written as

$$\mu_{x_i} \equiv E(y_i|x_i) \;=\; \beta_1 + \beta_2 x_i, \qquad y_i|x_i \;\sim\; N(\mu_{x_i}, \sigma^2)$$

so that

$$\begin{aligned} \mu_0 &= \beta_1 + \beta_2 \times 0 = \beta_1 \\ \mu_1 &= \beta_1 + \beta_2 \times 1 = \beta_1 + \beta_2 \end{aligned}$$

The intercept β_1 can now be interpreted as the expectation for the group coded 0, the *reference group* (here women), whereas the slope β_2 represents the difference in expectations $\beta_2 = \mu_1 - \mu_0$ between the group coded 1 (here men) and the reference group.

When a dichotomous variable, coded 0 and 1, is used in a regression model like this, it is referred to as a *dummy variable* or *indicator variable*. A useful convention is to give the dummy variable the name of the group for which it is 1 and to describe it as a dummy variable for being in that group, here a dummy variable for being male.

The null hypothesis that $\beta_2 = 0$ is equivalent to the null hypothesis that the population means are the same, $\mu_1 - \mu_0 = 0$. We can therefore use simple regression to obtain the same result as previously produced for the two-sided independent-samples t test with the equal-variance assumption:

```
. regress salary male
      Source |       SS       df       MS              Number of obs =     514
-------------+------------------------------           F(  1,   512) =   76.96
       Model |  1.0765e+10     1  1.0765e+10            Prob > F      =  0.0000
    Residual |  7.1622e+10   512   139887048            R-squared     =  0.1307
-------------+------------------------------           Adj R-squared =  0.1290
       Total |  8.2387e+10   513   160599133            Root MSE      =   11827

------------------------------------------------------------------------------
      salary |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
        male |   10582.63   1206.345     8.77   0.000     8212.636    12952.63
       _cons |    42916.6   1045.403    41.05   0.000      40862.8    44970.41
------------------------------------------------------------------------------
```

The t statistic has the same value as that previously shown for the independent-samples t test (with the equal-variance assumption) apart from the sign, which depends on whether $\mu_0 - \mu_1$ or $\mu_1 - \mu_0$ is estimated and is thus arbitrary.

We can also relax the homoskedasticity (and normality) assumption in linear regression by replacing the conventional *model-based estimator* for the standard errors with the so-called *sandwich estimator*. Simply add the `vce(robust)` option (where `vce` stands for "variance–covariance matrix of estimates") to the `regress` command:

```
. regress salary male, vce(robust)
Linear regression                               Number of obs =     514
                                                F(  1,   512) =  105.26
                                                Prob > F      =  0.0000
                                                R-squared     =  0.1307
                                                Root MSE      =   11827

------------------------------------------------------------------------------
             |               Robust
      salary |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
        male |   10582.63   1031.462    10.26   0.000     8556.213    12609.05
       _cons |    42916.6    808.184    53.10   0.000     41328.84    44504.37
------------------------------------------------------------------------------
```

The resulting t statistic is almost identical to that from the `ttest` command with the `unequal` option in section 1.3 (10.26 compared with 10.25). In the rest of this chapter, we will use model-based standard errors to facilitate comparisons between estimation methods. (Robust standard errors can perform worse than model-based standard errors in small samples.)

In this section, we entered a dummy variable into the model in the same way as we would enter a continuous covariate. However, it usually does not make sense to evaluate dummy variables at their mean or to report standardized regression coefficients for dummy variables, because a standard-deviation change in a dummy variable, such as `male`, is meaningless.

The utility of using a regression model with a dummy variable instead of the t test to compare two groups becomes evident in the next section, where we want to control or adjust for other variables, which is straightforward in a multiple regression model.

1.7 Multiple linear regression

An important question when investigating gender discrimination is whether the men and women being compared are similar in the variables that justifiably affect salaries. As we have seen, there is some variability in marketability, and marketability has an effect on salary. Could the lower mean salary for women be due to women tending to work in disciplines with lower marketability? This is a possible explanation only if women tend to work in disciplines with lower marketability than do men, which is indeed the case:

```
. tabstat marketc, by(male) statistics(mean sd)
Summary for variables: marketc
     by categories of: male
  male |      mean        sd
-------+--------------------
 Women | -.0469589  .1314393
   Men |  .0155718  .1518486
-------+--------------------
 Total | -2.96e-08    .14938
-------------------------------
```

A variable like marketability that is associated with both the covariate of interest (here gender) and the response variable is often called a *confounder*. The impact of ignoring one or more confounders on the estimated gender effect is called confounding.

We could render the comparison of salaries more fair by matching each woman to a man with the same value of marketability; however, this would be cumbersome, and we may not find matches for everyone. Instead, we can assume that marketability has the same, linear effect on salary for both genders and check whether gender has any additional effect after allowing for the effect of marketability.

This can be accomplished by specifying a multiple linear regression model,

$$y_i \;=\; \beta_1 + \beta_2 x_{2i} + \beta_3 x_{3i} + \epsilon_i, \qquad \epsilon_i | x_{2i}, x_{3i} \;\sim\; N(0, \sigma^2)$$

where we have multiple covariates or explanatory variables: a dummy variable x_{2i} for being a man and mean-centered marketability x_{3i}. (We number covariates beginning with 2 to correspond to the regression coefficients.)

For disciplines with mean marketability ($x_{3i} = 0$), the model specifies that the expected salary is β_1 for women ($x_{2i} = 0$) and $\beta_1 + \beta_2$ for men ($x_{2i} = 1$). Therefore, β_2 can be interpreted as the difference in population mean salary between men and women in disciplines with mean marketability. Fortunately, β_2 has an even more general interpretation as the difference in population mean salary between men and women in disciplines with any level of marketability, as long as both genders have the same value for marketability, $x_{3i} = a$:

$$E(y_i | x_{2i} = 1, x_{3i} = a) - E(y_i | x_{2i} = 0, x_{3i} = a) \;=\; (\beta_1 + \beta_2 + \beta_3 a) - (\beta_1 + \beta_3 a) \;=\; \beta_2$$

When comparing genders, we are now controlling for, adjusting for, partialling out, or keeping constant marketability.

Figure 1.8 shows model-implied regression lines for this model and how the lines depend on the coefficients. We see that β_2 determines the difference in means between men and women (vertical distance between the gender-specific regression lines) for any value of `marketc`.

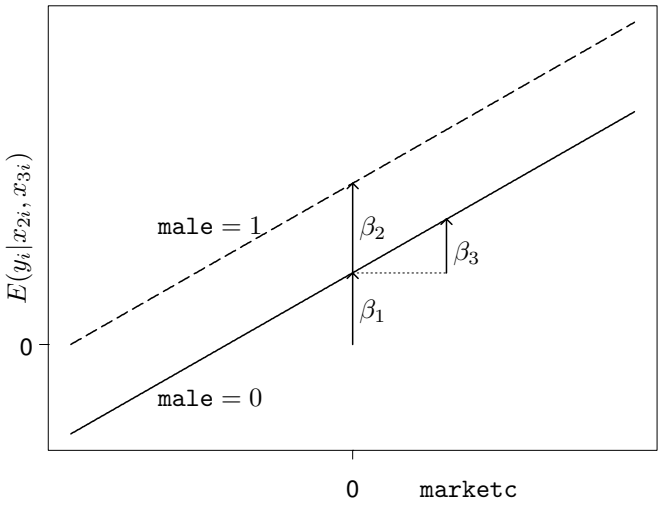


Figure 1.8: Illustration of multiple regression with a dummy variable for `male` (x_{2i}) and a continuous covariate, `marketc` (x_{3i})

The Stata command for the model is

```
. regress salary male marketc
```

Source	SS	df	MS	Number of obs =	514
				F(2, 511) =	85.80
Model	2.0711e+10	2	1.0356e+10	Prob > F =	0.0000
Residual	6.1676e+10	511	120696838	R-squared =	0.2514
				Adj R-squared =	0.2485
Total	8.2387e+10	513	160599133	Root MSE =	10986

salary	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
male	8708.423	1139.411	7.64	0.000	6469.917	10946.93
marketc	29972.6	3301.766	9.08	0.000	23485.89	36459.3
_cons	44324.09	983.3533	45.07	0.000	42392.17	46256

The difference in population mean salaries between men and women, controlling for marketability, is estimated as \$8,708, considerably smaller than the unadjusted difference of \$10,583 that we estimated in the previous section. The estimated coefficient of

`marketc` is also reduced and is now interpretable as the effect of marketability for a given gender or the within-gender effect of marketability. The coefficient of determination is now $R^2 = 0.251$ compared with $R^2 = 0.166$ for the model containing only `marketc` (R^2 cannot decrease when more covariates are added).

We can obtain predicted salaries $\widehat{y}_i$ and plot them with the observed salaries y_i against mean-centered marketability x_{3i} separately for each gender x_{2i} using

```
. predict yhat2, xb
. twoway (scatter salary marketc if male==1, msymbol(o))
>        (line yhat2 marketc if male==1, sort lpatt(dash))
>        (scatter salary marketc if male==0, msymbol(oh))
>        (line yhat2 marketc if male==0, sort lpatt(solid)),
>        ytitle(Academic salary) xtitle(Mean-centered marketability)
>        legend(order(1 " " 2 "Men" 3 " " 4 "Women"))
```

which produces the graph in figure 1.9.

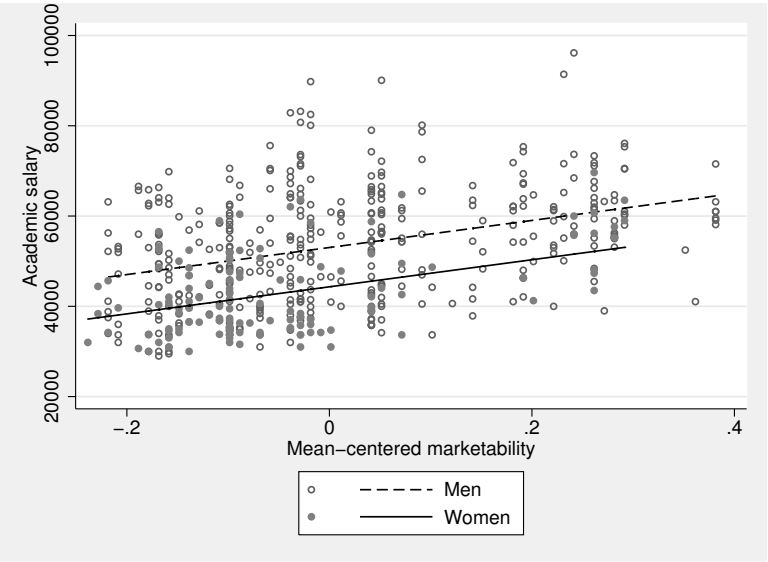


Figure 1.9: Scatterplot with predicted lines from multiple regression

In figure 1.9, The vertical distance between the regression lines is $\widehat{\beta}_2$, and the slope of both regression lines is $\widehat{\beta}_3$ (see also figure 1.8). The figure suggests that there is considerable overlap in the distributions of marketability for men and women. If there were little overlap (with men having higher values of marketability than women), the estimate of the coefficient of `male` would rely on extrapolating the regression line for males to low values of marketability and the regression line for females to high values of marketability. Such extrapolation beyond the range of data for each gender would hinge completely on the linearity assumption and would therefore be problematic. The

degree of overlap, or *common support*, can be better assessed by plotting estimated probability density functions of `marketc` for both genders on the same graph,

```
. twoway (kdensity marketc if male==0) (kdensity marketc if male==1),
>        legend(order(2 "Men" 1 "Women")) xtitle(Mean-centered marketability)
>        ytitle(Estimated density)
```

where `kdensity` uses a kernel density smoother to obtain a smooth version of a histogram. We see in figure 1.10 that there is very good overlap between the densities except beyond `marketc` equal to 0.3, which occurs only for a few men.

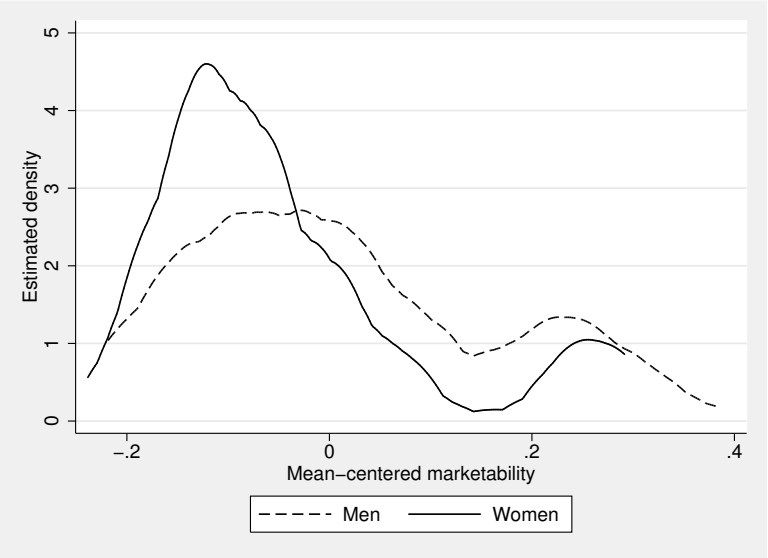


Figure 1.10: Estimated densities of `marketc` for men and women

Figure 1.11 illustrates the ideas of confounding using a hypothetical population model and simulated data. (To exaggerate the confounding, the data were simulated with little common support, but here we know that the relationships are linear.) There are two treatment groups, whose responses are represented by hollow and filled circles. The lines in the top panel represent the fixed part of the true regression model, which includes a dummy variable for treatment and a continuous covariate x_i that is correlated with treatment. The coefficient of treatment is given by the vertical distance between the regression lines. The OLS estimator of the regression coefficient for treatment in the model including both treatment and the covariate (that is, the true model) is an unbiased estimator of this coefficient.

In the bottom panel, the vertical distance between the lines instead represents the difference in marginal population means for the treatments. This difference might be the parameter of interest. However, if we are interested in the regression coefficient of

treatment in the true model, it is clear from the figure that x_i is a confounder, because x_i is associated with both the treatment (the mean of x_i is larger for the treatment represented by hollow circles) and the response (the mean of y_i is larger for larger values of x_i). Thus the conditional difference in population means, given x_i, represented by the vertical distance between the population regression lines in the top panel, is different from the unconditional counterpart in the lower panel. If the regression lines in the top panel had coincided (with no vertical distance between them), then the association between the response variable and the treatment would be said to be *spurious*. For a further discussion of confounding—relating the idea to the concepts of causality and exogeneity, and giving an expression for omitted variable bias—see section 1.13.

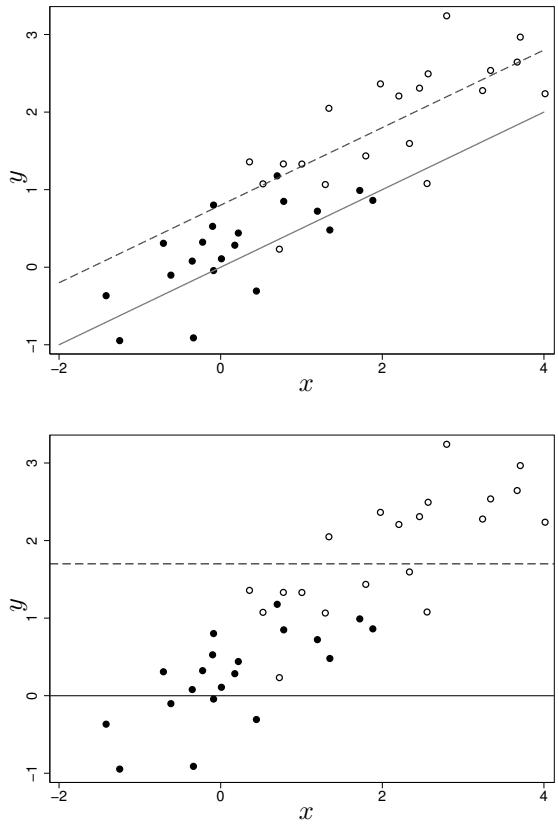


Figure 1.11: Illustration of confounding: Top panel shows conditional population means for the treatment groups, given x (true, data-generating model); bottom panel shows population means for two treatment groups, not conditioning on x

The model used in this section is sometimes called an analysis of covariance (ANCOVA) model because in addition to the categorical explanatory variable or *factor* (gender) used in one-way ANOVA, there is a continuous *covariate* marketability. Departing from the ANOVA/ANCOVA terminology, we use the word *covariate* for any observed explanatory variable, also including dummy variables, throughout this book.

Another covariate we should perhaps control for is time since the degree (in years), `yearsdg`, and we can do so using

```
. regress salary male marketc yearsdg
```

Source	SS	df	MS		
Model	5.6333e+10	3	1.8778e+10	Number of obs	= 514
Residual	2.6054e+10	510	51087083.4	F(3, 510)	= 367.56
				Prob > F	= 0.0000
Total	8.2387e+10	513	160599133	R-squared	= 0.6838
				Adj R-squared	= 0.6819
				Root MSE	= 7147.5

salary	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
male	2040.211	783.122	2.61	0.009	501.6684	3578.753
marketc	38402.39	2171.689	17.68	0.000	34135.83	42668.95
yearsdg	949.2583	35.94867	26.41	0.000	878.6326	1019.884
_cons	34834.3	733.7898	47.47	0.000	33392.68	36275.93

For a given marketability and time since degree, the estimated population mean salary for men is \$2,040 greater than for women, a substantial reduction in the estimated gender gap due to controlling for `yearsdg`. For a given gender and time since degree, the estimated effect of marketability is \$38,402 extra mean salary per unit increase in marketability. Comparing professors of the same gender from disciplines with the same marketability, the estimated effect of time since degree is \$949 extra mean salary per year since degree. It is tempting to interpret this coefficient as an effect of experience, but those with, for instance, `yearsdg`$=40$ differ from those with `yearsdg`$=0$ not only in terms of experience but also because they were recruited in a different epoch. As we will discuss in *Part III: Introduction to models for longitudinal and panel data*, we cannot separate such cohort effects from age or experience effects by using cross-sectional data.

We will now use Stata's `margins` command to obtain different kinds of predicted salaries for males and females based on the multiple regression model. To do this, we must first rerun the regression, this time declaring `male` as a categorical variable by using `i.male` (see section 1.8 for more information on factor variables). To suppress output, we use the `quietly` prefix.

```
. quietly regress salary i.male marketc yearsdg
```

We obtain predicted mean estimates for the two genders for certain values of the other covariates in the model, for instance, `marketc`$=0$ and `yearsdg`$=10$, by using

```
. margins male, at(marketc=0 yearsdg=10)
Adjusted predictions                              Number of obs   =        514
Model VCE    : OLS
Expression   : Linear prediction, predict()
at           : marketc         =           0
               yearsdg         =          10
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
male						
0	44326.89	639.7602	69.29	0.000	43072.98	45580.79
1	46367.1	444.0554	104.42	0.000	45496.77	47237.43

The difference in adjusted means is equal to the estimated coefficient of the male dummy variable.

Alternatively, we can predict the mean salaries that males and females would have if both genders had the same distribution of the covariates `marketc` and `yearsdg`, namely, the distribution of the combined sample of males and females:

```
. margins male
Predictive margins                                Number of obs   =        514
Model VCE    : OLS
Expression   : Linear prediction, predict()
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
male						
0	49331.73	667.2756	73.93	0.000	48023.89	50639.57
1	51371.94	370.7068	138.58	0.000	50645.37	52098.51

One way of obtaining this *predictive margin* for females ourselves would be to set `male` to 0 for the entire sample, obtain the predicted value $\widehat{y}_i$, and average it over the sample; we would do similarly for males. Because the predictions are linear in the covariates, the same results would be obtained by substituting the mean of `marketc` and `yearsdg` into the prediction formula, which can be achieved by using the command `margins male, atmeans`. Such predictions are also often referred to as *adjusted means*. We see that the difference between males and females is again equal to the estimated coefficient of the dummy variable for males.

1.8 Interactions

The models considered in the previous section assumed that the effects of different covariates were additive. For instance, if the dummy variable x_{2i} changes from 0 (women) to 1 (men), the mean salary increases by an amount β_2 regardless of the values of the other covariates (`marketc` and `yearsdg`).

However, this is a strong assumption that can be violated. The gender difference may depend on `yearsdg` if, for instance, starting salaries are similar for men and women but men receive larger or more frequent increases. We can investigate this possibility by including an *interaction* between gender and time since degree. An interaction between two variables implies that the effect of each variable depends on the value of the other variable: in our case, the effect of gender depends on time since degree and the effect of time since degree depends on gender.

We can incorporate the interaction in the regression model (with the usual assumptions) by simply including the product of `male` (x_{2i}) and `yearsdg` (x_{4i}) as a further covariate with regression coefficient β_5:

$$\begin{aligned} y_i &= \beta_1 + \beta_2 \texttt{male}_i + \beta_3 x_{3i} + \beta_4 \texttt{yearsdg}_i + \beta_5 \texttt{male}_i \times \texttt{yearsdg}_i + \epsilon_i \\ &= \beta_1 + (\beta_2 + \beta_5 \texttt{yearsdg}_i)\texttt{male}_i + \beta_3 x_{3i} + \beta_4 \texttt{yearsdg}_i + \epsilon_i \qquad (1.2) \\ &= \beta_1 + \beta_2 \texttt{male}_i + \beta_3 x_{3i} + (\beta_4 + \beta_5 \texttt{male}_i)\texttt{yearsdg}_i + \epsilon_i \qquad (1.3) \end{aligned}$$

From (1.2), we see that the effect of `male` (also called the gender gap) is given by $\beta_2 + \beta_5 \texttt{yearsdg}$ and hence depends on time since degree if $\beta_5 \neq 0$. From (1.3), we see that the effect of `yearsdg` is given by $\beta_4 + \beta_5 \texttt{male}$ and hence depends on gender if $\beta_5 \neq 0$. We can describe time since degree as a *moderator* or an *effect modifier* of the effect of gender or vice versa.

When including an interaction between two variables, it is usually essential to keep both variables in the model. For instance, dropping `male` or setting $\beta_2 = 0$ would force the gender gap to be exactly 0 when time since degree is 0, which is a completely arbitrary constraint unless it corresponds to a specific research question.

An illustration of the model is given in figure 1.12 (with `marketc` set to zero; $x_{3i} = 0$). If β_5 were 0, we would obtain two parallel regression lines with vertical distance β_2. We see that β_5 represents the additional slope for men compared with women, or the additional gender gap when `yearsdg` increases by one unit. We also see that β_2 is the gender gap when $\texttt{yearsdg} = 0$ and β_4 is the slope of `yearsdg` when $\texttt{male} = 0$.

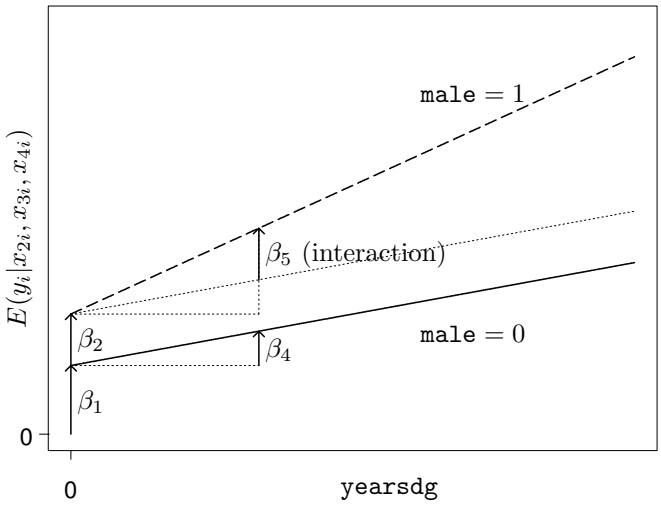


Figure 1.12: Illustration of interaction between `male` (x_{2i}) and `yearsdg` (x_{4i}) for `marketc` (x_{3i}) equal to 0 (not to scale)

To fit this model in Stata, we can generate the interaction as the product of the dummy variable for being male and years since degree:

```
. generate male_years = male*yearsdg
```

We can then include the interaction in the regression:

```
. regress salary male marketc yearsdg male_years
```

Source	SS	df	MS		Number of obs =	514
					F(4, 509) =	279.95
Model	5.6641e+10	4	1.4160e+10		Prob > F =	0.0000
Residual	2.5746e+10	509	50581607.4		R-squared =	0.6875
					Adj R-squared =	0.6850
Total	8.2387e+10	513	160599133		Root MSE =	7112.1

salary	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
male	-593.3088	1320.911	-0.45	0.654	-3188.418	2001.8
marketc	38436.65	2160.963	17.79	0.000	34191.14	42682.15
yearsdg	763.1896	83.4169	9.15	0.000	599.3057	927.0734
male_years	227.1532	91.99749	2.47	0.014	46.41164	407.8947
_cons	36773.64	1072.395	34.29	0.000	34666.78	38880.51

Here it is natural to interpret the interaction in terms of the effect of gender. When time since degree is 0 years, the population mean salary for men minus the population

mean salary for women (after adjusting for marketability) is estimated as −$593. For every additional year since completing the degree, we add $227 to the difference, giving a difference of $0 after a little over 2 years; a difference of about $-\$593.31+\$227.15\times 10 = \$1,678$ after 10 years; a difference of $-\$593.31+\$227.15\times 20 = \$3,949$ after 20 years; and a difference of $-\$593.31+\$227.15\times 30 = \$6{,}221$ after 30 years. Although the estimated gender gap at 0 years is not statistically significant at the 5% level ($t = -0.45$, df $= 509$, $p = 0.65$), the change in gender gap with years since degree (or interaction) is significant ($t = 2.47$, df $= 509$, $p = 0.01$).

We might wonder if the gender gap is statistically significant for faculty with 10 years of experience (adjusting for marketability), hence testing the null hypothesis H_0: $\beta_2 + \beta_5 \times 10 = 0$ against the two-sided alternative. This null hypothesis involves a linear combination of coefficients, and we can use the `lincom` command (which stands for "linear combination") to perform the test,

```
. lincom male + male_years*10
 ( 1)  male + 10*male_years = 0
```

salary	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
(1)	1678.223	792.9094	2.12	0.035	120.4449	3236.001

giving $t = 2.12$, df $= 509$, and $p = 0.04$. We also obtain a 95% confidence interval for the adjusted difference in population mean salaries 10 years since the degree that ranges from $120 to $3,236.

The regression model now includes three covariates, and it is difficult to represent it using a two-dimensional graph. However, as in figure 1.12, we can hold `marketc` constant and display the estimated population mean salary as a function of the other variables when `marketc` is zero. We could do this by setting `marketc` to zero and then using `predict`, or we can use Stata's `twoway function` command to produce figure 1.13:

```
. twoway (function Women = 36773 + 763.19*x, range(0 41) lpatt(dash))
>        (function Men = 36773 + -593.31 + (763.19 + 227.15)*x,
>        range(0 41) lpatt(solid)),
>        xtitle(Time since degree (years)) ytitle(Mean salary)
```

Here we have typed in the predicted regression lines for women and men as a function of `yearsdg` (here referred to as `x`), using (1.3) with `male` = 0 for women, `male` = 1 for men, and `marketc` = 0 (that is, $x_{3i} = 0$).

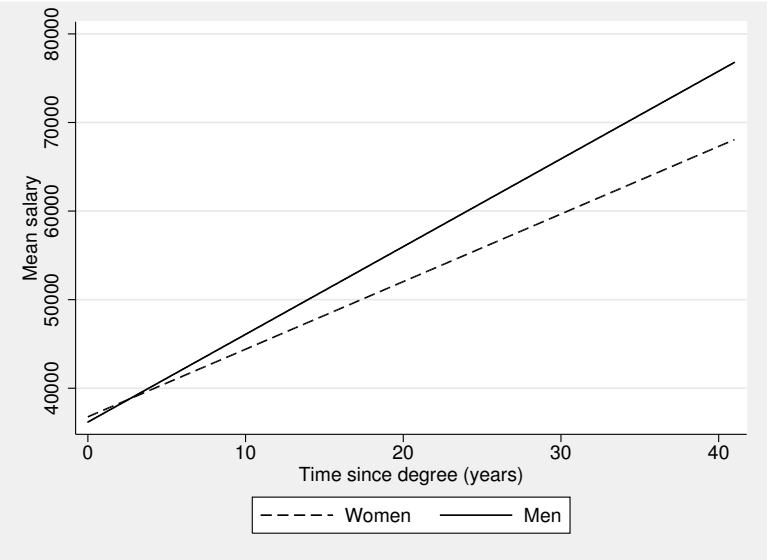


Figure 1.13: Estimated effect of gender and time since degree on mean salary for disciplines with mean marketability

Because we have just fit the model in Stata, we can also refer to the regression coefficients as `_b[_cons]` for the intercept, `_b[yearsdg]` for the coefficient of `yearsdg`, etc., saving us from having to type in all the coefficients, which is error-prone. The Stata command then looks like this:

```
twoway (function Women =_b[_cons] + _b[yearsdg]*x, range(0 41) lpatt(dash))
  (function Men =_b[_cons] + _b[male] + (_b[yearsdg] + _b[male_years])*x,
  range(0 41) lpatt(solid)), xtitle(Time since degree (years)) ytitle(Mean salary)
```

Instead of creating the interaction variable `male_years` first and then including it as a covariate in the regression model, we can also use *factor variables* to specify the interactions within the `regress` command (see also `help fvvarlist` for more information). To introduce an interaction between two variables, simply bind them together with a hash, `#`, making sure to declare their type: use the prefix `i.` for categorical variables (where `i.` stands for indicators, another term for dummy variables), and use `c.` for continuous variables. The command becomes

```
. regress salary male marketc yearsdg i.male#c.yearsdg
```

Source	SS	df	MS	Number of obs =	514
Model	5.6641e+10	4	1.4160e+10	F(4, 509) =	279.95
Residual	2.5746e+10	509	50581607.4	Prob > F =	0.0000
				R-squared =	0.6875
				Adj R-squared =	0.6850
Total	8.2387e+10	513	160599133	Root MSE =	7112.1

salary	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
male	-593.3088	1320.911	-0.45	0.654	-3188.418	2001.8
marketc	38436.65	2160.963	17.79	0.000	34191.14	42682.15
yearsdg	763.1896	83.4169	9.15	0.000	599.3057	927.0734
male# c.yearsdg						
1	227.1532	91.99749	2.47	0.014	46.41164	407.8947
_cons	36773.64	1072.395	34.29	0.000	34666.78	38880.51

By binding the two variables together with two hashes, `##`, we specify that in addition to the interaction, we would also like to include each variable on its own:

```
. regress salary marketc i.male##c.yearsdg
```

Source	SS	df	MS	Number of obs =	514
Model	5.6641e+10	4	1.4160e+10	F(4, 509) =	279.95
Residual	2.5746e+10	509	50581607.4	Prob > F =	0.0000
				R-squared =	0.6875
				Adj R-squared =	0.6850
Total	8.2387e+10	513	160599133	Root MSE =	7112.1

salary	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
marketc	38436.65	2160.963	17.79	0.000	34191.14	42682.15
1.male	-593.3088	1320.911	-0.45	0.654	-3188.418	2001.8
yearsdg	763.1896	83.4169	9.15	0.000	599.3057	927.0734
male# c.yearsdg						
1	227.1532	91.99749	2.47	0.014	46.41164	407.8947
_cons	36773.64	1072.395	34.29	0.000	34666.78	38880.51

In the output, the prefix "`1.`" in `1.male` stands for a dummy variable for the group of professors having the value 1 for the variable `male`, that is, men. The number `1` also appears in the interaction term to signify that it is an interaction between the dummy variable for `male`=1 and the continuous variable `yearsdg`.

In the `lincom` command, the coefficients are referred to by the names shown in the regression output, except that the number shown next to the interaction term (here `1`) comes before the categorical variable, followed by a "`.`"—for example, `1.male#c.yearsdg`. So, 10 years after the degree, the gender difference is estimated as

```
. lincom 1.male + 1.male#c.yearsdg*10
 ( 1)  1.male + 10*1.male#c.yearsdg = 0
```

salary	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
(1)	1678.223	792.9094	2.12	0.035	120.4449	3236.001

Similarly, in the `twoway` command for producing figure 1.13, we refer to the coefficients as `_b[1.male]` and `_b[1.male#c.yearsdg]`.

We could also include an interaction between `marketc` and `male` and, as will be discussed in section 1.10.1, an interaction between the two continuous covariates `marketc` and `yearsdg`. In addition to these *two-way interactions*, we could consider the *three-way interaction* represented by the product of all three covariates. However, such higher-order interactions are rarely used because they are difficult to interpret.

1.9 Dummy variables for more than two groups

Another important explanatory variable for salary is academic rank, coded in the variable `rank` as 1 for assistant professor, 2 for associate professor, and 3 for full professor.

Using `rank` as a continuous covariate in a simple regression model would force a constraint on the population mean salaries for the three groups, namely, that the mean salary of associate professors is halfway between the mean salaries of assistant and full professors:

$$E(y_i|x_i) \;=\; \beta_1 + \beta_2 x_i \;=\; \begin{cases} \beta_1 + \beta_2 \times 1 & \text{for assistant professors} \\ \beta_1 + \beta_2 \times 2 & \text{for associate professors} \\ \beta_1 + \beta_2 \times 3 & \text{for full professors} \end{cases}$$

Such linearity is a strong assumption for an ordinal variable, such as `rank`, and a meaningless assumption for unordered categorical covariates, such as ethnicity, where the ordering of the values assigned to categories is arbitrary. It thus makes sense to estimate the mean of each rank freely by treating one of the ranks, for instance, assistant professor, as the reference category and using dummy variables for the other two ranks.

We can create the dummy variables by typing

```
. generate associate = rank==2 if rank < .
. generate full = rank==3 if rank < .
```

Here the logical expression `rank==2` evaluates to 1 if it is true and zero otherwise. This expression yields a 0 when `rank` is 1, 3, or missing, but we do not want to interpret a missing value; therefore, the `if` condition is necessary to ensure that missing values in `rank` translate to missing values in the dummy variables. (We specify `rank < .` because Stata interprets all missing values, `.`, as very large numbers.)

Our preferred method for producing dummy variables is using the `tabulate` command with the `generate()` option, as follows:

```
. drop associate full
. tabulate rank, generate(r)
. rename r2 associate
. rename r3 full
```

The `generate(r)` option produces dummy variables for each unique value of `rank`, here named `r1`, `r2`, and `r3` for the values 1, 2, and 3. (The naming of the dummy variables would have been the same if the unique values had been 0, 1, and 4.) An advantage of using `tabulate` is that it places missing values into dummy variables whenever the original variable is missing—as shown above, this requires extra caution when using the `generate` command.

Denoting these dummy variables x_{2i} and x_{3i}, respectively, we specify the model

$$E(y_i|x_{2i}, x_{3i}) = \beta_1 + \beta_2 x_{2i} + \beta_3 x_{3i} = \begin{cases} \beta_1 & \text{for assistant professors} \\ \beta_1 + \beta_2 & \text{for associate professors} \\ \beta_1 + \beta_3 & \text{for full professors} \end{cases}$$

showing that the intercept β_1 represents the population mean salary for the reference category (assistant professors), β_2 represents the difference in mean salaries between associate and assistant professors, and β_3 represents the difference in mean salaries between full and assistant professors. Hence, the coefficient of each dummy variable represents the population mean of the corresponding group minus the population mean of the reference group. Figure 1.14 illustrates how the model-implied means for the three ranks are determined by the regression coefficients.

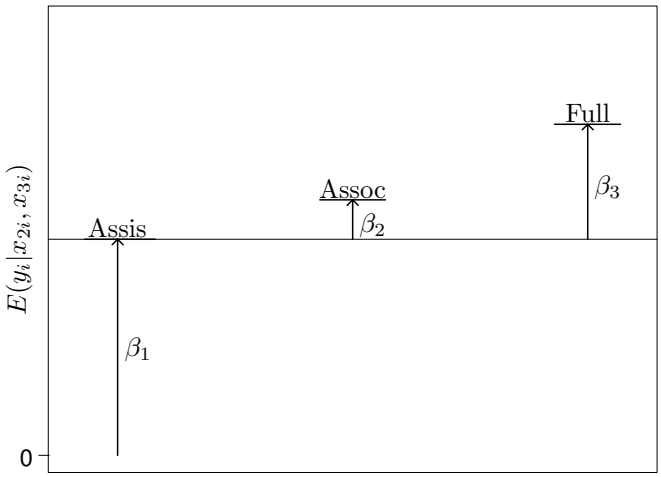


Figure 1.14: Illustration: Interpretations of coefficients of dummy variables x_{2i} and x_{3i} for associate and full professors, with assistant professors as the reference category

Estimates for the regression model with dummy variables for academic rank are obtained by using

```
. regress salary associate full
```

Source	SS	df	MS	Number of obs =	514
				F(2, 511) =	262.54
Model	4.1753e+10	2	2.0877e+10	Prob > F =	0.0000
Residual	4.0634e+10	511	79518710.1	R-squared =	0.5068
				Adj R-squared =	0.5049
Total	8.2387e+10	513	160599133	Root MSE =	8917.3

salary	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
associate	7285.121	1026.19	7.10	0.000	5269.049	9301.192
full	21267.11	965.8886	22.02	0.000	19369.51	23164.71
_cons	39865.86	745.7043	53.46	0.000	38400.84	41330.88

We see that the estimated difference in population means between associate professors and assistant professors is \$7,285 and that the estimated difference in population means between full professors and assistant professors is \$21,267. The mean salary for assistant professors is \$39,866. We can obtain the estimated population mean salary for associate professors, $\widehat{\beta}_1 + \widehat{\beta}_2$, by using

```
. lincom _cons + associate
 ( 1)  associate + _cons = 0
```

salary	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
(1)	47150.98	704.9766	66.88	0.000	45765.97	48535.99

We can obtain the estimated difference in population mean salary between full and associate professors, $(\widehat{\beta}_3 + \widehat{\beta}_1) - (\widehat{\beta}_2 + \widehat{\beta}_1) = \widehat{\beta}_3 - \widehat{\beta}_2$, by using

```
. lincom full - associate
 ( 1)  - associate + full = 0
```

salary	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
(1)	13981.99	934.8036	14.96	0.000	12145.45	15818.52

The difference in estimated population mean salaries between full and associate professors ($13,982) is considerably larger than the difference between associate and assistant professors ($7,285), suggesting that the constraint imposed if academic rank were treated as a continuous covariate is unreasonable.

We can fit the same regression model without forming dummy variables ourselves by using factor variables, that is, by simply preceding the categorical covariate(s) with the `i.` prefix:

```
. regress salary i.rank
```

Source	SS	df	MS		
Model	4.1753e+10	2	2.0877e+10	Number of obs	= 514
Residual	4.0634e+10	511	79518710.1	F(2, 511)	= 262.54
				Prob > F	= 0.0000
				R-squared	= 0.5068
				Adj R-squared	= 0.5049
Total	8.2387e+10	513	160599133	Root MSE	= 8917.3

salary	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
rank						
2	7285.121	1026.19	7.10	0.000	5269.049	9301.192
3	21267.11	965.8886	22.02	0.000	19369.51	23164.71
_cons	39865.86	745.7043	53.46	0.000	38400.84	41330.88

Here the `2` and `3` listed under `rank` denote the dummy variables for rank 2 (associate professor) and rank 3 (full professor), respectively. We can refer to the corresponding coefficients as `_b[2.rank]` and `_b[3.rank]`. The syntax for the `lincom` command to compare these coefficients is

```
. lincom 3.rank - 2.rank
 ( 1)  - 2.rank + 3.rank = 0
```

salary	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
(1)	13981.99	934.8036	14.96	0.000	12145.45	15818.52

The `i.` prefix treats the lowest value of a categorical variable as the reference category. For `rank`, the lowest value is 1 (assistant professor), and we wanted to treat assistant professors as the reference category. If we had instead wanted to treat the value 3 (full professors) as the reference category, we could have replaced `i.rank` by `ib3.rank` or `b3.rank`. Here the "`b`" stands for base level, another term for reference category. Although factor variables are very convenient, an advantage of constructing your own dummy variables is that you can give them meaningful names.

Instead of using regression with dummy variables, we could use one-way ANOVA with $g = 3$ groups (see table 1.1 on page 18). The one-way ANOVA model with g groups is sometimes written as

$$y_{ij} \;=\; \beta + \alpha_j + \epsilon_{ij}, \qquad \sum_{j=1}^{g} \alpha_j = 0, \quad \epsilon_{ij} \sim N(0, \sigma^2)$$

which corresponds to the model considered in section 1.3 with $\mu_j = \beta + \alpha_j$. The Stata command to fit this model is

```
. anova salary rank
```

```
                   Number of obs =     514     R-squared     =  0.5068
                   Root MSE      = 8917.33     Adj R-squared =  0.5049
```

Source	Partial SS	df	MS	F	Prob > F
Model	4.1753e+10	2	2.0877e+10	262.54	0.0000
rank	4.1753e+10	2	2.0877e+10	262.54	0.0000
Residual	4.0634e+10	511	79518710.1		
Total	8.2387e+10	513	160599133		

This command produces the same sums of squares, mean squares, and F statistic as given at the top of the regression output, but no estimates of population means or their differences. The F test is a test of the null hypothesis that all three population means are the same, or in other words, that the coefficients β_2 and β_3 of the dummy variables are both zero. The alternative hypothesis is that at least one of the coefficients differs from zero. Such joint or simultaneous hypotheses can also be tested by using `testparm` after fitting the regression model (see below).

Adding the dummy variables for academic rank to the regression model from the previous section, we obtain

```
. regress salary i.male##c.yearsdg marketc i.rank
```

Source	SS	df	MS		Number of obs =	514
					F(6, 507) =	242.32
Model	6.1086e+10	6	1.0181e+10		Prob > F =	0.0000
Residual	2.1301e+10	507	42014709.8		R-squared =	0.7414
					Adj R-squared =	0.7384
Total	8.2387e+10	513	160599133		Root MSE =	6481.9

salary	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
1.male	-1043.394	1215.034	-0.86	0.391	-3430.516	1343.727
yearsdg	405.2749	86.72844	4.67	0.000	234.8835	575.6663
male# c.yearsdg						
1	184.3764	85.06732	2.17	0.031	17.24853	351.5042
marketc	36987.08	1974.888	18.73	0.000	33107.11	40867.06
rank						
2	3349.005	871.6155	3.84	0.000	1636.582	5061.428
3	11168.26	1167.809	9.56	0.000	8873.923	13462.6
_cons	37493.09	988.658	37.92	0.000	35550.72	39435.46

The estimated coefficients of `associate` and `full` are considerably lower than before because they now represent the estimated adjusted or partial differences in population means, holding the other covariates in the model constant. However, interpreting the effect of rank, adjusted for `yearsdg`, may be problematic because rank and years since degree are inherently strongly associated. Therefore, estimating the adjusted difference between full and assistant professors effectively requires extrapolation for full professors to unrealistically low values of `yearsdg` and for assistant professors to unrealistically high values (there is little common support).

We can test the null hypothesis that the coefficients of these dummy variables are both zero by using the `testparm` command:

```
. testparm i.rank
 ( 1)  2.rank = 0
 ( 2)  3.rank = 0
       F(  2,   507) =   52.89
            Prob > F =    0.0000
```

The F statistic is equal to the difference in MSS between the models that do and do not contain the two dummy variables for academic rank (but contain all the other terms of the model), divided by the product of the difference in model degrees of freedom and the MSE of the larger model. (Had we used the dummy variables `associate` and `full` instead of the factor variable `i.rank`, the syntax for the above test would have been `testparm associate full`.)

After controlling for academic rank (and the other covariates), the difference in population mean salary between men and women is estimated as $-\$1043.39 + \$184.38 \times$

yearsdg, which is lower for every year since degree than the estimate of −$593.31 + $227.15 × yearsdg before adjusting for academic rank. For example, at 10 years since degree, the difference in mean salary is now estimated as about $800:

```
. lincom 1.male + 1.male#c.yearsdg*10
 ( 1)  1.male + 10*1.male#c.yearsdg = 0
```

salary	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
(1)	800.3697	727.9737	1.10	0.272	-629.8468	2230.586

The corresponding estimate not adjusting for academic rank was about $1,678.

We see that the estimated gender effect is smaller when it is adjusted for academic rank. However, adjusting for academic rank could be problematic if rank is a mediating or intervening variable on the causal pathway from gender to salary, that is, if gender affects promotions, which in turn affect salary. After controlling for rank, we obtain an estimate of the direct effect of gender on salary, not mediated by rank (although other intervening variables may be involved). Here we must decide whether we are interested in the direct effect or the total effect of gender on salary (the sum of the direct effect and the indirect effect mediated by rank). If we are interested in the direct effect, we should control for rank, whereas we should not control for rank if we are interested in the total effect. Boudreau et al. (1997) discuss a study arguing that gender does not affect academic rank at Bowling Green State University, in which case the direct effect should be the same as the total effect.

1.10 Other types of interactions

1.10.1 Interaction between dummy variables

Could the salary difference between ranks be gender specific? Equivalently, could the gender gap in salaries depend on academic rank? These questions can be answered by including the two interaction terms male×associate ($x_{2i}x_{5i}$) and male×full ($x_{2i}x_{6i}$) in the model. (We omit the male by yearsdg interaction here for simplicity.)

$$\begin{aligned} y_i &= \beta_1 + \beta_2\texttt{male}_i + \cdots + \beta_5\texttt{associate}_i + \beta_6\texttt{full}_i + \beta_7\texttt{male}_i\times\texttt{associate}_i \\ &\quad + \beta_8\texttt{male}_i\times\texttt{full}_i + \epsilon_i \\ &= \beta_1 + \beta_2\texttt{male}_i + \cdots + (\beta_5 + \beta_7\texttt{male}_i)\texttt{associate}_i + (\beta_6 + \beta_8\texttt{male}_i)\texttt{full}_i + \epsilon_i \qquad (1.4) \\ &= \beta_1 + (\beta_2 + \beta_7\texttt{associate}_i + \beta_8\texttt{full}_i)\texttt{male}_i + \cdots + \beta_5\texttt{associate}_i + \beta_6\texttt{full}_i + \epsilon_i \qquad (1.5) \end{aligned}$$

If the other terms denoted "$\cdots$" above are omitted, this model becomes a two-way ANOVA model with main effects and an interaction between academic rank and gender.

An interaction between dummy variables can be interpreted as a difference of a difference. For instance, we see from (1.4) that β_7 represents the difference between men and women of the difference between the mean salaries of associate and assistant professors.

We now construct the interactions

```
. generate male_assoc = male*associate
. generate male_full = male*full
```

and fit the regression model including these interactions:

```
. regress salary male marketc yearsdg associate full male_assoc male_full
      Source |       SS       df       MS              Number of obs =     514
-------------+------------------------------           F(  7,   506) =  205.77
       Model |  6.0969e+10     7  8.7099e+09           Prob > F      =  0.0000
    Residual |  2.1418e+10   506  42328437.6           R-squared     =  0.7400
-------------+------------------------------           Adj R-squared =  0.7364
       Total |  8.2387e+10   513   160599133           Root MSE      =    6506

------------------------------------------------------------------------------
      salary |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
        male |    465.2322   1118.953     0.42   0.678    -1733.133    2663.598
     marketc |    36950.82   1985.138    18.61   0.000     33050.69    40850.95
     yearsdg |    552.3409   51.93243    10.64   0.000     450.3112    654.3706
   associate |    3008.126   1306.744     2.30   0.022     440.8131    5575.438
        full |    9098.926   1894.294     4.80   0.000     5377.275    12820.58
  male_assoc |    284.0408    1574.62     0.18   0.857    -2809.557    3377.639
   male_full |    2539.387   1919.637     1.32   0.186    -1232.053    6310.826
       _cons |    36397.49   885.9509    41.08   0.000      34656.9    38138.09
------------------------------------------------------------------------------
```

From (1.5), we see that the estimated difference in population mean salaries between men and women is $\widehat{\beta}_2 + \widehat{\beta}_7$`associate` $+ \widehat{\beta}_8$`full`. In other words, the estimated coefficient $\widehat{\beta}_7$ of `male_assoc` can be interpreted as the difference in estimated gender gap between associate and assistant professors, and similarly for `male_full`. Neither interaction coefficient is significant at the 5% level. However, it is not considered good practice to include only some of the interaction terms for a group of dummy variables representing one categorical variable; hence, we should test both coefficients simultaneously:

```
. testparm male_assoc male_full
 ( 1)  male_assoc = 0
 ( 2)  male_full = 0
       F(  2,   506) =    0.95
            Prob > F =    0.3864
```

There is little evidence for an interaction between gender and academic rank $[F(2, 506) = 0.95,\ p = 0.39]$.

Using factor variables instead of constructing interaction terms ourselves, the `regress` command becomes

```
. regress salary marketc yearsdg i.male##i.rank
```

Source	SS	df	MS		
Model	6.0969e+10	7	8.7099e+09	Number of obs	= 514
Residual	2.1418e+10	506	42328437.6	F(7, 506)	= 205.77
				Prob > F	= 0.0000
Total	8.2387e+10	513	160599133	R-squared	= 0.7400
				Adj R-squared	= 0.7364
				Root MSE	= 6506

salary	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
marketc	36950.82	1985.138	18.61	0.000	33050.69	40850.95
yearsdg	552.3409	51.93243	10.64	0.000	450.3112	654.3706
1.male	465.2322	1118.953	0.42	0.678	-1733.133	2663.598
rank						
2	3008.126	1306.744	2.30	0.022	440.8131	5575.438
3	9098.926	1894.294	4.80	0.000	5377.275	12820.58
male#rank						
1 2	284.0408	1574.62	0.18	0.857	-2809.557	3377.639
1 3	2539.387	1919.637	1.32	0.186	-1232.053	6310.826
_cons	36397.49	885.9509	41.08	0.000	34656.9	38138.09

and the `testparm` command for testing the gender by rank interaction becomes

```
. testparm i.male#i.rank
 ( 1)  1.male#2.rank = 0
 ( 2)  1.male#3.rank = 0
       F(  2,   506) =    0.95
            Prob > F =    0.3864
```

The output above also shows how to refer to the two coefficients representing the interaction between gender and rank, namely, `_b[1.male#2.rank]` and `_b[1.male#3.rank]`.

1.10.2 Interaction between continuous covariates

The effect of marketability, `marketc` (x_{3i}), could increase or decrease with time since degree, `yearsdg` (x_{4i}). We can include an interaction between these two continuous covariates in a regression model:

$$\begin{aligned} y_i &= \beta_1 + \beta_2 x_{2i} + \beta_3 \texttt{marketc}_i + \beta_4 \texttt{yearsdg}_i + \cdots + \beta_7 \texttt{marketc}_i \times \texttt{yearsdg}_i + \epsilon_i \\ &= \beta_1 + \beta_2 x_{2i} + (\beta_3 + \beta_7 \texttt{yearsdg}_i)\texttt{marketc}_i + \beta_4 \texttt{yearsdg}_i + \cdots + \epsilon_i \qquad (1.6) \\ &= \beta_1 + \beta_2 x_{2i} + \beta_3 \texttt{marketc}_i + (\beta_4 + \beta_7 \texttt{marketc}_i)\texttt{yearsdg}_i + \cdots + \epsilon_i \qquad (1.7) \end{aligned}$$

We can then fit this model in Stata using the commands

```
. generate market_yrs = marketc*yearsdg
. regress salary male marketc yearsdg associate full market_yrs
```

Source	SS	df	MS		
Model	6.1397e+10	6	1.0233e+10	Number of obs	= 514
Residual	2.0990e+10	507	41401072	F(6, 507)	= 247.16
				Prob > F	= 0.0000
				R-squared	= 0.7452
				Adj R-squared	= 0.7422
Total	8.2387e+10	513	160599133	Root MSE	= 6434.4

salary	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
male	926.1298	712.2859	1.30	0.194	-473.2657	2325.525
marketc	46905.65	3455.747	13.57	0.000	40116.31	53695
yearsdg	540.73	51.40369	10.52	0.000	439.7395	641.7205
associate	3303.134	859.6452	3.84	0.000	1614.229	4992.04
full	11573.46	1165.936	9.93	0.000	9282.799	13864.12
market_yrs	-750.4151	214.1251	-3.50	0.000	-1171.097	-329.7334
_cons	36044.19	711.6195	50.65	0.000	34646.1	37442.28

Using (1.6), we see that the estimated effect of marketability, $\widehat{\beta}_3 + \widehat{\beta}_7$`yearsdg`, decreases from \$46,906 for faculty who have just completed their degree to \$46,906$-$\$750.41$\times$30 = \$24,394 for faculty who completed their degree 30 years ago.

Using factor variables, the model can be fit like this:

```
. regress salary i.male c.marketc##c.yearsdg i.rank
```

Source	SS	df	MS		
Model	6.1397e+10	6	1.0233e+10	Number of obs	= 514
Residual	2.0990e+10	507	41401072	F(6, 507)	= 247.16
				Prob > F	= 0.0000
				R-squared	= 0.7452
				Adj R-squared	= 0.7422
Total	8.2387e+10	513	160599133	Root MSE	= 6434.4

salary	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
1.male	926.1298	712.2859	1.30	0.194	-473.2657	2325.525
marketc	46905.65	3455.747	13.57	0.000	40116.31	53695
yearsdg	540.73	51.40369	10.52	0.000	439.7395	641.7205
c.marketc# c.yearsdg	-750.415	214.1251	-3.50	0.000	-1171.097	-329.7334
rank						
2	3303.134	859.6452	3.84	0.000	1614.229	4992.04
3	11573.46	1165.936	9.93	0.000	9282.799	13864.12
_cons	36044.19	711.6195	50.65	0.000	34646.1	37442.28

1.11 Nonlinear effects

We have assumed that the relationship between population mean salary and each of the continuous covariates `marketc` and `yearsdg` is linear after controlling for the other variables. However, the difference in population mean salary for each extra year is likely to increase with time since degree (for instance, if percentage increases are constant over time).

Such a nonlinear relationship can be modeled by including the square of `yearsdg` in the model in addition to `yearsdg` itself (adding the interaction `male_years` back in):

```
. generate yearsdg2 = yearsdg^2
. regress salary male marketc yearsdg male_years associate full
> market_yrs yearsdg2
```

Source	SS	df	MS	Number of obs =	514
				F(8, 505) =	192.04
Model	6.2005e+10	8	7.7507e+09	Prob > F =	0.0000
Residual	2.0382e+10	505	40360475	R-squared =	0.7526
				Adj R-squared =	0.7487
Total	8.2387e+10	513	160599133	Root MSE =	6353

salary	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
male	-1181.825	1251.647	-0.94	0.346	-3640.901	1277.251
marketc	46578.2	3544.482	13.14	0.000	39614.45	53541.95
yearsdg	39.04014	144.8758	0.27	0.788	-245.5933	323.6736
male_years	177.7129	89.36428	1.99	0.047	2.141361	353.2845
associate	4811.533	967.9374	4.97	0.000	2909.853	6713.213
full	12791	1230.256	10.40	0.000	10373.95	15208.05
market_yrs	-726.3863	222.4265	-3.27	0.001	-1163.382	-289.3911
yearsdg2	10.1092	3.970824	2.55	0.011	2.307829	17.91057
_cons	38837.69	1027.381	37.80	0.000	36819.23	40856.16

The estimated coefficient of `yearsdg2` is significantly different from 0 at, say, the 5% level ($t = 2.55$, df $= 505$, $p = 0.01$), whereas the coefficient of `yearsdg` is no longer statistically significant. It should nevertheless be retained to form a flexible quadratic curve because the minimum of the curve is otherwise arbitrarily forced to occur when `yearsdg` $= 0$.

After setting the covariates `marketc` (and hence `market_yrs`), `associate`, and `full` to zero, we can visualize the relationship between salary and time since degree for male and female assistant professors in disciplines with mean marketability by using the `twoway function` command, which produces figure 1.15:

```
. twoway (function Women = _b[_cons] + _b[yearsdg]*x + _b[yearsdg2]*x^2,
>        range(0 41) lpatt(dash))
>        (function Men = _b[_cons] + _b[male] + (_b[yearsdg] + _b[male_years])*x
>        + _b[yearsdg2]*x^2, range(0 41) lpatt(solid)),
>        xtitle(Time since degree (years)) ytitle(Mean salary)
```

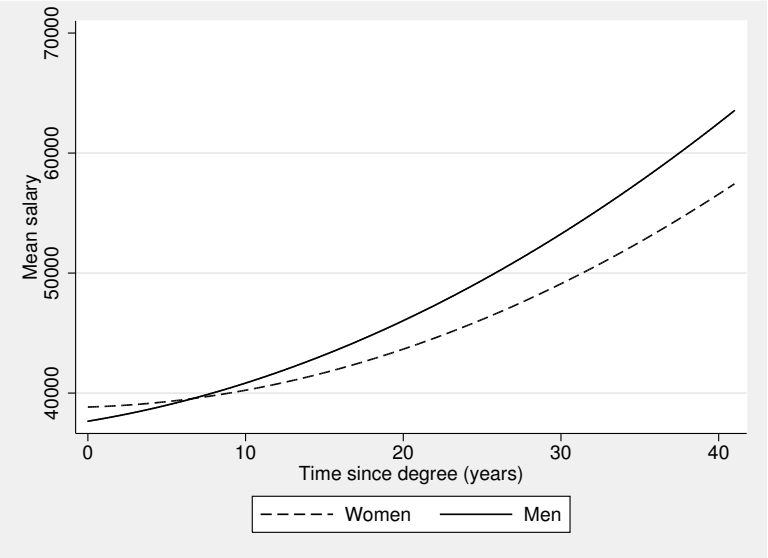


Figure 1.15: Estimated effects of gender and time since degree on mean salary for assistant professors in disciplines with mean marketability

The quadratic term for `yearsdg` can also be included in the regression by using factor variables, simply by using the expression `c.yearsdg#c.yearsdg`. We can therefore use the following command to fit the same model as before:

```
regress salary i.male##c.yearsdg c.marketc c.marketc#c.yearsdg i.rank
   c.yearsdg#c.yearsdg
```

Here we use a double-hash, `##`, in `i.male##c.yearsdg` to include `i.male`, `c.yearsdg`, and `i.male#c.yearsdg`. To avoid duplicating the term `c.yearsdg`, we use a single hash for `c.marketc#c.yearsdg` and then include the missing term `c.marketc`. In fact, it is not necessary to avoid duplication because Stata will drop any redundant terms. However, the terms are then listed in the output together with the label `omitted`. A preferred approach therefore is to factorize out all terms that interact with `c.yearsdg` using

```
. regress salary (i.male c.marketc c.yearsdg)##c.yearsdg i.rank
```

Source	SS	df	MS		
Model	6.2005e+10	8	7.7507e+09	Number of obs	= 514
Residual	2.0382e+10	505	40360475.1	F(8, 505)	= 192.04
				Prob > F	= 0.0000
				R-squared	= 0.7526
				Adj R-squared	= 0.7487
Total	8.2387e+10	513	160599133	Root MSE	= 6353

salary	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
1.male	-1181.825	1251.647	-0.94	0.346	-3640.901	1277.251
marketc	46578.2	3544.482	13.14	0.000	39614.45	53541.95
yearsdg	39.04014	144.8758	0.27	0.788	-245.5933	323.6736
male# c.yearsdg 1	177.7129	89.36428	1.99	0.047	2.141358	353.2845
c.marketc# c.yearsdg	-726.3863	222.4265	-3.27	0.001	-1163.382	-289.3911
c.yearsdg# c.yearsdg	10.1092	3.970824	2.55	0.011	2.307829	17.91057
rank 2	4811.533	967.9374	4.97	0.000	2909.853	6713.213
3	12791	1230.256	10.40	0.000	10373.95	15208.05
_cons	38837.69	1027.381	37.80	0.000	36819.23	40856.16

Stata now makes sure not to duplicate any terms. The estimated regression coefficients can be referred to as `_b[1.male]`, `_b[1.male#c.yearsdg]`, `_b[c.marketc#c.yearsdg]`, `_b[c.yearsdg#c.yearsdg]`, `_b[2.rank]`, and `_b[3.rank]`.

A more flexible curve can be produced by using *higher-order polynomials*, also including `yearsdg` cubed, which can be expressed as `c.yearsdg#c.yearsdg#c.yearsdg`, and possibly higher powers. Unless there are specific hypotheses about the shape of the curve, the coefficients of lower powers should be kept in the model. See section 7.3 for a further discussion of polynomials and for an alternative approach to modeling nonlinearity based on linear splines.

Finally, we note that the effect of gender becomes nonsignificant at the 5% level after adding `yearsrank`, the number of years spent at the current academic rank, to the final regression model presented here.

1.12 Residual diagnostics

Predicted residuals are defined as the differences between the observed responses y_i and the predicted responses $\widehat{y}_i$:

$$\widehat{\epsilon}_i \;=\; y_i - \underbrace{(\widehat{\beta}_1 + \widehat{\beta}_2 x_{2i} + \cdots + \widehat{\beta}_p x_{pi})}_{\widehat{y}_i}$$

Predicted standardized residuals are obtained as

$$r_i \;=\; \frac{\widehat{\epsilon}_i}{s_{ri}}$$

where s_{ri} is the estimated standard error of the residual.

Predicted residuals or standardized residuals can be used to investigate whether model assumptions, such as homoskedasticity and normally distributed errors, are violated. Predicted standardized residuals have the advantage that they have an approximate standard normal distribution if the model assumptions are true. For instance, a value greater than 3 should occur only about 0.1% of the time and may therefore be an outlier.

The postestimation command `predict` with the `residual` option provides predicted residuals for the last regression model that was fit.

```
. predict res, residual
```

Standardized residuals can be obtained by using the `rstandard` option of `predict`.

A histogram of the predicted residuals with an overlayed normal distribution is produced by the `histogram` command with the `normal` option,

```
. histogram res, normal
```

and is presented in figure 1.16.

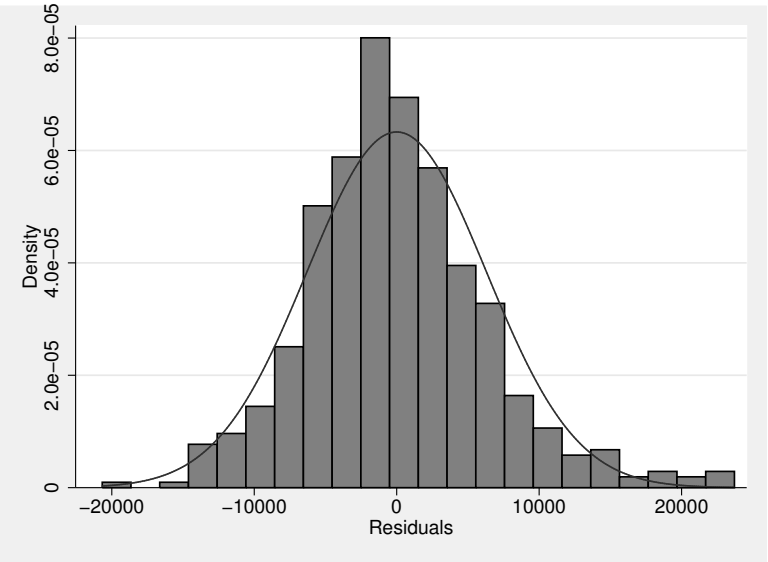


Figure 1.16: Predicted residuals with overlayed normal distribution

The distribution is somewhat skewed, suggesting that salary should perhaps be log-transformed as discussed in section 1.3. Again it may be advisable to use the `vce(robust)` option, which provides standard errors that are not just robust to heteroskedasticity but also to other violations of the distributional assumptions.

1.13 ❖ Causal and noncausal interpretations of regression coefficients

1.13.1 Regression as conditional expectation

Consider the regression model

$$y_i = \beta_1 + \beta_2 T_i + \epsilon_i$$

where y_i is income and T_i is a dummy variable for having a bachelor's degree (taking the value 1 for those with a degree and the value 0 for those without a degree). More generally, $T_i = 1$ could represent "treatment" and $T_i = 0$ could represent "control".

So far, we have followed the conventions of traditional statistics by not making causal interpretations of the regression coefficient β_2. β_2 is merely interpreted as the difference in the conditional expectation of income between those with and those without a degree:

$$\beta_2 = E(y_i|T_i = 1) - E(y_i|T_i = 0)$$

This difference can be due to the causal effect of having a degree on income or due to inherent differences that affect income, such as intelligence, between those who do and do not pursue and earn a degree. The reason for such differences is that subjects are not randomly assigned to getting a degree or not. Instead, there are various mechanisms at play that affect selection into the treatment, having a degree. Variables that affect both selection and income, such as intelligence, are called confounders or lurking variables. If there are confounders, then it is evident that β_2 is not a causal effect.

Some of the combined effect of the confounders on income contributes to β_2, and the remainder contributes to the error term ϵ_i. The part that contributes to β_2 is called the *linear projection* onto T_i, whereas the part that contributes to the error term is called orthogonal to (or uncorrelated with) T_i. In other words, β_2 absorbs all aspects of unobserved variables that are correlated with T_i, rendering ϵ_i uncorrelated with T_i by definition. This is the case for the true model, and consistent estimation refers to estimating the conflated parameter. Why would we want to estimate such a conflated parameter? The parameters β_1 and β_2 would give the best (smallest mean-squared prediction error) prediction $\widehat{y}_i = \beta_1 + \beta_2 T_i$ of the income y_i for someone who happens to have a degree ($T_i = 1$) or someone who happens not to have a degree ($T_i = 0$). In that sense, β_2 is a measure of association.

In many disciplines, confounding is implicitly viewed as inevitable, and the term "causation" is avoided at all cost. Many introductory statistics textbooks state that

regression or correlation does not imply causation, and that is the first and last time causality is mentioned.

1.13.2 Regression as structural model

In contrasts to traditional statistics, the regression coefficient of T_i is usually interpreted as causal in econometrics, and the assumptions under which the causal effect can be estimated consistently (or unbiasedly) are stated explicitly.

We will write the causal or *structural* model as

$$y_i = \beta_1^c + \beta_2^c T_i + \epsilon_i^c$$

where β_2^c is now the *causal effect* of having a degree on income, that is, the mean change in income produced by changing degree status, keeping all else constant. The error term ϵ_i^c represents the combined effects of all omitted variables, not just the component that is uncorrelated with T_i.

For unbiased estimation of β_2^c, the *strict exogeneity* assumption $E(\epsilon_i^c|T_i) = 0$ is required. This assumption implies lack of correlation between T_i and ϵ_i^c and this latter, weaker assumption is often loosely referred to as exogeneity. Endogeneity is due to confounders, such as intelligence that have been omitted from the model and are hence part of the error term ϵ_i^c and that are correlated with T_i. If assignment to the treatment and control groups is random, as in a randomized experiment, then T_i is strictly exogenous by design.

The top panel of figure 1.17 illustrates violation of exogeneity. Here x_i is intelligence, the hollow and filled circles represent observations from the group with a degree ($T_i = 1$) and group without a degree ($T_i = 0$), respectively, and the dashed and solid lines represent the corresponding fixed part of the structural model. The vertical distance between these lines is the causal treatment effect β_2^c. We see that the residuals tend to be positive for the degree group and negative for the nondegree group. This positive correlation between the degree dummy variable T_i and the error term ϵ_i is due to the omitted variable, intelligence x_i, which has a higher mean in the degree group than in the nondegree group and is positively correlated with income y_i.

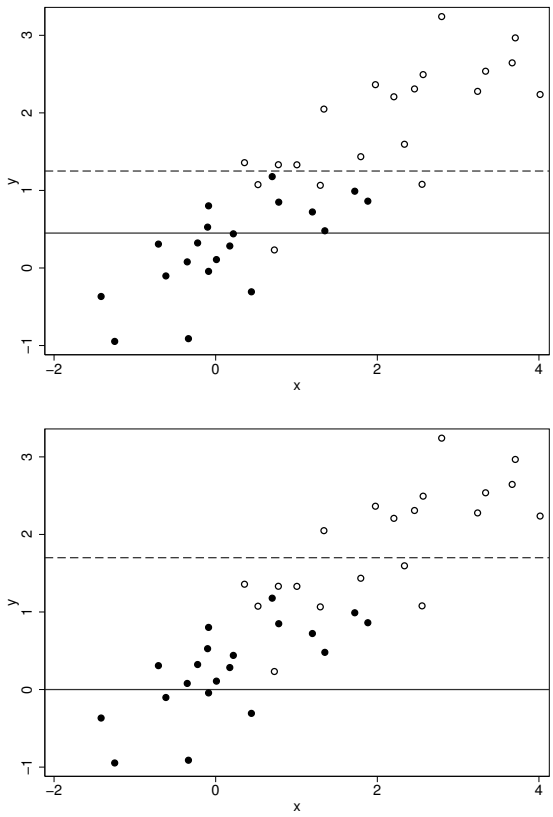


Figure 1.17: Illustration of violation of exogeneity: Top panel shows the structural model, where the errors are correlated with the treatments; bottom panel shows the estimated regression model when x_i is omitted

The bottom panel shows the least-squares regression lines when x_i is omitted. Here the vertical distance between the lines is the estimated effect of treatment, which is too large because of the positive correlation between the error term and the degree dummy variable. It can be shown that for given values of x_i and T_i, under repeated sampling of y_i from the model $y_i = \beta_1^c + \beta_2^c T_i + \beta_x^c x_i + \epsilon_i^c$, the bias of the OLS estimator of β_2^c for the model not containing x_i is given by $r_{Tx}\beta_x^c s_x/s_T$, where r_{Tx} is the correlation between x_i and T_i, β_x^c is the structural parameter of x_i, and s_x and s_T are the standard deviations of x_i and T_i, respectively.

1.14 Summary and further reading

In this chapter, we have shown how linear regression can be used to model the relationship between a continuous response variable and explanatory variables of different types, including continuous, dichotomous, and ordered or unordered polytomous (multicategory) variables. Special cases of such regression models are one-way ANOVA and the model underlying an independent-samples t test.

We have also demonstrated how dummy variables can be used to represent categories of categorical explanatory variables and how products of variables can be used to model interactions, where the effect of each variable is moderated by the other variable. We have shown how nonlinear relationships between the response and a continuous covariate can be modeled using polynomials. Specification of such models is greatly facilitated by Stata's factor variables, introduced in Stata release 11.

We have introduced the idea of a structural model representing the causal effect of covariates in contrast to a regression model for conditional means that makes no causal claims. Exogeneity assumptions that are required for using regression models to estimate causal effects have been briefly discussed. These issues become more complex in multilevel models and are revisited in chapter 3. We refer the interested reader to Morgan and Winship (2007) for a readable introduction to the modern literature on causal inference.

A good elementary introduction to linear regression models is provided by Agresti and Finlay (2007). More advanced, but accessible, introductions that also include regression for other response types, such as logistic regression, include DeMaris (2004) for social science, Vittinghoff et al. (2005) for biomedicine, and Stock and Watson (2011) and Wooldridge (2009) for economics.

The next section, 1.15, contains exercises designed to help reinforce the material discussed in this chapter. Exercises 1.1 to 1.5 involve analysis of four different datasets in Stata, whereas exercises 1.6 and 1.7 concern interpretation of estimated regression coefficients in models that include interactions. Exercise 1.5 concerns the interpretation of regression coefficients when the response variable is log-transformed, a topic not discussed in this chapter. Finally, exercise 1.8 is a self-assessment exercise (with solutions provided) that reviews many of the ideas discussed in this chapter. As indicated by the label Solutions, solutions to exercise 1.1 can be found on the website for this book (http://www.stata-press.com/books/mlmus3).

Brief introductions to logistic regression for dichotomous, ordinal, and nominal responses; discrete-time hazard models for survival or duration data; and Poisson regression for counts are given in the beginning of some chapters in volume 2, before we embark on multilevel versions of these models.

1.15 Exercises

1.1 High-school-and-beyond data Solutions

The data considered here are from the High School and Beyond Survey. They are discussed and analyzed in Raudenbush et al. (2004) and accompany the HLM program (Raudenbush et al. 2004).

The variables in the dataset `hsb.dta` that we will use here are

- `schoolid`: school identifier
- `mathach`: a measure of mathematics achievement
- `ses`: socioeconomic status based on parental education, occupation, and income
- `minority`: dummy variable for student being nonwhite

1. Keep only data on the five schools with the lowest values of `schoolid` (1224, 1288, 1296, 1308, and 1317). Also drop the variables not listed above.
2. Obtain the means and standard deviations for the continuous variables and frequency tables for the categorical variables. Also obtain the mean and standard deviation of the continuous variables for each of the five schools (using the `table` or `tabstat` command).
3. Produce a histogram and a box plot of `mathach`.
4. Produce a scatterplot of `mathach` versus `ses`. Also produce a scatterplot for each school (using the `by()` option).
5. Treating `mathach` as the response variable y_i and `ses` as an explanatory variable x_i, consider the linear regression of y_i on x_i:

$$y_i \;=\; \beta_1 + \beta_2 x_i + \epsilon_i, \quad \epsilon_i | x_i \sim N(0, \sigma^2)$$

   a. Fit the model.
   b. Report and interpret the estimates of the three parameters of this model.
   c. Interpret the confidence interval and p-value associated with β_2.

6. Using the `predict` command, create a new variable `yhat` that is equal to the predicted values $\widehat{y}_i$ of `mathach`:

$$\widehat{y}_i \;=\; \widehat{\beta}_1 + \widehat{\beta}_2 x_i$$

7. Produce a scatterplot of `mathach` versus `ses` with the regression line (`yhat` versus `ses`) superimposed. Produce the same scatterplot by school. Does it appear as if schools differ in their mean math achievement after controlling for `ses`?
8. Extend the regression model from step 5 by including dummy variables for four of the five schools.

   a. Fit the model with and without factor variables.

   b. Describe what the coefficients of the school dummies represent.
   c. Test the null hypothesis that the population coefficients of all four dummy variables are zero (use `testparm`).
9. Add interactions between the school dummies and `ses` using factor variables, and interpret the estimated coefficients.

See also exercise 3.7 for random-intercept models applied to this dataset.

1.2 Anorexia data

Hand et al. (1994) provide data on young girls with anorexia who were randomly assigned to three different treatments: cognitive behavioral therapy, family therapy, and control (treatment as usual). The response variable is the girls' weight in kilograms after treatment, and we also have their weights before treatment.

The variables in `anorexia.dta` are

- `treat`: treatment group (1: cognitive behavioral therapy; 2: control; 3: family therapy)
- `weight1`: weight before treatment (in kilograms)
- `weight2`: weight after treatment (in kilograms)

1. Produce a table of the means and standard deviations of `weight2`, as well as sample sizes by treatment group.
2. Plot box plots and histograms of `weight2` by group as shown in section 1.3.
3. Create dummy variables `cbt` and `ft` for cognitive behavioral therapy and family therapy, respectively.
4. Fit a regression model with `weight2` as the response variable and `weight1`, `cbt`, and `ft` as covariates.
5. Interpret the estimated regression coefficients.
6. For which of the three pairs of treatment groups is there any evidence, at the 5% level, that one treatment is better than the other?
7. Fit the model again, this time relaxing the homoskedasticity assumption. Does this alter your answer for step 6?
8. Plot a histogram of the estimated residuals for this model with a normal density curve superimposed.

1.3 Smoking-and-birthweight data

Here we consider a subset of data on birth outcomes, provided by Abrevaya (2006), which is analyzed in chapter 3. The data were derived from birth certificates by the U.S. National Center for Health Statistics.

The variables in `smoking.dta` that we will consider here are

- `momid`: mother identifier
- `idx`: chronological numbering of multiple children to the same mother in the database (1: first child; 2: second child; 3: third child)

- `birwt`: birthweight (in grams)
- `mage`: mother's age at the birth of the child (in years)
- `smoke`: dummy variable for mother smoking during pregnancy (1: smoking; 0: not smoking)
- `male`: dummy variable for baby being male (1: male; 0: female)
- `hsgrad`: dummy variable for mother having graduated from high school
- `somecoll`: dummy variable for mother having some college education (but no degree)
- `collgrad`: dummy variable for mother having graduated from college
- `black`: dummy variable for mother being black (1: black; 0: white)

1. Keep only the data on each mother's first birth, that is, where `idx` is 1.
2. Create the variable `education`, taking the value 1 if `hsgrad` is 1, the value 2 if `somecoll` is 1, the value 3 if `collgrad` is 1, and the value 0 otherwise.
3. Produce a table of the means and standard deviations of `birwt` for all the subgroups defined by `smoke`, `education`, `male`, and `black`. Hint: Use the `table` command with `smoke` as *rowvar*, `education` as *colvar*, and `male` and `black` as *superrowvars*; see `help table`.
4. Produce box plots for the same groups. Hint: Use the `asyvars` option and the `over()` option for each grouping variable except the last (starting with `over(education)`), and use the `by()` option for the last grouping variable. Use the `nooutsides` option to suppress the display of outliers, making the graph easier to interpret. What do you observe?
5. Regress `birwt` on `smoke` and interpret the estimated regression coefficients.
6. Add `mage`, `male`, `black`, `hsgrad`, `somecoll`, and `collgrad` to the model in step 5.
7. Interpret each of the estimated regression coefficients from step 6.
8. Discuss the difference in the estimated coefficient of `smoke` from steps 5 and 6.
9. Use the `margins` command to produce a table of estimated population means for girls born to white mothers of average age by smoking status and education. (This requires you to run the `regress` command again with the factor variables `i.smoke` and `i.education`.)
10. Extend the model from step 6 to investigate whether the adjusted difference in mean birthweight between boys and girls differs between black and white mothers. Is there any evidence at the 5% level that it does?

1.4 Class-attendance data

This dataset on college students is taken from Wooldridge (2010). The variables in `attend.dta` are

- `stndfnl`: standardized final exam score
- `atndrte`: percent of lectures attended
- `frosh`: dummy variable for being a freshman
- `soph`: dummy variable for being a sophomore
- `priGPA`: prior cumulative GPA (grade-point average)
- `ACT`: score on ACT test (a test used for admission to college)

The questions below are adapted from Wooldridge (2010, 86).

1. To assess the effect of lecture attendance on final exam performance, regress `stndfnl` on `atndrte` and the dummy variables `frosh` and `soph`. Interpret the estimated regression coefficient of `atndrte`.
2. Is the model suitable for estimating the causal effect of attendance? Explain.
3. Add `priGPA` and `ACT` to the regression model in step 1. Now what is the estimated coefficient of `atndrte`? Discuss how the estimate differs from that in step 1.
4. Add the squares of `priGPA` and `ACT` to the model in step 3 by using factor variables. What happens to the estimated coefficient of `atndrte`? Are the two quadratic terms jointly significant at the 5% level?
5. Retain the squares of `priGPA` and `ACT` only if they are jointly significant at the 5% level, and then add the square of `atndrte` to the model. What do you conclude?

1.5 ❖ Faculty salary data

In this exercise, we will revisit the data analyzed in this chapter. Instead of treating salary as the response variable, we will use the log-transform of salary as response. As shown in display 1.1 below, the exponentiated regression coefficients can then be interpreted as multiplicative effects on the mean salary.

1. Generate a variable equal to log-salary, and regress the new variable on a dummy variable for being male.
2. Calculate the exponential of the estimated coefficient of the male dummy variable and interpret it.
3. Add mean-centered marketability, `marketc`, as a further covariate and fit the extended model.
4. Interpret the exponentiated regression coefficients for the male dummy and for `marketc`.

Taking the exponential (antilogarithm) of the log-linear model

$$\ln(y_{ij}) \;=\; \beta_1 + \beta_2 x_{2ij} + \cdots + \beta_p x_{pij} + \zeta_j + \epsilon_{ij}$$

we obtain the multiplicative model

$$y_{ij} \;=\; \exp(\beta_1) \times \exp(\beta_2)^{x_{2ij}} \times \cdots \times \exp(\beta_p)^{x_{pij}} \times \exp(\zeta_j + \epsilon_{ij})$$

Taking the conditional expectation of y_{ij}, conditional on the covariates $\mathbf{x}_{ij} \equiv (x_{2ij}, \ldots, x_{pij})'$, we get

$$E(y_{ij}|\mathbf{x}_{ij}) \;=\; \exp(\beta_1) \times \exp(\beta_2)^{x_{2ij}} \times \cdots \times \exp(\beta_p)^{x_{pij}} \times E\{\exp(\zeta_j + \epsilon_{ij})|\mathbf{x}_{ij}\}$$

Using the fact that

$$E\{\exp(\zeta_j + \epsilon_{ij})|\mathbf{x}_{ij}\} \;=\; \exp\{(\psi + \theta)/2\}$$

for the log-normal distribution, we obtain

$$E(y_{ij}|\mathbf{x}_{ij}) \;=\; \exp\{\beta_1 + (\psi+\theta)/2\} \times \exp(\beta_2)^{x_{2ij}} \times \cdots \times \exp(\beta_p)^{x_{pij}}$$

Display 1.1: Log-linear models and multiplicative effects

1.6 Interaction I

The table below gives estimates for a multiple regression model fit to data from the 2000 Program for International Student Assessment (PISA). Specifically, the reading score for students from three of the countries was regressed on dummy variables for two of the countries (`country`=2 for the United Kingdom, `country`=3 the United States, and `country`=1 for Germany), a dummy variable `test_lan` for the test language (English or German depending on the country) being spoken at home, and the interactions between the country and test language dummy variables. The following output was obtained:

```
      Source |       SS       df       MS              Number of obs =    4528
-------------+------------------------------           F(  5,  4522) =   31.49
       Model |  1368555.21     5  273711.043            Prob > F      =  0.0000
    Residual |    39308808  4522  8692.79257            R-squared     =  0.0336
-------------+------------------------------           Adj R-squared =  0.0326
       Total |  40677363.2  4527  8985.50104            Root MSE      =  93.235

------------------------------------------------------------------------------
     wleread |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
     country |
           2 |   114.7891   17.88846     6.42   0.000     79.71894    149.8592
           3 |   42.36503   14.83595     2.86   0.004     13.27931    71.45075
             |
  1.test_lan |   98.53028   11.30737     8.71   0.000     76.36232    120.6982
             |
     country#|
   test_lan  |
         2 1 |  -98.53611   18.17351    -5.42   0.000    -134.1651   -62.90716
         3 1 |  -35.66298   15.32532    -2.33   0.020     -65.7081   -5.617867
             |
       _cons |   423.4007   11.06498    38.26   0.000     401.7079    445.0935
------------------------------------------------------------------------------
```

1. Interpret each estimated coefficient.
2. Plot the estimated relationship between mean reading score and `test_lan` for each of the countries. You may do this using the `twoway function` command in Stata.
3. Write down the Stata command to fit this model (using factor variables).

1.7 Interaction II

The following estimates were obtained by regressing a continuous measure y_i of fear of crime on the variables $\texttt{age}_i$, $\texttt{fem}_i$, and their interaction (using data from the British Crime Survey, 2001–2002):

$$\widehat{y}_i = -0.19 + 0.66\texttt{fem}_i - 0.02\texttt{age}_i - 0.07\texttt{fem}_i \times \texttt{age}_i$$

Here $\texttt{fem}_i$ is a dummy variable for being female, and $\texttt{age}_i$ is the number of 10-year intervals since age 16, that is, $(\texttt{age} - 16)/10$.

1. What is the predicted fear of crime for males and females at age 16?
2. What is the predicted fear of crime for males and females at age 80?
3. Interpret the estimated coefficient of $\texttt{fem}_i \times \texttt{age}_i$.
4. Plot the predicted relationship between fear of crime and age (for the age range 16–90 years) using a separate line for each gender. You may use Stata's `twoway function` command.
5. Adding $\texttt{age}_i^2$ to the model gave these estimates:

   $$\widehat{y}_i = -0.24 + 0.66\texttt{fem}_i + 0.02\texttt{age}_i - 0.006\texttt{age}_i^2 - 0.06\texttt{fem}_i \times \texttt{age}_i$$

   Use Stata to plot the predicted relationship between fear of crime and age (for the age range 16–90 years) using a separate curve for each gender.

1.8 Self-assessment exercise

1. In the simple linear regression model shown below, salary (y_i) is regressed on years of experience (x_i):

$$y_i = \beta_1 + \beta_2 x_i + \epsilon_i, \quad \epsilon_i | x_i \sim N(0, \sigma^2)$$

   a. What are the usual terms used to describe β_1, β_2, ϵ_i, and σ^2?
   b. State the assumptions of this model in words.
   c. If the variables are called `salary` (y_i) and `yearsexp` (x_i) in Stata, write down the command for fitting the model.

2. In a simple linear regression model for salary, the coefficient of a dummy variable for being male is estimated as \$3,623.

   a. Interpret the estimated coefficient.
   b. If a dummy variable for being female had been used instead of a dummy variable for being male, what would have been the value of the estimated regression coefficient?
   c. The estimated standard error for the estimated coefficient of the male dummy variable was \$1,912. Can you reject the null hypothesis that the population mean salary is the same for men and women by using a two-sided test at the 5% level?

3. What is the relationship between one-way ANOVA and multiple linear regression? Is one model a special case of the other? Explain.

4. In the output for a multiple linear regression model, an F test is given with $F(4, 268) = 12.63$. State the null and alternative hypotheses being tested.

5. In a regression of salary (in U.S. dollars) on age (in years), the intercept is estimated as $-$\$2,000. Explain how this is possible given that salary must be positive.

6. Using the United States sample of the 2000 Programme for International Student Assessment (PISA) study, the difference in population mean English reading score between those who do and do not speak English at home is estimated as 63 with a standard error of 10. When controlling for socioeconomic status, the adjusted difference in population mean reading score is estimated as 49 with a standard error of 10.

   a. What does it mean to "control" or "adjust for" socioeconomic status?
   b. Under what circumstances does controlling for a variable, x_1, alter the estimated regression coefficient of another variable, x_2?
   c. In the context of this example, explain why the adjusted estimate differs from the unadjusted estimate, paying attention to the direction of the difference.

7. The salaries of a company's employees were regressed on a dummy variable for being male, `male`, and years of experience, `yearsexp`, and their interaction, giving the following results:

$$\widehat{y}_i = \$30{,}000 + \$2{,}000\ \texttt{male}_i + \$600\ \texttt{yearsexp}_i - \$100\ \texttt{male}_i \times \texttt{yearsexp}_i$$

a. Interpret each estimated coefficient.
b. What is the estimated difference in population mean salary between men and women who have 10 years of experience?

8. Regression output for data from the 2000 PISA study is given below. The sample analyzed here included children from the United States, the United Kingdom, and Germany. `wleread` is the reading score, `usa` is a dummy variable for the child being from the United States, `uk` is a dummy variable for the child being from the United Kingdom, and `female` is a dummy variable for the child being female.

```
. regress wleread usa uk female
```

Source	SS	df	MS		Number of obs =	4528
					F(3, 4524) =	44.21
Model	1158538.51	3	386179.502		Prob > F =	0.0000
Residual	39518824.7	4524	8735.37239		R-squared =	0.0285
					Adj R-squared =	0.0278
Total	40677363.2	4527	8985.50104		Root MSE =	93.463

wleread	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
usa	4.00653	3.715402	1.08	0.281	-3.277473	11.29053
uk	20.30115	3.159347	6.43	0.000	14.10728	26.49501
female	26.13154	2.781327	9.40	0.000	20.67878	31.5843
_cons	504.7174	2.672635	188.85	0.000	499.4778	509.9571

a. Write down the linear regression model being fit.
b. Interpret the estimated coefficient of `uk`.
c. Estimate the difference in population mean reading scores between the United States and the United Kingdom.
d. What percentage of the variability in reading scores is explained by nationality and gender?
e. What is the magnitude of the estimated residual variance?
f. Write down the necessary Stata commands for investigating whether the difference in population mean reading scores between girls and boys differs between countries. Assume that the data contain a variable, `country`, taking the value 1 for Germany, 2 for United States, and 3 for United Kingdom. Give the commands with and without factor variables.

Solutions for self-assessment exercise

1. a. β_1 is the intercept, β_2 is the slope or coefficient of x_i, ϵ_i is the residual or error term for subject i, and σ^2 is the residual variance.
   b. For given x_i, the expectation of y_i is linearly related to x_i, the residuals ϵ_i are normally distributed with zero mean and variance σ^2, and the residuals ϵ_i are independent for different units i. The residual variance is constant for all values of x_i, an assumption called homoskedasticity.
   c. `regress salary yearsexp`
2. a. The estimated difference in population mean salaries between men and women is $3,623.
   b. −$3,623
   c. No, the t statistic is $t = 3,623/1,912 = 1.89$. The smallest t statistic that yields a two-sided p-value of $p \leq 0.05$ is 1.96, when the degrees of freedom are very large (larger t statistics are required for smaller degrees of freedom), so the test is not significant at the 5% level.
3. One-way ANOVA is a special case of multiple linear regression where the only explanatory variables are the dummy variables for each category of a categorical variable, except the reference category.
4. The null hypothesis is that all true regression coefficients, except the intercept, are zero. The alternative hypothesis is that at least one of the true regression coefficients (except the intercept) is nonzero.
5. The intercept is the estimated population mean salary, or predicted salary, at age 0. This is an extrapolation well outside the range of the data. Even if it were possible to have a salary at age 0, there would be no reason to believe that the relationship between salary and age is linear beginning with age 0.
6. a. Controlling for socioeconomic status means attempting to estimate the difference in mean reading score for two (sub)populations (native and nonnative speakers) having the same socioeconomic status.
   b. When x_1 is associated with both x_2 and y.
   c. Native speakers may have higher mean socioeconomic status, and socioeconomic status may be positively correlated with reading scores, so some of the apparent advantage of native speakers is actually due to their higher mean socioeconomic status.
7. a. The estimated population mean salary is $30,000 for females with no experience and $2,000 greater for males with no experience. For each extra year of experience, the estimated population mean salary increases $600 for females and $100 less (that is, $500) for males.
   b. The difference in population means for males and females after 10 years is estimated as $\$2{,}000 - \$100 \times 10 = \$1{,}000$.
8. a. $y_i = \beta_1 + \beta_2\,\texttt{usa}_i + \beta_3\,\texttt{uk}_i + \beta_4\,\texttt{female}_i + \epsilon_i$ where, for given covariates, ϵ_i has a normal distribution with mean 0 and constant variance σ^2, and is independent of $\epsilon_{i'}$ for another student i'.
   b. The estimated coefficient of `uk` represents the estimated difference in population mean reading scores between children in the United Kingdom and children in Germany.
   c. The estimated difference in population mean reading scores between children in the United States and children in the United Kingdom is the difference between the estimated coefficients of `usa` and `uk`, giving $4.01 - 20.30 = -16.29$.

d. 2.85%

e. $\widehat{\sigma^2} = 8735.37$ (under `MS` for `Residual`).

f. Without factor variables:

```
generate fem_usa = female*usa
generate fem_uk = female*uk
regress wleread usa uk female fem_usa fem_uk
testparm fem_usa fem_uk
```

With factor variables:

```
regress wleread i.country##i.female
testparm i.country#i.female
```

Part II

Two-level models

2 Variance-components models

2.1 Introduction

Units of observation often fall into groups or clusters. For example, individuals could be nested in families, hospitals, schools, neighborhoods, or firms. Longitudinal data also consist of clusters of observations made at different occasions for the same individual or cluster. For two examples of clustered data, the nesting structure is depicted in figure 2.1.

In clustered data, it is usually important to allow for dependence or correlations among the responses observed for units belonging to the same cluster. For example, the adult weights of siblings are likely to be correlated because siblings are genetically related to each other and have usually been raised within the same family. Variance-components models are designed to model and estimate such within-cluster correlations.

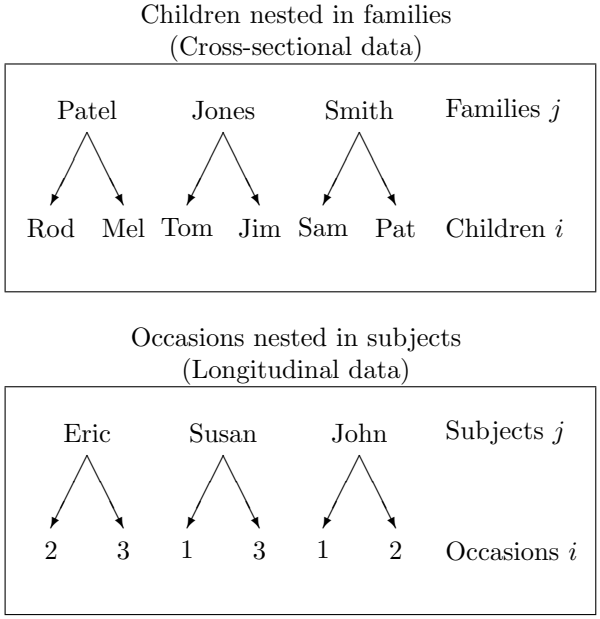


Figure 2.1: Examples of clustered data

In this chapter, we consider the simple situation of clustered data without covariates or explanatory variables. This situation is important in its own right and is also useful for introducing and motivating the notions of random effects and variance components. We also describe basic principles of estimation and prediction in this simple setting. However, this means that some parts of the chapter may be a bit demanding, and you might want to skip sections 2.10 and 2.11 on first reading.

In addition to describing variance-components models, we introduce the Stata commands `xtreg` and `xtmixed`, which will be used throughout volume 1.

2.2 How reliable are peak-expiratory-flow measurements?

The data come from a reliability study conducted by Professor Martin Bland using 17 of his family and colleagues as subjects. The purpose was to illustrate a way of assessing the quality of two instruments for measuring people's peak-expiratory-flow rate (PEFR). The PEFR, which is roughly speaking how strongly subjects can breathe out, is a central clinical measure in respiratory medicine.

The subjects had their PEFR measured twice (in liters per minute) using the standard Wright peak-flow meter and twice using the new Mini Wright peak-flow meter. The methods were used in random order to avoid confounding practice (prior experience) effects with method effects. If the new method agrees sufficiently well with the old, the old method may be replaced with the more convenient Mini meter. Interestingly, the paper reporting this study (Bland and Altman 1986) is the most cited paper in *The Lancet*, one of the most prestigious medical journals.

The data are presented in table 2.1 and are stored in `pefr.dta` in the same form as in the table, with the following variable names:

- `id`: subject identifier
- `wp1`: Wright peak-flow meter, occasion 1
- `wp2`: Wright peak-flow meter, occasion 2
- `wm1`: Mini Wright flow meter, occasion 1
- `wm2`: Mini Wright flow meter, occasion 2

Table 2.1: Peak-expiratory-flow rate measured on two occasions using both the Wright and the Mini Wright peak-flow meters

	Wright peak-flow meter		Mini Wright peak-flow meter	
Subject `id`	First `wp1`	Second `wp2`	First `wm1`	Second `wm2`
1	494	490	512	525
2	395	397	430	415
3	516	512	520	508
4	434	401	428	444
5	476	470	500	500
6	557	611	600	625
7	413	415	364	460
8	442	431	380	390
9	650	638	658	642
10	433	429	445	432
11	417	420	432	420
12	656	633	626	605
13	267	275	260	227
14	478	492	477	467
15	178	165	259	268
16	423	372	350	370
17	427	421	451	443

We load the data into Stata using the command

```
. use http://www.stata-press.com/data/mlmus3/pefr
```

In this chapter, we analyze the two sets of measurements from the Mini Wright peak-flow meter only. Analyses comparing the standard Wright and Mini Wright peak-flow meters are discussed in chapter 8.

2.3 Inspecting within-subject dependence

The first and second recordings on the Mini Wright peak-flow meter can be plotted against the subject identifier with a horizontal line representing the overall mean by using

```
. generate mean_wm = (wm1+wm2)/2
. summarize mean_wm
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
     mean_wm |         17    453.9118    111.2912       243.5        650
```

```
. twoway (scatter wm1 id, msymbol(circle))
>        (scatter wm2 id, msymbol(circle_hollow)),
>        xtitle(Subject id)  xlabel(1/17) ytitle(Mini Wright measurements)
>        legend( order(1 "Occasion 1" 2 "Occasion 2")) yline(453.9118)
```

The resulting graph is shown in figure 2.2.

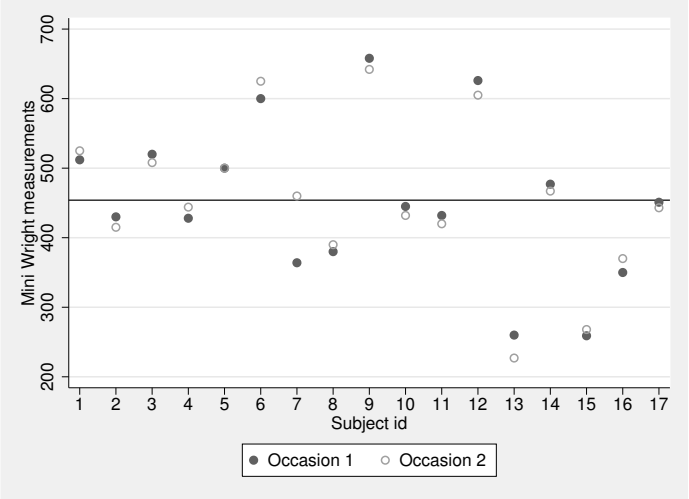


Figure 2.2: First and second measurements of peak-expiratory-flow using Mini Wright meter versus subject number (the horizontal line represents the overall mean)

It may be tempting to model the response y_{ij} of unit (here measurement occasion) i in cluster (here subject) j using a standard regression model without covariates

$$y_{ij} = \beta + \xi_{ij} \tag{2.1}$$

where ξ_{ij} are residuals or error terms that are uncorrelated over both subjects and occasions (the Greek letter ξ is pronounced "xi").

However, it is clear from the figure that repeated measurements on the same subject tend to be closer to each other than to the measurements on a different subject. Indeed, if this were not the case, the Mini Wright peak-flow meter would be useless as a tool for discriminating between the subjects in this sample. Because there are large differences between subjects (for example, compare subjects 9 and 15) and only small differences within subjects, the responses for occasions 1 and 2 on the same subject tend to lie on the same side of the overall mean, shown as a horizontal line in the figure, and are therefore positively correlated (that is, they have a positive covariance, defined as the expectation of products of deviations from the mean). See also section 2.4.4.

We can also see that there is within-subject dependence by considering prediction of a subject's response at occasion 2 if we only know all the subjects' responses at

occasion 1. If the response for a given subject at occasion 2 were independent of his or her response at occasion 1, a good prediction would be the mean response at occasion 1 across all subjects. However, it is clear that a much better prediction here is the subject's own response at occasion 1 because the responses are highly dependent within subject.

The within-subject dependence is due to between-subject heterogeneity. If all subjects were more or less alike (for example, pick subjects 2, 4, 10, 11, 14, and 17), there would be much less within-subject dependence.

2.4 The variance-components model

2.4.1 Model specification

As we saw in the previous section and in figure 2.2, it is unreasonable to assume that the deviations ξ_{ij} of y_{ij} from the population mean β are uncorrelated within subjects in the regression model

$$y_{ij} = \beta + \xi_{ij} \tag{2.2}$$

We can model the within-subject dependence by splitting the residual ξ_{ij} into two uncorrelated components: a permanent component ζ_j (ζ is pronounced "zeta"), which is specific to each subject j and constant across occasions i; and an idiosyncratic component ϵ_{ij}, which is specific to each occasion i for each subject j. We then obtain a variance-components model,

$$y_{ij} = \beta + \zeta_j + \epsilon_{ij} \tag{2.3}$$

as shown for subject j in figure 2.3.

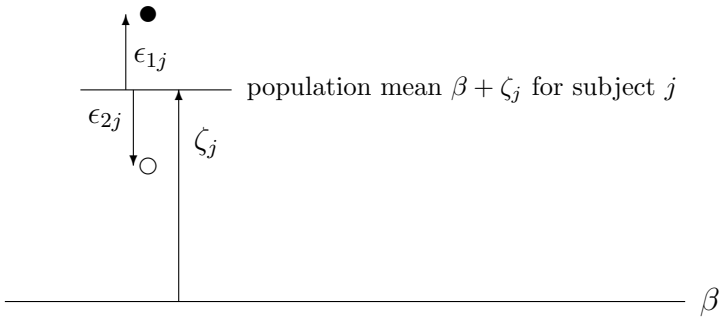


Figure 2.3: Illustration of variance-components model for a subject j

Here ζ_j is the random deviation of subject j's mean measurement (over a hypothetical population of measurement occasions) from the overall mean β. The component

ζ_j, often called a random effect of subject or a *random intercept*, has zero population mean and is uncorrelated across subjects. ζ_j can be viewed as representing individual differences due to personal characteristics not included as variables in the model. The component ϵ_{ij}, often called the level-1 residual or within-subject residual, is the random deviation of y_{ij} from subject j's mean. This residual has zero population mean and is uncorrelated across occasions and subjects.

In classical psychometric test theory, (2.3) represents a measurement model where $\beta + \zeta_j$ is the *true score* for subject j, defined as the long-term mean measurement, and ϵ_{ij} is the measurement error at occasion i for subject j.

The random intercept ζ_j has variance ψ (pronounced "psi"), interpretable as the between-subject variance, and the residual ϵ_{ij} has constant variance θ (pronounced "theta"), interpretable as the within-subject variance.

The model is a simple example of a two-level model, where occasions are level-1 units and subjects are level-2 units or clusters. The random intercept ζ_j is then referred to as the level-2 residual with level-2 (between-subject) variance ψ; ϵ_{ij} is referred to as the level-1 residual with level-1 (between-occasion, within-subject) variance θ.

2.4.2 Path diagram

We can display the random part of the model (every term except β) by using a path diagram or a directed acyclic graph (DAG), as shown in figure 2.4. Here the rectangles represent the observed responses y_{1j} and y_{2j} for each subject j, where the j subscript is implied by the label "subject j" inside the frame surrounding the diagram. The long arrows from ζ_j to the responses represent regressions with slopes equal to 1. The short arrows pointing at the responses from below represent the additive level-1 residuals ϵ_{1j} and ϵ_{2j}.

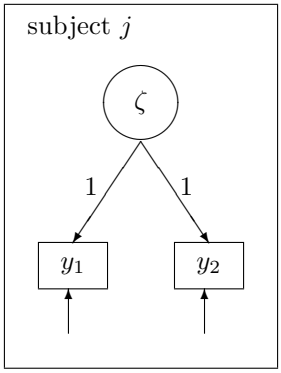


Figure 2.4: Path diagram of random part of random-intercept model

The path diagram makes it clear that the dependence between the two responses is solely due to the shared random intercept. The responses are *conditionally independent* given ζ_j because they are regressed on ζ_j and there is no arrow directly connecting them.[1] (There is also no two-way arrow connecting the level-1 errors ϵ_{1j} and ϵ_{2j} to indicate that they are correlated.) It follows that the responses are conditionally uncorrelated given ζ_j:

$$\text{Cor}(y_{ij}, y_{i'j}|\zeta_j) \;=\; 0$$

This can also be seen by imagining that the data in figure 2.2 were generated by the model depicted in figure 2.3, where the dependence is solely due to the measurements being shifted up or down by the shared random intercept ζ_j for each cluster j. One way of conditioning on ζ_j is to imagine a dataset consisting of just one cluster (or consisting of a subset of clusters with identical values of ζ_j). For that dataset, the responses would be uncorrelated. Another way of understanding conditional independence is to consider predicting the response y_{2j} at occasion 2 for a subject. Given that we know ζ_j (and β), knowing y_{1j} would not improve our prediction.

The (marginal) within-subject correlation is induced by ζ_j because this is shared by all responses for the same subject (see section 2.4.4). As we will see in later chapters, path diagrams are useful for conveying the structure of complex models involving several random effects.

2.4.3 Between-subject heterogeneity

Each response differs from the overall mean β by a total residual or error ξ_{ij}, the sum of two error terms or *error components*: ζ_j and ϵ_{ij}

$$\xi_{ij} \;\equiv\; \zeta_j + \epsilon_{ij}$$

The random intercept ζ_j is shared between measurement occasions for the same subject j, whereas ϵ_{ij} is unique for each occasion i (and subject).

The variance of the responses becomes $\psi + \theta$

$$\begin{aligned}\text{Var}(y_{ij}) &= E\{(y_{ij} - \underbrace{\beta}_{E(y_{ij})})^2\} \;=\; E\{(\zeta_j + \epsilon_{ij})^2\} \;=\; E(\zeta_j^2) + 2\underbrace{E(\zeta_j\epsilon_{ij})}_{\text{Cov}(\zeta_j,\epsilon_{ij})=0} + E(\epsilon_{ij}^2)\\ &= \psi + \theta\end{aligned}$$

which is the sum of *variance components* representing between-subject and within-subject variances. The proportion of the total variance that is between subjects is

$$\rho \;=\; \frac{\text{Var}(\zeta_j)}{\text{Var}(y_{ij})} = \frac{\psi}{\psi + \theta} \tag{2.4}$$

1. If the arrows between ζ_j and the y_{ij} were reversed, ζ_j would become a so-called "collider" and conditional independence would not hold (for example, Morgan and Winship [2007, chap. 3]).

The coefficient ρ is similar to the coefficient of determination R^2 in linear regression discussed in section 1.5, because it expresses how much of the total variability is "explained" by subjects.

In the measurement context, ψ is the variance of subjects' true scores $\beta + \zeta_j$, θ is the *measurement error variance* (the squared *standard error of measurement*), and ρ is a *reliability*, here a test–retest reliability. Note that the reliability is not just a characteristic of the method; it also depends on the between-subject variance, ψ, which can differ between populations.

2.4.4 Within-subject dependence

Intraclass correlation

The marginal (not conditional on ζ_j) covariance between the measurements on two occasions i and i' for the same subject j is defined as

$$\mathrm{Cov}(y_{ij}, y_{i'j}) \;=\; E[\{y_{ij} - E(y_{ij})\}\{y_{i'j} - E(y_{i'j})\}]$$

The corresponding marginal correlation is the above covariance divided by the product of the standard deviations:

$$\mathrm{Cor}(y_{ij}, y_{i'j}) \;=\; \frac{\mathrm{Cov}(y_{ij}, y_{i'j})}{\sqrt{\mathrm{Var}(y_{ij})}\sqrt{\mathrm{Var}(y_{i'j})}} \tag{2.5}$$

It follows from the variance-components model that the population means at both occasions are constrained to be equal to β and the standard deviations are constrained to be equal to $\sqrt{\psi + \theta}$. For the variance-components model, the marginal (not conditional on ζ_j) covariance between the measurements therefore equals ψ:

$$\begin{aligned}
\mathrm{Cov}(y_{ij}, y_{i'j}) &= E\{(y_{ij} - \underbrace{\beta}_{E(y_{ij})})(y_{i'j} - \underbrace{\beta}_{E(y_{i'j})})\} \;=\; E\{(\zeta_j + \epsilon_{ij})(\zeta_j + \epsilon_{i'j})\} \\
&= E(\zeta_j^2) + \underbrace{E(\zeta_j \epsilon_{i'j})}_{0} + \underbrace{E(\epsilon_{ij}\zeta_j)}_{0} + \underbrace{E(\epsilon_{ij}\epsilon_{i'j})}_{0} \;=\; E(\zeta_j^2) = \psi
\end{aligned}$$

The corresponding correlation, called the *intraclass correlation*, becomes

$$\mathrm{Cor}(y_{ij}, y_{i'j}) \;=\; \frac{\mathrm{Cov}(y_{ij}, y_{i'j})}{\sqrt{\mathrm{Var}(y_{ij})}\sqrt{\mathrm{Var}(y_{i'j})}} = \frac{\psi}{\sqrt{\psi + \theta}\sqrt{\psi + \theta}} = \frac{\psi}{\psi + \theta} \;=\; \rho$$

Thus ρ, previously given in (2.4), also represents the within-cluster correlation, which cannot be negative in the variance-components model because $\psi \geq 0$. We see that between-cluster heterogeneity and within-cluster correlations are different ways of describing the same phenomenon; both are zero when there is no between-cluster variance ($\psi = 0$), and both increase when the between-cluster variance increases relative to the within-cluster variance.

The intraclass correlation is estimated by simply plugging in estimates for the unknown parameters:

$$\widehat{\rho} \;=\; \frac{\widehat{\psi}}{\widehat{\psi}+\widehat{\theta}}$$

Figure 2.5 shows data with an estimated intraclass correlation of $\widehat{\rho} = 0.58$ (left panel) and data with an estimated intraclass correlation of $\widehat{\rho} = 0.87$ (right panel).

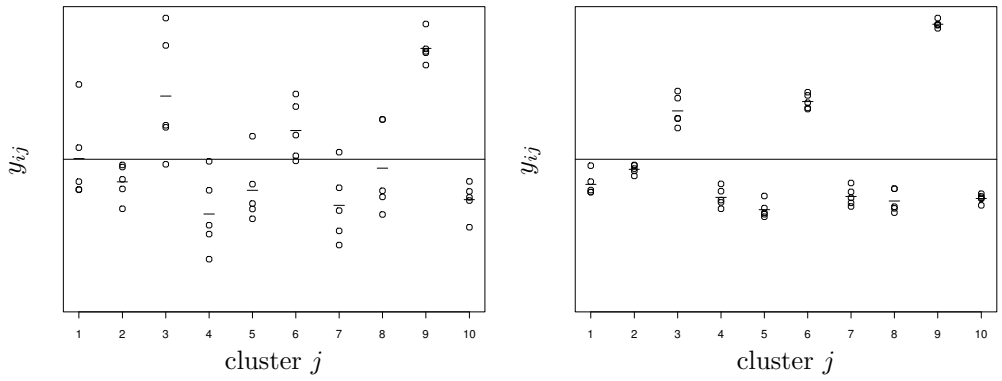


Figure 2.5: Illustration of lower intraclass correlation (left) and higher intraclass correlation (right)

Intraclass correlation versus Pearson correlation

In contrast to the estimated intraclass correlation, the Pearson correlation r is obtained by plugging in separate sample means $\overline{y}_{i\cdot}$ and $\overline{y}_{i'\cdot}$ and sample standard deviations s_{y_i} and $s_{y_{i'}}$ for the two occasions in the estimate of the marginal correlation (2.5),

$$r \;=\; \frac{\frac{1}{J-1}\sum_{j=1}^{J}(y_{ij}-\overline{y}_{i\cdot})(y_{i'j}-\overline{y}_{i'\cdot})}{s_{y_i}s_{y_{i'}}}$$

where J is the number of clusters. Here it is not assumed that the population means and standard deviations are constant across occasions.

To give more insight into the interpretation of the estimated intraclass correlation and Pearson correlation, consider what happens if we alter the second Mini Wright peak-flow measurements by adding 100 to them, as shown in figure 2.6. (Such a systematic increase could, for instance, be due to a practice effect.) For the variance-components model, it is obvious that the within-cluster variance has increased, giving a much smaller intraclass correlation than for the original data (estimated as 0.63 instead of 0.97). In contrast, the Pearson correlation r is 0.97 in both cases (figures 2.2 and 2.6) because it is based on deviations of the first and second measurements from their *respective* means. In contrast, the intraclass correlation is based on deviations from the *overall* or pooled mean.

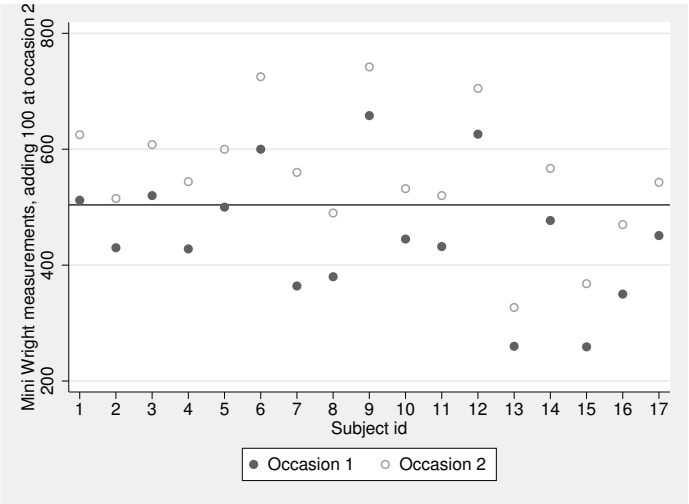


Figure 2.6: First recording of Mini Wright meter and second recording plus 100 versus subject number (the horizontal line represents the overall mean)

The Pearson correlation can be thought of as a measure of *relative agreement*, which refers to how well rankings of subjects based on each measure agree, and is therefore not affected by linear transformations of the measurements. In contrast, the intraclass correlation is a measure of *absolute agreement*.

The intraclass correlation is useful when the units i are *exchangeable* with identical means and standard deviations. For instance, for twin data, there may not even be such a thing as the first and second twin (presuming that birth order is either irrelevant or unknown). Whereas the Pearson correlation can only be obtained by making an arbitrary assignment to y_{1j} and y_{2j} for each twin-pair, the intraclass correlation does not require this. Twins are an example of exchangeable dyads, where the intraclass correlation is more appropriate; married couples are an example of nonexchangeable or distinguishable dyads, where the Pearson correlation between husbands y_{1j} and wives y_{2j} is more appropriate because it is usually difficult to justify that husbands and wives have the same population mean and the same variance. Another difference between the estimated intraclass correlation and the Pearson correlation is that the latter is only defined for pairs of variables, whereas the former summarizes dependence for clusters of size 2 and larger, and clusters of variable sizes; see, for example, exercise 2.4.

2.5 Estimation using Stata

In Stata, maximum likelihood estimates for variance-components models can be obtained using `xtreg` with the `mle` option or `xtmixed` with the `mle` option (the default for `xtmixed` since Stata 12). Restricted maximum likelihood (REML) estimates can be

obtained using `xtmixed, reml`, and feasible generalized least-squares (FGLS) estimates can be obtained using `xtreg, re` (the default method). See sections 2.10.2 and 3.10.1 for information on these estimation methods.

The `xtreg` command is the most computationally efficient for variance-components models. However, the postestimation command `predict` for `xtmixed` is more useful than `predict` for `xtreg`. The user-written command `gllamm` can also be used for maximum likelihood estimation of linear variance-components models and the other models discussed in this volume. However, we do not generally recommend using `gllamm` for these models because `xtreg` and `xtmixed` are more computationally efficient, and `gllamm` is sometimes less accurate for linear models for continuous responses. For readers interested in learning to use `gllamm`, either to apply it to noncontinuous responses or to use its extended modeling framework, a `gllamm` companion for this book is available from the `gllamm` website.

2.5.1 Data preparation: Reshaping to long form

We now set up the data for estimation in Stata. Currently, the responses for occasions 1 and 2 are in *wide form* as two separate variables, `wp1` and `wp2` for the Wright peak-flow meter, and `wm1` and `wm2` for the Mini Wright peak-flow meter

```
. list if id < 6, clean noobs
    id   wp1   wp2   wm1   wm2   mean_wm
     1   494   490   512   525     518.5
     2   395   397   430   415     422.5
     3   516   512   520   508       514
     4   434   401   428   444       436
     5   476   470   500   500       500
```

For model fitting, we need to stack the occasion 1 and 2 measurements using a given meter into one variable. We can use the `reshape` command to obtain such a *long form* with one variable, `wp`, for both Wright peak-flow meter measurements; one variable, `wm`, for both Mini Wright peak-flow meter measurements; and a variable, `occasion` (equal to 1 and 2), for the measurement occasion:

```
. reshape long wp wm, i(id) j(occasion)
(note: j = 1 2)
Data                               wide   ->   long
-----------------------------------------------------------------------------
Number of obs.                       17   ->      34
Number of variables                   6   ->       5
j variable (2 values)                     ->   occasion
xij variables:
                                wp1 wp2   ->   wp
                                wm1 wm2   ->   wm
-----------------------------------------------------------------------------
```

Note that `i()` is used to specify clusters, denoted j in this book, and `j()` is used to specify units within clusters, denoted i in this book.

The data for the first five subjects now look like this:

```
. list if id < 6, clean noobs
    id   occasion    wp    wm   mean_wm
     1          1   494   512     518.5
     1          2   490   525     518.5
     2          1   395   430     422.5
     2          2   397   415     422.5
     3          1   516   520       514
     3          2   512   508       514
     4          1   434   428       436
     4          2   401   444       436
     5          1   476   500       500
     5          2   470   500       500
```

2.5.2 Using xtreg

We can estimate the parameters of the variance-components model (2.3) using the `xtreg` command with the `mle` option, which stands for maximum likelihood estimation (see section 2.10.2).

Before using `xtreg` and many of the commands starting with `xt`, the data should be declared as clustered data (referred to as panel data in Stata documentation because longitudinal or panel data are a common example of clustered data) using the `xtset` command. Here it is sufficient to declare that `id` is the cluster identifier $j = 1, \ldots, 17$:

```
. xtset id
       panel variable:  id (balanced)
```

The output states that our data are balanced, meaning that the cluster size is constant (here two measurements per subject).

We are now ready to use the `xtreg` command. As in the `regress` command, the response variable `wm` and covariates are listed after the command name. In variance-components models, the fixed part is just the intercept β, which is included by default, so we do not specify any covariates. The random part includes a random intercept ζ_j for the clusters defined in the `xtset` command. The level-1 residual ϵ_{ij} need not be specified because it is always included. Therefore the command is

```
. xtreg wm, mle
Random-effects ML regression                    Number of obs      =        34
Group variable: id                              Number of groups   =        17
Random effects u_i ~ Gaussian                   Obs per group: min =         2
                                                               avg =       2.0
                                                               max =         2
                                                Wald chi2(0)       =      0.00
Log likelihood  = -184.57839                    Prob > chi2        =         .
```

wm	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
_cons	453.9118	26.18616	17.33	0.000	402.5878	505.2357
/sigma_u	107.0464	18.67858			76.0406	150.6949
/sigma_e	19.91083	3.414659			14.2269	27.8656
rho	.9665602	.0159494			.9210943	.9878545

```
Likelihood-ratio test of sigma_u=0: chibar2(01)=   46.27 Prob>=chibar2 = 0.000
```

We see in the output that there are 34 observations belonging to 17 groups (the clusters, here subjects) and that there are 2 observations in each group (the minimum, maximum, and hence average number are all 2). In the Stata output and in the Stata documentation for `xtreg`, the i subscript is used for clusters (instead of j used in this book), u_i is used for the random intercept (instead of ζ_j), and the t subscript is used for occasions (instead of i used in this book).

The estimate of the overall population mean β, given next to `_cons` in the output, is 453.91. The estimate of the between-subject standard deviation $\sqrt{\psi}$ of the random intercepts of subjects, referred to as `/sigma_u`, is 107.05, and the estimate of the within-subject standard deviation $\sqrt{\theta}$, referred to as `/sigma_e`, is 19.91. It follows that the intraclass correlation is estimated as

$$\widehat{\rho} = \frac{\widehat{\psi}}{\widehat{\psi} + \widehat{\theta}} = \frac{107.0464^2}{19.91083^2 + 107.0464^2} = 0.97$$

which is referred to as `rho` in the output. This estimate is close to 1, indicating that the Mini Wright peak-flow meter is very reliable. The parameter estimates are also given in table 2.2 below.

To be explicit about the structure of the model, we will run the `xtset` command every time we run `xtreg` although this is not required if the data have already been `xtset` in the current Stata session.

2.5.3 Using xtmixed

The variance-components model considered here is a simple special case of a linear mixed-effects model that can be fit using the `xtmixed` command (available as of Stata 9). The `xtmixed` command can be used for models with random slopes as well as models with more than one clustering variable (for example, three-level models). The structure of the model is completely specified in the `xtmixed` command instead of using the `xtset`

command to define any aspect of the model as for `xtreg`. A nice consequence is that it is completely transparent what model is being specified in `xtmixed`.

The fixed part of the model, here β, is specified as in any estimation command in Stata (the response variable followed by a list of covariates). The random part, except the residual ϵ_{ij}, is specified after two vertical bars (or pipes), `||`. The cluster identifier, here `id`, is first given to define the clusters j over which ζ_j varies. This is followed by a colon and nothing, because a random intercept ζ_j is included by default (it can be excluded using the `noconstant` option). Finally, we request maximum likelihood estimation by using the `mle` option (the default as of Stata 12).

```
. xtmixed wm || id:, mle
Mixed-effects ML regression                     Number of obs      =        34
Group variable: id                              Number of groups   =        17
                                                Obs per group: min =         2
                                                               avg =       2.0
                                                               max =         2
                                                Wald chi2(0)       =         .
Log likelihood = -184.57839                     Prob > chi2        =         .
```

wm	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
_cons	453.9118	26.18617	17.33	0.000	402.5878	505.2357

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
id: Identity				
sd(_cons)	107.0464	18.67858	76.04062	150.695
sd(Residual)	19.91083	3.414678	14.22687	27.86564

```
LR test vs. linear regression: chibar2(01) =    46.27 Prob >= chibar2 = 0.0000
```

The table of estimates for the fixed part of the model has the same form as that for `xtreg` and all Stata estimation commands. The random part is given under the `Random-effects Parameters` header. Here `sd(_cons)` is the estimate of the random-intercept standard deviation $\sqrt{\psi}$, and `sd(Residual)` is the estimate of the standard deviation $\sqrt{\theta}$ of the level-1 residuals. All of these estimates are identical to the estimates using `xtreg` given in table 2.2. We could also obtain estimated variances (instead of standard deviations) with their standard errors by using the `variance` option.

Table 2.2: Maximum likelihood estimates for Mini Wright peak-flow meter

	Est	(SE)
Fixed part		
β	453.91	(26.18)
Random part		
$\sqrt{\psi}$	107.05	
$\sqrt{\theta}$	19.91	
Log likelihood	−184.58	

2.6 Hypothesis tests and confidence intervals

2.6.1 Hypothesis test and confidence interval for the population mean

In the regression tables produced by `xtreg` and `xtmixed`, z statistics are reported for β instead of the t statistics given by the `regress` command.

Like the t statistic in ordinary linear regression, the z statistic for the null hypothesis

$$H_0\text{: } \beta = 0 \quad \text{against} \quad H_a\text{: } \beta \neq 0$$

is given by

$$z \;=\; \frac{\widehat{\beta}}{\widehat{\mathrm{SE}}(\widehat{\beta})}$$

(where the standard error takes a different form than in standard linear regression, as discussed in section 2.10.3).

The reason this statistic is called z instead of t is that a standard normal sampling distribution is assumed under the null hypothesis instead of a t distribution. The t distribution is a finite-sample distribution whose shape depends on the degrees of freedom. For the variance-components model, the finite-sample distribution does not have a simple form, so Stata's commands use the asymptotic (large-sample) sampling distribution. (Some other software packages approximate the finite-sample distribution by a t distribution where the degrees of freedom are some function of the data.) The null hypothesis that the population mean β is zero is not of interest in the peak-expiratory-flow example.

Squaring the z statistics gives the Wald statistic, an approximation to the likelihood-ratio statistic, described in section 2.6.2 for testing the between-cluster variance.

An asymptotic 95% confidence interval for β is given by

$$\widehat{\beta} \;\pm\; z_{0.975}\widehat{\mathrm{SE}}(\widehat{\beta})$$

where $z_{0.975}$ is the 97.5th percentile of the standard normal distribution, that is, $z_{0.975} = 1.96$. This kind of confidence interval based on assuming a normal sampling distribution is often called a Wald confidence interval. In the Mini Wright application, the 95% Wald confidence interval for the population mean β is from 402.59 to 505.24, as shown, for instance, in the output from `xtreg` on page 85.

As for linear regression, there are two versions of estimated standard errors: a model-based version and a robust version based on the so-called sandwich estimator. The latter can be obtained for the maximum likelihood estimator in `xtmixed` and for the feasible generalized least-squares (FGLS) estimator in `xtreg, re` with the `vce(robust)` option. However, it should be noted that robust standard errors are known to perform poorly in small samples (samples with a small number of clusters).

2.6.2 Hypothesis test and confidence interval for the between-cluster variance

We now consider testing hypotheses regarding the between-cluster variance, ψ. In particular, we are often interested in the hypothesis

$$H_0\text{: } \psi = 0 \quad \text{against} \quad H_a\text{: } \psi > 0$$

This null hypothesis is equivalent to the hypothesis that $\zeta_j = 0$ or that there is no random intercept in the model. If the null hypothesis is true, we can use ordinary regression instead of a variance-components model.

The test we will be using most in this book for testing variance components is the likelihood-ratio test.

Likelihood-ratio test

A likelihood-ratio test can be used by fitting the model with and without the random intercept. The likelihood-ratio test statistic then is

$$L \;=\; 2(l_1 - l_0)$$

where l_1 is the maximized log likelihood for the variance-components model (which includes ζ_j) and l_0 is the maximized log likelihood for the model without ζ_j. Importantly, the distribution of L under H_0 is not χ^2 with 1 degree of freedom (df) as usual. This is because the null hypothesis is on the boundary of the parameter space since $\psi \geq 0$, violating the regularity conditions of standard statistical test theory.

For datasets simulated under the null hypothesis, without the random intercept, we would expect positive within-cluster correlations in about half the datasets and negative within-cluster correlations in the other half. Thus ψ would be estimated as positive half the time and as zero (because ψ would have to be negative to produce negative correlations but is constrained to be nonnegative) the other half the time. The correct asymptotic sampling distribution under the null hypothesis hence takes a

simple form, being a 50:50 mixture of a spike at 0 and a χ^2 with 1 df, often written as $0.5\chi^2(0) + 0.5\chi^2(1)$, where $\chi^2(0)$ is spike of height 1 at 0. The correct p-value can be obtained by simply dividing the "naïve" p-value, based on the χ^2 with 1 df, by 2.

This p-value is given at the bottom of the `xtreg` and `xtmixed` output, where the correct sampling distribution is referred to as `chibar2(01)` (click on `chibar2(01)`, which is shown in blue in the Stata Results window to find an explanation). We can also perform the likelihood-ratio test ourselves by fitting the variance-components model, storing the estimates, then fitting the model without the random intercept, and finally comparing the models using the `lrtest` command:

```
. quietly xtmixed wm || id:, mle
. estimates store ri
. quietly xtmixed wm, mle
. lrtest ri .
Likelihood-ratio test                                 LR chi2(1)  =     46.27
(Assumption: . nested in ri)                          Prob > chi2 =    0.0000
Note: The reported degrees of freedom assumes the null hypothesis is not on
      the boundary of the parameter space.  If this is not true, then the
      reported test is conservative.
```

Here the `quietly` prefix command is used to suppress output from `xtmixed`. In the `lrtest` command, `ri` refers to the estimates stored under that name, and "`.`" refers to the current (or last) estimates. As the note in the output and the notation `LR chi2(1)` imply, we now have to divide the p-value by 2. We see that the test of the null hypothesis $\psi = 0$ has a very small p-value, and the null hypothesis is rejected at standard significance levels.

Recall that the number of clusters is only 17, perhaps too few to rely on the asymptotic distribution of the likelihood-ratio statistic. The same comment applies to the score test described below.

It does of course not make sense to test the null hypothesis that $\theta = 0$, or in other words that all $\epsilon_{ij} = 0$, because this would force all responses y_{ij} for the same cluster j to be identical.

❖ Score test

There are two approximations to the likelihood-ratio statistic: the Wald statistic and the score or Lagrange multiplier statistic (see display 2.1 below if you are interested in the details). For variance parameters, Wald tests do not perform well but score tests can be used. Breusch and Pagan's Lagrange multiplier test is a *score test* based on a quadratic approximation of the likelihood at $\psi = 0$. The implementation in Stata is based on the FGLS estimator (see section 2.10.2), obtained using the `re` option of `xtreg`:

```
. quietly xtset id
. quietly xtreg wm, re
```

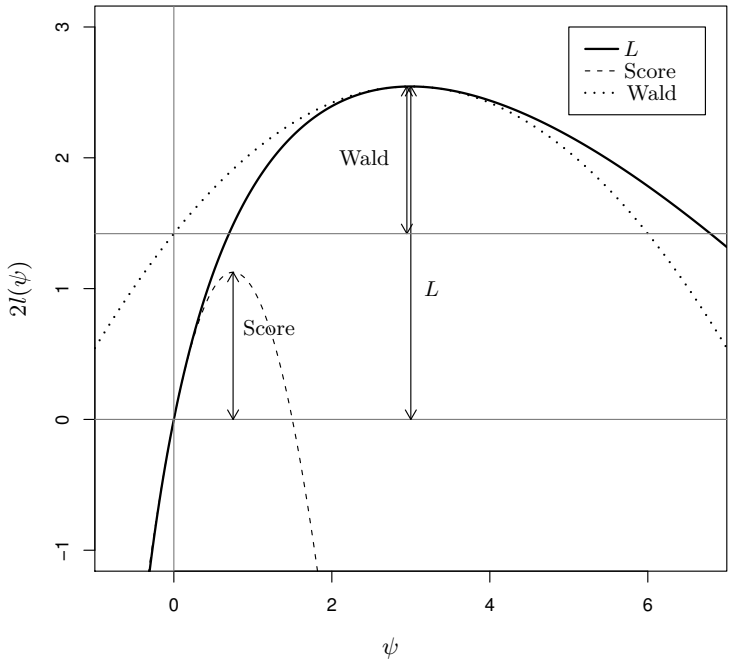
The test is then performed using the postestimation command `xttest0` for `xtreg`

```
. xttest0
Breusch and Pagan Lagrangian multiplier test for random effects
        wm[id,t] = Xb + u[id] + e[id,t]
        Estimated results:
                     |       Var     sd = sqrt(Var)
             ---------+-----------------------------
                  wm |   12214.63       110.5198
                   e |   396.4412       19.91083
                   u |   12187.51        110.397
        Test:   Var(u) = 0
                           chibar2(01) =    15.88
                           Prob > chi2 =     0.0000
```

leading to the same conclusion as before. Here the p-value has already been divided by 2, taking into account that the null hypothesis is on the boundary of the parameter space.

The graph below shows twice the log likelihood, $2l(\psi)$, as a function of the parameter ψ. (If there are other parameters, this is twice the profile likelihood, maximized with respect to the other parameters.) The maximum of this curve is at the maximum likelihood estimate $\widehat{\psi}$. We describe three statistics for testing H_0: $\psi = 0$:

- The *likelihood-ratio statistic* is given by $2\{l(\widehat{\psi}) - l(0)\}$ and is represented by the arrow labeled "L" pointing from $2l(\widehat{\psi})$ to $2l(0)$.
- The *Wald statistic* is based on approximating the function $2l(\psi)$ by the dotted quadratic curve at the maximum likelihood estimate $\widehat{\psi}$. The value of this curve at $\psi = 0$ is an approximation of $2l(0)$, and the Wald statistic is the decrease in the quadratic curve from $\widehat{\psi}$ to $\psi = 0$, as shown by the arrow labeled "Wald". Because the quadratic approximation to twice the log likelihood at the mode is $2l(\widehat{\psi}) - \frac{(\psi-\widehat{\psi})^2}{\mathrm{SE}(\widehat{\psi})^2}$, it follows that the Wald statistic is $\{\widehat{\psi}/\mathrm{SE}(\widehat{\psi})\}^2$.
- The *score statistic* is based on approximating $2l(\psi)$ by the dashed quadratic curve at the null hypothesis value, $\psi = 0$. The maximum value of this curve is an approximation of $2l(\widehat{\psi})$; the score statistic is the difference between that maximum and $2l(0)$, as shown by the arrow labeled "Score".



The Wald statistic is obtained by fitting only the unconstrained model, whereas the score statistic is obtained by fitting only the constrained model. A nice feature of the score statistic is that several model extensions can be tested by fitting only one model.

Adapted from Brian Ripley's notes for a course on Applied Statistics at the University of Oxford in 2005.

Display 2.1: Wald and score statistics as approximations to likelihood-ratio statistic

F test

We can also base the test for unexplained between-cluster heterogeneity on a regression model that includes dummy variables for clusters instead of including a random intercept for clusters. Such a model can be thought of as a one-way ANOVA model with clusters as a factor. As will be discussed in section 3.7.2, the model is often called a fixed-effects model because clusters are represented by fixed rather than random effects. The natural test in this setting is an F test for the joint null hypothesis that all clusters have the same mean (or that the coefficients of the 16 dummy variables are all zero). This F test can be obtained using `xtreg` with the `fe` (where `fe` stands for "fixed effects") option:

```
. quietly xtset id
. xtreg wm, fe
Fixed-effects (within) regression               Number of obs      =        34
Group variable: id                              Number of groups   =        17

R-sq:  within  = 0.0000                         Obs per group: min =         2
       between =      .                                       avg =       2.0
       overall =      .                                       max =         2

                                                F(0,17)            =      0.00
corr(u_i, Xb)  =      .                         Prob > F           =         .

------------------------------------------------------------------------------
          wm |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       _cons |    453.9118   3.414679   132.93   0.000     446.7074    461.1161
-------------+----------------------------------------------------------------
     sigma_u |  111.29118
     sigma_e |  19.910831
         rho |  .96898482   (fraction of variance due to u_i)
------------------------------------------------------------------------------
F test that all u_i=0:     F(16, 17) =    62.48                 Prob > F = 0.0000
```

We see from the bottom of the output that the null hypothesis is clearly rejected. (Use of the `xtreg` command with the `fe` option is discussed in more detail in section 3.7.2.)

If the uncertainty in the estimated level-1 residual variances is ignored and $\widehat{\theta}$ is treated as the true θ, then the F test can be replaced by a χ^2 test. A similar χ^2 test is described in Raudenbush and Bryk (2002) and implemented in the HLM software of Raudenbush et al. (2004). Instead of basing the χ^2 statistic on the estimated mean $\widehat{\beta}$ from the fixed-effects model, they base it on the estimated mean from the variance-components model.

Confidence intervals

Both `xtmixed` and `xtreg` report confidence intervals for the random-intercept standard deviation. These intervals are obtained by exponentiating the limits of the Wald confidence interval for the log standard deviation. The reason for this is that the sampling distribution of $\log(\widehat{\psi})$ approaches normality faster than that of $\widehat{\psi}$ as the number of clusters increases. The intervals may be adequate, as long as the lower limit is not too close to 0.

The estimated standard errors reported for the estimated between-cluster and within-cluster standard deviations $\sqrt{\psi}$ and $\sqrt{\theta}$ by `xtreg` and `xtmixed` and for the corresponding variances ψ and θ by `xtmixed` with the `variance` option should not be used to construct test statistics or confidence intervals. In particular, when the estimates are small or there are few clusters, the sampling distributions of the estimators may be very different from normal.

2.7 Model as data-generating mechanism

Figure 2.7 shows how the responses y_{ij} can be viewed as resulting from sequential (or hierarchical) sampling, first of ζ_j and then of y_{ij} given ζ_j. For concreteness, we consider normal distributions for ζ_j and ϵ_{ij}, but these distributional assumptions are usually not important for inferences. As seen in the top of the figure, the random intercept ζ_j has a normal distribution with mean zero (and variance ψ). Drawing a realization from this distribution for subject j determines the mean $\beta+\zeta_j$ of the distribution (with variance θ) from which responses y_{ij} for this subject are subsequently drawn. At a given measurement occasion i, a response y_{ij} is therefore sampled from a normal distribution with mean $\beta+\zeta_j$ and variance θ, $y_{ij} \sim N(\beta+\zeta_j, \theta)$ (see the bottom distribution in the figure). Equivalently, a residual (or measurement error) ϵ_{ij} is drawn from a normal distribution with mean zero and variance θ. The hierarchical sampling perspective is the reason why multilevel models are sometimes called hierarchical models.

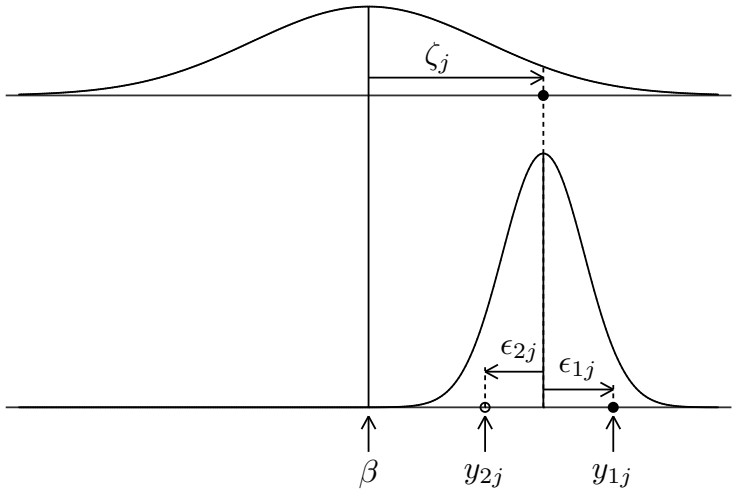


Figure 2.7: Illustration of hierarchical sampling in variance-components model

In this description, we have viewed the variance-components model as the data-generating mechanism for y_{ij} for given occasions and subjects.

The variance-components model is often motivated in terms of two-stage survey sampling, consisting of random sampling of clusters, such as schools, followed by random sampling of units (for example, students) from clusters. In this view, the top distribution of figure 2.7 represents the distribution of cluster means $\beta + \zeta_j$ in the population of clusters, where each cluster comes with a realized value of ζ_j. In stage 1, cluster j is sampled, and the bottom distribution represents the population of units in that cluster, where each unit in the cluster comes with a realized value of ϵ_{ij} and hence y_{ij}. We then randomly draw units from the cluster population, which determines the y_{ij} in our sample.

However, when motivating the model through survey sampling, it is important to remember that the sampling itself does not produce the within-cluster dependence. Such dependence must already exist in the population from which the sample was drawn, which we shall refer to as the finite population (because it is not infinite). Two-stage sampling merely guarantees that the sample contains multiple units per cluster, making it possible to separately estimate the between-cluster and within-cluster variance components ψ and θ. In contrast, a simple random sample of, say, 1,000 students from all U.S. high school students would be unlikely to contain any two students belonging to the same school, so we could only estimate the total variance, $\psi + \theta$, not the separate variance components.

Because the dependence preexists in the finite population, it is more useful to think of the variance-components model as the data-generating mechanism that generated the responses y_{ij} for the finite population. Furthermore, it is the model parameters—β, ψ, and θ—of this underlying variance-components model that we wish to estimate, not any finite population characteristic. Even if the sample contained the entire finite population, that is, all high school students in the U.S., we would still estimate the parameters with error, because all we have observed is one realization from the model, albeit for a large number of clusters and units. This imprecision of parameter estimates is even more pronounced if the finite population is small, for instance, all high school students in Monaco.

When the model is viewed as a data-generating mechanism, randomness comes from drawing the response from a distribution [the ζ_j from $N(0, \psi)$ and the ϵ_{ij} from $N(0, \theta)$, resulting in $y_{ij} = \beta + \zeta_j + \epsilon_{ij}$], not only from sampling units from a finite population. In the survey sampling literature, inference about the data-generating mechanism is referred to as superpopulation inference because data on the finite population (for example, all U.S. high school students) still represent only a sample from the model. Remembering that we wish to make inferences regarding the data-generating mechanism is particularly important in multilevel modeling, where it is not unusual to have data on the entire finite population of clusters (for example, all U.S. states) or the entire finite population of units within clusters (for example, both eyes on each head).

We can think of the randomness in the data as arising from two sources: the data-generating mechanism that produced the y_{ij} for the finite population and survey sampling of a subset of the finite population into the sample. When the parameters of interest are finite population characteristics, such as the proportion of eligible U.S. vot-

ers intending to vote for a given presidential candidate, the only randomness we need to care about when making inferences is randomness due to survey sampling, that is, sampling individuals from the finite population (as in an opinion poll). Such inferences, taking into account design features such as stratification, primary sampling units, and sample selection probabilities, are called design-based inferences. (In Stata, design-based inference is performed using the `svyset` command and the `svy` prefix command.)

When estimating model parameters of the data-generating mechanism (or superpopulation or infinite population parameters) rather than finite population characteristics, randomness due to drawing units from the finite population is often ignored, and the inferences are called "model based". For single-level data, ignoring randomness due to survey sampling is legitimate for simple (equal probability) random sampling (conditional on the covariates) because under such a design, the finite population distribution also holds in the sample. This means that the responses in the sample can be viewed as directly drawn from the model. For multilevel data, another design that preserves the distribution is two-stage sampling if simple random sampling (conditional on the covariates) is employed in each stage. Such sampling designs are called "ignorable".

To summarize, in this book we make inferences regarding the parameters of statistical models or data-generating mechanisms under the assumption that the sampling design is ignorable. We see no problem with applying this approach to data that contain the entire population of clusters or the entire population of units within clusters.

2.8 Fixed versus random effects

In the peak-expiratory-flow data, each subject j has a different effect ζ_j on the measured peak-expiratory-flow rates. In analysis of variance (ANOVA) terminology (see sections 1.4 and 1.9), the subjects can therefore be thought of as the levels of a *factor* or categorical explanatory variable. Because the effects of subjects are random, the variance-components model is therefore sometimes referred to as a one-way random-effects ANOVA model.

The one-way random-effects ANOVA model can be written as

$$y_{ij} = \beta + \zeta_j + \epsilon_{ij}, \qquad E(\epsilon_{ij}|\zeta_j)=0,\ E(\zeta_j)=0,\ \mathrm{Var}(\epsilon_{ij}|\zeta_j)=\theta,\ \mathrm{Var}(\zeta_j)=\psi \tag{2.6}$$

where ζ_j is a random intercept. In contrast, the one-way fixed-effects ANOVA model is

$$y_{ij} = \beta + \alpha_j + \epsilon_{ij}, \qquad E(\epsilon_{ij})=0,\ \mathrm{Var}(\epsilon_{ij})=\theta,\quad \sum_{j=1}^{J}\alpha_j = 0 \tag{2.7}$$

where α_j are unknown, fixed, cluster-specific parameters. In the random-effects model, the random intercepts are uncorrelated across clusters and uncorrelated with the level-1 residuals. In both models, the level-1 residuals are uncorrelated across units. Both random-effects models and fixed-effects models include cluster-specific intercepts—ζ_j and α_j, respectively—to account for unobserved heterogeneity. Thus a natural question is whether to use a random- or fixed-effects approach.

One way of answering this question is by being explicit about the target of inference, namely, whether interest concerns the *population* of clusters or the particular clusters in the *dataset*. Here the "population of clusters" refers to the infinite population, or the data-generating mechanism for the clusters. If we are interested in the population of clusters, the random-effects model is appropriate. In that model, β represents the population mean for the population of clusters (and for each cluster, the population of units in the cluster) and ψ represents the variance for the population of clusters. The model specifies how the cluster-specific means $\beta + \zeta_j$ are generated. In the variance-components model, ψ represents between-cluster variability due to cluster-level random (unexplained) processes that affect the response variable. As we will see in later chapters, the data-generating model for the cluster means can also contain cluster-level covariates to explain between-cluster variability.

If we do not wish to generalize beyond the particular clusters in the sample, the fixed-effects model is appropriate. In that model, β represents the mean for the sample of clusters (and for each cluster, the population of units in the cluster). The model allows each cluster to have a different mean $\beta + \alpha_j$ but does not specify how the means are generated. If the cluster means were generated by a random process, we merely condition on their realized values and do not learn about the process. It is not possible to include cluster-level covariates in fixed-effects models, so in this approach, no attempt is made to explain between-cluster variability.

Standard errors, confidence intervals, and p-values are based on the notion of repeated samples of the data from a model. For instance, the standard error for $\widehat{\beta}$ is the standard deviation of the estimates over repeated samples. In the random-effects approach, the random intercepts ζ_j change in repeated samples (in addition to ϵ_{ij}). In the fixed-effects approach, the fixed intercepts α_j remain constant in repeated samples (only ϵ_{ij} changes). As we will see in section 2.10.3, this leads to a larger standard error for $\widehat{\beta}$ in the random-effects approach (compared with the fixed-effects approach) because we are generalizing to the population of clusters and not just making inferences for the particular clusters in the data.

As we will see in section 2.11, the random-effects approach allows the ζ_j to be predicted after estimating the model parameters. In that sense, we can make inferences regarding the effects of clusters in the sample. These predictions can have better properties than the estimates of α_j in the fixed-effects approach, and this is sometimes the reason for adopting a random-effects approach.

A necessary assumption when treating the cluster effects as random is that they are exchangeable in the sense that their joint distribution (across clusters) does not change if the cluster labels j are permuted. In other words, there is no a priori ordering or grouping of the clusters. This assumption may appear unreasonable if the clusters are, for instance, countries. Sweden seems very different from Nigeria. While the same could be said about two individual people, an important difference is that the distinct nature of different countries is known to us a priori. In this case, we can include country-specific covariates in the model, as we will see in the next chapter, and exchangeability is then assumed conditional on the covariates. A fixed-effects approach should be used if it

does not make sense at all to think of the clusters in the sample merely as examples of possible clusters—for example, males and females as examples of possible genders—or if the clusters themselves are of such intrinsic interest that we do not want to model them as exchangeable even after conditioning on covariates.

A random-effects approach should be used only if there is a sufficient number of clusters in the sample, typically more than 10 or 20. The reason for this is that the between-cluster variance ψ is poorly estimated if there are few clusters. Poor estimation of ψ translates to poor estimation of the standard error of $\widehat{\beta}$. In two-level models, large-sample properties or asymptotics, such as consistency of point estimates and standard errors, rely on the number of clusters going to infinity, possibly for fixed cluster sizes. In contrast, the fixed-effects approach does not rely on a large number of clusters as long as the total sample size is large.

Regarding cluster sizes, these should be large in the fixed-effects approach if the α_j are of interest. This is also the case in the random-effects approach if prediction of the random effects is of interest, but prediction of ζ_j performs better with small cluster sizes than estimation of α_j because of "shrinkage" (see section 2.11). For parameter estimation in random-effects models, it is only required that there are a good number of clusters of size 2 or more; it does not matter if there are also "clusters" of size 1. Such singleton clusters do not provide information on the within-cluster correlation or on how the total variance is partitioned into ψ and θ, but they do contribute to the estimation of β and $\psi + \theta$.

In the peak-expiratory-flow application, the one-way fixed-effects ANOVA model has 19 parameters (β, $\alpha_1, \ldots, \alpha_{17}$, θ) and one constraint ($\sum_j \alpha_j = 0$). The one-way random-effects ANOVA model is thus much more parsimonious, having only 3 parameters (β, ψ, θ).

2.9 Crossed versus nested effects

So far, we have considered the random or fixed effects of a single cluster variable or factor, subjects. Another potential factor in the peak-expiratory-flow dataset is the measurement occasion with 2 levels, occasions 1 and 2. In the variance-components model, occasion was allowed to have an effect on the response variable only via the residual term ϵ_{ij}, which takes on a different value for each combination of subject and occasion and has mean zero for each occasion across subjects. We have therefore implicitly treated occasions as *nested* within subjects, meaning that occasion (2 versus 1) does not have a systematic effect for all subjects.

If all subjects had been measured and remeasured in the same sessions and if there were anything specific to the session (for example, time of day, temperature, or calibration of the measurement instrument) that could influence measurements on all subjects in a similar way, then subjects and occasions would be *crossed*. We would then include an occasion-specific term ("main effect of occasion") in the model that takes on the same value for all subjects.

The distinction between nested and crossed factors is illustrated in figure 2.8.

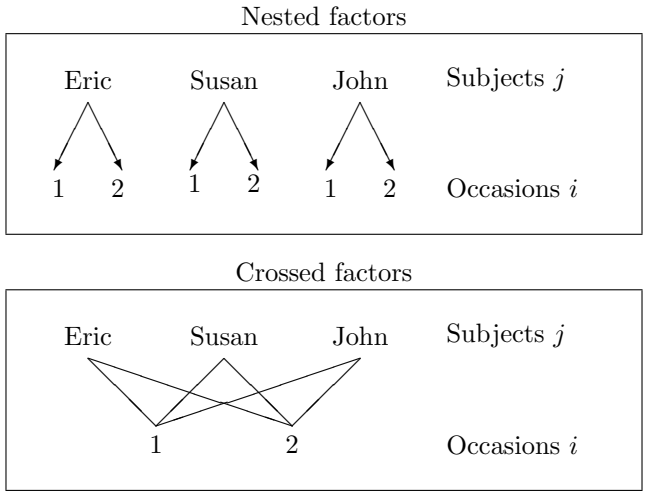


Figure 2.8: Illustration of nested and crossed factors

In the nested case, the effect of occasion 1 (or 2) is different for every subject; in the crossed case, there is a main effect of occasion that is the same for each subject (and possibly an occasion by subject interaction).

In the crossed case, the model can be described as a two-way ANOVA model. A subject-by-occasion interaction could in this case be included in addition to the main effects of each factor. However, because there are no replications for each subject–occasion combination in the peak-expiratory-flow application, an interaction term would be confounded with the error term ϵ_{ij}. If a random effect is specified for subjects and a fixed effect for occasion, we obtain a so-called *mixed-effects two-way* ANOVA *model*. Such a model can be fit by introducing a dummy variable for the second occasion in the fixed part of the model by using the commands

```
. generate occ2 = occasion==2
. xtmixed wm occ2 || id:, mle
Mixed-effects ML regression                     Number of obs      =        34
Group variable: id                              Number of groups   =        17
                                                Obs per group: min =         2
                                                               avg =       2.0
                                                               max =         2
                                                Wald chi2(1)       =      0.18
Log likelihood = -184.48885                     Prob > chi2        =    0.6714
```

wm	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
occ2	2.882353	6.793483	0.42	0.671	-10.43263	16.19734
_cons	452.4706	26.40555	17.14	0.000	400.7167	504.2245

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
id: Identity				
sd(_cons)	107.0561	18.67684	76.0523	150.6991
sd(Residual)	19.80624	3.396741	14.15214	27.71927

```
LR test vs. linear regression: chibar2(01) =    46.44 Prob >= chibar2 = 0.0000
```

We could alternatively have used the commands,

```
xtset id
xtreg wm occ2, mle
```

and instead of creating the dummy variable `occ2`, we could have used the factor-variable notation `i.occasion` within the `xtmixed` or `xtreg` commands.

We see that there is no evidence for an effect of occasion, which in this example could only be interpreted as a practice effect. If there had been considerably more than two occasions, we could have specified a random effect for occasion. Such models with crossed random effects are discussed in chapter 9.

2.10 Parameter estimation

2.10.1 Model assumptions

We now explicitly state a set of assumptions that are sufficient for everything we want to do in this chapter but are not always necessary. We briefly state which assumptions are needed for properties such as consistency and efficiency of the standard estimators for variance-components models discussed in section 2.10.2.

Mean structure and covariance structure

The total residual $\xi_{ij} = \zeta_j + \epsilon_{ij}$ is assumed to have zero expectation:

$$E(\zeta_j + \epsilon_{ij}) \;=\; 0$$

This assumption implies that the expectation or mean of the response, called the *mean structure*, is

$$E(y_{ij}) = \beta$$

If the mean structure is correctly specified, the point estimator $\widehat{\beta}$ of the parameter β will be *consistent*, meaning that $\widehat{\beta}$ approaches β as the sample size tends to infinity. A consistent estimator need not be unbiased in small samples, meaning that the average of $\widehat{\beta}$, over repeated samples, may not equal β. For $\widehat{\beta}$ to be unbiased, the distribution of $\zeta_j + \epsilon_{ij}$ must in general be symmetric (for instance, a normal distribution).

For the covariance structure, it is assumed that the random intercept ζ_j (with variance ψ) and the level-1 residual ϵ_{ij} (with variance θ) are uncorrelated, $\mathrm{Cor}(\epsilon_{ij}, \zeta_j) = 0$. From this it follows that the variance of the total residual is

$$\mathrm{Var}(\zeta_j + \epsilon_{ij}) \;=\; \psi + \theta$$

The ϵ_{ij} are assumed to be uncorrelated across units i, from which it follows that the covariance between total residuals for two units i and i' in the same cluster is

$$\mathrm{Cov}(\zeta_j + \epsilon_{ij}, \zeta_j + \epsilon_{i'j}) \;=\; \psi$$

Both ζ_j and ϵ_{ij} are also uncorrelated across different clusters so that there are no correlations between the total residuals of units in different clusters.

These assumptions imply that the *covariance structure* of the responses is

$$\begin{aligned}
\mathrm{Var}(y_{ij}) &= \psi + \theta \\
\mathrm{Cov}(y_{ij}, y_{i'j}) &= \psi \quad \text{if } i \neq i' \\
\mathrm{Cov}(y_{ij}, y_{i'j'}) &= 0 \quad \text{if } j \neq j'
\end{aligned}$$

If both the mean and covariance structure are correct, then the estimators of all parameters in the variance-components model are consistent and asymptotically efficient, and the model-based standard errors are consistent.

An *efficient* estimator is one that has a smaller standard error than any other estimator. Asymptotically efficient estimators acquire that property only asymptotically, as the sample size goes to infinity. For many estimators, the asymptotic sampling distribution is normal, making it easy to construct large-sample confidence intervals and tests. In variance-components models and other two-level models, "large sample" and "asymptotics" refer to the number of clusters going to infinity, possibly with fixed cluster size.

Consistent estimates for β can be obtained even if the covariance structure is not correct. In this case, model-based standard errors will be inconsistent, but robust standard errors can be used instead.

Distributional assumptions

The maximum likelihood estimator is based on the assumption that both ζ_j and $\epsilon_{ij}|\zeta_j$ are normally distributed. (Under normality, the assumptions above that the mean and variance of ϵ_{ij} do not depend on ζ_j actually imply that ϵ_{ij} and ζ_j are independent.) However, normality of the random intercepts and level-1 residuals is not required for consistent estimation of model parameters and standard errors, or for asymptotic normality of the estimators. The assumption does, however, matter in empirical Bayes prediction of the random effects (see section 2.11.2).

2.10.2 Different estimation methods

A classical method for estimating the parameters of statistical models is maximum likelihood (ML). The likelihood function is just the joint probability density of all the observed responses y_{ij}, $(i = 1, \ldots, n_j)$, $(j = 1, \ldots, J)$, as a function of the model parameters β, ψ, and θ. The likelihood contribution for cluster j can be obtained by integrating the joint distribution of the y_{ij} and ζ_j over the random intercept. The product of the likelihood contributions for all clusters is the likelihood, often called the *marginal likelihood* (averaged over ζ_j). The idea is to find parameter estimates $\widehat{\beta}$, $\widehat{\psi}$, and $\widehat{\theta}$ that maximize the likelihood function, thus making the responses appear as likely as possible.

When the data are balanced with the same number of units $n_j = n$ in each of the J clusters ($n = 2$ occasions in the current application), the ML estimators for the two-level variance-components model have relatively simple expressions. The expressions are in terms of the model sum of squares (MSS) and sum of squared errors (SSE) from a one-way ANOVA, treating subjects as a fixed factor (see section 1.4). Here the MSS is the sum of squared deviations of the cluster means $\overline{y}_{\cdot j}$ from the overall mean $\overline{y}_{\cdot\cdot}$,

$$\text{MSS} \;=\; \sum_{j=1}^{J}\sum_{i=1}^{n}(\overline{y}_{\cdot j} - \overline{y}_{\cdot\cdot})^2, \qquad \overline{y}_{\cdot j} = \frac{1}{n}\sum_{i=1}^{n} y_{ij}, \quad \overline{y}_{\cdot\cdot} = \frac{1}{Jn}\sum_{j=1}^{J}\sum_{i=1}^{n} y_{ij}$$

and the SSE is the sum of squared deviations of the responses from their cluster means,

$$\text{SSE} \;=\; \sum_{j=1}^{J}\sum_{i=1}^{n}(y_{ij} - \overline{y}_{\cdot j})^2$$

The population mean β is estimated by the sample mean,

$$\widehat{\beta} \;=\; \overline{y}_{\cdot\cdot}$$

and the ML estimator of the within-cluster variance θ is

$$\widehat{\theta} \;=\; \frac{1}{J(n-1)}\text{SSE} \;=\; \text{MSE}$$

where MSE is the mean squared error from the one-way ANOVA.

The ML estimator of the between-cluster variance ψ is given by

$$\widehat{\psi} \;=\; \begin{cases} \frac{\text{MSS}}{Jn} - \frac{\widehat{\theta}}{n} & \text{if positive} \\ 0 & \text{otherwise} \end{cases}$$

where the subtraction of the second term is required because the level-1 residuals contribute to the MSS. With a small number of clusters, boundary estimates of 0 can occur frequently. The ML estimators for β and θ are unbiased if the model is true, whereas the estimator for ψ has downward bias.

The unbiased moment estimator or ANOVA estimator of ψ is given by

$$\widehat{\psi}^M \;=\; \frac{\text{MSS}}{(J-1)n} - \frac{\widehat{\theta}}{n} \;=\; \frac{1}{n}\left(\text{MMS} - \text{MSE}\right)$$

where MMS is the model mean square from the one-way ANOVA. The estimate can be negative, making unbiasedness less attractive than it seems. The between-cluster sum of squares is now divided by n times the model degrees of freedom $J-1$ instead of n times J. The difference between the biased ML estimator $\widehat{\psi}$ and the unbiased moment estimator $\widehat{\psi}^M$ becomes small when the number of clusters J is large. In the example considered in this chapter, there are only $J=17$ clusters, so the difference between ML and ANOVA estimates will not be negligible (see exercise 2.10).

For balanced data, the ANOVA estimator is also the restricted maximum likelihood (REML) estimator. For unbalanced data, the ANOVA, REML, and ML estimators are all different; the latter two estimators are preferable because they are more efficient. The difference between REML and ML is that REML estimates the random-intercept variance taking into account the loss of 1 degree of freedom resulting from the estimation of the overall mean β. In models considered in the next chapters that include covariates, further degrees of freedom are lost because of estimation of additional regression coefficients. Contrary to common belief, REML is not unbiased for ψ when data are unbalanced. Furthermore, it is not clear which method has the smallest mean squared error (MSE).

Another estimation method, particularly popular in econometrics, is feasible generalized least squares (FGLS). For the simple model and the balanced case considered here, the variance-component estimates from FGLS are identical to the ANOVA and REML estimates.

Section 3.10.1 provides more details on ML, REML, and FGLS estimation of models with covariates.

2.10.3 Inference for β

Estimate and standard error: Balanced case

We first consider the balanced case where $n_j = n$. As mentioned in the previous section, the ML estimator $\widehat{\beta}$ of β in the variance-components model is simply the overall sample mean

$$\widehat{\beta} \;=\; \frac{1}{J\,n}\sum_{j=1}^{J}\sum_{i=1}^{n} y_{ij} = \frac{1}{J}\sum_{j=1}^{J}\overline{y}_{\cdot j}$$

an unweighted mean of the cluster means. The estimated standard error is given by

$$\widehat{\mathrm{SE}}(\widehat{\beta}) \;=\; \sqrt{\frac{n\widehat{\psi}+\widehat{\theta}}{J\,n}} = \sqrt{\frac{\widehat{\psi}+\widehat{\theta}/n}{J}}$$

Remember that β represents the mean of the cluster means for the population of clusters. When the cluster size n is infinite, the cluster means are known with complete precision and uncertainty about β comes only from having a finite sample of J clusters (rather than the infinite population of clusters). The estimated standard error therefore takes the familiar form $\sqrt{\widehat{\psi}/J}$—because $\widehat{\beta}$ is the sample mean of J (precisely known) cluster means, its estimated standard error is the variance of the cluster means divided by the number of clusters.

In the fixed-effects model (with the random ζ_j replaced with fixed α_j; see section 2.8), the estimator of β is the same, but now the estimated standard error is

$$\widehat{\mathrm{SE}}(\widehat{\beta}^{F}) \;=\; \sqrt{\frac{\widehat{\theta}}{J\,n}}$$

which is smaller than the standard error $\widehat{\mathrm{SE}}(\widehat{\beta})$ in the random-effects model if $\widehat{\psi} > 0$. Because β now represents the *sample* mean of the cluster means for the J clusters in the data, the standard error becomes zero when the cluster size n is infinite.

Now consider the model without cluster-specific random or fixed effects (no ζ_j or α_j) that assumes residuals to be independent. Such a single-level model would be used when the nesting of units in clusters is ignored. We refer to the corresponding estimator of β as the pooled ordinary least-squares (OLS) estimator $\widehat{\beta}^{\mathrm{OLS}}$. The estimator is the same as for the random- and fixed-effects models except the estimated standard error is now approximately

$$\widehat{\mathrm{SE}}(\widehat{\beta}^{\mathrm{OLS}}) \;\approx\; \sqrt{\frac{\widehat{\psi}+\widehat{\theta}}{J\,n}}$$

where we have approximated the OLS estimate of the residual variance $\widehat{\sigma^2}$ by the sum of the estimated variance components $\widehat{\psi}+\widehat{\theta}$ (the approximation is better for larger n).

We see that

$$\widehat{\mathrm{SE}}(\widehat{\beta}^{F}) \le \widehat{\mathrm{SE}}(\widehat{\beta}^{\mathrm{OLS}}) \le \widehat{\mathrm{SE}}(\widehat{\beta})$$

This relationship is best understood by remembering that the standard error is the standard deviation of the estimates over repeated samples (repeated random draws of y_{ij} for all units). In the fixed-effects case, only the ϵ_{ij} change from sample to sample (with variance θ). In the pooled OLS case, the total residuals change (with variance $\psi+\theta$), but they are drawn independently (because they are assumed to be independent). In contrast, the total residuals are not drawn independently in the random-effects case; they result from drawing ζ_j for all units in the cluster and drawing ϵ_{ij} for each unit. As a consequence, the total residuals $\zeta_j + \epsilon_{ij}$ for a cluster tend to change in the same direction, leading to larger variability in the resulting $\widehat{\beta}$. The difference between the pooled OLS and the random-effects standard error is particularly pronounced if the ζ_j vary considerably (large ψ), and if a change in a ζ_j affects a large number of units (large n).

For the peak-expiratory-flow application, we see from the output of `xtreg` with the `mle` option on page 85 that $\widehat{\mathrm{SE}}(\widehat{\beta}) = 26.19$ and from the output of `xtreg` with the `fe` option on page 92 that $\widehat{\mathrm{SE}}(\widehat{\beta}^{\mathrm{F}}) = 3.41$. We obtain the estimated model-based standard error for the OLS estimator by using the `regress` command,

```
. regress wm
      Source |       SS       df       MS              Number of obs =      34
-------------+------------------------------           F(  0,    33) =    0.00
       Model |           0     0           .            Prob > F      =       .
    Residual |  403082.735    33  12214.6283            R-squared     =  0.0000
-------------+------------------------------           Adj R-squared =  0.0000
       Total |  403082.735    33  12214.6283            Root MSE      =  110.52

------------------------------------------------------------------------------
          wm |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       _cons |    453.9118   18.95399    23.95   0.000     415.3496    492.4739
------------------------------------------------------------------------------
```

which gives $\widehat{\mathrm{SE}}(\widehat{\beta}^{\mathrm{OLS}}) = 18.95$. For the application, we see that $\widehat{\mathrm{SE}}(\widehat{\beta}) > \widehat{\mathrm{SE}}(\widehat{\beta}^{\mathrm{OLS}}) > \widehat{\mathrm{SE}}(\widehat{\beta}^{\mathrm{F}})$, as expected.

Although the clustered nature of the data is not taken into account in the OLS estimator $\widehat{\beta}^{\mathrm{OLS}}$ of the population mean, a *sandwich estimator* can be used to produce robust standard errors for $\widehat{\beta}^{\mathrm{OLS}}$, taking the clustering into account. Using the `regress` command with the `vce(cluster id)` option, we obtain the following:

```
. regress wm, vce(cluster id)
Linear regression                                     Number of obs =      34
                                                      F(  0,    16) =    0.00
                                                      Prob > F      =       .
                                                      R-squared     =  0.0000
                                                      Root MSE      =  110.52
                                    (Std. Err. adjusted for 17 clusters in id)
------------------------------------------------------------------------------
             |               Robust
          wm |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       _cons |    453.9118   26.99208    16.82   0.000     396.6911    511.1324
------------------------------------------------------------------------------
```

The estimated robust standard error is 26.99, which is close to the estimated model-based standard error of 26.19 from ML estimation of the variance-components model. (We have used a sandwich estimator before to obtain robust standard errors for nonclustered data in section 1.6.) By fitting an ordinary regression model with robust standard errors for clustered data instead of fitting variance-components models, we are taking into account within-cluster dependence but treating it as a nuisance, not as a phenomenon we are interested in. We learn nothing about the between and within-cluster variances or intraclass correlation.

Estimate: Unbalanced case

In the unbalanced case, the ML estimator of β under the variance-components model becomes a weighted mean of the cluster means:

$$\widehat{\beta} = \frac{\sum_{j=1}^{J} w_j \overline{y}_{\cdot j}}{\sum_{j=1}^{J} w_j} \qquad \text{where} \quad w_j = \frac{1}{\widehat{\psi} + \widehat{\theta}/n_j}$$

Small clusters have a weight similar to large clusters if $\widehat{\theta}$ is small compared with $\widehat{\psi}$. In contrast, the pooled OLS estimator, which disregards clustering and treats the data as single level, is

$$\widehat{\beta}^{\text{OLS}} = \frac{\sum_{j=1}^{J} n_j \bar{y}_{\cdot j}}{\sum_{j=1}^{J} n_j}$$

with cluster means given weights proportional to the cluster sizes n_j. Thus a variance-components model tends to give more weight to smaller clusters than does an ordinary regression model. In the random-effects case, one new observation for a new cluster adds more information regarding the mean for the *population* of clusters than one new observation for a cluster already included in the sample. In pooled OLS, whether the new observation is from a new or existing cluster is immaterial because clustering is ignored.

2.11 Assigning values to the random intercepts

Remember that the cluster-specific intercepts ζ_j are treated as random variables and not as model parameters in multilevel models. However, having obtained estimates $\widehat{\beta}$, $\widehat{\psi}$, and $\widehat{\theta}$ of the model parameters β, ψ, and θ, we may wish to assign values to the random intercepts ζ_j for individual clusters; this would be analogous to obtaining predicted residuals $\widehat{\epsilon}_i$ in ordinary linear regression.

There are a number of reasons why we may want to obtain values for the random intercepts ζ_j for individual clusters. For instance, we will use such assigned values for model diagnostics (see sections 3.9 and 4.8.4), for interpreting and visualizing models (see section 4.8.3), and for inference regarding individual clusters (see section 4.8.5), such as small area estimation (see exercise 3.9) and disease mapping (see section 13.13). An example of the last type would be to assign values to subjects' true expiratory flow $\beta + \zeta_j$ based on the fallible measurements.

It is easy to assign values to the total residuals because $\widehat{\xi}_{ij} = y_{ij} - \widehat{\beta}$. However, the total residuals are partitioned as $\xi_{ij} = \zeta_j + \epsilon_{ij}$, and different methods have been proposed for assigning values to its constituent components ζ_j and ϵ_{ij}. A common feature of the methods is that a value is first assigned to the ζ_j and then ϵ_{ij} is obtained by using the relation $\epsilon_{ij} = \xi_{ij} - \zeta_j$.

Values are assigned to the random intercepts ζ_j by either *prediction* or *estimation*. We continue treating ζ_j as a random variable when prediction is used, whereas the ζ_j are instead viewed as unknown fixed parameters when estimation is used. The predominant approaches to assigning values to the ζ_j are maximum "likelihood" estimation, described in section 2.11.1, and empirical Bayes prediction, described in section 2.11.2.

2.11.1 Maximum "likelihood" estimation

We first substitute the parameter estimate $\widehat{\beta}$ into the variance-components model (2.1), giving

$$y_{ij} = \widehat{\beta} + \underbrace{\zeta_j + \epsilon_{ij}}_{\xi_{ij}}$$

The ζ_j are now viewed as the only unknown parameters to be estimated. Specifically, for each subject j, we find the value of ζ_j that maximizes the conditional distribution or "likelihood" of the observed responses y_{1j} and y_{2j}, given the random intercept ζ_j,

$$\text{Likelihood}(y_{1j}, y_{2j}|\zeta_j)$$

treating the model parameters as known. This approach of treating ζ_j as an unknown (and fixed) parameter contradicts the original model specification, where ζ_j was treated as a random effect. We put "likelihood" in quotes because it differs from the marginal likelihood that is used to estimate the model parameters in three ways: 1) the model parameters are treated as known, 2) the random effect is treated as an unknown parameter, and 3) the likelihood is based on the data for just one cluster.

We can rearrange the above model by subtracting $\widehat{\beta}$ from y_{ij} to obtain estimated total residuals $\widehat{\xi}_{ij}$ and regard these as the responses:

$$\widehat{\xi}_{ij} \;=\; y_{ij} - \widehat{\beta} = \zeta_j + \epsilon_{ij} \tag{2.8}$$

The ML estimator of ζ_j is simply the cluster mean of the estimated total residual over the n_j occasions (here $n_j = 2$) for which we have data:

$$\widehat{\zeta}_j^{\mathrm{ML}} \;=\; \frac{1}{n_j}\sum_{i=1}^{n_j}\widehat{\xi}_{ij} = \frac{1}{2}(\widehat{\xi}_{1j} + \widehat{\xi}_{2j})$$

Implementation via OLS regression

The model in (2.8) has a different mean ζ_j for each subject, and we can estimate these means by regressing $\widehat{\xi}_{ij}$ on dummy variables for each of the subjects, excluding the overall intercept because this is now redundant. The OLS estimates of the regression coefficients for the subject dummies are the required ML estimates $\widehat{\zeta}_j^{\mathrm{ML}}$ of the ζ_j.

To obtain these estimates in Stata, we first refit the model by using `xtmixed` (with the `quietly` prefix to suppress the output), and then we subtract the predicted fixed part $\widehat{\beta}$, obtained using `predict` with the `xb` option, from the responses:

```
. quietly xtmixed wm || id:, mle
. predict pred, xb
. generate res = wm - pred
```

Next we regress the variable `res` on dummy variables for the 17 subjects, using the factor-variable notation for categorical variables with no base category, `ibn.id`, and with the `noconstant` option to suppress the overall constant:

```
. regress res ibn.id, noconstant
```

Source	SS	df	MS		
Model	396343.235	17	23314.308		
Residual	6739.5	17	396.441176		
Total	403082.735	34	11855.3746		

Number of obs = 34
F(17, 17) = 58.81
Prob > F = 0.0000
R-squared = 0.9833
Adj R-squared = 0.9666
Root MSE = 19.911

res	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
id						
1	64.58823	14.07908	4.59	0.000	34.88396	94.2925
2	-31.41177	14.07908	-2.23	0.039	-61.11604	-1.707504
3	60.08823	14.07908	4.27	0.001	30.38396	89.7925
4	-17.91177	14.07908	-1.27	0.220	-47.61604	11.7925
5	46.08823	14.07908	3.27	0.004	16.38396	75.7925
6	158.5882	14.07908	11.26	0.000	128.884	188.2925
7	-41.91177	14.07908	-2.98	0.008	-71.61604	-12.2075
8	-68.91177	14.07908	-4.89	0.000	-98.61604	-39.2075
9	196.0882	14.07908	13.93	0.000	166.384	225.7925
10	-15.41177	14.07908	-1.09	0.289	-45.11604	14.2925
11	-27.91177	14.07908	-1.98	0.064	-57.61604	1.792496
12	161.5882	14.07908	11.48	0.000	131.884	191.2925
13	-210.4118	14.07908	-14.94	0.000	-240.116	-180.7075
14	18.08823	14.07908	1.28	0.216	-11.61604	47.7925
15	-190.4118	14.07908	-13.52	0.000	-220.116	-160.7075
16	-93.91177	14.07908	-6.67	0.000	-123.616	-64.2075
17	-6.911774	14.07908	-0.49	0.630	-36.61604	22.7925

From the output, we see that, for instance, $\widehat{\zeta}_1^{\mathrm{ML}} = 64.58823$.

Alternatively, after first using `xtreg` with the `mle` option to estimate the model parameters by ML, we can obtain ML estimates of the random intercepts by using `predict` with the `u` option:

```
. quietly xtset id
. quietly xtreg wm, mle
. predict ml2, u
```

Implementation via the mean total residual

The subject-specific means can be calculated using the `egen` command:

```
. egen ml = mean(res), by(id)
```

For the first subject, we get the same result as before:

```
. sort id
. display ml[1]
64.588226
```

In this subsection, we have used all the terminology usually associated with estimating model parameters. However, it is important to remember that ζ_j is not a

parameter in the original model. It is only for the purpose of assigning values to ζ_j that we reformulate the problem by treating the original parameters β, ψ, and θ as known constants and the ζ_j as unknown parameters. The likelihood described here must hence be distinguished from the marginal likelihood used to estimate the model parameters.

2.11.2 Empirical Bayes prediction

Having obtained estimates $\widehat{\beta}$, $\widehat{\psi}$, and $\widehat{\theta}$ of the model parameters and treating them as the true parameter values, we can predict values of the random intercepts ζ_j for individual clusters (subjects in the application). Here we continue to treat ζ_j as a random variable, not as a fixed parameter as in ML estimation.

ML estimation of ζ_j uses the responses y_{ij} for subject j as the only information about ζ_j by maximizing the likelihood of observing these particular values:

$$\text{Likelihood}(y_{1j}, y_{2j}|\zeta_j)$$

In contrast, empirical Bayes prediction also uses the *prior distribution* of ζ_j, summarizing our knowledge about ζ_j before seeing the data for subject j:

$$\text{Prior}(\zeta_j)$$

This prior distribution is just the normal distribution specified for the random intercept with zero mean and estimated variance $\widehat{\psi}$. It represents what we know about ζ_j before we have seen the responses y_{1j} and y_{2j} for subject j. For instance, the most likely value of ζ_j is zero. (Obviously, we have already used all responses to obtain the estimate $\widehat{\psi}$, but we now pretend that ψ is known and not estimated.)

Once we have observed the responses, we can combine the prior distribution with the likelihood to obtain the *posterior distribution* of ζ_j given the observed responses y_{1j} and y_{2j}. According to Bayes theorem,

$$\text{Posterior}(\zeta_j|y_{1j}, y_{2j}) \;\propto\; \text{Prior}(\zeta_j) \times \text{Likelihood}(y_{1j}, y_{2j}|\zeta_j)$$

where $\propto$ means "proportional to". The posterior of ζ_j represents our updated knowledge regarding ζ_j after seeing the data y_{1j} and y_{2j} for subject j.

The empirical Bayes prediction is just the mean of the posterior distribution with parameter estimates ($\widehat{\beta}$, $\widehat{\psi}$, and $\widehat{\theta}$) plugged in. In a linear model with normal error terms, the posterior is normal and the mean is thus equal to the mode.

Figure 2.9 shows the prior, likelihood, and posterior for a hypothetical example of a subject with $n_j = 2$ responses. In both panels, the estimated total residuals $\widehat{\xi}_{ij}$ are 3 and 5, and the estimated total variance is $\widehat{\psi} + \widehat{\theta} = 5$. In the top panel, 80% of this variance is due to within-subject variability, whereas in the bottom panel, 80% is due to between-subject variability. In both cases, the likelihood (dotted curve) has its maximum at $\zeta_j = 4$, that is, the mode is 4 (see vertical dotted lines). The ML estimate therefore is $\widehat{\zeta}_j^{\text{ML}} = 4$. In contrast, the mode (and mean) of the posterior depends on the

relative sizes of the variance components and is 1.33 in the top panel and 3.56 in the bottom panel (see vertical dashed lines). The mean of the posterior lies between the mean of the prior (zero, vertical solid lines) and the mode of the likelihood.

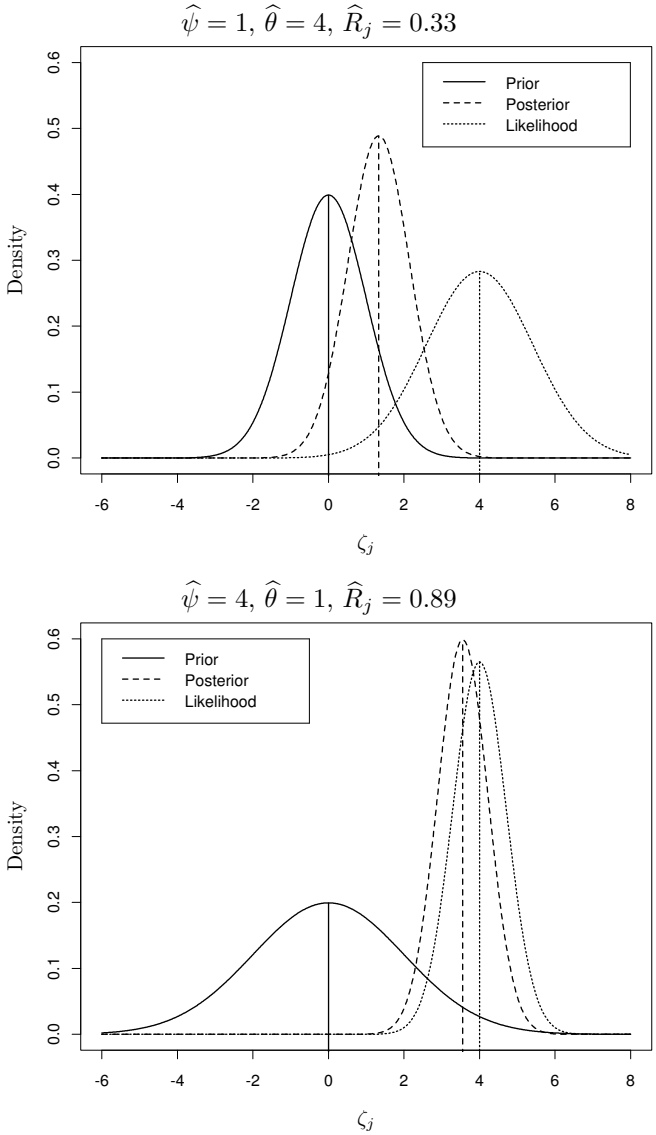


Figure 2.9: Prior distribution, likelihood (normalized), and posterior distribution for a hypothetical subject with $n_j = 2$ responses with total residuals $\widehat{\xi}_{1j} = 3$ and $\widehat{\xi}_{2j} = 5$ [the vertical lines represent modes (and means) of the distributions]

In fact, there is a simple formula relating the empirical Bayes prediction $\widetilde{\zeta}_j^{\mathrm{EB}}$ to the ML estimator $\widehat{\zeta}_j^{\mathrm{ML}}$ in linear random-intercept models:

$$\widetilde{\zeta}_j^{\mathrm{EB}} \;=\; \widehat{R}_j \widehat{\zeta}_j^{\mathrm{ML}}, \qquad \text{where} \qquad \widehat{R}_j \;=\; \frac{\widehat{\psi}}{\widehat{\psi} + \widehat{\theta}/n_j}$$

Here $\widehat{R}_j$ is similar to the estimated intraclass correlation, except that we divide the estimated level-1 variance $\widehat{\theta}$ by the number of responses n_j. $\widehat{R}_j$ can be interpreted as the *reliability* of the ML estimator of ζ_j, defined as the proportion of the variance of the ML estimator that is due to the variance of the random intercept. $\widehat{R}_j$ is also known as the *shrinkage factor* because $0 \leq \widehat{R}_j < 1$ so that the empirical Bayes prediction is shrunken toward 0 (the mean of the prior). There will be more shrinkage (that is, greater influence of the prior) if we have

- a small random-intercept variance ($\widehat{\psi}$) (an informative prior)
- a large level-1 residual variance ($\widehat{\theta}$) (uninformative data)
- a small cluster size (n_j) (uninformative cluster)

A nice feature of empirical Bayes prediction is that the prediction error, defined as the difference $\widetilde{\zeta}_j^{\mathrm{EB}} - \zeta_j$ between the prediction and the truth, has zero mean over repeated samples of ζ_j and ϵ_{ij} (or repeated samples of clusters and units from clusters) when model parameters are treated as fixed and known. Empirical Bayes predictions also have the smallest possible variance (for given model parameters). In linear mixed models, the empirical Bayes predictor is therefore also known as the best linear unbiased predictor (BLUP). When predictions are based on estimated model parameters, the term estimated best linear unbiased predictor (EBLUP) is sometimes used.

Empirical Bayes predictions are conditionally biased in the sense that their mean over repeated samples of ϵ_{ij} for a given ζ_j (or repeated samples of units from the same cluster) will be too close to zero because of shrinkage. In contrast, the ML estimator is conditionally unbiased but has a greater prediction-error variance.

In most applications, shrinkage is desirable because it only affects clusters that provide little information and it effectively downplays their influence, borrowing strength from other clusters. For instance, the empirical Bayes predictor for the cluster mean $\beta + \zeta_j$ becomes

$$\widehat{\beta} + \widetilde{\zeta}_j^{\mathrm{EB}} \;=\; \widehat{\beta} + \widehat{R}_j \widehat{\zeta}_j^{\mathrm{ML}} \;=\; \widehat{\beta} + \widehat{R}_j(\overline{y}_{.j} - \widehat{\beta}) \;=\; (1 - \widehat{R}_j)\widehat{\beta} + \widehat{R}_j \overline{y}_{.j}$$

We see that the empirical Bayes prediction can be expressed as a weighted average of the estimated population mean $\widehat{\beta}$, which is based on data for all clusters, and the cluster mean response $\overline{y}_{.j}$, based only on the data for cluster j. Hence, clusters with low reliabilities borrow more strength from other clusters than do clusters with high reliabilities. Since $\widehat{\beta}$ is based on total pooling of data across clusters, shrinkage estimation is sometimes described as partial pooling.

For the Mini Wright meter measurements, the shrinkage factor can be calculated from the estimates of $\sqrt{\psi}$ and $\sqrt{\theta}$ in table 2.2:

```
. display 107.05^2/(107.05^2+(19.91^2)/2)
.98299832
```

Instead of typing the rounded estimates, we can access the unrounded counterparts directly after estimation. For regression coefficients, we have already used the syntax `_b[`*varname*`]`. To find out how to access the standard deviations, we first refit the model using `xtmixed` with the `estmetric` option:

```
. xtmixed wm || id:, mle estmetric
Mixed-effects ML regression                     Number of obs      =        34
Group variable: id                              Number of groups   =        17
                                                Obs per group: min =         2
                                                               avg =       2.0
                                                               max =         2
                                                Wald chi2(0)       =         .
Log likelihood = -184.57839                     Prob > chi2        =         .
```

wm	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
wm						
_cons	453.9118	26.18617	17.33	0.000	402.5878	505.2357
lns1_1_1						
_cons	4.673263	.1744905	26.78	0.000	4.331268	5.015258
lnsig_e						
_cons	2.991264	.1714985	17.44	0.000	2.655133	3.327395

The estimation metric for each standard deviation is the logarithm of the standard deviation. We can access the estimated logarithms by using the syntax `[lns1_1_1]_cons` and `[lnsig_e]_cons`:

```
. display exp([lns1_1_1]_cons)
107.04643
. display exp([lnsig_e]_cons)
19.910826
```

We can compute the shrinkage factor by using

```
. display exp([lns1_1_1]_cons)^2/(exp([lns1_1_1]_cons)^2+ exp([lnsig_e]_cons)^2/2)
.98299582
```

We can now obtain empirical Bayes predictions in two ways: either by multiplying the ML estimates obtained in section 2.11.1 by the shrinkage factor,

```
. generate eb1 = .98299582*ml
```

or by using the `predict` command with the `reffects` (for "random effects") option after estimation using `xtmixed`,

```
. predict eb2, reffects
. sort id
. format eb1 eb2 %8.2f
. list id eb1 eb2 if occasion==1, clean noobs
```

id	eb1	eb2
1	63.49	63.49
2	-30.88	-30.88
3	59.07	59.07
4	-17.61	-17.61
5	45.30	45.30
6	155.89	155.89
7	-41.20	-41.20
8	-67.74	-67.74
9	192.75	192.75
10	-15.15	-15.15
11	-27.44	-27.44
12	158.84	158.84
13	-206.83	-206.83
14	17.78	17.78
15	-187.17	-187.17
16	-92.31	-92.31
17	-6.79	-6.79

Both methods give identical results.

It should be kept in mind that empirical Bayes predictions rely on the normality assumptions for the random intercepts unless the cluster sizes are very large.

2.11.3 Empirical Bayes standard errors

There are several different kinds of variances (squared standard errors) for empirical Bayes predictions that can be used to express uncertainty regarding the predictions. These variances do not take into account the uncertainty in the parameter estimates because the parameters are treated as known in empirical Bayes prediction; however, in practice, this only matters in small samples.

Comparative standard errors

The posterior variance is the variance of the random intercept ζ_j given the observed responses, the variance of the posterior distribution shown as a dashed curve in figure 2.9. For the model considered here, the posterior variance is

$$\mathrm{Var}(\zeta_j|y_{1j}, y_{2j}) \;=\; \frac{\theta/n_j}{\psi + \theta/n_j}\;\psi \;=\; (1 - R_j)\;\psi$$

As expected, the posterior variance is smaller than the prior variance ψ because of the information gained regarding the random intercept by knowing the responses y_{1j} and y_{2j} for cluster (here subject) j.

The posterior variance is also the conditional variance of the prediction errors $\widetilde{\zeta}_j^{\mathrm{EB}} - \zeta_j$, given the responses, $\mathrm{Var}(\widetilde{\zeta}_j^{\mathrm{EB}} - \zeta_j|y_{1j}, y_{2j})$. In the linear variance-components model,

the conditional variance equals the unconditional (or marginal) variance of the prediction errors,

$$\mathrm{Var}(\widetilde{\zeta}_j^{\mathrm{EB}} - \zeta_j)$$

over repeated samples of ζ_j and ϵ_{ij} (or repeated samples of clusters j and units i), but with parameters held constant and equal to the estimates. This variance is often referred to as the *mean squared error of prediction* (MSEP). Its square root is referred to as the *comparative standard error* because it can be used for inferences regarding differences between clusters' true random intercepts.

The comparative standard error can be estimated by plugging in estimates for θ and ψ. Such estimated standard errors are produced by the `predict` command after `xtmixed` with the `reses` (for "random effects standard errors") option

```
. predict comp_se, reses
```

These standard errors are identical for all clusters because the clusters have the same size $n_j = 2$ so that $\widehat{R}_j$ is the same for all clusters. We therefore display only the value for the first observation:

```
. display comp_se[1]
13.958865
```

Diagnostic standard errors

For linear variance-components models, the sampling distribution of the empirical Bayes predictions (over repeated samples of ζ_j and ϵ_{ij}, or of clusters and units from clusters) is normal with mean 0 and variance

$$\mathrm{Var}(\widetilde{\zeta}_j^{\mathrm{EB}}) \;=\; \frac{\psi}{\psi + \theta/n_j}\;\psi \;=\; R_j\;\psi$$

This variance is useful for deciding if the empirical Bayes prediction for a given cluster is aberrant. For instance, 95% of predictions should be no larger in absolute value than about two sampling standard deviations. Thus the sampling standard deviation is often called the *diagnostic standard error*.

We can estimate the diagnostic standard error from the estimated prior variance $\widehat{\psi}$ and posterior variance $\mathrm{Var}(\zeta_j|y_{1j}, y_{2j})$ obtained earlier, using the relationship

$$\mathrm{Var}(\widetilde{\zeta}_j^{\mathrm{EB}}) \;=\; R_j\psi \;=\; \psi - (1 - R_j)\;\psi \;=\; \psi - \mathrm{Var}(\zeta_j|y_{1j}, y_{2j})$$

The corresponding estimated standard error can be obtained using

```
. generate diag_se = sqrt(exp([lns1_1_1]_cons)^2 - comp_se^2)
. display diag_se[1]
106.13242
```

If $\widehat{R}_j > 0.5$, as is usually the case in practice, we obtain the following relation among the empirical Bayes variances:

$$\text{Var}(\zeta_j|y_{1j}, y_{2j}) \;=\; \text{Var}(\widetilde{\zeta}_j^{\text{EB}} - \zeta_j) \;<\; \text{Var}(\widetilde{\zeta}_j^{\text{EB}})$$

As we would expect, the relation is satisfied for the Mini Wright data because $\widehat{R}_j = 0.98$.

2.12 Summary and further reading

In this chapter, we introduced the idea of decomposing the total variance of the response variable into variance components, specifically the between-cluster variance ψ and the within-cluster variance θ. This was accomplished by specifying a model that includes corresponding error components; a level-2 random intercept ζ_j for clusters; and a level-1 residual ϵ_{ij} for units within clusters, where ϵ_{ij} is uncorrelated with ζ_j. The random intercept induces correlations among responses for units in the same cluster, known as the *intraclass correlation*.

The random intercept is a random variable and not a model parameter. The realizations of ζ_j change in repeated samples, either because clusters are sampled or because the random intercept is redrawn from the data-generating model for given clusters. An alternative to random intercepts are fixed intercepts. Some guidelines for choosing between random and fixed intercepts were given, and this issue will be revisited in the next chapter.

The concepts discussed in this chapter underlie all multilevel or hierarchical modeling. By considering the simplest case of a multilevel model, we have provided some insight into estimation of model parameters and prediction of random effects. We have also discussed how to conduct hypothesis testing and construct confidence intervals for variance-components models. Although the expressions for estimators and predictors become more complex for the models discussed in later chapters of this volume, the basic ideas remain the same.

For further reading about variance-components models, we recommend Snijders and Bosker (2012, chap. 3), as well as many of the books referred to in later chapters of this volume. Streiner and Norman (2008), Shavelson and Webb (1991), and Dunn (2004) are excellent books on linear measurement models.

The exercises cover a range of applications, such as measurement of peak expiratory flow (exercise 2.1), measurement of psychological distress (exercise 2.2), essay grading (exercise 2.5), neuroticism of twins (exercise 2.3), birthweights of siblings (exercise 2.7), head sizes of brothers (exercise 2.6), and achievement of children nested in neighborhoods and schools (exercise 2.4). Exercise 2.8 is about random-effects meta-analysis, a topic not discussed in this chapter.

2.13 Exercises

2.1 Peak-expiratory-flow data

1. Repeat the analysis of section 2.5 for the Wright peak-flow meter measurements (data are in `pefr.dta`) using `xtmixed`.
2. Compare the estimates with those obtained for the Mini Wright meter (see table 2.2). Does one measurement method appear to be better than the other?
3. Obtain empirical Bayes predictions for both methods, and compare the two sets of predictions graphically.
4. Which method has a smaller prediction-error variance (squared comparative standard error)?

2.2 General-health-questionnaire data

Dunn (1992) reported test–retest data for the 12-item version of Goldberg's (1972) General Health Questionnaire (GHQ) designed to measure psychological distress. Twelve clinical psychology students completed the questionnaire on two occasions, three days apart, giving the scores shown in table 2.3.

Table 2.3: GHQ scores for 12 students tested on two occasions

Student	GHQ1	GHQ2
1	12	12
2	8	7
3	22	24
4	10	14
5	10	8
6	6	4
7	8	5
8	4	6
9	14	14
10	6	5
11	2	5
12	22	16

Source: Dunn (1992).

1. Fit the variance-components model in (2.3) for these data using REML.
2. Obtain ML estimates and empirical Bayes predictions of ζ_j. Produce a scatterplot of empirical Bayes predictions versus ML estimates with a $y = x$ line superimposed. Describe how the graph would change if there were more shrinkage.

3. Extend the model to allow for different means at the two occasions instead of assuming a common mean β as shown in section 2.9. Is there any evidence for a change in mean GHQ scores over time?

2.3 Twin-neuroticism data

Sham (1998) analyzed data on 522 female monozygotic (identical) twin-pairs and 272 female dizygotic (nonidentical or fraternal) twin-pairs.

Specifically, the dataset (from MacDonald 1996) contains scores for the neuroticism dimension of the Eysenck Personality Questionnaire (EPQ). Such twin data are often used to find out to what degree a trait or phenotype (here neuroticism) is due to nature (genes) versus nurture (environment). According to the *equal environment assumption*, monozygotic (MZ) and dizygotic (DZ) twins share the same degree of similarity in their environments, so any excess similarity in neuroticism scores for MZ twins must be due to a greater proportion of shared genes (MZ twins share 100% of their genes, whereas DZ twins only share 50%); see Sham (1998) for a more detailed discussion.

The dataset `twin.dta` has the following variables:

- `twin1`: neuroticism score for twin 1 (the twin with the higher score)
- `twin2`: neuroticism score for twin 2
- `num2`: the number of twin-pairs with a given pair of neuroticism scores
- `dzmz`: a string variable for DZ versus MZ twins (`dz` and `mz`)

1. The data are in collapsed or aggregated form with `num2` representing the number of twin-pairs having a given pair of neuroticism scores. Expand the data by using `expand num2`.
2. Create an identifier for twin-pairs (for example, using `generate pair = _n`) and reshape the data to long form, stacking the neuroticism scores into one variable.
3. Fit the variance-components model in (2.3) separately for MZ and DZ twins by ML.
4. Compare the estimated variance components and total variances between MZ and DZ twins. Do these estimates suggest that there is a genetic contribution to the variability in neuroticism?
5. Obtain the estimated intraclass correlations. Again, do these estimates suggest that there is a genetic contribution to the variability in neuroticism?
6. Why should the Pearson correlation not be used for these data?

See also exercise 8.10 for biometrical genetic modeling of the same data.

2.4 Neighborhood-effects data

Garner and Raudenbush (1991), Raudenbush and Bryk (2002), and Raudenbush et al. (2004) considered neighborhood effects on educational attainment for young people who left school between 1984 and 1986 in one education authority in Scotland.

The dataset `neighborhood.dta` has the following variables:

- `attain`: a measure of end-of-school educational attainment, capturing both attainment and length of schooling (based on the number of O-grades and Higher SCE awards at the A–C levels)
- `neighid`: neighborhood identifier
- `schid`: school identifier

Educational attainment (`attain`) is the response variable.

1. Fit a variance-components model for students nested in schools by ML using `xtmixed`. Obtain the estimated intraclass correlation.
2. Fit a variance-components model for students nested in neighborhoods by ML using `xtmixed`. Obtain the estimated intraclass correlation.
3. Do neighborhoods or schools appear to have a greater influence on educational attainment?

See exercise 3.1 for random-intercept modeling with covariates, and see exercise 9.5 for crossed random-effects modeling using this dataset.

2.5 Essay-grading data

Here we consider a subset of data from Johnson and Albert (1999) on grades assigned to 198 essays by five experts. The grades are on a 10-point scale with 10 being "excellent".

The dataset `grader1.dta` has the following variables:

- `essay`: identifier for essays
- `grade1`: grade from grader 1 on 10-point scale
- `grade4`: grade from grader 4 on 10-point scale

1. Reshape the data to stack the grades from graders 1 and 4 into one variable.
2. Fit a linear variance-components model for the essay grades with variance components within and between graders. Use ML estimation in `xtmixed`.
3. Obtain the estimated intraclass correlation, here interpretable as an inter-rater reliability.
4. Include a dummy variable for grader 4 in the fixed part of the model to allow for bias between the graders, as shown in section 2.9. Does one grader appear to be more generous than the other?
5. Obtain empirical Bayes predictions (using `xtmixed` with the `reffects` option) and plot them using a histogram.

2.6 Head-size data

Frets (1921) analyzed data on the adult head sizes of the first two sons of 25 families. Both the length and breadth of each head were measured in millimeters (mm), and the data are provided by Hand et al. (1994).

The variables in the dataset `headsize.dta` are

- `length1`: length of head of first son (mm)
- `breadth1`: breadth of head of first son (mm)
- `length2`: length of head of second son (mm)
- `breadth2`: breadth of head of second son (mm)

1. We will use a variance-components model to estimate the intraclass correlation between the head lengths of sons nested in families. Why wouldn't it make sense to use this approach for obtaining the intraclass correlation between the head lengths and head breadths nested in heads (or men)?
2. Stack the head lengths of both sons into a variable, `length`, and the breadths into a variable, `breadth`.
3. Fit a linear variance-components model for head length by using `xtreg` and `xtmixed`, both with the `mle` option (the results from both commands should be the same).
4. Interpret the estimated intraclass correlation.
5. Extend the model to allow the mean head length to differ between the first-born and second-born sons (see section 2.9).
   a. Write down the model.
   b. Fit the model by using `xtmixed` with the `mle` option.
   c. Interpret the results.

2.7 Georgian-birthweight data Solutions

Adams et al. (1997) analyzed a dataset on all live births that occurred in Georgia, U.S.A, from 1980 to 1992 (regardless of maternal state of residence), or that occurred in other states to Georgia residents and for which birth certificates were sent to Georgia. They linked data on births to the same mother using 27 different variables (maternal social security number was often missing or inaccurately recorded; see the paper for details). Following Neuhaus and Kalbfleisch (1998) we will use a subset of the linked data, including only births to mothers for whom five births were identified.

We will use the following variables in `birthwt.dta`:

- `mother`: mother identifier
- `child`: child identifier
- `birthwt`: child's birthweight (in grams)

1. Fit a variance-components model to the birthweights by using `xtmixed` with the `mle` option, treating children as level 1 and mothers as level 2.
2. At the 5% level, is there significant between-mother variability in birthweights? Fully report the method and result of the test.
3. Obtain the estimated intraclass correlation and interpret it.

4. Obtain empirical Bayes predictions of the random intercept and plot a histogram of the empirical Bayes predictions.

See also exercise 3.5 for further analysis of these data.

2.8 ❖ Teacher expectancy meta-analysis data Solutions

According to Raudenbush and Bryk (2002, 210–211), "the hypothesis that teachers' expectations influence pupils' intellectual development as measured by IQ (intelligence quotient) scores has been the source of sustained and acrimonious controversy for over 20 years."

Raudenbush (1984) found 19 reports of experiments testing this hypothesis. In each study, children were assigned either to an experimental group or to a control group. Teachers were encouraged to have high expectations of the children in the experimental group, whereas no particular expectations were encouraged of the children in the control group.

Raudenbush (1984) analyzed the study results using a meta-analysis. The purpose of a meta-analysis is to pool data from several studies to obtain a more precise estimate of the effect of the intervention (effect size) than provided by any individual study. Typically, the data for a meta-analysis are the estimated effect sizes y_j for the individual studies j (because individual data are rarely published) and the estimated standard errors s_j of the estimated effect sizes. In the teacher expectancy meta-analysis, the effect size is the difference in mean IQ between the experimental and the control groups divided by the pooled within-group standard deviation.

The variables in `expectancy.dta` that we will use here are

- `est`: estimated effect size (y_j) (standardized mean difference)
- `se`: estimated standard error (s_j)

In a random-effects meta-analysis, it is acknowledged that there could be systematic differences between studies, such as target population, implementation of the intervention, or measurement of the outcome. Every study is therefore assumed to have a different true effect size $\beta+\zeta_j$, where β is the population mean effect size and ζ_j is a study-specific random intercept. The estimated effect size for study j differs from its true effect size by a random estimation error e_j with standard deviation estimated by s_j. The model therefore is

$$y_j = \beta + \zeta_j + e_j$$

where ζ_j and e_j are uncorrelated across studies and uncorrelated with each other. ζ_j has zero mean and variance τ^2 (the Greek letter τ is pronounced "tau") to be estimated. e_j has zero mean and variance set equal to the estimated squared standard error, s_j^2. A good book on meta-analysis is Borenstein et al. (2009).

1. Fit the model above by ML using the user-written command `metaan` (Kontopantelis and Reeves 2010). The program can be installed (if your computer is connected to the Internet) using `ssc install metaan`. The syntax is `metaan est se, ml`.
2. Find the estimated model parameters in the output and interpret them.
3. Fit a so-called fixed-effects meta-analysis that simply omits ζ_j from the model and assumes that all true effect sizes are equal to β. This can be accomplished by replacing the `ml` option with the `fe` option in the `metaan` command.
4. Explain how the model differs from what we have referred to as fixed-effects models in this chapter (apart from the fact that the data are in aggregated form and the level-1 variance is assumed known).
5. Compare the width of the confidence intervals for β between the random- and fixed-effects meta-analyses, and explain why they differ the way they do.

2.9 Reliability and empirical Bayes prediction

In a hypothetical test–retest study, the estimates for the measurement model in (2.3) were as shown in table 2.4.

Table 2.4: Estimates for hypothetical test–retest study

	Est
β	30
ψ	9
θ	8

1. What is the estimated test–retest reliability of these measurements?
2. For a person with measurements 34 and 36, obtain the ML estimate and empirical Bayes prediction of ζ_j and of the true score.
3. Two additional measurements of 37 and 33 are made on the same person. Using all four measurements, obtain the ML estimate and empirical Bayes prediction of ζ_j and of the true score. Compare the results with the results for step 2, and explain the reason for any differences.
4. What is the empirical Bayes prediction of ζ_j for a person who has not been measured yet?

2.10 ❖ Maximum likelihood and restricted maximum likelihood

For the Mini Wright meter, use the ML estimates in table 2.2 to calculate the REML or ANOVA estimate of ψ. Also obtain the corresponding REML or ANOVA estimate of the intraclass correlation.

3 Random-intercept models with covariates

3.1 Introduction

In this chapter, we extend the variance-components models introduced in the previous chapter by including observed explanatory variables or covariates x. Seen from another perspective, we extend the linear regression models discussed in chapter 1 by introducing random intercepts ζ_j to handle clustered data. As we will show, ignoring the clustering generally leads to incorrect estimated standard errors and hence incorrect p-values.

Although many of the features of the variance-components models persist, new issues arise in estimating regression coefficients. In particular, we discuss the distinction between within-cluster and between-cluster covariate effects, and the problem of omitted cluster-level covariates and endogeneity. We also discuss coefficients of determination or measures of variance explained by covariates.

3.2 Does smoking during pregnancy affect birthweight?

Abrevaya (2006) investigates the effect of smoking on birth outcomes with the Natality datasets derived from birth certificates by the U.S. National Center for Health Statistics. This is of considerable public health interest because many pregnant women in the U.S. continue to smoke during pregnancy. Indeed, it is estimated that only 18% to 25% of smokers quit smoking once they become pregnant, according to the 2004 Surgeon General's Report on The Health Consequences of Smoking.

Abrevaya identified multiple births from the same mothers in nine datasets from 1990–1998 by matching mothers across the datasets. Unlike, for instance, the Nordic countries, a unique person identifier such as a social security number or name is rarely available in U.S. datasets. Perfect matching is thus precluded, and matching must proceed by identifying mothers who have identical values on a set of variables in all datasets. In this study, matching was accomplished by considering mother's state of birth and child's state of birth, as well as mother's county and city of birth; mother's age, race, education, and marital status; and, if married, father's age and race. For the matching on mother's and child's states of birth to be useful, the data were restricted to combinations of states that occur rarely.

Here we consider the subset of the matches where the observed interval between births was consistent with the interval since the last birth recorded on the birth certifi-

cate. The data are restricted to births with complete data for the variables considered by Abrevaya (2006), singleton births (no twins or other multiple births), and births to mothers for whom at least two births between 1990 and 1998 could be matched and whose race was classified as white or black.

The birth outcome we will concentrate on is birthweight. Abrevaya (2006) motivates his study by citing a report from the U.S. Surgeon General:

> "Infants born to women who smoke during pregnancy have a lower average birthweight and are more likely to be small for gestational age than infants born to women who do not smoke ..."
> (*Women and Smoking: A Report of the Surgeon General*, Centers for Disease Control and Prevention, 2001).

The dataset used by Abrevaya (2006) is available from the Journal of Applied Econometrics Data Archive. Here we took a 10% random sample of the data, yielding 8,604 births from 3,978 mothers. We use the following variables from `smoking.dta`:

- `momid`: mother identifier
- `birwt`: birthweight (in grams)
- `mage`: mother's age at the birth of the child (in years)
- `smoke`: dummy variable for mother smoking during pregnancy (1: smoking; 0: not smoking)
- `male`: dummy variable for baby being male (1: male; 0: female)
- `married`: dummy variable for mother being married (1: married; 0: unmarried)
- `hsgrad`: dummy variable for mother having graduated from high school (1: graduated; 0: did not graduate)
- `somecoll`: dummy variable for mother having some college education, but no degree (1: some college; 0: no college)
- `collgrad`: dummy variable for mother having graduated from college (1: graduated; 0: did not graduate)
- `black`: dummy variable for mother being black (1: black; 0: white)
- `kessner2`: dummy variable for Kessner index = 2, or intermediate prenatal care (1: index=2; 0: otherwise)
- `kessner3`: dummy variable for Kessner index = 3, or inadequate prenatal care (1: index=3; 0: otherwise)
- `novisit`: dummy variable for no prenatal care visit (1: no visit; 0: at least 1 visit)
- `pretri2`: dummy variable for first prenatal care visit having occurred in second trimester (1: yes; 0: no)
- `pretri3`: dummy variable for first prenatal care visit having occurred in third trimester (1: yes; 0: no)

Smoking status was determined from the answer to the question asked on the birth certificate whether there was tobacco use during pregnancy. The dummy variables for mother's education—`hsgrad`, `somecoll`, and `collgrad`—were derived from the years of education given on the birth certificate. The Kessner index is a measure of the adequacy of prenatal care (1: adequate; 2: intermediate; 3: inadequate) based on the timing of the first prenatal visit and the number of prenatal visits, taking into account the gestational age of the fetus.

3.2.1 Data structure and descriptive statistics

The data have a two-level structure with births (or children or pregnancies) as units at level 1 and mothers as clusters at level 2. In multilevel models, the response variable always varies at the lowest level, taking on different values for different level-1 units within the same level-2 cluster. However, covariates can either vary at level 1 (and therefore usually also at level 2) or vary at level 2 only. For instance, while `smoke` can change from one pregnancy to the next, `black` is constant between pregnancies. `smoke` is therefore said to be a level-1 variable, whereas `black` is a level-2 variable. Among the variables listed above, `black` appears to be the only one that cannot in principle change between pregnancies. However, because of the way the matching was done, the education dummy variables (`hsgrad`, `somecoll`, and `collgrad`) and `married` also remain constant across births for the same mother and are thus level-2 variables.

We start by reading the smoking and birthweight data into Stata using the command

```
. use http://www.stata-press.com/data/mlmus3/smoking
```

A useful Stata command for exploring how much variables vary at level 1 and 2 is `xtsum`:

```
. quietly xtset momid
. xtsum birwt smoke black
```

Variable		Mean	Std. Dev.	Min	Max	Observations
birwt	overall	3469.931	527.1394	284	5642	N = 8604
	between		451.1943	1361	5183.5	n = 3978
	within		276.7966	1528.431	5411.431	T-bar = 2.1629
smoke	overall	.1399349	.3469397	0	1	N = 8604
	between		.3216459	0	1	n = 3978
	within		.1368006	-.5267318	.8066016	T-bar = 2.1629
black	overall	.0717108	.2580235	0	1	N = 8604
	between		.257512	0	1	n = 3978
	within		0	.0717108	.0717108	T-bar = 2.1629

The total number of observations is $N = 8604$; the number of clusters is $J = 3978$ (`n` in the output); and there are on average about 2.2 births per mother (`T-bar` in the output) in the dataset.

Three different sample standard deviations are given for each variable. The first is the *overall standard deviation*, s_{xO}, defined as usual as the square root of the mean squared deviation of observations from the overall mean:

$$s_{xO} = \sqrt{\frac{1}{N-1}\sum_{j=1}^{J}\sum_{i=1}^{n_j}(x_{ij}-\overline{x}_{..})^2}$$

The second is the *between standard deviation*, defined as the square root of the mean squared deviation of the cluster means from the overall mean:

$$s_{xB} = \sqrt{\frac{1}{J-1}\sum_{j=1}^{J}(\overline{x}_{.j}-\overline{x}_{..})^2}$$

This third is the *within standard deviation*, defined as the square root of the mean squared deviation of observations from the cluster means:

$$s_{xW} = \sqrt{\frac{1}{N-1}\sum_{j=1}^{J}\sum_{i=1}^{n_j}(x_{ij}-\overline{x}_{.j})^2}$$

We see that birthweight and smoking vary more between mothers than within mothers, whereas being black does not vary at all within mothers, as expected. It is important to be aware of how much level-1 variables vary within clusters because some estimators rely only on the within-cluster variability of covariates.

There are two different ways of expressing the mean or proportion for a level-2 variable: considering the summary either across units (with the level-1 units as unit of analysis) or across clusters (with the clusters as unit of analysis). For instance, the mean for `black` produced by `xtsum` is the mean (or proportion, because `black` is binary) across units, the proportion of children born to black mothers. We could also consider the mean across mothers, or the proportion of mothers who are black. To do so, we define a dummy variable equal to 1 for one child per mother using the `egen` command with the `tag()` function,

```
. egen pickone = tag(momid)
```

and summarize `black` across mothers by specifying `if pickone==1` in the command:

```
. summarize black if pickone==1
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
       black |       3978   .0713927     .257512          0          1
```

We see that the proportion of mothers who are black is very close to the proportion of children born to black mothers, probably because the number of children per mother does not vary much.

We can calculate the number of children per mother by using `egen` with the `count()` function:

```
. egen num = count(birwt), by(momid)
. tabulate num if pickone==1
```

num	Freq.	Percent	Cum.
2	3,330	83.71	83.71
3	648	16.29	100.00
Total	3,978	100.00	

Most mothers in the data have two children, and about 16% have three.

For categorical variables, including variables with more than two categories, `xttab` is a useful command. For the dichotomous variable `smoke`, the command produces the following table:

```
. quietly xtset momid
. xttab smoke
```

	Overall		Between		Within
smoke	Freq.	Percent	Freq.	Percent	Percent
Nonsmoke	7400	86.01	3565	89.62	95.69
Smoker	1204	13.99	717	18.02	79.03
Total	8604	100.00	4282	107.64	92.90
			(n = 3978)		

In the `Overall` table, we see that mothers smoked during their pregnancies for 14% of the children. According to the `Between` table, 90% of mothers had at least one pregnancy where they did not smoke, and 18% of mothers had at least one pregnancy where they did smoke. The `Within` table shows that the women who were ever nonsmokers during a pregnancy were nonsmokers for an average of 96% of their pregnancies. The women who ever smoked during a pregnancy did so for an average of 79% of their pregnancies.

3.3 The linear random-intercept model with covariates

3.3.1 Model specification

An obvious model to consider for the continuous response variable, birthweight, is a multiple linear regression model (discussed in chapter 1), including smoking status and various other variables as explanatory variables or covariates.

The model for the birthweight y_{ij} of child i of mother j is specified as

$$y_{ij} = \beta_1 + \beta_2 x_{2ij} + \cdots + \beta_p x_{pij} + \xi_{ij} \tag{3.1}$$

where x_{2ij} through x_{pij} are covariates and ξ_{ij} is a residual.

It may be unrealistic to assume that the birthweights of children born to the same mother are uncorrelated given the observed covariates, or in other words that the residuals ξ_{ij} and $\xi_{i'j}$ are uncorrelated. We can therefore use the idea introduced in the previous chapter to split the total residual or error into two error components: ζ_j, which is shared between children of the same mother, and ϵ_{ij}, which is unique for each child:

$$\xi_{ij} \equiv \zeta_j + \epsilon_{ij}$$

Substituting for ξ_{ij} into the multiple-regression model (3.1), we obtain a *linear random-intercept model with covariates*:

$$\begin{aligned} y_{ij} &= \beta_1 + \beta_2 x_{2ij} + \cdots + \beta_p x_{pij} + (\zeta_j + \epsilon_{ij}) \\ &= (\beta_1 + \zeta_j) + \beta_2 x_{2ij} + \cdots + \beta_p x_{pij} + \epsilon_{ij} \end{aligned} \tag{3.2}$$

This model can be viewed as a regression model with an added level-2 residual ζ_j, or with a mother-specific intercept $\beta_1 + \zeta_j$. The random intercept ζ_j can be considered a latent variable that is not estimated along with the fixed parameters β_1 through β_p, but whose variance ψ is estimated together with the variance θ of the ϵ_{ij}. The linear random-intercept model with covariates is the simplest example of a *linear mixed (effects) model* where there are both fixed and random effects.

The random intercept or level-2 residual ζ_j is a mother-specific error component, which remains constant across births, whereas the level-1 residual ϵ_{ij} is a child-specific error component, which varies between children i as well as mothers j. The ζ_j are uncorrelated over mothers, the ϵ_{ij} are uncorrelated over mothers and children, and the two error components are uncorrelated with each other.

The mother-specific error component ζ_j represents the combined effects of omitted mother characteristics or unobserved heterogeneity at the mother level. If ζ_j is positive, the total residuals for mother j, ξ_{ij}, will tend to be positive, leading to heavier babies than predicted by the covariates. If ζ_j is negative, the total residuals will tend to be negative. Because ζ_j is shared by all responses for the same mother, it induces within-mother dependence among the total residuals ξ_{ij}.

3.3.2 Model assumptions

We now explicitly state a set of assumptions that are sufficient for everything we want to do in this chapter but are not always necessary. For this purpose, all observed covariates for unit i in cluster j are placed in the vector $\mathbf{x}_{ij}$, and the covariates for all the units in cluster j are placed in the matrix $\mathbf{X}_j$.

It is assumed that the level-1 residual ϵ_{ij} has zero expectation or mean, given the covariates and the random intercept:

$$E(\epsilon_{ij}|\mathbf{X}_j, \zeta_j) = 0 \tag{3.3}$$

This mean-independence assumption implies that $E(\epsilon_{ij}|\mathbf{X}_j) = 0$ and that $\mathrm{Cor}(\epsilon_{ij}, \mathbf{x}_{ij}) = 0$. We call this lack of correlation between covariates and level-1 residual "level-1 exo-

geneity". (See also section 1.13 on the exogeneity assumption in ordinary linear regression.)

The random intercept ζ_j is assumed to have zero expectation given the covariates,

$$E(\zeta_j|\mathbf{X}_j) \;=\; 0 \tag{3.4}$$

and this mean-independence assumption implies that $\mathrm{Cor}(\zeta_j, \mathbf{x}_{ij}) = 0$. We call the lack of correlation between covariates and random intercept "level-2 exogeneity". Violations of the exogeneity assumptions are called level-1 endogeneity and level-2 endogeneity, respectively.

We assume that the variance of the level-1 residual is homoskedastic for given covariates and random intercept,

$$\mathrm{Var}(\epsilon_{ij}|\mathbf{X}_j, \zeta_j) \;=\; \theta \tag{3.5}$$

which implies that $\mathrm{Var}(\epsilon_{ij}) = \theta$ and that $\mathrm{Cor}(\epsilon_{ij}, \zeta_j) = 0$. It is also assumed that the variance of the random intercept is homoskedastic given the covariates,

$$\mathrm{Var}(\zeta_j|\mathbf{X}_j) \;=\; \psi \tag{3.6}$$

which implies that $\mathrm{Var}(\zeta_j) = \psi$.

It is assumed that the level-1 residuals are uncorrelated for two units i and i' (whether they are nested in the same cluster j or in different clusters j and j') given the covariates and random intercept(s),

$$\mathrm{Cov}(\epsilon_{ij}, \epsilon_{i'j'}|\mathbf{X}_j, \mathbf{X}_{j'}, \zeta_j, \zeta_{j'}) \;=\; 0 \qquad \text{if} \quad i \neq i' \quad \text{or} \quad j \neq j' \tag{3.7}$$

and that random intercepts are uncorrelated for different clusters j and j' given the covariates,

$$\mathrm{Cov}(\zeta_j, \zeta_{j'}|\mathbf{X}_j, \mathbf{X}_{j'}) \;=\; 0 \qquad \text{if} \quad j \neq j' \tag{3.8}$$

These assumptions imply the mean and residual covariance structure of the responses described in sections 3.3.3 and 3.3.4.

It is sometimes assumed that both $\epsilon_{ij}|\mathbf{X}_j, \zeta_j$ and $\zeta_j|\mathbf{X}_j$ have normal distributions. Together with the assumptions (3.3) and (3.5), this implies that ζ_j and ϵ_{ij} are independent (a stronger property than lack of correlation).

The assumptions necessary for consistency of the standard estimators for regression coefficients are a correct mean structure (correct functional form and correct covariates) and lack of correlation between covariates and the random part of the model (the random intercept and the level-1 residual). Consistency of model-based standard errors relies on the additional assumption that the covariance structure (the variances and covariances) of the total residuals is correctly specified. Likewise, efficient estimation of regression coefficients requires that both mean and covariance structures are correct. For unbiased estimation of regression coefficients, the mean structure must be correct and the distribution of the total residuals must be symmetric (such as normal).

3.3.3 Mean structure

Assumption (3.3) implies that the cluster-specific or conditional regression (averaged over ϵ_{ij} but given ζ_j and $\mathbf{X}_j$) is linear:

$$\begin{aligned} E(y_{ij}|\mathbf{X}_j,\zeta_j) &= E(\beta_1+\beta_2 x_{2ij}+\cdots+\beta_p x_{pij})+E(\zeta_j|\mathbf{X}_j,\zeta_j)+\underbrace{E(\epsilon_{ij}|\mathbf{X}_j,\zeta_j)}_{0} \\ &= \beta_1+\beta_2 x_{2ij}+\cdots+\beta_p x_{pij}+\zeta_j \end{aligned} \tag{3.9}$$

We see that the covariates for other units in the cluster do not affect the mean response for unit i once we control for the covariates $\mathbf{x}_{ij}$ for unit i and the random intercept ζ_j. The covariates for the cluster $\mathbf{X}_j$ are then said to be "strictly exogenous given the random intercept".

It follows from (3.4) that the population-averaged or marginal regression (averaged over ζ_j and ϵ_{ij} but given $\mathbf{X}_j$) is linear:

$$\begin{aligned} E(y_{ij}|\mathbf{X}_j) &= E(\beta_1+\beta_2 x_{2ij}+\cdots+\beta_p x_{pij})+\underbrace{E(\zeta_j|\mathbf{X}_j)}_{0}+\underbrace{E(\epsilon_{ij}|\mathbf{X}_j)}_{0} \\ &= \beta_1+\beta_2 x_{2ij}+\cdots+\beta_p x_{pij} \end{aligned} \tag{3.10}$$

We sometimes refer to this relationship between the mean and covariates as the mean structure.

3.3.4 Residual variance and intraclass correlation

It follows from assumptions (3.5) and (3.6) that total residuals or error terms are homoskedastic (having constant variance) given the covariates $\mathbf{X}_j$,

$$\mathrm{Var}(\xi_{ij}|\mathbf{X}_j) = \mathrm{Var}(\zeta_j+\epsilon_{ij}|\mathbf{X}_j)=\psi+\theta$$

or, equivalently, that the responses y_{ij} given the covariates are also homoskedastic,

$$\mathrm{Var}(y_{ij}|\mathbf{X}_j)=\psi+\theta$$

The conditional correlation between the total residuals for any two children i and i' of the same mother j given the covariates, also called the residual correlation, is

$$\rho \equiv \mathrm{Cor}(\xi_{ij},\xi_{i'j}|\mathbf{X}_j) = \frac{\psi}{\psi+\theta}$$

where ψ is the corresponding covariance. Thus ρ is also the conditional or residual intraclass correlation of responses y_{ij} and $y_{i'j}$ for mother j given the covariates:

$$\rho \equiv \mathrm{Cor}(y_{ij},y_{i'j}|\mathbf{X}_j) = \frac{\psi}{\psi+\theta}$$

It is important to distinguish between the intraclass correlation in a model not containing any covariates—sometimes called the *unconditional* intraclass correlation—and the *conditional* or *residual* intraclass correlation in a model containing covariates. The residual covariance structure is shown in matrix form in display 3.2.

3.3.5 Graphical illustration of random-intercept model

A graphical illustration of the random-intercept model with a single covariate x_{ij} for a mother j is given in figure 3.1.

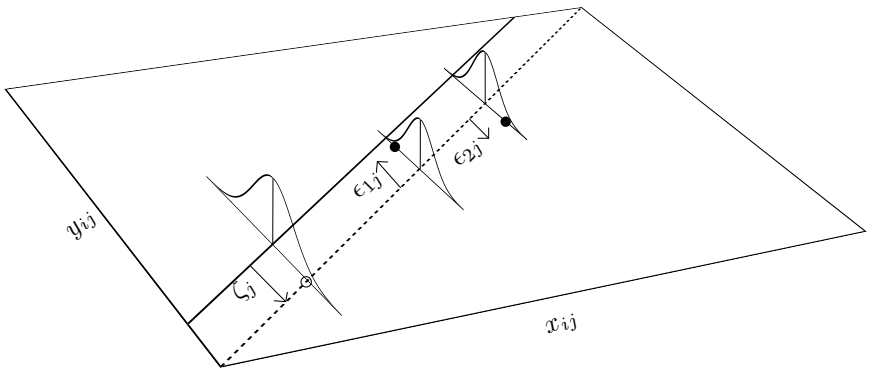


Figure 3.1: Illustration of random-intercept model for one mother

Here the solid line is $E(y_{ij}|x_{ij}) = \beta_1 + \beta_2 x_{ij}$, the population-averaged regression line for the population of all mothers j. The normal density curve centered on this line represents the random-intercept distribution with variance ψ and the hollow circle represents a realization ζ_j from this distribution for mother j (this could have been placed anywhere along the line). This negative random intercept ζ_j produces the dotted mother-specific regression line $E(y_{ij}|x_{ij}, \zeta_j) = (\beta_1 + \zeta_j) + \beta_2 x_{ij}$. This line is parallel to and below the population-averaged regression line. For a mother with a positive ζ_j, the mother-specific regression line would be parallel to and above the population-averaged regression line. Observed responses $y_{ij} = (\beta_1 + \zeta_j) + \beta_2 x_{ij} + \epsilon_{ij}$ are shown for two values of x_{ij}. The responses are sampled from the two normal distributions [with means $(\beta_1 + \zeta_j) + \beta_2 x_{ij}$ and variance θ] shown on the dotted curve.

3.4 Estimation using Stata

We can use `xtreg` or `xtmixed` to fit random-intercept models by maximum likelihood (ML). In addition, `xtreg` can be used to obtain feasible generalized least-squares estimates, and `xtmixed` can be used to obtain restricted ML estimates. Refer to section 3.10.1 for a brief description of these methods.

As discussed in chapter 2, `xtreg` is computationally more efficient than `xtmixed`, but `xtmixed` has a more useful `predict` command. Unless some special feature of `gllamm` or its prediction command `gllapred` are needed, we do not recommend using `gllamm` for linear models. A `gllamm` companion for this book is available from the `gllamm` website.

3.4.1 Using xtreg

The command for fitting the random-intercept model (3.2) by ML using `xtreg` is

```
. quietly xtset momid

. xtreg birwt smoke male mage hsgrad somecoll collgrad married black kessner2
> kessner3 novisit pretri2 pretri3, mle

Random-effects ML regression                    Number of obs      =      8604
Group variable: momid                           Number of groups   =      3978

Random effects u_i ~ Gaussian                   Obs per group: min =         2
                                                               avg =       2.2
                                                               max =         3

                                                LR chi2(13)        =    659.47
Log likelihood  = -65145.752                    Prob > chi2        =    0.0000

------------------------------------------------------------------------------
       birwt |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       smoke |  -218.3289   18.20988   -11.99   0.000    -254.0196   -182.6382
        male |   120.9375   9.558721    12.65   0.000     102.2027    139.6722
       mage |   8.100548   1.347266     6.01   0.000     5.459956    10.74114
     hsgrad |   56.84715   25.03538     2.27   0.023     7.778705    105.9156
   somecoll |   80.68607   27.30914     2.95   0.003     27.16115     134.211
   collgrad |   90.83273   27.99598     3.24   0.001     35.96162    145.7038
    married |    49.9202   25.50319     1.96   0.050    -.0651368    99.90554
      black |  -211.4138   28.27818    -7.48   0.000     -266.838   -155.9896
   kessner2 |  -92.91883   19.92624    -4.66   0.000    -131.9736   -53.86411
   kessner3 |  -150.8759   40.83414    -3.69   0.000    -230.9093   -70.84246
    novisit |  -30.03035   65.69213    -0.46   0.648    -158.7846    98.72387
    pretri2 |    92.8579   23.19258     4.00   0.000     47.40127    138.3145
    pretri3 |   178.7295   51.64145     3.46   0.001     77.51416    279.9449
      _cons |   3117.191   40.97597    76.07   0.000      3036.88    3197.503
-------------+----------------------------------------------------------------
    /sigma_u |   338.7674   6.296444                      326.6487    351.3358
    /sigma_e |   370.6654   3.867707                      363.1618     378.324
         rho |   .4551282   .0119411                      .4318152    .4785967
------------------------------------------------------------------------------
Likelihood-ratio test of sigma_u=0: chibar2(01)= 1108.77 Prob>=chibar2 = 0.000
```

The estimated regression coefficients are given next to the corresponding covariate name; for instance, the coefficient β_2 of `smoke` is estimated as -218 grams. This means that, according to the fitted model, the expected birthweight is 218 grams lower for a child of a mother who smoked during the pregnancy compared with a child of a mother who did not smoke, controlling or adjusting for the other covariates. The estimated regression coefficients for the other covariates make sense, although the coefficients for the prenatal care variables (`kessner2`, `kessner3`, `novisit`, `pretri2`, and `pretri3`) are not straightforward to interpret because their definitions are partly overlapping.

The estimate of the random-intercept standard deviation $\sqrt{\psi}$ is given under `/sigma_u` as 339 grams, and the estimate of the level-1 residual standard deviation $\sqrt{\theta}$ is given under `/sigma_e` as 371 grams.

The ML estimates for the random-intercept model are also presented under "Full model" in table 3.1. The estimated regression coefficients are reported under "Fixed part" in the table, and the estimated standard deviations for the random intercept and level-1 residual are given under "Random part".

Table 3.1: Maximum likelihood estimates for smoking data (in grams)

	Full model		Null model		Level-2 covariates	
	Est	(SE)	Est	(SE)	Est	(SE)
Fixed part						
β_1 [_cons]	3,117	(41)	3,468	(7)	3,216	(26)
β_2 [smoke]	−218	(18)				
β_3 [male]	121	(10)				
β_4 [mage]	8	(1)				
β_5 [hsgrad]	57	(25)			131	(25)
β_6 [somecoll]	81	(27)			181	(27)
β_7 [collgrad]	91	(28)			233	(26)
β_8 [married]	50	(26)			115	(25)
β_9 [black]	−211	(28)			−201	(29)
β_{10} [kessner2]	−93	(20)				
β_{11} [kessner3]	−151	(41)				
β_{12} [novisit]	−30	(66)				
β_{13} [pretri2]	93	(23)				
β_{14} [pretri3]	179	(52)				
Random part						
$\sqrt{\psi}$	339		368		348	
$\sqrt{\theta}$	371		378		378	
Derived estimates						
R^2	0.09		0.00		0.05	
ρ	0.46		0.49		0.46	

3.4.2 Using xtmixed

The random-intercept model (3.2) can also be fit by ML using `xtmixed` with the `mle` option:

```
. xtmixed birwt smoke male mage hsgrad somecoll collgrad married black
> kessner2 kessner3 novisit pretri2 pretri3 || momid:, mle
Mixed-effects ML regression                     Number of obs      =      8604
Group variable: momid                           Number of groups   =      3978
                                                Obs per group: min =         2
                                                               avg =       2.2
                                                               max =         3
                                                Wald chi2(13)      =    693.75
Log likelihood = -65145.752                     Prob > chi2        =    0.0000
```

birwt	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
smoke	-218.3291	18.15944	-12.02	0.000	-253.9209	-182.7372
male	120.9375	9.558013	12.65	0.000	102.2041	139.6708
mage	8.10054	1.344571	6.02	0.000	5.465229	10.73585
hsgrad	56.84715	25.03537	2.27	0.023	7.778723	105.9156
somecoll	80.68608	27.309	2.95	0.003	27.16142	134.2107
collgrad	90.83276	27.99491	3.24	0.001	35.96373	145.7018
married	49.9202	25.50303	1.96	0.050	-.0648328	99.90522
black	-211.4138	28.27757	-7.48	0.000	-266.8368	-155.9908
kessner2	-92.91884	19.92619	-4.66	0.000	-131.9734	-53.86423
kessner3	-150.876	40.83031	-3.70	0.000	-230.9019	-70.85002
novisit	-30.03037	65.69171	-0.46	0.648	-158.7837	98.72301
pretri2	92.85793	23.19069	4.00	0.000	47.40502	138.3108
pretri3	178.7296	51.63681	3.46	0.001	77.52332	279.9359
_cons	3117.192	40.88817	76.24	0.000	3037.052	3197.331

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
momid: Identity				
sd(_cons)	338.7669	6.296455	326.6481	351.3353
sd(Residual)	370.6656	3.867716	363.162	378.3242

```
LR test vs. linear regression: chibar2(01) =  1108.77 Prob >= chibar2 = 0.0000
```

The estimates are identical to those reported for `xtreg` in table 3.1.

The `reml` option can be used instead of `mle` to obtain restricted maximum likelihood (REML) estimates (see section 2.10.2 for the basic idea of REML). When there are many level-2 units J, as there are here, the REML and ML estimates will be almost identical. Robust standard errors can be obtained using the `vce(robust)` option.

3.5 Coefficients of determination or variance explained

In section 1.5, we motivated the coefficient of determination, or R-squared, as the proportional reduction in prediction error variance comparing the model without covariates (the null model) with the model of interest.

In ordinary linear regression without covariates, the predictions are $\widehat{y}_i = \overline{y}$, so the estimated prediction error variance is the mean squared error (MSE) for the null model,

$$\text{MSE}_0 \;=\; \frac{1}{N-1}\sum_i (y_i - \overline{y})^2 \;=\; \widehat{\sigma_0^2}$$

where $\widehat{\sigma_0^2}$ is an estimate of the residual variance in the null model. In the ordinary linear regression model including all covariates, the predictions are $\widehat{y}_i = \widehat{\beta}_1 + \widehat{\beta}_2 x_{2i} + \cdots + \widehat{\beta}_p x_{pi}$, and the estimated prediction error variance is the mean squared error in the regression model of interest,

$$\text{MSE}_1 \;=\; \frac{1}{N-p}\sum_i (y_i - \widehat{y}_i)^2 \;=\; \widehat{\sigma_1^2}$$

This is also an estimate of the residual variance σ_1^2 in the model of interest. The coefficient of determination is defined as

$$R^2 \;=\; \frac{\sum_i (y_i - \overline{y})^2 - \sum_i (y_i - \widehat{y}_i)^2}{\sum_i (y_i - \overline{y})^2} \;\approx\; \frac{\frac{\sum_i (y_i - \overline{y})^2}{N-1} - \frac{\sum_i (y_i - \widehat{y}_i)^2}{N-p}}{\frac{\sum_i (y_i - \overline{y})^2}{N-1}} \;=\; \frac{\widehat{\sigma_0^2} - \widehat{\sigma_1^2}}{\widehat{\sigma_0^2}}$$

where the approximation improves as N increases.

In a linear random-intercept model, the total residual variance is given by

$$\text{Var}(\zeta_j + \epsilon_{ij}) \;=\; \psi + \theta$$

An obvious definition of the coefficient of determination for two-level models, discussed by Snijders and Bosker (2012, chap. 7), is therefore the proportional reduction in the estimated total residual variance comparing the null model without covariates with the model of interest,

$$R^2 \;=\; \frac{\widehat{\psi}_0 + \widehat{\theta}_0 - (\widehat{\psi}_1 + \widehat{\theta}_1)}{\widehat{\psi}_0 + \widehat{\theta}_0}$$

where $\widehat{\psi}_0$ and $\widehat{\theta}_0$ are the estimates for the null model, and $\widehat{\psi}_1$ and $\widehat{\theta}_1$ are the estimates for the model of interest.

First, we fit the null model, also often called the *unconditional model*:

```
. quietly xtset momid

. xtreg birwt, mle

Random-effects ML regression                    Number of obs      =      8604
Group variable: momid                           Number of groups   =      3978

Random effects u_i ~ Gaussian                   Obs per group: min =         2
                                                               avg =       2.2
                                                               max =         3

                                                Wald chi2(0)       =      0.00
Log likelihood  = -65475.486                    Prob > chi2        =         .
```

birwt	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
_cons	3467.969	7.137618	485.87	0.000	3453.979	3481.958
/sigma_u	368.2866	6.45442			355.8509	381.1568
/sigma_e	377.6578	3.926794			370.0393	385.4331
rho	.4874391	.0114188			.4650901	.5098276

```
Likelihood-ratio test of sigma_u=0: chibar2(01)= 1315.66 Prob>=chibar2 = 0.000
```

The estimates for this model were also given under "Null model" in table 3.1. The total variance is estimated as

$$\widehat{\psi}_0 + \widehat{\theta}_0 \;=\; 368.2866^2 + 377.6578^2 = 278260.43$$

For the model including all covariates, whose estimates were given under "Full model" in table 3.1, the total residual variance is estimated as

$$\widehat{\psi}_1 + \widehat{\theta}_1 \;=\; 338.7674^2 + 370.6654^2 = 252156.19$$

It follows that

$$R^2 \;=\; \frac{278260.43 - 252156.19}{278260.43} = 0.09$$

so 9% of the variance is explained by the covariates.

Raudenbush and Bryk (2002, chap. 4) suggest considering the proportional reduction in each of the variance components separately. In our example, the proportion of level-2 variance explained by the covariates is

$$R_2^2 \;=\; \frac{\widehat{\psi}_0 - \widehat{\psi}_1}{\widehat{\psi}_0} = \frac{368.2866^2 - 338.7674^2}{368.2866^2} = 0.15$$

and the proportion of level-1 variance explained is

$$R_1^2 \;=\; \frac{\widehat{\theta}_0 - \widehat{\theta}_1}{\widehat{\theta}_0} = \frac{377.6578^2 - 370.6654^2}{377.6578^2} = 0.04$$

Let us now fit a random-intercept model that includes only the level-2 covariates:

```
. quietly xtset momid

. xtreg birwt hsgrad somecoll collgrad married black, mle
Random-effects ML regression                    Number of obs      =      8604
Group variable: momid                           Number of groups   =      3978

Random effects u_i ~ Gaussian                   Obs per group: min =         2
                                                               avg =       2.2
                                                               max =         3

                                                LR chi2(5)         =    290.48
Log likelihood  = -65330.247                    Prob > chi2        =    0.0000
```

birwt	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
hsgrad	131.4395	24.91149	5.28	0.000	82.61384	180.2651
somecoll	180.6879	26.50378	6.82	0.000	128.7414	232.6343
collgrad	232.8944	25.58597	9.10	0.000	182.7468	283.0419
married	114.765	25.45984	4.51	0.000	64.86465	164.6654
black	-201.4773	28.80249	-7.00	0.000	-257.9292	-145.0255
_cons	3216.482	25.82479	124.55	0.000	3165.866	3267.097
/sigma_u	348.1441	6.390242			335.8421	360.8968
/sigma_e	377.7638	3.929694			370.1397	385.5449
rho	.4592642	.0118089			.436201	.4824653

```
Likelihood-ratio test of sigma_u=0: chibar2(01)= 1146.40 Prob>=chibar2 = 0.000
```

In general, and as we can see from comparing the estimates for this model (given under "Level-2 covariates" in table 3.1) with the estimates from the null model, adding level-2 covariates will reduce mostly the level-2 variance. However, adding level-1 covariates can reduce both variances, as we can see by comparing the estimates for the above model with the full model. The reason is that many level-1 covariates vary both within and between clusters and can hence be decomposed as $x_{ij} = (x_{ij} - \overline{x}_{\cdot j}) + \overline{x}_{\cdot j}$, where $x_{ij} - \overline{x}_{\cdot j}$ only varies at level-1 and $\overline{x}_{\cdot j}$ only varies at level-2. Note that the estimated level-2 variance can increase when adding level-1 covariates, potentially producing a negative R_2^2.

Keep in mind that the coefficient of determination expresses to what extent the responses can be predicted from the covariates and not how appropriate the model is for the data. Indeed, a true model could very well have a large total residual variance.

For the intraclass correlation, we see that the unconditional intraclass correlation for the null model without covariates is estimated as 0.487. This reduces to a conditional or residual intraclass correlation of 0.459 when level-2 covariates are added and to 0.455 when all remaining covariates are added. The conditional intraclass correlation can also be larger than the unconditional intraclass correlation if the estimated level-1 variance decreases more than the level-2 variance does when covariates are added.

3.6 Hypothesis tests and confidence intervals

3.6.1 Hypothesis tests for regression coefficients

In ordinary linear regression, we use t tests for testing hypotheses regarding individual regression parameters and F tests for joint hypotheses regarding several regression parameters. Under the null hypothesis, these test statistics have t distributions and F distributions, respectively, with appropriate degrees of freedom in finite samples.

Because finite sample results are not readily available in the multilevel setting, hypothesis testing typically proceeds based on likelihood-ratio or Wald test statistics with asymptotic (large sample) $\chi^2(q)$ null distributions, with the number of restrictions q imposed by the null hypothesis as degrees of freedom. The Wald test and the less commonly used score test and Lagrange multiplier test are approximations of the likelihood-ratio test (see display 2.1). All three tests are asymptotically equivalent to each other but may produce different conclusions in small samples.

Hypothesis tests for individual regression coefficients

The most commonly used hypothesis test concerns an individual regression parameter, say, β_2, with null hypothesis

$$H_0\text{: } \beta_2 = 0$$

versus the two-sided alternative

$$H_a\text{: } \beta_2 \neq 0$$

The Wald statistic for testing the null hypothesis is

$$w \;=\; \left(\frac{\widehat{\beta}_2}{\widehat{\mathrm{SE}}(\widehat{\beta}_2)} \right)^2$$

which has an asymptotic $\chi^2(1)$ distribution under the null hypothesis, because the null hypothesis imposes one restriction. In practice, the test statistic

$$z \;=\; \frac{\widehat{\beta}_2}{\widehat{\mathrm{SE}}(\widehat{\beta}_2)}$$

is usually used. It has an asymptotic standard normal null distribution [because its square has a $\chi^2(1)$ distribution].

The z statistic is reported as `z` in the Stata output. For instance, in the output from `xtmixed` on page 134, the z statistic for the regression parameter of smoking is -12.02, which gives a two-sided p-value of less than 0.001. If robust standard errors are used in Stata, Wald tests and Wald-based confidence intervals will be based on them.

A likelihood-ratio test (described below) is less commonly used for testing individual regression parameters.

Joint hypothesis tests for several regression coefficients

Consider now the null hypothesis that the regression coefficients of two covariates x_{2ij} and x_{3ij} are both zero,

$$H_0\colon \beta_2 = \beta_3 = 0$$

versus the alternative hypothesis that at least one of the parameters is nonzero. For example, for the smoking and birthweight application, we may want to test the null hypothesis that the quality of prenatal care (as measured by the Kessner index) makes no difference to birthweight (controlling for the other covariates), where the Kessner index is represented by two dummy variables, `kessner2` and `kessner3`.

Let $\widehat{\beta}_2$ and $\widehat{\beta}_3$ be ML estimates from the model including the covariates x_{2ij} and x_{3ij}. The Wald statistic can be expressed as

$$\begin{aligned} w &= (\widehat{\beta}_2, \widehat{\beta}_3) \begin{Bmatrix} \widehat{\mathrm{SE}}(\widehat{\beta}_2)^2 & \widehat{\mathrm{Cor}}(\widehat{\beta}_2, \widehat{\beta}_3)\, \widehat{\mathrm{SE}}(\widehat{\beta}_2)\, \widehat{\mathrm{SE}}(\widehat{\beta}_3) \\ \widehat{\mathrm{Cor}}(\widehat{\beta}_2, \widehat{\beta}_3)\, \widehat{\mathrm{SE}}(\widehat{\beta}_2)\, \widehat{\mathrm{SE}}(\widehat{\beta}_3) & \widehat{\mathrm{SE}}(\widehat{\beta}_3)^2 \end{Bmatrix}^{-1} (\widehat{\beta}_2, \widehat{\beta}_3)' \\ &= \frac{1}{1 - \widehat{\mathrm{Cor}}(\widehat{\beta}_2, \widehat{\beta}_3)^2} \left\{ \left(\frac{\widehat{\beta}_2}{\widehat{\mathrm{SE}}(\widehat{\beta}_2)} \right)^2 + \left(\frac{\widehat{\beta}_3}{\widehat{\mathrm{SE}}(\widehat{\beta}_3)} \right)^2 - 2\, \widehat{\mathrm{Cor}}(\widehat{\beta}_2, \widehat{\beta}_3)\, \frac{\widehat{\beta}_2}{\widehat{\mathrm{SE}}(\widehat{\beta}_2)}\, \frac{\widehat{\beta}_3}{\widehat{\mathrm{SE}}(\widehat{\beta}_3)} \right\} \end{aligned}$$

and has an asymptotic $\chi^2(2)$ null distribution because the null hypothesis imposes two restrictions. We see that the Wald statistic for the joint null hypothesis H_0: $\beta_2 = \beta_3 = 0$ decomposes into the sum of the Wald statistics for $H_0\colon\ \beta_2 = 0$ and $H_0\colon\ \beta_3 = 0$ if $\widehat{\mathrm{Cor}}(\widehat{\beta}_2, \widehat{\beta}_3) = 0$, which would be the case if $\mathrm{Cor}(x_{2i}, x_{3i}) = 0$.

We can also test the simultaneous hypothesis that three or more regression coefficients are all zero, but the expression for the Wald statistic becomes convoluted unless matrix expressions are used.

The Wald test for the null hypothesis that coefficients of the dummy variables `kessner2` and `kessner3` are both zero can be performed by using the `testparm` command:

```
. quietly xtset momid
. quietly xtreg birwt smoke male mage hsgrad somecoll collgrad married
> black kessner2 kessner3 novisit pretri2 pretri3, mle
. testparm kessner2 kessner3
 ( 1)  [birwt]kessner2 = 0
 ( 2)  [birwt]kessner3 = 0
           chi2(  2) =   26.94
         Prob > chi2 =    0.0000
```

We reject the null hypothesis at the 5% level with $w = 26.94$, degrees of freedom (df) $= 2$, $p < 0.001$. A more robust version of the test is obtained by specifying robust standard errors in the estimation command by using the `vce(robust)` option for `xtmixed, mle` or `xtreg, re`.

The analogous likelihood-ratio test statistic is

$$L = 2(l_1 - l_0)$$

where l_1 and l_0 are now the maximized log likelihoods for the models including and excluding both `kessner2` and `kessner3`, respectively. Under the null hypothesis, the likelihood-ratio statistic also has an asymptotic $\chi^2(2)$ null distribution.

A likelihood-ratio test of the null hypothesis that the coefficients of the dummy variables `kessner2` and `kessner3` are both zero can be performed by using the `lrtest` command:

```
. estimates store full
. quietly xtset momid
. quietly xtreg birwt smoke male mage hsgrad somecoll collgrad married black
> novisit pretri2 pretri3, mle
. lrtest full .
Likelihood-ratio test                                 LR chi2(2)  =     26.90
(Assumption: . nested in full)                        Prob > chi2 =    0.0000
```

Note that likelihood-ratio tests for regression coefficients cannot be based on log likelihoods from REML estimation.

Sometimes it is required to test hypotheses regarding linear combinations of coefficients, as demonstrated in section 1.8. In section 3.7.4, we will encounter a special case of this when testing the null hypothesis that two regression coefficients are equal, or in other words that the difference between the coefficients is 0, a simple example of a *contrast*. Wald tests of such hypotheses can be performed in Stata using the `lincom` command.

3.6.2 Predicted means and confidence intervals

We can use the `margins` command (introduced in Stata 11) to obtain predicted means for mothers and pregnancies with particular covariate values, such as education and smoking status. If we evaluate the other covariates at particular values of our choice, we obtain adjusted means, called *adjusted predictions* in Stata. Alternatively, we can obtain what Stata calls *predictive margins*, the mean birthweight we would obtain if the distributions of the other covariates were the same for all combinations of education and smoking status. As mentioned in section 1.7, in linear models, predictive margins can be obtained by evaluating the other covariates at their means.

The `margins` command works only if factor notation is used for the categorical variables for which we want to make predictions (education and smoking status). We therefore define a categorical variable for level of education,

```
. generate education = hsgrad*1 + somecoll*2 + collgrad*3
```

and refit the model, declaring `education` and `smoke` as categorical variables using `i.education` and `i.smoke`:

```
. quietly xtset momid
. quietly xtreg birwt i.smoke male mage i.education married black
> kessner2 kessner3 novisit pretri2 pretri3, mle
```

We then use the `margins` command to obtain predictive margins for all combinations of `smoke` and `education`:

```
. margins i.smoke#i.education

Predictive margins                                Number of obs   =       8604
Model VCE    : OIM
Expression   : Linear prediction, predict()
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
smoke# education						
0 0	3430.916	23.4495	146.31	0.000	3384.956	3476.876
0 1	3487.763	13.22835	263.66	0.000	3461.836	3513.69
0 2	3511.602	14.11543	248.78	0.000	3483.936	3539.268
0 3	3521.749	12.16946	289.39	0.000	3497.897	3545.601
1 0	3212.587	25.18765	127.55	0.000	3163.22	3261.954
1 1	3269.434	19.62569	166.59	0.000	3230.969	3307.9
1 2	3293.273	21.13939	155.79	0.000	3251.841	3334.706
1 3	3303.42	21.2282	155.61	0.000	3261.813	3345.026

Here the interaction syntax `i.smoke#i.education` was used to specify that we want predictions for all combinations of the values of `smoke` and `education`. The standard errors of the predictions are based on the estimated standard errors from the random-intercept model.

We can plot these predictive margins using `marginsplot` (available from Stata 12),

```
. marginsplot, xdimension(education)
```

which gives the graph in figure 3.2.

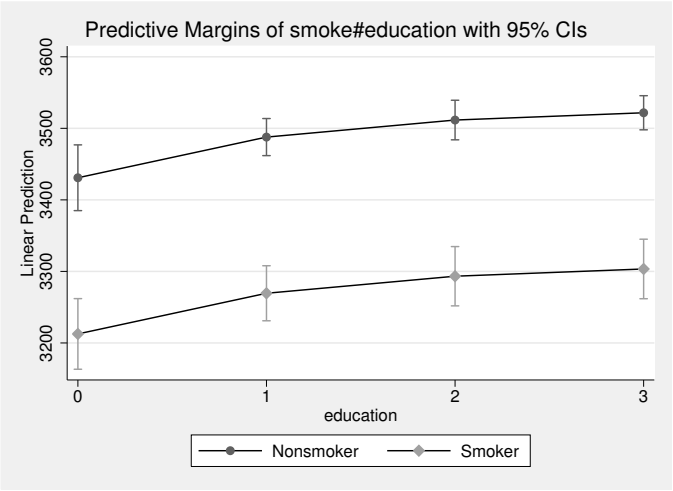


Figure 3.2: Predictive margins and confidence intervals for birthweight data

3.6.3 Hypothesis test for random-intercept variance

Consider testing the null hypothesis that the between-cluster variance is zero:

$$H_0\text{: } \psi = 0 \quad \text{against} \quad H_a\text{: } \psi > 0$$

This null hypothesis is equivalent to the hypothesis that $\zeta_j = 0$ or that there is no random intercept in the model. If this is true, a multilevel model is not required.

Likelihood-ratio tests are typically used with the test statistic,

$$L \;=\; 2(l_1 - l_0)$$

where l_1 is the maximized log likelihood for the random-intercept model (which includes ζ_j) and l_0 is the maximized log likelihood for an ordinary regression model (without ζ_j). A correct p-value is obtained by dividing the naïve p-value based on the $\chi^2(1)$ by 2, as was discussed in more detail in section 2.6.2. The result for the correct test procedure is provided in the last row of output from `xtreg` and `xtmixed`, giving $L = 1109$ and $p < 0.001$ for the full model.

Alternative tests for the random-intercept variance were described in section 2.6.2.

3.7 Between and within effects of level-1 covariates

We now turn to the estimated regression coefficients for the random-intercept model with covariates. For births where the mother smoked during the pregnancy, the population mean birthweight is estimated to be 218 grams lower than for births where the mother did not smoke, holding all other covariates constant. This estimate represents

either a comparison between children of *different* mothers, one of whom smoked during the pregnancy and one of whom did not (holding all other covariates constant), or a comparison between children of the *same* mother, where the mother smoked during one pregnancy and not during the other (holding all other covariates constant). This is neither purely a between-mother comparison (because smoking status can change between pregnancies) nor purely a within-mother comparison (because some mothers either smoke or do not smoke during *all* their pregnancies).

3.7.1 Between-mother effects

If we wanted to obtain purely between-mother effects of the covariates, we could average the response and covariates for each mother j over children i and perform the regression on the resulting means:

$$\frac{1}{n_j}\sum_{i=1}^{n_j} y_{ij} \quad = \quad \frac{1}{n_j}\sum_{i=1}^{n_j}(\beta_1 + \beta_2 x_{2ij} + \cdots + \beta_p x_{pij} + \zeta_j + \epsilon_{ij})$$

or

$$\overline{y}_{\cdot j} \quad = \quad \beta_1 + \beta_2 \overline{x}_{2\cdot j} + \cdots + \beta_p \overline{x}_{p\cdot j} + \zeta_j + \overline{\epsilon}_{\cdot j} \tag{3.11}$$

Here $\overline{y}_{\cdot j}$ is the mean response for mother j, $\overline{x}_{2\cdot j}$ is the mean of the first covariate `smoke` for mother j, etc., and $\overline{\epsilon}_{\cdot j}$ is the mean of the level-1 residuals in the original regression model (3.2). The error term $\zeta_j + \overline{\epsilon}_{\cdot j}$ has population mean zero, $E(\zeta_j + \overline{\epsilon}_{\cdot j}) = 0$, and heteroskedastic variance $\mathrm{Var}(\zeta_j + \overline{\epsilon}_{\cdot j}) = \psi + \theta/n_j$, unless the data are balanced with $n_j = n$. Any information on the regression coefficients from within-mother variability is eliminated, and the coefficients of covariates that do not vary between mothers are absorbed by the intercept.

Ordinary least-squares (OLS) estimates[1] $\widehat{\boldsymbol{\beta}}^B$ of the parameters $\boldsymbol{\beta}$ in the between regression (3.11) whose corresponding covariates vary between mothers (here all covariates) can be obtained using `xtreg` with the `be` (between) option:

1. For unbalanced data ($n_j \neq n$), *weighted* least-squares (WLS) estimates can be obtained using the `wls` option. Then the cluster weights $1/(\widehat{\psi} + \widehat{\theta}/n_j)$ are used, where $\widehat{\psi}$ and $\widehat{\theta}$ are obtained from OLS. OLS still produces consistent albeit inefficient estimators of the regression coefficients but inconsistent estimators of the corresponding standard errors under heteroskedasticity. We use OLS to estimate the between effects here because this estimator will be used when we spell out the relationships among different estimators later in the chapter.

```
. quietly xtset momid

. xtreg birwt smoke male mage hsgrad somecoll collgrad married black kessner2
> kessner3 novisit pretri2 pretri3, be

Between regression (regression on group means)  Number of obs      =      8604
Group variable: momid                           Number of groups   =      3978

R-sq:  within  = 0.0299                         Obs per group: min =         2
       between = 0.1168                                        avg =       2.2
       overall = 0.0949                                        max =         3

                                                F(13,3964)         =     40.31
sd(u_i + avg(e_i.))=  424.7306                  Prob > F           =    0.0000
```

birwt	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
smoke	-286.1476	23.22554	-12.32	0.000	-331.6828	-240.6125
male	104.9432	19.49531	5.38	0.000	66.72141	143.165
mage	4.398704	1.505448	2.92	0.003	1.447179	7.35023
hsgrad	58.80977	25.51424	2.30	0.021	8.787497	108.832
somecoll	85.07129	28.1348	3.02	0.003	29.91126	140.2313
collgrad	99.87509	29.35324	3.40	0.001	42.32622	157.424
married	41.91268	26.10719	1.61	0.108	-9.272101	93.09745
black	-218.4045	28.57844	-7.64	0.000	-274.4344	-162.3747
kessner2	-101.4931	37.65605	-2.70	0.007	-175.3202	-27.66607
kessner3	-201.9599	79.28821	-2.55	0.011	-357.4094	-46.51042
novisit	-51.02733	124.2073	-0.41	0.681	-294.5435	192.4889
pretri2	125.4776	44.72006	2.81	0.005	37.80114	213.1541
pretri3	241.1201	100.6567	2.40	0.017	43.77638	438.4637
_cons	3241.45	46.15955	70.22	0.000	3150.951	3331.948

The estimates of the between-mother effects are also shown under "Between effects" in table 3.2. The estimated coefficient $\widehat{\beta}_2^B$ of `smoke` of -286 grams is considerably larger, in absolute value, than the ML estimate $\widehat{\beta}_2^{\mathrm{ML}}$ for the random-intercept model of -218 grams, shown under "Random effects" in table 3.2. The between-effect can be interpreted as the difference in mean birthweight comparing two different mothers, one of whom smoked during pregnancy while the other did not, given the other covariates.

Table 3.2: Random-, between-, and within-effects estimates for smoking data (in grams); MLE of random-intercept model (3.2), OLS of (3.11), OLS of (3.12), and MLE of random-intercept model including all cluster means

	Random effects $\widehat{\boldsymbol{\beta}}^{\mathrm{ML}}$		Between effects $\widehat{\boldsymbol{\beta}}^{B}$		Within effects $\widehat{\boldsymbol{\beta}}^{W}$		Random effects +clust. mean $\widehat{\boldsymbol{\beta}}^{\mathrm{ML}}$	
	Est	(SE)	Est	(SE)	Est	(SE)	Est	(SE)
Fixed part								
β_1 [_cons]	3,117	(41)	3,241	(46)	2,768	(86)	3,238	(46)
β_2 [smoke]	−218	(18)	−286	(23)	−105	(29)	−105	(29)
β_3 [male]	121	(10)	105	(19)	126	(11)	126	(11)
β_4 [mage]	8	(1)	4	(2)	23	(3)	23	(3)
β_5 [hsgrad]	57	(25)	59	(26)			56	(25)
β_6 [somecoll]	81	(27)	85	(28)			83	(28)
β_7 [collgrad]	91	(28)	100	(29)			98	(29)
β_8 [married]	50	(26)	42	(26)			42	(26)
β_9 [black]	−211	(28)	−218	(29)			−219	(28)
β_{10} [kessner2]	−93	(20)	−101	(38)	−91	(23)	−91	(23)
β_{11} [kessner3]	−151	(41)	−202	(79)	−128	(48)	−128	(48)
β_{12} [novisit]	−30	(66)	−51	(124)	−5	(78)	−5	(78)
β_{13} [pretri2]	93	(23)	125	(45)	81	(27)	81	(27)
β_{14} [pretri3]	179	(52)	241	(101)	153	(60)	153	(60)
β_{15} [m_smok]							−183	(37)
β_{16} [m_male]							−20	(22)
β_{17} [m_mage]							−18	(3)
β_{18} [m_kessner2]							−9	(44)
β_{19} [m_kessner3]							−79	(92)
β_{20} [m_novisit]							−38	(146)
β_{21} [m_pretri2]							45	(52)
β_{21} [m_pretri3]							96	(117)
Random part								
$\sqrt{\psi}$	339				440 [a]		338	
$\sqrt{\theta}$	371				369 [a]		369	

[a] Not parameter estimates, but standard deviations of estimates $\widehat{\epsilon}_{ij}$ and $\widehat{\alpha}_j$.

3.7.2 Within-mother effects

If we wanted to obtain purely within-mother effects, we could subtract the between-mother regression (3.11) from the original model (3.2) to obtain the within model:

$$y_{ij} - \overline{y}_{\cdot j} \;=\; \beta_2(x_{2ij} - \overline{x}_{2\cdot j}) + \cdots + \beta_p(x_{pij} - \overline{x}_{p\cdot j}) + \epsilon_{ij} - \overline{\epsilon}_{\cdot j} \tag{3.12}$$

Here the response and all covariates have simply been centered around their respective cluster means. The error term $\epsilon_{ij} - \bar{\epsilon}_{\cdot j}$ has population mean zero, $E(\epsilon_{ij} - \bar{\epsilon}_{\cdot j}) = 0$, and heteroskedastic variance $\text{Var}(\epsilon_{ij} - \bar{\epsilon}_{\cdot j}) = \theta(1 - 1/n_j)$, unless the data are balanced. Covariates that do not vary within clusters drop out of the equation because the mean-centered covariate is zero. Importantly, this also includes the random intercept ζ_j.

OLS can be used to estimate the within effects $\boldsymbol{\beta}^W$ in (3.12). The standard errors of the estimated coefficients of covariates that vary little within clusters will be large because estimation is solely based on the within-cluster variability.

Identical estimates of within-mother effects can be obtained by replacing the random intercept ζ_j for each mother in the original model in (3.2) by a fixed intercept α_j. This could be accomplished by using dummy variables for each mother and omitting the intercept β_1 so that α_j represents the total intercept for mother j, previously represented by $\beta_1 + \zeta_j$. Letting d_{kj} be the dummy variable for the kth mother, $(k = 1, \ldots, 3{,}978)$, the fixed-effects model can be written as

$$\begin{aligned} y_{ij} &= \beta_2 x_{2ij} + \cdots + \beta_p x_{pij} + \sum_{k=1}^{3{,}978} d_{kj}\alpha_k + \epsilon_{ij} \\ &= \beta_2 x_{2ij} + \cdots + \beta_p x_{pij} + \alpha_j + \epsilon_{ij} \end{aligned} \tag{3.13}$$

and estimated by OLS. In this model, all mother-specific effects are accommodated by α_j, leaving only within-mother variation to be explained by covariates. The coefficients of level-2 covariates can therefore not be estimated, which can also be seen by considering that the set of dummy variables is collinear with any such covariates. In practice, it is more convenient to eliminate the intercepts by mean-centering all covariates, as in (3.12), instead of estimating 3,978 intercepts.

The within estimates $\widehat{\boldsymbol{\beta}}^W$ for the coefficients of covariates that vary within mothers can be obtained using `xtreg` with the `fe` (fixed effects) option:[2]

2. Here the overall constant (next to `_cons`) is obtained by adding the overall means $\overline{y}_{\cdot\cdot}$, $\overline{x}_{2\cdot\cdot}$, etc., and $\overline{\alpha}_{\cdot} + \overline{\epsilon}_{\cdot\cdot}$ back onto the corresponding differences:

$$y_{ij} - \overline{y}_{\cdot j} + \overline{y}_{\cdot\cdot} = \beta_1 + \beta_2(x_{2ij} - \overline{x}_{2\cdot j} + \overline{x}_{2\cdot\cdot}) + \cdots + \beta_p(x_{pij} - \overline{x}_{p\cdot j} + \overline{x}_{p\cdot\cdot}) + \epsilon_{ij} - \overline{\epsilon}_{\cdot j} + \overline{\alpha}_{\cdot} + \overline{\epsilon}_{\cdot\cdot}$$

```
. quietly xtset momid

. xtreg birwt smoke male mage kessner2 kessner3 novisit pretri2 pretri3, fe
Fixed-effects (within) regression               Number of obs      =      8604
Group variable: momid                           Number of groups   =      3978

R-sq:  within  = 0.0465                         Obs per group: min =         2
       between = 0.0557                                        avg =       2.2
       overall = 0.0546                                        max =         3

                                                F(8,4618)          =     28.12
corr(u_i, Xb)  = -0.0733                        Prob > F           =    0.0000

------------------------------------------------------------------------------
       birwt |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       smoke |  -104.5494   29.10075    -3.59   0.000    -161.6007   -47.49798
        male |   125.6355   10.92272    11.50   0.000     104.2217    147.0492
       mage |   23.15832   3.006667     7.70   0.000     17.26382    29.05282
    kessner2 |  -91.49483   23.48914    -3.90   0.000    -137.5448    -45.4449
    kessner3 |   -128.091   47.79636    -2.68   0.007    -221.7947   -34.38731
     novisit |  -4.805898    77.7721    -0.06   0.951    -157.2764    147.6646
     pretri2 |   81.29039   27.04974     3.01   0.003     28.25998    134.3208
     pretri3 |    153.059   60.08453     2.55   0.011     35.26462    270.8534
       _cons |   2767.504   86.23602    32.09   0.000      2598.44    2936.567
-------------+----------------------------------------------------------------
     sigma_u |  440.05052
     sigma_e |  368.91787
         rho |  .58725545   (fraction of variance due to u_i)
------------------------------------------------------------------------------
F test that all u_i=0:     F(3977, 4618) =     2.90          Prob > F = 0.0000
```

The estimates of the within-mother effects were also reported under "Within effects" in table 3.2. The estimated coefficient $\widehat{\beta}_2^W$ for `smoke` of -105 grams is dramatically smaller, in absolute value, than the estimate $\widehat{\beta}_2^R$ of -218 grams for the random-intercept model. The within-effect can be interpreted as the difference in mean birthweight between births for a given mother who changes smoking status between pregnancies, given the level-1 covariates. Level-2 covariates, whether observed or unobserved, are implicitly controlled for because mother is held constant in the comparison, along with all her characteristics. Therefore each mother truly serves as her own control.

In the output, `sigma_u` and `sigma_e` are standard deviations of estimated level-2 and level-1 residuals, $\widehat{\alpha}_j = \overline{y}_{\cdot j} - (\widehat{\beta}_1 + \widehat{\beta}_2\overline{x}_{2\cdot j} + \cdots + \widehat{\beta}_p\overline{x}_{p\cdot j})$ and $\widehat{\epsilon}_{ij} = y_{ij} - \widehat{\alpha}_j - (\widehat{\beta}_1 + \widehat{\beta}_2 x_{2ij} + \cdots + \widehat{\beta}_p x_{pij})$, the latter standard deviation adjusted for the number of estimated means.

3.7.3 ❖ Relations among within estimator, between estimator, and estimator for random-intercept model

We now show that an estimator for the random-intercept model can be expressed as a weighted average of the within estimator and the between estimator.

The original random-intercept model in (3.2) implicitly assumes that the between and within effects of the set of covariates that vary both between and within mothers are

identical because the between-mother model (3.11) and the within-mother model (3.12) derived from the random-intercepts model (3.2) have the same regression coefficients, $\boldsymbol{\beta} = (\beta_1, \beta_2, \ldots, \beta_p)'$. The estimators for the random-intercept model therefore use both within- and between-mother information. This can be seen explicitly for the feasible generalized least-squares (FGLS) estimator described in section 3.10.1 (obtained using `xtreg` with the `re` option), which is equivalent to the ML estimator in large samples. The relations among the estimators are most transparent for a single covariate x_{ij} with regression coefficient β_2 and balanced data $n_j = n$.

It can be shown that the sampling variance of the OLS between estimator $\widehat{\beta}_2^B$ can be consistently estimated as

$$\widehat{\mathrm{SE}}(\widehat{\beta}_2^B)^2 \;=\; \frac{\widehat{\mathrm{Var}}(\zeta_j + \overline{\epsilon}_{\cdot j})}{(J-1)s_{xB}^2} = \frac{\widehat{\psi} + \widehat{\theta}/n}{(J-1)s_{xB}^2}$$

where $\widehat{\mathrm{Var}}(\zeta_j + \overline{\epsilon}_{\cdot j})$ is the mean squared error from the between regression in (3.11) and $s_{xB}^2 = \frac{1}{J-1}\sum_{j=1}^{J}(\overline{x}_{\cdot j} - \overline{x}_{\cdot\cdot})^2$ is the between variance of x_{ij}, given in section 3.2.1. The sampling variance of the OLS within estimator $\widehat{\beta}_2^W$ can be consistently estimated as

$$\widehat{\mathrm{SE}}(\widehat{\beta}_2^W)^2 \;=\; \frac{\frac{Jn-1}{J(n-1)-1}\widehat{\mathrm{Var}}(\epsilon_{ij} - \overline{\epsilon}_{\cdot j})}{(Jn-1)s_{xW}^2} = \frac{\widehat{\theta}(1-1/n)}{\{J(n-1)-1\}s_{xW}^2} \tag{3.14}$$

where $\widehat{\mathrm{Var}}(\epsilon_{ij} - \overline{\epsilon}_{\cdot j})$ is the mean squared error from the within regression in (3.12) and $s_{xW}^2 = \frac{1}{Jn-1}\sum_{j=1}^{J}\sum_{i=1}^{n}(x_{ij} - \overline{x}_{\cdot j})^2$ is the within variance of x_{ij}, given in section 3.2.1. The term $\frac{Jn-1}{J(n-1)-1}$ is necessary in (3.14) because of the loss of J degrees of freedom due to mean-centering. The numerator after the first equality is the square of `sigma_e` reported by `xtreg` with the `fe` option.

The FGLS estimator $\widehat{\beta}_2^{\mathrm{FGLS}}$ for the random-intercept model can then be written as

$$\widehat{\beta}_2^{\mathrm{FGLS}} \;=\; (1-\widehat{\omega})\widehat{\beta}_2^B \;+\; \widehat{\omega}\widehat{\beta}_2^W$$

where

$$\widehat{\omega} \;=\; \frac{\widehat{\mathrm{SE}}(\widehat{\beta}_2^B)^2}{\widehat{\mathrm{SE}}(\widehat{\beta}_2^B)^2 + \widehat{\mathrm{SE}}(\widehat{\beta}_2^W)^2} \qquad \text{and} \qquad 1-\widehat{\omega} \;=\; \frac{\widehat{\mathrm{SE}}(\widehat{\beta}_2^W)^2}{\widehat{\mathrm{SE}}(\widehat{\beta}_2^B)^2 + \widehat{\mathrm{SE}}(\widehat{\beta}_2^W)^2}$$

We see that the FGLS estimator $\widehat{\beta}_2^{\mathrm{FGLS}}$ for the random-intercept model can be expressed as a weighted average of the between estimator $\widehat{\beta}_2^B$ and the within estimator $\widehat{\beta}_2^W$, where the weight of each estimator decreases as its standard error (imprecision) increases.

$\widehat{\beta}_2^{\mathrm{FGLS}}$ approaches the within estimator $\widehat{\beta}_2^W$ when $\widehat{\omega}$ approaches 1, that is, when the within standard error is much smaller than the between standard error. This happens when n becomes large, or $\widehat{\theta}$ becomes small, or $\widehat{\psi}$ becomes large, or s_{xB} becomes small.

$\widehat{\beta}_2^{\text{FGLS}}$ approaches the between estimator $\widehat{\beta}_2^B$ when $\widehat{\omega}$ approaches 0, that is, when the between standard error is much smaller than the within standard error. This happens when n becomes small, or $\widehat{\theta}$ becomes large, or $\widehat{\psi}$ becomes small, or s_{xW} becomes small. If $\widehat{\psi} = 0$, the FGLS estimator reduces to the OLS estimator, known as the pooled OLS estimator because there are several observations per cluster.

Although $\widehat{\beta}_2^{\text{FGLS}}$, $\widehat{\beta}_2^B$, and $\widehat{\beta}_2^W$ are all estimators of the same parameter β_2, the FGLS estimator $\widehat{\beta}_2^{\text{FGLS}}$ is more efficient (varies less in repeated samples) than the other estimators when the between effects equal the within effects because it exploits both within- and between-mother information.

3.7.4 Level-2 endogeneity and cluster-level confounding

The estimated between effect $\widehat{\beta}_2^B$ based on (3.11) may differ from the estimated within-effect $\widehat{\beta}_2^W$ from (3.12) because of omitted mother-specific explanatory variables that affect both $\overline{x}_{2\cdot j}$ and the mother-specific residual ζ_j and hence the mean response $\overline{y}_{\cdot j}$, given the included explanatory variables.

As discussed by Abrevaya (2006), mothers who smoke during their pregnancy may also adopt other behaviors such as drinking and poor nutritional intake. They are also likely to have lower socioeconomic status. The between-mother effect of smoking is thus confounded with the effects of these omitted level-2 covariates. Because the confounders adversely affect birthweight and have not been adequately controlled for, the between-effect is likely to be an overestimate of the true effect (in absolute value). We thus have cluster-level confounding or cluster-level omitted-variable bias. In contrast, each mother serves as her own control for the within estimate, so all mother-specific explanatory variables have been held constant. Indeed, this was the reason why Abrevaya (2006) constructed the matched dataset: to get closer to the causal effect of smoking by using within-mother estimates.

To illustrate the idea of different between and within effects, figure 3.3 shows data for hypothetical clusters and a continuous covariate where the between-cluster effect (slope of dashed line) is positive and the within-cluster effect (slope of dotted lines) is negative. Here the hollow circles represent the observed data, and the solid circles represent cluster means.

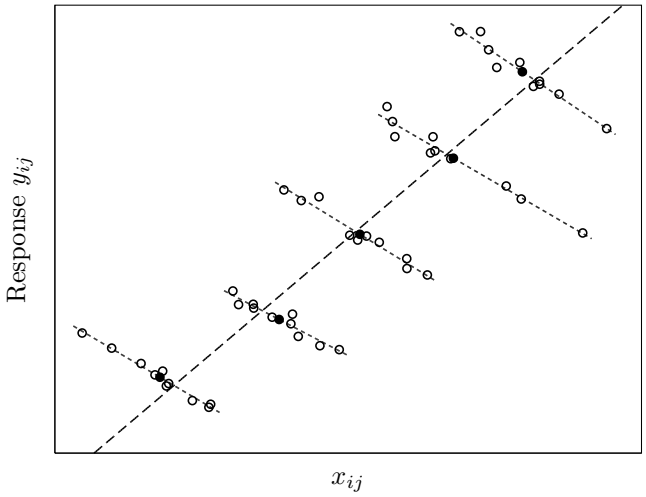


Figure 3.3: Illustration of different within-cluster and between-cluster effects of a covariate

The problem of cluster-level confounding can be described as correlation between the level-1 variable of interest—such as smoking x_{2ij}—and the random intercept ζ_j, which represents the effects of omitted level-2 covariates. In the figure, we see that clusters with larger (mean) values of x_{ij} tend to have larger (mean) values of y_{ij} because they have larger random intercepts. This problem is often referred to as *endogeneity* in econometrics. Specifically, the level-2 exogeneity assumption, discussed in section 3.3.2 is violated.

Cluster-level confounding can also be responsible for the *ecological fallacy*. This fallacy occurs when using aggregated data (cluster means, as in `xtreg, be`) and interpreting the estimated between effects as within effects. The *atomistic fallacy* occurs when ignoring clustering (by using ordinary regression) and interpreting the effects as between effects.

Figure 3.4 illustrates relationships between within and between effects where $\beta_2^W = \beta_2^B$ (left panel) and $\beta_2^W < \beta_2^B$ (right panel). The cluster-specific regression lines are shown for two clusters (solid and dashed lines for clusters 1 and 2, respectively) having the same value of the random intercept ζ_j but nonoverlapping ranges of x_{ij}. β_2^W, the slope of the cluster-specific lines, shown for cluster 1, is the within effect. The bullets represent the cluster means $(\overline{x}_{\cdot 1},\ \overline{y}_{\cdot 1})$ for cluster 1 and $(\overline{x}_{\cdot 2},\ \overline{y}_{\cdot 2})$ for cluster 2. The between effect β_2^B is the increase in the cluster mean of y_{ij} when the cluster mean of x_{ij} increases one unit (here shown for a change from 1.5 to 2.5).

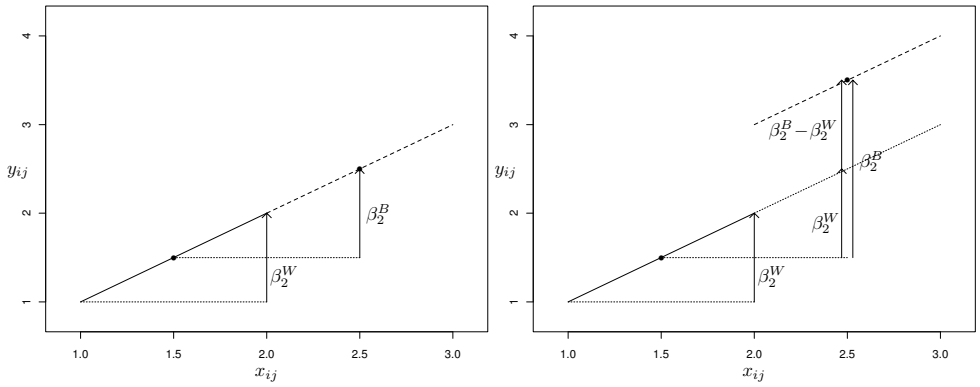


Figure 3.4: Illustration of different within and between effects for two clusters having the same value of ζ_j (β_2^W is the within effect and β_2^B is the between effect); in the left panel, $\beta_2^W = \beta_2^B$, whereas $\beta_2^W < \beta_2^B$ in the right panel

Let the clusters be schools with y_{ij} representing an achievement score for student i in school j and with x_{ij} representing the socioeconomic status (SES) of the student. In the left panel, the difference in school mean achievement is purely due to a *compositional effect*; within the schools, higher SES is associated with greater achievement, which completely explains why the school with greater mean SES has greater mean achievement. In the right panel, the compositional effect does not completely explain the difference in mean achievement between the schools. There is an additional, so-called *contextual effect* $\beta_2^B - \beta_2^W$, an additional increase of the second school's mean $\overline{y}_{\cdot j}$ after allowing for the within (or compositional) effect β_2^W. The contextual effect could be due to nonrandom assignment of high SES students to better schools (confounding), as well as direct peer effects.

It is common to include only the cluster-mean centered covariate in the model but not the cluster mean itself. However, as shown in figure 3.5, setting $\beta_2^B = 0$ makes the unrealistic assumption that the contextual effect equals the negative of the compositional effect. The original model that assumed equal between and within effects (no contextual effects) is no longer a special case if the cluster mean is omitted from the model.

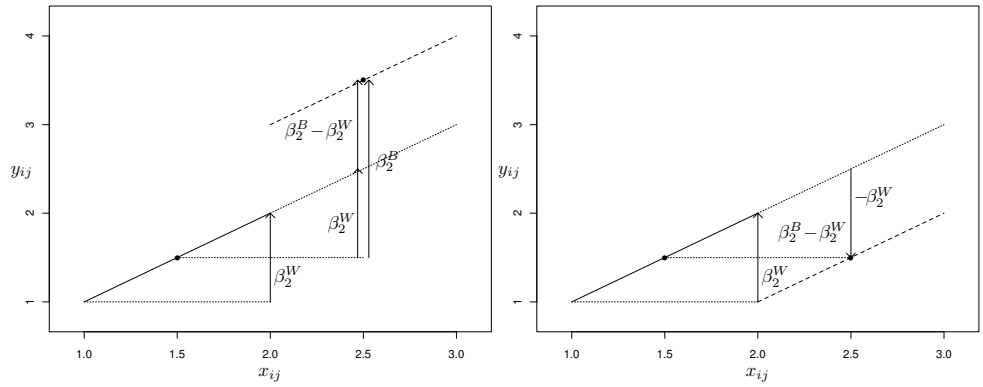


Figure 3.5: Illustration of assuming zero between effect for two clusters having the same value of ζ_j (β_2^W is the within effect and β_2^B is the between effect). The left panel is the same as the right panel of figure 3.4 with $\beta_2^W < \beta_2^B$ whereas in the right panel $\beta_2^B = 0$.

Including the cluster-mean centered covariate only (and not the cluster mean) is likely to lead to cluster-level confounding for other cluster-level covariates. For instance, including school-mean centered SES but not school-mean SES could have the consequence that the compositional effect is attributed to covariates correlated with school mean SES (due to selection effects), such as teacher qualifications. If students with high mean SES tend to have more highly educated teachers, the effect of teacher qualifications would then be overestimated due to confounding with SES. Only purely within-school covariates, such as other school-mean centered covariates and perhaps gender, have thus been controlled for SES.

3.7.5 Allowing for different within and between effects

We can easily relax the assumption that the between and within effects are the same for a particular covariate, say, x_{2ij}, by using the model

$$y_{ij} = \beta_1 + \beta_2^W(x_{2ij} - \overline{x}_{2\cdot j}) + \beta_2^B\overline{x}_{2\cdot j} + \beta_3 x_{3ij} + \cdots + \beta_p x_{pij} + \zeta_j + \epsilon_{ij} \quad (3.15)$$

which collapses to the original random-intercept model in (3.2) if $\beta_2^W = \beta_2^B = \beta_2$. The deviation from the cluster mean of smoking $x_{2ij} - \overline{x}_{2\cdot j}$ is uncorrelated with ζ_j because it does not vary between clusters (and ζ_j does not vary within clusters). We can also view the above model as relaxing the assumption that the random intercept is uncorrelated with x_{2ij} if we think of $\beta_2^B\overline{x}_{2\cdot j} + \zeta_j$ as the random intercept.

We do not need to subtract the cluster mean $\overline{x}_{2\cdot j}$ from x_{2ij} as long as we include the cluster mean in the model, because

$$\begin{aligned} y_{ij} &= \beta_1 + \beta_2^W(x_{2ij} - \overline{x}_{2\cdot j}) + \beta_2^B\overline{x}_{2\cdot j} + \beta_3 x_{3ij} + \cdots + \beta_p x_{pij} + \zeta_j + \epsilon_{ij} \\ &= \beta_1 + \beta_2^W x_{2ij} + (\beta_2^B - \beta_2^W)\overline{x}_{2\cdot j} + \beta_3 x_{3ij} + \cdots + \beta_p x_{pij} + \zeta_j + \epsilon_{ij} \end{aligned} \quad (3.16)$$

Whether x_{2ij} is cluster-mean centered affects only the interpretation of the coefficient of the cluster mean $\overline{x}_{2\cdot j}$. If x_{2ij} is cluster-mean centered, as in the first line of (3.16), the coefficient of the cluster mean represents the between effect. If x_{2ij} is not cluster-mean centered, as in the second line of (3.16), the coefficient represents the difference in between and within effects.

We will now fit (3.15) with the cluster mean of `smoke` (the proportion of pregnancies in which the mother smokes), as well as the child-specific deviation from the cluster mean of `smoke` as covariates. These covariates are produced by the commands

```
. egen mn_smok = mean(smoke), by(momid)
. generate dev_smok = smoke - mn_smok
```

We fit the resulting random-intercept model by ML using

```
. quietly xtset momid
. xtreg birwt dev_smok mn_smok male mage hsgrad somecoll collgrad married
> black kessner2 kessner3 novisit pretri2 pretri3, mle
Random-effects ML regression                    Number of obs      =      8604
Group variable: momid                           Number of groups   =      3978
Random effects u_i ~ Gaussian                   Obs per group: min =         2
                                                               avg =       2.2
                                                               max =         3
                                                LR chi2(14)        =    684.32
Log likelihood  = -65133.327                    Prob > chi2        =    0.0000
```

birwt	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
dev_smok	-104.2331	29.18164	-3.57	0.000	-161.4281	-47.03815
mn_smok	-289.904	23.12917	-12.53	0.000	-335.2364	-244.5717
male	121.1497	9.543995	12.69	0.000	102.4438	139.8556
mage	8.191991	1.345733	6.09	0.000	5.554404	10.82958
hsgrad	43.10052	25.15802	1.71	0.087	-6.208299	92.40934
somecoll	62.74526	27.51558	2.28	0.023	8.815722	116.6748
collgrad	66.89807	28.37807	2.36	0.018	11.27806	122.5181
married	35.21194	25.6433	1.37	0.170	-15.04801	85.47189
black	-218.9694	28.28467	-7.74	0.000	-274.4064	-163.5325
kessner2	-92.03346	19.89661	-4.63	0.000	-131.0301	-53.03683
kessner3	-149.2771	40.77281	-3.66	0.000	-229.1903	-69.36383
novisit	-23.3923	65.60531	-0.36	0.721	-151.9763	105.1917
pretri2	92.33952	23.15722	3.99	0.000	46.95221	137.7268
pretri3	176.774	51.56358	3.43	0.001	75.7112	277.8367
_cons	3154.8	41.57504	75.88	0.000	3073.314	3236.285
/sigma_u	338.4563	6.27314			326.3818	350.9775
/sigma_e	370.0488	3.856608			362.5666	377.6853
rho	.4554982	.0119054			.4322541	.4788957

```
Likelihood-ratio test of sigma_u=0: chibar2(01)= 1115.22 Prob>=chibar2 = 0.000
```

The estimated between effect of smoking (coefficient of `mn_smok`) is $\widehat{\beta}_2^B = -290$ grams and is different from $\widehat{\beta}_2^W = -104$ grams, the estimated within effect of smoking (coefficient of `dev_smok`). Comparing two mothers, one of whom smoked, the expected difference in birthweight is estimated as 290 grams, given the other covariates. Com-

paring two births of the same mother, where she smoked during one of the pregnancies, the expected difference is estimated as 104 grams, controlling for the other covariates. We can formally test the null hypothesis that the corresponding coefficients are the same, H_0: $\beta_2^W - \beta_2^B = 0$, using the postestimation command `lincom`:

```
. lincom mn_smok - dev_smok
 ( 1)  - [birwt]dev_smok + [birwt]mn_smok = 0
```

birwt	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
(1)	-185.6709	37.21887	-4.99	0.000	-258.6186	-112.7233

There is strong evidence that the within effect of smoking differs from the between effect.

As pointed out previously, $x_{2ij} - \overline{x}_{2\cdot j}$ is correlated with x_{2ij} but uncorrelated with the random intercept ζ_j per construction. However, ζ_j may be correlated with another within-mother covariate x_{3ij} and the inconsistency in estimating the corresponding regression coefficient β_3 can be transmitted to the estimator for β_2^W.

To address this problem, we can follow Mundlak (1978) and include the cluster means of all within-mother covariates. If there is level-1 exogeneity (lack of correlation between covariates and ϵ_{ij}), inclusion of the cluster means ensures consistent estimation of all within effects. The reason is that the deviations from the cluster means are uncorrelated with the cluster means themselves, with any between-mother covariate (such as x_{4j}), and with ζ_j. However, the coefficients of the between-mother covariates and the random-intercept variance ψ are in general not consistently estimated. This is because the cluster means of the within-mother covariates and the between-mother covariates are likely to be correlated with ζ_j. In contrast, the estimator for the level-1 residual variance θ is consistent.

We start by constructing the cluster means (apart from `mn_smok`, which already exists):

```
. egen mn_male = mean(male), by(momid)
. egen mn_mage = mean(mage), by(momid)
. egen mn_kessner2 = mean(kessner2), by(momid)
. egen mn_kessner3 = mean(kessner3), by(momid)
. egen mn_novisit = mean(novisit), by(momid)
. egen mn_pretri2 = mean(pretri2), by(momid)
. egen mn_pretri3 = mean(pretri3), by(momid)
```

A more elegant way of forming cluster means for such a large number of variables is to use a `foreach` loop:

```
foreach var of varlist male mage kessner* novisit pretri* {
   egen mn_‘var’ = mean(‘var’), by(momid)
}
```

Here the loop repeats the `egen` command for each of the variables in the variable list `male mage kessner* novisit pretri*`. Inside the curly braces, the local macro `var` (which we could have called whatever we like) evaluates to the current variable name (first `male`, then `mage`, etc.). This variable name is accessed by placing the macro name in single quotes (really, a left quote and an apostrophe). We therefore obtain exactly the same commands we previously ran one at a time.

If we include the cluster means of all level-1 covariates but leave the latter variables in the model without cluster-mean centering them, as in (3.16), the coefficients for the cluster means represent the differences in the between and within effects for the set of covariates having both between and within variation. We fit the model using

```
. quietly xtset momid
. xtreg birwt smok mn_smok male mn_male mage mn_mage hsgrad somecoll
> collgrad married black kessner2 mn_kessner2 kessner3 mn_kessner3 novisit
> mn_novisit pretri2 mn_pretri2 pretri3 mn_pretri3, mle
Random-effects ML regression                    Number of obs      =      8604
Group variable: momid                           Number of groups   =      3978
Random effects u_i ~ Gaussian                   Obs per group: min =         2
                                                               avg =       2.2
                                                               max =         3
                                                LR chi2(21)        =    719.28
Log likelihood  = -65115.846                    Prob > chi2        =    0.0000
```

birwt	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
smoke	-104.5494	29.1063	-3.59	0.000	-161.5967	-47.50206
mn_smok	-183.1657	37.19657	-4.92	0.000	-256.0696	-110.2617
male	125.6355	10.9248	11.50	0.000	104.2232	147.0477
mn_male	-20.22363	22.31026	-0.91	0.365	-63.95093	23.50367
mage	23.15832	3.007241	7.70	0.000	17.26424	29.0524
mn_mage	-18.59407	3.360264	-5.53	0.000	-25.18007	-12.00808
hsgrad	56.29698	25.38638	2.22	0.027	6.540583	106.0534
somecoll	83.07017	27.99083	2.97	0.003	28.20914	137.9312
collgrad	98.17599	29.18708	3.36	0.001	40.97037	155.3816
married	42.46127	26.03156	1.63	0.103	-8.559647	93.48219
black	-219.0013	28.41769	-7.71	0.000	-274.699	-163.3037
kessner2	-91.49483	23.49362	-3.89	0.000	-137.5415	-45.44819
mn_kessner2	-9.050791	44.22205	-0.20	0.838	-95.72442	77.62284
kessner3	-128.091	47.80548	-2.68	0.007	-221.788	-34.394
mn_kessner3	-79.42459	92.26946	-0.86	0.389	-260.2694	101.4202
novisit	-4.805899	77.78694	-0.06	0.951	-157.2655	147.6537
mn_novisit	-38.11621	146.3218	-0.26	0.794	-324.9017	248.6693
pretri2	81.29039	27.0549	3.00	0.003	28.26376	134.317
mn_pretri2	44.76713	52.06045	0.86	0.390	-57.26948	146.8037
pretri3	153.059	60.09599	2.55	0.011	35.27303	270.845
mn_pretri3	96.07044	116.707	0.82	0.410	-132.6711	324.8119
_cons	3238.407	45.98903	70.42	0.000	3148.271	3328.544
/sigma_u	338.4422	6.243867			326.423	350.9039
/sigma_e	368.9882	3.840715			361.5368	376.5932
rho	.4569014	.011855			.4337527	.4801973

```
Likelihood-ratio test of sigma_u=0: chibar2(01)= 1127.34 Prob>=chibar2 = 0.000
```

The estimates were shown under "Random effects + clust. mean" in table 3.2 on page 145. The estimated coefficients for the covariates varying within mothers are now identical to the within-effects and hence not susceptible to cluster-level confounding.

A Wald test of the joint null hypothesis that all coefficients for the cluster means in the above model are zero can be performed using the `testparm` command:

```
. testparm mn_*
 ( 1)  [birwt]mn_smok = 0
 ( 2)  [birwt]mn_male = 0
 ( 3)  [birwt]mn_mage = 0
 ( 4)  [birwt]mn_kessner2 = 0
 ( 5)  [birwt]mn_kessner3 = 0
 ( 6)  [birwt]mn_novisit = 0
 ( 7)  [birwt]mn_pretri2 = 0
 ( 8)  [birwt]mn_pretri3 = 0
           chi2(  8) =   60.04
         Prob > chi2 =    0.0000
```

The Wald statistic is 60.04 with df = 8, so the null hypothesis that the coefficients of the cluster means are all zero is rejected at the 5% level. The above null hypothesis is equivalent to the hypothesis of equal between and within effects (for the covariates having both within and between variation), which is thus also rejected.

A great advantage of clustered or multilevel data is that we can investigate and address level-2 endogeneity of level-1 covariates (correlation between ζ_j and x_{ij}). However, the approaches considered in this chapter do not produce consistent estimates of the coefficients of level-2 covariates and the random-intercept variance in this case. Furthermore, the approaches cannot handle level-2 endogeneity of level-2 covariates (correlation between ζ_j and x_j). Both problems are addressed in an approach suggested by Hausman and Taylor (1981), which we describe in section 5.2.

Unfortunately, it is not straightforward to check for level-1 endogeneity, that is, to check whether ϵ_{ij} is correlated with either cluster-level or unit-level covariates. To correct for level-1 endogeneity, external instrumental variables are usually required.

Fortunately, there is no endogeneity problem due to omitted covariates when estimating a treatment or intervention effect in a randomized experiment.

3.7.6 Hausman endogeneity test

The Hausman test (Hausman 1978), more aptly called the Durbin–Wu–Hausman test, can be used to compare two alternative estimators of $\boldsymbol{\beta}$, both of which are consistent if the model is true. In its standard form, one of the estimators is asymptotically efficient if the model is true, but is inconsistent when the model is misspecified. The other estimator is consistent also under misspecification but is not asymptotically efficient when the model is true.

For instance, if the random-intercept model is correctly specified, both the fixed-effects estimator $\widehat{\boldsymbol{\beta}}^{W}$ and the FGLS estimator $\widehat{\boldsymbol{\beta}}^{\mathrm{FGLS}}$ are consistent for coefficients of covariates that vary within clusters whereas only $\widehat{\boldsymbol{\beta}}^{\mathrm{FGLS}}$ is efficient. However, if the random intercept is correlated with any of the covariates (cluster-level endogeneity), the within effects will differ from the between effects and $\widehat{\boldsymbol{\beta}}^{\mathrm{FGLS}}$ becomes inconsistent, whereas $\widehat{\boldsymbol{\beta}}^{W}$ remains consistent.

Consider first the simple case of a model with a single covariate x_{ij} that varies both between and within clusters. The Hausman test statistic for endogeneity then takes the form

$$h \;=\; \frac{(\widehat{\beta}^{W} - \widehat{\beta}^{\mathrm{FGLS}})^2}{\widehat{\mathrm{SE}}(\widehat{\beta}^{W})^2 - \widehat{\mathrm{SE}}(\widehat{\beta}^{\mathrm{FGLS}})^2} \tag{3.17}$$

which has an asymptotic $\chi^2(1)$ null distribution. The denominator of the test statistic would usually take the form $\widehat{\mathrm{SE}}(\widehat{\beta}^{W})^2 + \widehat{\mathrm{SE}}(\widehat{\beta}^{\mathrm{FGLS}})^2 - 2\,\widehat{\mathrm{Cov}}(\widehat{\beta}^{W}, \widehat{\beta}^{\mathrm{FGLS}})$, where the covariance between the within and FGLS estimators would be hard to obtain. However, it can be shown that the denominator simplifies to the one in (3.17) because the FGLS estimator is efficient when the random-intercept model is true.

Consider now the case where there are several covariates that all vary both between and within clusters. Let the fixed effects and FGLS estimates be denoted $\widehat{\boldsymbol{\beta}}^{W}$ and $\widehat{\boldsymbol{\beta}}^{\mathrm{FGLS}}$, respectively, and let the corresponding estimated covariance matrices be denoted $\widehat{\mathrm{Cov}}(\widehat{\boldsymbol{\beta}}^{W})$ and $\widehat{\mathrm{Cov}}(\widehat{\boldsymbol{\beta}}^{\mathrm{FGLS}})$. The Hausman test statistic then takes the form

$$h \;=\; (\widehat{\boldsymbol{\beta}}^{W} - \widehat{\boldsymbol{\beta}}^{\mathrm{FGLS}}) \left\{ \widehat{\mathrm{Cov}}(\widehat{\boldsymbol{\beta}}^{W}) - \widehat{\mathrm{Cov}}(\widehat{\boldsymbol{\beta}}^{\mathrm{FGLS}}) \right\}^{-1} (\widehat{\boldsymbol{\beta}}^{W} - \widehat{\boldsymbol{\beta}}^{\mathrm{FGLS}})'$$

The h statistic has an asymptotic χ^2 null distribution with degrees of freedom given as the number of overlapping estimated regression coefficients from the two approaches, that is, the number of covariates with both between- and within-cluster variation.

We can use the `hausman` command to perform the Hausman test in Stata, following estimation of $\widehat{\boldsymbol{\beta}}^{W}$ using `xtreg` with the `fe` option and estimation of $\widehat{\boldsymbol{\beta}}^{\mathrm{FGLS}}$ using `xtreg` with the `re` option:

```
. quietly xtset momid
. quietly xtreg birwt smoke male mage hsgrad somecoll collgrad married
> black kessner2 kessner3 novisit pretri2 pretri3, fe
```

```
. estimates store fixed
. quietly xtreg birwt smoke male mage hsgrad somecoll collgrad married
> black kessner2 kessner3 novisit pretri2 pretri3, re
. estimates store random
. hausman fixed random
```

	——— Coefficients ———			
	(b) fixed	(B) random	(b-B) Difference	sqrt(diag(V_b-V_B)) S.E.
smoke	-104.5494	-217.7488	113.1995	22.71343
male	125.6355	120.9874	4.648084	5.297981
mage	23.15832	8.137158	15.02116	2.687211
kessner2	-91.49483	-92.89604	1.401212	12.44845
kessner3	-128.091	-150.6366	22.54563	24.87574
novisit	-4.805898	-29.9223	25.11641	41.66561
pretri2	81.29039	92.73087	-11.44048	13.94097
pretri3	153.059	178.4334	-25.37443	30.76114

```
                b = consistent under Ho and Ha; obtained from xtreg
     B = inconsistent under Ha, efficient under Ho; obtained from xtreg

Test:  Ho:  difference in coefficients not systematic

           chi2(8) = (b-B)'[(V_b-V_B)^(-1)](b-B)
                   =       60.07
         Prob>chi2 =      0.0000
```

There is strong evidence for model misspecification because the Hausman test statistic is 60.07 with df = 8. The Hausman statistic is practically identical to the Wald statistic for the joint null hypothesis that all regression coefficients of the cluster means are zero, shown in the previous section. This is what we would expect because the corresponding tests are asymptotically equivalent. In fact, equivalent variants of the Hausman test could have been constructed based on instead comparing the between and FGLS estimators, or the OLS and FGLS estimators, or the between and within estimators; but this is not implemented in Stata.

A significant Hausman test is often taken to mean that the random-intercept model should be abandoned in favor of a fixed-effects model that only uses within information. However, if there are covariates having the same within and between effects, we obtain more precise estimates of these coefficients by exploiting both within- and between-cluster information. The fixed-effects estimators are particularly imprecise if the covariates have little within-cluster variation. If the (true) between and within effects differ by a small amount, it may still be advisable to use the random-effects estimator because it may have a smaller mean squared error (some bias but considerably smaller variance) than the fixed-effects estimator.

3.8 Fixed versus random effects revisited

In section 2.8, we discussed whether the effects of clusters should be treated as random or fixed in models without covariates. We argued that this depends on whether inferences are for the population of clusters or only for the clusters included in the sample. In

table 3.3, we consider these as the main questions and then ask questions related to each main question. The answers to these questions delineate the main differences between fixed-effects and random-effects approaches.

Table 3.3: Overview of distinguishing features of fixed- and random-effects approaches for linear models that include covariates

	Answers	
Questions	**Fixed effects**	**Random effects**
Inference for population of clusters?	No	Yes
Minimum number of clusters required?	Any number	At least 10 or 20
What assumptions are required for ζ_j or α_j?		Level-2 exogeneity, constant variance ψ
Can estimate effects of cluster-level covariates?	No	Yes
Inference for clusters in particular sample?	Yes	No, not for βs, but yes, for ζ_j by using empirical Bayes
Minimum cluster size required?	At least 2, but large for est. α_j	Any sizes if many ≥ 2
Is the model parsimonious?	No, J parameters α_j	Yes, one variance parameter ψ for all J clusters
Can estimate within-cluster effects of covariates?	Yes	Yes, by including cluster means

Unlike the fixed-effects model, the random-effects model can be used to make inferences regarding the population of clusters, but at the cost of requiring many clusters and making additional assumptions regarding the random-intercept distribution. The additional assumptions include exogeneity of the observed covariates $\mathbf{x}_{ij}$ with respect to ζ_j (level-2 exogeneity) and a constant variance ψ. The standard assumption of a normal distribution for ζ_j is actually not required for consistent estimation of regression coefficients. Both the fixed-effects and random-effects models assume exogeneity of $\mathbf{x}_{ij}$ with respect to the level-1 residual ϵ_{ij} (level-1 exogeneity). An advantage of the random-effects model is that it can be used to estimate the effects of cluster-level covariates, in contrast to the fixed-effects model, although consistent estimation requires both level-1 and level-2 exogeneity.

While the fixed-effects model is designed for making inferences for the clusters in the sample, the random-effects model can also to some extent be used for this purpose

by predicting the ζ_j using empirical Bayes (EB). However, inferences regarding the regression coefficients from random-effects models, such as estimated standard errors, are for the population of clusters as discussed in section 2.10.3. Random-effects models can be used if there are clusters with only one unit as long as there are many clusters with at least two units.

In the fixed-effects approach, singleton clusters do not provide any information on any of the parameters except α_j. Furthermore, the fixed-effects approach requires large cluster sizes if we want to consistently estimate the intercepts α_j. The fixed-effects model is much less parsimonious than the random-intercept model because it includes one parameter α_j for each cluster, whereas the random-intercept model has only one parameter ψ for the variance of the random intercepts ζ_j. Eliminating the α_j by mean centering, as shown in section 3.7.2, simplifies the estimation problem but does not make the estimates of the remaining parameters any more efficient. Unlike the random-effects approach, the fixed-effects approach controls for clusters, providing estimates of within-cluster effects of covariates. The random-effects model can provide estimates of within-cluster effects only with extra effort, namely, by including cluster means of those covariates for which the between effect differs from the within effect.

3.9 Assigning values to random effects: Residual diagnostics

As discussed in section 2.11, we often want to assign values to random effects, for inferences regarding clusters, model visualization, or diagnostics. In data on institutions such as schools or hospitals, the predicted random intercepts can be viewed as measures of institutional performance if the covariates represent intake characteristics of individuals or "case-mix" of institutions (see section 4.8.5). Model visualization is demonstrated in section 4.8.3 and throughout the book.

We now consider residual diagnostics for assessing the normality assumptions for ζ_j and ϵ_{ij}. Inference generally does not hinge on normality, but severe skewness and outliers can pose problems. In contrast, EB prediction of random effects relies much more on normality.

In section 2.11.2, we discussed EB prediction of the random intercepts for different clusters j. Such predictions $\widetilde{\zeta}_j$ can be interpreted as predicted level-2 residuals for the mothers. We can obtain corresponding predicted level-1 residuals for birth i of mother j as

$$\widetilde{\epsilon}_{ij} \;=\; \widehat{\xi}_{ij} - \widetilde{\zeta}_j$$

where

$$\widehat{\xi}_{ij} \;=\; y_{ij} - (\widehat{\beta}_1 + \widehat{\beta}_2 x_{2ij} + \cdots + \widehat{\beta}_p x_{pij})$$

In linear mixed models (but not in the generalized linear mixed models discussed in volume 2), these predicted level-2 and level-1 residuals have normal sampling distributions if it is assumed that the random-intercept model has a normally distributed random

intercept and level-1 residual. We can therefore use histograms or normal quantile–quantile plots of the predicted residuals to assess the assumptions that ζ_j and ϵ_{ij} are normally distributed. However, the EB predictions are based on normality assumptions and will tend to look more normal than they are when normality is violated.

We can also try to find outliers by using standardized residuals and looking for values that are unlikely under the standard normal distribution, for example, values outside the range ± 4. In section 2.11.3, we discussed the diagnostic standard error of the EB predictions. A standardized level-2 residual can therefore be obtained as

$$r_j^{(2)} = \frac{\widetilde{\zeta}_j}{\sqrt{\widehat{\mathrm{Var}}(\widetilde{\zeta}_j)}}$$

For the level-1 residuals, we simply divide by the estimated level-1 standard deviation:

$$r_{ij}^{(1)} = \frac{\widetilde{\epsilon}_{ij}}{\sqrt{\widehat{\theta}}}$$

After using `xtmixed`, we can use the `predict` command with the `reffects` option to obtain $\widetilde{\zeta}_j$ and with the `rstandard` option to obtain $r_{ij}^{(1)}$. The standardized level-2 residual $r_j^{(2)}$ is, at the time of writing this book, not provided by `predict`, but we can calculate it by first estimating the comparative standard errors using the `reses` option and then estimating the required diagnostic standard error, as shown in section 2.11.3.

We begin by refitting the model in `xtmixed` without producing any output:

```
. quietly xtmixed birwt smoke male mage hsgrad somecoll collgrad
> married black kessner2 kessner3 novisit pretri2 pretri3 || momid: , mle
```

The steps necessary to obtain $r_j^{(2)}$ are (see section 2.11.3)

```
. predict lev2, reffects
. predict comp_se, reses
. generate diag_se = sqrt(exp(2*[lns1_1_1]_cons) - comp_se^2)
. replace lev2 = lev2/diag_se
```

and the $r_{ij}^{(1)}$ are obtained using

```
. predict lev1, rstandard
```

Histograms of the standardized level-1 residuals $r_{ij}^{(1)}$ and the standardized level-2 residuals $r_j^{(2)}$ can be plotted as follows:

```
. histogram lev1, normal xtitle(Standardized level-1 residuals)
. histogram lev2 if idx==1, normal xtitle(Standardized level-2 residuals)
```

These commands produce figures 3.6 and 3.7, respectively.

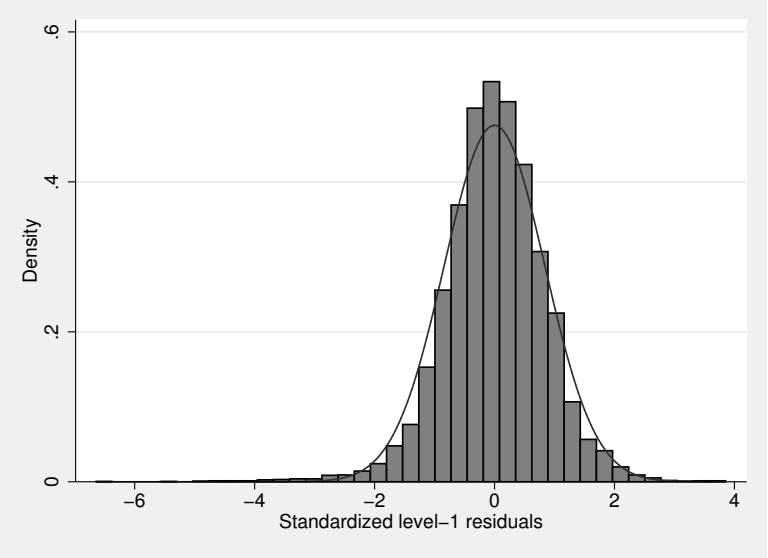


Figure 3.6: Histogram of standardized level-1 residuals

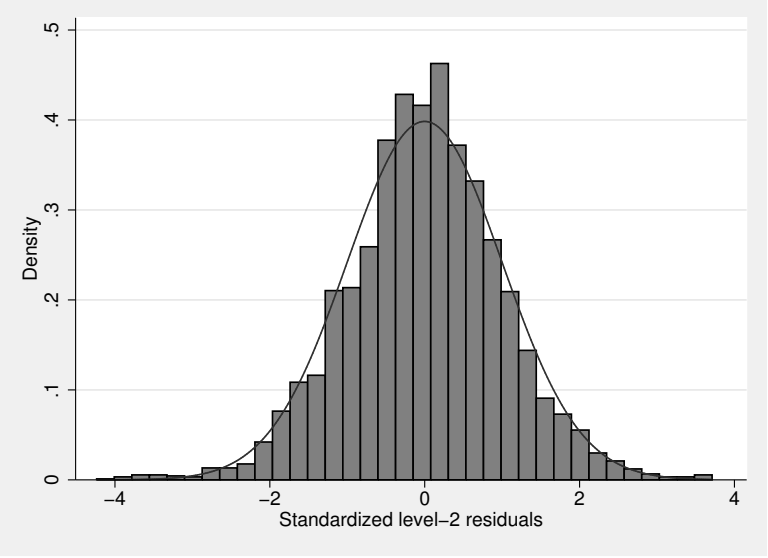


Figure 3.7: Histogram of standardized level-2 residuals

Both histograms look approximately normal, perhaps with thicker tails than the normal distribution. However, there are some extremely small level-1 residuals. The expected number of standardized level-1 residuals less than −4 is approximately 0.27 (=`8604*normal(-4)`).

It may in this case be judicious to use the sandwich estimator to obtain robust standard errors that do not rely on the model being correctly specified. Robust standard errors can be obtained using `xtmixed` (from Stata 12) with the `vce(robust)` option:

```
. quietly xtset momid

. xtreg birwt smoke male mage hsgrad somecoll collgrad married black
> kessner2 kessner3 novisit pretri2 pretri3, vce(robust) re

Random-effects GLS regression                   Number of obs      =      8604
Group variable: momid                           Number of groups   =      3978

R-sq:  within  = 0.0380                         Obs per group: min =         2
       between = 0.1128                                        avg =       2.2
       overall = 0.0949                                        max =         3

Random effects u_i ~ Gaussian                   Wald chi2(13)      =    623.99
corr(u_i, X)       = 0 (assumed)                Prob > chi2        =    0.0000

                                (Std. Err. adjusted for 3978 clusters in momid)
------------------------------------------------------------------------------
             |               Robust
       birwt |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       smoke |  -217.7488   19.15796   -11.37   0.000    -255.2977   -180.1999
        male |   120.9874   9.676186    12.50   0.000     102.0224    139.9524
        mage |   8.137158   1.406836     5.78   0.000      5.37981    10.89451
      hsgrad |   56.85672   25.83816     2.20   0.028     6.214852    107.4986
   somecoll |   80.64814   28.40641     2.84   0.005     24.97261    136.3237
   collgrad |   90.72697   29.14273     3.11   0.002     33.60827    147.8457
    married |   49.95895   26.63437     1.88   0.061    -2.243452    102.1613
      black |  -211.3336   29.32198    -7.21   0.000    -268.8037   -153.8636
   kessner2 |  -92.89604   21.66719    -4.29   0.000     -135.363   -50.42913
   kessner3 |  -150.6366   40.99285    -3.67   0.000    -230.9811   -70.29214
    novisit |   -29.9223   80.94521    -0.37   0.712     -188.572    128.7274
    pretri2 |   92.73087   24.76155     3.74   0.000     44.19912    141.2626
    pretri3 |   178.4334   52.90179     3.37   0.001     74.74785     282.119
      _cons |    3116.04   42.55804    73.22   0.000     3032.628    3199.452
-------------+----------------------------------------------------------------
    sigma_u |  340.64782
    sigma_e |  368.91787
        rho |  .46022181   (fraction of variance due to u_i)
------------------------------------------------------------------------------
```

Most of the standard errors are larger than before, but the basic conclusions remain the same.

3.10 More on statistical inference

3.10.1 ❖ Overview of estimation methods

The simplest approach for estimating the fixed part of the model is to use OLS, sometimes referred to as pooled OLS because data on all clusters is combined. The OLS estimator is unbiased and consistent, but the conventional estimated standard errors are invalid if the residuals are correlated (see section 3.10.2). The sandwich estimator for clustered data can be used to obtain standard errors that take the clustering into account without making any assumptions regarding the random part of the model, apart from exogeneity. Such an approach can be viewed as treating clustering as a nuisance because nothing is learned about the residual between-cluster variability or within-cluster dependence.

A disadvantage of the OLS approach is that it is generally not asymptotically efficient if the residuals are correlated. If the residual covariance matrix were known, the efficient estimator would be generalized least squares (GLS), where the inverse covariance matrix of the total residuals is used as a weight matrix.

Display 3.1 shows matrix expressions for the GLS estimator.

Let $\mathbf{y} = (y_{11}, \ldots, y_{n_1 1}, y_{12}, \ldots, y_{n_2 2}, \ldots, y_{1J}, \ldots, y_{n_J J})'$ denote the N-dimensional vector of all responses, $\mathbf{X}$ the $N \times p$ matrix of covariates, $\boldsymbol{\beta}$ the corresponding p-dimensional vector of regression coefficients, and $\boldsymbol{\xi}$ the N-dimensional vector of total residuals. A linear model can then be written as

$$\mathbf{y} \;=\; \mathbf{X}\boldsymbol{\beta} + \boldsymbol{\xi}$$

Letting $\mathbf{V}$ denote the $N \times N$ covariance matrix of the vector of residuals $\boldsymbol{\xi}$, the OLS and GLS estimators can be written, respectively, as

$$\widehat{\boldsymbol{\beta}}^{\mathrm{OLS}} \;=\; (\mathbf{X}'\mathbf{X})^{-1}\mathbf{X}'\mathbf{y}$$

and

$$\widehat{\boldsymbol{\beta}}^{\mathrm{GLS}} \;=\; (\mathbf{X}'\mathbf{V}^{-1}\mathbf{X})^{-1}\mathbf{X}'\mathbf{V}^{-1}\mathbf{y}$$

Display 3.1: Matrix expressions for generalized least-squares estimator

In practice, we know only the structure of the residual covariance matrix, assuming that our model is correct. Namely, according to the random-intercept model, the variance is constant, residuals are correlated within clusters with constant correlation and uncorrelated across clusters. See display 3.2 for the form of the covariance structure.

In FGLS, the regression coefficients are first estimated by OLS, yielding estimated residuals from which the residual covariance matrix is estimated as $\widehat{\mathbf{V}}$. The regression coefficients are then reestimated by substituting $\widehat{\mathbf{V}}$ for $\mathbf{V}$ in the GLS estimator, producing estimates $\widehat{\boldsymbol{\beta}}^{\mathrm{FGLS}}$.

The FGLS estimator is consistent for the regression coefficients even if the covariance structure is incorrectly specified. Under the model assumptions stated in section 3.3.2, the FGLS estimator is asymptotically normal and asymptotically efficient, and the model-based standard errors are valid, if a consistent estimator $\widehat{\mathbf{V}}$ is used for $\mathbf{V}$. Furthermore, the model assumptions imply that the FGLS estimator is unbiased in small samples if the total residuals have a symmetric distribution, such as normal.

In a random intercept model, the covariance matrix $\mathbf{V}$ of all total residuals in the dataset $(\xi_{11}, \ldots, \xi_{n_1 1}, \xi_{12}, \ldots, \xi_{n_2 2}, \ldots, \xi_{1J}, \ldots, \xi_{n_J J})'$ has the block-diagonal form

$$\mathbf{V} = \begin{pmatrix} \mathbf{V}_1 & \mathbf{0} & \cdots & \mathbf{0} \\ \mathbf{0} & \mathbf{V}_2 & \cdots & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \ddots & \vdots \\ \mathbf{0} & \mathbf{0} & \cdots & \mathbf{V}_J \end{pmatrix}$$

The blocks $\mathbf{V}_1$ to $\mathbf{V}_J$ on the diagonal are the within-cluster covariance matrices, and all other elements are zero. For a cluster with $n_j = 3$ units, the within-cluster covariance matrix has the structure

$$\mathbf{V}_j = \begin{pmatrix} \psi + \theta & \psi & \psi \\ \psi & \psi + \theta & \psi \\ \psi & \psi & \psi + \theta \end{pmatrix}$$

Display 3.2: Residual covariance structure for random-intercept model

The residuals based on FGLS are different from the residuals produced by OLS that were originally used to estimate $\mathbf{V}$. This suggests reestimating $\mathbf{V}$ based on the FGLS residuals and then reestimating the regression coefficients. Iterating this process until convergence yields so-called iterative generalized least squares (IGLS). The IGLS estimator maximizes the likelihood implied by the linear model assuming multivariate normal total residuals.

More commonly, the likelihood is maximized using gradient methods such as the Newton–Raphson algorithm. The basic idea is to find the maximum of the log likelihood iteratively, in each step updating the parameters based on derivatives of the log likelihood at the current parameter values. In Newton–Raphson, the next parameter values are at the maximum of the quadratic function matching the first and second derivatives at the current parameter values. Indeed, if the log likelihood is quadratic, one Newton–Raphson step suffices. It is remarkable how few iterations are often required even for quite complicated models. The negative *Hessian* (the matrix of second derivatives) of the log likelihood at the maximum is called the observed *information matrix*. Its inverse is a model-based estimator of the covariance matrix of the parameter estimates.

Another common approach for ML estimation of multilevel models is the expectation-maximization (EM) algorithm. Here the random effects are treated as missing data. If

the random effects (or missing data) were known, or in other words if we had the "complete data", estimation of the parameters would be straightforward.

For instance, in a random-intercept model, the random-intercept variance ψ could be estimated as

$$\widehat{\psi}^{\text{complete data}} = \frac{1}{J}\sum_{j=1}^{J}\zeta_j^2 \tag{3.18}$$

However, the random effects are not known, so in the expectation step, the posterior expectation of the complete data estimators is found. For ψ, this amounts to finding the mean of (3.18) over the posterior distribution of the random effects, given the observed data (where the current parameter estimates are substituted for the unknown parameters; see section 2.11.2):

$$E\left(\frac{1}{J}\sum_{j=1}^{J}\zeta_j^2\middle|\mathbf{y},\mathbf{X}\right)$$

In the maximization step, the parameters are updated by setting them equal to the posterior expectations of the complete data estimators. This yields an updated posterior distribution of the random intercepts, giving updated posterior expectations, etc., until convergence. It has been shown that the EM algorithm converges to a (local) maximum, but the number of iterations required can be large.

An alternative to ML estimation is restricted or residual maximum likelihood (REML) estimation. Here the responses are transformed in such a way that their distribution no longer depends on the regression parameters $\boldsymbol{\beta}$. The likelihood then depends only on the parameters of the random part of the model. Maximizing this residual likelihood produces REML estimates of the variance (and covariance) parameters. Having estimated these parameters by REML, the regression coefficients can be estimated by using the implied residual covariance matrix $\widehat{\mathbf{V}}$ in GLS. For balanced data, REML gives unbiased estimates of variance (and covariance) parameters (if variances are allowed to be negative), unlike ML. However, it is not clear which estimator has a smaller mean squared error (in balanced or unbalanced data).

Pooled OLS is obtained using the `regress` command, and the sandwich estimator for clustered data is obtained using the `vce(cluster` *clustvar*`)` option. FGLS is implemented in `xtreg` with the `re` option and in `xtgls` (see section 6.7.2 and exercise 6.4). The latter command uses IGLS when the `igls` option is specified.

By default, `xtmixed` uses ML (since Stata 12), but the `reml` option can be used for REML estimation. `xtmixed` starts with the EM algorithm and then switches to Newton–Raphson. The options `emiterate()` or `emonly` can be used to increase the number of EM steps or to use EM exclusively. The `technique()` option can be used to replace Newton–Raphson by another gradient method.

3.10.2 Consequences of using standard regression modeling for clustered data

In this section, we presume that the random-intercept model

$$y_{ij} \;=\; \beta_1 + \beta_2 x_{ij} + \underbrace{\zeta_j + \epsilon_{ij}}_{\xi_{ij}} \tag{3.19}$$

is the true model, with the assumptions stated in section 3.3.1 satisfied. However, the regression coefficient β_2 in the above random-intercept model is estimated using OLS, based on the assumptions stated in section 1.5, for the linear regression model

$$y_i \;=\; \beta_1 + \beta_2 x_i + \epsilon_i$$

which is *misspecified*.

The crucial difference between the two models is that there is a positive within-cluster correlation between the (total) residuals in the random-intercept model if $\psi > 0$, whereas there is no such within-cluster correlation in the linear regression model. For simplicity, we assume that the data are balanced ($n_j = n > 1$) and have large $N = Jn$.

The good news is that the OLS estimator is consistent (approaches the unknown parameter value in large samples) when the random-intercept model is true and $\psi > 0$. Indeed, even for a given dataset, the OLS estimates are usually close to the ML estimates for the correctly specified random-intercept model: $\widehat{\beta}_1^{\mathrm{OLS}} \approx \widehat{\beta}_1^{\mathrm{ML}}$, $\widehat{\beta}_2^{\mathrm{OLS}} \approx \widehat{\beta}_2^{\mathrm{ML}}$, and $\widehat{\sigma^2}^{\mathrm{OLS}} \approx \widehat{\psi}^{\mathrm{ML}} + \widehat{\theta}^{\mathrm{ML}}$.

The results are worse when it comes to fitted model-based standard errors and p-values for hypothesis tests. The estimated standard error of the OLS estimator $\widehat{\beta}_2^{\mathrm{OLS}}$ for the linear regression model is

$$\widehat{\mathrm{SE}}(\widehat{\beta}_2^{\mathrm{OLS}}) \;=\; \sqrt{\frac{\widehat{\sigma^2}^{\mathrm{OLS}}}{Jn\, s_{xO}^2}} \;\approx\; \sqrt{\frac{\widehat{\psi}^{\mathrm{ML}} + \widehat{\theta}^{\mathrm{ML}}}{Jn\, s_{xO}^2}}$$

where s_{xO}^2 is the overall sample variance of x_{ij} given in section 3.2.1.

For a purely between-cluster covariate (with $x_{ij} = \overline{x}_{\cdot j}$), the within-cluster variance s_{xW}^2 is zero ($s_{xO}^2 = s_{xB}^2$) and the estimated standard error of the ML estimator $\widehat{\beta}_2^{\mathrm{ML}}$ for the random-intercept model is

$$\widehat{\mathrm{SE}}(\widehat{\beta}_2^{\mathrm{ML}}) \;=\; \sqrt{\frac{n\widehat{\psi}^{\mathrm{ML}} + \widehat{\theta}^{\mathrm{ML}}}{Jn\, s_{xO}^2}} \;>\; \widehat{\mathrm{SE}}(\widehat{\beta}_2^{\mathrm{OLS}}) \qquad \text{if } n > 1,\ \widehat{\psi} > 0$$

Because the OLS standard error is smaller than it should be, the corresponding p-value is too small.

For a purely within-cluster covariate (with $\overline{x}_{.j} = \overline{x}_{..}$), the between-cluster variance s^2_{xB} is zero ($s^2_{xO} = s^2_{xW}$) and the estimated standard error of $\widehat{\beta}_2^{\mathrm{ML}}$ for the random-intercept model is

$$\widehat{\mathrm{SE}}(\widehat{\beta}_2^{\mathrm{ML}}) \;=\; \sqrt{\frac{\widehat{\theta}^{\mathrm{ML}}}{Jn\, s^2_{xO}}} \;<\; \widehat{\mathrm{SE}}(\widehat{\beta}_2^{\mathrm{OLS}}) \qquad \text{if } \widehat{\psi} > 0$$

Because the OLS standard error is larger than it should be, the p-value is now too large.

Thus assuming a standard regression model when the random-intercept model is true and $\psi > 0$ will produce too small or too large model-based standard errors and p-values depending on the nature of the covariate. This is contrary to the common belief that the estimated standard errors are always too small.

An important lesson is that robust standard errors for clustered data should be employed when standard regression models are used for clustered data. In Stata, such standard errors can be obtained using the `vce(cluster` *clustvar*`)` option, as demonstrated in section 2.10.3.

The above expressions for the fitted model-based standard errors also hold if the model includes other covariates that are uncorrelated with x_{ij}.

3.10.3 ❖ Power and sample-size determination

Here we consider power and sample-size determination for the random-intercept model in (3.19) with a single covariate that either varies only between clusters or varies only within clusters. A typical problem is to determine the sample size to achieve a required power γ at a given significance level α for the two-sided test of the null hypothesis H_0: $\beta_2 = 0$.

From the construction of the z test for the above null hypothesis, it follows that

$$\frac{\beta_2}{\mathrm{SE}(\widehat{\beta}_2)} \;\approx\; z_{1-\alpha/2} + z_{\gamma} \tag{3.20}$$

where $z_{1-\alpha/2}$ is the quantile of a standard normal distribution so that the area under the density curve from $-\infty$ to $z_{1-\alpha/2}$ is $1-\alpha/2$. Analogously, z_γ is a quantile, making the area equal to γ (see display 3.3 for a derivation).

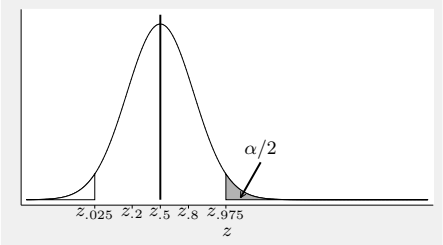
The above approximation is very accurate if $\gamma > 0.30$. Often the significance level and power are chosen as $\alpha = 0.05$ and $\gamma = 0.80$, respectively, which gives $z_{1-\alpha/2} + z_\gamma = 1.96 + 0.84 = 2.80$.

Under the null hypothesis, H_0: $\beta_2 = 0$, the test statistic z has a standard normal distribution (asymptotically). If the alternative hypothesis is two-sided, the null hypothesis is rejected at significance level $\alpha = 0.05$ if $z > z_{0.975}$ or $z < z_{0.025}$, where $z_{0.975}$ is the 97.5th percentile of the standard normal distribution (equal to 1.96) and $z_{0.025}$ is the 2.5th percentile (equal to -1.96). More generally, the null hypothesis is rejected at level α if $z > z_{1-\alpha/2}$ or $z < z_{\alpha/2}$. The right-tail probability, $P(z > z_{1-\alpha/2}|H_0)$, is shown as a light-shaded area under the standard normal density in the graph below for $\alpha = 0.05$:

Null hypothesis
$H_0 : z \sim N(0, 1)$

$P(z > z_{1-\alpha/2}|H_0) = \alpha/2$

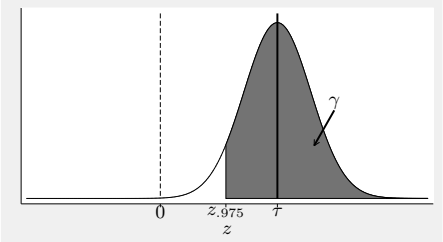
$P(z > z_{0.975}|H_0) = 0.025$



Alternative hypothesis
$H_a : z \sim N(\tau, 1)$

$P(z > z_{1-\alpha/2}|H_a) \approx \gamma$

$P(z < z_{\alpha/2}|H_a) \approx 0$



From now on we assume that the alternative hypothesis, H_a: $\beta_2 \neq 0$, is true and that the true coefficient β_2 equals some predetermined positive *effect size*. We let τ be the true coefficient divided by the standard error of its estimate, $\tau = \beta_2/\text{SE}(\widehat{\beta}_2)$. The test statistic $z = \widehat{\beta}_2/\text{SE}(\widehat{\beta}_2)$ now has an asymptotic normal distribution with mean τ and variance 1:

$$z \sim N(\tau, 1) \quad \Longleftrightarrow \quad z - \tau \sim N(0, 1)$$

The probability that H_0 is rejected because $z > z_{1-\alpha/2}$ is shown as the dark-shaded area in the graph above. This is approximately the power γ, defined as the probability of rejecting the null hypothesis for an assumed effect size under the alternative hypothesis, because the probability that $z < z_{\alpha/2}$ is negligible if τ is sufficiently large:

$$\text{Power} \equiv \gamma \approx P(z > z_{1-\alpha/2}|H_a) = P(z - \tau > z_{1-\alpha/2} - \tau|H_a)$$

Because $z - \tau$ is standard normal, we know how large $z_{1-\alpha/2} - \tau$ has to be for the probability in the above equation to equal γ, namely,

$$z_{1-\alpha/2} - \tau \approx z_{1-\gamma} \quad \Longleftrightarrow \quad \tau \equiv \frac{\beta_2}{\text{SE}(\widehat{\beta_2})} \approx z_{1-\alpha/2} - z_{1-\gamma} = z_{1-\alpha/2} + z_{\gamma}$$

where $z_{1-\gamma}$ is the appropriate percentile of $N(0, 1)$.

Display 3.3: Approximate relationship between power, significance level, effect size, and standard error for two-sided test

For a random-intercept model with a purely between-cluster covariate x_j, the standard error of the ML estimate of the coefficient is

$$\text{SE}(\widehat{\beta}_2^B) \;=\; \sqrt{\frac{n\psi+\theta}{Jn\,s_{xO}^2}}$$

We can then substitute this standard error into (3.20) and solve for the total number of clusters J for given cluster size n (or vice versa), with given values of the parameters β_2, ψ, and θ and with a given variance of the covariate s_{xO}^2.

For example, let $n=4$, $\beta_2=1$, $\psi=1$, $\theta=1$, and x_j be a between-cluster treatment dummy variable, equal to 0 for half the clusters and 1 for the other half so that $s_{xO}^2 = 0.5\times(1-0.5) = 0.25$. We then obtain

$$\text{SE}(\widehat{\beta}_2^B) \;=\; \sqrt{\frac{4\times 1+1}{J\times 4\times 0.25}} = \sqrt{5/J}$$

from which it follows that

$$\frac{\beta_2}{\text{SE}(\widehat{\beta}_2^B)} = \sqrt{\frac{1}{5/J}} = \sqrt{J/5}$$

Substituting for $\beta_2/\text{SE}(\widehat{\beta}_2^B)$ and $z_{1-\alpha/2}+z_\gamma$ in (3.20), we obtain the equation

$$\sqrt{J/5} \;=\; 2.80$$

which we solve to get $J = 39.2$. We see that about 40 clusters are needed (20 per treatment group) to achieve 80% power to detect the treatment effect at the 5% significance level.

For a random-intercept model with a purely within-cluster covariate x_{ij} that does not vary between clusters, the standard error of the ML estimate of the coefficient is

$$\text{SE}(\widehat{\beta}_2^W) \;=\; \sqrt{\frac{\theta}{Jn\,s_{xO}^2}}$$

Assuming that x_{ij} is a treatment dummy variable equal to 0 for half the units in each cluster and 1 for the other half, and keeping all other assumptions the same as in the example above, we obtain

$$\text{SE}(\widehat{\beta}_2^W) \;=\; \sqrt{\frac{1}{J\times 4\times 0.25}} = \sqrt{1/J}$$

and it follows that

$$\frac{\beta_2}{\text{SE}(\widehat{\beta}_2^W)} = \sqrt{\frac{1}{1/J}} = \sqrt{J}$$

Substituting in (3.20),

$$\sqrt{J} \;=\; 2.80$$

and solving for J, we see that only about 8 clusters are now needed in total, compared with about 40 if treatment is between clusters.

In randomized experiments, the designs where entire clusters are assigned to treatments are often called cluster-randomized trials whereas studies where units are assigned to treatments, stratified by cluster, are called multisite studies. Multisite studies have more power and thus require smaller sample sizes, particularly if $n\psi$ is large compared with θ as in our example. Sometimes, though, multisite studies are not feasible, for instance, if the clusters are classrooms and the treatment is a new curriculum. Another reason for a cluster-randomized trial is that it avoids "contamination", where units not assigned to the treatment may indirectly benefit from the treatment received by other units in the cluster.

3.11 Summary and further reading

We have discussed linear random-intercept models, which are important for investigating the relationship between a continuous response and a set of covariates when the data have a clustered or hierarchical structure. Topics included hypothesis testing, different kinds of coefficients of determination, the choice between fixed- and random-effects approaches, model diagnostics, consequences of using standard regression for clustered data, and power and sample-size determination.

An important problem in any regression model is the potential for bias due to omitted covariates. In clustered data, we can identify the problem of omitted cluster-level covariates by comparing within-cluster and between-cluster effects of covariates varying both within and between clusters. This problem of cluster-level confounding is the reason for the ecological fallacy and is referred to as an endogeneity problem in econometrics. Although the problem of endogeneity is emphasized in econometrics, where the Hausman test is routinely used, it is not usually considered in other disciplines. However, relatively nontechnical treatments with applications in biostatistics can be found in Neuhaus and Kalbfleisch (1998) and Begg and Parides (2003). Exercise 3.5 uses a dataset considered in the first paper.

Another area where within- and between-cluster effects are contrasted is education (Raudenbush and Bryk 2002, 135–141). Specifically, interest often concerns the difference in within-school and between-school effects of socioeconomic status (SES); see exercise 3.7. As discussed in section 3.7.4, the difference in the within-cluster effect of a covariate (such as students' individual SES) and the between-cluster effect of the aggregated covariate (such as school mean SES) is often called a *contextual effect* in contrast to the *compositional effect* (the within effect). The distinction between compositional and contextual effects on health is discussed by Bingenheimer and Raudenbush (2004) and Duncan, Jones, and Moon (1998). The book by Wooldridge (2010) provides a good but demanding treatment of within and between estimators and endogeneity from an

econometric perspective. More accessible discussions of this topic are given in the papers by Palta and Seplaki (2002) and Ebbes, Böckenholt, and Wedel (2004). The endogeneity problem is revisited in chapter 5, where more advanced methods are introduced in section 5.3.2.

An excellent discussion of linear random-intercept models can be found in Snijders and Bosker (2012, chap. 4), which is also a useful reference on model diagnostics and power analysis. A useful overview of power analysis and sample-size determination for multilevel models is provided in the encyclopedia entry by Snijders (2005). Swaminathan and Rogers (2008) give an excellent overview and detailed explanation of estimation methods for random-intercept and random-coefficient models. Many of the references mentioned above are collected in Skrondal and Rabe-Hesketh (2010), the first volume of a recent anthology on multilevel modeling.

In the exercises, random-intercept models are applied to data from different disciplines with clustering due to longitudinal data (exercises 3.2, 3.3, and 3.6), children nested in neighborhoods (exercise 3.1), rat pups nested in litters (exercise 3.4), children nested in mothers (exercise 3.5), and students nested in schools (exercises 3.7 and 3.8). Exercise 3.9 is about small-area estimation, a topic not covered in this chapter. Exercises 3.8 and 3.11 involve power analysis.

3.12 Exercises

3.1 Neighborhood-effects data

Garner and Raudenbush (1991), Raudenbush and Bryk (2002), and Raudenbush et al. (2004) considered neighborhood effects on educational attainment for young people who left school between 1984 and 1986 in one education authority in Scotland.

The dataset `neighborhood.dta` (previously used in exercise 2.4) has the following variables:

- Level 1 (students)
  - `attain`: a measure of end-of-school educational attainment capturing both attainment and length of schooling (based on the number of O-grades and Higher SCE awards at the A–C levels)
  - `p7vrq`: verbal-reasoning quotient (test at age 11–12 in primary school)
  - `p7read`: reading test score (test at age 11–12 in primary school)
  - `dadocc`: father's occupation scaled on the Hope–Goldthorpe scale in conjunction with the Registrar General's social-class index (Willms 1986)
  - `dadunemp`: dummy variable for father being unemployed (1: unemployed; 0: not unemployed)
  - `daded`: dummy variable for father's schooling being past the age of 15
  - `momed`: dummy variable for mother's schooling being past the age of 15
  - `male`: dummy variable for student being male

- Level 2 (neighborhoods)
  - `neighid`: neighborhood identifier
  - `deprive`: social-deprivation score derived from poverty concentration, health, and housing stock of local community

1. Fit a random-intercept model with `attain` as the response variable and without any covariates by ML using `xtmixed`. What are the estimated variance components between and within neighborhoods? Obtain the estimated intraclass correlation.
2. Include the covariate `deprive` in the model and interpret the estimates. Discuss the changes in the estimated standard deviations of the random intercept and level-1 residual.
3. Include the student-level covariates and interpret the estimates. Also comment on how the estimated standard deviations have changed.
4. Obtain the overall coefficient of determination R^2 for the model in step 3.

Crossed random-effects models are applied to the same data in exercise 9.5.

3.2 Grade-point-average data

Hox (2010) analyzed simulated longitudinal or panel data on 200 college students whose grade point average (GPA) was recorded over six successive semesters.

The variables in the dataset `gpa.dta` are

- `gpa1`–`gpa6`: grade point average (GPA) for semesters 1–6
- `student`: student identifier
- `highgpa`: high school GPA
- `job1`–`job6`: amount of time per week spent working for pay (0: not at all; 1: 1 hour; 2: 2 hours; 3: 3 hours; 4: 4 or more hours) in semesters 1–6
- `sex`: sex (1: male; 2: female)

1. Reshape the data to long form, stacking the time-varying variables `gpa1`–`gpa6` and `job1`–`job6` into two new variables, `gpa` and `job`, and generating a new variable, `time`, taking the values 1–6 for semesters 1–6.
2. Fit a random-intercept model with covariates `time`, `highgpa`, and `job`, and a dummy variable for males.
3. Assess whether the linearity assumptions for the three continuous covariates appear to be reasonable. You could use graphical methods, include quadratic terms, or use dummy variables for the different values of the covariates (if there are not too many).
4. Test whether there are interactions between each of the two student-level covariates and `time`.
5. For the chosen model, obtain empirical Bayes predictions of the random intercepts and produce graphs to assess their normality.

3.3 Jaw-growth data

In this jaw growth dataset from Potthoff and Roy (1964), eleven boys and sixteen girls had the distance between the center of the pituitary to the pterygomaxillary fissure recorded at ages 8, 10, 12, and 14.

The dataset `growth.dta` has the following variables:

- `idnr`: subject identifier
- `measure`: distance between pituitary and maxillary fissure in millimeters
- `age`: age in years
- `sex`: gender (1: boys; 2: girls)

1. Plot the observed growth trajectories—that is, plot `measure` against `age`—and connect successive observations on the same subject using the option `connect(ascending)`. Use the `by()` option to obtain separate graphs by sex.
2. Fit a linear random-intercept model with `measure` as the response variable and with `age` and a dummy variable for girls as explanatory variables.
3. Test whether there is a significant interaction between sex and age at the 5% level.
4. For the chosen model (with or without the interaction), add the predicted mean trajectories for boys and girls to the graph of the observed growth trajectories. (Hint: use `predict, xb`.)

Random-coefficient models are applied to the same data in exercise 7.3.

3.4 Rat-pups data

Dempster et al. (1984) analyzed data from a reproductive study on rats to assess the effect of an experimental compound on general reproductive performance and pup weights. Thirty dams (rat mothers) were randomized to three groups of 10 dams: control, low dose, and high dose of the compound. In the high-dose group, one female did not conceive, one cannibalized her litter, and one delivered one still birth, so that data on only seven litters were available for that group.

The dataset `pups.dta` has the following variables:

- `dam`: dam (pup's mother) identifier
- `sex`: sex of pup (0: male; 1: female)
- `dose`: dose group (0: controls; 1: low dose; 2: high dose)
- `w`: weight of pup in grams

1. Construct a variable, `size`, representing the size of each litter.
2. Construct a variable, `mnw`, representing the mean weight of each litter.
3. Plot `mnw` versus `size`, using different symbols for the three treatment groups. Describe the graph.

4. Fit a random-intercept model for pup weights with `sex`, `dose` (dummy variables for low and high doses), and `size` as covariates and a random intercept for `dam`. Use ML estimation.
5. Obtain level-1 and level-2 residuals, and produce graphs to assess the normality assumptions for ζ_j and ϵ_{ij}.

3.5 Georgian birthweight data

Here we use the data described in exercise 2.7. Following Neuhaus and Kalbfleisch (1998) and Pan (2002), we consider the relationship between the child's birthweight and his or her mother's age at the time of the birth, distinguishing between within-mother and between-mother effects of age.

The variables in `birthwt.dta` are

- `mother`: mother identifier
- `child`: child identifier
- `birthwt`: child's birthweight (in grams)
- `age`: mother's age at the time of the child's birth

1. Fit a random-intercept model with birthweight as the response variable and age as the explanatory variable.
2. Perform a Hausman specification test.
3. Modify the model to estimate both within-mother and between-mother effects of age.
4. Discuss what mother-level omitted covariates might be responsible for the difference between the estimated within-mother and between-mother effects.

We recommend reading either Neuhaus and Kalbfleisch (1998) or Pan (2002), the latter being less technical.

3.6 Wage-panel data

Vella and Verbeek (1998) analyzed panel data for 545 young males taken from the U.S. National Longitudinal Survey (Youth Sample) for the period 1980–1987.

The dataset `wagepan.dta` was supplied by Wooldridge (2010). The subset of variables considered here is

- `nr`: person identifier (j)
- `year`: 1980 to 1987 (i)
- `lwage`: log of hourly wage in U.S. dollars (y_{ij})
- `educ`: years of schooling (x_{2j})
- `black`: dummy variable for being black (x_{3j})
- `hisp`: dummy variable for being Hispanic (x_{4j})
- `exper`: labor-market experience defined as age$-6-$`educ` (x_{5ij})
- `expersq`: labor-market experience squared (x_{6ij})

- `married`: dummy variable for being married (x_{7ij})
- `union`: dummy variable for being a member of a union (that is, wage being set in collective bargaining agreement) (x_{8ij})

1. Ignore the clustered nature of the data, and use the `regress` command to fit the regression model

$$y_{ij} = \alpha_i + \beta_2 x_{2j} + \beta_3 x_{3j} + \beta_4 x_{4j} + \beta_5 x_{5ij} + \beta_6 x_{6ij} + \beta_7 x_{7ij} + \beta_8 x_{8ij} + \epsilon_{ij}$$

   where α_i are fixed year-specific intercepts and the covariates are defined in the bulleted list above.
2. Refit the above model using the `vce(cluster nr)` option to get standard errors taking the clustering into account. Compare the estimated standard errors with those from step 1.
3. Fit the random-intercept model

$$y_{ij} = \alpha_i + \beta_2 x_{2j} + \beta_3 x_{3j} + \beta_4 x_{4j} + \beta_5 x_{5ij} + \beta_6 x_{6ij} + \beta_7 x_{7ij} + \beta_8 x_{8ij} + \zeta_j + \epsilon_{ij}$$

   with the usual assumptions. How do the estimates of the βs compare with those from the models ignoring clustering?
4. Modify the random-intercept model to investigate whether the effect of education has increased linearly over time after controlling for the other covariates.

A wide range of longitudinal models are applied to this dataset in chapters 5 and 6.

3.7 High-school-and-beyond data Solutions

Raudenbush and Bryk (2002) and Raudenbush et al. (2004) analyzed data from the High School and Beyond Survey.

The variables in the dataset `hsb.dta` that we will use here are

- `schoolid`: school identifier (j)
- `mathach`: a measure of mathematics achievement (y_{ij})
- `ses`: socioeconomic status (SES) based on parental education, occupation, and income (x_{ij})

1. Use `xtreg` to fit a model for `mathach` with a fixed effect for SES and a random intercept for school.
2. Use `xtsum` to explore the between-school and within-school variability of SES.
3. Produce a variable, `mn_ses`, equal to the schools' mean SES and another variable, `dev_ses`, equal to the difference between the students' SES and the mean SES for their school.
4. The model in step 1 assumes that SES has the same effect within and between schools. Check this by using the covariates `mn_ses` and `dev_ses` instead of `ses` and comparing the coefficients using `lincom`.

5. Interpret the coefficients of `mn_ses` and `dev_ses`.
6. Returning to the model with `ses` as the only covariate, perform a Hausman specification test and comment on the result.

3.8 Cluster-randomized trial of sex education

Wight et al. (2002) reported on a randomized trial of sex education, and the data were also analyzed and provided by Hayes and Moulton (2009).

Twenty-five secondary schools in east Scotland were randomly assigned to a sex education program for adolescents called SHARE (Sexual Health and Relationships: Safe, Happy and Responsible) or to a control group (usual sex education). Trials in which the unit of randomization is a group are often called cluster-randomized trials.

Teachers in schools belonging to the intervention group received five days of training. They delivered 10 sessions in the third year of secondary school (at 13–14 years) and 10 sessions in the fourth year to two successive cohorts of students (students in their third year in 1996 and 1997). Out of 47 non-Catholic, qualifying schools, 25 agreed to participate. Eight thousand four hundred thirty students were recruited to the trial, and 5,854 were successfully followed up after two years.

The variables in the dataset `sex.dta` that we will use are

- `school`: school identifier
- `sex`: gender of the student (1: male; 2: female)
- `arm`: treatment group (0: control; 1: intervention)
- `scpar`: highest social class of mother or father, where social class is defined using the UK Registrar General's classification based on occupation (I is highest). (10: I; 20: II; 31: III nonmanual; 32: III manual; 40: IV; 50: V; 99: not coded)
- `kscore`: knowledge of sexual health at follow-up (score from −8 to +8)

1. Discuss whether you expect gender and social class to be approximately balanced between treatment groups (with similar frequency distributions).
2. Produce frequency tables for social class and gender by treatment group (with both absolute frequencies and percentages). Are the treatment groups adequately balanced in these variables?
3. Compare the knowledge of sexual health score at follow-up between students in the intervention and control groups. Include a random intercept for schools to allow for the cluster-randomized design. Interpret the estimated treatment effect.
4. Extend the model in step 3 by including dummy variables for gender and social class (using a dummy variable for the group for whom social class was not coded instead of discarding these data). Comment on any change in the estimated treatment effect.
5. Report the estimated residual intraclass correlation for the model in step 4, and use a likelihood-ratio test to test for zero intraclass correlation.

6. ❖ A similar trial is planned with an improved version of the sex education program. Assume that the estimated effect size from step 4 is a conservative estimate of the effect size for the new study. Also assume that the same covariates will be used and that the residual variances at the school and student levels are equal to the estimates from step 4. The new study will recruit 60 students per school; it will randomize half of the students in each school to the new sex education program and the other half to the control group. How many schools should be recruited to achieve 80% power to detect a treatment effect at the 5% level of significance, allowing for a 30% dropout rate per school?

3.9 ❖ Small-area estimation of crop areas Solutions

Here we consider the problem of estimating quantities for small areas by borrowing strength from other areas using empirical Bayes prediction. The classic reference is Rao (2003), and the classic example is introduced below.

Battese, Harter, and Fuller (1988) analyzed survey and LANDSAT satellite data on 12 Iowa counties. The counties were partitioned into segments of about 250 hectares. In the survey, farm operators reported the number of hectares within 36 of the segments that are devoted to corn. Also available are inaccurate satellite data classifying the crop for all pixels (a pixel is about 0.45 hectares) in the 12 counties as corn, soybean, or neither. The problem is to estimate the number of hectares of corn per segment for an entire county, based on accurate survey information on a small sample of segments within the county, combined with covariate information (satellite measurements) for all segments in the county. This type of problem is called *small-area estimation*.

Battese, Harter, and Fuller (1988) fit a two-level linear random-intercept model, regressing the hectares of corn reported in the survey y_{ij} for the 36 segments i for counties $j = 1, \ldots, 12$ on the number of pixels classified as corn x_{1ij} and soybean x_{2ij} from the satellite data:

$$y_{ij} = \beta_1 + \beta_2 x_{2ij} + \beta_3 x_{3ij} + \zeta_j + \epsilon_{ij}$$

They then predicted the number of hectares devoted to corn per segment for each of the counties by $\widehat{\beta}_1 + \widehat{\beta}_2 \overline{x}_{2\cdot j} + \widehat{\beta}_3 \overline{x}_{3\cdot j} + \widetilde{\zeta}_j$, where $\overline{x}_{2\cdot j}$ and $\overline{x}_{3\cdot j}$ are the county means of the pixel variables (for all segments in the counties, not just those for which survey data were available) and $\widetilde{\zeta}_j$ is the empirical Bayes prediction of ζ_j.

The dataset `cropareas.dta` contains the following variables:

- `county`: county identifier
- `name`: name of county
- `segment`: segment identifier
- `cornhec`: number of corn hectares in the segment (reported in the survey)
- `soyhec`: number of soybean hectares in the segment (reported in the survey)

- `cornpix`: number of corn pixels in the segment (from satellite data) (x_{2ij})
- `soypix`: number of soybean pixels in the segment (from satellite data) (x_{3ij})
- `mn_cornpix`: mean number of corn pixels per segment, averaged over all segments in the county ($\overline{x}_{2\cdot j}$)
- `mn_soypix`: mean number of soybean pixels per segment, averaged over all segments in the county ($\overline{x}_{3\cdot j}$)

1. Fit the model above by ML.
2. Obtain predictions following the method of Battese, Harter, and Fuller (1988). (The prediction for Cerro Gordo should be 122.28.)
3. Obtain the estimated comparative standard errors of $\widetilde{\zeta}_j$.
4. Are these standard errors appropriate for expressing the uncertainty in the small-area estimates? Explain.

3.10 ❖ Relations among within, between, and FGLS estimators

For the Georgian birthweight data used in exercise 3.5, the within-mother and between-mother standard deviations of mothers' ages x_{ij} at the birth of the child are $s_{xW} = 2.796$ years and $s_{xB} = 3.693$ years, respectively. Consider a random-intercept model for the child's birthweight (with the usual assumptions):

$$y_{ij} \;=\; \beta_1 + \beta_2 x_{ij} + \zeta_j + \epsilon_{ij}$$

The within-mother and between-mother estimates of the effect of age on birthweight are $\widehat{\beta}_2^W = 11.832$ grams/year and $\widehat{\beta}_2^B = 30.355$ grams/year, respectively. There are 878 mothers with $n=5$ births each, $\widehat{\mathrm{Var}}(\epsilon_{ij} - \overline{\epsilon}_{\cdot j}) = 150,631$ grams^2 and $\widehat{\mathrm{Var}}(\zeta_j + \overline{\epsilon}_{\cdot j}) = 161,457$ grams^2.

Based solely on the above information, obtain the following:

1. The estimated standard error of $\widehat{\beta}_2^W$.
2. The estimated standard error of $\widehat{\beta}_2^B$.
3. The FGLS estimate of β_2 for the random-intercept model.

3.11 ❖ Power analysis

1. For a random-intercept model with a single between-cluster covariate, calculate the total sample size Jn required to have 80% power to reject the null hypothesis that $\beta_2 = 0$ using a two-sided test at the 5% level. Assume that $n=20$, $\beta_2=1$, $\psi=1$, $\theta=5$, and $s_{xO}^2=0.25$.
2. Repeat the calculation in step 1 with the same assumptions except that $\psi=0$ and $\theta=6$, that is, keeping the total variance as before but setting the intraclass correlation to zero.
3. Now consider the general situation where there are two scenarios, each having the same total residual variance $\psi + \theta$, but one having $\psi > 0$ and the other $\psi=0$. Obtain an expression for the ratio of the required sample sizes Jn for these two scenarios in terms of the intraclass correlation ρ and the cluster size n. (This factor is sometimes called the "design effect" for clustered data.)

4 Random-coefficient models

4.1 Introduction

In the previous chapter, we considered linear random-intercept models where the overall level of the response was allowed to vary between clusters after controlling for covariates. In this chapter, we include random coefficients or random slopes in addition to random intercepts, thus also allowing the effects of covariates to vary between clusters. Such models involving both random intercepts and random slopes are often called *random-coefficient models*. In longitudinal settings, where the level-1 units are occasions and the clusters are typically subjects, random-coefficient models are also referred to as growth-curve models (see chapter 7).

4.2 How effective are different schools?

We start by analyzing a dataset on inner-London schools that accompanies the MLwiN software (Rasbash et al. 2009) and is part of the data analyzed by Goldstein et al. (1993).

At age 16, students took their Graduate Certificate of Secondary Education (GCSE) exams in a number of subjects. A score was derived from the individual exam results. Such scores often form the basis for school comparisons, for instance, to allow parents to choose the best school for their child. However, schools can differ considerably in their intake achievement levels. It may be argued that what should be compared is the "value added"; that is, the difference in mean GCSE score between schools after controlling for the students' achievement before entering the school. One such measure of prior achievement is the London Reading Test (LRT) taken by these students at age 11.

The dataset `gcse.dta` has the following variables:

- `school`: school identifier
- `student`: student identifier
- `gcse`: Graduate Certificate of Secondary Education (GCSE) score (z score, multiplied by 10)
- `lrt`: London Reading Test (LRT) score (z score, multiplied by 10)
- `girl`: dummy variable for student being a girl (1: girl; 0: boy)
- `schgend`: type of school (1: mixed gender; 2: boys only; 3: girls only)

One purpose of the analysis is to investigate the relationship between GCSE and LRT and how this relationship varies between schools. The model can then be used to address the question of which schools appear to be most effective, taking prior achievement into account.

We read the data using

```
. use http://www.stata-press.com/data/mlmus3/gcse
```

4.3 Separate linear regressions for each school

Before developing a model for all 65 schools combined, we consider a separate model for each school. For school j, an obvious model for the relationship between GCSE and LRT is a simple regression model,

$$y_{ij} = \beta_{1j} + \beta_{2j}x_{ij} + \epsilon_{ij}$$

where y_{ij} is the GCSE score for the ith student in school j, x_{ij} is the corresponding LRT score, β_{1j} is the school-specific intercept, β_{2j} is the school-specific slope, and ϵ_{ij} is a residual error term with school-specific variance θ_j.

For school 1, OLS estimates of the intercept $\widehat{\beta}_{11}$ and the slope $\widehat{\beta}_{21}$ can be obtained using `regress`,

```
. regress gcse lrt if school==1
```

Source	SS	df	MS		Number of obs =	73
					F(1, 71) =	59.44
Model	4084.89189	1	4084.89189		Prob > F =	0.0000
Residual	4879.35759	71	68.7233463		R-squared =	0.4557
					Adj R-squared =	0.4480
Total	8964.24948	72	124.503465		Root MSE =	8.29

gcse	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
lrt	.7093406	.0920061	7.71	0.000	.5258856	.8927955
_cons	3.833302	.9822377	3.90	0.000	1.874776	5.791828

where we have selected school 1 by specifying the condition `if school==1`.

To assess whether this is a reasonable model for school 1, we can obtain the predicted (ordinary least squares) regression line for the school,

$$\widehat{y}_{i1} = \widehat{\beta}_{11} + \widehat{\beta}_{21}x_{i1}$$

by using the `predict` command with the `xb` option:

```
. predict p_gcse, xb
```

We superimpose this line on the scatterplot of the data for the school, as shown in figure 4.1.

```
. twoway (scatter gcse lrt) (line p_gcse lrt, sort) if school==1,
> xtitle(LRT) ytitle(GCSE)
```

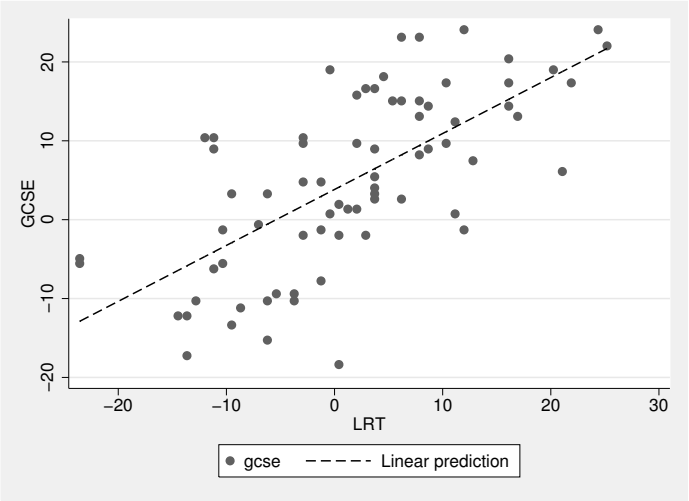


Figure 4.1: Scatterplot of `gcse` versus `lrt` for school 1 with ordinary least-squares regression line

We can also produce a *trellis graph* containing such plots for all 65 schools by using

```
. twoway (scatter gcse lrt) (lfit gcse lrt, sort lpatt(solid)),
> by(school, compact legend(off) cols(5))
> xtitle(LRT) ytitle(GCSE) ysize(3) xsize(2)
```

with the result shown in figure 4.2. The resulting graphs suggest that the model assumptions are reasonably met.

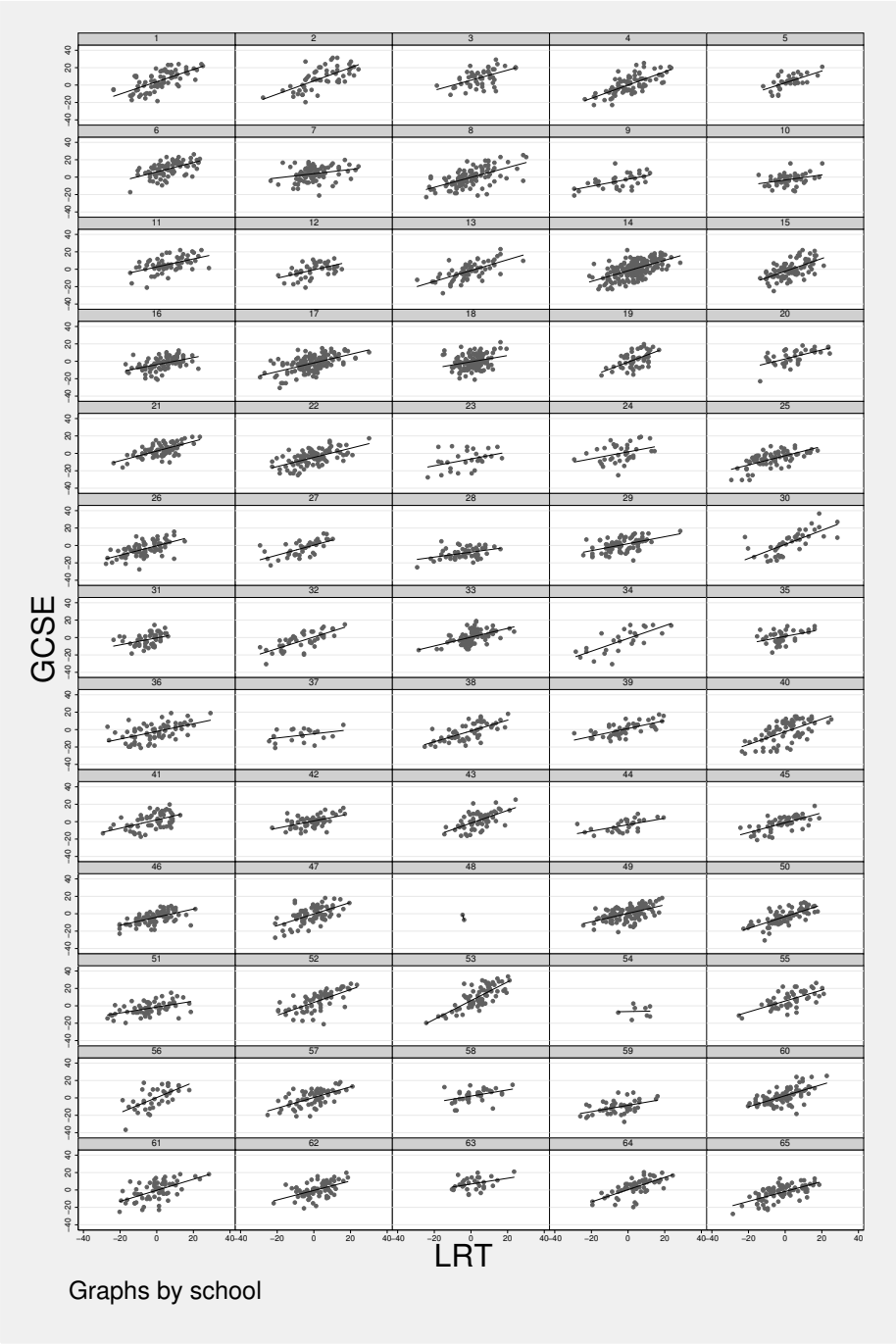


Figure 4.2: Trellis of scatterplots of `gcse` versus `lrt` with fitted regression lines for all 65 schools

We will now fit a simple linear regression model for each school, which is easily done using Stata's prefix command `statsby`. Then we will examine the variability in the estimated intercepts and slopes.

We first calculate the number of students per school by using `egen` with the `count()` function to preclude fitting lines to schools with fewer than five students:

```
. egen num = count(gcse), by(school)
```

We then use `statsby` to create a new dataset, `ols.dta`, in the local directory with the variables `inter` and `slope` containing OLS estimates of the intercepts (`_b[_cons]`) and slopes (`_b[lrt]`) from the command `regress gcse lrt if num>4` applied to each school (as well as containing the variable `school`):

```
. statsby inter=_b[_cons] slope=_b[lrt], by(school) saving(ols):
> regress gcse lrt if num>4
(running regress on estimation sample)
      command:  regress gcse lrt if num>4
        inter:  _b[_cons]
        slope:  _b[lrt]
           by:  school
Statsby groups
-----+--- 1 ---+--- 2 ---+--- 3 ---+--- 4 ---+--- 5
.....................................................    50
.............
```

We can merge the estimates `inter` and `slope` into the `gcse` dataset by using the `merge` command (after sorting the "master data" that are currently loaded by `school`; the "using data" created by `statsby` are already sorted by `school`):

```
. sort school
. merge m:1 school using ols
    Result                           # of obs.
    -----------------------------------------
    not matched                             2
        from master                         2  (_merge==1)
        from using                          0  (_merge==2)
    matched                             4,057  (_merge==3)
    -----------------------------------------
. drop _merge
```

Here we have specified `m:1` in the `merge` command, which stands for "many-to-one merging" (observations for several students per school in the master data, but only one observation per school in the using data). We see that two of the schools in the master data did not have matches in the using data (because they had fewer than five students per school, so we did not compute OLS estimates for them). We have deleted the variable `_merge` produced by the `merge` command to avoid error messages when we run the `merge` command in the future.

A scatterplot of the OLS estimates of the intercept and slope is produced using the following command and given in figure 4.3:

```
. twoway scatter slope inter, xtitle(Intercept) ytitle(Slope)
```

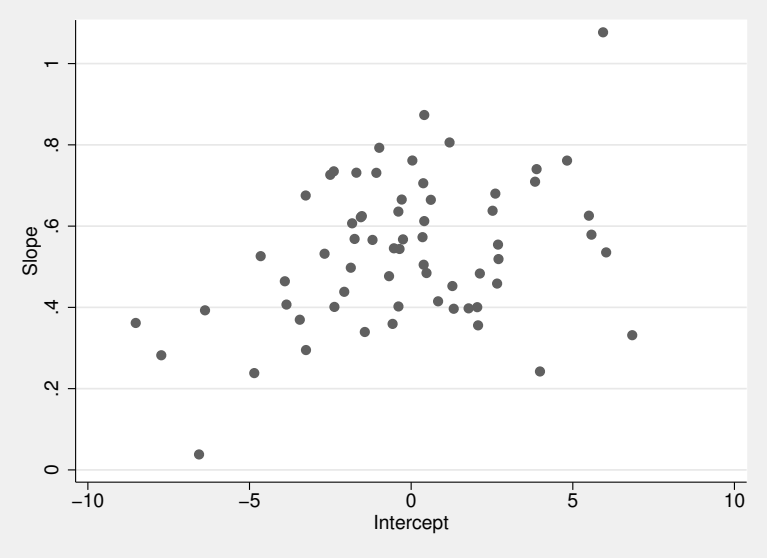


Figure 4.3: Scatterplot of estimated intercepts and slopes for all schools with at least five students

We see that there is considerable variability between the estimated intercepts and slopes of different schools. To investigate this further, we first create a dummy variable to pick out one observation per school,

```
. egen pickone = tag(school)
```

and then we produce summary statistics for the schools by using the `summarize` command:

```
. summarize inter slope if pickone == 1
    Variable |       Obs        Mean    Std. Dev.       Min        Max
-------------+--------------------------------------------------------
       inter |        64   -.1805974    3.291357  -8.519253   6.838716
       slope |        64    .5390514    .1766135   .0380965   1.076979
```

To allow comparison with the parameter estimates obtained from the random-coefficient model considered later on, we also obtain the covariance matrix of the estimated intercepts and slopes:

```
. correlate inter slope if pickone == 1, covariance
(obs=64)
             |    inter    slope
-------------+------------------
       inter |   10.833
       slope |  .208622  .031192
```

The diagonal elements, 10.83 and 0.03, are the sample variances of the intercepts and slopes, respectively. The off-diagonal element, 0.21, is the sample covariance between the intercepts and slopes, equal to the correlation times the product of the intercept and slope standard deviations.

We can also obtain a *spaghetti plot* of the predicted school-specific regression lines for all schools. We first calculate the fitted values $\widehat{y}_{ij} = \widehat{\beta}_{1j} + \widehat{\beta}_{2j}x_{ij}$,

```
. generate pred = inter + slope*lrt
(2 missing values generated)
```

and sort the data so that `lrt` increases within a given school and then jumps to its lowest value for the next school in the dataset:

```
. sort school lrt
```

We then produce the plot by typing

```
. twoway (line pred lrt, connect(ascending)), xtitle(LRT)
> ytitle(Fitted regression lines)
```

The `connect(ascending)` option is used to connect points only as long as `lrt` is increasing; it ensures that only data for the same school are connected. The resulting graph is shown in figure 4.4.

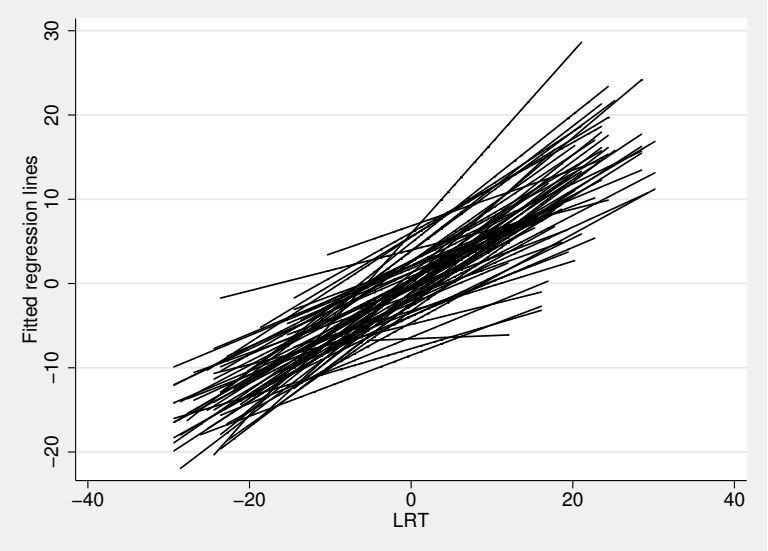


Figure 4.4: Spaghetti plot of ordinary least-squares regression lines for all schools with at least five students

4.4 Specification and interpretation of a random-coefficient model

4.4.1 Specification of a random-coefficient model

How can we develop a joint model for the relationships between `gcse` and `lrt` in all schools?

One way would be to use dummy variables for all schools (omitting the overall constant) to estimate school-specific intercepts and interactions between these dummy variables and `lrt` to estimate school-specific slopes. The only difference between the resulting model and separate regressions is that a common residual error variance $\theta_j = \theta$ is assumed. However, this model has 130 regression coefficients! Furthermore, if the schools are viewed as a (random) sample of schools from a population of schools, we are not interested in the individual coefficients characterizing each school's regression line. Rather, we would like to estimate the mean intercept and slope as well as the (co)variability of the intercepts and slopes in the population of schools.

A parsimonious model for the relationships between `gcse` and `lrt` can be obtained by specifying a school-specific random intercept ζ_{1j} and a school-specific random slope ζ_{2j} for `lrt` (x_{ij}):

$$\begin{aligned} y_{ij} &= \beta_1 + \beta_2 x_{ij} + \zeta_{1j} + \zeta_{2j} x_{ij} + \epsilon_{ij} \\ &= (\beta_1 + \zeta_{1j}) + (\beta_2 + \zeta_{2j}) x_{ij} + \epsilon_{ij} \end{aligned} \tag{4.1}$$

Here ζ_{1j} represents the deviation of school j's intercept from the mean intercept β_1, and ζ_{2j} represents the deviation of school j's slope from the mean slope β_2.

Given all covariates $\mathbf{X}_j$ in cluster j, it is assumed that the random effects ζ_{1j} and ζ_{2j} have zero expectations:

$$E(\zeta_{1j}|\mathbf{X}_j) = 0$$

$$E(\zeta_{2j}|\mathbf{X}_j) = 0$$

It is also assumed that the level-1 residual ϵ_{ij} has zero expectation, given the covariates and the random effects:

$$E(\epsilon_{ij}|\mathbf{X}_j, \zeta_{1j}, \zeta_{2j}) = 0$$

It follows from these mean-independence assumptions that the random terms ζ_{1j}, ζ_{2j}, and ϵ_{ij} are all uncorrelated with the covariate x_{ij} and that ϵ_{ij} is uncorrelated with both ζ_{1j} and ζ_{2j}. Both the intercepts ζ_{1j} and slopes ζ_{2j} are assumed to be uncorrelated across schools, and the level-1 residuals ϵ_{ij} are assumed to be uncorrelated across schools and students.

An illustration of this random-coefficient model with one covariate x_{ij} for one cluster j is shown in the bottom panel of figure 4.5. A random-intercept model is shown for comparison in the top panel.

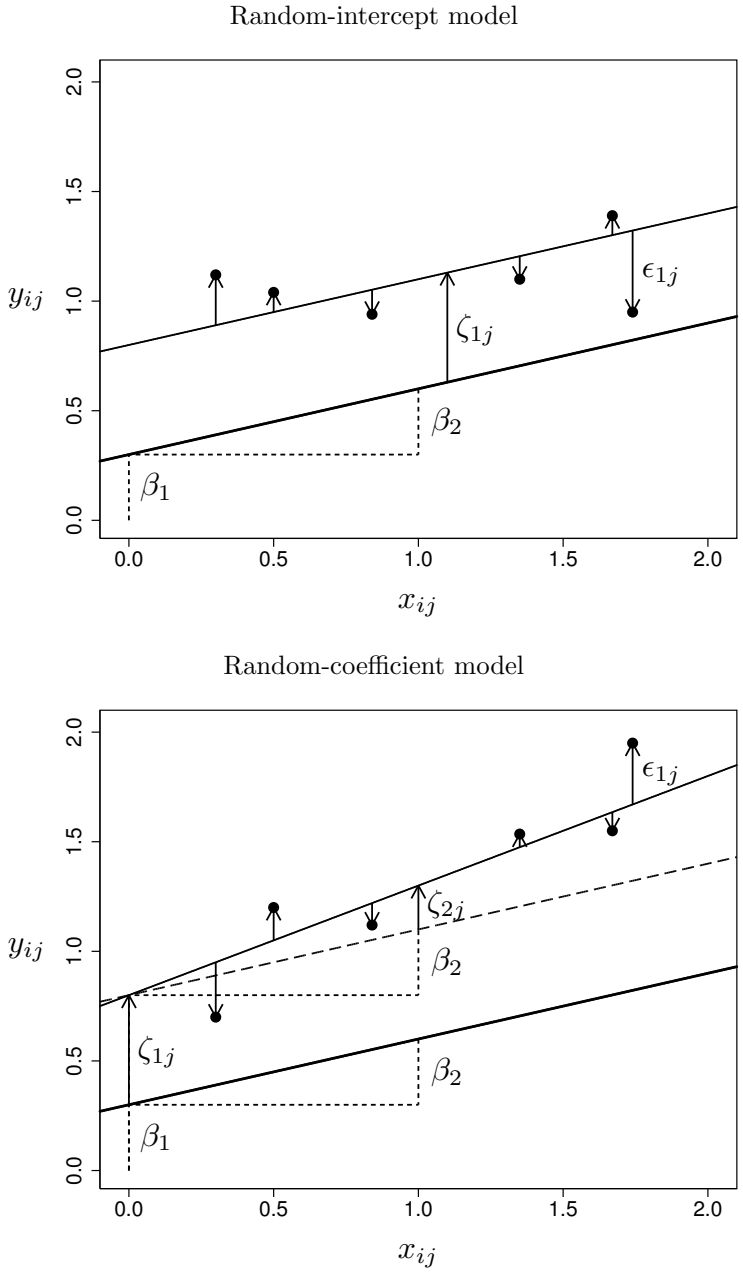


Figure 4.5: Illustration of random-intercept and random-coefficient models

In each panel, the lower bold and solid line represents the population-averaged or marginal regression line

$$E(y_{ij}|x_{ij}) = \beta_1 + \beta_2 x_{ij}$$

across all clusters. The thinner solid line represents the cluster-specific regression line for cluster j. For the random-intercept model, this is

$$E(y_{ij}|x_{ij}, \zeta_{1j}) = (\beta_1 + \zeta_{1j}) + \beta_2 x_{ij}$$

which is parallel to the population-averaged line with vertical displacement given by the random intercept ζ_{1j}. In contrast, in the random-coefficient model, the cluster-specific or conditional regression line

$$E(y_{ij}|x_{ij}, \zeta_{1j}, \zeta_{2j}) = (\beta_1 + \zeta_{1j}) + (\beta_2 + \zeta_{2j})x_{ij}$$

is not parallel to the population-averaged line but has a greater slope because the random slope ζ_{2j} is positive in the illustration. Here the dashed line is parallel to the population-averaged regression line and has the same intercept as cluster j. The vertical deviation between this dashed line and the line for cluster j is $\zeta_{2j}x_{ij}$, as shown in the diagram for $x_{ij}=1$. The bottom panel illustrates that the total intercept for cluster j is $\beta_1 + \zeta_{1j}$ and the total slope is $\beta_2 + \zeta_{2j}$. The arrows from the cluster-specific regression lines to the responses y_{ij} are the within-cluster residual error terms ϵ_{ij} (with variance θ). It is clear that $\zeta_{2j}x_{ij}$ represents an *interaction* between the clusters, treated as random, and the covariate x_{ij}.

Given $\mathbf{X}_j$, the random intercept and random slope have a bivariate distribution assumed to have zero means and covariance matrix $\mathbf{\Psi}$:

$$\mathbf{\Psi} = \begin{bmatrix} \psi_{11} & \psi_{12} \\ \psi_{21} & \psi_{22} \end{bmatrix} \equiv \begin{bmatrix} \mathrm{Var}(\zeta_{1j}|\mathbf{X}_j) & \mathrm{Cov}(\zeta_{1j}, \zeta_{2j}|\mathbf{X}_j) \\ \mathrm{Cov}(\zeta_{2j}, \zeta_{1j}|\mathbf{X}_j) & \mathrm{Var}(\zeta_{2j}|\mathbf{X}_j) \end{bmatrix}, \qquad \psi_{21} = \psi_{12}$$

Hence, given the covariates, the variance of the random intercept is ψ_{11}, the variance of the random slope is ψ_{22}, and the covariance between the random intercept and the random slope is ψ_{21}. The correlation between the random intercept and random slope given the covariates becomes

$$\rho_{21} \equiv \mathrm{Cor}(\zeta_{1j}, \zeta_{2j}|\mathbf{X}_j) \;=\; \frac{\psi_{21}}{\sqrt{\psi_{11}\psi_{22}}}$$

It is sometimes assumed that given $\mathbf{X}_j$, the random intercept and random slope have a bivariate normal distribution. An example of a bivariate normal distribution with $\psi_{11}=\psi_{22}=4$ and $\psi_{21}=\psi_{12}=1$ is shown as a perspective plot in figure 4.6. Specifying a bivariate normal distribution implies that the (marginal) univariate distributions of the intercept and slope are also normal.

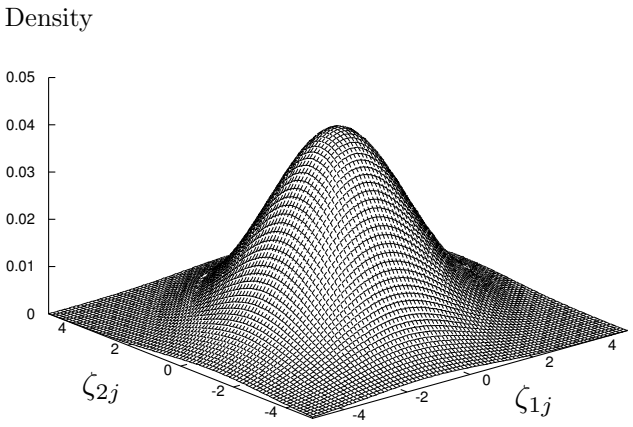


Figure 4.6: Perspective plot of bivariate normal distribution

4.4.2 Interpretation of the random-effects variances and covariances

Interpreting the covariance matrix $\mathbf{\Psi}$ of the random effects (given the covariates $\mathbf{X}_j$) is not straightforward.

First, the random-slope variance ψ_{22} and the covariance between random slope and intercept ψ_{21} depend not just on the scale of the response variable but also on the scale of the covariate, here `lrt`. Let the units of the response and explanatory variable be denoted as u_y and u_x, respectively. For instance, in an application considered in chapter 7 on children's increase in weight, u_y is kilograms and u_x is years. The units of ψ_{11} are u_y^2, the units of ψ_{21} are u_y^2/u_x, and the units of ψ_{22} are u_y^2/u_x^2. It therefore does not make sense to compare the magnitude of random-intercept and random-slope variances.

Another issue is that the total residual variance is no longer constant as in random-intercept models. The total residual is now

$$\xi_{ij} \equiv \zeta_{1j} + \zeta_{2j}x_{ij} + \epsilon_{ij}$$

and the conditional variance of the responses given the covariate, or the conditional variance of the total residual, is

$$\mathrm{Var}(y_{ij}|\mathbf{X}_j) = \mathrm{Var}(\xi_{ij}|\mathbf{X}_j) = \psi_{11} + 2\psi_{21}x_{ij} + \psi_{22}x_{ij}^2 + \theta \tag{4.2}$$

This variance depends on the value of the covariate x_{ij}, and the total residual is therefore *heteroskedastic*. The conditional covariance for two students i and i' with covariate values x_{ij} and $x_{i'j}$ in the same school j is

$$\begin{aligned}\mathrm{Cov}(y_{ij}, y_{i'j}|\mathbf{X}_j) &= \mathrm{Cov}(\xi_{ij}, \xi_{i'j}|\mathbf{X}_j) \\ &= \psi_{11} + \psi_{21}x_{ij} + \psi_{21}x_{i'j} + \psi_{22}x_{ij}x_{i'j} \qquad (4.3)\end{aligned}$$

and the conditional intraclass correlation becomes

$$\mathrm{Cor}(y_{ij}, y_{i'j}|\mathbf{X}_j) = \frac{\mathrm{Cov}(\xi_{ij}, \xi_{i'j}|\mathbf{X}_j)}{\sqrt{\mathrm{Var}(\xi_{ij}|\mathbf{X}_j)\mathrm{Var}(\xi_{i'j}|\mathbf{X}_j)}}$$

When $x_{ij} = x_{i'j} = 0$, the expression for the intraclass correlation is the same as for the random-intercept model and represents the correlation of the residuals (from the overall mean regression line) for two students in the same school who both have `lrt` scores equal to 0 (the mean). However, for pairs of students in the same school with other values of `lrt`, the intraclass correlation is a complicated function of `lrt` (x_{ij} and $x_{i'j}$).

Due to the heteroskedastic total residual variance, it is not straightforward to define coefficients of determination—such as R^2, R_2^2, and R_1^2, discussed in section 3.5—for random-coefficient models. Snijders and Bosker (2012, 114) suggest removing the random coefficient(s) for the purpose of calculating the coefficient of determination because this will usually yield values that are close to the correct version (see their section 7.2.2 for how to obtain the correct version).

Finally, interpreting the parameters ψ_{11} and ψ_{21} can be difficult because their values depend on the translation of the covariate or, in other words, on how much we add or subtract from the covariate. Adding a constant to `lrt` and refitting the model would result in different estimates of ψ_{11} and ψ_{21} (see also exercise 4.9). This is because the intercept variance is the variability in the vertical positions of school-specific regression lines where `lrt`=0 (which changes when `lrt` is translated) and the covariance or correlation is the tendency for regression lines that are higher up where `lrt`=0 to have higher slopes. This lack of invariance of ψ_{11} and ψ_{21} to translation of the covariate x_{ij} is illustrated in figure 4.7. Here identical cluster-specific regression lines are shown in the two panels, but the covariate $x'_{ij} = x_{ij} - 3.5$ in the lower panel is translated relative to the covariate x_{ij} in the upper panel. The intercepts are the intersections of the regression lines with the vertical lines at zero. Clearly these intercepts vary more in the upper panel than the lower panel, whereas the correlation between intercepts and slopes is negative in the upper panel and positive in the lower panel.

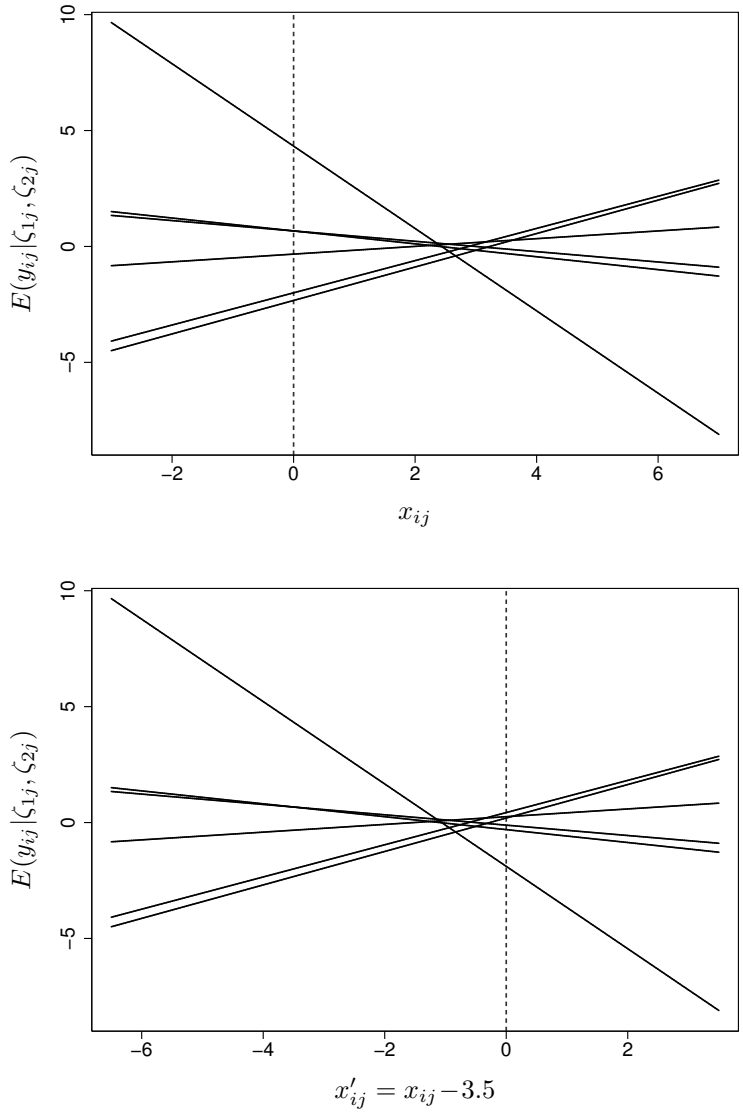


Figure 4.7: Cluster-specific regression lines for random-coefficient model, illustrating lack of invariance under translation of covariate (*Source:* Skrondal and Rabe-Hesketh 2004a)

To make ψ_{11} and ψ_{21} interpretable, it makes sense to translate x_{ij} so that the value $x_{ij} = 0$ is a useful reference point in some way. Typical choices are either mean centering (as for `lrt`) or, if x_{ij} is time, as in growth-curve models, defining 0 to be the initial time in some sense. Because the magnitude and interpretation of ψ_{21} depend on the location

(or translation) of x_{ij}, which is often arbitrary, it generally does not make sense to set ψ_{21} to 0 by specifying uncorrelated intercepts and slopes.

A useful way of interpreting the magnitude of the estimated variances $\widehat{\psi}_{11}$ and $\widehat{\psi}_{22}$ is by considering the intervals $\widehat{\beta}_1 \pm 1.96\sqrt{\widehat{\psi}_{11}}$ and $\widehat{\beta}_2 \pm 1.96\sqrt{\widehat{\psi}_{22}}$, which contain about 95% of the intercepts and slopes in the population, respectively. To aid interpretation of the random part of the model, it is also useful to produce plots of school-specific regression lines, as discussed in section 4.8.3.

4.5 Estimation using xtmixed

`xtmixed` can be used to fit linear random-coefficient models by maximum likelihood (ML) estimation or restricted maximum likelihood (REML) estimation. (`xtreg` can only fit two-level random-intercept models.)

4.5.1 Random-intercept model

We first consider the random-intercept model discussed in the previous chapter:

$$y_{ij} = (\beta_1 + \zeta_{1j}) + \beta_2 x_{ij} + \epsilon_{ij}$$

This model is a special case of the random-coefficient model in (4.1) with $\zeta_{2j} = 0$ or, equivalently, with zero random-slope variance and zero random intercept and slope covariance, $\psi_{22} = \psi_{21} = 0$.

Maximum likelihood estimates for the random-intercept model can be obtained using `xtmixed` with the `mle` option (the default):

```
. xtmixed gcse lrt || school:, mle
```

```
Mixed-effects ML regression                     Number of obs      =      4059
Group variable: school                          Number of groups   =        65
                                                Obs per group: min =         2
                                                               avg =      62.4
                                                               max =       198
                                                Wald chi2(1)       =   2042.57
Log likelihood = -14024.799                     Prob > chi2        =    0.0000
```

gcse	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
lrt	.5633697	.0124654	45.19	0.000	.5389381	.5878014
_cons	.0238706	.4002255	0.06	0.952	-.760557	.8082982

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
school: Identity				
sd(_cons)	3.035269	.3052513	2.492261	3.696587
sd(Residual)	7.521481	.0841759	7.358295	7.688285

```
LR test vs. linear regression: chibar2(01) =   403.27 Prob >= chibar2 = 0.0000
```

To allow later comparison with random-coefficient models using likelihood-ratio tests, we store these estimates using

```
. estimates store ri
```

The random-intercept model assumes that the school-specific regression lines are parallel. The common coefficient or slope β_2 of `lrt`, shared by all schools, is estimated as 0.56 and the mean intercept as 0.02. Schools vary in their intercepts with an estimated standard deviation of 3.04. Within the schools, the estimated residual standard deviation around the school-specific regression lines is 7.52. The within-school correlation, after controlling for `lrt`, is therefore estimated as

$$\widehat{\rho} \;=\; \frac{\widehat{\psi}_{11}}{\widehat{\psi}_{11}+\widehat{\theta}} \;=\; \frac{3.035^2}{3.035^2+7.521^2} = 0.14$$

The ML estimates for the random-intercept model are also given under "Random intercept" in table 4.1.

Table 4.1: Maximum likelihood estimates for inner-London schools data

	Random intercept		Random coefficient		Rand. coefficient & level-2 covariates		
Parameter	Est	(SE)	Est	(SE)	Est	(SE)	γ_{xx}
Fixed part							
β_1 [_cons]	0.02	(0.40)	−0.12	(0.40)	−1.00	(0.51)	γ_{11}
β_2 [lrt]	0.56	(0.01)	0.56	(0.02)	0.57	(0.03)	γ_{21}
β_3 [boys]					0.85	(1.09)	γ_{12}
β_4 [girls]					2.43	(0.84)	γ_{13}
β_5 [boys_lrt]					−0.02	(0.06)	γ_{22}
β_6 [girls_lrt]					−0.03	(0.04)	γ_{23}
Random part							
$\sqrt{\psi_{11}}$	3.04		3.01		2.80		
$\sqrt{\psi_{22}}$			0.12		0.12		
ρ_{21}			0.50		0.60		
$\sqrt{\theta}$	7.52		7.44		7.44		
Log likelihood	−14,024.80		−14,004.61		−13,998.83		

4.5.2 Random-coefficient model

We now relax the assumption that the school-specific regression lines are parallel by introducing random school-specific slopes $\beta_2 + \zeta_{2j}$ of `lrt`:

$$y_{ij} = (\beta_1 + \zeta_{1j}) + (\beta_2 + \zeta_{2j})x_{ij} + \epsilon_{ij}$$

To introduce a random slope for `lrt` using `xtmixed`, we simply add that variable name in the specification of the random part, replacing `school:` with `school: lrt`. We must also specify the `covariance(unstructured)` option because `xtmixed` will otherwise set the covariance, ψ_{21} (and the corresponding correlation), to zero by default. ML estimates for the random-coefficient model are then obtained using

```
. xtmixed gcse lrt || school: lrt, covariance(unstructured) mle
Mixed-effects ML regression                     Number of obs      =      4059
Group variable: school                          Number of groups   =        65
                                                Obs per group: min =         2
                                                               avg =      62.4
                                                               max =       198
                                                Wald chi2(1)       =    779.79
Log likelihood = -14004.613                     Prob > chi2        =    0.0000
```

gcse	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
lrt	.556729	.0199368	27.92	0.000	.5176535	.5958044
_cons	-.115085	.3978346	-0.29	0.772	-.8948264	.6646564

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
school: Unstructured				
sd(lrt)	.1205646	.0189827	.0885522	.1641498
sd(_cons)	3.007444	.3044148	2.466258	3.667385
corr(lrt,_cons)	.4975415	.1487427	.1572768	.7322094
sd(Residual)	7.440787	.0839482	7.278058	7.607155

```
LR test vs. linear regression:       chi2(3) =   443.64   Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference.
```

Because the `variance` option was not used, the output shows the standard deviations, `sd(lrt)`, of the slope and `sd(_cons)` of the intercept instead of variances. It also shows the correlation between intercepts and slopes, `corr(lrt,_cons)`, instead of the covariance. We can obtain the estimated covariance matrix either by replaying the estimation results with the `variance` option,

```
xtmixed, variance
```

or by using the postestimation command `estat recovariance`:

```
. estat recovariance
Random-effects covariance matrix for level school
             |        lrt      _cons
-------------+----------------------
         lrt |   .0145358
       _cons |   .1804042    9.04472
```

The ML estimates for the random-coefficient model were also given under "Random coefficient" in table 4.1 and will be interpreted in section 4.7. We store the estimates under the name `rc` for later use:

```
. estimates store rc
```

Restricted maximum likelihood (REML) estimation is obtained by specifying the `reml` option. Robust standard errors can be obtained using the `vce(robust)` option.

4.6 Testing the slope variance

Before interpreting the parameter estimates, we may want to test whether the random slope is needed in addition to the random intercept. Specifically, we test the null hypothesis

$$H_0\text{: } \psi_{22} = 0 \quad \text{against} \quad H_a\text{: } \psi_{22} > 0$$

Note that H_0 is equivalent to the hypothesis that the random slopes ζ_{2j} are all zero. The null hypothesis also implies that $\psi_{21} = 0$, because a variable that does not vary also does not covary with other variables. Setting $\psi_{22} = 0$ and $\psi_{21} = 0$ gives the random-intercept model.

A naïve likelihood-ratio test can be performed using the `lrtest` command in Stata:

```
. lrtest rc ri
Likelihood-ratio test                                 LR chi2(2)  =     40.37
(Assumption: ri nested in rc)                         Prob > chi2 =    0.0000
Note: The reported degrees of freedom assumes the null hypothesis is not on the
      boundary of the parameter space.  If this is not true, then the reported
      test is conservative.
```

However, the null hypothesis lies on the boundary of the parameter space because the variance ψ_{22} must be nonnegative, and as discussed in section 2.6.2, the likelihood-ratio statistic L does not have a simple χ^2 distribution under the null hypothesis.

Since Stata 11, the default estimation metric (transformation used during estimation) for the covariance matrix of the random effects is the square root or Cholesky decomposition (which is requested by the `matsqrt` option). This parameterization forces the covariance matrix to be *positive semidefinite* (estimates on the boundary of parameter space, for example, zero variance or perfect correlations, are allowed). It can be shown that the asymptotic null distribution for testing the null hypothesis that the variance of the q+1th random effect is zero becomes $0.5\,\chi^2(q) + 0.5\,\chi^2(q+1)$. For our case

of testing the random slope variance in a model with a random intercept and a random slope, $q=1$; it follows that the asymptotic null distribution is $0.5\,\chi^2(1)+0.5\,\chi^2(2)$. The correct p-value can be obtained as

```
. display 0.5*chi2tail(1,40.37) + 0.5*chi2tail(2,40.37)
9.616e-10
```

We see that the conclusion remains the same as for the naïve approach for this application.

If the `matlog` option is used (which was the default in Stata 10), the estimation metric for the covariance matrix of the random effects is matrix logarithms, which forces the covariance matrix to be *positive definite* (estimates on the boundary of the parameter space are not allowed). Consequently, convergence is not achieved if the ML estimates are on the boundary of the parameter space. If this leads to reverting to the model under the null hypothesis, giving a likelihood-ratio statistic equal to zero, then the asymptotic null distribution for testing the null hypothesis that the variance of the $q+1$th random effect is zero becomes $0.5\,\chi^2(0)+0.5\,\chi^2(q+1)$, where $\chi^2(0)$ has a probability mass of 1 at 0. For testing the random slope variance in a model with a random intercept and a random slope, the asymptotic null distribution is $0.5\,\chi^2(0)+0.5\,\chi^2(1)$; the correct p-value can simply be obtained by dividing the naïve p-value based on the $\chi^2(2)$ by 2.

Keep in mind that the naïve likelihood-ratio test for testing the slope variance is conservative, as is acknowledged at the bottom of the output from `lrtest`. Hence, if the null hypothesis of a zero slope variance is rejected by the naïve approach, it would also have been rejected if a correct approach had been used.

Unfortunately, there is no straightforward procedure available for testing several variances simultaneously, unless the random effects are independent (see section 8.8), and simulations must be used in this case to obtain the correct null distribution.

4.7 Interpretation of estimates

The population-mean intercept and slope are estimated as -0.12 and 0.56, respectively. These estimates are similar to those for the random-intercept model (see table 4.1) and also similar to the means of the school-specific least-squares regression lines given on page 186.

The estimated random-intercept standard deviation and level-1 residual standard deviation are somewhat lower than for the random-intercept model. The latter is because of a better fit of the school-specific regression lines for the random-coefficient model, which relaxes the restriction of parallel regression lines. The estimated covariance matrix of the intercepts and slopes is similar to the sample covariance matrix of the ordinary least-squares estimates reported on page 186.

As discussed in section 4.4.2, the easiest way to interpret the estimated standard deviations of the random intercept and random slope (conditional on the covariates) is to form intervals within which 95% of the schools' random intercepts and slopes are

expected to lie assuming normality. Remember that these intervals represent ranges within which 95% of the realizations of a *random variable* are expected to lie, a concept different from confidence intervals, which are ranges within which an *unknown parameter* is believed to lie.

For the intercepts, we obtain $-0.115 \pm 1.96 \times 3.007$, so 95% of schools have their intercept in the range -6.0 to 5.8. In other words, the school mean GCSE scores for children with average (`lrt`=0) LRT scores vary between -6.0 and 5.8. For the slopes, we obtain $0.557 \pm 1.96 \times 0.121$, giving an interval from 0.32 to 0.80. Thus 95% of schools have slopes between 0.32 and 0.80.

This exercise of forming intervals is particularly important for slopes because it is useful to know whether the slopes have different signs for different schools (which would be odd in the current example). The range from 0.32 to 0.80 is fairly wide and the regression lines for schools may cross: one school could add more value (produce higher mean GCSE scores for given LRT scores) than another school for students with low LRT scores and add less value than the other school for students with high LRT scores.

The estimated correlation $\widehat{\rho}_{21} = 0.50$ between random intercepts and slopes (given the covariates) means that schools with larger mean GCSE scores for students with average LRT scores than other schools also tend to have larger slopes than those other schools. This information, combined with the random-intercept and slope variances and the range of LRT scores, determines how much the lines cross, something that is best explored by plotting the predicted regression lines for the schools, as demonstrated in section 4.8.3.

The variance of the total residual ξ_{ij} (equal to the conditional variance of the responses y_{ij} given the covariates $\mathbf{X}_j$) was given in (4.2). We can estimate the corresponding standard deviation by plugging in the ML estimates:

$$\begin{aligned}\sqrt{\widehat{\mathrm{Var}}(\xi_{ij}|\mathbf{X}_j)} &= \sqrt{\widehat{\psi}_{11} + 2\widehat{\psi}_{21}x_{ij} + \widehat{\psi}_{22}x_{ij}^2 + \widehat{\theta}} \\ &= \sqrt{9.0447 + 2 \times 0.1804 \times x_{ij} + 0.0145 \times x_{ij}^2 + 55.3653}\end{aligned}$$

A graph of the estimated standard deviation of the total residual against the covariate `lrt` (x_{ij}) can be obtained using the following `twoway function` command, which is graphed in figure 4.8:

```
. twoway function sqrt(9.0447+2*0.1804*x+0.0145*x^2+55.3653), range(-30 30)
> xtitle(LRT) ytitle(Estimated standard deviation of total residual)
```

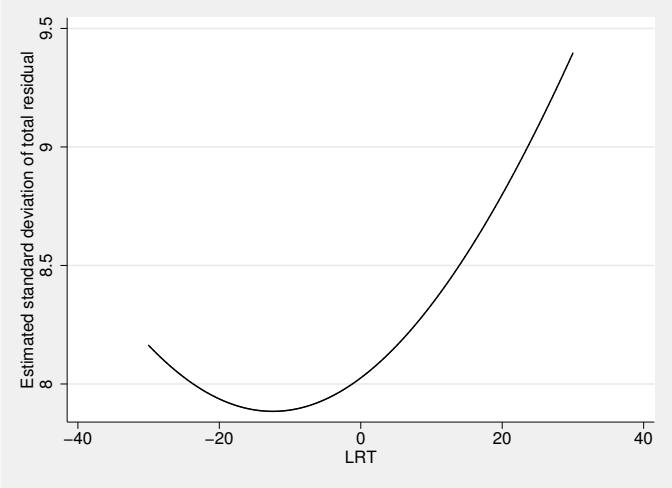


Figure 4.8: Heteroskedasticity of total residual ξ_{ij} as function of `lrt`

The estimated standard deviation of the total residual varies between just under 8 and just under 9.5.

4.8 Assigning values to the random intercepts and slopes

Having obtained estimated model parameters $\widehat{\beta}_1$, $\widehat{\beta}_2$, $\widehat{\psi}_{11}$, $\widehat{\psi}_{22}$, $\widehat{\psi}_{21}$, and $\widehat{\theta}$, we now assign values to the random intercepts and slopes, treating the estimated parameters as known (see also section 2.11). This is useful for model visualization, residual diagnostics, and inference for individual clusters, as will be demonstrated.

4.8.1 Maximum "likelihood" estimation

Maximum likelihood estimates of the random intercepts and slopes can be obtained by first predicting the total residuals $\widehat{\xi}_{ij} = y_{ij} - (\widehat{\beta}_1 + \widehat{\beta}_2 x_{ij})$ and then fitting individual regressions of $\widehat{\xi}_{ij}$ on x_{ij} for each school by OLS. As explained in section 2.11.1, we put "likelihood" in quotes in the section heading because it differs from the marginal likelihood that is used to estimate the model parameters.

We can fit the individual regression models using the `statsby` prefix command. We first retrieve the `xtmixed` estimates stored under `rc`,

```
. estimates restore rc
(results rc are active now)
```

and obtain the predicted total residuals,

```
. predict fixed, xb
. generate totres = gcse - fixed
```

We can then use `statsby` to produce the variables `mli` and `mls`, which contain the ML estimates $\widehat{\zeta}_{1j}$ and $\widehat{\zeta}_{2j}$ of the random intercepts and slopes, respectively:

```
. statsby mli=_b[_cons] mls=_b[lrt], by(school) saving(ols, replace):
> regress totres lrt
(running regress on estimation sample)
      command:  regress totres lrt
          mli:  _b[_cons]
          mls:  _b[lrt]
           by:  school
Statsby groups
----+--- 1 ----+--- 2 ----+--- 3 ----+--- 4 ----+--- 5
..................................................    50
..............
. sort school
. merge m:1 school using ols
    Result                           # of obs.
    -----------------------------------------
    not matched                             0
    matched                             4,059  (_merge==3)
    -----------------------------------------
. drop _merge
```

Maximum likelihood estimates will not be available for schools with only one observation or for schools within which x_{ij} does not vary. There are no such schools in the dataset, but school 48 has only two observations, and the ML estimates of the intercept and slope look odd:

```
. list lrt gcse mli mls if school==48, clean noobs
       lrt      gcse       mli         mls
   -4.5541   -1.2908   -32.607   -7.458484
   -3.7276   -6.9951   -32.607   -7.458484
```

Because there are only two students, the fitted line connects the points perfectly. Its intercept and slope are determined by ϵ_{1j} and ϵ_{2j} roughly as much as they are by the true intercept and slope. The intercept and slope are therefore extreme, the so-called "bouncing beta" phenomenon often encountered when using ML estimation of random effects for clusters that provide little information. In general, we therefore do not recommend using this method and suggest using empirical Bayes prediction instead.

4.8.2 Empirical Bayes prediction

As discussed for random-intercept models in section 2.11.2, empirical Bayes (EB) predictions have a smaller prediction error variance than ML estimates because of shrinkage toward the mean (for given model parameters). Furthermore, EB predictions are available for schools with only one observation or only one unique value of x_{ij}.

Empirical Bayes predictions $\widetilde{\zeta}_{1j}$ and $\widetilde{\zeta}_{2j}$ of the random intercepts ζ_{1j} and slopes ζ_{2j}, respectively, can be obtained using the `predict` command with the `reffects` option after estimation with `xtmixed`:

```
. estimates restore rc
. predict ebs ebi, reffects
```

Here we specified the variable names `ebs` and `ebi` for the EB predictions $\widetilde{\zeta}_{2j}$ and $\widetilde{\zeta}_{1j}$ of the random slopes and intercepts. The intercept variable comes last because `xtmixed` treats the intercept as the last random effect, as reflected by the output. This order is consistent with Stata's convention of treating the fixed intercept as the last regression parameter in estimation commands.

To compare the EB predictions with the ML estimates, we list one observation per school for schools 1–9 and school 48:

```
. list school mli ebi mls ebs if pickone==1 & (school<10 | school==48), noobs
```

school	mli	ebi	mls	ebs
1	3.948387	3.749336	.1526116	.1249761
2	4.937838	4.702127	.2045585	.1647271
3	5.69259	4.797687	.0222565	.0808662
4	.1526221	.3502472	.2047174	.1271837
5	2.719525	2.462807	.1232876	.0720581
6	6.147151	5.183819	-.0213858	.0586235
7	4.100312	3.640948	-.314454	-.1488728
8	-.136885	-.1218853	.0106781	.0068856
9	-2.258599	-1.767985	-.1555332	-.0886202
48	-32.607	-.4098203	-7.458484	-.0064854

Most of the time, the EB predictions are closer to zero than the ML estimates because of shrinkage, as discussed for random-intercept models in section 2.11.2. However, for models with several random effects, the relationship between EB predictions and ML estimates is somewhat more complex than for random-intercept models. The benefit of shrinkage is apparent for school 48, where the EB predictions appear more reasonable than the ML estimates.

We can see shrinkage more clearly by plotting the EB predictions against the ML estimates and superimposing a $y = x$ line. For the random intercept, the command is

```
. twoway (scatter ebi mli if pickone==1 & school!=48, mlabel(school))
> (function y=x, range(-10 10)), xtitle(ML estimate)
> ytitle(EB prediction) legend(off) xline(0)
```

and for the random slope, it is

```
. twoway (scatter ebs mls if pickone==1 & school!=48, mlabel(school))
> (function y=x, range(-0.6 0.6)), xtitle(ML estimate)
> ytitle(EB prediction) legend(off) xline(0)
```

These commands produce the graphs in figure 4.9 (we excluded school 48 from the graphs because the ML estimates are so extreme).

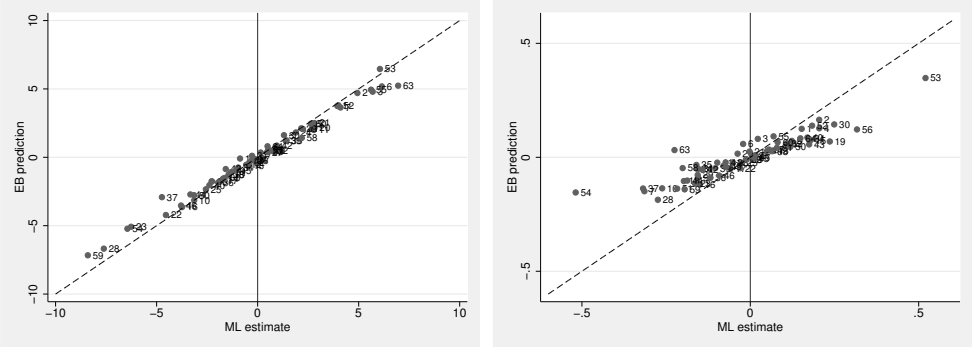


Figure 4.9: Scatterplots of empirical Bayes (EB) predictions versus maximum likelihood (ML) estimates of school-specific intercepts (left) and slopes (right); equality of EB and ML shown as dashed reference lines and ML estimates of 0 shown as solid reference lines

For ML estimates above zero, the EB prediction tends to be smaller than the ML estimate; the reverse is true for ML estimates below zero.

4.8.3 Model visualization

To better understand the random-intercept and random-coefficient models—and in particular, the variability implied by the random part—it is useful to produce graphs of predicted model-implied regression lines for the individual schools.

This can be achieved using the `predict` command with the `fitted` option to obtain school-specific fitted regression lines, with ML estimates substituted for the regression parameters (β_1 and β_2) and EB predictions substituted for the random effects (ζ_{1j} for the random-intercept model, and ζ_{1j} and ζ_{2j} for the random-coefficient model). For instance, for the random-coefficient model, the predicted regression line for school j is

$$\widehat{y}_{ij} \;=\; \widehat{\beta}_1 + \widehat{\beta}_2 x_{ij} + \widetilde{\zeta}_{1j} + \widetilde{\zeta}_{2j} x_{ij}$$

These predictions are obtained by typing

```
. predict murc, fitted
```

and a spaghetti plot is produced as follows:

```
. sort school lrt
. twoway (line murc lrt, connect(ascending)), xtitle(LRT)
> ytitle(Empirical Bayes regression lines for model 2)
```

To obtain predictions for the random-intercept model, we must first restore the estimates stored under the name `ri`:

```
. estimates restore ri
(results ri are active now)
. predict muri, fitted
. sort school lrt
. twoway (line muri lrt, connect(ascending)), xtitle(LRT)
> ytitle(Empirical Bayes regression lines for model 1)
```

The resulting spaghetti plots of the school-specific regression lines for both the random-intercept model and the random-coefficient model are given in figure 4.10.

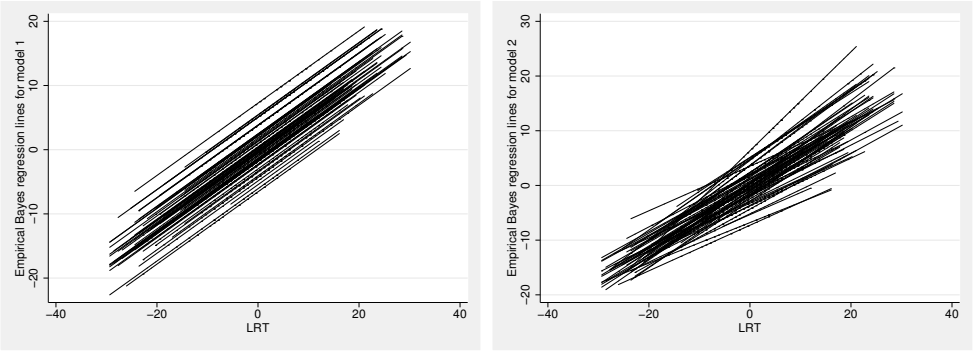


Figure 4.10: Spaghetti plots of empirical Bayes (EB) predictions of school-specific regression lines for the random-intercept model (left) and the random-intercept and random-slope model (right)

The predicted school-specific regression lines are parallel for the random-intercept model (with vertical shifts given by the $\widetilde{\zeta}_{1j}$) but are not parallel for the random-coefficient model, where the slopes $\beta_2 + \widetilde{\zeta}_{2j}$ also vary across schools. Because of shrinkage, the predicted lines vary somewhat less than implied by the estimated variances and covariance.

4.8.4 Residual diagnostics

If normality is assumed for the random intercepts ζ_{1j}, random slopes ζ_{2j}, and level-1 residuals ϵ_{ij}, the corresponding EB predictions should also have normal distributions.

To plot the distributions of the predicted random effects, we must pick one prediction per school, and we can accomplish this using the `pickone` variable created earlier. We can now plot the distributions using

```
. histogram ebi if pickone==1, normal xtitle(Predicted random intercepts)
. histogram ebs if pickone==1, normal xtitle(Predicted random slopes)
```

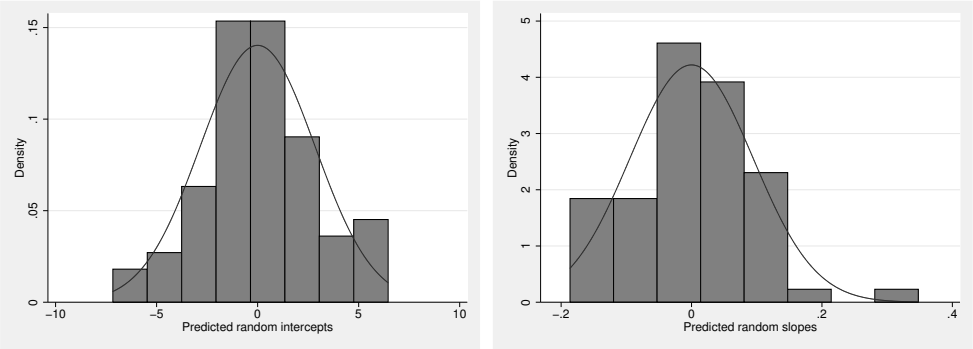


Figure 4.11: Histograms of predicted random intercepts and slopes

The histograms in figure 4.11 look approximately normal although the one for the slopes is perhaps a little positively skewed.

It is also useful to look at the bivariate distribution of the predicted random intercepts and slopes using a scatterplot, or to display such a scatterplot together with the two histograms:

```
. scatter ebs ebi if pickone==1, saving(yx, replace)
> xtitle("Random intercept") ytitle("Random slope") ylabel(, nogrid)
. histogram ebs if pickone==1, freq horizontal saving(hy, replace) normal
> yscale(alt) ytitle(" ") fxsize(35) ylabel(, nogrid)
. histogram ebi if pickone==1, freq saving(hx, replace) normal
> xscale(alt) xtitle(" ") fysize(35) ylabel(, nogrid)
. graph combine hx.gph yx.gph hy.gph, hole(2) imargin(0 0 0 0)
```

Here the scatterplot and histograms are first plotted separately and then combined using the `graph combine` command. In the first `histogram` command, the `horizontal` option is used to produce a rotated histogram of the random slopes. In both histogram commands, the `yscale(alt)` and `xscale(alt)` options are used to put the corresponding axes on the other side, and the `normal` option is used to overlay normal density curves. The `fysize(35)` and `fxsize(35)` options change the aspect ratios of the histograms, making them more flat so that they use up a smaller portion of the combined graph. Finally, in the `graph combine` command, the graphs are listed in lexicographic order, the `hole(2)` option denotes that there should be a hole in the second position—that is, the top-right corner—and the `imargin(0 0 0 0)` option reduces the space between the graphs. The resulting graph is shown in figure 4.12.

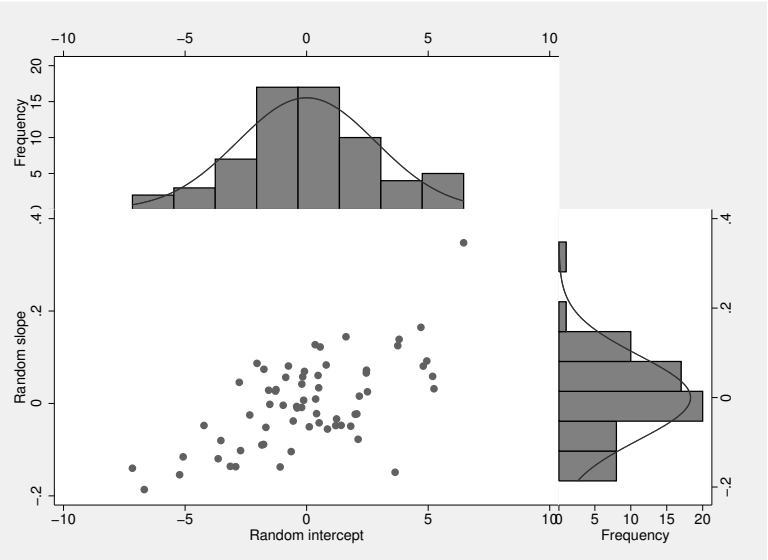


Figure 4.12: Scatterplot and histograms of predicted random intercepts and slopes

After estimation with `xtmixed`, we obtain the predicted level-1 residuals,

$$\widetilde{\epsilon}_{ij} \;=\; y_{ij} - (\widehat{\beta}_1 + \widehat{\beta}_2 x_{ij} + \widetilde{\zeta}_{1j} + \widetilde{\zeta}_{2j} x_{ij})$$

using

```
. predict res1, residuals
```

We plot the residuals using the following command, which produces the graph in figure 4.13:

```
. histogram res1, normal xtitle(Predicted level-1 residuals)
```

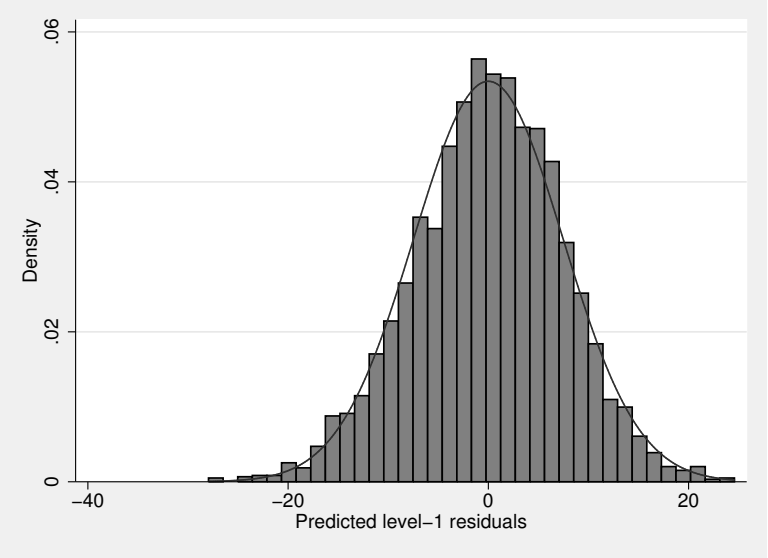


Figure 4.13: Histogram of predicted level-1 residuals

To obtain standardized level-1 residuals, use the `rstandard` option in the `predict` command after estimation using `xtmixed`.

4.8.5 Inferences for individual schools

Random-intercept predictions $\widetilde{\zeta}_{1j}$ are sometimes viewed as measures of institutional performance—in the present context, how much value the schools add for children with LRT scores equal to zero (the mean). However, we may not have adequately controlled for covariates correlated with achievement that are outside the control of the school, such as student SES. Furthermore, the model assumes that the random intercepts are uncorrelated with the LRT scores, so if schools with higher mean LRT scores add more value, their value added would be underestimated. Nevertheless, predicted random intercepts shed some light on the research question: Which schools are most effective for children with LRT $= 0$?

It does not matter whether we add the predicted fixed part of the model because the ranking of schools is not affected by this.

Returning to the question of comparing the schools' effectiveness for children with LRT scores equal to 0, we can plot the predicted random intercepts with approximate 95% confidence intervals based on the comparative standard errors (see section 2.11.3). These standard errors can be obtained using

```
. estimates restore rc
. predict slope_se inter_se, reses
```

We only need `inter_se`. We first produce ranks for the schools in ascending order of the random intercept predictions `ebi`:

```
. gsort + ebi - pickone
. generate rank = sum(pickone)
```

Here the `gsort` command is used to sort in ascending order of `ebi` (indicated by "`+ ebi`") and, within `ebi`, in descending order of `pickone` (indicated by "`- pickone`"). The `sum()` function forms the cumulative sum, so the variable `rank` increases by one every time a new school with higher value of `ebi` is encountered. Before producing the graph, we generate a variable, `labpos`, for the vertical positions in the graph where the school identifiers should go:

```
. generate labpos = ebi + 1.96*inter_se + .5
```

We are now ready to produce a so-called *caterpillar plot*:

```
. serrbar ebi inter_se rank if pickone==1, addplot(scatter labpos rank,
> mlabel(school) msymbol(none) mlabpos(0)) scale(1.96) xtitle(Rank)
> ytitle(Prediction) legend(off)
```

The school labels were added to the graph by superimposing a scatterplot onto the error bar plot with the `addplot()` option, where the vertical positions of the labels are given by the variable `labpos`. The resulting caterpillar plot is shown in figure 4.14.

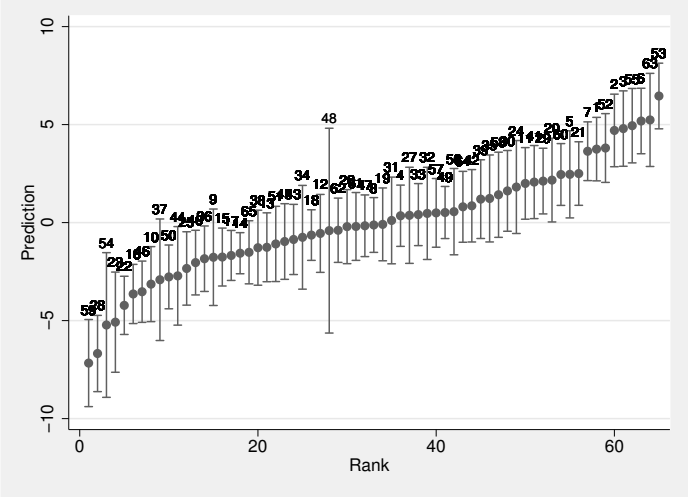


Figure 4.14: Caterpillar plot of random-intercept predictions and approximate 95% confidence intervals versus ranking (school identifiers shown on top of confidence intervals)

The interval for school 48 is particularly wide because there are only two students from this school in the dataset. It is clear from the large confidence intervals that the rankings are not precise and that perhaps only a coarse classification into poor, medium, and good schools can be justified.

An alternative method for producing a caterpillar plot is to first generate the confidence limits `lower` and `upper`,

```
. generate lower = ebi - 1.96*inter_se
. generate upper = ebi + 1.96*inter_se
```

and then use the `rcap` plot type to produce the intervals:

```
. twoway (rcap lower upper rank, blpatt(solid) lcol(black))
> (scatter ebi rank)
> (scatter labpos rank, mlabel(school) msymbol(none) mlabpos(0)
> mlabcol(black) mlabsiz(medium)),
> xtitle(Rank) ytitle(Prediction) legend(off)
> xscale(range(1 65)) xlabel(1/65) ysize(1)
```

Here `scatter` is first used to overlay the point estimates and then the labels. The `ysize()` option is used to change the aspect ratio and obtain the horizontally stretched graph shown in figure 4.15.

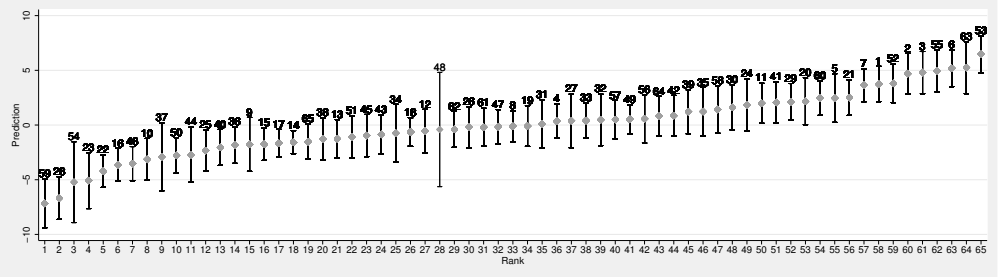


Figure 4.15: Stretched caterpillar plot of random-intercept predictions and approximate 95% confidence intervals versus ranking (school identifiers shown on top of confidence intervals)

We could also produce similar plots for children with different values x^0 of the LRT scores:

$$\widehat{\beta}_1 + \widehat{\beta}_2 x^0 + \widetilde{\zeta}_{1j} + \widetilde{\zeta}_{2j} x^0$$

For instance, in a similar application, Goldstein et al. (2000) substitute the 10th percentile of the intake measure to compare school effectiveness for poorly performing children. (To obtain confidence intervals for different values of x^0 requires posterior correlations that are produced by `gllapred`, the prediction command for `gllamm`.)

4.9 Two-stage model formulation

In this section, we describe an alternative way of specifying random-coefficient models that is popular in some areas such as education (for example, Raudenbush and Bryk 2002). As shown below, models are specified in two stages (for levels 1 and 2), necessitating a distinction between level-1 and level-2 covariates. Many people find this formulation helpful for interpreting and specifying models. Identical models can be formulated using either the approach discussed up to this point or the two-stage formulation.

To express the random-coefficient model using a two-stage formulation, Raudenbush and Bryk (2002) specify a level-1 model:

$$y_{ij} = \beta_{0j} + \beta_{1j}x_{ij} + r_{ij}$$

where the intercept β_{0j} and slope β_{1j} are school-specific coefficients. Their level-2 models have these coefficients as responses:

$$\begin{aligned} \beta_{0j} &= \gamma_{00} + u_{0j} \\ \beta_{1j} &= \gamma_{10} + u_{1j} \end{aligned} \tag{4.4}$$

Sometimes the first of these level-2 models is referred to as a "means as outcomes" or "intercepts as outcomes" model, and the second as a "slopes as outcomes" model. It is typically assumed that given the covariate(s), the residuals or disturbances u_{0j} and u_{1j} in the level-2 model have a bivariate normal distribution with zero mean and covariance matrix

$$\mathbf{T} = \begin{bmatrix} \tau_{00} & \tau_{01} \\ \tau_{10} & \tau_{11} \end{bmatrix}, \qquad \tau_{10} = \tau_{01}$$

The level-2 models cannot be fit on their own because the random effects β_{0j} and β_{1j} are not observed. Instead, we must substitute the level-2 models into the level-1 model to obtain the *reduced-form* model for the observed responses, y_{ij}:

$$\begin{aligned} y_{ij} &= \underbrace{\gamma_{00} + u_{0j}}_{\beta_{0j}} + \underbrace{(\gamma_{10} + u_{1j})}_{\beta_{1j}} x_{ij} + r_{ij} \\ &= \underbrace{\gamma_{00} + \gamma_{10}x_{ij}}_{\text{fixed}} + \underbrace{u_{0j} + u_{1j}x_{ij} + r_{ij}}_{\text{random}} \\ &\equiv \beta_1 + \beta_2 x_{ij} + \zeta_{1j} + \zeta_{2j}x_{ij} + \epsilon_{ij} \end{aligned}$$

In the reduced form, the fixed part is usually written first, followed by the random part. We can return to our previous notation by defining $\beta_1 \equiv \gamma_{00}$, $\beta_2 \equiv \gamma_{10}$, $\zeta_{1j} \equiv u_{0j}$, $\zeta_{2j} \equiv u_{1j}$, and $\epsilon_{ij} \equiv r_{ij}$. The above model is thus equivalent to the model in (4.1).

Any level-2 covariates (covariates that do not vary at level 1) are included in the level-2 models. For instance, we could include dummy variables for type of school: w_{1j} for boys schools and w_{2j} for girls schools, with mixed schools as the reference category. If we include these dummy variables in the model for the random intercept,

$$\beta_{0j} = \gamma_{00} + \gamma_{01}w_{1j} + \gamma_{02}w_{2j} + u_{0j}$$

the reduced form becomes

$$\begin{aligned} y_{ij} &= \underbrace{\gamma_{00} + \gamma_{01}w_{1j} + \gamma_{02}w_{2j} + u_{0j}}_{\beta_{0j}} + \underbrace{\left(\gamma_{10} + u_{1j}\right)}_{\beta_{1j}} x_{ij} + r_{ij} \\ &= \underbrace{\gamma_{00} + \gamma_{01}w_{1j} + \gamma_{02}w_{2j} + \gamma_{10}x_{ij}}_{\text{fixed}} + \underbrace{u_{0j} + u_{1j}x_{ij} + r_{ij}}_{\text{random}} \end{aligned}$$

If we also include the dummy variables for type of school in the model for the random slope,

$$\beta_{1j} = \gamma_{10} + \gamma_{11}w_{1j} + \gamma_{12}w_{2j} + u_{1j}$$

we obtain so-called *cross-level interactions* between covariates varying at different levels—w_{1j} and x_{ij} as well as w_{2j} and x_{ij}—in the reduced form

$$\begin{aligned} y_{ij} &= \underbrace{\gamma_{00} + \gamma_{01}w_{1j} + \gamma_{02}w_{2j} + u_{0j}}_{\beta_{0j}} + \underbrace{\left(\gamma_{21} + \gamma_{22}w_{2j} + \gamma_{23}w_{3j} + u_{1j}\right)}_{\beta_{1j}} x_{ij} + r_{ij} \\ &= \underbrace{\gamma_{00} + \gamma_{01}w_{1j} + \gamma_{02}w_{2j} + \gamma_{10}x_{ij} + \gamma_{11}w_{1j}x_{ij} + \gamma_{12}w_{2j}x_{ij}}_{\text{fixed}} + \underbrace{u_{0j} + u_{1j}x_{ij} + r_{ij}}_{\text{random}} \end{aligned}$$

The effect of `lrt` now depends on the type of school, with γ_{11} representing the additional effect of `lrt` on `gcse` for boys schools compared with mixed schools and γ_{12} representing the additional effect for girls schools compared with mixed schools.

For estimation in `xtmixed`, it is necessary to convert the two-stage formulation to the reduced form because the fixed part of the model is specified first, followed by the random part of the model. Using factor variables in `xtmixed`, the command is

```
. xtmixed gcse i.schgend##c.lrt || school: lrt, covariance(unstructured) mle
Mixed-effects ML regression                     Number of obs      =      4059
Group variable: school                          Number of groups   =        65
                                                Obs per group: min =         2
                                                               avg =      62.4
                                                               max =       198
                                                Wald chi2(5)       =    803.89
Log likelihood = -13998.825                     Prob > chi2        =    0.0000
```

gcse	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
schgend						
2	.8546715	1.085021	0.79	0.431	-1.271931	2.981274
3	2.43341	.8433413	2.89	0.004	.7804919	4.086329
lrt	.5712361	.0271256	21.06	0.000	.5180708	.6244014
schgend# c.lrt						
2	-.0230098	.0573895	-0.40	0.688	-.1354911	.0894716
3	-.029544	.0447032	-0.66	0.509	-.1171606	.0580726
_cons	-.9976073	.506809	-1.97	0.049	-1.990935	-.0042799

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
school: Unstructured				
sd(lrt)	.1199154	.0189129	.0880287	.1633525
sd(_cons)	2.797934	.28868	2.285672	3.425005
corr(lrt,_cons)	.5967727	.1381314	.2614253	.8035676
sd(Residual)	7.441831	.0839662	7.279067	7.608235

```
LR test vs. linear regression:       chi2(3) =   381.45   Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference.
```

Here `schgend` is 1 for mixed schools, 2 for boys schools and 3 for girls schools. We see that students from girls schools perform significantly better at the 5% level than students from mixed schools, whereas students from boys schools do not perform significantly better than students from mixed schools. The effect of `lrt` does not differ significantly between boys schools and mixed schools or between girls schools and mixed schools. The estimates and the corresponding parameters in the two-stage formulation are given under "Rand. coefficient & level-2 covariates" in the last three columns of table 4.1 on page 195.

Although equivalent models can be specified using either the reduced-form (used by `xtmixed`) or the two-stage formulation (used in the HLM software of Raudenbush et al. [2004]), in practice, model specification to some extent depends on the approach adopted. For instance, cross-level interactions are easily included using the two-stage specification in the HLM software, whereas same-level interactions must be created outside the program. Papers using HLM tend to include more cross-level interactions and more random

coefficients in the models (because the level-2 models look odd without residuals) than papers using, for instance, Stata.

4.10 Some warnings about random-coefficient models

4.10.1 Meaningful specification

It rarely makes sense to include a random slope if there is no random intercept, just like interactions between two covariates usually do not make sense without including the covariates themselves in standard regression models. Similarly, it is seldom sensible to include a random slope without including the corresponding fixed slope because it is usually strange to allow the slope to vary randomly but constrain its population mean to zero.

It is generally not a good idea to include a random coefficient for a covariate that does not vary at a lower level than the random coefficient itself. For example, in the inner-London schools data, it does not make sense to include a random slope for type of school because type of school does not vary within schools. Because we cannot estimate the effect of type of school for individual schools, it also appears impossible to estimate the variability of the effect of type of school between schools. However, level-2 random coefficients of level-2 covariates can be used to construct heteroskedastic random intercepts (see section 7.5.2).

4.10.2 Many random coefficients

It may be tempting to allow many different covariates to have random slopes. However, the number of parameters for the random part of the model increases rapidly with the number of random slopes because there is a variance parameter for each random effect (intercept or slope) and a covariance parameter for each *pair* of random effects. If there are k random slopes (plus one random intercept), then there are $(k+2)(k+1)/2+1$ parameters in the random part (for example, $k=3$ gives 11 parameters).

Another problem is that clusters may not provide much information on cluster-specific slopes and hence on the slope variance either if the clusters are small, or if x_{ij} does not vary much within clusters or varies only in a small number of clusters. Perhaps a useful rule is to consider the random part of the model (ignoring the fixed part) and replace the random effects with fixed regression coefficients. It should be possible (even if not very sensible) to fit the resulting model to a good number of clusters (say, 20 or more). Note, however, that it does not matter if some of the clusters have insufficient data as long as there are an adequate number of clusters that do have sufficient data. It is never a good idea to discard clusters merely because they provide little information on some of the parameters of the model.

In general, it makes sense to allow for more flexibility in the fixed part of the model than in the random part. For instance, the fixed part of the model may include a dummy variable for each occasion in longitudinal data, but in the random part of the model it may be sufficient to allow for a random intercept and a random slope of time, keeping in mind that in this case it is only assumed that the *deviation* from the population-average curve is linear in time, not that the relationship itself is linear.

The overall message is that random slopes should be included only if strongly suggested by the subject-matter theory related to the application *and* if the data provide sufficient information.

4.10.3 Convergence problems

Convergence problems can manifest themselves in different ways. Either estimates are never produced, or standard errors are missing, or `xtmixed` produces messages such as "nonconcave", or "backed-up", or "standard error calculation has failed". Sometimes none of these things happen, but the confidence intervals for some of the correlations cover the full permissible range from -1 to 1 (see sections 7.3 and 8.13.2 for examples).

Convergence problems can occur because the estimated covariance matrix "tries" to become negative definite, meaning, for instance, that variances try to become negative or correlations try to be greater than 1 or less than -1. All the commands in Stata force the covariance matrix to be positive (semi)definite, and when parameters approach nonpermissible values, convergence can be slow or even fail. It may help to translate and rescale x_{ij} because variances and covariances are not invariant to these transformations. Often a better remedy is to simplify the model by removing some random slopes. Convergence problems can also occur because of lack of identification, and again, a remedy is to simplify the model.

However, before giving up on a model, it is worth attempting to achieve convergence by trying both the `mle` and the `reml` options, specifying the `difficult` option, trying the `matlog` option (which parameterizes the random part differently during maximization), or increasing the number of EM iterations using either the `emiterate()` option or even the `emonly` option. It can also be helpful to monitor the iterations more closely by using `trace`, which displays the parameter estimates at the end of each iteration (unfortunately, not for the EM iterations). Lack of identification of a parameter might be recognized by that parameter changing wildly between iterations without much of a change in the log likelihood. Problems with variances approaching zero can be detected by noticing that the log-standard deviation takes on very large negative values.

4.10.4 Lack of identification

Sometimes random-coefficient models are simply not identified (or in other words, underidentified). As an important example, consider balanced data with clusters of size $n_j = 2$ and with a covariate x_{ij} taking the same two values $t_1 = 0$ and $t_2 = 1$ for each

cluster (an example would be the peak-expiratory-flow data from chapter 2). A model including a random intercept, a random slope of x_{ij}, and a level-1 residual, all of which are normally distributed, is not identified in this case. This can be seen by considering the two distinct variances (for $i = 1$ and $i = 2$) and one covariance of the total residuals when $t_1 = 0$ and $t_2 = 1$:

$$\begin{aligned} \mathrm{Var}(\xi_{1j}) &= \psi_{11} + \theta \\ \mathrm{Var}(\xi_{2j}) &= \psi_{11} + 2\psi_{21} + \psi_{22} + \theta \\ \mathrm{Cov}(\xi_{1j}, \xi_{2j}) &= \psi_{11} + \psi_{21} \end{aligned}$$

The marginal distribution of y_{ij} given the covariates is normal and therefore completely characterized by the fixed part of the model and these three model-implied moments (two variances and a covariance). However, the three moments are determined by four parameters of the random part (ψ_{11}, ψ_{22}, ψ_{21}, and θ), so fitting the model-implied moments to the data would effectively involve solving three equations for four unknowns. The model is therefore not identified. We could identify the model by setting $\theta = 0$, which does not impose any restrictions on the covariance matrix (however, such a constraint is not allowed in `xtmixed`). The original model becomes identified if the covariate x_{ij}, which has a random slope, varies also between clusters because the model-implied covariance matrix of the total residuals then differs between clusters, yielding more equations to solve for the four parameters.

Still assuming that the random effects and level-1 residual are normally distributed, consider now the case of balanced data with clusters of size $n_j = 3$ and with a covariate x_{ij} taking the same three values t_1, t_2, and t_3 for each cluster. An example would be longitudinal data with three occasions at times t_1, t_2, and t_3. Instead of including a random intercept and a random slope of time, it may be tempting to specify a random-coefficient model with a random-intercept and two random coefficients for the dummy variables for occasions two and three. In total, such a model would contain seven (co)variance parameters: six for the three random effects and one for the level-1 residual variance. Because the covariance matrix of the responses for the three occasions given the covariates only has six elements, it is impossible to solve for all unknowns. The same problem could occur when attempting to fit this kind of model for more than three occasions.

4.11 Summary and further reading

In this chapter, we have introduced the notion of slopes or regression coefficients varying randomly between clusters in linear models. Linear random-coefficient models are parsimonious representations of situations where each cluster has a separate regression model with its own intercept and slope. The linear random-coefficient model was applied to a cross-sectional study of school effectiveness. Here students were nested in schools, and we considered school-specific regressions.

An important consideration when using random-coefficient models is that the interpretation of the covariance matrix of the random effects depends on the scale and location of the covariates having random slopes. One should thus be careful when interpreting the variance and covariance estimates. We briefly demonstrated a two-stage formulation of random-coefficient models that is popular in some fields. This formulation can be used to specify models that are equivalent to models specified using the reduced-form formulation used in this book.

The utility of empirical Bayes prediction was demonstrated for visualizing the model, making inferences for individual clusters, and for diagnostics. See Skrondal and Rabe-Hesketh (2009) for a detailed discussion of prediction of random effects.

Introductory books discussing random-coefficient models include Snijders and Bosker (2012, chap. 5), Kreft and de Leeuw (1998, chap. 3), and Raudenbush and Bryk (2002, chap. 2, 4). Papers and chapters with good overviews of much of the material we covered in chapters 2–4 include Snijders (2004), Duncan, Jones, and Moon (1998), and Steenbergen and Jones (2002); a useful list of multilevel terminology is provided by Diez Roux (2002). These papers and chapters are among those collected in Skrondal and Rabe-Hesketh (2010).

The first six exercises are on standard random-coefficient models applied to data from different disciplines, whereas exercises 4.7 and 4.8 use random-coefficient models to fit biometrical genetic models to nuclear family data. Random-coefficient models for longitudinal data, often called growth-curve models, are considered in chapter 7. Exercises 7.2, 7.5, 7.6, and 7.7, and parts of the other exercises in that chapter can be viewed as supplementary exercises for the current chapter. Parts of exercises 6.1 and 6.2 are also relevant.

4.12 Exercises

4.1 ❖ Inner-London schools data

1. Fit the random-coefficient model fit on page 212.
2. Write down a model with the same covariates as in step 1 that also allows the mean for mixed schools to differ between boys and girls. (The variable `girl` is a dummy variable for the student being a girl.) Write down null hypotheses in terms of linear combinations of regression coefficients for the following research questions:
   a. Do girls do better in girls schools than in mixed schools (after controlling for the other covariates)?
   b. Do boys do better in boys schools than in mixed schools (after controlling for the other covariates)?
3. Fit the model from step 2, and test the null hypotheses from step 2. Discuss whether there is evidence that children of a given gender do better in single-sex schools.

4.2 High-school-and-beyond data

Raudenbush and Bryk (2002) and Raudenbush et al. (2004) analyzed data from the High School and Beyond Survey.

The dataset `hsb.dta` has the following variables:

- Level 1 (student)
  - `mathach`: a measure of mathematics achievement
  - `minority`: dummy variable for student being nonwhite
  - `female`: dummy variable for student being female
  - `ses`: socioeconomic status (SES) based on parental education, occupation, and income
- Level 2 (school)
  - `schoolid`: school identifier
  - `sector`: dummy variable for school being Catholic
  - `pracad`: proportion of students in the academic track
  - `disclim`: scale measuring disciplinary climate
  - `himinty`: dummy variable for more than 40% minority enrollment

Raudenbush et al. (2004) specify a two-level model. We will use their model and notation here. At level 1, math achievement Y_{ij} is regressed on student's SES, centered around the school mean:

$$Y_{ij} \;=\; \beta_{0j} + \beta_{1j}(X_{1ij} - \overline{X}_{1.j}) + r_{ij}, \quad r_{ij} \sim N(0, \sigma^2)$$

where X_{1ij} is the student's SES, $\overline{X}_{1.j}$ is the school mean SES, and r_{ij} is a level-1 residual. At level 2, the intercepts and slopes are regressed on the dummy variable W_{1j} for the school being a Catholic school (`sector`) and on the school mean SES

$$\beta_{pj} \;=\; \gamma_{p0} + \gamma_{p1}W_{1j} + \gamma_{p2}\overline{X}_{1.j} + u_{pj}, \quad p=0,1, \quad (u_{0j}, u_{1j})' \sim N(\mathbf{0}, \mathbf{T})$$

where u_{pj} is a random effect (a random intercept if $p=0$ and a random slope if $p=1$). The covariance matrix

$$\mathbf{T} = \begin{bmatrix} \tau_{00} & \tau_{01} \\ \tau_{10} & \tau_{11} \end{bmatrix}$$

has three unique elements with $\tau_{10}=\tau_{01}$.

1. Substitute the level-2 models into the level-1 model, and write down the resulting reduced form using the notation of this book.
2. Construct the variables `meanses`, equal to the school-mean SES ($\overline{X}_{1.j}$), and `devses`, equal to the deviations of the student's SES from their school means ($X_{1ij} - \overline{X}_{1.j}$).
3. Fit the model considered by Raudenbush et al. (2004) using `xtmixed` and interpret the coefficients. In particular, interpret the estimate of γ_{12}.

4. Fit the model that also includes `disclim` in the level-2 models and `minority` in the level-1 model.

4.3 Homework data

Kreft and de Leeuw (1998) consider a subsample of students in eighth grade from the National Education Longitudinal Study of 1988 (NELS–88) collected by the National Center for Educational Statistics of the U.S. Department of Education. The students are viewed as nested in schools.

The data are given in `homework.dta`. In this exercise, we will use the following subset of the variables:

- `schid`: school identifier
- `math`: continuous measure of achievement in mathematics (standardized to have a mean of 50 and a standard deviation of 10)
- `homework`: number of hours of homework done per week
- `white`: student's race (1: white; 0: nonwhite)
- `ratio`: class size as measured by the student–teacher ratio
- `meanses`: school mean socioeconomic status (SES)

1. Write down and state the assumptions of a random-coefficient model with `math` as response variable and `homework`, `white`, and `ratio` as covariates. Let the intercept and the effect of `homework` vary between schools.
2. Fit the model by ML and interpret the estimated parameters.
3. Derive an expression for the estimated variance of math achievement conditional on the covariates.
4. How would you extend the model to investigate whether the effect of homework on math achievement depends on the mean SES of schools? Write down both the two-stage and the reduced-form formulation of your extended model.
5. Fit the model from step 4.

4.4 Wheat and moisture data

Littell et al. (2006) describe data on ten randomly chosen varieties of winter wheat. Each variety was planted on six randomly selected 1-acre plots of land in a 60-acre field. The amount of moisture in the top 36 inches of soil was determined for each plot before planting the wheat. The response variable is the yield in bushels per acre.

The data, `wheat.dta`, contain the following variables:

- `variety`: variety (or type) of wheat (j)
- `plot`: plot (1 acre) on which wheat was planted (i)
- `yield`: yield in bushels per acre (y_{ij})
- `moist`: amount of moisture in top 36 inches of soil prior to planting (x_{ij})

In this exercise, variety of wheat will be treated as the cluster.

1. Write down the model for `yield` with a fixed and random intercept for variety of wheat and a fixed and variety-specific random slope of `moist`. State all model assumptions.
2. Fit the random-coefficient model using ML estimation.
3. Use a likelihood-ratio test to test the null hypothesis that the random-coefficient variance is zero.
4. For the chosen model, obtain the predicted yields for each variety (with EB predictions substituted for the random effects).
5. Produce a trellis graph of predicted yield versus moisture, using the `by()` option to obtain a separate graph for each variety.
6. Produce the same graphs as above but with observed values of yield added as dots.

4.5 Well-being in the U.S. army data Solutions

Bliese (2009) provides the data analyzed by Bliese and Halverson (1996). The data are on soldiers (with the lowest five enlisted ranks) from 99 U.S. army companies in noncombat environments stationed in the U.S. and Europe.

The variables in the dataset `army.dta` are the following:

- `grp`: army company identification number
- `wbeing`: well-being assessed using the General Well-Being Schedule (Dupuy 1978), an 18-item scale measuring depression, anxiety, somatic complaints, positive well-being, and emotional control
- `hrs`: answer to the question "How many hours do you usually work in a day?"
- `cohes`: score on horizontal cohesion scale consisting of eight items, including "My closest relationships are with people I work with"
- `lead`: score on an 11-item leadership consideration (vertical cohesion) scale with a typical item being "The noncommissioned officer in this company would lead well in combat"

1. Fit a random-intercept model for `wbeing` with fixed coefficients for `hrs`, `cohes`, and `lead`, and a random intercept for `grp`. Use ML estimation.
2. Form the cluster means of the three covariates from step 1, and add them as further covariates to the random-intercept model. Which of the cluster means have coefficients that are significant at the 5% level?
3. Refit the model from step 2 after removing the cluster means that are not significant at the 5% level. Interpret the remaining coefficients and obtain the estimated intraclass correlation.
4. We have included soldier-specific covariates x_{ij} in addition to the cluster means $\overline{x}_{.j}$. The coefficient of the cluster means represents the contextual

effects (see section 3.7.5). Use `lincom` to estimate the corresponding between effects.

5. Add a random slope for `lead` to the model in step 3, and compare this model with the model from step 3 using a likelihood-ratio test.
6. Add a random slope for `cohes` to the model chosen in step 5, and compare this model with the model from step 3 using a likelihood-ratio test. Retain the preferred model.
7. Perform residual diagnostics for the level-1 errors, random intercept, and random slope(s). Do the model assumptions appear to be satisfied?

4.6 Dialyzer data

Vonesh and Chinchilli (1997) analyzed data on low-flux dialyzers used to treat patients with end-stage renal disease (kidney disease) to remove excess fluid and waste from their blood. In low-flux hemodialysis, the ultrafiltration rate at which fluid is removed (volume per time) is thought to follow a straight-line relationship with the transmembrane pressure applied across the dialyzer membrane. In a study to investigate this relationship, three centers measured the ultrafiltration rate at several transmembrane pressures for each of several dialyzers, or patients.

The variables in `dialyzer.dta` are as follows:

- `subject`: subject (or dialyzer) identifier
- `tmp`: transmembrane pressure (mmHg)
- `ufr`: ultrafiltration rate (ml/hr)
- `center`: center at which study was conducted

1. For each center, plot a graph of `ufr` versus `tmp` with separate lines for each subject. You may want to use the `by(center)` option.
2. Write down a model that assumes a linear relationship between `ufr` and `tmp` (denoted y_{ij} and x_{ij}, respectively), with mean intercepts and mean slopes differing between the three centers. In the random part of the model, include a random intercept and a random slope of x_{ij}.
3. Fit the model by ML estimation.
4. Test whether the mean slopes differ significantly at the 5% level for each pair of centers.
5. Plot the estimated mean line for each center on one graph, using `twoway function`.
6. For center 1, produce a trellis graph of the data and fitted subject-specific regression lines.

4.7 ❖ Family-birthweight data Solutions

Rabe-Hesketh, Skrondal, and Gjessing (2008) analyzed a random subset of the birthweight data from the Medical Birth Registry of Norway described in Magnus

et al. (2001). There are 1,000 nuclear families each comprising mother, father, and one child (not necessarily the only child in the family).

The data are given in `family.dta`. In this exercise, we will use the following variables:

- `family`: family identifier (j)
- `member`: family member (i) (1: mother; 2: father; 3: child)
- `bwt`: birthweight in grams (y_{ij})
- `male`: dummy variable for being male (x_{1ij})
- `first`: dummy variable for being the first child (x_{2ij})
- `midage`: dummy variable for mother of family member being aged 20–35 at time of birth (x_{3ij})
- `highage`: dummy variable for mother of family member being older than 35 at time of birth (x_{4ij})
- `birthyr`: year of birth minus 1967 (1967 was the earliest birth year in the birth registry) (x_{5ij})

In this dataset, family members are nested within families. Because of additive genetic and environmental influences, there will be a particular covariance structure between the members of the same family. Rabe-Hesketh, Skrondal, and Gjessing (2008) show that the following random-coefficient model can be used to induce the required covariance structure (see also exercise 4.8):

$$y_{ij} = \beta_1 + \zeta_{1j}(M_i + K_i/2) + \zeta_{2j}(F_i + K_i/2) + \zeta_{3j}(K_i/\sqrt{2}) + \epsilon_{ij} \qquad (4.5)$$

where M_i is a dummy variable for mothers, F_i is a dummy variable for fathers, and K_i is a dummy variable for children. The random coefficients ζ_{1j}, ζ_{2j}, and ζ_{3j} are constrained to have the same variance ψ and to be uncorrelated with each other. As usual, we assume normality with $\zeta_{1j} \sim N(0, \psi)$, $\zeta_{2j} \sim N(0, \psi)$, $\zeta_{3j} \sim N(0, \psi)$, and $\epsilon_{ij} \sim N(0, \theta)$. The variances ψ and θ can be interpreted as genetic and environmental variances, respectively, and the total residual variance is $\psi + \theta$.

1. Produce the required dummy variables M_i, F_i, and K_i.
2. Generate variables equal to the terms in parentheses in (4.5).
3. Which of the correlation structures available in `xtmixed` should be specified for the random coefficients?
4. Fit the model given in (4.5). Note that the model does not include a random intercept.
5. Obtain the estimated proportion of the total variance that is attributable to additive genetic effects.
6. Now fit the model including all the covariates listed above and having the same random part as the model in step 3.
7. Interpret the estimated coefficients from step 6.

8. Conditional on the covariates, what proportion of the residual variance is estimated to be due to additive genetic effects?

4.8 ❖ Covariance structure for nuclear family data

This exercise concerns family data such as those of exercise 4.7 consisting of a mother, father, and child. Here we consider three types of influences on birthweight: additive genetic effects (due to shared genes), common environmental effects (due to shared environment), and unique environmental effects. These random effects have variances σ_A^2, σ_C^2, and σ_E^2, respectively.

The additive genetic effects have the following properties:

- The parents share no genes by descent, so their additive genetic effects are uncorrelated.
- The child shares half its genes with each parent by decent, giving a correlation of 1/2 with each parent.
- The additive genetic variance should be the same for each family member.

For birth outcomes, no two family members share a common environment because they all developed in different wombs. We therefore cannot distinguish between common and unique environmental effects.

Rabe-Hesketh, Skrondal, and Gjessing (2008) show that we can use the following random-coefficient model to produce the required covariance structure:

$$y_{ij} = \beta_1 + \zeta_{1j}(M_i + K_i/2) + \zeta_{2j}(F_i + K_i/2) + \zeta_{3j}(K_i/\sqrt{2}) + \epsilon_{ij} \qquad (4.6)$$

where M_i, F_i, and K_i are dummy variables for mothers, fathers, and children, respectively. The random coefficients ζ_{1j}, ζ_{2j}, and ζ_{3j} produce the required additive genetic correlations and variances. These random coefficients are constrained to have the same variance $\psi = \sigma_A^2$ and to be uncorrelated with each other. As usual, we assume normality with $\zeta_{1j} \sim N(0, \sigma_A^2)$, $\zeta_{2j} \sim N(0, \sigma_A^2)$, $\zeta_{3j} \sim N(0, \sigma_A^2)$, and $\epsilon_{ij} \sim N(0, \theta)$.

1. By substituting the appropriate numerical values for the dummy variables M_i, F_i, and K_i in (4.6), write down three separate models, one for mothers, one for fathers, and one for children. It is useful to substitute $i = 1$ for mothers, $i = 2$ for fathers, and $i = 3$ for children in these equations.
2. Using the equations from step 1, demonstrate that the total variance is the same for mothers, fathers, and children.
3. Using the equations from step 1, demonstrate that the covariance between mothers and fathers from the same families is zero.
4. Using the equations from step 1, demonstrate that the correlation between the additive genetic components (terms involving ζ_{1j}, ζ_{2j}, or ζ_{3j}) of mothers and their children is 1/2.
5. What is the relationship between θ, σ_C^2, and σ_E^2?

4.9 ❖ Effect of covariate translation on random-effects covariance matrix

Using (4.2) and the estimates for the random-coefficient model without level-2 covariates given in section 4.5.2, calculate what values $\widehat{\psi}_{11}$ and $\widehat{\psi}_{21}$ would take if you were to subtract 5 from the variable `lrt` and refit the model.

Part III

Models for longitudinal and panel data

Introduction to models for longitudinal and panel data (part III)

In this part, we focus on multilevel models and other methods for longitudinal and panel data. In longitudinal data, subjects have observations at several occasions or time points. Most commonly, longitudinal data are collected prospectively by following a group of subjects over time. Such data are referred to as *panel data*, *repeated measures*, or *cross-sectional time-series data* (the latter term explains the `xt` prefix in Stata's commands for longitudinal modeling). Longitudinal data can also be collected retrospectively, from archival data or by asking subjects to recall their history. We assume that the data have been collected in a way that makes it reasonable to treat them as prospective longitudinal data. We concentrate on "short panels", where there are many more subjects than occasions per subject. Other types of data that resemble longitudinal data are *time-series* data, where one unit is followed over time (usually at many occasions), and duration or survival data, which are discussed in volume 2 (chapters 14 and 15).

It is useful to distinguish between different types of longitudinal studies. In *panel studies*, all subjects are typically followed up at the same occasions (called "panel waves") leading to balanced or fixed-occasion data, although there may be missing data at some occasions for a subject. Usually, the occasions are also equally spaced with constant time intervals between them. In *cohort studies* (as defined in epidemiology), a group of subjects—sometimes of the same age, as in a birth cohort—may be followed up at subject-specific occasions, which produces unbalanced or variable-occasion data. Intervention studies and clinical trials are special cases of cohort studies with the important difference that subjects are assigned to treatments by researchers. In these studies, the intention is usually to collect balanced data; in practice, however, the data are often unbalanced because it is not feasible to assess all subjects exactly at the intended time points.

Longitudinal data can be viewed as two-level or clustered data with occasions nested in subjects, in which case subjects become clusters. Indeed, we have already applied random-intercept models to longitudinal data, such as the smoking and birthweight data, in previous chapters and exercises. We use the term "occasions" i for level-1 units and the term "subjects" j for level-2 units or clusters. We denote the timing associated with occasion i for subject j by a variable with subscripts i and j, such as t_{ij}, dropping the j subscript for balanced data. Note that the Stata documentation uses the indices t for occasions and i for subjects, and refers to subjects or units as "panels".

A special feature of longitudinal data is that the level-1 units or occasions are ordered in time and not necessarily exchangeable (where permuting units within clusters leaves the multivariate distribution unchanged) unlike, for example, students nested in schools. For this reason, there are a variety of different models designed specifically for longitudinal data. Broadly speaking, these models fall into the following categories:

Random-effects models, where unobserved between-subject heterogeneity is represented by subject-specific effects that are randomly varying.

Random-effects models are useful for exploring and explaining average trends as well as individual differences by allowing subject-specific relationships to vary randomly around average relationships. Typical application areas are psychological development, physical growth, or learning, where both the nature and reasons for variability are of major interest. Growth-curve models are a special case of random-effects models. In this archetypal multilevel approach to longitudinal data analysis, the focus is on modeling growth (or decline) over time by including random coefficients of time (or functions of time) to represent individual growth trajectories. Random-effects models are discussed in chapter 5. Chapter 7 is devoted to growth-curve models.

Fixed-effects models, where unobserved between-subject heterogeneity is represented by fixed subject-specific effects.

Fixed-effects models are used to estimate average within-subject relationships between time-varying covariates and the response variable, where every subject acts as its own control. Such models eliminate subject-level confounding and therefore facilitate causal inference. An example was considered in chapter 3, where the effect of smoking on birthweight was investigated by comparing births where the mother smoked with births where the same mother did not smoke. Fixed-effects models are revisited in chapter 5, where several new topics from econometrics are considered, particularly, approaches for handling different kinds of endogeneity or subject-level unmeasured confounding.

Dynamic models, where the response at a given occasion depends on previous or lagged responses.

Dynamic or lagged-response models allow previous responses to affect future responses directly; for instance, the wages a year ago affect current wages. When combined with random- or fixed-effects approaches, dynamic models allow us to distinguish between two explanations of wage-dependence over time: 1) state dependence, where previous wages cause future wages (either due to fixed percentage salary increases within a job or due to the importance of past wages when negotiating salary in a new job) and 2) individual differences, where ability affected past wages and continues to affect future wages. Dynamic models are discussed in chapter 5.

Marginal models, where within-subject dependence is modeled by direct specification of the residual covariance structure across occasions.

Marginal or population-averaged models focus on average trends while accounting for longitudinal dependence. In these models, a covariance structure is directly specified for (total) residuals, instead of including random effects in the model that imply a certain covariance structure. Such models are often used in randomized controlled clinical trials to estimate average treatment effects. In this case, there are no subject-level confounders by design, and individual differences are of secondary concern. Chapter 6 discusses marginal models.

Which of the approaches to longitudinal modeling outlined above is adopted in practice depends largely on the discipline. In the biomedical sciences, random-effects and marginal models are most common, whereas random-effects models are popular in most of the social sciences. In economics, fixed-effects models and dynamic models are predominant. Repeated measures or split-plot analysis of variance (ANOVA) can in some ways be viewed as a fixed-effects model; this approach is used mostly for experimental designs in areas such as agriculture and psychology but is increasingly being replaced by random-effects models. Growth-curve modeling is particularly popular in education and psychology. We hope that our chapters on longitudinal and panel modeling will make you aware of strengths and weaknesses of methods used in a range of disciplines and encourage you to explore tools not commonly used in your own field.

The rest of this introduction discusses special features and challenges of longitudinal data and provides prerequisite information for all chapters in part III. The ideas are illustrated using a dataset that will be analyzed throughout chapters 5 and 6.

How and why do wages change over time?

Labor economists are interested in research questions such as how hourly wage depends on union membership, labor-market experience, and education, and how hourly wages change over time.

To address these questions, we will use data from the U.S. National Longitudinal Survey of Youth 1979. The original sample is representative of noninstitutionalized civilian youth who were aged 14–21 on December 31, 1978. Here we consider the subsample of the data previously analyzed by Vella and Verbeek (1998) and provided by Wooldridge (2010). The data comprise 545 full-time working males who completed schooling by 1980 and who had complete data for 1980–1987 (note that we would not recommend discarding subjects with incomplete data).

The variables in the dataset, `wagepan.dta`, that we will use here are

- `nr`: person identifier (j)
- `lwage`: log hourly wage in U.S. dollars (y_{ij})
- `black`: dummy variable for being black (x_{2j})

- `hisp`: dummy variable for being Hispanic (x_{3j})
- `union`: dummy variable for being a member of a union (that is, wage being set in collective bargaining agreement) (x_{4ij})
- `married`: dummy variable for being married (x_{5ij})
- `exper`: labor-market experience, defined as age−6−`educ` (L_{ij})
- `year`: calendar year 1980–1987 (P_i)
- `educ`: years of schooling (E_j)

We start by reading in the wage-panel data:

```
. use http://www.stata-press.com/data/mlmus3/wagepan
```

Longitudinal data structure and descriptives

Long and wide form

The wage-panel data are in long form, with one row of data per occasion for each subject. Table III.1 shows data for some of these variables (and two additional variables, C_j and A_{ij}) for two subjects. Longitudinal data are often in wide form, with a separate variable for each occasion and only one row of data per subject. For all analyses discussed in this part, data should be in long form. Stata's `reshape` command is convenient for converting data from long form to wide form and vice versa.

Table III.1: Illustration of longitudinal data in long form

Subject j	Occ. i	Cohort C_j	Age A_{ij}	Period P_i	Black x_{2j}	Hispanic x_{3j}	Union x_{4ij}	Log wage y_{ij}
45	1	1960	20	1980	0	0	1	1.89
45	2	1960	21	1981	0	0	1	1.47
45	3	1960	22	1982	0	0	0	1.47
45	4	1960	23	1983	0	0	0	1.74
45	5	1960	24	1984	0	0	0	1.82
45	6	1960	25	1985	0	0	0	1.91
45	7	1960	26	1986	0	0	0	1.74
45	8	1960	27	1987	0	0	0	2.14
847	1	1959	21	1980	1	0	1	1.56
847	2	1959	22	1981	1	0	1	1.66
847	3	1959	23	1982	1	0	0	1.77
847	4	1959	24	1983	1	0	0	1.79
847	5	1959	25	1984	1	0	0	2.00
847	6	1959	26	1985	1	0	1	1.65
847	7	1959	27	1986	1	0	0	2.13
847	8	1959	28	1987	1	0	1	1.69

To illustrate the `reshape` command, we first delete all unnecessary variables by using the `keep` command:

```
. keep nr lwage black hisp union married exper year educ
```

In the `reshape wide` command, we must list all time-varying variables and give the subject and occasion identifiers in the `i()` and `j()` options, respectively:

```
. reshape wide lwage union married exper, i(nr) j(year)
(note: j = 1980 1981 1982 1983 1984 1985 1986 1987)
Data                               long   ->   wide
-----------------------------------------------------------------------------
Number of obs.                     4360   ->    545
Number of variables                   9   ->     36
j variable (8 values)              year   ->   (dropped)
xij variables:
                                  lwage   ->   lwage1980 lwage1981 ... lwage1987
                                  union   ->   union1980 union1981 ... union1987
                                married   ->   married1980 married1981 ... married1987
                                  exper   ->   exper1980 exper1981 ... exper1987
-----------------------------------------------------------------------------
```

We see that the values in the `year` variable have been appended to `lwage` to make eight new variables, `lwage1980` to `lwage1987`, containing the log hourly wages for the eight panel waves, and similarly for the other time-varying variables. Instead of eight rows per subject, a single row is now produced. To see what happened, we list the new log

hourly wage variables together with the subject identifier for the first five subjects in the dataset (formatting the variable to make the list fit on the page)

```
. format lwage* %5.3f
. list nr lwage* in 1/5, clean noobs abbreviate(6)
     nr   l~1980   l~1981   l~1982   l~1983   l~1984   l~1985   l~1986   l~1987
     13    1.198    1.853    1.344    1.433    1.568    1.700   -0.720    1.669
     17    1.676    1.518    1.559    1.725    1.622    1.609    1.572    1.820
     18    1.516    1.735    1.632    1.998    2.184    2.267    2.070    2.873
     45    1.894    1.471    1.473    1.741    1.823    1.908    1.742    2.136
    110    1.949    1.962    1.963    2.203    2.135    2.126    1.991    2.112
```

To reshape the data back to long form, we use the `reshape` command again with identical syntax, except for replacing `wide` with `long`:

```
. reshape long lwage union married exper, i(nr) j(year)
(note: j = 1980 1981 1982 1983 1984 1985 1986 1987)
Data                               wide   ->   long
-----------------------------------------------------------------------------
Number of obs.                      545   ->    4360
Number of variables                  36   ->       9
j variable (8 values)                     ->   year
xij variables:
      lwage1980 lwage1981 ... lwage1987   ->   lwage
      union1980 union1981 ... union1987   ->   union
married1980 married1981 ... married1987   ->   married
      exper1980 exper1981 ... exper1987   ->   exper
-----------------------------------------------------------------------------
```

We can then list `lwage` for all eight years for the first subject to have a look at the long form of the data:

```
. list nr year lwage in 1/8, clean noobs
    nr   year    lwage
    13   1980    1.198
    13   1981    1.853
    13   1982    1.344
    13   1983    1.433
    13   1984    1.568
    13   1985    1.700
    13   1986   -0.720
    13   1987    1.669
```

Declaring the data as longitudinal using xtset

As we have already seen in chapters 2 and 3, some Stata commands, such as `xtreg`, require the data to be declared as longitudinal by using the `xtset` command to specify a cluster identifier (called a "panel variable" in Stata) and a time variable

```
. xtset nr year
       panel variable:  nr (strongly balanced)
        time variable:  year, 1980 to 1987
                delta:  1 unit
```

Stata's powerful time-series operators (similar to factor variables) can then be used to refer to lags and other transformations of time-varying variables as will be seen in section 5.7. Note that `xtset` does not affect the behavior of `xtmixed`.

For clarity, we will repeat the `xtset` command (with the `quietly` prefix to suppress output) whenever we rely on the cluster identifier and the time variable to be defined.

Balance, strong balance, and constant spacing of occasions

When the occasions for all subjects occur at the same sets of points in time so that $t_{ij} = t_i$, the data are called *balanced*. The data are *strongly balanced* if there are no missing data. It also sometimes matters whether the time intervals between occasions are the same across subjects and occasions with $t_{ij} - t_{i-1,j} = \Delta$, where the Greek letter Δ is pronounced "delta". We will refer to this property as *constant spacing of occasions*. We see from the output from `xtset` that the wage-panel data are strongly balanced with constant spacing of occasions; that is, $\Delta = 1$.

If we had specified a different time variable, such as `age`, in the `xtset` command, the data would not be balanced. As we will see later, we can consider several time scales simultaneously, but when first exploring the data, it is best to concentrate on a time scale that is at least approximately balanced.

Missing data

If we did not know that the data are strongly balanced, we might wonder whether `lwage` was missing at any occasion for any of the subjects. We can investigate missingness patterns by using `xtdescribe`:

```
. xtdescribe if lwage < .
      nr:  13, 17, ..., 12548                                 n =        545
    year:  1980, 1981, ..., 1987                              T =          8
           Delta(year) = 1 unit
           Span(year)  = 8 periods
           (nr*year uniquely identifies each observation)

Distribution of T_i:   min      5%     25%       50%       75%     95%     max
                         8       8       8         8         8       8       8

     Freq.  Percent    Cum. |  Pattern
----------------------------+---------
       545   100.00  100.00 |  11111111
----------------------------+---------
       545   100.00         |  XXXXXXXX
```

Here `Pattern` could be any sequence of eight characters consisting of "`1`" (for not missing) and "`.`" (for missing). The only pattern in these data is "`11111111`" corresponding to complete data for everyone (see section 7.7.2 for an example with missing data). For such patterns to be interpretable, it is necessary to specify a time variable or occasion identifier in the `xtset` command that takes on the same values for all subjects when not missing.

The `xtdescribe` command checks whether there is a row of data for a given subject at a given occasion. Generally, we do not want to count rows where the response variable is missing; we should therefore apply the command only to observations where the response is not missing, here by using the condition `if lwage < .` (The dot, `.`, in Stata is a very large number denoting a missing observation.)

Time-varying and time-constant variables

Whenever a variable changes over time for some subjects, it is called *time varying*. The response variable in longitudinal data is always time-varying (here log wage y_{ij}). Some explanatory variables or covariates are *subject-specific* or *time-constant* (education E_j and the ethnicity dummies x_{2j} and x_{3j}).

Time-varying covariates can be further classified into (a) occasion-specific (and not subject-specific) covariates (here year P_i) or (b) both subject- and occasion-specific covariates (here labor-market experience L_{ij}, union membership x_{4ij}, and marital status x_{5ij}).

For longitudinal data, it is useful to investigate the within-subject, between-subject, and total variability of the variables, shown here for only some of the variables. (For precise definitions of the different kinds of standard deviations, see section 3.2.1.)

```
. quietly xtset nr
. xtsum lwage union educ year
```

Variable		Mean	Std. Dev.	Min	Max	Observations
lwage	overall	1.649147	.5326094	-3.579079	4.05186	N = 4360
	between		.3907468	.3333435	3.174173	n = 545
	within		.3622636	-2.467201	3.204687	T = 8
union	overall	.2440367	.4295639	0	1	N = 4360
	between		.3294467	0	1	n = 545
	within		.2759787	-.6309633	1.119037	T = 8
educ	overall	11.76697	1.746181	3	16	N = 4360
	between		1.747585	3	16	n = 545
	within		0	11.76697	11.76697	T = 8
year	overall	1983.5	2.291551	1980	1987	N = 4360
	between		0	1983.5	1983.5	n = 545
	within		2.291551	1980	1987	T = 8

As expected, `lwage` and `union` vary both within and between subjects. `educ` does not vary within subjects, and `year` does not vary between subjects (that is, it has the same mean for all subjects). It is especially important to examine how much a variable varies within subjects because some estimation methods, such as fixed-effects approaches (see section 5.4), rely exclusively on within-subject variability for estimation of regression coefficients. We see from the fact that `T` is given in the output instead of `T-bar` that the number of occasions n_j is constant over subjects j as we already know.

For time-varying categorical or binary variables, like `union`, the `xttab` command also provides useful information:

```
. quietly xtset nr
. xttab union
```

union	Overall Freq.	Overall Percent	Between Freq.	Between Percent	Within Percent
0	3296	75.60	511	93.76	80.63
1	1064	24.40	280	51.38	47.50
Total	4360	100.00	791 (n = 545)	145.14	68.90

We see from the `Overall` columns that `union` takes the value one 24.4% of the time across all subjects and occasions. From the `Between` columns, we see that 93.8% of subjects were nonunion members for at least one occasion, and 51.4% of subjects were union members for at least one occasion. Finally, the `Within` column shows that among those who were ever nonunion members the average percentage of occasions for which they were nonunion members is 80.6%. Those who were ever union members were union members for an average of 47.5% of occasions. Whenever the total percentage in the `Between` columns is greater than 100%, the variable changes over time for some subjects.

Graphical displays for longitudinal data

Box plots of the response variable at each occasion are useful for inspecting the distribution of the variable and detecting outliers:

```
. graph box lwage, over(year) intensity(0) medtype(line)
> marker(1,mlabel(nr) mlabsize(vsmall) msym(i) mlabpos(0)
> mlabcol(black)) ytitle(Log hourly wage)
```

Here we used the `mlabel()` suboption to show the subject identifiers for extreme log hourly wages (smaller than the lower quartile minus 1.5 interquartile ranges, or greater than the upper quartile plus 1.5 interquartile ranges). We see in figure III.1 that subject 813 had a very low reported log hourly wage in 1984, corresponding to just a few cents. Subject 813 may therefore merit special attention because he may have had a very bad year, the reported wage may be wrong, or an error may have been committed in the coding of the data. (Using box plots requires that there are sufficiently many observations at each occasion.)

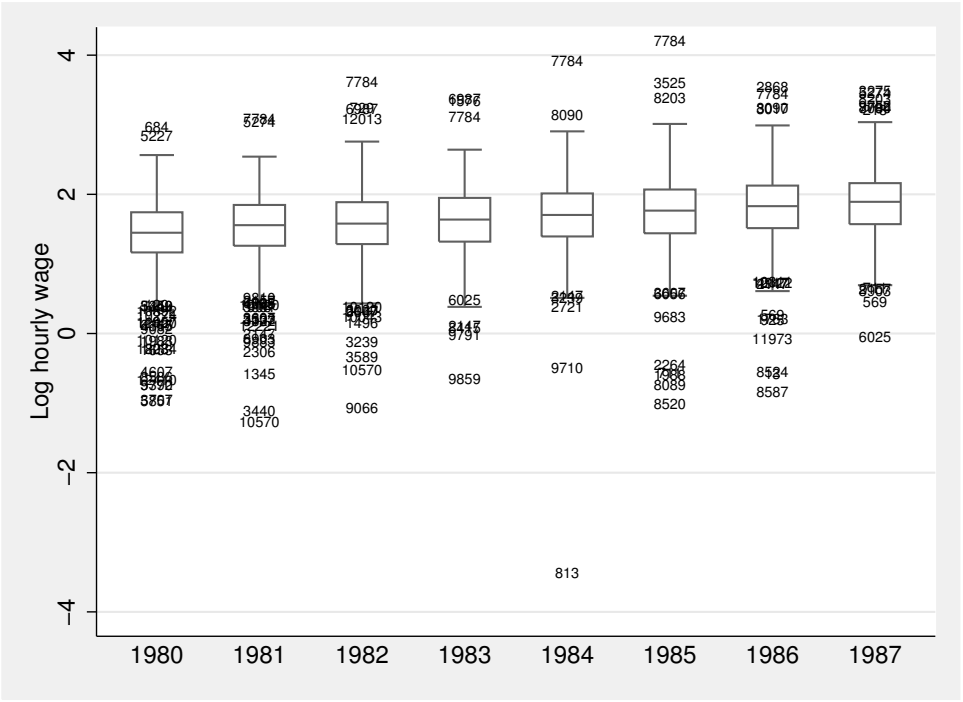


Figure III.1: Box plots of log hourly wages at each occasion

It is also important to get an idea of how log hourly wages change over time for individual subjects. Plotting observed trajectories for all subjects becomes messy, so we will draw a random sample of subjects. We do this by generating a random number, `r`, for each subject for 1980, with values of `r` for all other years missing:

```
. format lwage* %9.0g
. sort nr year
. set seed 132144
. generate r = runiform() if year==1980
```

A random sample of 12 subjects can be obtained by choosing the subjects with the 12 largest random numbers `r`, and similarly for any other required number of subjects. We therefore rank order the random numbers by using `egen` with the `rank()` function:

```
. egen num = rank(r) if r<.
```

We then generate a variable, `number`, that contains the nonmissing value of the rank order, `num`, for each subject:

```
. egen number = mean(num), by(nr)
```

(The `mean()` function finds the mean of all nonmissing values; here there is only one per subject, so that number is placed in all rows for the subject.) It is now easy to plot the trajectories of log hourly wage for the 12 randomly chosen subjects in a trellis graph:

```
. twoway line lwage year if number<=12, by(nr, compact)
> ytitle(Log hourly wage) xtitle(Year) xlabel(,angle(45))
```

The resulting graph is shown in figure III.2. In the first row, we clearly see the common phenomenon of *tracking*, whereby some individuals consistently remain higher or lower than other individuals. This pattern is consistent with subject-specific random or fixed intercepts, where individual curves are vertically shifted by subject-specific constants. Column 2 of the figure illustrates that the slope of `year` varies between subjects, and column 3 shows that the log hourly wage is volatile for some subjects.

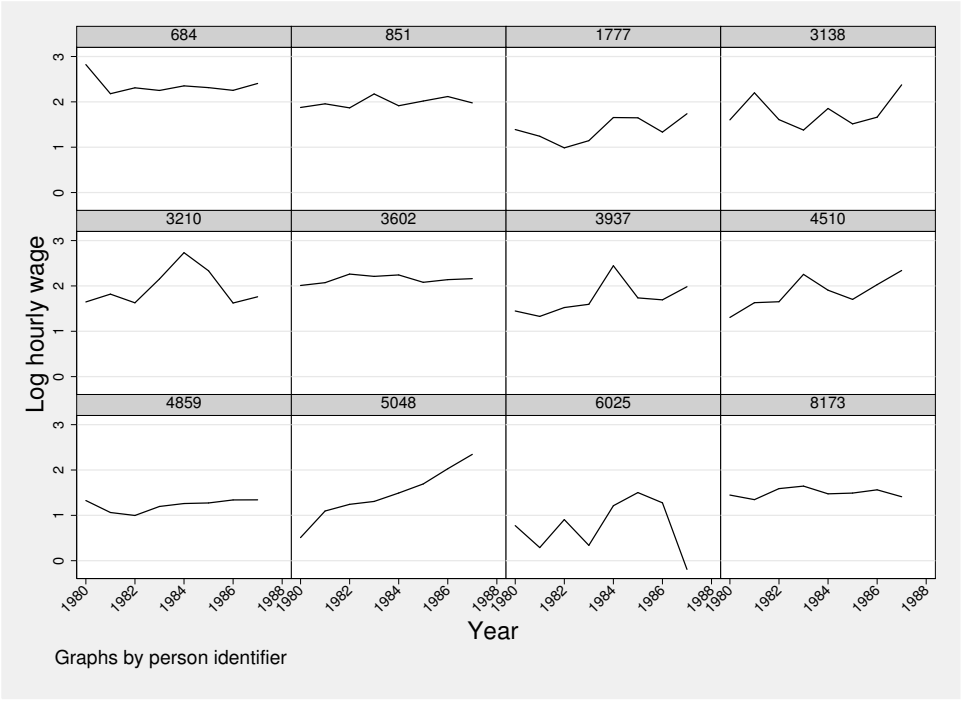


Figure III.2: Trellis graph of trajectories for log hourly wage for 12 randomly chosen subjects

To see these trajectories within the context of the entire sample of subjects, we can add them to a scatterplot for all subjects. We also display the average trajectory on the same graph. First, we find the mean log hourly wage for each year,

```
. egen mn_lwage = mean(lwage), by(year)
```

and then we produce the graph, which is displayed in figure III.3:

```
. sort nr year
. twoway (scatter lwage year, jitter(2) msym(o) msize(tiny))
> (line lwage year if number<=12, connect(ascending)
> lwidth(vthin) lpatt(solid))
> (line mn_lwage year, sort lpatt(longdash)) if lwage>-2,
> ytitle(Log hourly wage) xtitle(Year)
> legend(order(2 "Individual trajectories" 3 "Mean trajectory"))
```

By first sorting the data by `year` within `nr` and then using the `connect(ascending)` option, we ensure that successive observations for a subject are connected, but that the last observation for a subject is not connected to the first observation for the next subject. The outlying observation for subject 813 was discarded by plotting only observations with `lwage>-2` to obtain a better resolution. A small amount of jitter was used for the scatterplot to prevent overlap of data points.

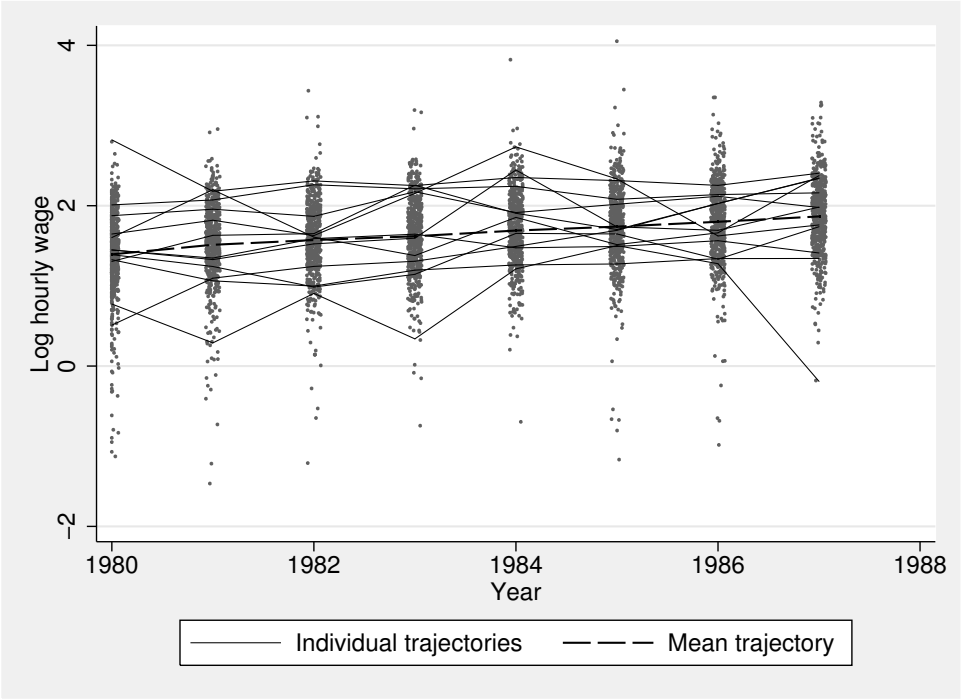


Figure III.3: Scatterplot of log hourly wages versus occasions; individual trajectories for 12 randomly chosen subjects (thin solid lines) and mean trajectory (thick dashed line)

The population-mean trajectory appears to be linear.

Time scales in longitudinal data: Age-period-cohort effects

Consider the longitudinal data on subjects 45 and 847 from the wage-panel data given in table III.1 on page 231. We refer to the birth year as "cohort" and to the calendar year as "period". We have calculated age and cohort from other variables in the data (see below for the relationship among the variables).

When investigating change in the response variable using *age-period-cohort* data, such as those in table III.1, any of three different time scales may be of interest: age, period, or cohort. (The term cohort usually refers to a group of people such as a birth cohort, but here it refers to the birth year associated with the birth cohort.) In our example, the definitions of both cohort and age are in terms of the time of birth; this reference point is important in many investigations. However, for some applications, the reference point could be an occurrence of some other event, such as graduation from university. Then a particular cohort may be referred to as "the class of 2011", and the age-like time scale becomes time since graduation.

The relationship between age, period, and cohort is given by

$$A_{ij} = P_i - C_j$$

as illustrated in figure III.4 for four subjects for the first five waves of the wage-panel data. The top two lines represent subjects 847 and 45 in table III.1. For example, we see that subject 847 was born in 1959 and hence belongs to the 1959 cohort (referred to as C59 in the figure), and his age is 21 years in 1980. In 1984, any member of the 1959 cohort is 25 years old.

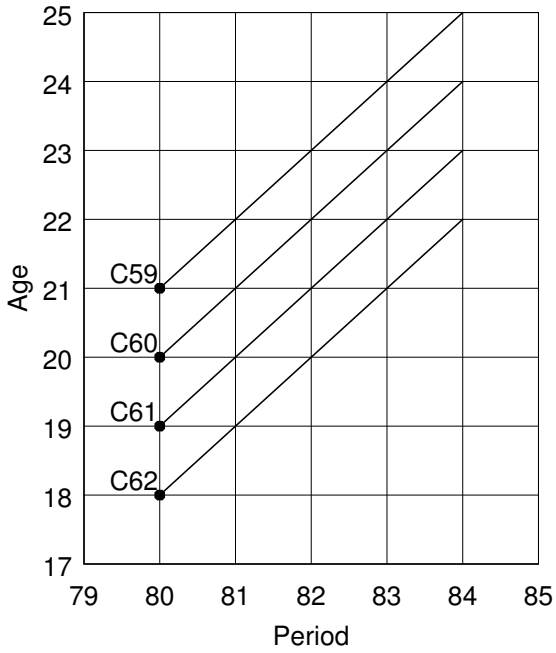


Figure III.4: Illustration of the relationship between age, period, and cohort

A great advantage of this kind of longitudinal study with several cohorts is that we can investigate the effects of more than one time scale simultaneously. In contrast, a cross-sectional study provides data for just one period P, which obviously makes it impossible to estimate the effect of period. Furthermore, we cannot separate the effects of age and cohort in a cross-sectional study because each subject's age A_j is determined by the cohort, $A_j = P - C_j$. For example, there are two competing explanations for older people being more conservative: 1) they are in later stages in life with increased A_j or 2) they were born longer ago (in a different era) with smaller C_j. Cross-sectional data cannot be used to distinguish between these explanations.

A longitudinal study with one cohort C also does not allow us to investigate the effect of more than one time scale. We obviously cannot estimate the effect of cohort, and age is determined by period, $A_i = P_i - C$. For instance, we cannot distinguish between two explanations for salary increases: 1) people get more experience as they get older with increased A_i or 2) there is inflation over calendar time P_i.

Longitudinal studies with several cohorts are sometimes said to have a *cohort-sequential design* or *accelerated longitudinal design*, where the term "accelerated" refers to the range of ages covered exceeding the length of the study. From the relation $A_{ij} = P_i - C_j$, we see that it is possible to estimate the effects of two time scales, but these will be confounded with the third scale. Thus it is necessary to pick the time scales that are believed to be most important. For example, conservatism may be viewed as

depending on age and cohort (ignoring period), and salary may be viewed as depending on age and period (ignoring cohort).

To resolve the collinearity among A_{ij}, C_j, and P_i in the wage-panel data, we choose to eliminate C_j. However, other time scales are also of interest because there are two other relevant subject-specific events: entering education (assumed to occur at age 6) and leaving education. The relationship between age A_{ij}, years of education E_j, and number of years in the labor market L_{ij} is

$$A_{ij} \;=\; 6 + E_j + L_{ij}$$

We see that we have to eliminate one of the collinear variables, for instance, A_{ij}. We are then left with three time scales: P_i, E_j, and L_{ij}. (We have ignored two other time scales that are collinear with P_i, E_j, and L_{ij}: age at entry into the labor market, $6+E_j$, and calendar year at entry into the labor market, $C_j + 6 + E_j$.)

Several time scales can be relevant in longitudinal studies, and the prospect of disentangling the effects of different time scales depends on the research design. Within the limitations of the chosen research design, the time scales that are deemed most relevant for the research problem should be included in the models. These time scales are not necessarily present in the dataset and may have to be constructed from the data.

Pooled ordinary least-squares estimation

The simplest approach to longitudinal modeling is to ignore the longitudinal structure of the data and proceed as if each row of the data (in long form) corresponds to a different unit of observation. We can then consider a standard linear regression model that includes the three time scales L_{ij}, P_i, and E_j (`exper`, `yeart`, and `educt`) as covariates as well as `black`, `hisp`, `union`, and `married`:

$$y_{ij} \;=\; \beta_1 + \beta_2 x_{2j} + \beta_3 x_{3j} + \beta_4 x_{4ij} + \beta_5 x_{5ij} + \beta_6 L_{ij} + \beta_7 P_i + \beta_8 E_j + \xi_{ij}$$

where ξ_{ij} is a residual. We can estimate the parameters by ordinary least squares (OLS), often called pooled ordinary least squares.

First, we translate the time scales to make the intercept more interpretable here and in later analyses:

```
. generate educt = educ - 12
. generate yeart = year - 1980
```

The variable `educt` is the number of years of education beyond the usual time (12 years) required to complete high school, and `yeart` is the number of years since 1980. For simplicity, we will henceforth refer to the translated variables as E_j and P_i, respectively.

We now fit the model by pooled OLS using `regress` with the `vce(cluster nr)` option to obtain appropriate standard errors for clustered data:

```
. regress lwage black hisp union married exper yeart educt, vce(cluster nr)
Linear regression                                      Number of obs =    4360
                                                       F(  7,   544) =   84.63
                                                       Prob > F      =  0.0000
                                                       R-squared     =  0.1870
                                                       Root MSE      =  .48064
                                     (Std. Err. adjusted for 545 clusters in nr)
------------------------------------------------------------------------------
             |               Robust
       lwage |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       black |  -.1371356   .0503591    -2.72   0.007    -.2360577   -.0382134
        hisp |   .0136874   .0386814     0.35   0.724    -.0622959    .0896707
       union |   .1863618   .0274214     6.80   0.000     .1324971    .2402265
     married |   .1119207   .0257939     4.34   0.000     .0612529    .1625885
       exper |   .0302751   .0111744     2.71   0.007     .0083249    .0522253
       yeart |   .0267888   .0117137     2.29   0.023     .0037791    .0497985
       educt |   .0928443   .0110632     8.39   0.000     .0711124    .1145762
       _cons |   1.298895   .0397477    32.68   0.000     1.220818    1.376973
------------------------------------------------------------------------------
```

The estimated coefficients of `exper` and `yeart` suggest that the mere passage of time is associated with a similar effect as each extra year of experience, probably because of inflation. Each additional year of education is associated with an estimated increase in the expectation of log hourly wage of 0.09, controlling for the other covariates. The exponential of this coefficient, 1.10, therefore represents the estimated multiplicative effect of each extra year of education on the expectation of the hourly wage, as shown in display 1.1 on page 64. In other words, there is a 10% [$0.10 = \exp(0.0928443) - 1$] estimated increase in expected wages per year of education, compared with a 3% [$0.03 = \exp(0.0302751) - 1$] increase due to experience, when controlling for other covariates. We also estimate that given the other covariates, black men's mean wages are 13% lower than white men's [$-0.13 = \exp(-0.1371356) - 1$].

Pooled OLS produces consistent estimates for the regression coefficients under the assumption that the mean structure is correctly specified (basically, that the correct covariates are included and that the correct functional form is specified) and that the residuals ξ_{ij} are uncorrelated with the covariates. Furthermore, the sandwich estimator of the standard errors, requested by the `vce(cluster nr)` option, produces consistent estimates of the standard errors even if the residuals are correlated within subjects and have nonconstant variance. However, an important but rarely acknowledged limitation of this approach is the tacit assumption either that there are no missing data or that the probability that a response is missing does not depend on observed or unobserved responses after controlling for the covariates. See section 5.8.1 for a simulation where this assumption is violated.

Correlated residuals

In longitudinal data, the response variable is invariably correlated within subjects even after controlling for covariates. To demonstrate this phenomenon, we now obtain the within-subject correlation matrix of the estimated residuals from pooled OLS using

```
. predict res, residuals
```

To form the within-subject correlation matrix for pairs of occasions, we must reshape the data to wide form, treating the residuals at times 0–7 as variables `res0`–`res7`. We first preserve and later restore the data because we will require them in long form when fitting models. (If running the subsequent commands from a do-file, all the commands from `preserve` to `restore` must be run in one block, not one command at a time.)

```
. preserve
. keep nr res yeart
. reshape wide res, i(nr) j(year)
(note: j = 0 1 2 3 4 5 6 7)
Data                               long   ->   wide
-----------------------------------------------------------------------------
Number of obs.                     4360   ->    545
Number of variables                   3   ->      9
j variable (8 values)            yeart   ->   (dropped)
xij variables:
                                   res   ->   res0 res1 ... res7
-----------------------------------------------------------------------------
```

The standard deviations and correlations of the residuals are then obtained using

```
. tabstat res*, statistics(sd) format(%3.2f)
   stats |  res0  res1  res2  res3  res4  res5  res6  res7
---------+------------------------------------------------
      sd |  0.53  0.50  0.46  0.45  0.50  0.49  0.49  0.43
----------------------------------------------------------
```

and

```
. correlate res*, wrap
(obs=545)
             |     res0     res1     res2     res3     res4     res5     res6     res7
-------------+------------------------------------------------------------------------
        res0 |   1.0000
        res1 |   0.3855   1.0000
        res2 |   0.3673   0.5525   1.0000
        res3 |   0.3298   0.5220   0.6263   1.0000
        res4 |   0.2390   0.4451   0.5740   0.6277   1.0000
        res5 |   0.2673   0.4071   0.5230   0.5690   0.6138   1.0000
        res6 |   0.2084   0.3220   0.4622   0.4710   0.5020   0.5767   1.0000
        res7 |   0.2145   0.4019   0.4232   0.4976   0.5349   0.6254   0.6337   1.0000
. restore
```

We see that there are substantial within-subject correlations among the residuals, ranging from 0.21 to 0.63 for pairs of occasions. The correlations tend to decrease down the columns, meaning, for instance, that residuals at occasion 0 (column 1), are more corre-

lated with residuals at occasion 1 than with residuals at occasion 7. As the time interval between occasions increases, the correlation between the corresponding residuals tends to decrease.

Within-subject correlations over time are sometimes referred to as *longitudinal correlations*, *serial correlations*, or *autocorrelations*, and these terms also suggest that correlations may depend on the time interval between occasions. The correlations could be partly due to between-subject heterogeneity in the intercept and possibly in the slopes of covariates, which is not accommodated in the standard linear regression model. Alternatively, the responses at an occasion could depend on previous responses, but lagged responses are mistakenly omitted from the model. Finally, the residuals could be governed by slowly varying processes that induce correlations that decay as the time interval between occasions increases. Within-subject correlations among the residuals could, of course, be due to a combination of these reasons.

Why do we need special models for longitudinal data?

Because pooled OLS with robust standard errors for clustered data gives consistent estimates of regression coefficients and standard errors (assuming a correctly specified mean structure), the question is, why are there three chapters on longitudinal modeling in this part of the book?

In the discussion section of papers based on cross-sectional data, it is often stated that longitudinal data would be required for causal inference. The reason for this is that causal effects are based on comparisons of a subject's hypothetical (potential or counterfactual) responses for different treatments or exposures. It is evident that comparing actual observed responses within subjects is closer to this ideal than comparing observed responses between subjects. Indeed, the great advantage of longitudinal data as compared with cross-sectional data is that each subject can serve as his or her own control. Unfortunately, pooled OLS treats longitudinal data as repeated cross-sectional data (where independent samples of subjects are drawn at each occasion) and conflates within- and between-subject comparisons. Between-subject comparisons are susceptible to omitted variable bias or unmeasured confounding, due to time-constant subject-specific variables that are not included in the model. Within-subject comparisons are free from such bias because subjects truly act as their own controls. In chapter 5, we discuss methods that reap the benefits of longitudinal data for causal inference.

When the causal effects of previous responses are of interest, lagged responses are included as covariates. In this case, pooled OLS is no longer consistent if there are time-constant omitted covariates, which will typically be the case. In chapter 5, we describe methods that address this problem.

Another limitation of pooled OLS is that estimates of regression coefficients are no longer consistent if there are missing data and if missingness depends on observed responses for the same subject, given the covariates. In this common scenario, it becomes necessary to model the within-subject residual covariance matrix to obtain consistent estimates.

If we can model the residual covariance structure appropriately, estimates of regression coefficients that are based on the covariance structure will be more precise or efficient than pooled OLS estimates. Modeling the covariance matrix can also be of interest in its own right because it sheds light on the kinds of processes that lead to within-subject dependence. An estimated residual covariance matrix is also needed, in addition to estimates of regression coefficients, to make forecasts for individual subjects. Modeling the residual covariance matrix is the focus of chapter 6.

Finally, pooled OLS estimates only the population-averaged relationship between the response variable and covariates. Subject-specific effects can be investigated using random-effects and fixed-effects models as discussed in chapter 5. When the nature of changes in the response variable over time is of interest, we can use growth-curve models to investigate how subject-specific growth trajectories vary around the population-averaged trajectory. Such models are discussed in chapter 7.

5 Subject-specific effects and dynamic models

5.1 Introduction

In this chapter, we discuss models where the intercept and possibly some of the coefficients can vary between subjects. In sections 5.2, 5.3, and 5.4, models with subject-specific intercepts are treated, where the intercepts are either random or fixed. As we saw in chapter 3, the random-effects approach treats the intercepts as (unobserved) random variables that can be viewed as residuals, whereas the fixed-effects approach treats the intercepts as model parameters that can be estimated by including dummy variables for subjects. In both cases, the intercepts can be viewed as representing the effects of omitted covariates that are constant over time.

As pointed out in section 3.7.4, an advantage of the fixed-effects approach is that it relaxes the assumption that the covariates are uncorrelated with the subject-specific intercept. For this reason, any estimator that relaxes this exogeneity assumption is called a "fixed-effects estimator" in econometrics, and the assumption is therefore referred to as the random-effects assumption in that literature. However, in modern econometrics, the subject-specific intercept is usually viewed as random even if a fixed-effects approach is used. In fact, some fixed-effects estimators, such as the Hausman–Taylor estimator described in section 5.3, relax the exogeneity assumption for some covariates while explicitly treating the subject-specific intercept as random (by providing an estimate of the random-intercept variance).

Sections 5.5 and 5.6 discuss models where the coefficients of time-varying covariates vary between subjects in addition to the subject-specific intercepts. Again we can distinguish between random-coefficient models where the slopes are treated as random variables and fixed-coefficient models where the slopes are treated as unknown parameters.

Finally, *dynamic models*, where the current response is regressed on previous or lagged responses, are introduced in section 5.7. When these models include random intercepts, they pose special challenges that will be addressed.

Throughout this chapter, we analyze the wage-panel data described in *Introduction to models for longitudinal and panel data (part III)*. We first read in the data

```
. use http://www.stata-press.com/data/mlmus3/wagepan
```

and construct the required variables:

```
. generate educt = educ - 12
. generate yeart = year - 1980
```

5.2 Conventional random-intercept model

Random-intercept models were discussed in detail in chapter 3. For the wage-panel data, a conventional random-intercept model is specified as

$$y_{ij} = (\beta_1 + \zeta_j) + \beta_2 x_{2j} + \beta_3 x_{3j} + \beta_4 x_{4ij} + \beta_5 x_{5ij} + \beta_6 L_{ij} + \beta_7 P_i + \beta_8 E_j + \epsilon_{ij}$$

In econometrics, the error components ζ_j and ϵ_{ij} are sometimes referred to as "permanent" and "transitory" components, respectively. To be poetic, Crowder and Hand (1990) referred to the fixed part of the model as the "immutable constant of the universe", to ζ_j as the "lasting characteristic of the individual", and to ϵ_{ij} as the "fleeting aberration of the moment".

Recall from section 3.7.4 that exogeneity assumptions—such as no correlation between the covariates and either the random intercept ζ_j or the level-1 residuals ϵ_{ij}—are required for consistent estimation of the parameters in the conventional random-intercept model. As we did there, we make the somewhat stronger assumptions that $E(\zeta_j|\mathbf{X}_j) = 0$ and $E(\epsilon_{ij}|\mathbf{X}_j, \zeta_j) = 0$, where $\mathbf{X}_j$ contains the covariates at all occasions for subject j. We also define $\psi \equiv \mathrm{Var}(\zeta_j|\mathbf{X}_j)$ and $\theta \equiv \mathrm{Var}(\epsilon_{ij}|\mathbf{X}_j, \zeta_j)$. It is assumed that the ζ_j are uncorrelated across subjects, that the ϵ_{ij} are uncorrelated across both subjects and occasions, and that the ζ_j and ϵ_{ij} are uncorrelated.

Maximum likelihood (ML) estimation is based on the usual assumptions that given the covariates, the random intercept ζ_j, and the level-1 residual ϵ_{ij} are both normally distributed. However, the normality assumptions are not required for consistent estimation of the parameters and standard errors.

The random-intercept model can be fit by ML using `xtmixed`:

```
. xtmixed lwage black hisp union married exper yeart educt || nr:, mle
Mixed-effects ML regression                     Number of obs      =      4360
Group variable: nr                              Number of groups   =       545
                                                Obs per group: min =         8
                                                               avg =       8.0
                                                               max =         8
                                                Wald chi2(7)       =    894.85
Log likelihood = -2214.3572                     Prob > chi2        =    0.0000
```

lwage	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
black	-.1338495	.0479549	-2.79	0.005	-.2278395	-.0398595
hisp	.0174169	.0428154	0.41	0.684	-.0664998	.1013336
union	.1105923	.0179007	6.18	0.000	.0755075	.1456771
married	.0753674	.0167345	4.50	0.000	.0425684	.1081664
exper	.0331593	.0112023	2.96	0.003	.0112031	.0551154
yeart	.0259133	.0114064	2.27	0.023	.0035571	.0482695
educt	.0946864	.0107047	8.85	0.000	.0737055	.1156673
_cons	1.317175	.0373979	35.22	0.000	1.243877	1.390474

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
nr: Identity				
sd(_cons)	.3271344	.0114153	.3055088	.3502908
sd(Residual)	.3535088	.0040494	.3456606	.3615351

```
LR test vs. linear regression: chibar2(01) =  1547.76 Prob >= chibar2 = 0.0000
```

The estimates, which are also shown under "Random intercept" in table 5.1 on page 260, are stored for later use:

```
. estimates store ri
```

We can exponentiate the estimated regression coefficients to obtain estimated multiplicative effects on the expected hourly wages (see display 1.1 on page 64). Controlling for the other variables, expected hourly wages increase by about 3% per year of experience and per year of calendar time. Each additional year of education is associated with an estimated 10% increase in expected wages when controlling for other covariates. We also estimate that given the other covariates, black men's mean wages are 13% lower than white men's, although this estimate is likely to be prone to subject-level confounding or bias due to omitted subject-level variables.

From the random part of the model, we see that the residual between-subject standard deviation is estimated as 0.33 compared with an estimate of 0.35 for the residual within-subject standard deviation. The corresponding estimated residual intraclass correlation is

$$\widehat{\rho} = \frac{\widehat{\psi}}{\widehat{\psi}+\widehat{\theta}} = \frac{0.327^2}{0.327^2+0.354^2} = 0.46$$

which is also the within-subject correlation between the residuals. Thus 46% of the variance in log wage that is not explained by the covariates is due to unobserved time-invariant subject-specific characteristics (strictly speaking, the component of the omitted covariates that is uncorrelated with the included covariates—not an issue if the covariates are exogenous).

5.3 Random-intercept models accommodating endogenous covariates

In this section, we discuss methods for accommodating different kinds of endogenous covariates that are correlated with the random intercept ζ_j. It is still assumed that $E(\epsilon_{ij}|\mathbf{X}_j, \zeta_j) = 0$, which implies that all covariates are uncorrelated with the level-1 residual ϵ_{ij}.

5.3.1 Consistent estimation of effects of endogenous time-varying covariates

We now accommodate endogenous time-varying covariates that are correlated with the random-intercept ζ_j by allowing for different within and between effects for time-varying covariates. As discussed in section 3.7.4, subject-mean centered covariates are uncorrelated with ζ_j by construction, and the corresponding coefficients can be consistently estimated. After subtracting the subject mean from `yeart` and `exper`, both deviation variables would be identical because

$$\texttt{yeart}_i = t_j + \texttt{exper}_{ij}$$

where t_j is the time (in years since 1980) when the subject entered the labor market. We therefore omit `yeart` from the model.

Denoting the subject mean of a variable x_{ij} as $\overline{x}_{\cdot j} = \sum_{i=1}^{n_j} x_{ij}/n_j$, the random-intercept model with different within and between effects can be written as

$$\begin{aligned} y_{ij} = {} & (\beta_1 + \zeta_j) + \beta_2 x_{2j} + \beta_3 x_{3j} + \beta_4(x_{4ij} - \overline{x}_{4\cdot j}) + \beta_5(x_{5ij} - \overline{x}_{5\cdot j}) + \beta_6(L_{ij} - \overline{L}_{\cdot j}) \\ & + \beta_8 E_j + \beta_9 \overline{x}_{4\cdot j} + \beta_{10}\overline{x}_{5\cdot j} + \beta_{11}\overline{L}_{\cdot j} + \epsilon_{ij} \end{aligned} \tag{5.1}$$

where β_7 is missing because `yeart` was removed.

We first construct the subject means of the time-varying covariates `union`, `married`, and `exper` by using the commands

```
. egen mn_union = mean(union), by(nr)
. egen mn_married = mean(married), by(nr)
. egen mn_exper = mean(exper), by(nr)
```

We then construct the occasion-specific deviations from the subject means:

```
. generate dev_union = union - mn_union
. generate dev_married = married - mn_married
. generate dev_exper = exper - mn_exper
```

We fit model (5.1) by ML using `xtmixed` with the `vce(robust)` option, which has the advantage that the estimated standard errors are valid even if the level-1 errors are heteroskedastic or autocorrelated:

```
. xtmixed lwage black hisp dev_union dev_married dev_exper educt
> mn_union mn_married mn_exper || nr:, mle vce(robust)
Mixed-effects regression                        Number of obs      =      4360
Group variable: nr                              Number of groups   =       545
                                                Obs per group: min =         8
                                                               avg =       8.0
                                                               max =         8
                                                Wald chi2(9)       =    597.05
Log pseudolikelihood = -2206.1344               Prob > chi2        =    0.0000
                                  (Std. Err. adjusted for 545 clusters in nr)
------------------------------------------------------------------------------
             |               Robust
       lwage |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       black |   -.1414313   .0508596    -2.78   0.005    -.2411144   -.0417482
        hisp |    .0100387   .0384598     0.26   0.794     -.065341    .0854184
   dev_union |     .083791   .0231021     3.63   0.000     .0385117    .1290702
 dev_married |    .0610384   .0212003     2.88   0.004     .0194866    .1025902
   dev_exper |    .0598672   .0033705    17.76   0.000     .0532611    .0664734
       educt |    .0912614   .0111498     8.19   0.000     .0694082    .1131147
    mn_union |    .2587162   .0425155     6.09   0.000     .1753873    .3420451
  mn_married |    .1416358   .0400085     3.54   0.000     .0632206    .2200509
    mn_exper |    .0278124    .011318     2.46   0.014     .0056296    .0499952
       _cons |    1.378695   .0753624    18.29   0.000     1.230988    1.526403
------------------------------------------------------------------------------

------------------------------------------------------------------------------
  Random-effects Parameters |   Estimate   Robust Std. Err.     [95% Conf. Interval]
----------------------------+-------------------------------------------------
nr: Identity                |
                  sd(_cons) |    .3224087    .0133976      .2971907    .3497665
----------------------------+-------------------------------------------------
               sd(Residual) |    .3533891    .0132959      .3282672    .3804336
------------------------------------------------------------------------------
```

The within effects of the time-varying covariates `union`, `married`, and `exper` are consistently estimated, as long as relevant time-varying covariates are not omitted from the model (and the functional form is correct). Importantly, this is true whether the time-constant covariates are exogenous or not.

Unfortunately, this approach produces inconsistent estimates for the effects of the time-constant covariates `black`, `hisp`, and `educt`, even if they are exogenous. The estimator for the random-intercept variance is also inconsistent.

We can test the joint hypothesis that all the between and within effects are equal using the `test` command (which in this case is robust against heteroskedastic or autocorrelated level-1 errors because we used the `vce(robust)` option for `xtmixed`):

```
. test (dev_union=mn_union) (dev_married=mn_married) (dev_exper=mn_exper)
 ( 1)  [lwage]dev_union - [lwage]mn_union = 0
 ( 2)  [lwage]dev_married - [lwage]mn_married = 0
 ( 3)  [lwage]dev_exper - [lwage]mn_exper = 0
           chi2(  3) =   21.22
         Prob > chi2 =    0.0001
```

We conclude that the between and within effects are significantly different from each other, which suggests that one or more of the time-varying covariates are endogenous. This test is numerically identical to a simultaneous test that the coefficients for all the cluster means are zero in a random-intercept model that includes the cluster means of the time-varying covariates as well as the noncentered covariates (the approach taken in section 3.7.4). The test is also asymptotically equivalent to the Hausman test discussed in section 3.7.6.

As a next step, it is useful to consider the evidence against exogeneity for each of the time-varying covariates by performing separate tests of equal between and within effects, for instance, using `lincom`:

```
. lincom dev_union-mn_union
 ( 1)  [lwage]dev_union - [lwage]mn_union = 0
```

lwage	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
(1)	-.1749252	.0474094	-3.69	0.000	-.267846	-.0820045

```
. lincom dev_married-mn_married
 ( 1)  [lwage]dev_married - [lwage]mn_married = 0
```

lwage	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
(1)	-.0805974	.0452476	-1.78	0.075	-.1692811	.0080864

```
. lincom dev_exper-mn_exper
 ( 1)  [lwage]dev_exper - [lwage]mn_exper = 0
```

lwage	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
(1)	.0320548	.0119636	2.68	0.007	.0086067	.055503

We see that there is most evidence against `union` being exogenous. This is not surprising, because one might expect the random intercept to be correlated with union membership. For instance, if the random intercept is interpreted as unmeasured ability, then high ability subjects might have higher mean earnings than expected given their observed covariates and be more likely to be union members. Interestingly, the research

focus of Vella and Verbeek (1998), who made the wage-panel data available, was to develop an approach for handling the endogeneity of `union`.

5.3.2 Consistent estimation of effects of endogenous time-varying and endogenous time-constant covariates

A limitation of the approach with different within and between effects is that the coefficients of time-constant exogenous or endogenous covariates are not consistently estimated. Fortunately, Hausman and Taylor (1981) developed a method, implemented in Stata's `xthtaylor` command, that makes it possible to fit models with some endogenous time-constant covariates in addition to some endogenous time-varying covariates [still assuming that $E(\epsilon_{ij}|\mathbf{X}_j, \zeta_j) = 0$ so that all covariates are uncorrelated with ϵ_{ij}].

A requirement for using the Hausman–Taylor approach is that both time-varying and time-constant covariates can be classified as either endogenous or exogenous (correlated or not with the random intercept ζ_j). We hence have four kinds of covariates:

1. Exogenous time-varying covariates x_{ij}
2. Endogenous time-varying covariates x_{ij}^{end}
3. Exogenous time-constant covariates x_j
4. Endogenous time-constant covariates x_j^{end}

Furthermore, a necessary condition for identification is that there are at least as many exogenous time-varying covariates as there are endogenous time-constant covariates.

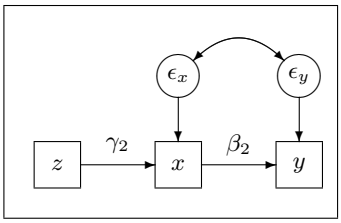
The basic idea of the Hausman–Taylor method is as follows. First, consistent estimates of the within effects for the time-varying covariates (and the variance of the level-1 residual) are obtained using a standard fixed-effects estimator (see sections 3.7.2 and 5.4). Residuals are then produced by predicting the response using uncentered time-varying covariates and the estimated coefficients from the first step. The subject-mean residuals are then regressed on the time-constant covariates, using the exogenous covariates as *instrumental variables*, to obtain consistent estimates of the coefficients for the time-constant covariates (if you are unfamiliar with instrumental-variables estimation you may want to consult display 5.1, which provides the basic ideas).

Consider a simple linear model for cross-sectional data (no clustering):

$$y_i = \beta_1 + \beta_2 x_i + \epsilon_{yi} \quad (1)$$

We want to estimate β_2, but x_i is endogenous because it is correlated with ϵ_{yi}, and the ordinary least squares (OLS) estimator $\widehat{\beta}_2^{\text{OLS}}$ is therefore inconsistent.

We can overcome this problem and obtain a consistent estimator of β_2 if we can find an *instrumental variable* (IV) z_i. The requirements for an instrumental variable are that it is 1) correlated with x_i and 2) uncorrelated with ϵ_{yi}. An example is the problem of estimating the effect of smoking x_i on health y_i. There may be omitted covariates, such as socioeconomic status, that affect both smoking and health, and hence x_i may be endogenous. A possible instrumental variable z_i in this case is the price of cigarettes (if this varies in the sample) because price affects smoking but not health. To understand the instrumental-variable estimator, consider the model shown in the path diagram below:



This model also involves the regression (treated as a linear projection)

$$x_i = \gamma_1 + \gamma_2 z_i + \epsilon_{xi} \quad (2)$$

A double-headed arrow connects ϵ_{xi} and ϵ_{yi} because x_i is endogenous, whereas z_i and ϵ_{yi} are not connected because of the second property above of an instrumental variable. The reduced-form model for y_i is

$$y_i = \beta_1 + \beta_2(\underbrace{\gamma_1 + \gamma_2 z_i + \epsilon_{xi}}_{x_i}) + \epsilon_{yi} = (\beta_1 + \beta_2\gamma_1) + (\beta_2\gamma_2)z_i + \underbrace{\beta_2\epsilon_{xi} + \epsilon_{yi}}_{\epsilon_i^*} \quad (3)$$

The following OLS estimators are consistent because ϵ_{xi} and ϵ_i^* are uncorrelated with z_i:

$$(2)\ x \text{ on } z: \quad \widehat{\gamma}_2^{\text{OLS}} = \frac{\text{Cov}(x,z)}{\text{Var}(z)} \qquad (3)\ y \text{ on } z: \quad \widehat{\beta_2\gamma_2}^{\text{OLS}} = \frac{\text{Cov}(y,z)}{\text{Var}(z)}$$

From these estimators, we see that a consistent (but not unbiased) estimator for β_2 is

$$\widehat{\beta}_2^{\text{IV}} = \frac{\widehat{\beta_2\gamma_2}^{\text{OLS}}}{\widehat{\gamma}_2^{\text{OLS}}} = \frac{\text{Cov}(y,z)}{\text{Cov}(x,z)}$$

In practice, this estimator can be obtained using two-stage least squares (2SLS), where x_i is first regressed on z_i and then the prediction $\widehat{x}_i$ from this regression is used as a covariate in the model for y_i instead of the original x_i. This method can also be generalized to linear models with several covariates, possibly with multiple instruments; see Wooldridge (2010, sec. 5.1).

A problem with instrumental variables is that they are often weak in the sense that $\text{Cor}(z_i, x_i)$ is small, and in this case the instrumental-variable estimator is inefficient.

Display 5.1: Instrumental-variables estimation

We could stop here because we have consistent estimates of all regression parameters, but Hausman and Taylor proceed by using further instrumental-variable methods to obtain a more efficient estimator and perform valid statistical inference using that estimator. Specifically, a new set of residuals is formed by plugging in the estimated regression parameters from the previous stages, and simple moment estimators are used to estimate θ and ψ based on these residuals. Using these estimated variance parameters a so-called generalized least squares (GLS) transform is performed to make the responses uncorrelated across occasions, whereby standard instrumental-variables estimation becomes feasible. The Hausman–Taylor estimator is finally obtained by using three sets of instruments: the deviations from the cluster means of the time-varying covariates, the cluster means of exogenous time-varying covariates, and the exogenous time-constant covariates.

If the random-intercept model is correctly specified (including the designation of exogenous and endogenous covariates), the Hausman–Taylor method will produce consistent and asymptotically efficient estimators for all model parameters, including the regression coefficients of time-constant covariates and the random-intercept variance.

Subsequent work has improved on the finite-sample efficiency of the Hausman–Taylor estimator by including more instruments. Stata provides one of these approaches, due to Amemiya and MaCurdy (1986), which is invoked by the `amacurdy` option of the `xthtaylor` command.

As pointed out in the previous section, the most obvious candidate for an endogenous time-varying covariate is `union`, and we will stick to this here. Regarding endogenous time-constant covariates, we have chosen `educt` because the random intercept is likely to be correlated with education. For instance, if the random intercept is interpreted as unmeasured ability, then high ability subjects might have higher earnings than expected given their observed covariates and higher education, leading to a positive correlation between education and the random intercept. Conversely, it could be that high ability subjects are less educated (perhaps because they know that they do not need high education to succeed), producing a negative correlation. To illustrate the Hausman–Taylor approach, the covariates `married` and `exper` are treated as exogenous time-varying covariates, whereas `black` and `hisp` are treated as exogenous time-constant covariates.

The resulting random-intercept model with `union` x_{4ij}^{end} and `educt` E_j^{end} as endogenous covariates can be written as (we omit `yeart` because it is collinear with `exper` after mean-centering in the first step of the Hausman–Taylor estimator)

$$y_{ij} = (\beta_1 + \zeta_j) + \beta_2 x_{2j} + \beta_3 x_{3j} + \beta_4 x_{4ij}^{\text{end}} + \beta_5 x_{5ij} + \beta_6 L_{ij} + \beta_8 E_j^{\text{end}} + \epsilon_{ij}$$

where ϵ_{ij} is a level-1 residual with mean zero and variance θ.

We use the `xthtaylor` command to fit the model, specifying the endogenous covariates in the `endog()` option (Stata keeps track of whether covariates are time varying or time constant):

```
. quietly xtset nr
. xthtaylor lwage black hisp union married exper educt, endog(union educt)
Hausman-Taylor estimation                       Number of obs      =      4360
Group variable: nr                              Number of groups   =       545
                                                Obs per group: min =         8
                                                               avg =         8
                                                               max =         8
Random effects u_i ~ i.i.d.                     Wald chi2(6)       =    801.99
                                                Prob > chi2        =    0.0000
```

lwage	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
TVexogenous						
married	.0715925	.0168862	4.24	0.000	.0384962	.1046888
exper	.0593827	.0025624	23.17	0.000	.0543605	.0644049
TVendogenous						
union	.0844763	.0194014	4.35	0.000	.0464503	.1225023
TIexogenous						
black	-.1255779	.049431	-2.54	0.011	-.2224608	-.028695
hisp	.0513715	.0459801	1.12	0.264	-.0387478	.1414908
TIendogenous						
educt	.1424144	.0161925	8.80	0.000	.1106777	.174151
_cons	1.249935	.0237772	52.57	0.000	1.203332	1.296537
sigma_u	.33790949					
sigma_e	.35338912					
rho	.47761912	(fraction of variance due to u_i)				

```
Note:  TV refers to time varying; TI refers to time invariant.
```

The prefixes `TV` and `TI` in the headings in the table of coefficients stand for "time varying" and "time invariant" (same as time-constant), respectively.

Although only `union` is treated as an endogenous time-varying covariate here, the estimated coefficients of time-varying covariates are quite similar to those produced by the approach based on different within and between effects in the previous section (where all time-varying covariates were treated as endogenous but no time-constant covariates were treated as endogenous). The estimate of the covariate designated as endogenous time constant, `educt`, is considerably higher than when it was treated as exogenous. This suggests that there is a negative correlation between education and the random intercept.

The estimates produced by `xthtaylor` are highly dependent on which covariates are designated as endogenous. Hence, subject-matter considerations regarding endogeneity should be combined with sensitivity analyses to try to ensure sensible estimates. The Hausman–Taylor estimator produces consistent and asymptotically efficient estimates of the coefficients of endogenous time-varying covariates if the model specification is correct. A Hausman test can therefore be used to compare the estimates for the time-varying covariates with their consistent (but possibly inefficient) counterparts from the fixed-effects approach (see exercises 5.7 and 5.8).

5.4 Fixed-intercept model

In the fixed-intercept model, often called the fixed-effects model in econometrics, subject-specific intercepts are treated as fixed, unknown parameters α_j. The model can be written as

$$y_{ij} = \alpha_j + \beta_2 x_{2j} + \beta_3 x_{3j} + \beta_4 x_{4ij} + \beta_5 x_{5ij} + \beta_6 L_{ij} + \beta_7 P_i + \beta_8 E_j + \epsilon_{ij}$$

It is assumed that given the covariates $\mathbf{X}_j$ of a subject, the level-1 residual ϵ_{ij} has mean zero, variance θ, and is uncorrelated across occasions and subjects. Because the subject-specific intercepts are treated as fixed, this model relaxes all assumptions made in the random-intercept model regarding the subject-specific intercepts.

As previously discussed in section 3.7.2, we can fit this model by OLS by including dummy variables for each subject in the model and omitting the overall constant (using the `noconstant` option of `regress`). This produces consistent estimates of the coefficients β_4, β_5, and β_6 of the time-varying covariates `union`, `married`, and `exper`, as long as relevant time-varying covariates (confounders) are not omitted from the model. These estimated within effects are numerically identical to the corresponding ML estimates for the random-intercept model (5.1) with different within and between effects.

However, the coefficients β_2, β_3, and β_8 for the time-constant covariates `black`, `hisp`, and `educt` cannot be estimated because all between-subject variability is explained by the fixed intercepts. To see this, think of the subject-specific effects as coefficients of dummy variables for subjects. The problem is that the time-constant covariates are perfectly collinear with these dummy variables. It also turns out that the coefficient β_7 of the time-varying covariate `yeart` cannot be estimated because `yeart` differs from `exper` (L_{ij}) only by a subject-specific constant t_j: $\texttt{yeart}_i = t_j + \texttt{exper}_{ij}$, where t_j is the time (in years since 1980) at which the subject entered the labor market. The linear combination `yeart`$-$`exper` is therefore collinear with dummy variables for subjects.

The α_j are not consistently estimated if the number of occasions remains fixed and the number of subjects increases. This is an incidental parameter problem that is due to the number of parameters α_j increasing as the number of subjects increases. Usually, the subject-specific effects are not of interest, and they can be eliminated by subject-mean centering the responses and covariates (which is what the `xtreg` command with the `fe` option does). From this perspective, α_j can also be viewed as random intercepts.

Because these intercepts are eliminated, it is not necessary to assume that they are uncorrelated with covariates or that they have a constant variance or a normal distribution. The random intercepts could also be correlated across subjects, for instance, because of clustering in states.

To see this, we first obtain the subject means of the model

$$y_{ij} = \alpha_j + \beta_2 x_{2j} + \beta_3 x_{3j} + \beta_4 x_{4ij} + \beta_5 x_{5ij} + \beta_6 L_{ij} + \beta_7 P_i + \beta_8 E_j + \epsilon_{ij}$$

which are

$$\overline{y}_{\cdot j} \;=\; \alpha_j + \beta_2 x_{2j} + \beta_3 x_{3j} + \beta_4 \overline{x}_{4\cdot j} + \beta_5 \overline{x}_{5\cdot j} + \beta_6 \overline{L}_{\cdot j} + \beta_7 \overline{P}_{\cdot} + \beta_8 E_j + \overline{\epsilon}_{\cdot j}$$

Subtracting these subject means from the model, we get

$$y_{ij} - \overline{y}_{\cdot j} \;=\; \beta_4(x_{4ij} - \overline{x}_{4\cdot j}) + \beta_5(x_{5ij} - \overline{x}_{5\cdot j}) + \beta_6(L_{ij} - \overline{L}_{\cdot j}) + \cancel{\beta_7(P_i - \overline{P}_{\cdot})} + \epsilon_{ij} - \overline{\epsilon}_{\cdot j}$$

The subject-specific intercepts α_j are eliminated from this model as desired, but the coefficients for the time-constant covariates cannot be estimated because the terms involving these are also eliminated. As pointed out above, `yeart` has to be omitted because the mean-centered `yeart` ($P_i - \overline{P}_{\cdot}$) is identical to the mean-centered `exper` ($L_{ij} - \overline{L}_{\cdot j}$). The estimated coefficient of `exper` will then be an estimate of the sum $\beta_6 + \beta_7$.

Alternatively, we could eliminate the intercepts α_j by taking first-differences:

$$y_{ij} - y_{i-1,j} \;=\; (\beta_6 + \beta_7) + \beta_4(x_{4ij} - x_{4,i-1,j}) + \beta_5(x_{5ij} - x_{5,i-1,j}) + \epsilon_{ij} - \epsilon_{i-1,j} \quad (5.2)$$

The terms involving time-constant variables are again eliminated. Because $L_{ij} - L_{i-1,j} = 1$ and $P_i - P_{i-1} = 1$, $\beta_6 + \beta_7$ becomes an intercept. The differencing approach is preferable if the residuals ϵ_{ij} in the fixed-effects model are correlated over time (see exercise 5.4, question 2.b.iii).

As discussed in section 3.7.2, the estimates based on the fixed-intercept approach represent the within-subject effects of the covariates. A great advantage of these estimates is that they are not susceptible to bias due to omitted subject-level covariates (level-2 endogeneity). Each subject truly serves as its own control when using this approach.

Keep in mind, however, that the fixed-effects approach is no panacea. It requires sufficient within-subject variability of the response and covariates to obtain reliable estimates (this is one of the reasons for investigating the within and between variability of variables using `xtsum`). In practice, the consistency of the within estimator is often purchased at the cost of large mean squared errors and low power. Griliches and Hausman (1986) also point out that measurement error bias is likely to be exacerbated using the conventional fixed-effects approach as compared with the random-effects approach. Finally, as is the case for the random-effects approach, the problem of level-1 endogeneity—where covariates are correlated with the level-1 residual ϵ_{ij}—is not addressed.

5.4.1 Using xtreg or regress with a differencing operator

The fixed-intercept model can be fit by OLS using `xtreg` with the `fe` option (where we have not included covariates whose effects cannot be estimated):

```
. quietly xtset nr
. xtreg lwage union married exper, fe
Fixed-effects (within) regression               Number of obs      =      4360
Group variable: nr                              Number of groups   =       545

R-sq:  within  = 0.1672                         Obs per group: min =         8
       between = 0.0001                                        avg =       8.0
       overall = 0.0513                                        max =         8

                                                F(3,3812)          =    255.03
corr(u_i, Xb)  = -0.1575                        Prob > F           =    0.0000

------------------------------------------------------------------------------
       lwage |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       union |    .083791   .019414     4.32   0.000      .045728    .1218539
     married |   .0610384   .0182929     3.34   0.001     .0251736    .0969032
       exper |   .0598672   .0025835    23.17   0.000      .054802    .0649325
       _cons |   1.211888   .0169244    71.61   0.000     1.178706     1.24507
-------------+----------------------------------------------------------------
     sigma_u |  .40514496
     sigma_e |  .35352815
         rho |  .56772216   (fraction of variance due to u_i)
------------------------------------------------------------------------------
F test that all u_i=0:     F(544, 3812) =    10.08           Prob > F = 0.0000
```

We store the estimates using

```
. estimates store fi
```

and report them under "Fixed intercept" in table 5.1. (`sigma_u` in the output is the sample standard deviation of the estimated intercepts $\widehat{\alpha}_j$.)

Table 5.1: Estimates for subject-specific models for wage-panel data

	Subject-specific intercepts								Subject-specific slopes			
	Random intercept		Random int. & w/b†		Hausman–Taylor		Fixed intercept		Random coefficient		Fixed coefficient	
	Est	(SE)	Est	(SE)	Est	(SE)	Est	(SE)	Est	(SE)	Est	(SE)
Fixed part												
β_1 [_cons]	1.32	(0.04)	1.37	(0.02)	1.25	(0.02)	1.21	(0.02)	1.31	(0.04)		
β_2 [black]	−0.13	(0.05)	−0.14	(0.05)	−0.13	(0.05)			−0.14	(0.05)		
β_3 [hisp]	0.02	(0.04)	0.01	(0.04)	0.05	(0.05)			0.01	(0.04)		
β_4 [union]	0.11	(0.02)	0.08	(0.02)	0.08	(0.02)	0.08	(0.02)	0.11	(0.02)	0.04	(0.02)
β_5 [married]	0.08	(0.02)	0.06	(0.02)	0.07	(0.02)	0.06	(0.02)	0.08	(0.02)	0.04	(0.03)
β_6 [exper]	0.03	(0.01)							0.04	(0.01)		
β_7 [yeart]	0.03	(0.01)							0.02	(0.01)		
$\beta_6 + \beta_7$			0.06	(0.00)	0.06	(0.00)	0.06	(0.00)			0.07	(0.01)
β_8 [educt]	0.09	(0.01)	0.09	(0.01)	0.14	(0.02)			0.10	(0.01)		
Random part												
$\sqrt{\psi_{11}}$	0.33		0.32		0.34				0.45			
$\sqrt{\psi_{22}}$									0.05			
ρ_{21}									−0.68			
$\sqrt{\theta}$ or res. SD	0.35		0.35		0.35		0.35		0.33		0.47‡	

† Separate within and between effects; coefficients of cluster means not shown
‡ Estimated standard deviation (SD) of first-differenced residual

We see that union membership, being married, and having more experience are all beneficial for wages, according to the fitted model. For instance, each extra year of experience is associated with an estimated increase in the expectation of log hourly wage of 0.06, controlling for the other covariates. In other words, mean hourly wages increase 6% [$= 100\%\{\exp(1.06) - 1\}$] for each extra year of experience. However, this actually represents the combined effect of experience and period, which cannot be disentangled here. Interestingly, the estimated coefficients of `exper` and `yeart` for the random-intercept model approximately add up to the present coefficient of `exper`. In contrast to the random-intercept model, cohort effects have been controlled for because they are subject specific. For a given subject, becoming a member of a union increases his or her mean hourly wages by about 8%, controlling for the other covariates. Importantly, this is a within effect and differs from the between effect that compares different subjects who are either union members or not. If a subject becomes married, this increases his or her mean hourly wages by about 6% according to the fitted model, controlling for the other covariates.

The above estimates are obtained by subject-mean centering. For estimation using first-differencing, it is very convenient to use Stata's time-series operators, where the required differences are simply obtained by using the prefix "D." (for first-differencing) for the variables included in the estimation command.

We can fit the first-differenced model by OLS by typing

```
regress D.lwage D.union D.married
```

or using the more compact syntax

```
regress D.(lwage union married)
```

(output not shown).

The Hausman test described in section 3.7.6 can be used to investigate endogeneity of the time-varying covariates by comparing the estimates from the fixed-intercept model (stored as `fi`) with those from the random-intercept model. We cannot use the estimates for the random-intercept model obtained in section 5.2 because that model included `yeart` as a covariate and was fit by ML and not by feasible generalized least squares (FGLS), as required by the `hausman` command. We therefore first fit the appropriate random-intercept model by FGLS using `xtreg` with the `re` option:

```
. quietly xtset nr
. quietly xtreg lwage black hisp union married exper educt, re
```

We then store the estimates using

```
. estimates store ri2
```

and perform a Hausman test:

```
. hausman fi ri2
                 ---- Coefficients ----
                |      (b)          (B)            (b-B)     sqrt(diag(V_b-V_B))
                |       fi          ri2         Difference          S.E.
----------------+----------------------------------------------------------------
          union |     .083791     .1100027       -.0262118        .0074711
        married |    .0610384     .0757698       -.0147314        .0073449
          exper |    .0598672     .0579462          .001921        .0006418
------------------------------------------------------------------------------
                           b = consistent under Ho and Ha; obtained from xtreg
            B = inconsistent under Ha, efficient under Ho; obtained from xtreg

    Test:  Ho:  difference in coefficients not systematic

                  chi2(3) = (b-B)'[(V_b-V_B)^(-1)](b-B)
                          =       22.69
                Prob>chi2 =      0.0000
```

As expected, the Hausman statistic is similar to the test statistic for the joint hypothesis of equal within and between effects, shown in section 5.3.1. An advantage of the latter test (based on robust standard errors) is that it can be used even if there are heteroskedastic or autocorrelated level-1 errors.

5.4.2 ❖ Using anova

Using the language of experimental design, subjects can be viewed as blocks or plots to which different treatments are applied. In a split-plot design, some treatments are applied to the entire plots (subjects)—these are the whole-plot, between-subject, or level-2 variables (`black`, `hisp`, and `educt`). The plots are split into subplots (subjects at different occasions) to which other treatments can be applied—these are the split-plot, within-subject, or level-1 variables (`union`, `married`, `exper`, and `yeart`).

One-way analysis of variance (ANOVA) was briefly discussed in section 1.4, where we showed how the total sum of squares is partitioned into the sum of squares attributed to a factor (a categorical covariate) and the sum of squared errors. An F statistic is then constructed by dividing the mean squares due to the factor by the mean squared error.

ANOVA with continuous covariates is often called ANCOVA (analysis of covariance). In a split-plot design, the important thing to remember is that a different mean squared error is used in the denominator of the F statistic for testing the whole-plot (between-subject) variables than for the split-plot (within-subject) variables. For the between-subject variables, the denominator is given by the (unique or partial) mean squares due to subjects. For the within-subject variables, the denominator is given by the mean squared error after allowing for fixed effects of subjects. Subjects are often viewed as random, and an estimator of the between-subject variance can be derived from the mean squares, but the estimators of the effects of within-subject variables are fixed-effects estimators.

In Stata's `anova` command, a categorical explanatory variable is entered directly instead of the corresponding dummy variables. We must therefore first construct the categorical variable `ethnic` (with values 0: white; 1: black; and 2: Hispanic) from the dummy variables `black` and `hisp`:

```
. generate ethnic = black*1 + hisp*2
```

For simplicity, we initially fit the model with only one time-constant variable, `ethnic`, omitting `educt` (after first increasing `matsize`):

```
. set matsize 800
. anova lwage ethnic / nr|ethnic union married c.exper, dropemptycells
                          Number of obs =    4360     R-squared     =  0.6147
                          Root MSE      = .353528     Adj R-squared =  0.5594
    Source | Partial SS    df       MS           F     Prob > F
-----------+----------------------------------------------------
     Model |  760.097675   547  1.38957527      11.12     0.0000
           |
    ethnic |  15.5566098     2  7.77830491       6.46     0.0017
nr|ethnic |  652.885925   542  1.20458658
-----------+----------------------------------------------------
     union |  2.32814565     1  2.32814565      18.63     0.0000
   married |  1.39152302     1  1.39152302      11.13     0.0009
     exper |  67.1116346     1  67.1116346     536.97     0.0000
           |
  Residual |  476.431967  3812  .124982153
-----------+----------------------------------------------------
     Total |  1236.52964  4359  .283672779
```

(Without the `dropemptycells` option, the command would require a very large matrix size.)

The model includes the main effects `ethnic`, `nr|ethnic`, `union`, `married`, and `exper`, where `nr|ethnic` denotes that subjects are nested within ethnicities in the sense that each subject can have only one ethnicity. The term `ethnic` represents the main effect of ethnicity, whereas the term `nr|ethnic` represents the main effect of subject, where subject is nested in ethnicities. The prefix `c.` in `c.exper` denotes that `exper` should be treated as continuous by assuming the conditional expectation of the log wages to be linearly related to `exper`. The purpose of the forward slash, `/`, is to declare that the denominator for the F statistic(s) for the preceding term(s) is the mean square for subjects (nested in ethnicity) and not the mean squared error for the entire model, after subtracting the sums of squares due to all terms, including subjects nested within ethnicities. Using the latter "within-subject" mean squared error in the F test for `ethnic` would produce a p-value that is too small and ignores the longitudinal nature of the data. The within-subject mean squared error is used for the denominator in the F statistic for the time-varying variables `union`, `married`, and `exper`.

The F-test statistic for `ethnic` is $F(2, 542) = 6.46$, with $p = 0.002$. This can be interpreted as a test for the between-subject effect of ethnicity after removing the within-subject effects of the time-varying variables. The F tests for the within-subject variables are equivalent to the t-tests obtained using `xtreg` with the `fe` option (see

page 259). Because each F test has one numerator degree of freedom, taking the square roots of the F statistics gives the corresponding t statistics:

```
. display sqrt(18.63)
4.3162484
. display sqrt(11.13)
3.3361655
. display sqrt(536.97)
23.172613
```

Including further time-constant variables is relatively straightforward, but remember that subject is now nested in the combinations of the values of these variables. For ethnicity and education, this means that every ethnicity may be combined with every possible number of years of education. The syntax for nesting within such a cross-classification is `nr|ethnic#educt`, and the syntax for the full model is

```
anova lwage ethnic c.educt / nr|ethnic#educt union married c.exper, dropemptycells
```

The ANOVA model assumes that the responses are uncorrelated given the explanatory variables (which include the factor subject). This assumption, together with constant variance, implies *compound symmetry* of the variance–covariance matrix of the responses given the explanatory variables (but not given the factor subject) when subject is treated as random. Compound symmetry means that the responses have the same conditional variances across occasions and the same conditional covariances between all pairs of occasions (not necessarily positive). This covariance structure is the same as for a random-intercept model except that the covariances can also be negative.

A less strict assumption that all pairwise differences between responses have the same variance, called *sphericity*, is sufficient for the F test for within-subject variables to be valid. When this assumption is violated, the `repeated()` option can be used in the `anova` command to correct the p-values for within-subject variables. Unfortunately, this option works only for categorical within-subject variables (but `exper` is continuous). By default, it also requires that there be only one observation per cell in the cross-tabulation of within-subject variables for each subject. So, omitting `exper` because it is continuous would not help because a subject can have a given combination of the values of `union` and `married`—for example, 0, 0—for several waves of data.

The version of repeated-measures ANOVA discussed here is sometimes referred to as *univariate* or as applicable to a split-plot design. There is also a multivariate version, called multivariate analysis of variance (MANOVA) and implemented in Stata's `manova` command, that specifies an unstructured covariance matrix for the repeated measures (see section 6.3.1). A great disadvantage of that approach is that it uses listwise deletion, dropping entire subjects if one or more of their responses are missing. Furthermore, the MANOVA approach requires that the within-subject variables take on identical values for all subjects; for instance, the variable `yeart` can be used but `union` cannot.

5.5 Random-coefficient model

We could in principle include random coefficients for any of the time-varying variables in the wage-panel data to allow the effect of these variables to vary between subjects (but remember the warnings in section 4.10). The data provide no information on subject-specific effects of time-constant variables x_j, and it therefore does not make sense to include random coefficients for these variables unless we want to model heteroskedasticity (see section 7.5.2)

It may well be that different subjects' wages increase at different rates with each extra year of experience. We can investigate this by including a random coefficient ζ_{2j} of labor-market experience L_{ij} in the model

$$\begin{aligned} y_{ij} &= \beta_1 + \beta_2 x_{2j} + \beta_3 x_{3j} + \beta_4 x_{4ij} + \beta_5 x_{5ij} + \beta_6 L_{ij} + \beta_7 P_i + \beta_8 E_j + \zeta_{1j} + \zeta_{2j} L_{ij} + \epsilon_{ij} \\ &= (\beta_1 + \zeta_{1j}) + \beta_2 x_{2j} + \beta_3 x_{3j} + \beta_4 x_{4ij} + \beta_5 x_{5ij} + (\beta_6 + \zeta_{2j}) L_{ij} + \beta_7 P_i + \beta_8 E_j + \epsilon_{ij} \end{aligned}$$

Given the covariates $\mathbf{X}_j$ for a subject, the random intercept ζ_{1j} has mean zero and variance ψ_{11}, the random slope ζ_{2j} has mean zero and variance ψ_{22}, and the covariance between ζ_{1j} and ζ_{2j} is ψ_{21}. The random effects ζ_{1j} and ζ_{2j} are uncorrelated across subjects. Given the covariates and random effects, the level-1 residuals ϵ_{ij} have zero means, variance θ, and are mutually uncorrelated across both occasions and subjects.

We fit the random-coefficient model by ML using `xtmixed` with the `mle` option:

```
. xtmixed lwage black hisp union married exper yeart educt || nr: exper,
> covariance(unstructured) mle
Mixed-effects ML regression                     Number of obs      =      4360
Group variable: nr                              Number of groups   =       545
                                                Obs per group: min =         8
                                                               avg =       8.0
                                                               max =         8
                                                Wald chi2(7)       =    573.88
Log likelihood = -2130.4677                     Prob > chi2        =    0.0000
------------------------------------------------------------------------------
       lwage |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       black |   -.139996   .0489058    -2.86   0.004    -.2358496   -.0441423
        hisp |    .009267   .0437623     0.21   0.832    -.0765055    .0950396
       union |   .1098184    .017896     6.14   0.000     .0747429     .144894
     married |   .0757788   .0173732     4.36   0.000      .041728    .1098296
       exper |   .0418495   .0119737     3.50   0.000     .0183815    .0653175
       yeart |   .0171964   .0118898     1.45   0.148    -.0061072    .0405001
       educt |    .097203   .0109324     8.89   0.000     .0757758    .1186302
       _cons |   1.307388   .0404852    32.29   0.000     1.228039    1.386738
------------------------------------------------------------------------------
```

```
------------------------------------------------------------------------------
  Random-effects Parameters |   Estimate   Std. Err.      [95% Conf. Interval]
----------------------------+-------------------------------------------------
nr: Unstructured            |
                  sd(exper) |   .0539497   .0030854       .048229    .0603489
                  sd(_cons) |   .4514402   .0215257       .411162    .4956641
           corr(exper,_cons) |  -.6801072   .0348441     -.7426584   -.6057911
----------------------------+-------------------------------------------------
                sd(Residual) |   .3266336   .0040591       .318774    .3346871
------------------------------------------------------------------------------
LR test vs. linear regression:       chi2(3) =  1715.54   Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference.
```

Then we store the estimates:

```
. estimates store rc
```

The estimates were also shown under "Random coefficient" in table 5.1. We note that the coefficient for `exper` varies quite considerably, with 95% of the effects being in the range from about -0.06 to 0.15 ($0.0418495 \pm 1.96 \times 0.0539497$). Negative effects of `exper` are therefore not uncommon.

We can perform a likelihood-ratio test comparing the random-intercept and random-coefficient models:

```
. lrtest ri rc
Likelihood-ratio test                                 LR chi2(2)  =    167.78
(Assumption: ri nested in rc)                         Prob > chi2 =    0.0000
Note: The reported degrees of freedom assumes the null hypothesis is not on
      the boundary of the parameter space.  If this is not true, then the
      reported test is conservative.
```

The correct p-value from this test should be obtained by using a 50:50 mixture of a $\chi^2(1)$ and a $\chi^2(2)$ as null distribution (see section 4.6), which makes no difference to the conclusion that the random-intercept model is rejected in favor of the random-coefficient model.

We could alternatively have included a random slope for `yeart`. However, if different subjects grow at different rates after 1980 (when `yeart`=0), it makes sense to assume that they have grown at different rates ever since they entered the labor market, which could be before 1980. The variance in wages in the year 1980 must then be larger for those who entered the labor market long before that time (and have grown at different rates for a long time) than for those who entered recently. However, a model with a random coefficient for `yeart` would assume a constant variance when `yeart` is zero.

5.6 Fixed-coefficient model

The fixed-effects version of the model with subject-specific intercepts and slopes is

$$\begin{aligned} y_{ij} &= \beta_1 + \beta_2 x_{2j} + \beta_3 x_{3j} + \beta_4 x_{4ij} + \beta_5 x_{5ij} + \beta_6 L_{ij} + \beta_7 P_i \\ &\quad + \beta_8 E_j + \alpha_{1j} + \alpha_{2j} L_{ij} + \epsilon_{ij} \\ &= (\beta_1 + \alpha_{1j}) + \beta_2 x_{2j} + \beta_3 x_{3j} + \beta_4 x_{4ij} + \beta_5 x_{5ij} + (\beta_6 + \alpha_{2j}) L_{ij} \\ &\quad + \beta_7 P_i + \beta_8 E_j + \epsilon_{ij} \end{aligned}$$

where α_{1j} and α_{2j} are fixed subject-specific intercept and slope parameters, respectively. Conditional on the covariates $\mathbf{X}_j$, ϵ_{ij} has mean zero, variance θ, and is uncorrelated across occasions and subjects. The estimated coefficients represent within-subject effects of the covariates and are not susceptible to bias due to omitted subject-level covariates.

If the covariate that has a subject-specific slope increases by constant amounts across occasions (as does L_{ij}) and if there are no missing data, first-differences can be used to turn the slope into an intercept. Specifically, we obtain

$$\begin{aligned} y_{ij} - y_{i-1,j} &= (\beta_6 + \beta_7 + \alpha_{2j}) + \beta_4 (x_{4ij} - x_{4,i-1,j}) + \beta_5 (x_{5ij} - x_{5,i-1,j}) \\ &\quad + \epsilon_{ij} - \epsilon_{i-1,j} \end{aligned}$$

The original intercepts α_{1j} disappear as do the terms involving time-constant covariates. Because $L_{ij} - L_{i-1,j} = 1$, the original subject-specific slopes α_{2j} now become subject-specific intercepts. The coefficient β_6 for L_{ij} becomes part of a fixed intercept, as does the coefficient β_7 because $P_i - P_{i-1} = 1$. The resulting fixed subject-specific intercept model can then be fit using the approach described in section 5.4 to produce consistent estimates of the coefficients β_4 and β_5 for the time-varying covariates `union` and `married`. As for the first-difference approach to fitting fixed-intercept models, this approach also handles serially correlated (nonexchangeable) residuals to some extent.

To implement the first-difference approach, we once again use Stata's time-series operators, where first-differences are obtained by using the prefix "D." for the variables. We can then use `xtreg, fe` to fit the fixed-coefficient model (we only include the covariates `union` and `married`, whose coefficients can be estimated by this approach here):

```
. quietly xtset nr yeart
. xtreg D.(lwage union married), fe
Fixed-effects (within) regression               Number of obs      =      3815
Group variable: nr                              Number of groups   =       545
R-sq:  within  = 0.0020                         Obs per group: min =         7
       between = 0.0073                                        avg =       7.0
       overall = 0.0022                                        max =         7
                                                F(2,3268)          =      3.26
corr(u_i, Xb)  = 0.0075                         Prob > F           =    0.0387
------------------------------------------------------------------------------
     D.lwage |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       union |
        D1.  |   .0402949   .0212656     1.89   0.058    -.0014003    .0819901
             |
     married |
        D1.  |   .0427839   .0250491     1.71   0.088    -.0063296    .0918974
             |
       _cons |   .0648842   .0077594     8.36   0.000     .0496704     .080098
-------------+----------------------------------------------------------------
     sigma_u |  .08632664
     sigma_e |  .46977158
         rho |  .03266576   (fraction of variance due to u_i)
------------------------------------------------------------------------------
F test that all u_i=0:     F(544, 3268) =     0.24           Prob > F = 1.0000
```

The estimated coefficients of `union` and `married` (reported under "Fixed coefficient" in table 5.1) are considerably smaller than the corresponding estimates in the random-coefficient model. This is likely to be because of subject-level confounding in the latter model. The estimated intercept is quite close to the sum of $\widehat{\beta}_6$ and $\widehat{\beta}_7$ (the estimated coefficients for L_{ij} and P_i) from the random-coefficient model.

Alternatively, both the fixed intercept α_{1j} and the fixed slope α_{2j} can be eliminated by *double*-differencing, for instance, using $(y_{ij}-y_{i-1,j})-(y_{i-1,j}-y_{i-2,j})$, and analogous double-differencing of the covariates. Estimation can then proceed by simply using OLS for the resulting regression model. Again, serially correlated residuals are handled to some extent by this approach.

Using the `regress` command, this approach can be implemented by using the prefix "D2." (for double-differencing) for the variables included in the model:

```
regress D2.(lwage union married)
```

Wooldridge (2010, sec. 11.7.2) discusses estimation of models with fixed subject-specific slopes for several covariates, also accommodating covariates that do not necessarily change by the same amount from occasion to occasion for every subject.

5.7 Lagged-response or dynamic models

5.7.1 Conventional lagged-response model

We now consider *lagged-response* models where responses at previous occasions are treated as covariates (usually in addition to other covariates). Lagged-response models are sometimes referred to as autoregressive-response models, Markov models, or conditional autoregressive models in statistics. In econometrics, the term *dynamic models* is invariably used. Note that when there are more than two occasions, lagged-response models are different from models that include the response at the first occasion (baseline) as a covariate for subsequent responses, as is often done, for instance, in clinical trials.

The most prevalent lagged-response model is the autoregressive lag-1 (AR(1)) model, where the current response y_{ij} is regressed on the previous response $y_{i-1,j}$:

$$\begin{aligned} y_{ij} &= \beta_1 + \gamma y_{i-1,j} + \beta_2 x_{2j} + \beta_3 x_{3j} + \beta_4 x_{4ij} \\ &\quad + \beta_5 x_{5ij} + \beta_6 L_{ij} + \beta_7 P_i + \beta_8 E_j + \epsilon_{ij} \end{aligned} \tag{5.3}$$

Here γ is the coefficient associated with the lagged response. It is assumed that given $\mathbf{z}_{ij}$, ϵ_{ij} has zero mean and variance σ^2, where $\mathbf{z}_{ij} = (\mathbf{x}'_{ij}, y_{i-1,j})'$ contains all covariates for subject j at occasion i. There is no conditional cross-sectional or longitudinal correlation between the residuals given the covariates; $\mathrm{Cov}(\epsilon_{ij}, \epsilon_{i'j'}|\mathbf{z}_{ij}, \mathbf{z}_{i'j'}) = 0$. A stationary model results if the process has been ongoing long before the first occasion in the dataset and $|\gamma| < 1$. A graphical representation of an AR(1) lagged-response model is shown in figure 5.1.

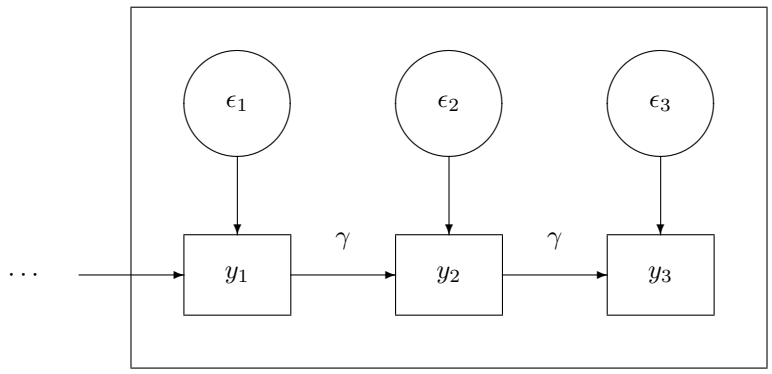


Figure 5.1: Path diagram of AR(1) lagged-response model

Lagged-response models should be used only if it really makes sense to control the effects of the other covariates for the previous response or if the effect of the lagged response is itself of scientific interest. For instance, in the context of the wage-panel data, it may make some sense to investigate the effect of previous wage on the current

wage, because having experienced a high salary in the past could place subjects in a good bargaining position.

The previous response or "lag-1 response" can be obtained in Stata using

```
. by nr (yeart), sort: generate lag1 = lwage[_n-1]
(545 missing values generated)
```

On the right-hand side of the command, we see that the lag is produced by referring to the previous observation of `lwage` using the row counter `_n` minus 1. The `by` prefix command is used with the subject identifier `nr` to cause the counter `_n` to be reset to 1 every time `nr` increases. Otherwise, the lag-1 response for the second subject in the data would be the last response of the first subject. For this command to work, we must also sort by `nr` as specified by the `sort` option. `yeart` is also given in parentheses to sort the data by `yeart` within `nr` before defining the counter so that the counter increases in tandem with `yeart`. (If `yeart` were not in parentheses, the counter would reset to 1 each time `yeart` increases.)

To see the result of this command, we list the first nine observations (all panel waves or occasions for subject 13 and the first wave for subject 17):

```
. sort nr yeart
. list nr yeart lwage lag1 in 1/9, clean noobs
    nr   yeart       lwage        lag1
    13       0     1.19754           .
    13       1     1.85306     1.19754
    13       2    1.344462     1.85306
    13       3    1.433213    1.344462
    13       4    1.568125    1.433213
    13       5    1.699891    1.568125
    13       6   -.7202626    1.699891
    13       7    1.669188   -.7202626
    17       0    1.675962           .
```

Obviously, there is no lag-1 response for the first wave of data when `yeart` is 0, and `lag1` is hence missing at the first occasion.

We can now fit the lagged-response model by OLS using the `regress` command:

```
. regress lwage lag1 black hisp union married exper yeart educt
```

Source	SS	df	MS		
Model	455.410767	8	56.9263459	Number of obs	= 3815
Residual	571.325295	3806	.150111743	F(8, 3806)	= 379.23
				Prob > F	= 0.0000
Total	1026.73606	3814	.269201904	R-squared	= 0.4436
				Adj R-squared	= 0.4424
				Root MSE	= .38744

lwage	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
lag1	.5572532	.0128673	43.31	0.000	.5320257	.5824807
black	-.0721592	.0204291	-3.53	0.000	-.1122123	-.0321062
hisp	.0092496	.0179206	0.52	0.606	-.0258854	.0443846
union	.0755261	.0149509	5.05	0.000	.0462135	.1048388
married	.0482021	.0132629	3.63	0.000	.022199	.0742051
exper	.0028574	.0047477	0.60	0.547	-.0064509	.0121657
yeart	.0175801	.0056328	3.12	0.002	.0065365	.0286237
educt	.0389675	.0046551	8.37	0.000	.0298409	.0480942
_cons	.6683362	.0253468	26.37	0.000	.6186417	.7180308

A more elegant (but perhaps less transparent) way of including the lagged response as a covariate, without explicitly constructing it as above, is to use Stata's very powerful time-series operators within the estimation command.

If the data have been `xtset`, we can refer to the lag-1 of a variable simply by using the prefix `L.` before the relevant variable name (and `L2.` for lag-2 etc.), so the results presented above could alternatively have been produced by the commands

```
xtset nr
regress lwage L.lwage black hisp union married exper yeart educt
```

The estimates for the lagged-response model are placed under "OLS" in table 5.2. We see that $\widehat{\gamma} = 0.56$ and that all the other estimated regression coefficients are now closer to zero than for the models considered in table 5.1. Such a change in estimated effects is typical in lagged-response models because the estimates now have a different interpretation, as the estimated effects of the covariates on the response *after controlling for the previous response*. Reexpressing the model as

$$y_{i,j} - \gamma y_{i-1,j} \;=\; \beta_1 + \beta_2 x_{2j} + \beta_3 x_{3j} + \beta_4 x_{4ij} + \beta_5 x_{5ij} + \beta_6 L_{ij} + \beta_7 P_i + \beta_8 E_j + \epsilon_{ij}$$

it is clear that this is similar to a change-score approach because the left-hand side becomes $y_{i,j} - y_{i-1,j}$ if $\gamma = 1$.

Table 5.2: Estimates for AR(1) lagged-response models for wage-panel data

	Exogenous lag		Endogenous lag			
	OLS		Anderson–Hsiao IV		Arellano–Bond GMM	
	Est	(SE)	Est	(SE)	Est	(SE)
Fixed part						
β_1 [_cons]	0.67	(0.03)				
β_2 [black]	-0.07	(0.02)				
β_3 [hisp]	0.01	(0.02)				
β_4 [union]	0.08	(0.01)	0.02	(0.02)	0.02	(0.03)
β_5 [married]	0.05	(0.01)	0.04	(0.03)	0.04	(0.02)
β_6 [exper]	0.00	(0.00)				
β_7 [yeart]	0.02	(0.01)				
$\beta_6 + \beta_7$			0.05	(0.01)	0.04	(0.00)
β_8 [educt]	0.04	(0.00)				
γ	0.56	(0.01)	0.12	(0.04)	0.13	(0.04)
Random part						
$\sqrt{\theta}$	0.39		0.44			

Model (5.3) makes the strong assumption that all within-subject dependence is due to the lagged response. If the true model also includes a subject-specific intercept, the estimators of the regression coefficients are likely to be inconsistent, as discussed in the next section. The lagged-response model is only sensible if the occasions are approximately equally spaced in time. Otherwise, it would be strange to assume that the lagged response has the same effect on the current response regardless of the time interval between them. Also remember that the sample size is reduced when using a lagged-response approach because lags are missing for the first occasion (here 545 observations are lost). Furthermore, the problem of missing data becomes exacerbated because not just the missing response itself is discarded but also the subsequent response because its lagged response is missing.

A natural extension of the AR(1) model considered above is the general AR(k) model that includes k lagged responses as covariates. For instance, in the AR(2) model, the current response y_{ij} is regressed on both the previous response $y_{i-1,j}$ and the response preceding the previous response, $y_{i-2,j}$. Another extension of the lagged-response model is the *antedependence model*, where the coefficient associated with a lagged response is occasion specific γ_i (accommodating unequal spacing in time). The antedependence model could have several lags, each with occasion-specific coefficients.

5.7.2 ❖ Lagged-response model with subject-specific intercepts

We now specify a model for the wage-panel data that includes both a random intercept ζ_j and a lagged response $y_{i-1,j}$ as a covariate (in addition to the original covariates):

$$\begin{aligned} y_{ij} &= (\beta_1 + \zeta_j) + \gamma y_{i-1,j} + \beta_2 x_{2j} + \beta_3 x_{3j} + \beta_4 x_{4ij} \\ &\quad + \beta_5 x_{5ij} + \beta_6 L_{ij} + \beta_7 P_i + \beta_8 E_j + \epsilon_{ij} \end{aligned} \tag{5.4}$$

where γ is still the coefficient of the lagged response. It is assumed that given $\mathbf{z}_{ij}$ and ζ_j, the ϵ_{ij} have zero mean, variance σ^2, and are uncorrelated across subjects and occasions.

A useful feature of such models is that they can be used to distinguish between two competing explanations of within-subject dependence: *unobserved heterogeneity* (represented by the random intercepts) or *state dependence* (represented by the lagged responses). For instance, the within-subject dependence of salaries over time, over and above that explained by observed covariates, may be due to some subjects being especially gifted and thus more valued or subjects with high previous salaries having a better bargaining position for future salaries.

The model assumptions discussed in section 3.3.2 imply that covariates at other occasions than i do not affect the response y_{ij} given the random intercept ζ_j (see section 3.3.3). Because this contradicts the lagged-response model where $y_{i-1,j}$ is treated as a covariate, we can instead assume that covariates other than the lagged response are "strictly exogenous given the random intercept" as before but that the lagged response is "sequentially exogenous given the random intercept":

$$E(\epsilon_{ij}|\zeta_j, \mathbf{X}_j, y_{i-1,j}, \ldots, y_{1j}) \;=\; 0$$

where $\mathbf{X}_j$ now represents all observed covariates, apart from the lagged response, for all occasions i for subject j. Together with model (5.4), this implies that

$$\begin{aligned} E(y_{ij}|\zeta_j, \mathbf{X}_j, y_{i-1,j}, \ldots, y_{1j}) &= \beta_1 + \gamma y_{i-1,j} + \beta_2 x_{2j} + \beta_3 x_{3j} + \beta_4 x_{4ij} \\ &\quad + \beta_5 x_{5ij} + \beta_6 L_{ij} + \beta_7 P_i + \beta_8 E_j + \zeta_j \\ &= E(y_{ij}|\zeta_j, \mathbf{x}_{ij}, y_{i-1,j}) \end{aligned}$$

Hence, after conditioning on the random intercept ζ_j, past values of the covariates, apart from the lagged response, do not affect the mean response at an occasion.

It would be tempting to fit the model using any of the commands for random-intercept models, such as `xtreg` and `xtmixed`, by simply including the lagged responses as covariates. However, a major problem with that approach is that it would produce inconsistent estimates of the regression coefficients because lagged responses such as $y_{i-1,j}$, which are included as covariates, are correlated with the random intercept ζ_j. This is because all responses are affected by the random intercept. When fitting the model using a standard random-intercept model that includes a lagged response, as demonstrated above, we are falsely assuming that the first or initial response (the 1980 response in the wage-panel data) is not affected by the random intercept. Inconsistent parameter estimates are produced by this *initial-conditions problem*.

A standard fixed-intercept approach does not address the initial-conditions problem and will also give inconsistent estimators. To see this, it is instructive to consider estimating the parameters of model (5.4) by using a first-differences approach (assuming that there are at least three occasions in the data). It follows from that model that the model for the response $y_{i-1,j}$ at occasion $i-1$ becomes

$$\begin{aligned} y_{i-1,j} &= (\beta_1+\zeta_j)+\gamma y_{i-2,j}+\beta_2 x_{2j}+\beta_3 x_{3j}+\beta_4 x_{4,i-1,j} \\ &\quad +\beta_5 x_{5,i-1,j}+\beta_6 L_{i-1,j}+\beta_7 P_{i-1}+\beta_8 E_j+\epsilon_{i-1,j} \end{aligned}$$

Taking the difference between the models for y_{ij} and $y_{i-1,j}$, we obtain

$$\begin{aligned} y_{ij}-y_{i-1,j} &= \gamma(y_{i-1,j}-y_{i-2,j})+\beta_4(x_{4ij}-x_{4,i-1,j})+\beta_5(x_{5ij}-x_{5,i-1,j}) \\ &\quad +\beta_6+\beta_7+\epsilon_{ij}-\epsilon_{i-1,j} \end{aligned} \tag{5.5}$$

which sweeps out the ζ_j as desired (as well as the terms corresponding to the time-constant covariates). The intercept in this model becomes the sum of the coefficients β_6 of `exper` and β_7 of `yeart`. The first term on the right-hand side is called a lagged first-difference; the first-difference of the response is $y_{ij}-y_{i-1,j}$, and taking the lag of this difference gives the lagged difference $y_{i-1,j}-y_{i-2,j}$.

Unfortunately, this attempt to address one endogeneity problem creates another endogeneity problem. Specifically, the lagged difference of the responses $y_{i-1,j}-y_{i-2,j}$, which is a covariate here, becomes correlated with the residual $\epsilon_{ij}-\epsilon_{i-1,j}$, because $y_{i-1,j}$ (which is part of the lagged difference) is obviously correlated with its own error term $\epsilon_{i-1,j}$. Hence, proceeding by fitting the model by OLS would lead to inconsistent estimates, in contrast to the case without lagged responses, (5.2).

Anderson and Hsiao (1981, 1982) pointed out that either the second lag of the response $y_{i-2,j}$ or the second lag of the *first-difference* of the responses $y_{i-2,j}-y_{i-3,j}$ can be used as an *instrumental variable* (IV) for the endogenous covariate $y_{i-1,j}-y_{i-2,j}$, because both these variables are correlated with $y_{i-1,j}-y_{i-2,j}$ but uncorrelated with the error term $\epsilon_{ij}-\epsilon_{i-1,j}$ (you may want to consult display 5.1 on page 254 for the basic ideas of instrumental-variables estimation). The instrumental-variables estimator suggested by Anderson and Hsiao is consistent for the coefficients of the time-varying covariates and the coefficient of the lagged response (and for a simple function of the level-1 residual variance, as we will see below), but it does not provide estimators for the coefficients of the time-constant covariates or the random-intercept variance. However, Hsiao (2003, sec. 4.3.3.c) demonstrates how consistent estimators can also be obtained for the level-2 residual variance ψ and the coefficients for time-constant covariates.

The estimator used by Stata's dedicated panel-data command `xtivreg, fd` for instrumental-variables estimation uses the second lag of the difference as an instrument, but because the performance of this estimator can be problematic, the use of the second lag of the response as instrument is recommended instead. For this purpose, we can use Stata's `ivregress` command, combined with Stata's powerful time-series operators for specifying the required lags of responses and differences of lagged responses (after using the `xtset` command to define the variables representing subjects and occasions).

In Stata's time-series operators, the `D.` prefix before a variable name produces a first-difference (it can also be used for a list of variables, as in `D.(union married)` above), the `LD.` prefix produces a lagged difference, and the `L2.` prefix produces a second lag (see table 5.3 for an overview).

Table 5.3: Prefix for different lags and lagged differences in Stata's time-series operators

#	Lag L#.	Lagged Difference L#D.
0	y_{ij} (lag-0)	$y_{ij} - y_{i-1,j}$ (first-difference)
1	$y_{i-1,j}$ (lag-1)	$y_{i-1,j} - y_{i-2,j}$ (lagged difference)
2	$y_{i-2,j}$ (lag-2)	$y_{i-2,j} - y_{i-3,j}$ (lag-2 difference)
3	$y_{i-3,j}$ (lag-3)	$y_{i-3,j} - y_{i-4,j}$ (lag-3 difference)

We can fit model (5.5) using the Anderson–Hsiao approach, with the second lag of the responses $y_{i-2,j}$ (`L2.lwage`) as instrumental variable for the lagged difference (`LD.lwage`) by including the expression `(LD.lwage = L2.lwage)` in the `ivregress` command:

```
. quietly xtset nr yeart
. ivregress 2sls D.lwage D.(union married) (LD.lwage = L2.lwage)
Instrumental variables (2SLS) regression              Number of obs =    3270
                                                      Wald chi2(3)  =   14.38
                                                      Prob > chi2   =  0.0024
                                                      R-squared     =       .
                                                      Root MSE      =   .4429
------------------------------------------------------------------------------
     D.lwage |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       lwage |
         LD. |   .1150229   .0382794     3.00   0.003     .0399966    .1900492
             |
       union |
         D1. |   .0246217   .0217933     1.13   0.259    -.0180925    .0673359
             |
     married |
         D1. |   .0444829   .0251453     1.77   0.077     -.004801    .0937668
             |
       _cons |   .0486734   .0082742     5.88   0.000     .0324564    .0648904
------------------------------------------------------------------------------
Instrumented:  LD.lwage
Instruments:   D.union D.married L2.lwage
```

As shown at the bottom of the output, the instrumental-variables estimator has used `L2.wage` as instrumental variable for the lagged difference of log wage `LD.lwage`. The variables `D.union` and `D.married` are used as instruments for themselves because `union` and `married` are assumed to be exogenous variables. Note that $2 \times 545 = 1090$ observations are lost when using this estimator.

The estimates were shown under "Anderson–Hsiao IV" in table 5.2. A striking feature is that the estimated coefficient of the lagged response ($\widehat{\gamma} = 0.12$) is considerably reduced compared with the corresponding estimate previously obtained for the lagged-response model without random effects ($\widehat{\gamma} = 0.56$). This confirms that the subject-specific intercept is positively correlated with the lagged response as expected. The `Root MSE` of 0.44 reported in the output represents the estimated standard deviation of the differenced level-1 errors $\epsilon_{ij} - \epsilon_{i-1,j}$. Because ϵ_{ij} and $\epsilon_{i-1,j}$ are assumed to be uncorrelated, the variance of this difference is equal to the sum of the variances of each term 2θ. It follows that the estimated variance of the level-1 error becomes $\widehat{\theta} = 0.44^2/2 = 0.19$. The reduced magnitude of the estimated γ and θ is due to the current model accommodating dependence among the responses in two different ways: by incorporating a random intercept that is shared among the responses and by conditioning on previous responses.

It has been suggested to use more lags as instruments than in the Anderson–Hsiao approach to increase efficiency. Arellano and Bond (1991), among others, apply an extension of instrumental-variables estimation called generalized method of moments (GMM) for this purpose, and this approach is implemented in Stata's `xtabond, twostep` command. Fitting model (5.5) by the Arellano–Bond approach is accomplished by using the `lags(1)` option (for a lag-1 response) and the `noconstant` option (for only using instruments for the differenced model). We also use the `vce(robust)` option because the estimated standard errors from GMM otherwise tend to be underestimated:

```
. xtabond lwage union married exper, lags(1) twostep noconstant vce(robust)
Arellano-Bond dynamic panel-data estimation  Number of obs         =      3270
Group variable: nr                           Number of groups      =       545
Time variable: yeart
                                             Obs per group:    min =         6
                                                               avg =         6
                                                               max =         6
Number of instruments =     24               Wald chi2(4)          =    352.02
                                             Prob > chi2           =    0.0000
Two-step results
                                    (Std. Err. adjusted for clustering on nr)
------------------------------------------------------------------------------
             |               WC-Robust
       lwage |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       lwage |
         L1. |   .1304084   .0373708     3.49   0.000      .057163    .2036538
             |
       union |    .015568   .0252765     0.62   0.538     -.033973    .0651089
     married |   .0448827   .0224378     2.00   0.045     .0009055    .0888599
       exper |   .0447144   .0041293    10.83   0.000     .0366212    .0528077
------------------------------------------------------------------------------
Instruments for differenced equation
        GMM-type: L(2/.).lwage
        Standard: D.union D.married D.exper
```

The estimates were shown under "Arellano–Bond GMM" in table 5.2. The coefficient for the lagged response is now estimated as $\widehat{\gamma} = 0.13$. The estimated coefficient for `exper`, 0.0447144, corresponds to the intercept in the Anderson–Hsiao approach, estimated as 0.048. This is because `exper` increases by the constant 1 between adjacent occasions. Both estimates are estimates of the sum of the effects of `exper` and `yeart`, $\beta_6 + \beta_7$. We see from the output that 24 instruments are used.[1]

The Anderson–Hsiao and the Arellano–Bond approaches both produce estimates ($\widehat{\gamma} = 0.12$ and $\widehat{\gamma} = 0.13$, respectively) that are considerably lower than the $\widehat{\gamma} = 0.56$ reported for the naïve lagged-response model without a subject-specific intercept.

Even more instruments than those used by Arellano and Bond are used in Stata's `xtdpdsys` command to increase efficiency. However, a potential problem, particularly when many instruments are used, is *weak instruments* that have low correlations with the instrumented lagged differences of the responses. In this case, GMM estimators may suffer from quite severe finite-sample bias.

1. In 1987, the six instruments $\texttt{lwage}_{1985,j}$ to $\texttt{lwage}_{1980,j}$ are used for $\texttt{lwage}_{1986,j}-\texttt{lwage}_{1985,j}$. In 1986, the five instruments $\texttt{lwage}_{1984,j}$ to $\texttt{lwage}_{1980,j}$ are used for $\texttt{lwage}_{1985,j}-\texttt{lwage}_{1984,j}$. In 1985, the four instruments $\texttt{lwage}_{1983,j}$ to $\texttt{lwage}_{1980,j}$ are used for $\texttt{lwage}_{1984,j}-\texttt{lwage}_{1983,j}$. In 1984, the three instruments $\texttt{lwage}_{1982,j}$ to $\texttt{lwage}_{1980,j}$ are used for $\texttt{lwage}_{1983,j}-\texttt{lwage}_{1982,j}$. In 1983, the two instruments $\texttt{lwage}_{1981,j}$ to $\texttt{lwage}_{1980,j}$ are used for $\texttt{lwage}_{1982,j}-\texttt{lwage}_{1981,j}$. And in 1982, the instrument $\texttt{lwage}_{1980,j}$ is used for $\texttt{lwage}_{1981,j}$. In addition, the exogenous variables `D.union`, `D.married`, and `D.exper` are used as instruments for themselves.

All the estimators discussed so far for lagged-response models have assumed that the residuals ϵ_{ij}, and hence the differenced residuals $\epsilon_{ij} - \epsilon_{i-1,j}$, are uncorrelated. If this assumption is violated, these estimators become inconsistent. We can test the assumption of no correlation between differenced residuals up to lag-2 (the default) using `xtabond`'s postestimation command `estat abond`. Stata's `xtdpd` command implements a GMM estimator that accommodates correlated residuals at the cost of more convoluted command statements.

Endogeneity also becomes an issue if the response at the first occasion (baseline) is included as a covariate at all subsequent occasions instead of lagged responses. However, if the baseline is viewed as a *proxy* for omitted covariates (as when using a pretest when studying educational achievement), the target of inference would not be the causal effect of baseline and this kind of endogeneity should be ignored.

5.8 Missing data and dropout

A ubiquitous problem in longitudinal and panel modeling is missing data. When data for a subject are missing from some time onward, the situation is called *dropout* or *attrition*. Often subjects do not exhibit monotone missingness patterns like this but rather *intermittent missingness* where, for instance, a response is given at an occasion, missing at the next occasion, but given again at a future occasion.

All the methods discussed so far use data for those subjects j and occasions i where neither the response y_{ij} nor the covariates $\mathbf{x}_{ij}$ are missing. This is in contrast to more old-fashioned approaches to longitudinal data, such as MANOVA, where subjects with any missing responses or covariates are discarded altogether, an approach often referred to as "listwise deletion" or "complete-case analysis". Using all available data does not waste information and is less susceptible to bias.

Using ML estimation, as we did for random-intercept and random-coefficient models, has the advantage that consistency (estimates approaching parameter values in large samples) is retained for correctly specified models, as long as the missing data are *missing at random* (MAR). This means that the probability of being missing may only depend on the covariates $\mathbf{x}_{ij}$ or responses at previous occasions (or future occasions, although this seems strange), but not on the responses we would have observed had they not been missing.

In practice, dependence of missingness on previous responses is only allowed if missingness is monotone, meaning that subjects drop out (never return) when missing an occasion. For intermittent missing data, if missingness at occasion 2, say, can depend on the response at occasion 1, this becomes a problem for subjects for whom the response at occasion 1 is missing (because for them missingness at occasion 2 depends on a response that is not observed). In the case of monotone missing data or dropout, this problem does not occur because the response at occasion 2 is missing with certainty if the response at occasion 1 is missing.

In a random-intercept model, an example of *not missing at random* (NMAR) is when missingness depends on the random intercept. In contrast, such missingness is MAR in a fixed-intercept model because missingness can be viewed as depending on subjects, and dummy variables for subjects are included as covariates, making missingness covariate-dependent. (This still holds if the fixed-effects estimator is implemented by mean-centering or first-differencing, because the estimates are identical.)

5.8.1 ❖ Maximum likelihood estimation under MAR: A simulation

We now use a simulation to investigate how well ML estimation works when data are MAR.

We first simulate complete data from a random-intercept model,

$$y_{ij} = 2 + \zeta_j + \epsilon_{ij}, \qquad \zeta_j \sim N(0,1),\ \epsilon_{ij} \sim N(0,1) \tag{5.6}$$

for $J = 100{,}000$ subjects and $n_j = 2$ occasions. The random intercepts ζ_j are independent across subjects, the level-1 residuals ϵ_{ij} are independent across subjects and occasions, and ζ_j and ϵ_{ij} are independent.

It is convenient to simulate the data in wide form, generating a row of data for each subject with variables `y1` and `y2` for the two occasions:

```
. clear
. set obs 100000
. set seed 123123123
. generate zeta = rnormal(0,1)
. generate y1 = 2 + zeta + rnormal(0,1)
. generate y2 = 2 + zeta + rnormal(0,1)
```

Here the `rnormal(0,1)` function draws a pseudorandom variable from a standard normal distribution (as required for ζ_j, ϵ_{1j}, and ϵ_{2j}). We have set the seed of the pseudorandom-number generator to an arbitrary number so that you can get the same results as we do, but you can also try other seeds if you like.

Among those subjects who have a value of `y1` greater than 2, we now randomly sample about 90% of subjects and replace their `y2` with a missing value:

```
. replace y2 = . if y1>2 & runiform()<0.9
(45104 real changes made, 45104 to missing)
```

where `runiform()` generates pseudorandom numbers from a uniform distribution. Here we used the fact that the probability that a (pseudo)random number with a uniform distribution (on the interval from 0 to 1) is less than 0.9 is 0.9. This selection mechanism is of course rather extreme but nicely illustrates the ideas. The responses are MAR because the probability of dropout or attrition depends only on the previous response.

The sample means at the two occasions are

```
. tabstat y1 y2
   stats |        y1        y2
---------+--------------------
    mean |  1.997182  1.532937
------------------------------
```

We see that the sample mean at the second occasion is 1.53, much lower than the population mean of 2. This is because subjects with larger than average values at occasion 1 ($y_{1j} > 2$) are likely to have larger than average values at occasion 2 as well (because of an intraclass correlation of 0.5), but about 90% of these values are missing at occasion 2.

To see if such a difference in estimated means is also found using ML estimation, we fit a slightly more general model than the true model (5.6), which allows the means at the two occasions to be different:

$$y_{ij} = \beta_1 x_{1i} + \beta_2 x_{2i} + \zeta_j + \epsilon_{ij} \tag{5.7}$$

where x_{1i} is a dummy variable for occasion $i = 1$ and x_{2i} is a dummy variable for occasion $i = 2$. According to the true model (5.6) used to generate the complete data, the population means at both occasions are $\beta_1 = \beta_2 = 2$.

We must first reshape the data and generate the dummy variables:

```
. generate id = _n
. reshape long y, i(id) j(occasion)
(note: j = 1 2)
Data                               wide   ->   long
-----------------------------------------------------------------------------
Number of obs.                   100000   ->  200000
Number of variables                   4   ->       4
j variable (2 values)                     ->   occasion
xij variables:
                                  y1 y2   ->   y
-----------------------------------------------------------------------------
. quietly tabulate occasion, generate(occ)
```

Now we can use the `xtreg` command to fit the random-intercept model (5.7) using the `noconstant` option because the model does not include an intercept:

```
. quietly xtset id
. xtreg y occ1 occ2, noconstant mle
Random-effects ML regression                    Number of obs      =    154896
Group variable: id                              Number of groups   =    100000
Random effects u_i ~ Gaussian                   Obs per group: min =         1
                                                               avg =       1.5
                                                               max =         2
                                                Wald chi2(2)       = 223725.11
Log likelihood  = -265985.81                    Prob > chi2        =    0.0000
```

y	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
occ1	1.997182	.004485	445.30	0.000	1.988392	2.005973
occ2	1.998877	.0066523	300.48	0.000	1.985839	2.011916
/sigma_u	1.003776	.0049132			.9941921	1.013452
/sigma_e	1.001969	.0033497			.9954253	1.008556
rho	.5009008	.0036862			.4936763	.508125

```
Likelihood-ratio test of sigma_u=0: chibar2(01)= 9845.55 Prob>=chibar2 = 0.000
```

All parameter estimates, including $\widehat{\beta}_2$, are almost identical to the true parameter values. The standard error for $\widehat{\beta}_2$ is larger than for $\widehat{\beta}_1$ because of the missing values at the second occasion. The reason these estimates are so good is that the random-intercept model takes the intraclass correlation into account.

In comparison, consider now using pooled OLS (see *Introduction to models for longitudinal and panel data (part III)*) to fit the analogous regression model

$$y_{ij} \;=\; \beta_1 x_{1i} + \beta_2 x_{2i} + \xi_{ij}$$

This is accomplished by using the following `regress` command, where we have used the `vce(cluster id)` option to obtain robust standard errors taking the dependence into account:

```
. regress y occ1 occ2, noconstant vce(cluster id)
Linear regression                               Number of obs =  154896
                                                F(  2, 99999) =       .
                                                Prob > F      =  0.0000
                                                R-squared     =  0.6378
                                                Root MSE      =   1.391
                                   (Std. Err. adjusted for 100000 clusters in id)
```

y	Coef.	Robust Std. Err.	t	P>|t|	[95% Conf.	Interval]
occ1	1.997182	.0044854	445.26	0.000	1.988391	2.005973
occ2	1.532937	.005718	268.09	0.000	1.52173	1.544144

In contrast to ML, the pooled OLS estimator of β_2 is based on assuming zero intraclass correlation and is just the sample mean at the second occasion with $\widehat{\beta}_2^{\text{OLS}} = 1.54$.

We see that the pooled OLS estimator can perform very badly when missingness at an occasion depends on responses at other occasions. Falsely assuming that units are uncorrelated is unproblematic for the pooled OLS estimator if missingness only depends on covariates and not on responses.

In general, it is important to get the covariance structure right (in addition to the mean structure) when there are missing data. In this case, ML produces consistent estimators if responses are MAR. See also exercise 6.6.

5.9 Summary and further reading

In this chapter, we focused on models with random or fixed subject-specific effects. The random-effects models can be extended to allow level-1 residuals to be correlated or heteroskedastic (see section 6.4). Chapter 7 is dedicated to random-effects models that include random slopes of time.

A weakness of conventional random-effects approaches is the possibility of subject-level confounding. For time-varying covariates, this problem can be eliminated by extending random-effects models to include subject means of time-varying covariates or alternatively by using fixed-effects approaches. However, neither approach gives consistent estimators of coefficients of time-constant covariates, not even for exogenous time-constant covariates. The Hausman–Taylor approach can be used to obtain consistent estimators of all model parameters if we can correctly classify the covariates as being exogenous or endogenous.

Dynamic or lagged-response models should in general be used only if dependence on previous responses is of substantive interest. Such models can generally not be fit consistently by simply including the lagged response as a covariate because the (total) residual is correlated with the lagged response whenever the correct model includes subject-specific effects (whenever there are time-constant omitted variables). We discussed methods addressing this problem.

Good, but somewhat demanding, books on the topics covered in this chapter include Cameron and Trivedi (2005, chap. 21–22), Wooldridge (2010, chap. 10–11), and Frees (2004), with the first two written from an explicit econometric perspective. Hsiao (2003) and Baltagi (2008) are technical books on the econometrics of panel data. Random-effects models are also treated in the books by the biostatisticians Fitzmaurice, Laird, and Ware (2011) and Verbeke and Molenberghs (2000).

The exercises cover almost all topics discussed in this chapter. Specifically, exercises 5.1, 5.2, 5.5, and 5.6 are about random- and fixed-intercept models, and exercises 5.4 and 5.5 involve lagged-response models. Exercise 5.3 introduces the difference-in-difference approach, not covered in this chapter, that is often used for estimating treatment effects in quasi-experiments or natural experiments. See also exercises 3.2 and 3.3 in chapter 3 for further examples with random intercepts; see also exercises 6.2 and 6.3 in chapter 6, as well as the exercises of chapter 7, for further examples with random intercepts and slopes.

5.10 Exercises

5.1 Tax-preparer data

Frees (2004) analyzed panel or repeated-measurement data on tax returns filed by 258 taxpayers for the years 1982, 1983, 1984, 1986, and 1987. (The data come from the Statistics of Income panel of individual returns.)

The dataset `taxprep.dta` has the following variables:

- `subject`: subject identifier
- `time`: identifier for the panel wave or occasion
- `lntax`: natural logarithm of tax liability in 1983 dollars
- `prep`: dummy variable for using a tax preparer for the tax return
- `ms`: dummy variable for being married
- `hh`: dummy variable for being the head of the household
- `depend`: number of dependents claimed by taxpayer
- `age`: dummy variable for being at least 65 years old
- `lntpi`: natural logarithm of the sum of all positive income line items on return in 1983 dollars
- `mr`: marginal tax rate computed on total income minus exemptions and standard deductions
- `emp`: dummy variable for schedule C or F being present on the return, a proxy for self-employment income

1. Fit a random-intercept model for `lntax` with all the subsequent variables given above as covariates and with a random intercept for subjects.
2. Obtain between and within estimates for all the covariates using `xtreg` with the `fe` and `be` options. Compare the estimates for the effect of tax preparer.
3. Perform a Hausman specification test.
4. Obtain histograms for the level-1 and level-2 residuals. Do the normality assumptions appear plausible?

5.2 Antisocial-behavior data

Allison (2005) considered a sample of 581 children who were interviewed in 1990, 1992, and 1994 as part of the U.S. National Longitudinal Survey of Youth. The children were between 8 and 10 years old in 1990.

The dataset `antisocial.dta` includes the following variables:

- `id`: child identifier (j)
- `occ`: year of interview (90, 92, 94)
- `anti`: a measure of the child's antisocial behavior (y_{ij}) (higher values mean more antisocial behavior)
- `pov`: dummy variable for child being from a poor family (x_{2ij}) (1: poor; 0: otherwise); this covariate varies both between and within children

- `momage`: mother's age at birth of child in years (x_{3j})
- `female`: dummy variable for child being female (x_{4j}) (1: female; 0: male)
- `childage`: child's age in years in 1990 (x_{5j})
- `hispanic`: dummy variable for child being Hispanic (x_{6j}) (1: Hispanic; 0: otherwise)
- `black`: dummy variable for child being black (x_{7j}) (1: black; 0: otherwise)
- `momwork`: dummy variable for mother being employed in 1990 (x_{8j}) (1: employed; 0: not employed)
- `married`: dummy variable for mother being married in 1990 (x_{9j}) (1: married; 0: otherwise)

1. Fit the random-intercept model

$$\begin{aligned} y_{ij} &= \beta_1 + \beta_2 x_{2ij} + \beta_3 x_{3j} + \beta_4 x_{4j} + \beta_5 x_{5j} + \beta_6 x_{6j} + \beta_7 x_{7j} + \beta_8 x_{8j} + \beta_9 x_{9j} \\ &\quad + \zeta_j + \epsilon_{ij} \end{aligned}$$

   (with the usual assumptions) and interpret the estimated regression coefficients that are significant at the 5% level.
2. Test the null hypothesis that the random-intercept variance is zero.
3. State the expression for the residual intraclass correlation in terms of the model parameters and give the estimate.
4. Replace x_{2ij} in the random-intercept model with the covariates

$$x_{10,j} = \frac{1}{n_j} \sum_{i=1}^{n_j} x_{2ij}$$

   where n_j is the number of units in cluster j, and

$$x_{11,ij} = x_{2ij} - x_{10,j}$$

   Fit the resulting model and interpret the estimates $\widehat{\beta}_{10}$ and $\widehat{\beta}_{11}$ corresponding to $x_{10,j}$ and $x_{11,ij}$, respectively.
5. Test the null hypothesis $\beta_{10} = \beta_{11}$ against the alternative $\beta_{10} \neq \beta_{11}$. Explain why this test can be interpreted as an endogeneity test.

See also exercise 6.1.

5.3 Unemployment-claims data I Solutions

Papke (1994) analyzed panel data on Indiana's enterprise zone program, which provided tax credits for areas with high unemployment and high poverty levels. One of the purposes was to investigate whether inclusion in an enterprise zone would reduce the number of unemployment claims. Here we consider data from 1983 and 1984 on 22 unemployment claims offices (serving a zone and the surrounding city), 6 of which were included as enterprise zones in 1984.

The dataset `papke_did.dta`, extracted from a dataset supplied by Wooldridge (2010), contains the following variables from the 1983 and 1984 waves of the panel study:

- `city`: unemployment claims office identifier (j)
- `year`: year (i)
- `luclms`: logarithm of number of unemployment claims (y_{ij})
- `ez`: dummy variable for unemployment claims office being in an enterprise zone (x_{ij})

1. Use a "posttest-only design with nonequivalent groups", which is based on comparing those receiving the intervention with those not receiving the intervention at the second occasion only.
   a. Use an appropriate t test to test the hypothesis of no intervention effect on the log-transformed number of unemployment claims in 1984.
   b. Consider the model

$$\ln(y_{2j}) \;=\; \beta_1 + \beta_2 x_{2j} + \epsilon_{2j}$$

   where the usual assumptions are made. Estimate the intervention effect and test the null hypothesis that there is no intervention effect.
2. Use a "one-group pretest–posttest design", which is based on comparing the second occasion (posttest) with the first occasion (pretest) for the intervention group only. To do this, first construct a new variable for intervention group, taking the value 1 if an unemployment claims office is ever in an enterprise zone and 0 for the control group (consider using `egen`).
   a. Use an appropriate t test to test the hypothesis of no intervention effect on the log-transformed number of unemployment claims. (It may be useful to reshape the data to wide form for the t test and then reshape them to long form again for the next questions.)
   b. For the intervention group, consider the model

$$\ln(y_{ij}) \;=\; \beta_1 + \alpha_j + \beta_2 x_{ij} + \epsilon_{ij}$$

   where α_j is an office-specific parameter (fixed effect). Estimate the intervention effect and test the null hypothesis that there is no intervention effect.
3. Discuss the pros and cons of the "posttest-only design with nonequivalent groups" and the "one-group pretest–posttest design".
4. Use an "untreated control group design with dependent pretest and posttest samples", which is based on data from both occasions and both intervention groups.
   a. Find the difference between the following two differences:
      i. the difference in the sample means of `luclms` for the intervention group between 1984 and 1983

ii. the difference in the sample means of `luclms` for the control group between 1984 and 1983

The resulting estimator is called the *difference-in-difference estimator* and is commonly used for the analysis of intervention effects in quasi-experiments and natural experiments.

b. Consider the model

$$\ln(y_{ij}) \;=\; \beta_1 + \alpha_j + \tau z_i + \beta_2 x_{ij} + \epsilon_{ij}$$

where α_j is an office-specific parameter (fixed effect) and τ is the coefficient of a dummy variable z_i for 1984. Estimate the intervention effect and test the null hypothesis that there is no intervention effect. Note that the estimate $\widehat{\beta}_2$ is identical to the difference-in-difference estimate. The advantage of using a model is that statistical inference regarding the intervention effect is straightforward, as is extension to many occasions, several intervention groups, and inclusion of extra covariates.

c. What are the advantages of using the "untreated control group design with dependent pretest and posttest samples" compared with the "posttest-only design with nonequivalent groups" and the "one-group pretest–posttest design"?

The full dataset is used in exercises 5.4 and 7.8.

5.4 Unemployment-claims data II Solutions

The full dataset used by Papke (1994) has annual panel waves from 1980 to 1988 on 22 unemployment claims offices, 6 of which were included as enterprise zones in 1984 and 4 in 1985. A subset of this dataset was used in exercise 5.3.

The dataset `ezunem.dta` supplied by Wooldridge (2010) contains the following variables:

- `city`: unemployment claims office identifier (j)
- `year`: year (i)
- `uclms`: number of unemployment claims (y_{ij})
- `ez`: dummy variable for office being in an enterprise zone (x_{2ij})
- `t`: time 1, ..., 9 (x_{3i})

1. Use the `xtset` command to specify the variables representing the clusters and units for this application. This enables you to use Stata's time-series operators, which should be used within the estimation commands in this exercise. Interpret the output.
2. Consider the fixed-intercept model

$$\ln(y_{ij}) \;=\; \tau_i + \beta_2 x_{2ij} + \alpha_j + \epsilon_{ij}$$

where τ_i and α_j are year-specific and office-specific parameters, respectively. (Use dummy variables for years to include τ_i in the model.) This gives the

difference-in-difference estimator for more than two panel waves (see exercise 5.3).

a. Fit the model using `xtreg` with the `fe` option.
b. Fit the first-difference version of the model using OLS.
   i. Do the estimates of the intervention effect differ much?
   ii. Papke (1994) actually assumed a linear trend of year instead of year-specific intercepts as specified above. Write down the first-difference version of Papke's model.
   iii. ❖ A random walk is the special case of an AR(1) process where $\alpha = 1$. Show that the first-difference approach accommodates a random walk for the residuals ϵ_{ij}.

3. Fit the lagged-response model

$$\ln(y_{ij}) \;=\; \tau_i + \beta_2 x_{2ij} + \gamma \ln(y_{i-1,j}) + \epsilon_{ij}$$

where γ is the regression coefficient for the lagged response $\ln(y_{i-1,j})$. Compare the estimated intervention effect with that for the fixed-intercept model. Interpret β_2 in the two models.

4. Consider a lagged-response model with an office-specific intercept b_j:

$$\ln(y_{ij}) \;=\; \tau_i + \beta_2 x_{2ij} + \gamma \ln(y_{i-1,j}) + b_j + \epsilon_{ij}$$

   a. Treat b_j as a random intercept, and fit a random-intercept model by ML using `xtmixed`. Are there any problems associated with this random-intercept model?
   b. Fit the model using the Anderson–Hsiao approach with the second lag of the response as an instrumental variable. Compare the estimated intervention effect with that from step 4a.
   c. Papke (1994) used the Anderson–Hsiao approach with the second lag of the first-difference of the response as an instrumental variable. Does the choice of instruments matter in this case?

Growth-curve models are applied to this dataset in exercise 7.8.

5.5 Hours-worked data

In this exercise, we use panel data on 532 men with annual panel waves from 1979 to 1988 from Ziliak (1997). The dataset can be downloaded from the website of *Journal of Business and Economic Statistics* and accompanies the book by Cameron and Trivedi (2005).

The file `hours.dta` contains the following variables:

- `id`: identification number for man (j)
- `year`: years 1979–1988 of panel wave (i)
- `lnhr`: natural logarithm of annual hours worked (y_{ij})
- `lnwg`: natural logarithm of hourly wage in U.S. dollars (x_{2ij})

- `kids`: number of children (x_{3ij})
- `ageh`: age of man (x_{4ij})
- `agesq`: age of man squared (x_{5ij})
- `disab`: dummy variable for having a disability (x_{6ij})

The model we will consider is of the form

$$y_{ij} = \beta_1 + \beta_2 x_{2ij} + \beta_3 x_{3ij} + \beta_4 x_{4ij} + \beta_5 x_{5ij} + \beta_2 x_{6ij} + c_j + \epsilon_{ij}$$

where c_j is a man-specific intercept and ϵ_{ij} is a level-1 residual with mean zero. The main interest concerns β_2, which is called the "intertemporal substitution wage elasticity of labor supply" by economists. (See display 6.2 for information on elasticities.)

1. First have a look at the data:
   a. Use `xtdescribe` to describe the longitudinal structure of the dataset. Are the data balanced?
   b. Use `xtsum` to investigate the within, between, and total variability of the response and the covariates. Are there any covariates that only have within variability, and are there any covariates that only have between variability?
2. Treating c_j as a random intercept, use FGLS to fit a random-intercept model. Store the estimates. What is the estimated residual intraclass correlation of log hours worked?
3. Now treat c_j as a fixed intercept.
   a. Fit the model by using `xtreg` with the `fe` option. Store the estimates.
   b. Estimate the regression coefficients by using OLS for the transformed model where all variables are first-differences.

   Do the estimates of the regression coefficients differ appreciably?
4. Perform a Hausman test to compare the fixed-intercept model with the random-intercept model.
   a. What is the null hypothesis of the Hausman test? What is the alternative hypothesis?
   b. What is the conclusion at the 5% significance level?
5. Use FGLS to fit a random-intercept model where the cluster means of all covariates and the deviations from these cluster means are included as covariates, making sure to obtain robust standard errors. Test the null hypothesis that the coefficients of the cluster means equal the coefficients of the deviations from the cluster means at the 5% significance level.
   a. How do you interpret this test?
   b. Is your conclusion the same as for the Hausman test?
   c. Are there any advantages of this test compared with the Hausman test?

6. Now also include the lag-1 of the response, $y_{i-1,j}$, as a covariate in the model.
   a. Fit a lagged-response model with a subject-specific intercept using the Anderson–Hsiao method and obtain robust standard errors.
   b. Does the estimate of β_2 change much compared with the estimate for the fixed-intercept model?
   c. Is the coefficient of the lagged response significant at the 5% level?

5.6 Cognitive-style data

Here we consider classic repeated-measures data described and made available by Broota (1989). The data have also been analyzed by Crowder and Hand (1990), Everitt (1995), and others. Subjects selected at random from a large group of potential subjects were identified as having either field-independent or field-dependent cognitive styles. They read two types of words (color and form names) under three cue conditions: normal, congruent, and incongruent. The order in which the six reading tasks were carried out was randomized. The response variable is the time in milliseconds taken to read the stimulus words.

The data `cogstyle.dta` are in wide form and the variables are

- `subj`: subject identifier
- `dependent`: dummy variable for being field dependent
- `rfn`: form word, normal cue
- `rfc`: form word, congruent cue
- `rfi`: form word, incongruent cue
- `rcn`: color word, normal cue
- `rcc`: color word, congruent cue
- `rci`: color word, incongruent cue

1. Reshape the data to long form so that there are six rows per subject with variables `word` and `cue` identifying the word type and cue condition, respectively. (Use `reshape` twice, first to obtain three rows of data for form and color words and then to stack the word types into a single variable. In each `reshape` command, use the `string` option to handle the fact that word type and cue condition are indicated by letters instead of numbers in the variable names.)
2. Create numeric variables `words` and `cues` for words and cues, with cues labeled 1 for normal, 2 for congruent, and 3 for incongruent. Take the logarithm of the response variable after subtracting 134 and call the new variable `lnr`.
3. Produce box plots using the command

```
graph box lnr, over(cues) over(words) asyvars by(dependent) legend(row(1))
```

4. Fit a random-intercept model with three main effects, three two-way interactions, and one three-way interaction among the three covariates `dependent`, `words`, and `cues`. Use `xtmixed` with factor variables.

5. Test whether the three-way interaction is significant at the 5% level, and fit the model without the three-way interaction.
6. Test all pairwise interactions at the 5% level, and fit the model with non-significant two-way interactions removed.
7. Also remove any main effects that are not significant for variables not involved in any two-way interactions. For this final model, obtain predicted means for all combinations of the values of the covariates included in the model using the `margins` command. Run the command `marginsplot, xdim(cues)` to produce a graph of these means with confidence intervals.

5.7 Returns-to-schooling data

In this exercise, we consider data from the Panel Study of Income Dynamics used by Cornwell and Rupert (1988). The subjects are 595 heads of household who were between 18 and 65 years old in 1976 and report a positive wage in some private, nonfarm employment in 1976–1982, the years included in the dataset. The main research question concerns the causal effect of years of schooling on wage.

The datafile `returns.dta` (based on the data supplied by Baltagi [2008]) contains the following variables:

- `nr`: person identifier
- `year`: year of survey
- `lwage`: log hourly wage in U.S. dollars
- `exp`: years of full-time work experience
- `wks`: weeks worked
- `occ`: dummy variable for having blue-collar occupation
- `ind`: dummy variable for working in manufacturing industry
- `south`: dummy variable for residing in the south of the U.S.A.
- `smsa`: dummy variable for residing in standard metropolitan statistical area
- `ms`: dummy variable for being married
- `union`: dummy variable for being a member of a union (that is, wage being set in collective bargaining agreement)
- `fem`: dummy variable for being female
- `ed`: years of schooling
- `blk`: dummy variable for being black

1. The variables from `exp` to `blk` above are used as covariates. Also generate a new covariate, `exp2`, which is equal to `exp` squared. Which of the covariates are time varying and which are time constant?
2. Fit a fixed-intercept model that includes all covariates and store the estimates. Does this analysis address the research question?

3. Fit a random-intercept model that includes all covariates using FGLS and store the estimates. Which kind of information is used to estimate the effect of years of schooling in this analysis?
4. Perform a Hausman test to investigate if the random intercepts are correlated with the covariates. Which of the models in steps 2 and 3 are preferable according to the test?
5. Following Cornwell and Rupert (1988), suppose that the covariates can be partitioned in the following way: `wks`, `south`, `smsa`, `ms`, `exp`, `exp2`, `occ`, `ind`, and `union` are exogenous covariates, and `fem`, `blk`, and `ed` are endogenous covariates. Fit a random-intercept model that allows for endogenous time-varying and endogenous time-constant covariates using the Hausman–Taylor estimator and store the estimates. Has the estimated effect of years of schooling changed appreciably compared with step 3 (you need not perform a formal test to answer this question)?
6. Perform a Hausman test to assess whether the partitioning into exogenous and endogenous covariates in step 5 appears to be appropriate. What do you conclude?
7. Fit the same model as in step 5 but now with the `amacurdy` option. Do you gain much efficiency compared with the Hausman–Taylor estimator?

5.8 Hausman test for Hausman–Taylor estimator

Consider the data in `wagepan.dta` from the U.S. National Longitudinal Survey of Youth 1979 that we introduced on page 229 and have used throughout the current chapter. Perform a Hausman test to assess whether the partitioning of covariates into time-varying exogenous covariates, time-varying exogenous covariates, time-constant exogenous covariates, and time-constant endogenous covariates used in section 5.3.2 seems reasonable.

6 Marginal models

6.1 Introduction

Instead of specifying multilevel linear models for longitudinal data—from which we can *derive* the marginal or population-averaged expectations, variances, and covariances of the responses (averaged over the random effects but conditional on the observed covariates)—we can *directly specify* a model for the marginal expectations and the marginal covariance matrix.

In both multilevel and marginal linear models, the population-averaged relationship between the response variable and the covariates is the fixed part of the model. The regression coefficients therefore have the same meaning, and the estimates tend to be similar if the fixed part of the model is the same. (As we will see in volume 2, this is not the case for most other generalized linear mixed models.)

However, in contrast to marginal models, multilevel models also provide subject-specific relationships. For instance, for a model with a random-intercept ζ_{1j} and a random slope ζ_{2j} of x_{2ij}, the subject-specific relationships are $E(y_{ij}|\mathbf{x}_{ij}, \zeta_{1j}, \zeta_{2j}) = E(y_{ij}|\mathbf{x}_{ij}) + \zeta_{1j} + \zeta_{2j}x_{2ij}$. In the *multilevel approach*, the focus is on modeling such subject-specific relationships and how they vary around the population average, as summarized by the covariance matrix of the random effects. Although it is possible to derive a marginal covariance matrix, that is, the covariance matrix of the total residuals $\xi_{ij} = \zeta_{1j} + \zeta_{2j}x_{2ij} + \epsilon_{ij}$, that matrix is generally not of interest in multilevel modeling. In contrast, in the *marginal approach*, we are only interested in the marginal residual covariance matrix and the marginal relationship $E(y_{ij}|\mathbf{x}_{ij})$ between the response variable and the covariates.

6.2 Mean structure

The *mean structure* is the fixed part of the model because this part represents the mean of the response variable given the covariates, as a function of the regression coefficients.

In this chapter, we will consider marginal models for the wage-panel data described in *Introduction to models for longitudinal and panel data (part III)*. The marginal model can be written as

$$y_{ij} = \beta_1 + \beta_2 x_{2j} + \beta_3 x_{3j} + \beta_4 x_{4ij} + \beta_5 x_{5ij} + \beta_6 L_{ij} + \beta_7 P_i + \beta_8 E_j + \xi_{ij}$$

where the (total) residuals ξ_{ij} have zero means given the covariates.

The mean structure of the marginal model for each of the $n_j = 8$ occasions i for subject j is then

$$E(y_{ij}|\mathbf{x}_{ij}) = \beta_1 + \beta_2 x_{2j} + \beta_3 x_{3j} + \beta_4 x_{4ij} + \beta_5 x_{5ij} + \beta_6 L_{ij} + \beta_7 P_i + \beta_8 E_j$$

We will keep this mean structure for the wage-panel data throughout the chapter.

6.3 Covariance structures

In this section, we will make different assumptions regarding the covariance matrix of the $n_j = 8$ residuals for a subject j in the wage-panel data. To write these structures in a compact form using matrices, we think of the responses and total residuals for subject j as being assembled in column vectors:

$$\mathbf{y}_j = \begin{bmatrix} y_{1j} \\ y_{2j} \\ \vdots \\ y_{8j} \end{bmatrix} \qquad \boldsymbol{\xi}_j = \begin{bmatrix} \xi_{1j} \\ \xi_{2j} \\ \vdots \\ \xi_{8j} \end{bmatrix}$$

The covariate matrix $\mathbf{X}_j$ has the covariates $(x_{2j}, x_{3j}, x_{4ij}, x_{5ij}, L_{ij}, P_i, E_j)$ for subject j at occasion i placed in row i.

Different structures will be specified for the residual covariance matrix $\mathbf{V}_j$ (conditional on the covariates):

$$\mathbf{V}_j \equiv \begin{bmatrix} \mathrm{Var}(\xi_{1j}|\mathbf{X}_j) & & & & \\ \mathrm{Cov}(\xi_{2j},\xi_{1j}|\mathbf{X}_j) & \mathrm{Var}(\xi_{2j}|\mathbf{X}_j) & & & \\ \mathrm{Cov}(\xi_{3j},\xi_{1j}|\mathbf{X}_j) & \mathrm{Cov}(\xi_{3j},\xi_{2j}|\mathbf{X}_j) & \mathrm{Var}(\xi_{3j}|\mathbf{X}_j) & & \\ \vdots & \vdots & \vdots & \ddots & \\ \mathrm{Cov}(\xi_{8j},\xi_{1j}|\mathbf{X}_j) & \mathrm{Cov}(\xi_{8j},\xi_{2j}|\mathbf{X}_j) & \mathrm{Cov}(\xi_{8j},\xi_{3j}|\mathbf{X}_j) & \cdots & \mathrm{Var}(\xi_{8j}|\mathbf{X}_j) \end{bmatrix}$$

Sometimes we use the expression "within-subject" residual covariance matrix to emphasize that it is the covariance matrix for residuals of the same subject and not across subjects. The covariances are longitudinal, not cross-sectional. This matrix is also the covariance matrix of the responses given the covariates:

$$\mathrm{Cov}(\mathbf{y}_j|\mathbf{X}_j) \;=\; \mathrm{Cov}(\boldsymbol{\xi}_j|\mathbf{X}_j) \;=\; \mathbf{V}_j$$

Viewed as a function of model parameters (and sometimes of covariates), this is the *covariance structure* of the marginal model.

We will generally not present estimated residual covariance matrices directly, but rather will show the standard deviations (the square roots of the diagonal elements of the covariance matrix) and the correlation matrix (each covariance divided by the product of the relevant standard deviations). We have already seen an example of this on page 243.

Possible assumptions about the residual within-subject covariance matrix would be that all variances are equal and all covariances are equal. In clustered data, such a structure is the only appropriate choice if units within clusters are exchangeable. For instance, for students nested in schools, in the absence of student-level covariates, the students are exchangeable and there is no reason to believe that the responses for one pair of students are more or less correlated than those for another pair of students within the same school. The exchangeability assumption would generally be inappropriate for longitudinal data because the occasions are ordered in time.

The ordering and also the timing and spacing of occasions is relevant when considering the covariance structure. Usually, we would expect pairs of responses to be more correlated if the time interval between them is small than if the interval is large. When describing covariance structures, we will therefore refer to the time t_{ij} associated with occasion i for subject j, where t_{ij} is the (time-varying) time scale of interest, such as age, period, or time since some event of interest.

The residual covariance matrix is typically assumed to be the same for all subjects; $\mathbf{V}_j = \mathbf{V}$. Generally, such models are appropriate only if the data are quite balanced, in the sense that occasion i means approximately the same thing across subjects, which we denote as $t_{ij} = t_i$. An example of imbalance would be if the timing of occasions varies considerably between subjects so that it does not make sense to assume that all subjects have the same covariance between a given pair of occasions (such as occasions 1 and 2). For some subjects, the occasions may be distant in time and for others they may be close. Some covariance structures require *constant spacing* of occasions for each pair of occasions across subjects, which is denoted as $t_{ij} - t_{i-1,j} = \Delta$. In this case, the timing of the first occasion t_{1j} can differ between subjects. Other models allow the residual covariance matrix to differ between subjects. In these models (for example, random-coefficient models), the variances and covariances are typically functions of the subject-specific timing of occasions or other covariates.

Some popular covariance structures for marginal modeling are shown in table 6.1. In addition to showing the different structures, the table shows the corresponding number of parameters as a function of the number of occasions n, whether balance is required ($t_{ij} = t_i$) and whether equal spacing is required ($t_{ij} - t_{i-1,j} = \Delta$) for the structure to make sense.

Table 6.1: Common marginal covariance structures for longitudinal data ($n = 3$). The number of parameters and requirements for timing of occasions are also given. (In Stata, missing data are allowed for all structures.) Whenever the variance is constant, it is denoted σ^2 and factored out.

Unstructured $\{n(n+1)/2$ parameters$\}$ $(t_{ij} = t_i)$

$$\begin{bmatrix} V_{11} & & \\ V_{21} & V_{22} & \\ V_{31} & V_{32} & V_{33} \end{bmatrix}$$

Random-intercept ($\psi_{11} \geq 0$) or
Compound symmetric or Exchangeable (2 parameters) (any t_{ij})

$$\begin{bmatrix} \psi_{11}+\theta & & \\ \psi_{11} & \psi_{11}+\theta & \\ \psi_{11} & \psi_{11} & \psi_{11}+\theta \end{bmatrix} \quad \text{or} \quad \sigma^2 \begin{bmatrix} 1 & & \\ \rho & 1 & \\ \rho & \rho & 1 \end{bmatrix}$$

Random-coefficient (intercept and slope, t=0,1,2) (4 parameters) (any t_{ij})

$$\begin{bmatrix} \psi_{11}+\theta & & \\ \psi_{11}+\psi_{21} & \psi_{11}+2\psi_{21}+\psi_{22}+\theta & \\ \psi_{11}+2\psi_{21} & \psi_{11}+3\psi_{21}+2\psi_{22} & \psi_{11}+4\psi_{21}+4\psi_{22}+\theta \end{bmatrix}$$

Autoregressive residual AR(1) (2 parameters) $(t_{ij} - t_{i-1,j} = \Delta)$

$$\sigma^2 \begin{bmatrix} 1 & & \\ \alpha & 1 & \\ \alpha^2 & \alpha & 1 \end{bmatrix}$$

Exponential(1) (2 parameters) (any t_{ij})

$$\sigma^2 \begin{bmatrix} 1 & & \\ \exp(-\phi|t_{2j}-t_{1j}|) & 1 & \\ \exp(-\phi|t_{3j}-t_{1j}|) & \exp(-\phi|t_{3j}-t_{2j}|) & 1 \end{bmatrix}$$

Moving average MA(1) (2 parameters) $(t_{ij} - t_{i-1,j} = \Delta)$

$$\sigma^2 \begin{bmatrix} 1 & & \\ \phi/(1+\phi^2) & 1 & \\ 0 & \phi/(1+\phi^2) & 1 \end{bmatrix}$$

Banded(1) $(2n-1$ parameters$)$ $(t_{ij} = t_i)$

$$\begin{bmatrix} V_{11} & & \\ V_{21} & V_{22} & \\ 0 & V_{32} & V_{33} \end{bmatrix}$$

Table 6.1: Common marginal covariance structures for longitudinal data ($n = 3$). The number of parameters and requirements for timing of occasions are also given. (In Stata, missing data are allowed for all structures.) Whenever the variance is constant, it is denoted σ^2 and factored out. (cont.)

Toeplitz(1) (2 parameters) $(t_{ij} - t_{i-1,j} = \Delta)$

$$\sigma^2 \begin{bmatrix} 1 & & \\ \rho_1 & 1 & \\ 0 & \rho_1 & 1 \end{bmatrix}$$

Independence (n parameters) $(t_{ij} = t_i)$

$$\begin{bmatrix} V_{11} & & \\ 0 & V_{22} & \\ 0 & 0 & V_{33} \end{bmatrix}$$

We will describe each of these structures in detail in the following subsections. When reading these subsections, it may be useful to refer to figure 6.1, which shows how the models are related to each other assuming balance and constant spacing. An arrow pointing from model A to model B means that model B is nested in (a special case of) model A. Therefore, any model that can be reached by following arrows from model A is nested in model A. For example, the identity structure (zero correlations and equal variances) is nested in the exchangeable structure, which is nested in the unstructured model. In fact, all models are nested in the unstructured model, and the identity structure is nested in all models.

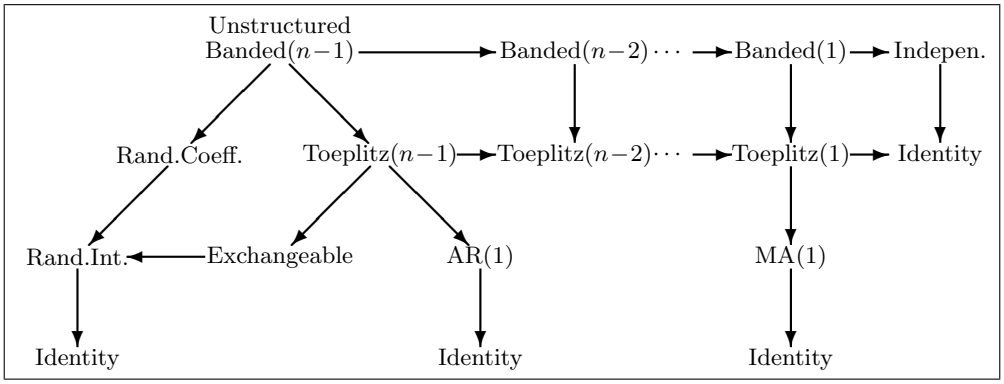


Figure 6.1: Relationships between covariance structures assuming balance and constant spacing; arrows point from a more general model to a model nested within it

In this chapter, we assume that $E(\xi_{ij}|\mathbf{X}_j) = 0$. This kind of exogeneity assumption is invariably (usually implicitly) made in the literature on marginal modeling, possibly because of the popularity of this approach in clinical trials where treatments are exogenous per design since subjects are randomized to treatments. Alternatively, the coefficients are not interpreted causally, but the mean structure is viewed merely as a linear projection (see section 1.13).

When the model is fit by maximum likelihood (ML), as we will do throughout most of this chapter, the likelihood is based on assuming multivariate normality of the total residuals. When this assumption is violated, point estimates of regression coefficients remain consistent (if the mean structure is correctly specified) as do model-based standard errors (if the covariance structure is also correctly specified). The residual covariance matrix is also consistently estimated if its structure, and the mean structure, are correctly specified. It is not widely known that as long as the distribution of the residuals is symmetric (for example, normal), ML and feasible generalized least squares (FGLS) estimators of regression coefficients are not only consistent but also small-sample unbiased, even if the covariance structure is incorrectly specified.

Model-based standard errors are valid only if the covariance structure is correctly specified. Furthermore, even for the point estimates of the regression coefficients, consistency relies on correct specification of the covariance structure if responses are missing, and missingness depends on observed responses at other occasions (see section 5.8 and exercise 6.6). Therefore, it is important to specify a good (close to correct) covariance structure if there are missing data. A good choice of covariance structure also improves efficiency (precision of estimation) for regression coefficients. Finally, understanding the nature of the longitudinal dependence may be of interest in its own right.

6.3.1 Unstructured covariance matrix

The most obvious approach is not to impose any structure on the residual covariance matrix and to estimate the variance at each occasion and the covariances between each pair of occasions freely. This is the most general example of a covariance structure that is constant across subjects. If there are n occasions, such an *unstructured* covariance matrix has $n(n+1)/2$ parameters—namely, n variances and $n(n-1)/2$ unique covariances [keeping in mind that $\text{Cov}(\xi_{ij}, \xi_{i'j}) = \text{Cov}(\xi_{i'j}, \xi_{ij})$, that is, covariance matrices are symmetric].

An unstructured covariance matrix should be used only if $t_{ij} = t_i$ (or in practice if the equality holds approximately and the time variable is rounded to obtain the same integer values across subjects), but gaps due to missing data are permitted. However, there must be sufficient numbers of subjects who have nonmissing responses at each occasion to make it feasible to estimate a separate variance parameter for each occasion and separate covariance parameters for each pair of occasions.

We will fit the model to the wage-panel data described in *Introduction to models for longitudinal and panel data (part III)*. We first read in the data and generate the necessary variables:

```
. use http://www.stata-press.com/data/mlmus3/wagepan
. generate educt = educ - 12
. generate yeart = year - 1980
```

Previously, we have used Stata's `xtmixed` command for multilevel modeling and now use `xtmixed` for marginal modeling. As for multilevel models, the double pipe, `||`, is used to separate the fixed and random parts of the model. The cluster identifier is given, followed by a colon, to specify the clusters (here subjects) within which the residuals should be correlated. By default, `xtmixed` includes a random intercept, so we use the `noconstant` option in the random part to omit the random intercept. What would ordinarily be the level-1 residual ϵ_{ij} then becomes the total residual ξ_{ij}. The `residuals()` option allows covariance structures to be specified for ϵ_{ij} and hence for ξ_{ij}. In contrast, covariance structures for random effects (such as ζ_{1j} and ζ_{2j}) are specified by using the `covariance()` option.

We now use `xtmixed` with the `noconstant` and `mle` options for ML estimation of marginal models. The `residuals(unstructured, t())` option is used to specify an unstructured covariance matrix where `t()` is used to specify the time variable t_i, which should be integer-valued here. For brevity, we display the random part of the model only and omit cluster information by using the `nofetable` and `nogroup` options (the model takes a long time to estimate).

```
. xtmixed lwage black hisp union married exper yeart educt || nr:,
> noconstant residuals(unstructured, t(yeart)) nofetable nogroup mle
Mixed-effects ML regression                     Number of obs      =      4360
                                                Wald chi2(7)       =    569.40
Log likelihood = -1977.7961                     Prob > chi2        =    0.0000
```

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
nr: (empty)				
Residual: Unstructured				
sd(e0)	.5310578	.0163	.5000524	.5639856
sd(e1)	.5032696	.0153426	.4740793	.5342571
sd(e2)	.4615847	.0140538	.4348456	.489968
sd(e3)	.4481479	.0136054	.4222597	.4756232
sd(e4)	.4990527	.0151449	.4702349	.5296367
sd(e5)	.4878995	.0148655	.4596165	.5179228
sd(e6)	.4859753	.0147864	.4578417	.5158377
sd(e7)	.4332586	.013296	.4079671	.4601181
corr(e0,e1)	.3930551	.036518	.3192001	.4621645
corr(e0,e2)	.3699349	.0372008	.2948549	.4404751
corr(e0,e3)	.3413282	.0381116	.2645994	.4137627
corr(e0,e4)	.2489353	.0403531	.168344	.3262208
corr(e0,e5)	.2813188	.0396332	.2019437	.3570224
corr(e0,e6)	.2216649	.04092	.1401321	.3002119
corr(e0,e7)	.2272449	.0407984	.1459159	.3055229
corr(e1,e2)	.5634612	.0293651	.5031855	.618281
corr(e1,e3)	.5320892	.0308314	.4689796	.5897928
corr(e1,e4)	.4559925	.0340303	.3868009	.5200785
corr(e1,e5)	.4125282	.0355852	.340453	.4797838
corr(e1,e6)	.3359342	.0381591	.259151	.4084978
corr(e1,e7)	.4156282	.0355712	.3435559	.4828333
corr(e2,e3)	.6392672	.0254606	.5866517	.6865085
corr(e2,e4)	.5816768	.0283895	.523317	.6346054
corr(e2,e5)	.5309919	.030854	.4678444	.5887455
corr(e2,e6)	.466369	.0335636	.3980685	.5295275
corr(e2,e7)	.4295472	.0350594	.3584261	.495711
corr(e3,e4)	.6351057	.025611	.5822074	.6826498
corr(e3,e5)	.5756103	.0286975	.5166483	.6291385
corr(e3,e6)	.4851861	.0329002	.4181174	.5469937
corr(e3,e7)	.5045518	.0320256	.439159	.5646266
corr(e4,e5)	.6217451	.0263582	.5673651	.6707257
corr(e4,e6)	.512188	.0317281	.4473563	.5716651
corr(e4,e7)	.5413647	.0303945	.4790993	.5982091
corr(e5,e6)	.5838479	.0283346	.5255848	.6366597
corr(e5,e7)	.629591	.0259946	.5759177	.6778598
corr(e6,e7)	.6453735	.0251813	.5933006	.6920676

```
LR test vs. linear regression:      chi2(35) =  2020.88   Prob > chi2 = 0.0000

Note: The reported degrees of freedom assumes the null hypothesis is not on
      the boundary of the parameter space.  If this is not true, then the
      reported test is conservative.

. estimates store un
```

The `variance` option could have been used to display estimated variances and covariances instead of standard deviations and correlations. We can use the program `xtmixed_corr` by Bobby Gutierrez (2011)[1] to display the model-implied standard deviations and correlation matrix for one of the subjects (here the same for all subjects). The program can be downloaded using

```
ssc install xtmixed_corr, replace
```

and run using

```
. xtmixed_corr
Standard deviations and correlations for nr = 13:
Standard Deviations:
```

yeart	0	1	2	3	4	5	6	7
sd	0.531	0.503	0.462	0.448	0.499	0.488	0.486	0.433

```
Correlations:
```

yeart	0	1	2	3	4	5	6	7
0	1.000							
1	0.393	1.000						
2	0.370	0.563	1.000					
3	0.341	0.532	0.639	1.000				
4	0.249	0.456	0.582	0.635	1.000			
5	0.281	0.413	0.531	0.576	0.622	1.000		
6	0.222	0.336	0.466	0.485	0.512	0.584	1.000	
7	0.227	0.416	0.430	0.505	0.541	0.630	0.645	1.000

Because the number and timing of occasions can vary between subjects in some datasets, `xtmixed_corr` displays the results for the first subject in the data (here subject 13) by default. The `at()` option can be used to specify a different subject (see also section 6.4.3).

The estimated residual standard deviations and correlation matrix are also shown in the top left panel of figure 6.2.

1. We thank Bobby for writing this program as a result of seeing an earlier draft of our chapter where we presented Mata code to produce this output.

Unstructured

```
|| nr:, noconstant
   residuals(unstructured, t(yeart))
```

.53	.50	.46	.45	.50	.49	.49	.43

1							
.39	1						
.37	.56	1					
.34	.53	.64	1				
.25	.46	.58	.64	1			
.28	.41	.53	.58	.62	1		
.22	.34	.47	.49	.51	.58	1	
.23	.42	.43	.50	.54	.63	.65	1

Random-intercept

```
|| nr:
```

.48	.48	.48	.48	.48	.48	.48	.48

1							
.46	1						
.46	.46	1					
.46	.46	.46	1				
.46	.46	.46	.46	1			
.46	.46	.46	.46	.46	1		
.46	.46	.46	.46	.46	.46	1	
.46	.46	.46	.46	.46	.46	.46	1

Random-coefficient

```
|| nr:  yeart, cov(unstructured)
```

.49	.48	.47	.46	.47	.48	.49	.51

1							
.55	1						
.52	.52	1					
.48	.49	.50	1				
.43	.46	.48	.50	1			
.38	.42	.46	.49	.52	1		
.33	.38	.43	.47	.51	.54	1	
.28	.34	.40	.45	.50	.54	.58	1

AR(1)

```
|| nr:, noconstant
   residuals(ar 1, t(yeart))
```

.48	.48	.48	.48	.48	.48	.48	.48

1							
.58	1						
.33	.58	1					
.19	.33	.58	1				
.11	.19	.33	.58	1			
.06	.11	.19	.33	.58	1		
.04	.06	.11	.19	.33	.58	1	
.02	.04	.06	.11	.19	.33	.58	1

MA(1)

```
|| nr:, noconstant
   residuals(ma 1, t(yeart))
```

.46	.46	.46	.46	.46	.46	.46	.46

1							
.36	1						
0	.36	1					
0	0	.36	1				
0	0	0	.36	1			
0	0	0	0	.36	1		
0	0	0	0	0	.36	1	
0	0	0	0	0	0	.36	1

Banded(1)

```
|| nr:, noconstant
   residuals(banded 1, t(yeart))
```

.53	.49	.43	.42	.47	.48	.47	.43

1							
.31	1						
0	.31	1					
0	0	.44	1				
0	0	0	.26	1			
0	0	0	0	.50	1		
0	0	0	0	0	.13	1	
0	0	0	0	0	0	.59	1

Figure 6.2: Estimated residual standard deviations and correlation matrices from `xtmixed`

Toeplitz(2)

```
|| nr:, noconstant
   residuals(toeplitz 2, t(yeart))
```

.46	.46	.46	.46	.46	.46	.46	.46

1							
.44	1						
.26	.44	1					
0	.26	.44	1				
0	0	.26	.44	1			
0	0	0	.26	.44	1		
0	0	0	0	.26	.44	1	
0	0	0	0	0	.26	.44	1

Random-intercept & AR(1)

```
|| nr:
   residuals(ar 1, t(yeart))
```

.48	.48	.48	.48	.48	.48	.48	.48

1							
.57	1						
.45	.57	1					
.41	.45	.57	1				
.40	.41	.45	.57	1			
.40	.40	.41	.45	.57	1		
.40	.40	.40	.41	.45	.57	1	
.40	.40	.40	.40	.41	.45	.57	1

Figure 6.2: Estimated residual standard deviations and correlation matrices from `xtmixed` (cont.)

Models with an unstructured covariance matrix can also be used when there are several different response variables, such as weight and height, instead of longitudinal data. In this case, it seems necessary to allow for different residual variances and covariances for different (pairs) of variables because the variables are measured in different units. In addition, the effects of covariates would typically be allowed to differ between the response variables (see exercise 6.5 for an example). In such situations, the models are referred to as multivariate regression models or seemingly unrelated regressions.

Specifying an unstructured covariance matrix may appear to be ideal because it seems to make no assumptions about the covariance structure. However, the covariance structure is not completely unrestricted because it is assumed to be constant across subjects. Also, unless there are relatively few occasions, the number of parameters becomes large (for example, 36 (co)variance parameters for the wage-panel data for $n = 8$ and 120 parameters for $n = 15$), which may lead to unreliable estimation. Therefore, structured covariance matrices are often used that depend on a smaller number of parameters.

The regression parameters will be more precisely estimated if a structured covariance matrix is specified, assuming that the structure is correct. Another reason for specifying structured covariance matrices is that unstructured covariance matrices cannot be used if different timings are associated with occasions for different subjects. For these two reasons, a large variety of covariance structures have been proposed.

6.3.2 Random-intercept or compound symmetric/exchangeable structure

In a random-intercept model, the total residual ξ_{ij} is partitioned as

$$\xi_{ij} \;=\; \zeta_{1j} + \epsilon_{ij}$$

where ζ_{1j} and ϵ_{ij} have zero means, variances ψ_{11} and θ, and are uncorrelated with each other. The ζ_{1j} are uncorrelated across subjects, and the ϵ_{ij} are uncorrelated across both subjects and occasions.

In section 3.3.1, we discussed the marginal residual covariance matrix implied by this model; see table 6.2. The marginal variances are $\psi_{11} + \theta$ at all occasions, and the covariances are ψ_{11} for all pairs of occasions. The corresponding correlation is often referred to as an intraclass correlation. This structure does not require balance or constant spacing of occasions.

Table 6.2: Conditional variances and covariances of total residuals for random-intercept model

Conditional or subject-specific			Marginal or population-averaged		
$\mathrm{Var}(\xi_{ij}\vert\zeta_{1j})$	$=$	θ	$\mathrm{Var}(\xi_{ij})$	$=$	$\psi_{11}+\theta$
$\mathrm{Cov}(\xi_{ij},\xi_{i'j}\vert\zeta_{1j})$	$=$	0	$\mathrm{Cov}(\xi_{ij},\xi_{i'j})$	$=$	ψ_{11}

When a random-intercept structure is used in the marginal modeling approach, it could be argued that ψ_{11} and θ need not both be positive as long as their sum $\psi_{11} + \theta$ is nonnegative. Only this sum is interpreted as a variance, and ψ_{11} is interpreted as a covariance, so ψ_{11} could be negative. This more general covariance structure, with possibly negative covariances, is called the *compound symmetric* or *exchangeable* structure. All variances are equal and all covariances (and thus correlations) are also equal.

The random-intercept model fit to the wage-panel data using `xtmixed` in section 5.2 can be viewed as a marginal model with a random-intercept structure. The residual intraclass correlation was estimated as 0.46, and the total standard deviation was estimated as $\sqrt{0.327^2 + 0.354^2} = 0.48$. The model therefore implies that all pairwise correlations are equal to 0.46 and all standard deviations are equal to 0.48 (as shown in the top-right panel of figure 6.2).

A model with the compound symmetric or exchangeable covariance structure can be fit in `xtmixed` with the `residuals(exchangeable)` option:

```
. quietly xtmixed lwage black hisp union married exper yeart educt || nr:,
> noconstant residuals(exchangeable) mle
```

where the `noconstant` option after the double pipe ensures that no random intercept is included. No `t()` option is needed here because the covariance structure does not depend on the order or timing of occasions. Because the estimated covariance is positive, all estimates are identical to those reported for the random-intercept model (see section 5.2 and see table 5.1 on page 260), and we therefore used the `quietly` prefix command to omit the output. We store the estimates as `ri` for later use:

```
. estimates store ri
```

6.3.3 Random-coefficient structure

Consider now a random-coefficient model with a random slope for a time-varying covariate, such as the time t_{ij} associated with occasion i for subject j. In this case, the total residual becomes

$$\xi_{ij} \;=\; \zeta_{1j} + \zeta_{2j} t_{ij} + \epsilon_{ij}$$

where the random effects ζ_{1j} and ζ_{2j} and the level-1 error ϵ_{ij} have zero means and variances ψ_{11}, ψ_{22}, and θ, respectively. The random effects ζ_{1j} and ζ_{2j} have covariance ψ_{21} within subjects and are uncorrelated across subjects. The level-1 errors are uncorrelated with the random effects and uncorrelated across subjects and occasions.

An overview of the relationship between conditional and marginal (with respect to ζ_{1j} and ζ_{2j}) variances and covariances of y_{ij} for this model is given in table 6.3. As discussed in section 4.4.2, the variances and covariances (as well as correlations) now depend on the variable having a random coefficient, here t_{ij}. Balance and equal spacing are not required. We see that the marginal covariance matrix differs between subjects if there is no balance, $t_{ij} \neq t_i$. (The random-coefficient structure is also shown in matrix form in display 6.1.)

Table 6.3: Conditional and marginal variances and covariances of total residuals for random-coefficient model

Conditional or subject-specific	Marginal or population-averaged
$\mathrm{Var}(\xi_{ij}\vert t_{ij},\zeta_{1j},\zeta_{2j}) = \theta$	$\mathrm{Var}(\xi_{ij}\vert t_{ij}) = \psi_{11} + 2\psi_{21}t_{ij} + \psi_{22}t_{ij}^2 + \theta$
$\mathrm{Cov}(\xi_{ij},\xi_{i'j}\vert t_{ij},t_{i'j},\zeta_{1j},\zeta_{2j}) = 0$	$\mathrm{Cov}(\xi_{ij},\xi_{i'j}\vert t_{ij},t_{i'j}) = \psi_{11} + \psi_{21}(t_{ij}+t_{i'j}) + \psi_{22}t_{ij}t_{i'j}$

We first write a general two-level linear mixed model for the n_j-dimensional vector of responses $\mathbf{y}_j$ for subject j as

$$\mathbf{y}_j \;=\; \mathbf{X}_j\boldsymbol{\beta} + \mathbf{Z}_j\boldsymbol{\zeta}_j + \boldsymbol{\epsilon}_j$$

where $\mathbf{X}_j$ is the $n_j \times p$ covariate matrix for the fixed part and $\mathbf{Z}_j$ is the $n_j \times q$ covariate matrix for the random part, consisting of rows $(1, z_{1ij}, \ldots, z_{q-1,ij})$, where z_{1ij}, etc., are covariates that have random slopes. Analogous to the p-dimensional fixed coefficient vector $\boldsymbol{\beta}$, there is a q-dimensional random coefficient vector $\boldsymbol{\zeta}_j = (\zeta_{1j}, \ldots, \zeta_{qj})'$, and $\boldsymbol{\epsilon}_j$ is an n_j-dimensional vector of level-1 residuals. Under the usual assumption that $\boldsymbol{\zeta}_j$ is uncorrelated with $\boldsymbol{\epsilon}_j$, we obtain

$$\mathrm{Cov}(\mathbf{y}_j\vert\mathbf{X}_j,\mathbf{Z}_j) \;=\; \mathbf{Z}_j\boldsymbol{\Psi}\mathbf{Z}_j' + \mathbf{R}_j$$

where $\boldsymbol{\Psi} = \mathrm{Cov}(\boldsymbol{\zeta}_j)$ and $\mathbf{R}_j = \mathrm{Cov}(\boldsymbol{\epsilon}_j)$, usually specified as $\mathbf{R}_j = \theta\mathbf{I}_{n_j}$ where $\mathbf{I}_{n_j}$ is the $n_j \times n_j$ identity matrix.

Display 6.1: Covariance structure induced by random-coefficient model

To get a better idea of the correlation pattern induced by random-coefficient models, consider examples of balanced longitudinal data. Figure 6.3 gives two examples with five time points and $t_{ij} = t_i$ given by 0, 1, 2, 3, and 4. The two examples differ from each other only in terms of the correlation between intercept and slope, equal to 0.2 on the left and -0.8 on the right.

As can be seen from the randomly drawn subject-specific regression lines for 10 subjects, the variances increase as a function of time on the left, whereas they change much less, first decreasing and then increasing, on the right. On the left, the correlations between adjacent time points (or lag-1 correlations) are 0.63 between occasions 1 and 2, 0.76 between occasions 2 and 3, then 0.84, and finally 0.90. Similarly, the lag-2 and lag-3 correlations increase over time. We see that the correlation between occasions 1 and 2 is greater than that between occasions 1 and 3. In general, at a given occasion, the correlations with other occasions decrease as the time lag increases. The correlation matrix on the right is very different, illustrating that the random-coefficient model can produce a wide range of different correlation patterns.

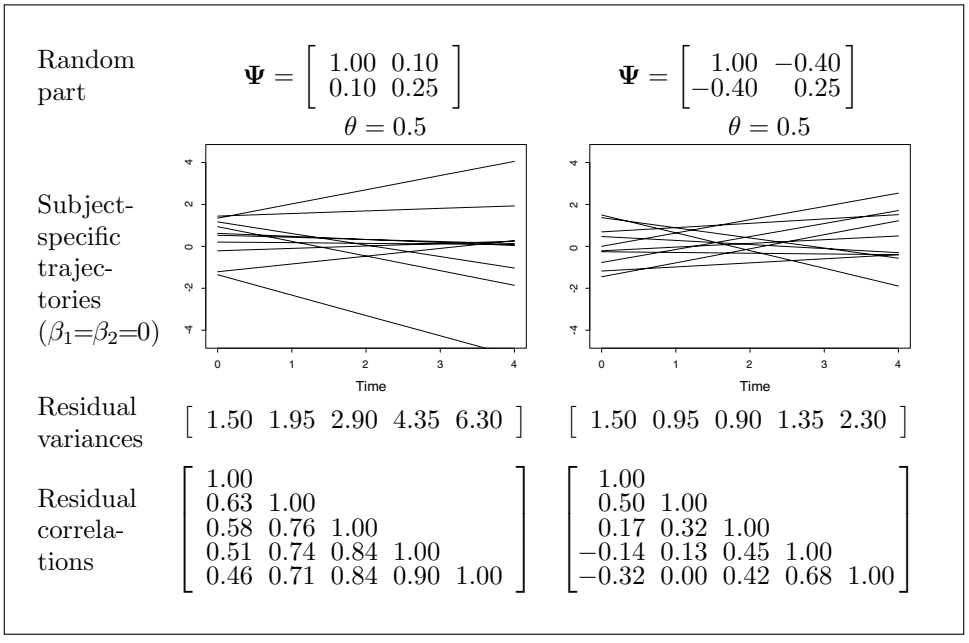


Figure 6.3: Illustration of marginal variances and correlations induced by random-coefficient models ($t = 0, 1, 2, 3, 4$)

When the random-coefficient structure is used in a marginal modeling approach, it can be argued that it is acceptable to relax the usual restriction that the covariance matrix of the random effects is positive semidefinite (for example, with nonnegative variances $0 \leq \psi_{11}$ and $0 \leq \psi_{22}$ and valid correlation $-1 \leq \rho_{21} \leq 1$) and that the

level-1 residual variance is nonnegative as long as the marginal covariance matrix is positive semidefinite. In this case, the parameters are no longer interpreted as variances and covariances but merely as parameters structuring the residual covariance matrix. Relaxing the restrictions (not currently possible in Stata) makes the random-coefficient structure even more flexible but no longer interpretable as being induced by random intercepts and slopes.

A random-coefficient model with a random intercept and a random coefficient of `yeart` can be fit using `xtmixed` with the random part `|| nr: yeart` and with the `covariance(unstructured)` option:

```
. xtmixed lwage black hisp union married exper yeart educt || nr: yeart,
> covariance(unstructured) nofetable nogroup mle
Mixed-effects ML regression                     Number of obs      =      4360
                                                Wald chi2(7)       =    542.92
Log likelihood = -2120.9657                     Prob > chi2        =    0.0000
```

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
nr: Unstructured				
sd(yeart)	.0562206	.0031127	.0504392	.0626646
sd(_cons)	.3720286	.0151849	.3434261	.4030132
corr(yeart,_cons)	-.4626367	.050111	-.5550306	-.3589666
sd(Residual)	.3255862	.0040282	.3177859	.3335779

```
LR test vs. linear regression:       chi2(3) =  1734.54   Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference.
. estimates store rc
```

The marginal standard deviations and correlation matrix can be obtained using

```
. xtmixed_corr
Standard deviations and correlations for nr = 13:
Standard Deviations:
```

obs	1	2	3	4	5	6	7	8
sd	0.494	0.478	0.467	0.463	0.466	0.476	0.492	0.514

```
Correlations:
```

obs	1	2	3	4	5	6	7	8
1	1.000							
2	0.545	1.000						
3	0.515	0.518	1.000					
4	0.477	0.493	0.503	1.000				
5	0.432	0.461	0.485	0.502	1.000			
6	0.382	0.423	0.460	0.491	0.516	1.000		
7	0.330	0.381	0.430	0.475	0.512	0.541	1.000	
8	0.278	0.339	0.398	0.454	0.503	0.544	0.575	1.000

and were shown in row 2, column 1 of figure 6.2 on page 302.

More complex covariance structures can be produced by adding random coefficients of the square, the cube, and possibly higher powers of `yeart`.

6.3.4 Autoregressive and exponential structures

Autoregressive residual covariance structures can be derived from a model where the residuals are regressed on themselves ("auto" in Greek means "self") in the sense that the residual at an occasion is regressed on residuals at previous or lagged occasions. This makes the correlations between the residuals fall off as the number of occasions between them increases.

A popular special case is the first-order or autoregressive lag-1 structure, AR(1). This structure is produced by a model where the residual at occasion i is regressed on the residual at the previous occasion $i-1$:

$$\xi_{ij} \;=\; \alpha\xi_{i-1,j} + v_{ij}, \qquad \mathrm{Cov}(\xi_{i-1,j}, v_{ij}) = 0, \quad E(v_{ij}) = 0, \quad \mathrm{Var}(v_{ij}) = \sigma_v^2$$

The disturbances v_{ij} are independent across occasions and subjects. An AR(1) process is displayed in figure 6.4.

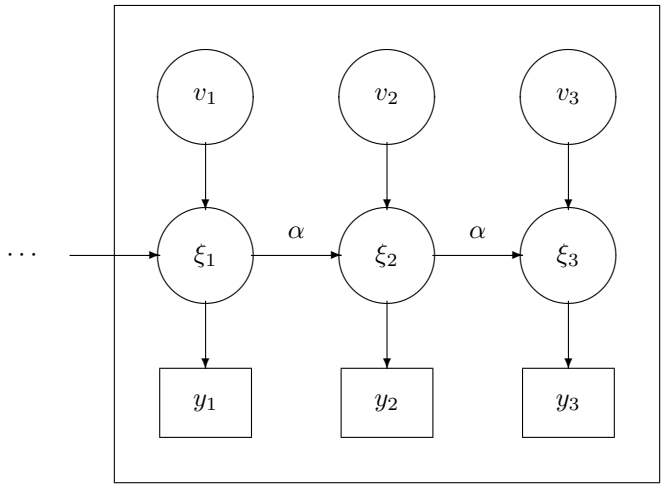


Figure 6.4: Path diagram of AR(1) process

The residual at a given occasion is determined partly by the residual at the previous occasion and partly by independent random noise. As a result of such inertia, where the present depends to some extent on the immediate past, AR(1) residuals change less from one occasion to the next than independent "white noise" residuals that have the same variance. This phenomenon is clearly seen in the simulated AR(1) and white noise time series shown in figure 6.5. In the figure, the parameters for the AR(1) process were set to $\alpha = 0.8$ and $\sigma_v^2 = 0.04$, whereas the white noise was independently distributed. Both processes were simulated from normal distributions with the same marginal variance.

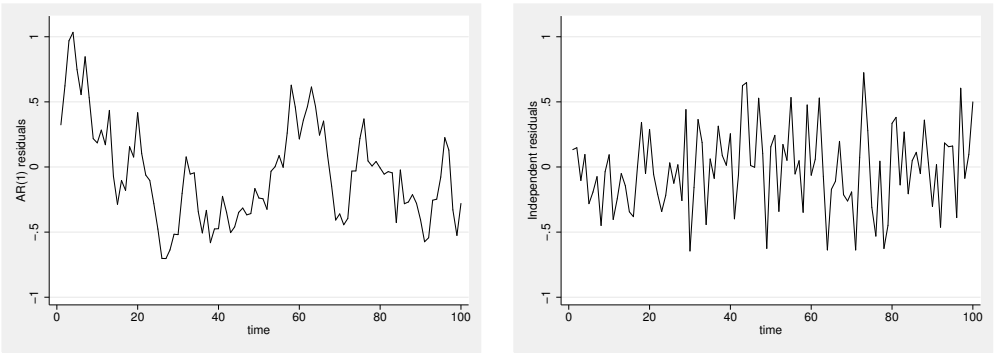


Figure 6.5: Simulated AR(1) process (left panel) and white noise (right panel) where both processes have the same mean and variance

The AR(1) model makes sense only if the time intervals between successive occasions are constant across time and across subjects, $t_{ij} - t_{i-1,j} = \Delta$ (although Stata can handle gaps, assumed to be unobserved realizations from the process). Higher-order autoregressive residual structures are produced by including further lags in the model.

A weakly or second-order *stationary* process for ξ_{ij} has expectations that are identical at all occasions, variances that are identical at all occasions, and covariances that are identical between all residuals at occasions a given time interval apart. An AR(1) process is stationary (and therefore also weakly stationary) if the process has been ongoing long before the first occasion in the dataset and $|\alpha| < 1$. For a stationary AR(1) process, the variances of the total residual at all occasions i are

$$\sigma^2 \equiv \mathrm{Var}(\xi_{ij}) \;=\; \frac{\sigma_v^2}{1-\alpha^2}$$

and the covariances and correlations between the residuals at occasions i and i' are

$$\mathrm{Cov}(\xi_{ij}, \xi_{i'j}) \;=\; \sigma^2 \alpha^{|i-i'|} \qquad \text{and} \qquad \mathrm{Cor}(\xi_{ij}, \xi_{i'j}) \;=\; \alpha^{|i-i'|}$$

respectively. We see that the correlations decrease as the time interval between the occasions increases.

For the wage-panel data, an AR(1) residual correlation structure can be fit using `xtmixed` with the `residuals(ar 1, t())` option. Here the time variable `yeart` is given in the `t()` option to determine the ordering and spacing of the occasions (the time variable must be integer valued). It is necessary to specify the cluster identifier `nr:` to identify the groups of observations that are to follow the specified structure. The `noconstant` option is used to omit the random intercept, which is otherwise included by default in `xtmixed`:

```
. xtmixed lwage black hisp union married exper yeart educt || nr:, noconstant
> residuals(ar 1, t(yeart)) nofetable nogroup mle
Mixed-effects ML regression                     Number of obs      =      4360
                                                Wald chi2(7)       =    468.26
Log likelihood = -2237.6188                     Prob > chi2        =    0.0000

------------------------------------------------------------------------------
  Random-effects Parameters |   Estimate   Std. Err.      [95% Conf. Interval]
----------------------------+-------------------------------------------------
nr:                   (empty)
----------------------------+-------------------------------------------------
Residual: AR(1)
                        rho |   .575936   .0126414      .5506306    .6001838
                     sd(e) |   .4821976   .0069132      .4688365    .4959394
------------------------------------------------------------------------------
LR test vs. linear regression:       chi2(1) =  1501.23   Prob > chi2 = 0.0000

Note: The reported degrees of freedom assumes the null hypothesis is not on
      the boundary of the parameter space.  If this is not true, then the
      reported test is conservative.

. estimates store ar1
```

The standard deviation σ of the (total) residuals (called `sd(e)` in the output) is estimated as 0.48, and the autoregressive parameter α (called `rho` in the output) is estimated as 0.58. We can obtain the standard deviations and correlation matrix by using

```
. xtmixed_corr
Standard deviations and correlations for nr = 13:
Standard Deviations:
       yeart |      0       1       2       3       4       5       6       7
-------------+--------------------------------------------------------------
          sd |  0.482   0.482   0.482   0.482   0.482   0.482   0.482   0.482
Correlations:
       yeart |      0       1       2       3       4       5       6       7
-------------+--------------------------------------------------------------
           0 |  1.000
           1 |  0.576   1.000
           2 |  0.332   0.576   1.000
           3 |  0.191   0.332   0.576   1.000
           4 |  0.110   0.191   0.332   0.576   1.000
           5 |  0.063   0.110   0.191   0.332   0.576   1.000
           6 |  0.036   0.063   0.110   0.191   0.332   0.576   1.000
           7 |  0.021   0.036   0.063   0.110   0.191   0.332   0.576   1.000
```

These standard deviations and correlations were shown in row 2 and column 2 of figure 6.2 on page 302.

When the occasions are irregularly spaced or the times t_{ij} associated with occasions i for subject j are nonintegers, a correlation structure of the form

$$\mathrm{Cor}(\xi_{ij}, \xi_{i'j} | t_{ij}, t_{i'j}) = \rho^{|t_{ij} - t_{i'j}|}$$

is sometimes specified. The covariance structure is no longer constant across subjects if the data are not balanced ($t_{ij} \neq t_i$). It is called the *exponential structure* in Stata

and is fit by using the `residuals(exponential, t())` option in `xtmixed`. Because the wage-panel data are balanced, identical results are produced as for the AR(1) structure and therefore not shown here.

6.3.5 Moving-average residual structure

A first-order *moving-average*, MA(1), residual covariance structure can be derived from a model where the total residual depends on the current and previous value of a random variable u_{ij} that is uncorrelated between occasions.

$$\xi_{ij} \;=\; \phi u_{i-1,j} + u_{ij}, \qquad \mathrm{Cov}(u_{i-1,j}, u_{ij}) = 0, \quad E(u_{ij}) = 0, \quad \mathrm{Var}(u_{ij}) = \sigma_u^2$$

The process makes sense only if the time intervals are constant, $t_{ij} - t_{i-1,j} = \Delta$. The MA(1) process is displayed in figure 6.6.

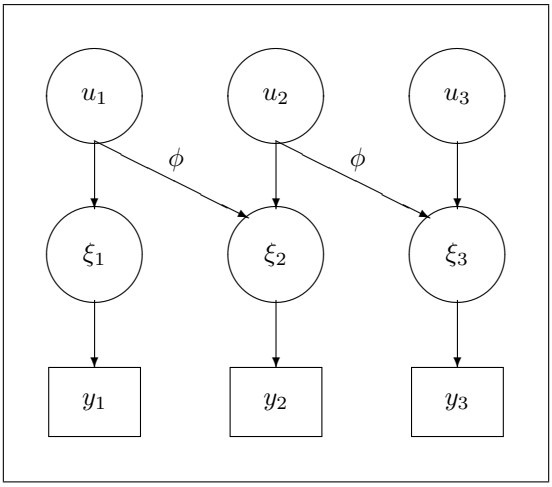


Figure 6.6: Path diagram of MA(1) process

Moving-average processes can be interpreted as arising from random shocks u_{ij}—such as strikes or government decisions or personal experiences—that affect residuals for a fixed number of occasions before disappearing. For the MA(1) process, the shock affects the current and next occasion. Higher-order moving-average structures allow shocks to affect more future occasions. An AR(1) process can be generated by letting the order k of the MA(k) process tend to infinity.

For the MA(1) process, the variance of the (total) residual at all occasions i becomes

$$\sigma^2 \equiv \mathrm{Var}(\xi_{ij}) \;=\; \sigma_u^2(1+\phi^2)$$

The covariances and correlations between residuals at occasions i and i' become

$$\mathrm{Cov}(\xi_{ij}, \xi_{i'j}) \;=\; \begin{cases} \sigma_u^2\phi & \text{if } |i-i'| = 1 \\ 0 & \text{otherwise} \end{cases}$$

and

$$\mathrm{Cor}(\xi_{ij}, \xi_{i'j}) = \begin{cases} \phi/(1+\phi^2) & \text{if } |i-i'|=1 \\ 0 & \text{otherwise} \end{cases}$$

respectively. We see that the process is weakly or second-order stationary.

For the wage-panel data, an MA(1) process can be estimated using `xtmixed` with the `residuals(ma 1, t())` option:

```
. xtmixed lwage black hisp union married exper yeart educt || nr:,
> noconstant residuals(ma 1, t(yeart)) nofetable nogroup mle
Mixed-effects ML regression                     Number of obs      =      4360
                                                Wald chi2(7)       =    707.90
Log likelihood =   -2522.49                     Prob > chi2        =    0.0000
```

Random-effects Parameters		Estimate	Std. Err.	[95% Conf.	Interval]
nr:	(empty)				
Residual: MA(1)					
	theta1	.4219844	.013202	.3957695	.4475122
	sd(e)	.4626877	.0052703	.4524726	.4731335

```
LR test vs. linear regression:       chi2(1) =   931.49   Prob > chi2 = 0.0000

Note: The reported degrees of freedom assumes the null hypothesis is not on
      the boundary of the parameter space.  If this is not true, then the
      reported test is conservative.

. estimates store ma1
```

The standard deviation of the (total) residual σ (called `sd(e)` in the output) is estimated as 0.46, and the weight parameter ϕ (called `theta1` in the output) is estimated as 0.42, corresponding to a correlation of 0.36 [$= 0.4219844/(1+0.4219844^2)$]. The standard deviations and correlation matrix can be obtained using

```
. xtmixed_corr
Standard deviations and correlations for nr = 13:
Standard Deviations:
```

yeart	0	1	2	3	4	5	6	7
sd	0.463	0.463	0.463	0.463	0.463	0.463	0.463	0.463

```
Correlations:
```

yeart	0	1	2	3	4	5	6	7
0	1.000							
1	0.358	1.000						
2	0.000	0.358	1.000					
3	0.000	0.000	0.358	1.000				
4	0.000	0.000	0.000	0.358	1.000			
5	0.000	0.000	0.000	0.000	0.358	1.000		
6	0.000	0.000	0.000	0.000	0.000	0.358	1.000	
7	0.000	0.000	0.000	0.000	0.000	0.000	0.358	1.000

and were shown in row 3 and column 1 of figure 6.2 on page 302.

6.3.6 Banded and Toeplitz structures

The *banded* covariance structure is a special case of the unstructured covariance structure with covariances between pairs of occasions further than some lag apart set to zero. For instance, the banded(1) structure allows all variances to be freely estimated as well as all covariances on the first off-diagonal (lag 1), whereas all other covariances are set to zero. A banded(2) structure also allows the second off-diagonal (lag 2) to be free, and so forth. See table 6.1 for an example of a banded(1) structure for three occasions. This structure only makes sense for balanced data with $t_{ij} = t_i$.

We fit a model with a banded(1) structure for the wage-panel data using `xtmixed` with the `residuals(banded 1, t())` option:

```
. xtmixed lwage black hisp union married exper yeart educt || nr:, noconstant
> residuals(banded 1, t(yeart)) nofetable nogroup mle
Mixed-effects ML regression                     Number of obs      =      4360
                                                Wald chi2(7)       =    674.54
Log likelihood = -2470.0904                     Prob > chi2        =    0.0000
```

Random-effects Parameters		Estimate	Std. Err.	[95% Conf.	Interval]
nr:	(empty)				
Residual: Banded(1)					
	sd(e0)	.5298451	.01615	.4991185	.5624631
	sd(e1)	.488302	.0141587	.4613252	.5168563
	sd(e2)	.4336913	.0121559	.4105088	.4581831
	sd(e3)	.4249331	.0121275	.4018161	.44938
	sd(e4)	.4690608	.0133869	.4435432	.4960464
	sd(e5)	.4758399	.0142071	.4487937	.5045161
	sd(e6)	.4655073	.0141701	.4385467	.4941255
	sd(e7)	.4323662	.0131472	.407351	.4589176
	corr(e0,e1)	.3072858	.0401419	.2266593	.3837294
	corr(e1,e2)	.3065635	.0437078	.2186103	.3895758
	corr(e2,e3)	.4440175	.0453184	.3510051	.5283533
	corr(e3,e4)	.262966	.045426	.1719201	.3495574
	corr(e4,e5)	.499973	.0402668	.416992	.5746881
	corr(e5,e6)	.1341619	.0375518	.0599544	.2068946
	corr(e6,e7)	.594792	.0319827	.5284894	.6538825

```
LR test vs. linear regression:      chi2(14) =  1036.29   Prob > chi2 = 0.0000

Note: The reported degrees of freedom assumes the null hypothesis is not on
      the boundary of the parameter space.  If this is not true, then the
      reported test is conservative.

. estimates store ba1
```

The estimated residual standard deviations and correlations are

```
. xtmixed_corr
Standard deviations and correlations for nr = 13:
Standard Deviations:
```

yeart	0	1	2	3	4	5	6	7
sd	0.530	0.488	0.434	0.425	0.469	0.476	0.466	0.432

```
Correlations:
```

yeart	0	1	2	3	4	5	6	7
0	1.000							
1	0.307	1.000						
2	0.000	0.307	1.000					
3	0.000	0.000	0.444	1.000				
4	0.000	0.000	0.000	0.263	1.000			
5	0.000	0.000	0.000	0.000	0.500	1.000		
6	0.000	0.000	0.000	0.000	0.000	0.134	1.000	
7	0.000	0.000	0.000	0.000	0.000	0.000	0.595	1.000

We see that only the correlations on the first off-diagonal of the correlation matrix are estimated (see also row 3 and column 2 of figure 6.2 on page 302).

Comparing these correlations with the first off-diagonal of the estimated unstructured correlation matrix, it is at first surprising that the correlations for the banded structure are all lower than in the unstructured case, because one might expect them to be identical. However, setting, for instance, the correlation between residuals at occasions 1 and 3 to zero is incompatible with a high correlation between occasions 1 and 2 and a high correlation between occasions 2 and 3. An extreme case would be where $\text{Cor}(\xi_{1j}, \xi_{2j}) = 1$ and $\text{Cor}(\xi_{2j}, \xi_{3j}) = 1$, from which it follows that $\text{Cor}(\xi_{1j}, \xi_{3j})$ is one and not zero. By setting all but lag-1 correlations to zero, we are therefore imposing a constraint on the lag-1 correlations. Formally, such constraints on the correlation matrix follow from the fact that such matrices are positive semidefinite.

The *Toeplitz* structure is similar to the banded structure in the sense that covariances outside the bands are set to zero. However, this structure constrains the parameters on the main diagonal to be equal and the parameters on each of the off-diagonals to be equal. For instance, the Toeplitz(1) structure constrains all variance parameters to be equal and all covariance parameters in the first off-diagonal to be equal, whereas all other covariances are set to zero; see table 6.1 for the case of three occasions. This structure appears to be equivalent to an MA(1) structure, but MA(1) forces the correlation to be at most 0.5, whereas in three dimensions, the Toeplitz(1) structure allows the correlation to be as large as $\sqrt{0.5} = 0.71$. The Toeplitz(2) structure extends Toeplitz(1) by specifying a common covariance parameter in the second off-diagonal instead of zeros, still setting all covariances on the third and further off-diagonals to zero. This structure makes sense only if the spacing between occasions is constant, $t_{ij} - t_{i-1,j} = \Delta$.

Because the estimated Toeplitz(1) covariance structure in the present application turns out to be identical to that previously reported for the MA(1) structure (because the correlation is estimated as 0.36, which is less than 0.5), we instead fit a Toeplitz(2) structure by using `xtmixed` with the `residuals(toeplitz 2, t())` option:

```
. xtmixed lwage black hisp union married exper yeart educt || nr:, noconstant
> residuals(toeplitz 2, t(yeart)) nofetable nogroup mle
Mixed-effects ML regression                     Number of obs      =      4360
                                                Wald chi2(7)       =    607.48
Log likelihood =  -2325.486                     Prob > chi2        =    0.0000
```

Random-effects Parameters		Estimate	Std. Err.	[95% Conf.	Interval]
nr:	(empty)				
Residual: Toeplitz(2)					
	rho1	.4359403	.012634	.4108515	.4603694
	rho2	.258459	.0116724	.2354403	.281188
	sd(e)	.4583503	.0055387	.4476222	.4693355

```
LR test vs. linear regression:       chi2(2) =  1325.50   Prob > chi2 = 0.0000
Note: The reported degrees of freedom assumes the null hypothesis is not on
      the boundary of the parameter space.  If this is not true, then the
      reported test is conservative.
. estimates store to2
```

Here `rho_1` and `rho_2` represent the common correlation on the first and second off-diagonal of the correlation matrix, respectively, and `sd(e)` represents the standard deviation parameter that is common for all occasions. The implied standard deviations and correlations are

```
. xtmixed_corr
Standard deviations and correlations for nr = 13:
Standard Deviations:
```

yeart	0	1	2	3	4	5	6	7
sd	0.458	0.458	0.458	0.458	0.458	0.458	0.458	0.458

```
Correlations:
```

yeart	0	1	2	3	4	5	6	7
0	1.000							
1	0.436	1.000						
2	0.258	0.436	1.000					
3	0.000	0.258	0.436	1.000				
4	0.000	0.000	0.258	0.436	1.000			
5	0.000	0.000	0.000	0.258	0.436	1.000		
6	0.000	0.000	0.000	0.000	0.258	0.436	1.000	
7	0.000	0.000	0.000	0.000	0.000	0.258	0.436	1.000

(see row 4 and column 1 of figure 6.2). Again the correlations are lower than in the unstructured case to satisfy positive semidefiniteness.

6.4 Hybrid and complex marginal models

6.4.1 Random effects and correlated level-1 residuals

In many of the covariance structures discussed so far, the correlations are zero for large lags or approach zero in the case of autoregressive processes. However, if there are unobserved subject-specific characteristics or individual differences that affect the response variable, we would expect nonzero correlations no matter how large the lag. More realistic covariance structures can often be produced by combining a random-intercept model with a covariance structure for the level-1 residuals.

An appealing and quite commonly used hybrid specification is a random-intercept model in which the level-1 residuals have a first-order autoregressive correlation structure. This produces a correlation matrix with serial correlations that do not approach zero as the time lag increases (when occasions are not equally spaced, an exponential structure can be used).

For the wage-panel data, we can fit a random-intercept model with AR(1) residuals using `xtmixed` by no longer including the `noconstant` option after the double pipe (as done repeatedly in this chapter) and by using the `residuals(ar 1, t())` option:

```
. xtmixed lwage black hisp union married exper yeart educt || nr:,
> residuals(ar 1, t(yeart)) nofetable nogroup mle
Mixed-effects ML regression                     Number of obs      =      4360
                                                Wald chi2(7)       =    656.72
Log likelihood = -2123.5033                     Prob > chi2        =    0.0000
```

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
nr: Identity				
sd(_cons)	.3045101	.0124286	.2810994	.3298705
Residual: AR(1)				
rho	.2774511	.0213005	.2352016	.3186541
sd(e)	.3722109	.0054527	.3616757	.3830529

```
LR test vs. linear regression:       chi2(2) =  1729.46   Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference.
. estimates store ri_ar1
```

The estimated marginal residual standard deviations and correlation matrix are obtained using

```
. xtmixed_corr
Standard deviations and correlations for nr = 13:
Standard Deviations:
```

yeart	0	1	2	3	4	5	6	7
sd	0.481	0.481	0.481	0.481	0.481	0.481	0.481	0.481

```
Correlations:
```

yeart	0	1	2	3	4	5	6	7
0	1.000							
1	0.567	1.000						
2	0.447	0.567	1.000					
3	0.414	0.447	0.567	1.000				
4	0.404	0.414	0.447	0.567	1.000			
5	0.402	0.404	0.414	0.447	0.567	1.000		
6	0.401	0.402	0.404	0.414	0.447	0.567	1.000	
7	0.401	0.401	0.402	0.404	0.414	0.447	0.567	1.000

and shown in bottom right panel of figure 6.2 on page 302 (obtained using the matrix expressions given in display 6.1, where $\mathbf{R}$ now has an AR(1) structure). As the lag increases, the estimated correlations approach $\widehat{\psi}_{11}/(\widehat{\psi}_{11}+\widehat{\theta}) = 0.40$ (see also exercise 6.8).

There are of course many different covariance structures for the level-1 residuals that could be specified for models with random intercepts and possibly random slopes of time. This offers great flexibility at the cost of potential identification problems if the implied covariance structure for the responses, given the observed covariates, becomes complex. For instance, with n occasions, a random-intercept model with a Toeplitz$(n-1)$ structure for the level-1 residuals is not identified. To see this, consider the covariance matrix of the total residual, which is the Toeplitz$(n-1)$ covariance matrix with ψ_{11} added to each element. We can add a constant to ψ_{11} and subtract the same constant from Toeplitz$(n-1)$ without changing the covariance matrix of the total residual, and therefore ψ_{11} is a redundant parameter. However, for Toeplitz$(n-2)$, ψ_{11} becomes the covariance $\mathrm{Cov}(\xi_{1j}, \xi_{nj})$ between the first and last occasions and is therefore identified. Following this logic, Toeplitz and banded matrices of order $n-2$ or lower can be combined with a random intercept.

6.4.2 Heteroskedastic level-1 residuals over occasions

We now combine a random-coefficient structure with heteroskedastic level-1 residuals, letting the standard deviations of these residuals be occasion specific by using the `residuals(independent, by())` option:

```
. xtmixed lwage black hisp union married exper yeart educt || nr: yeart,
> covariance(unstructured) residuals(independent, by(yeart)) nofetable nogroup
> mle
Mixed-effects ML regression                     Number of obs      =      4360
                                                Wald chi2(7)       =    548.74
Log likelihood =  -2036.413                     Prob > chi2        =    0.0000
```

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
nr: Unstructured				
sd(yeart)	.053767	.0030945	.0480315	.0601873
sd(_cons)	.3804544	.0161599	.350064	.413483
corr(yeart,_cons)	-.472357	.0509171	-.5659588	-.3667326
Residual: Independent, by yeart				
0: sd(e)	.4568489	.0164572	.4257057	.4902705
1: sd(e)	.3558621	.0131617	.3309784	.3826165
2: sd(e)	.2880905	.010939	.2674289	.3103484
3: sd(e)	.2794221	.0100623	.2603802	.2998565
4: sd(e)	.3334089	.0112416	.312088	.3561864
5: sd(e)	.3089093	.0107731	.2884999	.3307625
6: sd(e)	.321404	.0116002	.2994535	.3449634
7: sd(e)	.2348136	.0125032	.2115432	.2606439

```
LR test vs. linear regression:      chi2(10) =  1903.64   Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference.
. estimates store rc_het
```

The estimated occasion-specific standard deviations of the level-1 errors range from 0.23 to 0.46. The model-implied marginal residual standard deviations and correlations are

```
. xtmixed_corr
Standard deviations and correlations for nr = 13:
Standard Deviations:
```

obs	1	2	3	4	5	6	7	8
sd	0.595	0.505	0.448	0.437	0.474	0.465	0.486	0.454

```
Correlations:
```

obs	1	2	3	4	5	6	7	8
1	1.000							
2	0.450	1.000						
3	0.471	0.537	1.000					
4	0.446	0.520	0.581	1.000				
5	0.376	0.451	0.517	0.540	1.000			
6	0.349	0.432	0.509	0.546	0.525	1.000		
7	0.300	0.385	0.469	0.517	0.510	0.554	1.000	
8	0.286	0.382	0.483	0.548	0.554	0.616	0.637	1.000

6.4.3 Heteroskedastic level-1 residuals over groups

We can also let the level-1 residuals have different variances for different groups of subjects, such as ethnic groups. Based on the dummy variables `black` and `hisp`, we

first construct the categorical variable `ethnic`, taking the values 0 for white, 1 for black, and 2 for Hispanic:

```
. generate ethnic = black*1 + hisp*2
```

A random-intercept model with level-1 residuals that have different variances for ethnic groups can be fit by using `xtmixed` with the `residuals(independent, by())` option:

```
. xtmixed lwage black hisp union married exper yeart educt || nr:,
> residuals(independent, by(ethnic)) nofetable nogroup mle
Mixed-effects ML regression                     Number of obs      =      4360
                                                Wald chi2(7)       =    896.36
Log likelihood = -2213.0207                     Prob > chi2        =    0.0000
```

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
nr: Identity				
sd(_cons)	.3270843	.0114203	.3054497	.3502513
Residual: Independent, by ethnic				
0: sd(e)	.3548746	.0047629	.3456612	.3643336
1: sd(e)	.3634011	.0122687	.3401332	.3882608
2: sd(e)	.3394479	.0098302	.3207177	.359272

```
LR test vs. linear regression:       chi2(3) =  1550.43   Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference.
. estimates store ri_het2
```

We see that the estimated standard deviations (and hence variances) of the level-1 residuals are very similar for the different ethnic groups. To display the model-implied marginal residual standard deviations and correlations for the three groups, we first find one subject per group, for example, the subject with the smallest identifier in the variable `nr`,

```
. table ethnic, contents(min nr)
```

ethnic	min(nr)
0	13
1	383
2	1142

and then display the results for these three subjects by using the `at()` option in `xtmixed_corr` (within each group all subjects have the same standard deviations and the same correlations). For white, we obtain

```
. xtmixed_corr, at(nr=13)
Standard deviations and correlations for nr = 13:
Standard Deviations:
```

obs	1	2	3	4	5	6	7	8
sd	0.483	0.483	0.483	0.483	0.483	0.483	0.483	0.483

```
Correlations:
```

obs	1	2	3	4	5	6	7	8
1	1.000							
2	0.459	1.000						
3	0.459	0.459	1.000					
4	0.459	0.459	0.459	1.000				
5	0.459	0.459	0.459	0.459	1.000			
6	0.459	0.459	0.459	0.459	0.459	1.000		
7	0.459	0.459	0.459	0.459	0.459	0.459	1.000	
8	0.459	0.459	0.459	0.459	0.459	0.459	0.459	1.000

For black, we get

```
. xtmixed_corr, at(nr=383)
Standard deviations and correlations for nr = 383:
Standard Deviations:
```

obs	1	2	3	4	5	6	7	8
sd	0.489	0.489	0.489	0.489	0.489	0.489	0.489	0.489

```
Correlations:
```

obs	1	2	3	4	5	6	7	8
1	1.000							
2	0.448	1.000						
3	0.448	0.448	1.000					
4	0.448	0.448	0.448	1.000				
5	0.448	0.448	0.448	0.448	1.000			
6	0.448	0.448	0.448	0.448	0.448	1.000		
7	0.448	0.448	0.448	0.448	0.448	0.448	1.000	
8	0.448	0.448	0.448	0.448	0.448	0.448	0.448	1.000

For Hispanic, we have

```
. xtmixed_corr, at(nr=1142)
Standard deviations and correlations for nr = 1142:
Standard Deviations:
```

obs	1	2	3	4	5	6	7	8
sd	0.471	0.471	0.471	0.471	0.471	0.471	0.471	0.471

```
Correlations:
```

obs	1	2	3	4	5	6	7	8
1	1.000							
2	0.481	1.000						
3	0.481	0.481	1.000					
4	0.481	0.481	0.481	1.000				
5	0.481	0.481	0.481	0.481	1.000			
6	0.481	0.481	0.481	0.481	0.481	1.000		
7	0.481	0.481	0.481	0.481	0.481	0.481	1.000	
8	0.481	0.481	0.481	0.481	0.481	0.481	0.481	1.000

6.4.4 Different covariance matrices over groups

Stata can also fit marginal models where the covariance matrix is different for groups of subjects. We illustrate this by fitting an AR(1) structure stratified by ethnicity, using `xtmixed` with the `residuals(ar(1), t() by())` option:

```
. xtmixed lwage black hisp union married exper yeart educt || nr:, noconstant
> residuals(ar 1, t(yeart) by(ethnic)) nofetable nogroup mle
Mixed-effects ML regression                     Number of obs      =      4360
                                                Wald chi2(7)       =    472.11
Log likelihood = -2233.2874                     Prob > chi2        =    0.0000
```

Random-effects Parameters		Estimate	Std. Err.	[95% Conf.	Interval]
nr:	(empty)				
Residual: AR(1), by ethnic					
	0: rho	.5894316	.0144551	.5603749	.6170392
	sd(e)	.485829	.0082504	.4699246	.5022716
	1: rho	.5600764	.0374796	.4822492	.6291319
	sd(e)	.5025142	.020865	.4632393	.5451191
	2: rho	.5114246	.0352765	.4390287	.5772225
	sd(e)	.4470734	.015431	.4178296	.478364

```
LR test vs. linear regression:       chi2(5) =  1509.90   Prob > chi2 = 0.0000
Note: The reported degrees of freedom assumes the null hypothesis is not on
      the boundary of the parameter space.  If this is not true, then the
      reported test is conservative.
```

The estimated parameters of the AR(1) structure are somewhat smaller for Hispanics (group 2) than for whites and blacks. We could again display the group-specific marginal residual standard deviations and correlations using

```
xtmixed_corr, at(nr=13)
xtmixed_corr, at(nr=383)
xtmixed_corr, at(nr=1142)
```

Random effects whose covariance matrix differs between groups can also be accommodated, but we defer discussion of this to section 7.5.2 in the chapter on growth curves.

6.5 Comparing the fit of marginal models

We have fit a large number of marginal models with the same mean structure (fixed part of the model) and a wide range of covariance structures.

For balanced data, an informal comparison of the fit of these different models consists of eyeballing the estimated standard deviations and correlations for each model to see how much they differ from the corresponding estimates for the unstructured case. This way, it can be judged how reasonable the restrictions are. For instance, in figure 6.2, it is immediately apparent that the restrictions imposed by the MA(1) structure are unreasonable. Correlations for lag greater than 1 are set to zero though the corresponding estimates for the unstructured case are as large as 0.63 and never smaller than 0.22. A correlation as high as 0.63 is unlikely to occur by chance.

All covariance structures that are constant across subjects (the only restriction for the unstructured case) can be obtained by imposing restrictions on the unstructured model and are hence nested in the unstructured model. (For nesting relationships between other pairs of models, refer to figure 6.1.) Therefore, we could conduct a likelihood-ratio test to compare a structured model, for example, MA(1), to the unstructured model:

```
. lrtest un ma1
Likelihood-ratio test                                 LR chi2(34) =   1089.39
(Assumption: ma1 nested in un)                        Prob > chi2 =    0.0000
Note: The reported degrees of freedom assumes the null hypothesis is not on
      the boundary of the parameter space.  If this is not true, then the
      reported test is conservative.
```

As expected, the MA(1) structure is rejected at any reasonable significance level. The note at the end of the output is a useful reminder of the problem of testing a null hypothesis that restricts parameters to lie on the boundary of the parameter space. We have discussed this problem before in the context of testing the null hypothesis that a variance parameter is zero in a random-intercept or random-coefficient model. For the null hypothesis just tested here, there does not appear to be a boundary issue, but sometimes this is not transparent.

Performing likelihood-ratio tests to compare each of the structures with the unstructured model, we reject each of the structures at the 5% level. However, it should be kept in mind that any structure that is not exactly correct will be rejected as the sample size and hence the power of the tests increases. It could be argued that models should be simplifications of reality (parsimonious, with few parameters) as long as prominent features are not smoothed away (good fit or large log likelihood). Therefore, other criteria for model selection have been proposed that are not based on statistical significance.

For a given dataset, the fit can usually be improved by increasing the number of parameters that are estimated. There is therefore an unavoidable trade-off between desired model fit and undesired model complexity. Information criteria, such as AIC and BIC (described below), have been developed in an attempt to provide a rational trade-off between fit and complexity. The idea is to choose the model with the smallest "badness", where badness is defined as twice the log likelihood, a measure of misfit, plus a penalty for model complexity (a function of the number of model parameters).

An additional reason for using information criteria in favor of likelihood-ratio tests is that they can be used to choose between models that are not nested.

We can obtain information criteria for the models we have fit (ignoring models that allow covariance matrices to differ between ethnic groups) by using `estimates stats` as follows:

```
. estimates stats un ri rc ar1 ma1 ba1 to2 rc_het
```

Model	Obs	ll(null)	ll(model)	df	AIC	BIC
un	4360	.	-1977.796	44	4043.592	4324.322
ri	4360	.	-2214.357	10	4448.714	4512.517
rc	4360	.	-2120.966	12	4265.931	4342.494
ar1	4360	.	-2237.619	10	4495.238	4559.04
ma1	4360	.	-2522.49	10	5064.98	5128.782
ba1	4360	.	-2470.09	23	4986.181	5132.926
to2	4360	.	-2325.486	11	4672.972	4743.155
rc_het	4360	.	-2036.413	19	4110.826	4232.05

```
Note:  N=Obs used in calculating BIC; see [R] BIC note
```

In addition to the log likelihoods, `ll(model)`, and the number of estimated parameters, `df`, the output shows the Akaike information criterion (AIC) and the Bayesian information criterion (BIC) for each of the models.

The AIC for a particular model is defined as

$$\text{AIC} \;=\; -2\log\text{ likelihood} + 2\,k$$

where "log likelihood" is the maximum log likelihood for the model and k is the number of parameters estimated. BIC is defined as

$$\text{BIC} \;=\; -2\log\text{ likelihood} + \ln(N)\,k$$

where N is the number of observations. For both the AIC and the BIC, the model that has the smallest value of the criterion is preferred, but the best model according to the AIC may differ from the best model according to the BIC.

For the wage-panel data, the unstructured model (with 44 parameters) is best according to the AIC, whereas the random-coefficient model with heteroskedastic level-1 residuals (with 19 parameters) is best according to the BIC. In general, the BIC tends to select more parsimonious models than does the AIC.

When two models have the same number of parameters, both criteria will lead to the same choice between the models. Note that we have fit some models [for example, the banded(1) model] that are clearly bad in the sense that they have a lower log likelihood than a model with fewer parameters (for example, the random-intercept model). In such cases, any sensible criterion would prefer the simpler and better-fitting model.

Whenever log likelihoods or information criteria are being compared, the log likelihood must be based on the same data and therefore the same number of observations. As shown in the output, the number of observations analyzed for each model was 4,360. (When comparing models with different sets of covariates, different missingness patterns for different covariates will often result in different estimation samples for different models.)

A theoretical justification for the AIC can be given in terms of cross-validation, and the BIC can be motivated as an approximation to Bayes factors used by Bayesians for model selection. Unfortunately, the AIC and BIC given above were derived for models with independent observations, not for longitudinal or clustered data, and there does not appear to be any theoretical justification for their use in longitudinal (or multilevel) models. For instance, the BIC depends on the sample size N, but it is not clear what the sample size should be for clustered data. Should it be the number of clusters J, the total number of observations $\sum_{j=1}^{J} n_j$ (used by Stata), or something in between? Nevertheless, AIC and BIC are quite commonly used for model selection in longitudinal and multilevel modeling. In this setting, the criteria are best viewed as informal indices of lack of fit, with the smallest value suggesting the preferred model.

In this chapter on marginal modeling, we have concentrated on specifying the correct covariance structure. However, research questions usually concern the relationships between response and explanatory variables, so regression coefficients are the main focus. These coefficients can be estimated consistently even if the covariance structure is misspecified, as long as the mean structure (fixed part of the model) is correctly specified. (This is true here because the models are linear and there are no missing data; see section 5.8 and exercise 6.6.) However, in finite samples, the estimates will of course differ.

We can obtain a table of estimated regression coefficients and their standard errors for the models compared here by using the following `estimates table` command:

```
. estimates table un ri rc ar1 ma1 ba1 to2 ri_ar1 rc_het,
> b(%4.3f) se(%4.3f) keep(lwage:)
```

Variable	un	ri	rc	ar1	ma1	ba1	to2	ri_ar1	rc_het
black	-0.134	-0.134	-0.130	-0.133	-0.137	-0.141	-0.131	-0.133	-0.141
	0.047	0.048	0.048	0.039	0.029	0.029	0.032	0.048	0.048
hisp	0.017	0.017	0.017	0.020	0.018	0.019	0.014	0.019	0.020
	0.042	0.043	0.043	0.035	0.025	0.025	0.028	0.042	0.043
union	0.094	0.111	0.111	0.099	0.136	0.127	0.131	0.097	0.103
	0.017	0.018	0.018	0.018	0.018	0.017	0.018	0.018	0.017
married	0.077	0.075	0.076	0.081	0.100	0.093	0.092	0.074	0.075
	0.017	0.017	0.017	0.019	0.017	0.017	0.018	0.018	0.017
exper	0.036	0.033	0.036	0.035	0.033	0.031	0.033	0.034	0.031
	0.011	0.011	0.011	0.009	0.007	0.007	0.007	0.011	0.011
yeart	0.022	0.026	0.023	0.026	0.026	0.027	0.027	0.026	0.026
	0.011	0.011	0.012	0.010	0.008	0.008	0.008	0.011	0.012
educt	0.096	0.095	0.095	0.095	0.094	0.094	0.094	0.095	0.095
	0.010	0.011	0.011	0.009	0.006	0.006	0.007	0.011	0.011
_cons	1.313	1.317	1.308	1.300	1.301	1.314	1.298	1.313	1.334
	0.037	0.037	0.038	0.033	0.025	0.026	0.028	0.038	0.039

legend: b/se

The overall impression is that the estimates of the regression coefficients (first line for each covariate) are quite similar for the different covariance structures.

However, the model-based standard errors rely on correct specification of the covariance structure. We see that the estimated standard errors (second line for each covariate) differ somewhat across covariance structures and appear to be larger for the unstructured, random-intercept, and random-coefficient structures than for the other structures. We could of course use robust standard errors by specifying the `vce(robust)` option in the `xtmixed` commands. However, these standard errors can perform poorly in small samples (when there are few subjects).

Because inferences for regression coefficients depend on the specified covariance structure, it is usually recommended to select the covariance structure before selecting the mean structure. However, the *residual* covariance structure depends on the residuals and hence on the specified mean structure. Therefore it is often recommended to include all potentially relevant covariates and interactions when selecting the covariance structure and then keep the chosen covariance structure when refining the mean structure.

6.6 Generalized estimating equations (GEE)

Recall from section 3.10.1 that for a known residual covariance matrix, maximum likelihood (ML) estimation of the regression coefficients can be accomplished by generalized least squares (GLS). Feasible generalized least squares (FGLS) substitutes estimates for the covariance matrix based on residuals from pooled ordinary least squares (OLS). In iteratively reweighted generalized least squares (IGLS), estimation proceeds by iterating between estimating the covariance matrix based on residuals from FGLS and using FGLS

based on this covariance matrix to estimate new regression coefficients and hence new residuals, until convergence is achieved.

For linear marginal models with continuous responses, the `xtgee` command for generalized estimating equations (GEE) works essentially in the same way as IGLS, iterating between estimation of the residual covariance matrix and the regression coefficients. The only difference between GEE and IGLS is the estimator for the residual correlation matrix, which is called the "working correlation matrix" in GEE. The residual variance is assumed to be constant across occasions.

Stata's `xtgee` command offers all the correlation structures corresponding to the covariance structures discussed in this chapter except the random-coefficient and moving-average structures. Note that banded correlation structures are called "nonstationary" and Toeplitz correlation structures are called "stationary" in `xtgee`. Specifying the "independent" structure simply produces the pooled OLS estimator.

The correlation structure is what is specified in GEE, not the covariance structure. Even in the unstructured case, the variances are all constrained to be equal in GEE, which may be very restrictive. For instance, when modeling children's weights as a function of age, it seems obvious that their weights are less variable at age 0 than they are at age 5.

We now briefly demonstrate how a marginal model with an AR(1) working correlation structure can be fit using `xtgee` with the `corr(ar 1)` option:

```
. quietly xtset nr yeart
. xtgee lwage black hisp union married exper yeart educ, corr(ar 1) vce(robust)
GEE population-averaged model                   Number of obs      =      4360
Group and time vars:              nr yeart      Number of groups   =       545
Link:                             identity      Obs per group: min =         8
Family:                           Gaussian                     avg =       8.0
Correlation:                         AR(1)                     max =         8
                                               Wald chi2(7)       =    547.37
Scale parameter:                  .2322738     Prob > chi2        =    0.0000
                                    (Std. Err. adjusted for clustering on nr)
------------------------------------------------------------------------------
             |               Robust
       lwage |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       black |  -.1329348   .0487983    -2.72   0.006    -.2285776   -.0372919
        hisp |   .0195104   .0398453     0.49   0.624     -.058585    .0976058
       union |   .0995969   .0195432     5.10   0.000      .061293    .1379008
     married |   .0813371   .0190996     4.26   0.000     .0439026    .1187715
       exper |   .0351937   .0107019     3.29   0.001     .0142183    .0561691
       yeart |    .025618   .0113301     2.26   0.024     .0034115    .0478246
       educ  |   .0952535   .0107629     8.85   0.000     .0741586    .1163485
       _cons |   1.300357   .0381552    34.08   0.000     1.225574     1.37514
------------------------------------------------------------------------------
```

As is invariably done in practice, we have also used the `vce(robust)` option to produce robust standard errors based on the sandwich estimator. Robust standard errors for the estimated regression coefficients do not rely on correct specification of

the correlation structure, although the mean structure must be correctly specified. The estimates of the regression coefficients are nearly identical to the ML estimates with the same covariance structure, but the standard errors are a little different. With the `vce(robust)` option in `xtmixed`,

```
xtmixed lwage black hisp union married exper yeart educt || nr:, noconstant
   residuals(ar 1, t(yeart)) vce(robust)
```

the standard errors are practically identical to those produced by `xtgee` with the `vce(robust)` option above.

The estimated correlation matrix of the residuals or working correlation matrix can be displayed using

```
. estat wcorrelation, format(%4.3f)
Estimated within-nr correlation matrix R:
```

	c1	c2	c3	c4	c5	c6	c7	c8
r1	1.000							
r2	0.575	1.000						
r3	0.330	0.575	1.000					
r4	0.190	0.330	0.575	1.000				
r5	0.109	0.190	0.330	0.575	1.000			
r6	0.063	0.109	0.190	0.330	0.575	1.000		
r7	0.036	0.063	0.109	0.190	0.330	0.575	1.000	
r8	0.021	0.036	0.063	0.109	0.190	0.330	0.575	1.000

We see that the estimated correlation matrix is identical, to two decimal places, to the one using ML estimation shown in figure 6.2 (partly because of the balanced nature of the data). The estimated residual standard deviation is the square root of the scale parameter, here estimated as 0.48 ($= \sqrt{0.2322738}$).

Identical results can also be obtained using `xtreg` with the `pa` (for "population averaged") and `vce(robust)` (for "robust standard errors") options:

```
xtset nr yeart
xtreg lwage black hisp union married exper yeart educt, pa corr(ar 1) vce(robust)
```

followed by

```
matrix list e(R)
```

GEE was actually developed for noncontinuous responses, such as dichotomous responses and counts (see volume 2, sections 10.14.2 and 13.11.3), and is rarely used for continuous responses.

6.7 Marginal modeling with few units and many occasions

So far we have considered longitudinal data with short panels, where there are far more units (or subjects) than occasions. In data with long panels, there are nearly as

many or more occasions than there are units. Political scientists tend to call such data "time-series–cross-sectional data". Usually, the units are states or countries, and cross-sectional correlations are expected between responses for different (possibly neighboring) units at a given occasion, which should be taken into account when estimating standard errors.

6.7.1 Is a highly organized labor market beneficial for economic growth?

The political scientist Garrett (1998) argues that a highly organized labor market is beneficial for economic growth when left-wing parties are powerful, whereas a less organized labor market is beneficial when right-wing parties are powerful.

The data analyzed here are from 14 OECD countries that were observed annually in the 25-year period from 1966 to 1990. The dataset `garrett.dta` contains the following variables:

- `country`: country identifier (j)
- `year`: year (i)
- `gdp`: annual real (adjusted for inflation) growth in gross domestic product (GDP) in percent (y_{ij})
- `oildep`: price of oil in U.S. dollars weighted by dependence on imported oil (as a proportion of all energy requirements) (x_{2ij})
- `demand`: overall real GDP growth in the OECD, weighted by national exposure to trade (x_{3ij})
- `leftpow`: left-wing power, an index that weights party groupings by their shares of legislative seats and cabinet portfolios; more left-wing power gives a higher index (x_{4ij})
- `organ`: degree of organization of the labor market; an index that is increasing in union density and major confederation share but decreasing in public sector share and the number of confederation-affiliated unions (x_{5ij})

To address the research question, we include `leftpow`, `organ`, and their interaction in the model. In addition, we control for `gdp`, `oildep`, and `demand`. The model then is

$$\begin{aligned} y_{ij} &= \beta_1 + \beta_2 x_{2ij} + \beta_3 x_{3ij} + \beta_4 x_{4ij} + \beta_5 x_{5ij} + \beta_6 x_{4ij} x_{5ij} + \xi_{ij} \\ &= \beta_1 + \beta_2 x_{2ij} + \beta_3 x_{3ij} + \beta_4 x_{4ij} + \underbrace{(\beta_5 + \beta_6 x_{4ij})}_{\text{effect of } \texttt{organ}} x_{5ij} + \xi_{ij} \end{aligned} \tag{6.1}$$

where the total residual ξ_{ij} has zero mean given the covariates.

If Garrett (1998) is right, we would expect a negative coefficient β_5 of `organ` (a detrimental effect of organization when the left-wing power index `leftpow` is 0) and a positive interaction β_6 (an increase in the beneficial effect of `organ` as `leftpow` increases) such that for high values of `leftpow`, the slope of `organ`, $\beta_5 + \beta_6 x_{4ij}$, is positive.

The data are clearly long panel because there are as many as 25 occasions but only 14 countries.

6.7.2 Marginal modeling for long panels

Until now in this book, we have assumed that the number of units (or more generally clusters) is large and that there are relatively few occasions. It was therefore possible to use many occasion-specific parameters to model the longitudinal covariance structure. In this short panel case, large-sample properties (asymptotics), such as the consistency of estimators, refer to the number of units going to infinity for a fixed number of occasions.

Now we will consider models where the roles of units and occasions are reversed. Residuals for different units at an occasion are now allowed to be correlated, possibly with an unstructured covariance matrix. In addition to such cross-sectional correlations, some of the models can also handle longitudinal correlations by including unit-specific autocorrelation parameters (and unit-specific residual variances). There are now a large number of unit-specific parameters and few occasion-specific parameters. Estimation therefore requires a large number of occasions. Because the number of parameters increases when the number of units increases, large-sample results are now based on the number of occasions going to infinity for a fixed number of units.

To accommodate both cross-sectional and longitudinal dependence of the residuals, Parks (1967) proposed using FGLS to fit a model with unstructured cross-sectional covariances and an AR(1) structure longitudinally with unit-specific autocorrelation parameters. If there are many more occasions than units, we can use Stata's `xtgls` command to fit these models using FGLS or IGLS, the latter with the `igls` option.

The number of variance and covariance parameters becomes large when flexible covariance structures are specified both cross-sectionally and longitudinally. Unfortunately, Beck and Katz (1995) have shown that estimated standard errors from FGLS can exhibit downward finite-sample bias in this case. Instead of fitting the Parks model by FGLS, Beck and Katz advocate estimating regression parameters using pooled OLS, assuming both cross-sectional and longitudinal independence. "Panel-corrected standard errors" are then obtained, which are robust to misspecification of the cross-sectional correlation but are not robust to misspecification of the longitudinal correlation structure (independence). To accommodate longitudinal dependence in the random part of the model, Beck and Katz also consider a model with a common autocorrelation parameter for all units; they suggest estimating the regression parameters using pooled OLS after applying a Prais–Winsten transformation to make the observations uncorrelated across occasions.

6.7.3 Fitting marginal models for long panels in Stata

These methods are implemented in Stata's `xtpcse` command. To investigate the research question, we follow Garrett (1998) and fit time-series–cross-sectional models because we have a long panel with 25 occasions and 14 units.

First, we read in the data and construct the interaction term `left_org` between `leftpow` and `organ`:

```
. use http://www.stata-press.com/data/mlmus3/garrett
. generate left_org = leftpow*organ
```

We then `xtset` the data using

```
. xtset country year
       panel variable:  country (strongly balanced)
        time variable:  year, 1966 to 1990
                delta:  1 year
```

We note that the data are strongly balanced with observations for each year for every country. We are then ready to use the `xtpcse` command to fit model (6.1) by pooled OLS and obtain panel-corrected standard errors:

```
. xtpcse gdp oild demand leftpow organ left_org
Linear regression, correlated panels corrected standard errors (PCSEs)
Group variable:   country                       Number of obs      =       350
Time variable:    year                          Number of groups   =        14
Panels:           correlated (balanced)         Obs per group: min =        25
Autocorrelation:  no autocorrelation                           avg =        25
                                                               max =        25
Estimated covariances      =       105          R-squared          =    0.1410
Estimated autocorrelations =         0          Wald chi2(5)       =     42.01
Estimated coefficients     =         6          Prob > chi2        =    0.0000
```

gdp	Panel-corrected Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
oildep	-15.2321	5.228694	-2.91	0.004	-25.48015	-4.98405
demand	.0049977	.0015394	3.25	0.001	.0019804	.0080149
leftpow	-1.483548	.2755847	-5.38	0.000	-2.023684	-.9434123
organ	-1.139716	.2234088	-5.10	0.000	-1.577589	-.7018423
left_org	.4547182	.0839526	5.42	0.000	.2901741	.6192624
_cons	5.919865	.583395	10.15	0.000	4.776432	7.063298

According to the fitted model, when left-wing power is zero, a unit increase in organization of the labor market produces a decrease of 1.14 in the mean growth of GDP (in percent), controlling for the other covariates. A unit increase in left-wing power decreases the mean by 1.48 when labor-market organization is zero, controlling for the other covariates. As the power of left-wing parties increases, the negative impact of organization of the labor market on GDP is reduced because the estimated interaction parameter associated with `left_org` is positive (equal to 0.45). When left-wing power is greater than 2.5 (= 1.139716/0.4547183), the effect of increasing organization of the labor market on growth becomes positive. Using a test based on panel-corrected standard errors, the interaction is significantly different from zero at the 5% level. Garrett's (1998) theory is hence supported by these data.

Identical estimates of the regression coefficients and almost identical estimated standard errors are obtained by using the `regress` command with the `vce(robust year)` option (output not shown).

Instead of assuming lack of longitudinal correlation when estimating the regression coefficients, we can let the total residual in model (6.1) have an AR(1) structure, $\xi_{ij} = \rho\xi_{i-1,j}+u_{ij}$, where ρ is a common autocorrelation parameter for all countries (previously, we referred to this autocorrelation parameter as α). We fit this model using the `xtpcse` command with the `correlation(ar1)` option:

```
. xtpcse gdp oild demand leftpow organ left_org, correlation(ar1)
Prais-Winsten regression, correlated panels corrected standard errors (PCSEs)
Group variable:   country                     Number of obs      =       350
Time variable:    year                        Number of groups   =        14
Panels:           correlated (balanced)       Obs per group: min =        25
Autocorrelation:  common AR(1)                               avg =        25
                                                             max =        25
Estimated covariances      =       105        R-squared          =    0.1516
Estimated autocorrelations =         1        Wald chi2(5)       =     31.55
Estimated coefficients     =         6        Prob > chi2        =    0.0000
```

gdp	Panel-corrected Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
oildep	-13.77227	6.587739	-2.09	0.037	-26.684	-.8605331
demand	.0060806	.0016414	3.70	0.000	.0028635	.0092977
leftpow	-1.46776	.3623476	-4.05	0.000	-2.177948	-.7575716
organ	-1.177444	.2934019	-4.01	0.000	-1.752502	-.6023872
left_org	.448846	.1112233	4.04	0.000	.2308524	.6668396
_cons	5.814019	.8076921	7.20	0.000	4.230971	7.397066
rho	.2958842					

We see that the autocorrelation parameter, called `rho` in the output, is estimated as 0.30. The estimate of the interaction is very similar to that produced by pooled OLS, and the interaction is still significant at the 5% level.

Garrett (1998) also included country-specific dummy variables in the model so that the estimated regression coefficients represent within-country effects. Instead of using an AR(1) structure to accommodate longitudinal dependence, he included the lag-1 of the response as a covariate in the fixed part of the model. However, he did not address the initial-conditions problem discussed in section 5.7.2.

When an exchangeable correlation structure is adequate both longitudinally and cross-sectionally, it is possible to specify a random intercept for occasion in addition to a random intercept for units. Such two-way error-components models or crossed random-effects models are discussed in chapter 9 (see also exercise 9.9). Asymptotics in this case rely on both the number of units and the number of occasions getting large.

6.8 Summary and further reading

In this chapter, we focused mostly on short panel data or longitudinal data; we summarize the issues concerning modeling of such data below. We also introduced methods for long panel data with few units and many occasions, where the challenge is to allow for cross-sectional correlations in addition to longitudinal correlations.

Three different marginal approaches for longitudinal data have been discussed: pooled OLS, GEE, and ML estimation. Pooled OLS corresponds to assuming uncorrelated residuals with constant variances when estimating regression coefficients and then making valid inferences regarding the coefficients based on robust standard errors. The covariance structure is not modeled but is treated as a nuisance. The original idea behind generalized estimating equations (GEE) is to do one better than pooled OLS by assuming a working correlation structure that may lead to efficiency improvements. However, due to robust standard errors invariably being used in GEE, the choice of correlation structure is not an important consideration in this approach either. In contrast, traditional ML estimation is accompanied by model-based standard errors, which explains the greater importance attached to specifying a reasonable covariance structure in ML estimation compared with GEE.

In linear models, all three approaches usually give nearly identical estimates of regression coefficients except when there are missing data and the probability of missingness depends on other responses. In the latter case, correct specification of the covariance structure is necessary for consistent estimation of regression coefficients (see exercise 6.6).

There is an overwhelming range of covariance structures available to choose from. When there are few (no more than 4) occasions with balance, an unstructured covariance matrix might be a good choice unless there are only a small number of subjects. With more occasions, a structured covariance matrix should generally be used to improve efficiency. The smaller the interval between occasions and the larger the number of occasions, the more likely it is that a decaying correlation structure is needed. However, correlations are unlikely to decay to zero, so combining random intercepts with autoregressive or Toeplitz structures may be a good idea. The combination of random intercept and exponential covariance structures is particularly attractive because it can be used with nonconstant time intervals. For balanced data and when there are not too many occasions, it may be worth checking whether the variance changes over time.

Marginal approaches are susceptible to the problem of subject-level confounding or level-2 endogeneity discussed in chapters 3 and 5, so inconsistent estimators of regression coefficients are produced if relevant covariates at the subject level are omitted.

Good books on marginal approaches to the analysis of panel and longitudinal data include Diggle et al. (2002), Hedeker and Gibbons (2006), and Fitzmaurice, Laird, and Ware (2011). Frees (2004, sec. 8.3) discusses methods for long panels (few units and many occasions). Weiss (2005) provides a particularly extensive discussion of different covariance structures for marginal modeling.

Exercises 6.1, 6.2, and 6.3 consider marginal modeling, and exercises 6.2 and 6.3 also consider random-intercept and random-coefficient models. More exercises on random-coefficient models can be found in the next chapter. Exercise 6.4 concerns the cross-sectional time-series approach to long panel data, and exercise 6.5 demonstrates the use of `xtmixed` for fitting multivariate regression models or seemingly unrelated regressions. Exercise 6.6 is a simulation study to investigate the consequences of misspecifying the covariance structure with and without missing data.

6.9 Exercises

6.1 Antisocial-behavior data

Consider the data from Allison (2005) that are described in exercise 5.2.

1. Find out if there are any missing values for the response variable `anti`.
2. Calculate a new variable, `time`, taking the values 0, 1, and 2 for the three time points.
3. Use pooled OLS to fit a linear model for `anti` with `time`, `pov`, `momage`, `female`, `childage`, `hispanic`, `black`, `momwork`, and `married` as covariates. Obtain robust standard errors that take the clustering of the data into account.
4. Now use GEE, again with robust standard errors.
   a. Use GEE with the same covariates as in step 3 but with the following correlation structures: unstructured, exchangeable, and AR(1). Store each set of estimates.
   b. Obtain the corresponding estimated correlation matrices and standard deviations. Comparing the two restricted correlation matrices with the unstructured ones, which restricted structure seems to be more reasonable?
   c. Do the estimated regression coefficients change appreciably when different working correlation structures are used? Does their significance at the 5% level change? (Hint: Use `estimates table` with the `star` option to compare the estimates.)
   d. How would you use GEE to obtain the pooled OLS estimates in step 2?
5. Use `xtmixed` to fit the models in step 4 by ML and obtain the estimated residual standard deviations and correlations.
6. Fit a random-coefficient model with the same covariates as in step 3 and with a child-specific random intercept and slope of `time`.
7. ❖ Derive the three residual variances and correlations implied by the random-coefficient model (by hand) and compare them with the estimates from step 5.

6.2 Postnatal-depression data Solutions

The dataset to be analyzed in this exercise comes from a clinical trial of the use of estrogen patches in the treatment of postnatal depression; full details are given in Gregoire et al. (1996).

In total, 61 women with major depression, which began within 3 months of childbirth and persisted for up to 18 months postnatally, were randomly assigned to the active treatment (an estrogen patch) or a placebo (a dummy patch). Thirty-four women received the former and the remaining 27 received the latter.

The women were assessed pretreatment and monthly for six months after treatment using the Edinburgh postnatal depression scale (EPDS), with possible scores from 0 to 30 and with a score of 10 or greater interpreted as possible depression. Noninteger depression scores result from missing questionnaire items (in this case, the average of all available items was multiplied by the total number of items).

The main research question is whether the estrogen patch is effective at reducing postnatal depression compared with the placebo.

The following variables are in the dataset `postnatal.dta` that was supplied by Rabe-Hesketh and Everitt (2007):

- `subj`: patient identifier
- `group`: treatment group (1: estrogen patch; 0: placebo patch)
- `pre`: pretreatment or baseline EPDS depression score
- `dep1` to `dep6`: EPDS depression scores for months 1 to 6

The mean structure of all models considered in this exercise should include a term for treatment group and a term for a linear time trend (where time starts at 0 for the first posttreatment visit). Note that the treatment by time interaction is not significant at the 5% level. Use `xtmixed` to fit each of the models mentioned below by ML, followed by `estimates store` to store the results.

1. Start by preparing the data for analysis.
   a. Reshape the data to long form.
   b. Missing values for the depression scores are coded as -9 in the dataset. Recode these to Stata's missing-value code. (You may want to use the `mvdecode` command.)
   c. Use the `xtdescribe` command to investigate missingness patterns. Is there any intermittent missingness?
2. Fit a model with an unstructured residual covariance matrix. Store the estimates (also store estimates for each of the models below).
3. Fit a model with an exchangeable residual covariance matrix. Use a likelihood-ratio test to compare this model with the unstructured model.
4. Fit a random-intercept model and compare it with the model with an exchangeable covariance matrix.

5. Fit a random-intercept model with AR(1) level-1 residuals. Compare this model with the ordinary random-intercept model using a likelihood-ratio test.
6. Fit a model with a Toeplitz(5) covariance structure (without a random intercept). Use likelihood-ratio tests to compare this model with each of the models fit above that are either nested within this model or in which this model is nested. (Stata may refuse to perform a test if it thinks the models are not nested. If you are sure the models are nested, use the `force` option.)
7. Fit a random-coefficient model with a random slope of time. Use a likelihood-ratio test to compare the random-intercept and random-coefficient models.
8. Specify an AR(1) process for the level-1 residuals in the random-coefficient model. Use likelihood-ratio tests to compare this model with the models you previously fit that are nested within it.
9. Use the `estimates stats` command to obtain a table including the AIC and BIC for the fitted models. Which models are best and second best according to the AIC and BIC?

6.3 Adolescent-alcohol-use data

Singer and Willett (2003) analyzed a dataset from Curran, Stice, and Chassin (1997). As part of a larger study of substance abuse, 82 adolescents were interviewed yearly from ages 14–16 and asked about their alcohol consumption during the previous year. Specifically, they were asked to report the frequency in the past 12 months of each of the following behaviors on an 8-point scale from 0 (not at all) to 7 (every day):

1. drinking wine or beer
2. drinking hard liquor
3. drinking five or more drinks in a row
4. getting drunk

Following Singer and Willett, we will use the square root of the mean of these four items as the response variable.

At age 14, the adolescents were also asked how many of their peers drank alcohol 1) occasionally and 2) regularly over the past 12 months, with each answer scored on a 6-point rating scale from 0 (none) to 5 (all). The square root of the mean of these two items was used as a covariate.

The original sample comprised 246 children of alcoholics (recruited through court records, wellness questionnaires from health maintenance organizations, and community telephone surveys) and 208 demographically matched controls. For the children of alcoholics, at least one biological and custodial parent had to have a lifetime Diagnostic Interview Schedule III (DSM-III) diagnosis of alcohol abuse or dependence.

The dataset `alcuse.dta` has the following variables:

- `id`: identifier for the adolescents

- `alcuse`: frequency of alcohol use (square root of mean on four alcohol items)
- `age_14`: age − 14, number of years since first interview (t_i)
- `coa`: dummy variable for being a child of an alcoholic (w_{1j})
- `peer`: alcohol use among peers at age 14 (square root of mean of two items) w_{2j}

In this exercise, we will consider a sequence of models with different marginal covariance structures. All models have the same mean structure, which includes the adolescent-level covariates `coa` and `peer` and their interaction with `age_14`.

1. Fit the following sequence of models using ML in `xtmixed` and store the estimates for each model:
   a. An AR(1) model for the total residuals.
   b. A random-intercept model.
   c. A random-intercept model with an AR(1) process for the level-1 residuals.
   d. A random-intercept model allowing the level-1 residuals to be heteroskedastic over years since first interview.
   e. A random-coefficient model with a random slope of number of years since first interview.
   f. A random-coefficient model with an AR(1) process for the level-1 residuals.
   g. A random-coefficient model with heteroskedastic level-1 residuals over years since first interview.
   h. A model with an unstructured residual covariance matrix.
2. Use the `estimates stats` command to obtain a table that includes the AIC and BIC for the fitted models. Which model is the best according to the AIC and BIC?

Growth-curve models are applied to this dataset in exercise 7.7.

6.4 ❖ Cigarette-consumption data

Baltagi, Griffin, and Xiong (2000) investigated how cigarette prices and disposable income affect cigarette consumption using annual data for 1963 to 1992 for 46 U.S. states.

The dataset `cigar.dta` from Baltagi (2008) includes the following variables:

- `state`: identifier for U.S. state (j)
- `name`: abbreviated name of U.S. state
- `year`: year from 1963–1992 (i)
- `price`: average retail price of pack of cigarettes in U.S. dollars
- `pop`: population size
- `pop16`: population size above 16 years
- `CPI`: consumer price index (reference value of 100 in 1983)
- `NDI`: per capita annual disposable income in U.S. dollars

- `c`: cigarette sales in packs per capita per year (by persons of smoking age; 14 years or older)
- `pimin`: minimum price per pack of cigarettes in adjoining states in U.S. dollars

In this kind of long panel data for macro units, it is often of interest to accommodate potential cross-sectional dependence between states when estimating standard errors. All models will be fit using `xtpcse` but with different approaches to handling cross-sectional and longitudinal correlations.

1. `xtset` the data.
2. The consumer price index is a weighted average of prices of a basket of consumer goods and services. In this dataset, `CPI` is 100 times the consumer price index in a given year divided by the consumer price index in 1983. Convert `price`, `pimin` and `NDI` to 1983 U.S. dollars using the consumer price index. Such real prices and real income are adjusted for inflation over years. In the analyses below, you will use the natural logarithms of real prices and real disposable income.
3. Let the response variable be the logarithm of the number of packs of cigarettes sold per person of smoking age. Consider models where the mean structure contains the following covariates: the logarithm of real cigarette price, the logarithm of real disposable income, the logarithm of real minimum price in adjoining states (a proxy for casual smuggling across states), and year (treated as continuous).
    a. Fit a regression model with estimated standard errors based on assuming that there are neither cross-sectional nor longitudinal correlations. First use the `regress` command and then use `xtpcse` with the `correlation(independent)` and `independent` options; the first option implies longitudinal independence and the second option implies cross-sectional independence. Also specify the `nmk` option to base standard errors on 'n minus k' (number of observations minus number of estimated parameters) as in standard linear regression. The parameter estimates and the estimated standard errors produced by the two commands should be identical.
    b. Use `xtpcse` with the `correlation(independent)` option but not the `independent` option to accommodate cross-sectional correlations among states when estimating standard errors. (Regression coefficients are estimated by pooled OLS.) Compare the magnitude of the estimated standard errors to those assuming no correlations.
    c. Use `xtpcse` with the `correlation(ar1)` option to fit a model with longitudinal correlation, specified as an AR(1) process with autocorrelation parameter ρ for the residuals. This accommodates cross-sectional as well as longitudinal correlations among states.
        i. Why have the estimated coefficients changed compared with step 3b above?

ii. Interpret the estimated coefficients. When the response variable is a logarithmic transformation, the coefficients associated with covariates that are logarithmic transformations can be interpreted as elasticities (% change in the expectation of response for a 1% change in the covariate); see display 6.2.

d. Use `xtgls` with the `panels(correlated)` and `corr(ar1)` options to fit the same model as in step 3c by FGLS.
   i. How many variance and covariance (or correlation) parameters are estimated?
   ii. Compare the estimated coefficients and their estimated standard errors with those from the previous step.

Consider a linear regression model where the response variable y_i and a covariate x_i are both log-transformed:

$$\ln y_i = \beta_1 + \beta_2 \ln x_i + \cdots + \epsilon_i$$

The logarithm of the conditional expectation of y_i given the covariates then is (see display 1.1 on page 64)

$$\ln\{E(y_i|\mathbf{x}_i)\} \;=\; \beta_1 + \sigma^2/2 + \beta_2 \ln x_i + \cdots$$

Taking derivatives with respect to x_i (using the chain rule), we find that

$$\frac{\partial \ln E(y_i|\mathbf{x}_i)}{\partial x_i} \;=\; \frac{1}{E(y_i|\mathbf{x}_i)} \frac{\partial E(y_i|\mathbf{x}_i)}{\partial x_i} \;=\; \beta_2 \frac{1}{x_i}$$

so that the elasticity is

$$\frac{\partial E(y_i|\mathbf{x}_i)}{E(y_i|\mathbf{x}_i)} \Big/ \frac{\partial x_i}{x_i} \;=\; \beta_2$$

The regression coefficient can therefore be interpreted as the relative change in the conditional expectation of y_i associated with unit relative change in x_i. Note, however, that this is the correct effect only for small changes in x_i.

Display 6.2: Elasticities

See exercise 9.9 for further analysis of this dataset.

6.5 ❖ Wages-and-fringe-benefits data

Wooldridge (2010) analyzed and provided a subset of data from the 1977 Quality of Employment Survey. The survey recruited workers aged 16 and older who were working for pay for 20 or more hours per week.

The variables in `fringe.dta` that we will use here are the following:

- `hrearn`: hourly wages in U.S. dollars

- `hrbens`: hourly fringe benefits in U.S. dollars, including value of vacation days, sick leave, employee insurance, and employee pension
- `educ`: years of schooling
- `exper`: years of work experience
- `expersq`: years of work experience squared
- `tenure`: number of years with the current employer
- `tenuresq`: number of years with the current employer squared
- `union`: dummy variable for being a union member
- `south`: dummy variable for living in the south of the U.S.
- `nrtheast`: dummy variable for living in the northeast of the U.S.
- `nrthcen`: dummy variable for living in the north central U.S.
- `married`: dummy variable for being married
- `white`: dummy variable for being white
- `male`: dummy variable for being male

Wooldridge considered a bivariate model for wages and fringe benefits, where fringe benefits are the total value of employee benefits including vacation days, sick leave, insurance, and pension. Annual wages and annual fringe benefits were divided by the total number of hours worked per year to obtain hourly wages, `hrearn`, and hourly benefits, `hrbens`. Each response variable was regressed on `educ`, `exper`, `expersq`, `tenure`, `tenuresq`, `union`, `south`, `nrtheast`, `nrthcen`, `married`, `white`, and `male`, giving two regression equations, each with its own set of regression coefficients. The residual error terms for the two regressions had different variances and were allowed to be correlated (a positive correlation would be expected because ability and other unobserved covariates that increase wages would also be expected to increase fringe benefits).

The model is a bivariate linear regression model (because of the correlation between the two response variables). Econometricians often call such models seemingly unrelated regression (SUR) models because the only aspect connecting the equations is the residual correlation (neither response variable appears as a covariate in the other equation, and there are typically no constraints across equations).

An advantage of joint instead of separate modeling of the two response variables is that hypotheses across equations can be tested. For instance, we can test the joint null hypothesis that there is no gender gap for earnings and that there is no gender gap for benefits. Using one such joint test for two or more response variables has the advantage that multiple testing (one test for each response variable) and the resulting increase in type I error are avoided.

1. Fit the model using `mvreg` with the `corr` option (see `help mvreg`). What is the estimated residual correlation? Interpret the relationship between experience and wages, and compare it with the relationship between experience and benefits.
2. Fit the model using `sureg` with the `corr` option (see `help sureg`). Are there any differences between the estimates from step 1 and step 2?

3. Fit the model using `xtmixed`.
   a. Stack `hrearn` and `hrbens` into one variable by using the `reshape` command.
   b. Form dummy variables `e_` for the observations corresponding to `hrearn` and `f_` for the observations corresponding to `hrbens`.
   c. Form interactions between all the covariates and the two dummy variables, `e_` and `f_`. (To avoid a large block of commands, you can use `foreach var of` *varlist*; see page 154 for an example.)
   d. Now fit the model by ML using `xtmixed`, treating subjects as clusters and the identifier for the two response variables as the `t()` variable in the `residuals()` option.
4. Compare the estimates from step 3 with those from steps 1 and 2. Note that in contrast to `mvreg` and `sureg`, `xtmixed` uses ML estimation. Unlike the other commands, `xtmixed` uses the response for wages if someone's response for benefits is missing and vice versa, which yields consistent estimates under the missing at random (MAR) assumption (see section 5.8).
5. Use `testparm` to test whether there is a gender gap in wages or benefits (that is, simultaneously test two hypotheses for both response variables) after controlling for the other covariates.
6. Test whether there are regional differences in wages or benefits after controlling for the other covariates.

See also exercise 8.9 for an example of a multivariate multilevel model.

6.6 Simulation study

In this exercise, we simulate data with a particular covariance structure and then fit marginal models by ML with both the correct and several incorrect covariance structures. We also use pooled OLS. We then repeat the exercise, this time creating missing data where missingness depends on the response at the first occasion. (See also section 5.8.1 for a simulation study.)

1. Simulate data for 1,000 subjects and three occasions with mean structure

$$E(y_{ij}|t_{ij}) \;=\; \beta_1 + \beta_2 t_{ij}$$

   setting $\beta_1 = 0$ and $\beta_2 = 0$, and with an exchangeable residual covariance matrix with standard deviations equal to 2 and correlations equal to 0.5. You may use the following commands:

```
clear
set seed 1231214
set obs 1000
matrix define R = (1, .5, .5 \ .5, 1, .5 \ .5, .5, 1)
matrix list R
matrix define s = (2,2,2)
drawnorm y1 y2 y3, sds(s) corr(R)
generate id = _n
reshape long y, i(id) j(time)
```

Here the `drawnorm` command simulates variables—with names `y1`, `y2`, and `y3`—from a multivariate normal distribution with zero means (the default), standard deviations 2 (given in the row matrix `s`), and correlation matrix `R`. The `matrix define` commands are used to define the matrices `R` and `s` element by element. For the `R` matrix, the elements are given in the order R_{11}, R_{12}, R_{13}, R_{21}, etc., with elements separated by commas and rows separated by backslashes. We can think of this model as having the mean structure $\beta_1 + \beta_2 t_{ij}$ when both coefficients are zero because this gives zero mean at each occasion. (If you have a fast computer, you can also simulate 10,000 or more subjects to be able to better judge consistency of point estimates.)

2. Fit models with the same mean structure as the simulated data, treating β_1 and β_2 as parameters to be estimated.
   a. Use ML estimation with the correct covariance structure.
   b. Use ML estimation with a Toeplitz(1) covariance structure.
   c. Use ML estimation with an AR(1) covariance structure.
   d. Use pooled OLS with robust standard errors.
3. Compare the estimated slope of `time` with the true slope for each model. Are there important differences? Do the estimated standard errors of the slope differ substantially between models? Explain the findings.
4. Now create missing values by dropping observations at occasions 2 and 3 with probability 0.8 if the subject's response at occasion 1 is greater than 1. You may use these commands:

```
generate rand = runiform()
by id (time): generate firsty = y[1]
drop if firsty>1 & rand<.8 & time>1
```

5. Investigate the missingness patterns using `xtdescribe`.
6. Produce a table of means and sample sizes at the three occasions. Explain what you find.
7. Fit models with the same mean structure as the simulated data, treating β_1 and β_2 as parameters to be estimated.
   a. Use ML estimation with the correct covariance structure.
   b. Use ML estimation with a Toeplitz(1) covariance structure.
   c. Use ML estimation with an AR(1) covariance structure.
   d. Use pooled OLS with robust standard errors.
8. Compare the estimated slope of `time` with the true slope for each model. Are there important differences? Explain the findings, including the direction of any difference between estimate and truth, and how this may have come about, taking into account the estimated correlation matrix.
9. ❖ Design your own simulation study, for instance, simulating with an AR(1) structure and fitting the models above, or changing the probability of missingness.

6.7 Variances and correlations of total residual in random-coefficient model

Consider a random-coefficient model with a random intercept and random slope of time, where time takes on the values $t_{1j} = 0$, $t_{2j} = 1$, and $t_{3j} = 2$. The covariance matrix of the intercept and slope is estimated as

$$\widehat{\boldsymbol{\Psi}} = \begin{bmatrix} 4 & 1 \\ 1 & 2 \end{bmatrix}$$

and the level-1 residual variance is estimated as

$$\widehat{\theta} = 1$$

1. Calculate the estimated model-implied variance of the total residual

$$\xi_{ij} \;=\; \zeta_{1j} + \zeta_{2j} t_{ij} + \epsilon_{ij}$$

   for the three time points.
2. Calculate the estimated model-implied correlation matrix.

6.8 ❖ Covariance structure for random-intercept model with AR(1) errors

Consider a random-intercept model with level-1 errors following an AR(1) process.

1. Using the information that $\text{Var}(\epsilon_{ij}) = \frac{\sigma_e^2}{1-\alpha^2}$ and $\text{Cov}(\epsilon_{ij}, \epsilon_{i'j}) = \frac{\sigma_e^2}{1-\alpha^2}\alpha^{|i-i'|}$, derive an expression for the variance $\text{Var}(\xi_{ij})$ and covariance $\text{Cov}(\xi_{ij}, \xi_{i'j})$, where $\xi_{ij} = \zeta_j + \epsilon_{ij}$ and $\text{Var}(\zeta_j) = \psi$. ($\zeta_j$ and ϵ_{ij} are uncorrelated with each other and across subjects j and occasions i.)
2. Describe the covariance and correlation structure.
3. Calculate the standard deviations and correlation matrix for four equally spaced occasions for the case $\alpha = 0.6$, $\sigma_e^2 = 1$, and $\psi = 1$.

7 Growth-curve models

7.1 Introduction

In this chapter, we discuss perhaps the most prominent multilevel approach to longitudinal data, so-called *growth-curve models*, also sometimes referred to as *latent-trajectory models* or *latent growth-curve models*. Many people find this approach to longitudinal or panel modeling attractive because it explicitly models the shape of trajectories of individual subjects over time and how these trajectories vary, both systematically, due to occasion-level and subject-level covariates, and randomly. A somewhat flamboyant expression for this kind of modeling is to study *interindividual differences in intraindividual change*.

Growth-curve models are a special case of random-coefficient models where it is the coefficient of time that varies randomly between subjects. Random-coefficient models were discussed in chapter 4 and in sections 5.5 and 6.3.3 of the previous two chapters. That material can be viewed as sufficient background for standard linear growth-curve modeling, whereas the present chapter covers more advanced topics.

We first use growth-curve models to study children's physical growth, and we illustrate two different ways of modeling nonlinear growth, using polynomial functions and piecewise linear functions. How to handle heteroskedasticity or complex variation is also discussed both for the level-1 residuals and for random effects. Growth-curve models are subsequently applied to balanced panel data on growth in reading ability from kindergarten through third grade. In the balanced case, we show how growth-curve models can alternatively be expressed as structural equation models with latent variables and can be fit using Stata's `sem` command.

7.2 How do children grow?

The dataset considered here is on Asian children in a British community who were weighed on up to four occasions, roughly at ages 6 weeks, and then 8, 12, and 27 months. The dataset `asian.dta` is a 12% random sample, stratified by gender, from the dataset `asian.dat` available from the webpage of the Centre for Multilevel Modelling.[1] The full data were previously analyzed by Prosser, Rasbash, and Goldstein (1991).

1. See http://www.cmm.bristol.ac.uk/learning-training/multilevel-m-support/datasets.shtml.

The dataset `asian.dta` has the following variables:

- `id`: child identifier (j)
- `weight`: weight in kilograms (y_{ij})
- `age`: age in years (t_{ij})
- `gender`: gender (1: male; 2: female) (w_j)

The data are read in using

```
. use http://www.stata-press.com/data/mlmus3/asian
```

We want to investigate the growth trajectories of childrens' weights as they get older. Both the shape of the trajectories and the degree of variability in growth among the children are of interest.

7.2.1 Observed growth trajectories

We start by plotting the observed growth trajectories (connecting the observations by straight lines) by gender, after defining value labels for `gender` to make them appear on the graph:

```
. label define g 1 "Boy" 2 "Girl"
. label values gender g
. sort id age
. graph twoway (line weight age, connect(ascending)),
> by(gender) xtitle(Age in years) ytitle(Weight in Kg)
```

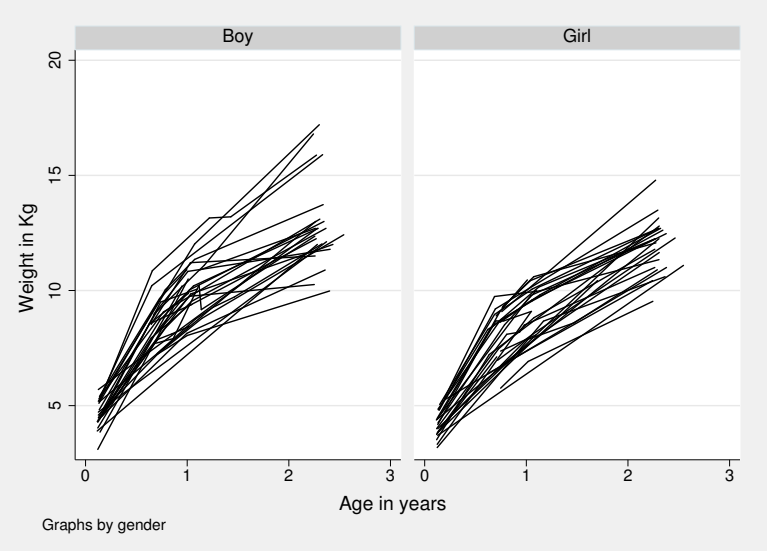


Figure 7.1: Observed growth trajectories for boys and girls

From figure 7.1, it is clear that the growth trajectories are nonlinear; growth is initially fast and then slows down. We will consider two methods of modeling this nonlinearity: polynomials and piecewise linear functions.

7.3 Models for nonlinear growth

7.3.1 Polynomial models

Growth trajectories can take a variety of shapes. A flexible approach to modeling possibly nonlinear growth in y_{ij} is to use a pth degree polynomial function of time t_{ij},

$$y_{ij} = \underbrace{\beta_1}_{\text{constant}} + \underbrace{\beta_2 t_{ij}}_{\text{linear}} + \underbrace{\beta_3 t_{ij}^2}_{\text{quadratic}} + \underbrace{\beta_4 t_{ij}^3}_{\text{cubic}} + \underbrace{\beta_5 t_{ij}^4}_{\text{quartic}} + \cdots + \beta_{p+1} t_{ij}^p + \xi_{ij}$$

where the names of the most commonly used terms are given below the braces and the random part of the model is represented by the term ξ_{ij}. A quadratic function will include a quadratic term and all terms of lower degree (a linear term and a constant), a cubic function includes a cubic term and all terms of lower degree, and so on.

An illustration of linear, quadratic, cubic, and quartic functions fit to the same data is given in figure 7.2. The largest number of extrema (maxima and minima) that can occur is $p - 1$, and they may not all occur within the range of the data. So a quadratic curve can have at most one maximum or minimum, a cubic curve can have at most one maximum and one minimum, etc. For low-degree polynomials, rapid changes in curvature are not possible. We see that these restrictions can cause artifacts in the fitted curve, such as the quadratic and cubic curves in figure 7.2 declining much sooner than the quartic curve.

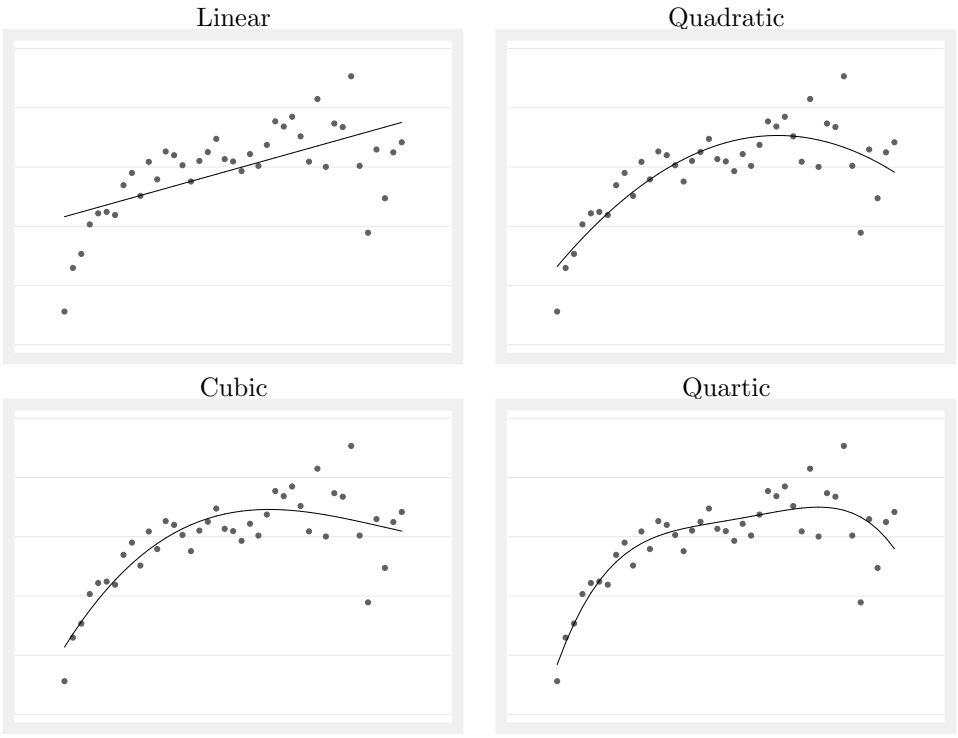


Figure 7.2: Illustration of different polynomial functions

It generally does not make sense to set the coefficients of lower-degree terms to zero while retaining higher-degree terms. This is because the implied restriction on the shape of the curve is usually not of interest and would only hold if the origin of the time scale is in a certain position. For instance, in a linear function, setting the intercept to zero implies that the line is at zero when time is zero; in a quadratic function, setting the coefficient of the linear term to zero implies that the minimum or maximum of the curve occurs when time is zero.

For balanced data with the same timing of occasions across subjects and a maximum of n occasions per subject (the number per person may vary because of missing data), a polynomial of degree $n-1$ will produce fitted means that are equal to the corresponding sample means at each occasion. It is therefore not possible to fit higher than $(n-1)$-degree polynomials in this case.

Fitting the models

We first model the nonlinearity in the growth trajectories by including a quadratic term for `age` in the model, giving a second-degree polynomial. It is also expected that boys and girls differ in their mean weight at any given age and that children vary in the initial weight and rate of growth. We therefore consider the model

$$y_{ij} = \beta_1 + \beta_2 w_j + \beta_3 t_{ij} + \beta_4 t_{ij}^2 + \zeta_{1j} + \zeta_{2j} t_{ij} + \epsilon_{ij} \tag{7.1}$$

where y_{ij} is the weight, t_{ij} is the age of child j at occasion i, w_j is a dummy variable for being a girl, and ζ_{1j} and ζ_{2j} are a random intercept and random slope, respectively. The occasion-specific error term ϵ_{ij} allows the responses y_{ij} to deviate from the perfectly quadratic trajectories defined by the first four terms.

The usual assumptions for random-coefficient models (discussed in section 4.4.1) are made throughout this chapter. Point estimates and standard errors of regression coefficients are consistent if the mean structure (the fixed part of the model) and the covariance structure of the total residual are correctly specified.

We construct a dummy variable, `girl`, for the child being a girl:

```
. recode gender 2=1 1=0, generate(girl)
```

We also construct the variable `age2` for age squared:

```
. generate age2 = age^2
```

The model can then be fit in `xtmixed` using

```
. xtmixed weight girl age age2 || id: age, covariance(unstructured) mle
Mixed-effects ML regression                     Number of obs      =       198
Group variable: id                              Number of groups   =        68
                                                Obs per group: min =         1
                                                               avg =       2.9
                                                               max =         5
                                                Wald chi2(3)       =   1975.44
Log likelihood = -253.86692                     Prob > chi2        =    0.0000
```

weight	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
girl	-.5960093	.196369	-3.04	0.002	-.9808854	-.2111332
age	7.697967	.2382121	32.32	0.000	7.23108	8.164854
age2	-1.657843	.0880529	-18.83	0.000	-1.830423	-1.485262
_cons	3.794769	.1655053	22.93	0.000	3.470385	4.119153

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
id: Unstructured				
sd(age)	.5097091	.0871791	.3645319	.7127041
sd(_cons)	.5947313	.128989	.3887827	.9097764
corr(age,_cons)	.1571078	.3240797	-.4564673	.6694134
sd(Residual)	.57233	.0496273	.4828786	.678352

```
LR test vs. linear regression:       chi2(3) =   104.17   Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference.
```

and we store the estimates using

```
. estimates store rc
```

We see that girls weigh on average about 0.6 kg less than boys of the same age. The coefficients of both `age` and `age2` are significant at the 5% level. The growth curve moves up at 0 (because of the positive coefficient of `age`) but the rate of growth declines (because of the negative coefficient of `age2`). There is a considerable estimated random-intercept standard deviation of 0.59 kg. The mean increase in weight per month varies with a standard deviation of 0.51 kg per month. The estimates are also shown under "Model 1: Polynomial" in table 7.1.

Note that we have included a higher-degree polynomial in the fixed part of the model than in the random part. This is often a good idea because there may be insufficient within-subject information to estimate the variability in the coefficients of higher powers of time, here the variability in the curvature of the relationships. If we also include a random slope for `age2`, which implies three extra parameters for the random part (one variance and two covariances), we obtain the following:

```
. xtmixed weight girl age age2 || id: age age2, covariance(unstructured) mle
Mixed-effects ML regression                     Number of obs      =       198
Group variable: id                              Number of groups   =        68
                                                Obs per group: min =         1
                                                               avg =       2.9
                                                               max =         5
                                                Wald chi2(3)       =   2159.56
Log likelihood = -241.01654                     Prob > chi2        =    0.0000
```

weight	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
girl	-.450187	.1582819	-2.84	0.004	-.7604139	-.1399602
age	7.790089	.2585223	30.13	0.000	7.283395	8.296784
age2	-1.700954	.1017658	-16.71	0.000	-1.900412	-1.501497
_cons	3.703218	.1200624	30.84	0.000	3.4679	3.938536

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
id: Unstructured				
sd(age)	1.350001	.3137402	.8560894	2.128898
sd(age2)	.5173013	.1234178	.3240886	.8257021
sd(_cons)	.1911551	.2846017	.0103293	3.537521
corr(age,age2)	-.9193943	.0427844	-.9719891	-.7791064
corr(age,_cons)	.7019993	1.97522	-.9999973	.9999999
corr(age2,_cons)	-.4414962	1.581981	-.9996501	.9976714
sd(Residual)	.4706363	.0497117	.3826273	.5788885

```
LR test vs. linear regression:       chi2(6) =   129.87   Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference.
```

The model converges (after 13 iterations, not shown), but the confidence intervals for the last two correlations cover nearly the entire range. There seems to be insufficient information to reliably estimate these correlations, and we will return to the model with a quadratic fixed part and linear random part:

```
. estimates restore rc
```

In general, it is perfectly reasonable to allow only the lower-order terms of the polynomial used in the fixed part of the model to vary randomly between subjects.

Table 7.1: Maximum likelihood estimates of random-coefficient models for children's growth data (in kilograms)

	Model 1: Polynomial		Model 2: Piecewise linear	
	Est	(SE)	Est	(SE)
Fixed part				
β_1 [`_cons`]	3.79	(0.17)	3.37	(0.22)
β_2 [`girl`]	−0.60	(0.20)	-0.64	(0.19)
β_3 [`age`] or [`ages1`]	7.70	(0.24)	9.94	(1.07)
β_4 [`age2`] or [`ages2`]	−1.66	(0.09)	4.44	(0.75)
β_5 [`ages3`]			2.34	(0.64)
β_6 [`ages4`]			2.21	(0.36)
Random part				
$\sqrt{\psi_{11}}$	0.59		0.66	
$\sqrt{\psi_{22}}$ [`age`]	0.51		0.57	
ρ_{21}	0.16		−0.04	
$\sqrt{\theta}$	0.57		0.49	
Log likelihood	−253.87		−242.00	

Predicting the mean trajectory

Except in the linear case, it is not easy to understand the shape of a polynomial without plotting it. To visualize the mean curve for boys, we produce a graph, shown in figure 7.3:

```
. twoway (function Weight=_b[_cons]+_b[age]*x+_b[age2]*x^2,
>        range(0.1 2.6)), xtitle(Age in years) ytitle(Weight in Kg)
>        yscale(range(0 20)) ylab(0(5)20)
```

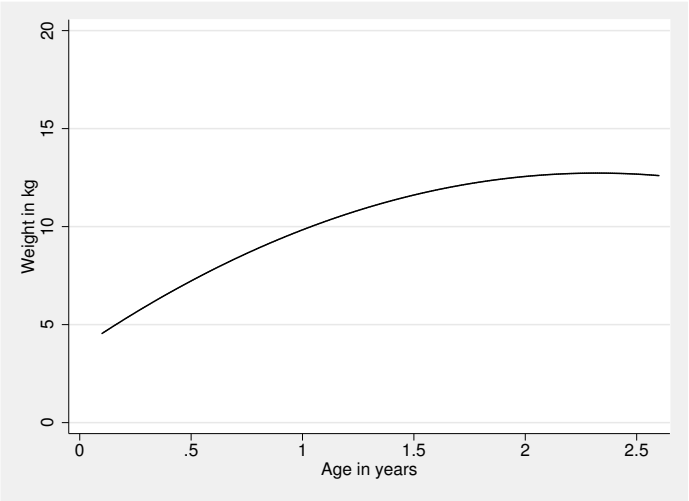


Figure 7.3: Mean trajectory for boys from quadratic model

(We have scaled the y axis from 0 to 20 to facilitate comparison with curves we will produce later.)

To visualize the variability in the growth curves implied by the model, we add the limits of the range within which 95% of the subject-specific growth curves are expected to lie. We first calculate the estimated standard deviation of $\zeta_{1j}+\zeta_{2j}t_{ij}$ which is given by $\sqrt{\widehat{\psi}_{11}+2\widehat{\psi}_{21}t_{ij}+\widehat{\psi}_{22}t_{ij}^2}$. We can display the required variance and covariance estimates to plug into this expression by using

```
. estat recovariance
Random-effects covariance matrix for level id
```

	age	_cons
age	.2598033	
_cons	.0476257	.3537053

A more elegant approach is to access the logarithms of the standard deviations by using `[lns1_1_1]_cons` and `[lns1_1_2]_cons` and access the arc tanh of the correlation (often called Fisher's z transformation) by using `[atr1_1_1_2]_cons` (to find out which labels to use, run `xtmixed` with the `estmetric` option, as shown in section 2.11.2). We calculate the variances and covariance below, storing the values in the *scalars* `var1`, `var2`, and `cov`:

```
. scalar var1 = exp(2*[lns1_1_1]_cons)
. scalar var2 = exp(2*[lns1_1_2]_cons)
. scalar cov = tanh([atr1_1_1_2]_cons)*sqrt(var1*var2)
```

We can now use these scalars within the `twoway function` command, which produces figure 7.4 for boys:

```
. twoway (function Weight=_b[_cons]+_b[age]*x+_b[age2]*x^2,
>         range(0.1 2.6) lwidth(medium))
>        (function upper=_b[_cons]+_b[age]*x+_b[age2]*x^2
>         +1.96*sqrt(var1+2*cov*x+var2*x^2), range(0.1 2.6) lpatt(dash))
>        (function lower=_b[_cons]+_b[age]*x+_b[age2]*x^2
>         -1.96*sqrt(var1+2*cov*x+var2*x^2), range(0.1 2.6) lpatt(dash)),
>        legend(order(1 "Mean" 2 "95% range")) xtitle(Age in years)
>        ytitle(Weight in kg) yscale(range(0 20)) ylab(0(5)20)
```

To obtain the corresponding figure for girls, add `_b[girl]` to the fixed part of the model.

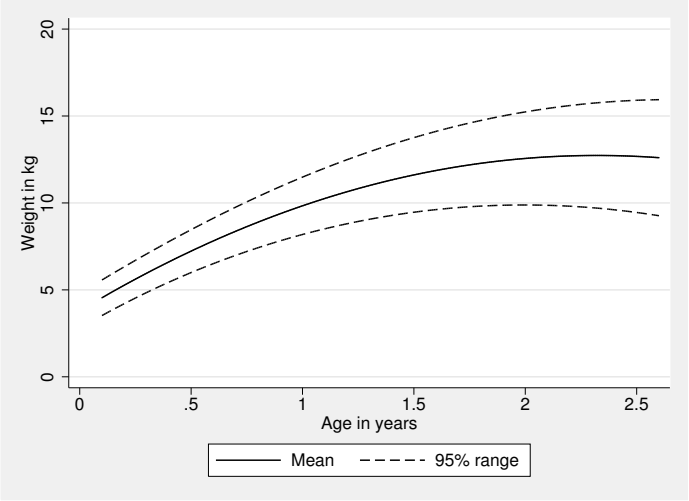


Figure 7.4: Mean trajectory and 95% range of subject-specific trajectories for boys from quadratic model

Predicting trajectories for individual children

After estimation with `xtmixed`, the predicted trajectories—based on substituting empirical Bayes (EB) predictions $\widetilde{\zeta}_{1j}$ and $\widetilde{\zeta}_{2j}$ for the random intercepts and random slopes—can be obtained using `predict` with the `fitted` option:

```
. predict traj, fitted
```

We can plot these predicted trajectories together with the observed responses using a *trellis graph*, a graph containing a separate two-way plot for each subject. This is accomplished using the `by(id)` option. For girls, we use the command

```
. twoway (scatter weight age) (line traj age, sort) if girl==1,
>        by(id, compact legend(off))
```

and similarly for boys. The graphs are shown in figures 7.5 and 7.6 for girls and boys, respectively, and suggest that the model fits well.

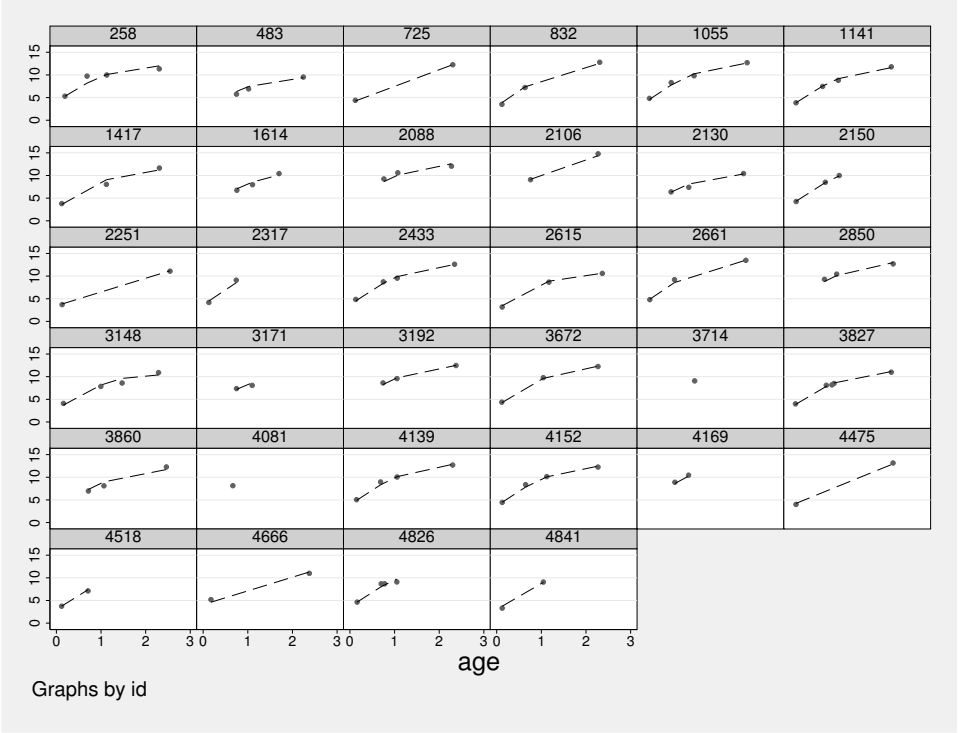


Figure 7.5: Trellis graph of observed responses (dots) and predicted trajectories (dashed lines) from quadratic model for girls

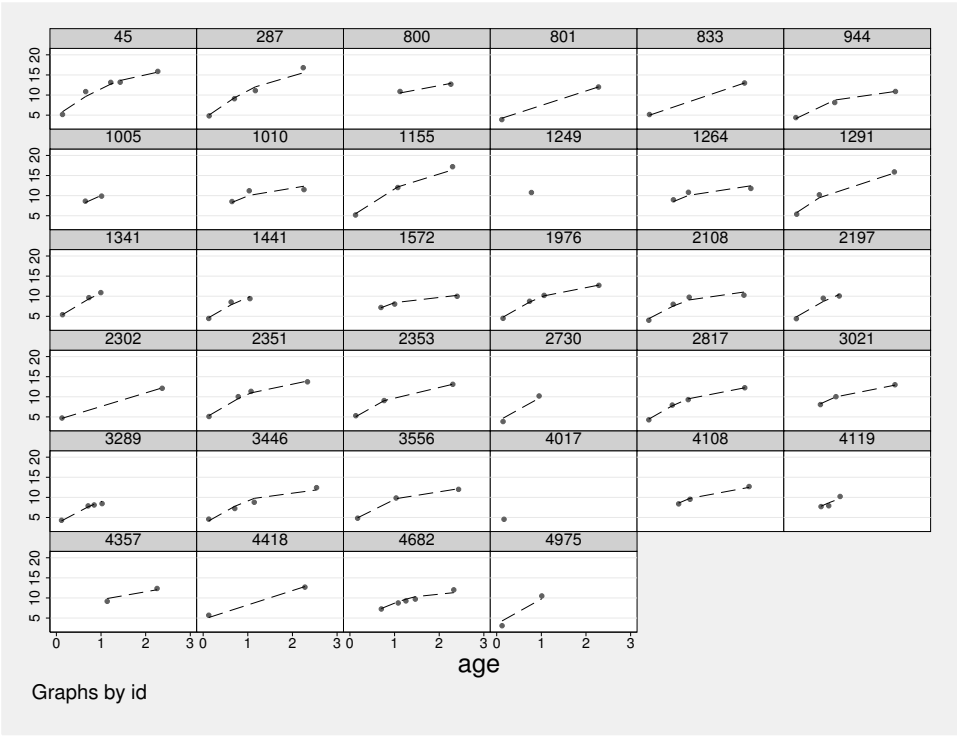


Figure 7.6: Trellis graph of observed responses (dots) and fitted trajectories (dashed lines) for boys

7.3.2 Piecewise linear models

Instead of using a polynomial to model the nonlinear relationship between weight and age, we can also split the age range into intervals, at *knots*, and fit straight line-segments between the knots, giving a piecewise linear model. Such a piecewise linear curve is an example of a *spline*, specifically a linear spline. As for polynomials, the piecewise linear function can be written as a linear model, $\beta_1 + \beta_2 z_{1ij} + \beta_3 z_{2ij} + \cdots$, where the variables z_{1ij}, z_{2ij}, etc., are called linear spline basis functions.

To see this, refer to the illustration in figure 7.7. The bottom panel shows the spline basis functions, which start at zero, increase with a slope of 1 between two knots, and then remain constant. The function in the top panel is a linear combination of these basis functions. We see that the function up to the first knot at 2 is simply $1 + z_{1ij}$. Between the knots at 2 and 6, the slope is only 0.25, so the second basis function z_{2ij} is multiplied by 0.25 before being added to $1 + z_{1ij}$. Finally, the slope in the last interval, from 6 to the maximum (here 7), is 2, so the final term in the model is $2z_{3ij}$.

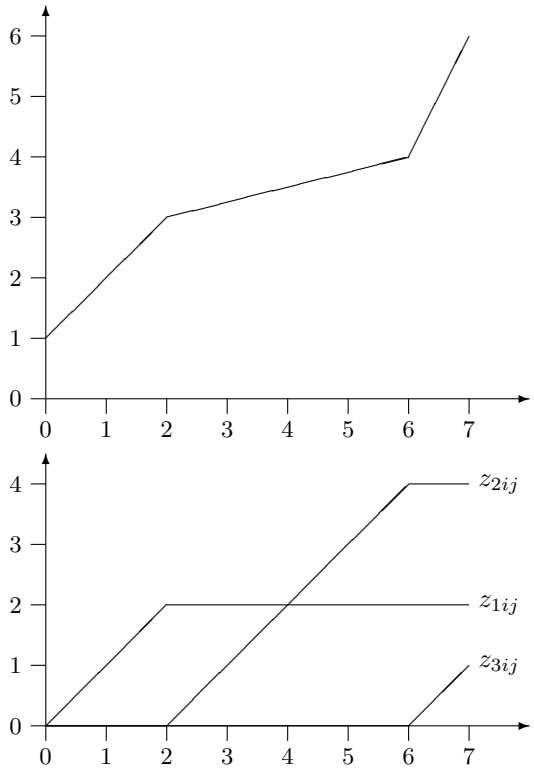


Figure 7.7: Illustration of piecewise linear function $1 + z_{1ij} + 0.25z_{2ij} + 2z_{3ij}$ with knots at 2 and 6

Fitting the models

For the children's growth data, we will arbitrarily let the knots be located at ages 0.4, 0.9, and 1.5 years. It is of course preferable to base the choice of knots on subject-matter considerations when possible (see exercise 7.6 for an example).

To fit a linear spline, we must create basis functions to include in the model as covariates. To produce nice graphs, we first add the knot values to the data so that we can later display the basis functions (generally, this is not something you would have to do).

There are 198 observations in the data:

```
. display _N
198
```

We increase the number of observations by 3 and substitute the values 0.4, 0.9, and 1.5 for age:

```
. set obs 201
obs was 198, now 201
. replace age = 0.4 in 199
(1 real change made)
. replace age = 0.9 in 200
(1 real change made)
. replace age = 1.5 in 201
(1 real change made)
```

(Note that we do not risk accidentally treating these invented data as real data during model fitting because the response variable is missing in rows 199 to 201.)

The spline basis functions are created using the Stata command `mkspline`,

```
. mkspline ages1 .4 ages2 .9 ages3 1.5 ages4 = age
```

and we can plot them using

```
. twoway (line ages1 age, sort) (line ages2 age, sort)
>        (line ages3 age, sort) (line ages4 age, sort),
>        xscale(range(0 2.5)) xlabel(0 .4 .9 1.5)
```

giving the graph in figure 7.8.

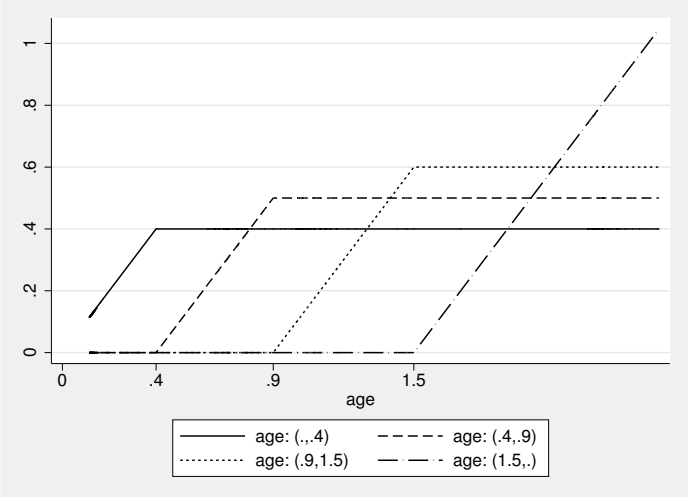


Figure 7.8: Spline basis functions for piecewise-linear model for children's growth data

We see that the first basis function (`ages1`) increases linearly from 0 (although the plotted line starts at the lowest age that occurs in the data), with a slope of 1, up to the first knot, and then stays constant. The second basis function, `ages2`, increases

linearly from 0, between the first and second knots, and then stays constant, etc. We can include these basis functions as covariates, and their coefficients will represent the slopes in the corresponding intervals. We can fit the piecewise-linear random-coefficient model using

```
. xtmixed weight girl ages1 ages2 ages3 ages4 || id: age,
> covariance(unstructured) mle
Mixed-effects ML regression                     Number of obs      =       198
Group variable: id                              Number of groups   =        68
                                                Obs per group: min =         1
                                                               avg =       2.9
                                                               max =         5
                                                Wald chi2(5)       =   2075.53
Log likelihood = -242.00811                     Prob > chi2        =    0.0000
```

weight	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
girl	-.6358097	.1947046	-3.27	0.001	-1.017424	-.2541958
ages1	9.936391	1.065415	9.33	0.000	7.848216	12.02457
ages2	4.441785	.7492172	5.93	0.000	2.973346	5.910224
ages3	2.344885	.6430038	3.65	0.000	1.084621	3.605149
ages4	2.209955	.3629384	6.09	0.000	1.498609	2.921301
_cons	3.374523	.2216652	15.22	0.000	2.940067	3.808979

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
id: Unstructured				
sd(age)	.5678807	.0818571	.4281153	.7532747
sd(_cons)	.6608931	.1158728	.468697	.9319021
corr(age,_cons)	-.0431119	.2332324	-.4629951	.3925743
sd(Residual)	.4878942	.0445727	.4079079	.583565

```
LR test vs. linear regression:       chi2(3) =   121.88   Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference.
```

Estimates for this model were shown under "Model 2: Piecewise linear" in table 7.1. The estimates of the gender difference and the random part of the model are similar to the estimates for the quadratic function. The slope in the first interval, up to 0.4 months, is estimated as 9.94 kg/month; the slope between 0.4 and 0.9 months is estimated as 4.44 kg/month; and the last two slopes are estimated as about 2.3 kg/month and 2.2 kg/month. The intercept, estimated as 3.37 kg, represents the mean initial weight (at birth), but this is an extrapolation outside the range of the data. An advantage of the piecewise linear model is that it is easier to interpret the relationship between mean birthweight and age than for the quadratic model.

The random part of the model is linear (with a random slope of `age`), so for a given child the same amount is added to the slope of each line segment. The estimated residual random-intercept standard deviation is 0.66 kg, and the mean increase in weight per month varies with an estimated standard deviation of 0.49 kg per month.

Predicting the mean trajectory

As for the quadratic model, we see that the slope decreases with age. We can obtain a graph of the mean trajectory for boys and the 95% range of trajectories as before. Here, it is easier to use the `predict` command to produce the mean curve. To make predictions for the three invented datapoints at the spline knots, we first set `girl` equal to 0 for these three observations:

```
. replace girl = 0 in 199/201
(3 real changes made)
. predict mean, xb
```

We produce scalars for the variances and covariance as before,

```
. scalar var1 = exp(2*[lns1_1_1]_cons)
. scalar var2 = exp(2*[lns1_1_2]_cons)
. scalar cov = tanh([atr1_1_1_2]_cons)*sqrt(var1*var2)
```

and then we generate variables `upper` and `lower` containing the limits of the 95% range:

```
. generate upper = mean + 1.96*sqrt(var1+2*cov*age+var2*age^2)
. generate lower = mean - 1.96*sqrt(var1+2*cov*age+var2*age^2)
```

We can then plot the ranges in addition to the mean by using the `twoway` command:

```
. twoway (line mean age, sort lwidth(medium))
>        (line lower age, sort lpatt(dash))
>        (line upper age, sort lpatt(dash)) if girl==0,
>        legend(order(1 "Mean" 2 "95% range")) xtitle(Age in years)
>        ytitle(Weight in kg) xtick(.4 .9 1.5, grid) ylabel(,nogrid)
>        yscale(range(0 20)) ylab(0(5)20)
```

The resulting graph in figure 7.9 clearly shows the kinks at the first two knots (helped by having made predictions at the generated ages at the spline knots).

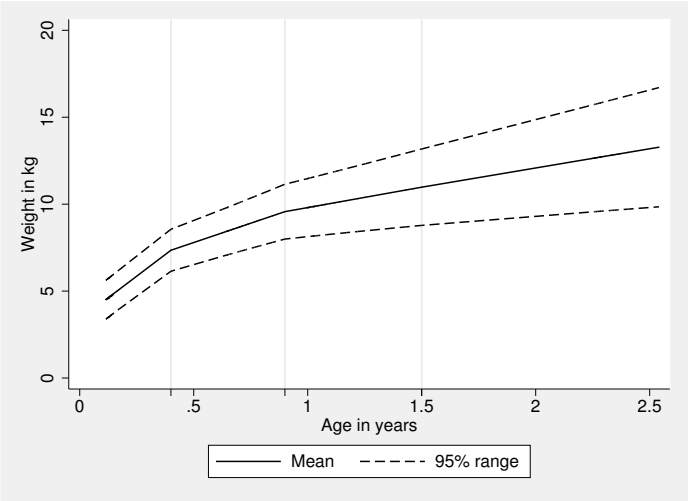


Figure 7.9: Mean trajectory and 95% range of subject-specific trajectories for boys from piecewise-linear model

Trellis graphs can be produced as shown for the quadratic model.

7.4 Two-stage model formulation

As is often done in the literature, we now express the polynomial random-coefficient model in (7.1) using the two-stage formulation described in section 4.9. The level-1 model is written as

$$y_{ij} = \pi_{0j} + \pi_{1j}t_{ij} + \pi_2 t_{ij}^2 + \epsilon_{ij}$$

where the intercept π_{0j} and slope π_{1j} are child-specific coefficients. The level-2 model has these coefficients as responses:

$$\begin{aligned} \pi_{0j} &= \gamma_{00} + \gamma_{01}w_j + r_{0j} \\ \pi_{1j} &= \gamma_{10} + r_{1j} \end{aligned} \tag{7.2}$$

where `girl` (w_j) is a covariate only in the intercept equation. As usual, r_{0j} and r_{1j} are assumed to have a bivariate distribution with zero means and unstructured covariance matrix.

Substituting the level-2 models into the level-1 model, we obtain the reduced form

$$\begin{aligned} y_{ij} &= \underbrace{\gamma_{00} + \gamma_{01}w_j + r_{0j}}_{\pi_{0j}} + \underbrace{(\gamma_{10} + r_{1j})}_{\pi_{1j}}t_{ij} + \pi_2 t_{ij}^2 + \epsilon_{ij} \\ &= \gamma_{00} + \gamma_{01}w_j + \gamma_{10}t_{ij} + \pi_2 t_{ij}^2 + r_{0j} + r_{1j}t_{ij} + \epsilon_{ij} \\ &\equiv \beta_1 + \beta_2 w_j + \beta_3 t_{ij} + \beta_4 t_{ij}^2 + \zeta_{1j} + \zeta_{2j}t_{ij} + \epsilon_{ij} \end{aligned}$$

where $\beta_1 \equiv \gamma_{00}$, $\beta_2 \equiv \gamma_{01}$, $\beta_3 \equiv \gamma_{10}$, $\beta_4 \equiv \pi_2$, $\zeta_{1j} \equiv r_{0j}$, and $\zeta_{2j} \equiv r_{1j}$. This reduced-form model is equivalent to model (7.1).

In the two-stage formulation, a natural extension of this model is to include `girl` as a covariate also in the level-2 model for π_{1j} in (7.2) by adding the term $\gamma_{11} w_j$ there. This results in a *cross-level interaction* $\gamma_{11} w_j t_{ij}$, between the level-2 covariate w_j and the level-1 covariate t_{ij}.

After constructing the interaction term for `age` and `girl`,

```
. generate age_girl = age*girl
```

the model can be fit using

```
. xtmixed weight girl age_girl age age2 || id: age, covariance(unstructured) mle
Mixed-effects ML regression                     Number of obs      =       198
Group variable: id                              Number of groups   =        68
                                                Obs per group: min =         1
                                                               avg =       2.9
                                                               max =         5
                                                Wald chi2(4)       =   2023.53
Log likelihood = -252.99486                     Prob > chi2        =    0.0000
```

weight	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
girl	-.5040553	.2071801	-2.43	0.015	-.9101208	-.0979897
age_girl	-.2303089	.1731563	-1.33	0.183	-.569689	.1090712
age	7.814711	.2526441	30.93	0.000	7.319538	8.309885
age2	-1.658569	.087916	-18.87	0.000	-1.830881	-1.486257
_cons	3.748607	.1682409	22.28	0.000	3.418861	4.078353

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
id: Unstructured				
sd(age)	.4969469	.0875711	.3518137	.7019517
sd(_cons)	.5890289	.1291188	.3833081	.9051599
corr(age,_cons)	.1870199	.3361438	-.4569593	.7023664
sd(Residual)	.5729779	.0498678	.4831206	.679548

```
LR test vs. linear regression:       chi2(3) =   104.77   Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference.
```

The estimates are shown under "Model 3" in table 7.2, next to the previous model that had no cross-level interaction, repeated here as "Model 1". Because the interaction is not significant at the 5% level, we retain Model 1 in the next section.

Table 7.2: Maximum likelihood estimates for quadratic models for children's growth data. "Model 3" includes cross-level interaction. "Model 4" and "Model 5" allow the random part of the model at level 1 and level 2, respectively, to differ between boys (B) and girls (G).

	Model 1		Model 3		Model 4		Model 5	
	Est	(SE)	Est	(SE)	Est	(SE)	Est	(SE)
Fixed part								
β_1 [_cons]	3.79	(0.17)	3.75	(0.17)	3.83	(0.17)	3.82	(0.16)
β_2 [girl]	−0.60	(0.20)	−0.50	(0.21)	−0.60	(0.20)	−0.61	(0.20)
β_3 [girl×age]			−0.23	(0.17)				
β_4 [age]	7.70	(0.24)	7.81	(0.25)	7.63	(0.23)	7.61	(0.23)
β_5 [age2]	−1.66	(0.09)	−1.66	(0.09)	−1.64	(0.09)	−1.65	(0.09)
Random part								
							B	G
$\sqrt{\psi_{11}}$	0.59		0.59		0.63		0.54	0.70
$\sqrt{\psi_{22}}$ [age]	0.51		0.50		0.49		0.69	0.22
ρ_{21}	0.16		0.19		0.15		0.05	0.39
					B	G		
$\sqrt{\theta}$	0.57		0.57		0.64	0.49	0.57†	0.57
Log likelihood	−253.87		−252.99		−252.41		−249.71	

†Constrained equal across genders

7.5 Heteroskedasticity

7.5.1 Heteroskedasticity at level 1

In all models considered so far in this chapter, we have assumed that the random intercept, random slope, and level-1 residual all have constant variance for all children. However, it is sometimes necessary to allow variances to depend on covariates.

We first allow the level-1 residual variance θ to differ between boys and girls by introducing gender-specific parameters $\theta^{(B)}$ and $\theta^{(G)}$, respectively. This is easily accomplished in `xtmixed` using the `residuals(independent, by(gender))` option to let the level-1 residuals be independent over occasions and have different variances for each gender:

```
. xtmixed weight girl age age2 || id: age, covariance(unstructured) mle
> residuals(independent, by(gender))
Mixed-effects ML regression                     Number of obs      =       198
Group variable: id                              Number of groups   =        68
                                                Obs per group: min =         1
                                                               avg =       2.9
                                                               max =         5
                                                Wald chi2(3)       =   2093.69
Log likelihood = -252.40553                     Prob > chi2        =    0.0000
```

weight	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
girl	-.6026741	.2011077	-3.00	0.003	-.9968378	-.2085103
age	7.629066	.2327022	32.78	0.000	7.172978	8.085154
age2	-1.635112	.0859732	-19.02	0.000	-1.803617	-1.466608
_cons	3.829123	.1731333	22.12	0.000	3.489788	4.168458

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
id: Unstructured				
sd(age)	.4857393	.0889252	.339291	.6953993
sd(_cons)	.6271286	.1180433	.4336471	.9069362
corr(age,_cons)	.1457196	.2996523	-.4245955	.6332441
Residual: Independent, by gender				
Boy: sd(e)	.6397179	.0697704	.5165981	.7921805
Girl: sd(e)	.4937988	.0581918	.3919585	.6220996

```
LR test vs. linear regression:       chi2(4) =   107.09   Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference.
```

The level-1 residual standard deviations $\sqrt{\theta^{(\mathrm{B})}}$ and $\sqrt{\theta^{(\mathrm{G})}}$ are estimated as 0.64 and 0.49, respectively. The point estimates look quite similar to each other, but we can use a likelihood-ratio test to formally test the null hypothesis that both residual variances (and hence standard deviations) are the same, H_0: $\theta^{(\mathrm{B})} = \theta^{(\mathrm{G})}$, using

```
. lrtest rc .
Likelihood-ratio test                                 LR chi2(1)  =      2.92
(Assumption: rc nested in .)                          Prob > chi2 =    0.0873
Note: The reported degrees of freedom assumes the null hypothesis is not on
      the boundary of the parameter space.  If this is not true, then the
      reported test is conservative.
```

There is no strong evidence against the null hypothesis, and we retain a common level-1 variance or homoskedastic level-1 residual. (We can ignore the note in the output for the likelihood-ratio test because our null hypothesis is not on the boundary of parameter space.)

For balanced data with a sufficient number of observations at each occasion, we can also let the level-1 residuals be heteroskedastic over occasions, as will be described in section 7.6.

7.5.2 Heteroskedasticity at level 2

We can also allow the random-intercept variance ψ_{11} and random-slope variance ψ_{22}, and their covariance ψ_{21}, to differ between boys and girls, with parameters $\psi_{11}^{(\mathrm{B})}$, $\psi_{22}^{(\mathrm{B})}$, and $\psi_{21}^{(\mathrm{B})}$ for boys and $\psi_{11}^{(\mathrm{G})}$, $\psi_{22}^{(\mathrm{G})}$, and $\psi_{21}^{(\mathrm{G})}$ for girls.

This is most easily done by specifying four different random effects—a random intercept ζ_{1j} and slope ζ_{2j} for boys, and a random intercept ζ_{3j} and slope ζ_{4j} for girls—giving level-2 random parts $\zeta_{1j}+\zeta_{2j}t_{ij}$ for boys and $\zeta_{3j}+\zeta_{4j}t_{ij}$ for girls. These level-2 random parts must be multiplied by dummy variables for boys and girls, respectively, to switch them on for the appropriate gender. The model can be written as

$$\begin{aligned} y_{ij} &= \beta_1 + \beta_2 \texttt{girl}_j + \beta_3 t_{ij} + \beta_4 t_{ij}^2 + (\zeta_{1j} + \zeta_{2j} t_{ij})\texttt{boy}_j + (\zeta_{3j} + \zeta_{4j} t_{ij})\texttt{girl}_j + \epsilon_{ij} \\ &= \cdots + (\zeta_{1j}\texttt{boy}_j + \zeta_{2j} t_{ij}\texttt{boy}_j) + (\zeta_{3j}\texttt{girl}_j + \zeta_{4j} t_{ij}\texttt{girl}_j) + \epsilon_{ij}, \end{aligned}$$

where the dummy variable `girl`, previously denoted w_j in equations, already exists and the dummy variable for boys, `boy`, can be created using

```
. generate boy = 1-girl
```

The model includes random coefficients of the gender dummies, as well as random coefficients of the products, $t_{ij}\texttt{boy}_j$ and $t_{ij}\texttt{girl}_j$. The latter variable already exists and is called `age_girl`. We create $t_{ij}\texttt{boy}_j$ using

```
. generate age_boy = age*boy
```

In the `xtmixed` command, we first specify random coefficients for `age_boy` and `boy`. After that, we specify a new random part, also with `id` as cluster variable, but this time with random coefficients for `age_girl` and `girl`. Specifying two random parts for the same cluster is a way of estimating two separate covariance matrices, hence achieving zero correlations between the random effects for boys and girls. Such correlations cannot be estimated because no child can be both a boy and a girl. Because the coefficients of `boy` and `girl` play the role of random intercepts, we must use the `noconstant` option for each random part:

```
. xtmixed weight girl age age2
> || id: age_boy boy, noconstant covariance(unstructured)
> || id: age_girl girl, noconstant covariance(unstructured)  mle
Mixed-effects ML regression                     Number of obs      =       198
Group variable: id                              Number of groups   =        68
                                                Obs per group: min =         1
                                                               avg =       2.9
                                                               max =         5
                                                Wald chi2(3)       =   2413.70
Log likelihood = -249.70684                     Prob > chi2        =    0.0000
```

weight	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
girl	-.6066394	.1996813	-3.04	0.002	-.9980075	-.2152713
age	7.613015	.2335188	32.60	0.000	7.155326	8.070703
age2	-1.646256	.0869013	-18.94	0.000	-1.81658	-1.475933
_cons	3.820121	.157553	24.25	0.000	3.511323	4.128919

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
id: Unstructured				
sd(age_boy)	.6891223	.1350621	.4693189	1.01187
sd(boy)	.5364599	.1807413	.2771755	1.038292
corr(age_boy,boy)	.0501319	.3995425	-.6260466	.6832774
id: Unstructured				
sd(age_girl)	.218154	.1450495	.0592657	.8030133
sd(girl)	.6987662	.1611978	.4445995	1.098234
corr(age_girl,girl)	.388837	.7897376	-.8881593	.9773197
sd(Residual)	.567544	.049112	.4790065	.6724465

```
LR test vs. linear regression:       chi2(6) =   112.49   Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference.
```

A likelihood-ratio test can be performed to compare this model with the one that constrained the covariance matrices of the random effects to be equal between boys and girls, H_0: $\psi_{11}^{(\mathrm{B})} = \psi_{11}^{(\mathrm{G})}$, $\psi_{22}^{(\mathrm{B})} = \psi_{22}^{(\mathrm{G})}$, $\psi_{21}^{(\mathrm{B})} = \psi_{21}^{(\mathrm{G})}$, using

```
. lrtest rc .
Likelihood-ratio test                                 LR chi2(3)  =      8.32
(Assumption: rc nested in .)                          Prob > chi2 =    0.0398
Note: The reported degrees of freedom assumes the null hypothesis is not on
      the boundary of the parameter space.  If this is not true, then the
      reported test is conservative.
```

The null hypothesis is not on the boundary, so the p-value is 0.04.

7.6 How does reading improve from kindergarten through third grade?

We now consider data from the 1986, 1988, 1990, and 1992 panel waves of the U.S. National Longitudinal Survey of Youth (NLSY) provided by Bollen and Curran (2006). The children were in kindergarten, grade 1, or grade 2 in 1986. Here the time-scale of interest is the grade the child is in (see Bollen and Curran [2006, 82]); we will consider grades 0 (kindergarten), 1, 2, and 3. The data have a considerable amount of missing values because they were collected only every other year; some children were already in year 3 at the first wave, and therefore contributed no further data in subsequent waves. The response variable used here is the reading recognition subscore of the Peabody Individual Achievement Test, scaled as the percentage of 84 items that were answered correctly.

The variables in the dataset `reading.dta` are as follows:

- `id`: child identifier
- `read0`, `read1`, `read2`, `read3`: reading scores in kindergarten (grade 0), grade 1, grade 2, and grade 3
- `age0`, `age1`, `age2`, `age3`: ages in months in kindergarten and grades 1 through 3
- `math0`, `math1`, `math2`, `math3`: math scores in kindergarten and grades 1 through 3 (not used here)
- `female`: dummy variable for being female (1: female; 0: male)
- `minority`: dummy variable for being a minority (1: minority; 0: nonminority)

Unlike the Asian child growth data, these data are balanced with constant spacing of occasions (apart from gaps due to missing data).

7.7 Growth-curve model as a structural equation model

When the data are balanced, the responses y_{ij} at different occasions i can be viewed as different variables or in other words as a multivariate response for child j. A growth-curve model can then be set up as a structural equation model (SEM) with latent (unobserved) variables. Such models are also called covariance structure models and are a special case of latent variable models. When applied to longitudinal data, SEMs are sometimes referred to as *latent growth-curve models* because the smooth growth curves for individual children (with the error ϵ_{ij} removed) are unobserved.

A linear growth-curve model for four occasions (as in the reading data) can be written as

$$\begin{bmatrix} y_{1j} \\ y_{2j} \\ y_{3j} \\ y_{4j} \end{bmatrix} = \begin{bmatrix} 1 & 0 \\ 1 & 1 \\ 1 & 2 \\ 1 & 3 \end{bmatrix} \begin{bmatrix} \eta_{1j} \\ \eta_{2j} \end{bmatrix} + \begin{bmatrix} \epsilon_{1j} \\ \epsilon_{2j} \\ \epsilon_{3j} \\ \epsilon_{4j} \end{bmatrix} = \begin{bmatrix} \eta_{1j} + 0\eta_{2j} + \epsilon_{1j} \\ \eta_{1j} + 1\eta_{2j} + \epsilon_{2j} \\ \eta_{1j} + 2\eta_{2j} + \epsilon_{3j} \\ \eta_{1j} + 3\eta_{2j} + \epsilon_{4j} \end{bmatrix}$$

This is just the level-1 model in a two-stage formulation (see section 7.4), written out for each occasion i, using matrix algebra and the notation $\eta_{1j} \equiv \pi_{0j}$ and $\eta_{2j} \equiv \pi_{1j}$. Here the values of t_i are 0, 1, 2, and 3 (note that the time variable does not vary between children here because the data are balanced). For a conventional SEM, it is not possible to have different sets of time points or occasions for different children.

In SEM terminology, this part of the model is called the *measurement model*. The child-specific intercept η_{1j} and slope η_{2j} are called common factors (or latent variables), and the matrix multiplying these factors on the left is the factor-loading matrix. The factor loadings (elements of the factor-loading matrix) are usually parameters to be estimated in SEM, but for linear growth-curve models they are constrained equal to fixed constants. The errors ϵ_{1j} to ϵ_{4j} have zero means and a diagonal 4×4 covariance matrix, with variances θ_{11} to θ_{44} and covariances set to zero. A diagonal covariance matrix means that the pairwise correlations are all zero. Typically, the residual variances are not constrained equal, and this is usually the only difference between SEM and multilevel approaches to growth-curve modeling.

The *structural model* is just matrix notation for the level-2 models in the two-stage formulation

$$\begin{bmatrix} \eta_{1j} \\ \eta_{2j} \end{bmatrix} = \begin{bmatrix} \gamma_{11} \\ \gamma_{21} \end{bmatrix} + \begin{bmatrix} \zeta_{1j} \\ \zeta_{2j} \end{bmatrix} = \begin{bmatrix} \gamma_{11} + \zeta_{1j} \\ \gamma_{21} + \zeta_{2j} \end{bmatrix}$$

(with the notation $\gamma_{11} \equiv \gamma_{00}$, $\gamma_{21} \equiv \gamma_{10}$, $\zeta_{1j} \equiv r_{0j}$, and $\zeta_{2j} \equiv r_{1j}$). The disturbances ζ_{1j} and ζ_{2j} have zero means and covariance matrix $\mathbf{\Psi}$.

A path diagram of the linear growth-curve model is shown in figure 7.10. As usual in SEM, observed variables are represented by rectangles and latent variables by circles. The four responses are regressed on the random intercept η_{1j} (as indicated by the long arrows from η_{1j} to the responses), with regression coefficients or factor loadings set to 1 (as indicated by the labels attached to the arrows). The responses are also regressed on the random slope η_{2j} with regression coefficients set equal to the time points t_i, here 0, 1, 2, and 3. The short arrows represent the occasion-specific error terms ϵ_{1j} to ϵ_{4j}. The curved double-headed arrow connecting η_{1j} and η_{2j} indicates that these latent variables (random effects), or the corresponding disturbances ζ_{1j} and ζ_{2j}, are correlated.

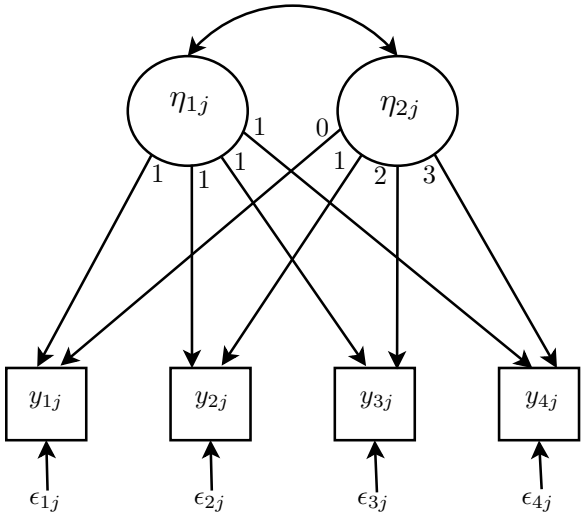


Figure 7.10: Path diagram of linear growth-curve model with four time points

Although we have written the model as an SEM, it can equivalently be fit as a multilevel model, as long as we allow the residual variances to differ between occasions. Allowing such heteroskedastic variances is possible if we have balanced data, such as those used here, but becomes unfeasible with unbalanced data if there are insufficient observations at any of the occasions.

7.7.1 Estimation using sem

The data are in wide form with responses at the four occasions represented by different variables `read0`, `read1`, `read2`, and `read3`. Because SEM is a method designed for multivariate data, the `sem` command (introduced in Stata 12) requires the data to be in wide form.

We start by reading in the data:

```
. use http://www.stata-press.com/data/mlmus3/reading, clear
```

In wide form, we can investigate the missingness patterns by using the `misstable` command (introduced in Stata 11):

```
. misstable patterns read*
  Missing-value patterns
    (1 means complete)

                 |  Pattern
  Percent        |  1  2  3  4
-----------------+------------
      <1%        |  1  1  1  1
                 |
      15         |  1  0  0  0
      14         |  1  0  1  0
      12         |  0  1  0  0
      10         |  0  0  1  0
       8         |  1  0  0  1
       8         |  1  1  0  0
       8         |  0  1  0  1
       7         |  0  0  0  1
       6         |  0  1  1  0
       5         |  0  0  0  0
       3         |  1  0  1  1
       2         |  1  1  0  1
       2         |  0  0  1  1
      <1         |  0  1  1  1
      <1         |  1  1  1  0
-----------------+------------
     100%        |
Variables are  (1) read0  (2) read1  (3) read2  (4) read3
```

In this table, a "1" means that the variable is observed and a "0" represents missing. We see, for instance, that 15% of the children only have observations for the reading score at the first occasion (kindergarten) and that fewer than 1% of children have observations at the first three occasions.

We can also produce box plots of the observations at each occasion using

```
. graph box read0 read1 read2 read3, ascategory intensity(0) medtype(line)
```

with the result shown in figure 7.11.

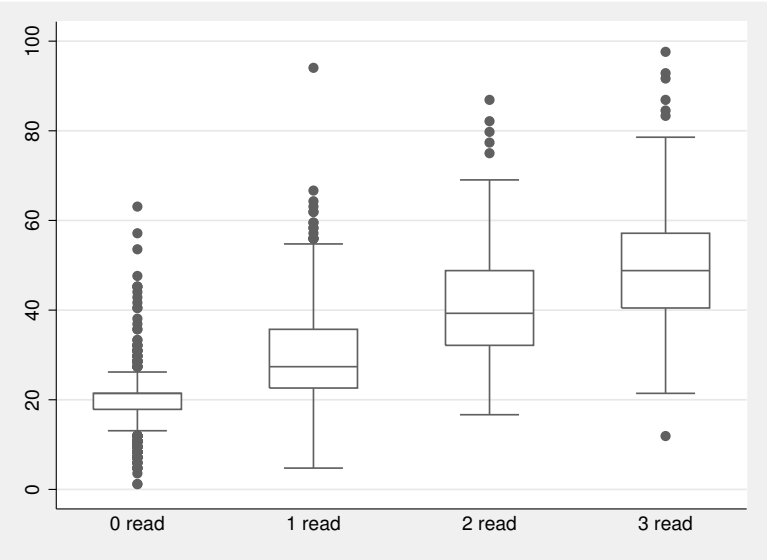


Figure 7.11: Box plots of reading scores for each grade

There does not seem to be much cause for concern. For instance, there is no sign of a ceiling effect by grade 3 (which occurs if a substantial proportion of the children get a perfect score). However, there appears to be an outlier for grade 1.

Note that traditional software for SEM, based on fitting model-implied covariance matrices to empirical covariance matrices, could only handle complete data, but modern software applies ML estimation to all available data. Hence, consistent estimates are produced if missing responses are missing at random (MAR) and the growth-curve model is correctly specified (see section 5.8.1 for more on MAR). In the `sem` command, ML estimation is obtained using the `method(mlmv)` option (`mlmv` stands for ML with missing values).

In the `sem` syntax, latent variables can be referred to using any label of our choosing as long as it begins with a capital letter. We use `L1` and `L2` for the latent variables η_{1j} and η_{2j}. For the measurement model, we want to regress the reading scores on the latent variables or, in other words, include paths from the latent variables to the response variables (see figure 7.10). Such paths are specified using arrows, `<-` or `->`. For example, the reading score in second grade is regressed on both latent variables, denoted as `(read2 <- L1 L2)` (the level-1 error ϵ_{2j} is implicit).

By default, all regression coefficients (factor loadings) and intercepts in the measurement model are free parameters, but we constrain all intercepts to zero using the `noconstant` option and constrain the factor loadings to 1 and 2, respectively, using the syntax `(read2 <- L1@1 L2@2)`.

For the structural model, we want to allow the latent variables to have nonzero means (γ_{11}) and (γ_{21}). By default, `sem` sets means of latent variables to zero, so we relax this constraint by using the `means(L1 L2)` option.

Putting it all together, the `sem` command becomes

```
. sem (read0 <- L1@1 L2@0)
>     (read1 <- L1@1 L2@1)
>     (read2 <- L1@1 L2@2)
>     (read3 <- L1@1 L2@3), means(L1 L2) noconstant method(mlmv)
(90 all-missing observations excluded)
Endogenous variables
Measurement:  read0 read1 read2 read3
Exogenous variables
Latent:       L1 L2
Structural equation model                       Number of obs      =      1677
Estimation method  = mlmv
Log likelihood     =   -9594.51
 ( 1)  [read0]L1 = 1
 ( 2)  [read1]L1 = 1
 ( 3)  [read1]L2 = 1
 ( 4)  [read2]L1 = 1
 ( 5)  [read2]L2 = 2
 ( 6)  [read3]L1 = 1
 ( 7)  [read3]L2 = 3
 ( 8)  [read0]_cons = 0
 ( 9)  [read1]_cons = 0
 (10)  [read2]_cons = 0
 (11)  [read3]_cons = 0
```

	OIM Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
Measurement						
read0 <-						
L1	1	(constrained)				
_cons	0	(constrained)				
read1 <-						
L1	1	(constrained)				
L2	1	(constrained)				
_cons	0	(constrained)				
read2 <-						
L1	1	(constrained)				
L2	2	(constrained)				
_cons	0	(constrained)				
read3 <-						
L1	1	(constrained)				
L2	3	(constrained)				
_cons	0	(constrained)				
Mean						
L1	19.86971	.1915621	103.72	0.000	19.49426	20.24517
L2	10.25926	.1508238	68.02	0.000	9.963652	10.55487
Variance						
e.read0	18.44756	5.410867			10.38179	32.77973
e.read1	61.00465	4.689062			52.47304	70.92343
e.read2	72.7696	7.215578			59.9167	88.37963
e.read3	42.8985	11.88719			24.92148	73.84318
L1	17.98089	5.403334			9.977496	32.40417
L2	7.925603	1.933835			4.912929	12.78569
Covariance						
L1						
L2	2.887407	2.615503	1.10	0.270	-2.238885	8.0137

LR test model vs. saturated: chi2(5) = 71.97, Prob > chi2 = 0.0000

In the output, the constraints are listed first, followed by the parameters (here all constrained) for the regressions of each of the response variables. This is followed by the estimated means of `L1` and `L2`, and then the residual variances of the response variables and the variances and covariance for `L1` and `L2`.

The intercept η_{1j} therefore has an estimated mean of 19.9 and variance of 18.0, and the slope η_{2j} has an estimated mean of 10.3 and variance of 7.9. The correlation between intercepts and slopes is estimated as 0.24 ($= 2.887407/\sqrt{7.925603 \times 17.98089}$). It is therefore estimated that the reading score increases, on average, by 10.3 units per grade level, and for 95% of children, it increases between 4.7 and 15.8 units per grade level ($10.25926 \pm 1.96 \times \sqrt{7.925603}$). The estimated residual variance is much lower in kindergarten than in grades 1 and 2, but it decreases somewhat again in year 3. The estimates are also reported in table 7.3.

Table 7.3: Maximum likelihood estimates for reading data

	Est	(SE)
Fixed part		
γ_{11} [_cons]	19.87	(0.19)
γ_{21} [grade]	10.26	(0.15)
Random part		
ψ_{11}	17.98	
ψ_{22}	7.93	
ψ_{21}	2.89	
θ_{11}	18.45	
θ_{22}	61.00	
θ_{33}	72.77	
θ_{44}	42.90	
Log likelihood	−9594.51	

An alternative syntax for the same model is

```
sem (L1 -> read0@1 read1@1 read2@1 read3@1)
    (L2 -> read1@1 read2@2 read3@3), means(L1 L2) nocons method(mlmv)
```

We can obtain EB predictions of the child-specific intercepts and slopes by using

```
. predict l1 l2, latent
(latent(L1 L2) assumed)
```

These predictions are called factor scores in SEM. There are two methods for factor scoring: the regression method (used by `sem`) corresponds to EB prediction, whereas the Bartlett method corresponds to ML estimation, as described in section 2.11.1 for variance-components models and in section 4.8.1 for random-coefficient models.

7.7.2 Estimation using xtmixed

We now demonstrate how the same growth-curve model can be fit using `xtmixed`. For analysis using `xtmixed`, the data should be in long form, so we begin by reshaping the data using the `reshape` command:

```
. reshape long read math age, i(id) j(grade)
(note: j = 0 1 2 3)
Data                               wide   ->   long
-----------------------------------------------------------------------------
Number of obs.                     1767   ->    7068
Number of variables                  15   ->       7
j variable (4 values)                     ->   grade
xij variables:
                  read0 read1 ... read3   ->   read
                  math0 math1 ... math3   ->   math
                     age0 age1 ... age3   ->   age
-----------------------------------------------------------------------------
```

In long form, we can use `xtdescribe` to explore the missing data patterns

```
. quietly xtset id grade
. drop if read >= .
(4392 observations deleted)
. xtdescribe
      id:  301, 401, ..., 1266701                             n =       1677
   grade:  0, 1, ..., 3                                       T =          4
           Delta(grade) = 1 unit
           Span(grade)  = 4 periods
           (id*grade uniquely identifies each observation)
Distribution of T_i:   min      5%     25%       50%       75%     95%     max
                         1       1       1         2         2       3       3
     Freq.  Percent    Cum. |  Pattern
-----------------------------+---------
       268    15.98   15.98 |  1...
       249    14.85   30.83 |  1.1.
       215    12.82   43.65 |  .1..
       170    10.14   53.79 |  ..1.
       144     8.59   62.37 |  1..1
       136     8.11   70.48 |  11..
       133     7.93   78.41 |  .1.1
       119     7.10   85.51 |  ...1
       112     6.68   92.19 |  .11.
       131     7.81  100.00 |  (other patterns)
-----------------------------+---------
      1677   100.00         |  XXXX
```

Note that children with missing responses at all four occasions are not counted here, unlike in the `misstable` command. We see that at least 92.19% of children (with at least one nonmissing response) have fewer than three observations.

Because of the balanced nature of the data, we have sufficient data per occasion to plot the mean trajectory,

```
. egen mn_read = mean(read), by(grade)
. twoway (connected mn_read grade, sort), xtitle(Grade)
> ytitle(Mean reading score)
```

giving the graph in figure 7.12, where the mean growth trajectory is remarkably linear. (Using the plot type `connected` is useful because it shows where the observations occurred.)

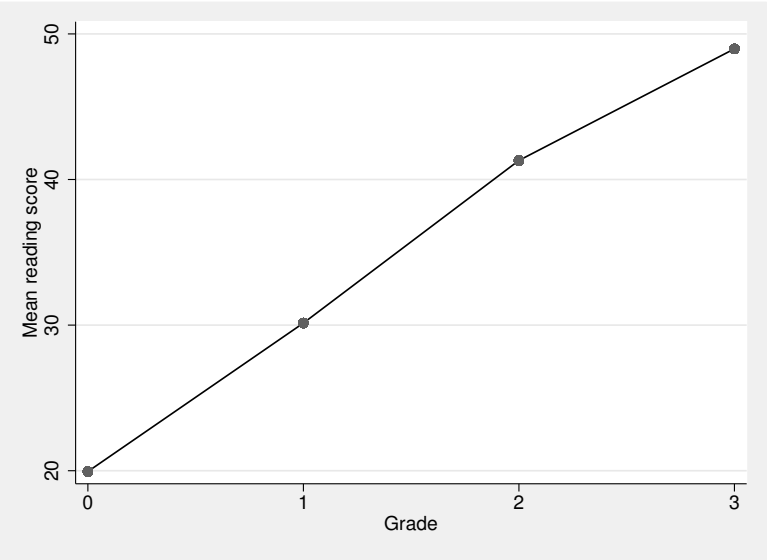


Figure 7.12: Sample mean growth trajectory for reading score

Box plots such as those shown in figure 7.11 can be produced using the command

```
graph box read, over(grade) ytitle(Reading score) intensity(0) medtype(line)
```

We can now fit a linear growth model using `grade` as the time variable and using the `residuals()` option to let the residual variance differ between occasions or, in other words, to allow heteroskedastic level-1 residuals over occasions. Specifically, we request an independence correlation structure (uncorrelated residuals) and estimate a separate variance parameter for each occasion by using the `residuals(independent, by())` option with `grade` as stratification variable:

```
. xtmixed read grade || id: grade, covariance(unstructured) mle
> variance residuals(independent, by(grade))
Mixed-effects ML regression                     Number of obs      =      2676
Group variable: id                              Number of groups   =      1677
                                                Obs per group: min =         1
                                                               avg =       1.6
                                                               max =         3
                                                Wald chi2(1)       =   4917.74
Log likelihood =   -9594.51                     Prob > chi2        =    0.0000
```

read	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
grade	10.25926	.1462962	70.13	0.000	9.972526	10.546
_cons	19.86971	.1887822	105.25	0.000	19.49971	20.23972

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
id: Unstructured				
var(grade)	7.925667	1.933749	4.913092	12.78547
var(_cons)	17.9805	5.403015	9.977499	32.40275
cov(grade,_cons)	2.887511	2.615339	-2.238458	8.013481
Residual: Independent, by grade				
0: var(e)	18.448	5.410546	10.38254	32.77895
1: var(e)	61.0048	4.689077	52.47316	70.92361
2: var(e)	72.76976	7.215601	59.91681	88.37983
3: var(e)	42.89778	11.88699	24.92107	73.84193

```
LR test vs. linear regression:       chi2(6) =   580.77   Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference.
```

As expected, the estimates agree almost perfectly with those obtained using the `sem` command.

We can compare the sample mean reading scores with the estimated model-implied means graphically (shown in figure 7.13) using

```
. predict fixed, xb
. twoway (connected mn_read grade, sort lpatt(solid))
>        (connected fixed grade, sort lpatt(dash)), xtitle(Grade)
>        ytitle(Mean reading score) legend(order(1 "Raw mean" 2 "Fitted mean"))
```

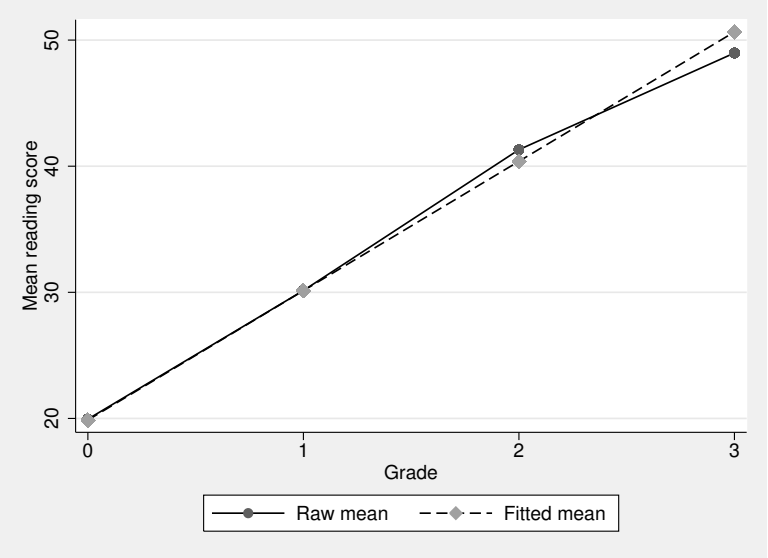


Figure 7.13: Fitted mean trajectory and sample mean trajectory for reading scores

The fitted means of the reading scores from the model are close to the sample means.

We can obtain EB predictions of the latent variables η_{1j} and η_{2j} by first predicting the corresponding disturbances,

```
. predict zeta2 zeta1, reffects
```

and then adding these to the estimated means:

```
. generate eta1 = _b[_cons] + zeta1
. generate eta2 = _b[grade] + zeta2
```

These predictions agree to at least three decimal places with the predictions `l1` and `l2` produced by `predict` after the `sem` command.

7.8 Summary and further reading

In this chapter, we have discussed growth-curve models, demonstrating how to model nonlinear growth using either polynomial or piecewise linear functions. We have also shown how heteroskedasticity can be modeled for both level-1 residuals and random effects. Serial correlations for the level-1 residuals can also be modeled; see section 6.4.1 and exercise 7.8. Keep in mind that adding more parameters to a model can render the model unidentified for a given data structure, as discussed for random-coefficient models in section 4.10.4. Importantly, the standard linear growth-curve model is not identified with two balanced occasions.

We also described how growth-curve models can alternatively be viewed as SEMs with latent variables and fit using the `sem` command. Whether a growth-curve model is viewed as a multilevel model or an SEM is mostly a question of tradition, but there are some differences. In practice, structural equation modelers invariably allow for occasion-specific residual variances, whereas multilevel modelers (implicitly) tend to constrain these variances to be equal. Another difference is that conventional structural equation modeling requires balanced data. A great advantage of SEM is that it is possible to include latent variables measured by multiple indicators. When the response variable in a growth-curve model is latent, such models are sometimes called curve-of-factors growth models or second-order latent growth models. Another advantage of SEM is that it is straightforward to include intervening variables or mediators in the model.

Useful introductions to linear growth-curve models include the book by Singer and Willett (2003, chap. 3–8), the articles by Bryk and Raudenbush (1987) and Willett, Singer, and Martin (1998), and the encyclopedia entry by Singer and Willett (2005). The book by Bollen and Curran (2006) takes a structural equation modeling perspective.

The exercises apply growth-curve models to problems from a range of disciplines. Whereas exercises 7.1 and 7.4 consider heteroskedasticity of the level-1 error over time, exercise 7.3 considers heteroskedasticity of both the level-1 and the level-2 random part between groups, and exercise 7.8 introduces an AR(1) process for the level-1 error (see section 6.4.1). Exercise 7.6 involves a piecewise linear spline with the knot occurring at different times for different individuals. Exercises 7.4 and 7.7 use both the two-stage model formulation and the reduced form. In exercise 7.4, the data come from a randomized experiment.

Growth-curve models for subjects nested in clusters are discussed in section 8.13 and exercises 8.1, 8.4, and 8.7 of the next chapter on higher-level models with nested random effects.

7.9 Exercises

7.1 Growth-in-math-achievement data Solutions

Consider the math outcome in the National Longitudinal Survey of Youth data, `reading.dta`, provided by Bollen and Curran (2006) and described in section 7.6. The math outcome, `math0` to `math3`, is the percentage of correctly answered items on a math achievement test (the same test was used in every grade).

1. Reshape the data to long form, and plot the mean math trajectory over time by minority status.
2. Fit a linear growth-curve model using `xtmixed` with `minority`, a dummy variable for being a minority, as a covariate. The fixed part should include an intercept and a slope for `grade`, and the random part should include random intercepts and random slopes of `grade`. Allow the residual variances to differ between grades.

3. By extending the model from step 2, test whether there is any evidence for a narrowing or widening of the minority gap over time.
4. Plot the mean fitted trajectories for minority and nonminority students.
5. Plot fitted and observed growth trajectories for the first 20 children (`id` less than 15900).
6. Fit the model in step 2, but without `minority` as a covariate, using `sem`.

7.2 Children's growth data

In this exercise, we revisit the Asian children's growth data used in the first part of this chapter.

1. Fit the model in (7.1) using `xtmixed`.
2. For the model and estimates from step 1, obtain EB predictions for the random intercepts and slopes.
3. Perform some residual diagnostics.
4. ❖ Also obtain ML (or OLS) estimates of ζ_{1j} and ζ_{2j} by first subtracting the predicted fixed part of the model and then using the `statsby` command. Merge these estimates into the data. Compare the ML estimates with the EB predictions using scatterplots by sex.

7.3 Jaw-growth data

In this exercise, we use the jaw-growth data `growth.dta`, previously considered in exercise 3.3.

1. Extend the model from exercise 3.3 (with an interaction between age and a dummy variable for girl) to investigate whether there is significant between-subject variability in the growth rate. Retain the simpler model if the likelihood-ratio test is not significant at the 5% level.
2. For the model chosen in step 1, investigate whether the child-level random-effects variances (and covariance if applicable) differ between boys and girls, again using a 5% level of significance.
3. For the model chosen in step 2, relax the assumption that the level-1 errors have the same variance for boys and girls, and test this assumption at the 5% level.
4. For the model selected in step 3, plot the fitted growth trajectories by sex and compare them with the corresponding observed growth trajectories.

7.4 Calcium-supplementation data

Lloyd et al. (1993) describe a study to evaluate the effect of calcium supplementation on bone acquisition in adolescent white girls. Ninety-four girls with a mean age of 11.9 years were randomized to receive 18 months of calcium supplementation (500 mg per day of calcium as calcium citrate malate) or placebo pills. Total body bone mineral density was measured approximately at six-month intervals for about 30 months using a bone absorptiometer.

The data in `calcium.dta` are provided by Vonesh and Chinchilli (1997) and Demidenko (2004), and contain the following variables:

- `id`: subject identifier
- `treat`: treatment group (1: calcium group; 0: placebo group)
- `time`: time in weeks after first intake
- `y`: total body bone mineral density (g/cm^2)

1. Convert the time scale to years after first intake (there are on average 52.177457 weeks per year) and call the new variable `years`.
2. Plot the observed growth trajectories by treatment group.
3. Consider a linear growth-curve model with a random intercept and random slope of `years` and with fixed effects of `years`, `treat`, and the `years` by `treat` interaction.
   a. Write down the model using a two-stage formulation.
   b. Write down the model in reduced form.
   c. Fit the model and interpret the estimated treatment effect.
4. Perform a likelihood-ratio test for the random slope of `years`, and retain it if significant at the 5% level.
5. For the model selected in step 4, relax the assumption that the level-1 residual variance is the same across occasions (create a variable, `visit`, for the occasion or visit number). Use a 5% significance level to decide whether the assumption should be rejected.
6. For the model chosen in step 5, obtain the fitted growth trajectories and plot them for comparison with the observed growth trajectories from step 1.
7. Plot the predicted mean growth trajectories for the two treatment groups.

7.5 Diffusion-of-innovations data

In some U.S. states, the introduction of new medical technology requires a certificate-of-need review to prevent unnecessary capital expenditure by health care facilities. Caudill, Ford, and Kaserman (1995) investigated whether such certificate-of-need regulation has an effect on the diffusion of innovations. Specifically, they considered the adoption of hemodialysis (blood filtering) for kidney failure in 50 U.S. states between 1977 and 1990.

Many states implemented certificate-of-need review of dialysis clinics' investments in the late 1970s and early 1980s, and many states eliminated such a review in the late 1980s. This change in policy allowed Caudill, Ford, and Kaserman to examine whether certificate-of-need regulation has slowed the rate of diffusion of hemodialysis technology.

They let L_i be the number of dialysis machines in state i in the most recent period in the sample and P_{it} be the number of dialysis machines in state i at time t. Using

the transformation $\ln\{P_{it}/(L_i - P_{it})\}$, Caudill, Ford, and Kaserman specified the following model (using their notation):

$$\ln\{P_{it}/(L_i - P_{it})\} \;=\; a_i + c_i T_t + d_i T_t \times \mathrm{Con}_{it} + \epsilon_{it}$$

where T_t is an index of the time period that begins at $T_1 = 1$ in 1977 and Con_{it} is a dummy variable indicating that certificate-of-need regulation was in effect in state i at time t.

The random intercept a_i and the random coefficients c_i and d_i are assumed to be independently distributed with means μ_a, μ_c, and μ_d, respectively, and variances σ_a^2, σ_c^2, and σ_d^2, respectively. ϵ_{it} has zero mean, variance σ_ϵ^2, and is independent of a_i, c_i, and d_i.

The dataset `data.cfk` from the *Journal of Applied Econometrics Data Archive* has the following variables:

- `state`: an identifier for the U.S. states
- `T`: the time index T_t
- `TCon`: the interaction $T_t \times \mathrm{Con}_{it}$
- `resp`: the response variable $\ln\{P_{it}/(L_i - P_{it})\}$

1. Read the data using the `infile` command (the variables are in the same order as listed above).
2. Fit the model specified by Caudill, Ford, and Kaserman using the `xtmixed` command, noting that they specified the random effects as uncorrelated. The random effects have nonzero means, whereas `xtmixed` assumes zero means. You can accommodate the means in the fixed part of the model.
3. Do the estimates suggest that certificate-of-need legislation slows the rate of diffusion of hemodialysis technology?
4. If you can get hold of the paper, compare your estimates with the ML estimates in table 1 of Caudill, Ford, and Kaserman (1995).
5. Perform a likelihood-ratio test for the null hypothesis

   $$\mathrm{H}_0\text{: } \sigma_c^2 = \sigma_d^2 = 0$$

   Note that the "naïve" test is conservative because the null hypothesis involves two parameters on the border of the parameter space. (You could use the correct asymptotic null distribution given in display 8.1.)
6. Does the conclusion for the effect of certificate-of-need-legislation change when the restricted model (with $\sigma_c^2 = \sigma_d^2 = 0$) is used?
7. Perform residual diagnostics for the selected model, as described in section 3.9.

7.6 Fat-accretion data

Fitzmaurice, Laird, and Ware (2011) analyzed data on the influence of menarche (onset of menstruation) on body fat accretion. They used longitudinal data

from a prospective study on body fat accretion in a cohort of 162 girls from the MIT Growth and Development Study (Bandini et al. 2002; Phillips et al. 2003; Naumova, Must, and Laird 2001). (Fitzmaurice, Laird, and Ware [2011] point out that the data represent a subset of the full study and should not be used to draw substantive conclusions.)

At the start of the study, all the girls were premenarcheal and nonobese, as determined by a triceps skinfold thickness less than the 85th percentile. The girls were examined annually until four years after menarche. The response variable is a measure of body fatness based on bioelectric impedance analysis from which a measure of percent body fat was derived.

The variables in the dataset `fat.dta` are the following:

- `id`: subject identifier
- `time`: time since menarche in years (negative if before menarche) (t_{ij})
- `fat`: percent body fat (y_{ij})
- `age`: age in years
- `menarche`: age at menarche (in years)

Fitzmaurice (1998) considers the following model:

$$y_{ij} = \beta_1 + \beta_2 t_{ij} + \beta_3 (t_{ij})_+ + \zeta_{1j} + \zeta_{2j} t_{ij} + \zeta_{3j} (t_{ij})_+ + \epsilon_{ij},$$

where t_{ij} is time since menarche and $(t_{ij})_+ = t_{ij}$ if $t_{ij} > 0$ and $(t_{ij})_+ = 0$ if $t_{ij} \leq 0$. The usual assumptions are made regarding the random effects and error term.

1. Interpret the following terms:
   - $\beta_1 + \zeta_{1j}$
   - $\beta_2 + \zeta_{2j}$
   - $\beta_3 + \zeta_{3j}$
2. Fit the model by ML and interpret the estimates.
3. Produce a scatterplot of the percent body fat measurements versus time, with the fitted mean curve superimposed.

7.7 Adolescent-alcohol-use data

Consider the data described in exercise 6.3. Using Singer and Willett's (2003) two-stage formulation (in their notation except that i is occasion and j is subject), consider the level-1 model

$$Y_{ij} = \pi_{0j} + \pi_{1j} t_i + \epsilon_{ij}$$

and the level-2 models

$$\begin{aligned} \pi_{0j} &= \gamma_{00} + \gamma_{01} w_{1j} + \gamma_{02} w_{2j} + \zeta_{0j} \\ \pi_{1j} &= \gamma_{10} + \gamma_{11} w_{1j} + \gamma_{12} w_{2j} + \zeta_{1j} \end{aligned}$$

1. Substitute the level-2 models into the level-1 model to obtain the reduced-form model.
2. Interpret each of the parameters in terms of initial status at age 14, π_{0j}, and the rate of growth π_{1j}.
3. Fit the model by ML using `xtmixed` and interpret the estimates.
4. Separately for children of alcoholics and other children, plot the fitted trajectories together with the data using trellis graphs.
5. Obtain the estimated marginal variances and correlation matrix of the total residuals. You can use the `xtmixed_corr` command described in section 6.3.1. Note that `xtmixed_corr` stores the covariance matrix as `r(V)`.
6. Fit latent growth-curve models using `sem`.
   a. Fit a standard latent growth-curve model without covariates as shown in section 7.7.1.
   b. Include covariates by specifying equations for the latent variables. For example, if the random intercept is called `L1`, add `(L1 <- coa peer _cons)`. Also add `cov(e.L1*e.L2)` to specify that the residuals ζ_{0j} and ζ_{1j} are correlated, and remove the `means()` option.
   c. Why are the estimates not the same as in step 3?
   d. ❖ Modify the model so that it corresponds exactly to the model fit in step 3 (with practically identical estimates).

7.8 Unemployment-claims data

Papke (1994) analyzed panel data on Indiana's enterprise zone program which provided tax credits for areas of cities with high unemployment and high poverty levels. One of the purposes was to investigate whether inclusion in an enterprise zone would reduce the number of unemployment claims (see also exercises 5.3 and 5.4). Data were from 22 unemployment claims offices (serving a zone and the surrounding city), 6 of which were included as enterprise zones in 1984 and 4 more of which were included as zones in 1985.

The dataset `ezunem.dta` supplied by Wooldridge (2010) contains the following variables:

- `city`: unemployment claims office identifier (j)
- `year`: year (i)
- `uclms`: number of unemployment claims (y_{ij})
- `ez`: dummy variable for office being in an enterprise zone (x_{2ij})
- `t`: time 1, ..., 9 (x_{3i})

Use ML to fit the models in this exercise.

1. Fit the random-intercept model

$$\ln(y_{ij}) \;=\; \tau_i + \beta_2 x_{2ij} + \zeta_j + \epsilon_{ij}$$

   where τ_i is a fixed year-specific intercept and ζ_j is an office-specific random intercept.

a. Interpret the estimated regression coefficients and random-intercept variance.
b. Does the enterprise zone program appear to reduce unemployment claims?

2. Fit the random-intercept model

$$\ln(y_{ij}) = \tau_i + \beta_2(x_{2ij} - \overline{x}_{2\cdot j}) + \beta_3\overline{x}_{2\cdot j} + \zeta_j + \epsilon_{ij}$$

where $\overline{x}_{2\cdot j}$ is the proportion of the panel waves when unemployment claims office j is in an enterprise zone.

a. Interpret the estimated regression coefficients β_2 and β_3.
b. Use the fitted model to test for level-2 endogeneity or office-level confounding.

3. Fit a random-coefficient model with a random intercept and random slope of time:

$$\ln(y_{ij}) = \tau_i + \beta_2 x_{2ij} + \zeta_{1j} + \zeta_{2j}x_{3i} + \epsilon_{ij}$$

Note that time is treated as a categorical variable in the fixed part of the model and as a continuous variable in the random part.

a. Is the random slope required? Use a 5% level of significance.
b. Interpret the fixed and random effects of time in this model.
c. Instead of treating `year` as continuous in the random part of the model, consider a model where the random part consists of a random intercept and random coefficients of eight dummy variables for the years. Explain why such a model is not identified (see section 4.10.4).

4. Fit a random-coefficient model including a random intercept, a random slope of time, and an AR(1) process for the residuals

$$\ln(y_{ij}) = \tau_i + \beta_2 x_{2ij} + \zeta_{1j} + \zeta_{2j}x_{3i} + \epsilon_{ij}, \qquad \epsilon_{ij} = \alpha\epsilon_{i-1,j} + u_{ij}$$

under the usual assumptions.

a. Which features of the random part of this model induce dependence of claims within offices over time?
b. Check whether setting $\alpha = 0$ or $\psi_{22} = 0$ produces a significant deterioration in model fit.

Part IV

Models with nested and crossed random effects

8 Higher-level models with nested random effects

8.1 Introduction

We have until now considered two-level data where units are nested in groups or clusters. In three-level data,the clusters themselves are nested in superclusters, forming a hierarchical structure. For example, we may have repeated measurement occasions (at level 1) for patients (at level 2) who are clustered in hospitals (at level 3). This three-level design is displayed in figure 8.1. It seems reasonable to expect that measurements on different patients within the same hospital are correlated and that measurements on the same patient are even more correlated.

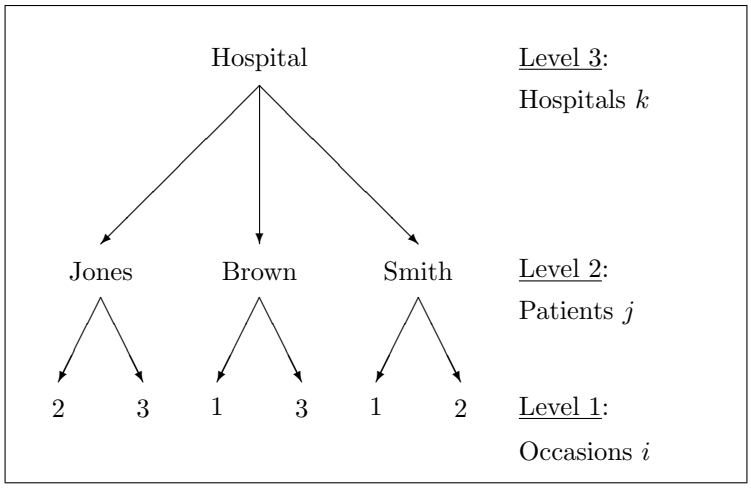


Figure 8.1: Illustration of three-level design

Other examples of three-level longitudinal designs include repeated measures on students nested in schools, and repeated measures on employees nested in firms. Examples of three-level cross-sectional designs include data on students nested in classes nested in schools, teeth nested in patients nested in dentists, and patients nested in physicians nested in hospitals.

In these examples, the level-1 units can be thought of as being grouped according to two classifications, for instance, students are grouped into both classes and schools. Nesting refers to the fact that the lower-level classification (here classes at level 2) results from subdividing units belonging to the same higher-level classification (here schools at level 3). All units belonging to the same level-2 clusters (for example, all students belonging to the same class) must also belong to the same level-3 supercluster (here school). Such data structures are referred to as *hierarchical*.

Violations of an apparently hierarchical structure are not uncommon. For instance, for patients nested in physicians nested in hospitals, some physicians may treat patients in multiple hospitals. For longitudinal data on students nested in schools, some students may switch schools. If the violations are rare, we can handle them by discarding some of the data or assigning units to the group to which they belong most often. Otherwise, models with *crossed* random effects may be necessary, as discussed in chapter 9.

A factor or classification such as school constitutes a *level* only if it is treated as random. It does not matter if students are cross-classified by ethnicity and school because ethnicity will typically be treated as fixed. Sometimes two factors are cross-classified and one factor is treated as the higher level, whereas the *interaction* between the two factors is treated as the lower level. For instance, in a study of house prices, houses may be classified by U.S. state and by whether they are in an urban or rural area. Then state may be treated as random at level 3, and the interaction between state and a dummy variable for urban area (versus rural area) treated as random at level 2. The level-2 random effect is nested in states because it takes on a different value for each combination of state and urban (versus rural) area to allow the effect of urban area to be different in different states. The model may also include a fixed main effect of a dummy variable for urban to represent the average difference in house prices between urban and rural areas across states.

8.2 Do peak-expiratory-flow measurements vary between methods within subjects?

In chapter 2, we considered test–retest data for peak-expiratory-flow measurements taken using only the Mini Wright meter. Here we will analyze the full dataset shown in table 2.1 on page 75, where two methods were used: the Mini Wright peak-flow meter and the standard Wright peak-flow meter, each on two occasions. The full dataset can be used for a method comparison study to investigate the performance of the measurement methods.

We first read in the data,

```
. use http://www.stata-press.com/data/mlmus3/pefr
```

and stack the measurements at the two occasions into one variable for each method, as shown in section 2.5:

```
. reshape long wp wm, i(id) j(occasion)
(note: j = 1 2)
Data                               wide   ->   long
-----------------------------------------------------------------------------
Number of obs.                       17   ->      34
Number of variables                   5   ->       4
j variable (2 values)                     ->   occasion
xij variables:
                                 wp1 wp2   ->   wp
                                 wm1 wm2   ->   wm
-----------------------------------------------------------------------------
```

We then stack the responses `wm` for the Mini Wright peak-flow meter and `wp` for the Wright peak-flow meter into a single response, `w`, producing a string variable, `meth`, equal to the suffixes `m` and `p`. To do this using Stata's `reshape long` command with the `string` option, we must first create a new variable, `i`, for the `i()` option that takes on a different value for each observation in the wide dataset:

```
. generate i = _n
. reshape long w, i(i) j(meth) string
(note: j = m p)
Data                               wide   ->   long
-----------------------------------------------------------------------------
Number of obs.                       34   ->      68
Number of variables                   5   ->       5
j variable (2 values)                     ->   meth
xij variables:
                                  wm wp   ->   w
-----------------------------------------------------------------------------
. sort id meth occasion
. list id meth occasion w in 1/8, clean noobs
    id   meth   occasion     w
     1      m          1   512
     1      m          2   525
     1      p          1   494
     1      p          2   490
     2      m          1   430
     2      m          2   415
     2      p          1   395
     2      p          2   397
```

We can convert the *string variable* `meth` to a numeric variable by using the `encode` command, which assigns successive integer values to the strings sorted in alphabetical order (here `m` becomes 1 and `p` becomes 2):

```
. encode meth, generate(method)
```

A dummy variable for `method` equal to 2 (the Mini Wright meter, `meth` equal to `m`) is then easy to create using the `recode` command:

```
. recode method 2=0
```

8.3 Inspecting sources of variability

We can plot all four peak-expiratory-flow measurements against the subject identifier using different symbols for the methods, giving the graph in figure 8.2:

```
. twoway (scatter w id if method==0, msymbol(circle))
> (scatter w id if method==1, msymbol(circle_hollow)),
> xtitle(Subject id) ytitle(Peak-expiratory-flow measurements)
> legend( order(1 "Wright" 2 "Mini Wright")) xlabel(1/17)
```

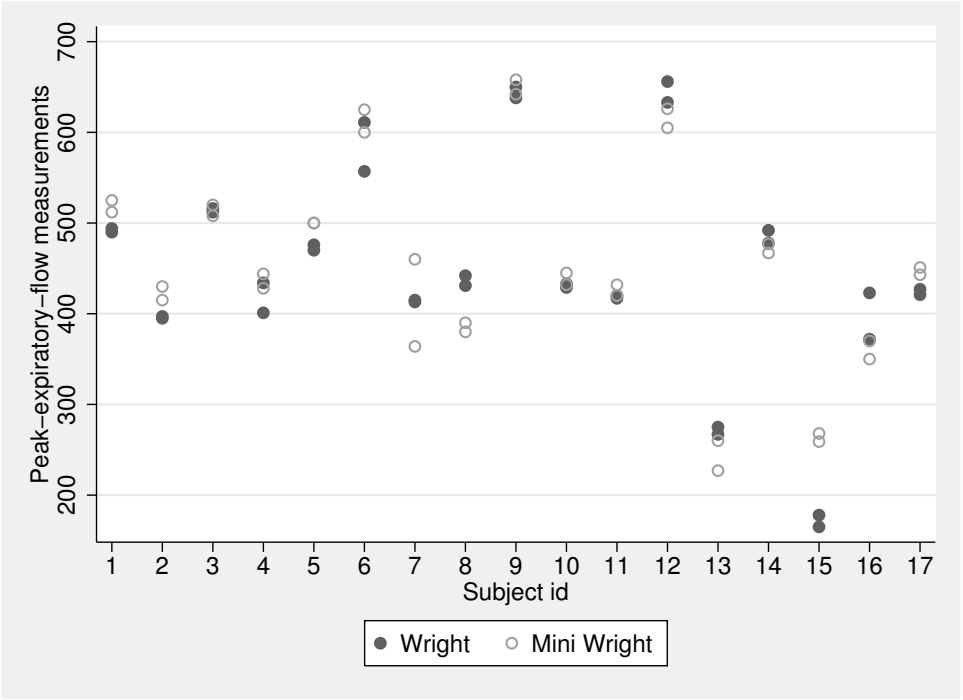


Figure 8.2: Scatterplot of peak expiratory flow measured by two methods versus subject

As would be expected, measurements on the same subjects are more similar than measurements on different subjects. This between-subject heterogeneity can be modeled by a subject-level random intercept, as we did in chapter 2. However, the figure also suggests that for a given subject, the measurements using the same method tend to resemble each other more than measurements using the other method, so that the responses for the same method are not conditionally independent given the subject-level random intercept. The phenomenon can also be described as between-method heterogeneity within subjects because the measurements made by the same instrument (or method) tend to be shifted up or down relative to the measurements made by the other instrument, with shifts that vary between subjects. For some subjects (for example, the first two), the Wright peak-flow meter measurements are lower, whereas

for other subjects (for example, subjects 8 and 12) the Mini Wright meter measurements are lower. Furthermore, the difference between methods is large for some subjects (for example, subject 15) and small for others (for example, subjects 3, 9, 10, and 11). In a measurement context, this kind of method by subject interaction is sometimes referred to as subject-specific bias of the methods (see Dunn [1992]).

8.4 Three-level variance-components models

We can accommodate the between-method within-subject heterogeneity apparent in figure 8.2 by including a random intercept for each combination of method and subject in addition to a random intercept for subject. The random intercept for method is nested within subjects in the sense that it does not take on the same value for a given method across all subjects, but takes on a different value for each combination of method and subject. We will therefore think of occasions as level 1, methods as level 2, and subjects as level 3.

The three-level variance-components model can be written as

$$y_{ijk} \;=\; \beta + \zeta^{(2)}_{jk} + \zeta^{(3)}_{k} + \epsilon_{ijk}$$

where $\zeta^{(2)}_{jk}$ is the random intercept for method j and subject k, and $\zeta^{(3)}_{k}$ is the random intercept for subject k. Here the superscripts denote the levels at which the random intercepts vary.

The error components ϵ_{ijk}, $\zeta^{(2)}_{jk}$, and $\zeta^{(3)}_{k}$ are assumed to have zero means and to be mutually uncorrelated so that their variances add up to the total variance. The corresponding variance components are the variance θ of the level-1 residuals, the variance $\psi^{(2)}$ of the level-2 random intercepts, and the variance $\psi^{(3)}$ of the level-3 random intercepts. The level-1 variance θ can be interpreted as the between-occasion, within-method, and within-subject variance. The level-2 variance $\psi^{(2)}$ is the between-methods, within-subjects variance. And the level-3 variance $\psi^{(3)}$ is the between-subjects variance. A large between-methods within-subjects variance would mean that there is a large method by subject interaction. All three error components are uncorrelated across subjects, the level-2 random intercepts and level-1 residuals are uncorrelated across methods, and the level-1 residuals are uncorrelated across occasions.

The error components for the three-level variance-components model are shown for a subject k in figure 8.3.

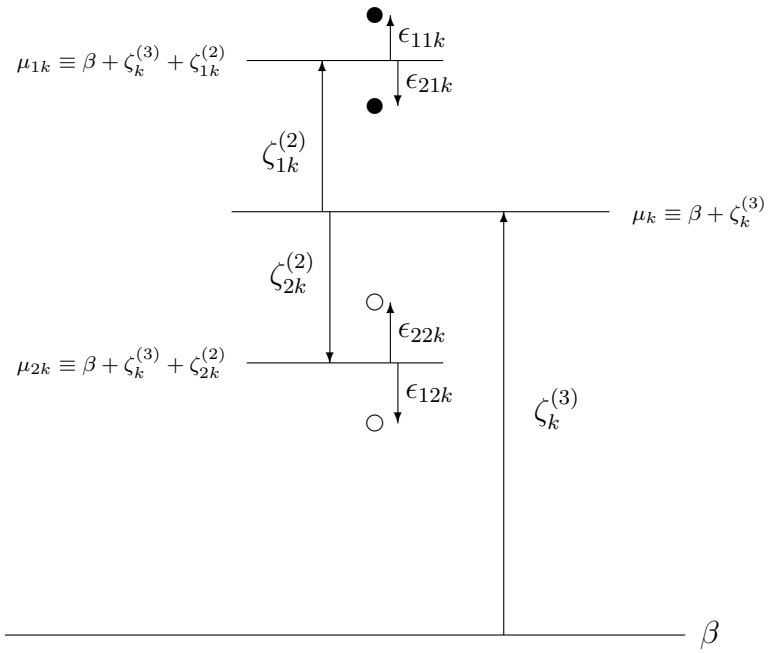


Figure 8.3: Illustration of error components for the three-level variance-components model for a subject k

The overall expectation or mean peak-expiratory-flow measurement for the population of subjects is $E(y_{ijk}) = \beta$, given as the bottom line in the figure. In the first stage, a random intercept $\zeta_k^{(3)}$ is drawn for a subject k from a distribution with mean 0 and variance $\psi^{(3)}$, resulting in a mean measurement for subject k equal to $\mu_k \equiv E(y_{ijk}|\zeta_k^{(3)}) = \beta + \zeta_k^{(3)}$. (In the measurement context, μ_k is the subject's true score.) In the second stage, a random intercept $\zeta_{1k}^{(2)}$ is drawn for the first method $j=1$ from a distribution with mean 0 and variance $\psi^{(2)}$. This produces a method-1-specific mean measurement for subject k equal to $\mu_{1k} \equiv E(y_{ijk}|\zeta_k^{(3)}, \zeta_{1k}^{(2)}) = \beta + \zeta_k^{(3)} + \zeta_{1k}^{(2)}$. For the second method $j=2$, a random intercept $\zeta_{2k}^{(2)}$ is drawn from the same distribution as for the first method, producing a method-2-specific mean measurement for subject k equal to $\mu_{2k} \equiv E(y_{ijk}|\zeta_k^{(3)}, \zeta_{2k}^{(2)}) = \beta + \zeta_k^{(3)} + \zeta_{2k}^{(2)}$. Finally, in the third stage, level-1 residuals ϵ_{11k} and ϵ_{21k} are drawn from a distribution with mean 0 and variance θ, resulting in the two observed measurements y_{11k} and y_{21k} (represented by the filled dots) for method $j=1$. Similarly, the two observed measurements y_{12k} and y_{22k} (represented by the hollow dots) for method $j=2$ are obtained by drawing level-1 residuals ϵ_{12k} and ϵ_{22k} from the same distribution.

The random part of the model is represented by a path diagram in figure 8.4. The rectangles represent observed variables, here the responses y_{11k}, y_{21k}, y_{12k}, and y_{22k} for subject k. The k subscript is implied by the label "subject k" inside the frame surrounding the diagram. The circles represent the random effects $\zeta_{1k}^{(2)}$ for method 1 and subject k, $\zeta_{2k}^{(2)}$ for method 2 and subject k, and $\zeta_k^{(3)}$ for subject k, again with k subscripts not shown. The long arrows represent regressions, here with regression coefficients set to 1, and the short arrows from below represent additive error terms ϵ_{ijk} (also with coefficients set to 1). For instance, y_{12k} (with $i=1$ and $j=2$) is regressed on $\zeta_{2k}^{(2)}$ and $\zeta_k^{(3)}$ with additive error term ϵ_{12k}

$$y_{12k} \;=\; \zeta_{2k}^{(2)} + \zeta_k^{(3)} + \epsilon_{12k} + \cdots$$

where the "$\cdots$" indicates that the fixed part of the model (here β) is not shown.

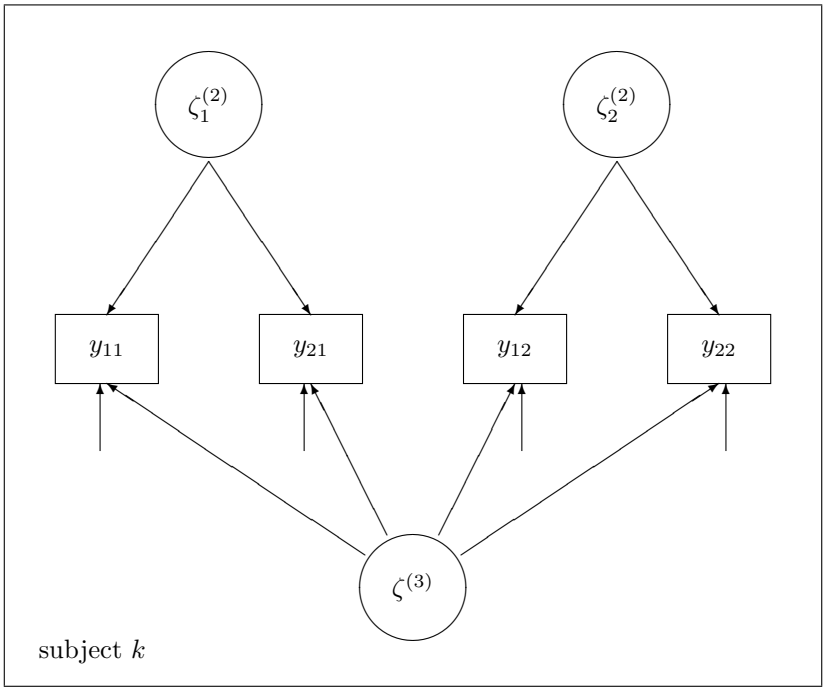


Figure 8.4: Path diagram of random part of three-level model

We see that responses (here measurements) for the same subject are correlated because they all depend on the shared level-3 random intercept $\zeta_k^{(3)}$. Conditional on $\zeta_k^{(3)}$,

responses for the same method are not independent but correlated because they depend on the shared level-2 random intercepts $\zeta_{1k}^{(2)}$ or $\zeta_{2k}^{(2)}$. However, responses for different methods, such as y_{11k} and y_{12k}, are conditionally independent given the subject-level random intercept $\zeta_k^{(3)}$.

8.5 Different types of intraclass correlation

For three-level models, we can consider several types of intraclass correlations. For measurements i and i' on the same subject k, using *different* methods j and j', the intraclass correlation becomes

$$\rho(\text{subject}) \equiv \text{Cor}(y_{ijk}, y_{i'j'k}) = \frac{\psi^{(3)}}{\psi^{(2)} + \psi^{(3)} + \theta}$$

The denominator is the product of standard deviations of y_{ijk} and $y_{i'j'k}$ (each equal to the square root of the denominator), and the numerator is the covariance between these responses. We can derive this covariance by taking the expectation of the product of the random parts for each variable,

$$\begin{aligned} E\{(\zeta_k^{(3)} + \zeta_{jk}^{(2)} + \epsilon_{ijk})(\zeta_k^{(3)} + \zeta_{j'k}^{(2)} + \epsilon_{i'j'k})\} &= E\{(\zeta_k^{(3)})^2\} + E(\zeta_k^{(3)}\zeta_{j'k}^{(2)}) + E(\zeta_k^{(3)}\epsilon_{i'j'k}) \\ &\quad + E(\zeta_{jk}^{(2)}\zeta_k^{(3)}) + E(\zeta_{jk}^{(2)}\zeta_{j'k}^{(2)}) + E(\zeta_{jk}^{(2)}\epsilon_{i'j'k}) \\ &\quad + E(\epsilon_{ijk}\zeta_k^{(3)}) + E(\epsilon_{ijk}\zeta_{j'k}^{(2)}) + E(\epsilon_{ijk}\epsilon_{i'j'k}) \\ &= E\{(\zeta_k^{(3)})^2\} = \psi^{(3)} \end{aligned}$$

All terms except the first are zero because the error components in the product are uncorrelated, either because the error components are at different levels or because they are not for the same level-2 unit [in the case of $E(\zeta_{jk}^{(2)}\zeta_{j'k}^{(2)})$] or the same level-1 unit [in the case of $E(\epsilon_{ijk}\epsilon_{i'j'k})$].

For measurements on the same subject k, using the *same* method j, we get

$$\rho(\text{method}, \text{subject}) \equiv \text{Cor}(y_{ijk}, y_{i'jk}) = \frac{\psi^{(2)} + \psi^{(3)}}{\psi^{(2)} + \psi^{(3)} + \theta}$$

We can derive the numerator by substituting j for j' in the derivation above. Then we see that another nonzero term now contributes to the covariance, namely, $E(\zeta_{jk}^{(2)}\zeta_{jk}^{(2)}) = \psi^{(2)}$. This intraclass correlation can be thought of as the test–retest reliability for each method. The models considered here assume that both methods are equally reliable, an assumption we relax in exercise 8.11.

In both intraclass correlations, the numerator is equal to the variance shared by the measurements, and the denominator is just the total variance. In a proper three-level model, the variances of the random intercepts are positive, $\psi^{(2)} > 0$ and $\psi^{(3)} > 0$, and it follows that $\rho(\text{method}, \text{subject}) > \rho(\text{subject})$. This relationship makes sense because,

as we saw in figure 10.2, measurements for the same subject are more correlated if they use the same method than if they use different methods.

We also saw in figure 8.4 that responses for the same method (for example, y_{11k} and y_{21k}) are connected via two paths, one through $\zeta_{1k}^{(2)}$ and the other through $\zeta_k^{(3)}$, whereas responses for different methods (for example, y_{21k} and y_{12k}) are connected via only one of these paths, through $\zeta_k^{(3)}$, making them less correlated.

8.6 Estimation using xtmixed

When there are several nested levels, we simply specify an equation for the random part at each level, starting with the highest level and working our way down.

Here we start with the random part `|| id:` for subjects at level 3, followed by the random part `|| method:` for methods within subject at level 2:

```
. xtmixed w || id: || method:, mle
Mixed-effects ML regression                     Number of obs      =        68
```

Group Variable	No. of Groups	Observations per Group Minimum	Average	Maximum
id	17	4	4.0	4
method	34	2	2.0	2

```
                                                Wald chi2(0)       =         .
Log likelihood = -345.29005                     Prob > chi2        =         .
```

w	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
_cons	450.8971	26.63839	16.93	0.000	398.6868	503.1074

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
id: Identity				
sd(_cons)	108.6037	19.05411	77.00246	153.1739
method: Identity				
sd(_cons)	19.47623	4.829488	11.97937	31.66474
sd(Residual)	17.75859	2.153545	14.00184	22.52329

```
LR test vs. linear regression:       chi2(2) =   143.81   Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference.
```

At the top of the output, we see that there are 17 subjects with 4 observations each and 34 methods-within-subjects (combinations of 2 methods with 17 subjects) with 2 observations each. The mean peak-expiratory-flow measurement is estimated as 450.9. In the random part of the model, the between-subject standard deviation $\sqrt{\psi^{(3)}}$ is estimated as 108.6, and the between-methods within-subjects standard deviation $\sqrt{\psi^{(2)}}$

is estimated as 19.5. Finally, the standard deviation $\sqrt{\theta}$ between occasions, within methods and subjects, is estimated as 17.8. We could obtain the corresponding variances using the `variance` option. The estimates for this variance-components model are also presented under "VC" in table 8.1.

Table 8.1: Maximum likelihood estimates for two-level and three-level variance-components (VC) and random-intercept (RI) models for peak-expiratory-flow data

	VC		RI	
	Est	(SE)	Est	(SE)
Fixed part				
β_1	450.90	(26.6)	447.9	(26.9)
β_2			6.0	(7.8)
Random part				
$\sqrt{\psi^{(2)}}$	19.5		19.0	
$\sqrt{\psi^{(3)}}$	108.6		108.6	
$\sqrt{\theta}$	17.8		17.8	
Log likelihood	−345.29		−345.00	

The number of highest-level units, subjects, is quite small, so the subject-level variance is not very precisely estimated. Perhaps the parameters should be estimated by REML instead of ML to avoid a downward-biased variance estimate. In higher-level models, asymptotics rely on the number of highest-level units becoming large, so tests and confidence intervals may not perform well in this application.

Plugging in estimates for the variance components in the expressions for the intraclass correlations, the estimated intraclass correlation between measurements on the same subject using the same method is

$$\widehat{\rho}(\text{method},\text{subject}) = \frac{19.476^2 + 108.604^2}{19.476^2 + 108.604^2 + 17.759^2} = 0.97$$

and the corresponding estimated intraclass correlation using different methods is

$$\widehat{\rho}(\text{subject}) = \frac{108.604^2}{19.476^2 + 108.604^2 + 17.759^2} = 0.94$$

We see that the peak-expiratory-flow measurements are extremely reliable, whether the same or different methods are used.

8.7 Empirical Bayes prediction

Empirical Bayes prediction of the random intercepts $\zeta_{jk}^{(2)}$ for the combination of methods and subjects and the random intercepts $\zeta_k^{(3)}$ for subjects is straightforward after

estimation with `xtmixed`. We simply use the `predict` command with the `reffects` option, specifying as many variables as there are random effects (here 2), keeping in mind the ordering of random effects from the highest to the lowest levels:

```
. predict subj instr, reffects
```

We can list the predictions for the first seven subjects (after defining labels for the values of `method`):

```
. sort id method
. label define m 0 "Wright" 1 "Mini Wright"
. label values method m
. list id method subj instr if id<8 & occasion==1, noobs sepby(id)
```

id	method	subj	instr
1	Wright	53.14315	-8.504796
1	Mini Wright	53.14315	10.2139
2	Wright	-40.72008	-10.01413
2	Mini Wright	-40.72008	8.704561
3	Wright	61.6984	.9921208
3	Mini Wright	61.6984	.9921208
4	Wright	-23.60959	-6.91353
4	Mini Wright	-23.60959	6.154238
5	Wright	34.81049	-8.97618
5	Mini Wright	34.81049	10.0957
6	Wright	144.0732	-7.748992
6	Mini Wright	144.0732	12.38243
7	Wright	-37.05355	.1105384
7	Mini Wright	-37.05355	-1.302193

We see from the predictions $\widetilde{\zeta}_{jk}^{(2)}$ in the last column that, just as suggested by figure 8.2, for subjects 1, 2, 4, 5, and 6 the Mini Wright meter appears to be positively biased compared with the Wright peak-flow meter; this bias is reversed for subject 7. For subject 3, the empirical Bayes predictions for both methods are small because all four measurements nearly coincide.

8.8 Testing variance components

Is the between-methods within-subjects variance significantly different from zero? We can answer this question by testing

$$H_0\text{: } \psi^{(2)} = 0 \qquad \text{against} \qquad H_a\text{: } \psi^{(2)} > 0$$

using a likelihood-ratio test. We first save the estimates from the three-level model:

```
. estimates store thrlev
```

Then we fit the two-level model in which the level-2 random intercept no longer appears (equivalent to setting its variance $\psi^{(2)}$ to zero)

```
. quietly xtmixed w || id:, mle
```

where the `quietly` prefix command suppressed the display of output. We perform a likelihood-ratio test using

```
. lrtest thrlev .
Likelihood-ratio test                                 LR chi2(1)  =      9.20
(Assumption: . nested in thrlev)                      Prob > chi2 =    0.0024
Note: The reported degrees of freedom assumes the null hypothesis is not on
      the boundary of the parameter space.  If this is not true, then the
      reported test is conservative.
```

The test is conservative because the null hypothesis is on the boundary of the parameter space. We have encountered this problem in previous chapters when testing a random-intercept variance in a random-intercept model (section 2.6.2) or when testing a random-slope variance in a model containing a random intercept and random slope (section 4.6). Although the latter situation seems similar to our current one in the sense that we are testing the variance of one random effect when another random effect is in the model, the situation is different here because the random effects are *uncorrelated*. Display 8.1 shows the asymptotic null distributions for various testing situations when all the random effects in the model are mutually uncorrelated. For testing one variance when another uncorrelated random effect is in the model, the asymptotic null distribution is $0.5\chi^2(0)+0.5\chi^2(1)$ and we can simply divide the p-value by 2, giving 0.0012.

The asymptotic null distribution for testing the null hypothesis of k *uncorrelated* random effects (where k could be zero) against the alternative of $k+\ell$ *uncorrelated* random effects is

$$\sum_{m=0}^{\ell} \frac{1}{2^\ell} \binom{\ell}{m} \chi^2(m)$$

(see also Verbeke and Molenberghs [2003]).

We give the asymptotic null distributions for $\ell = 1, 2, 3$:

- The asymptotic null distribution for testing k uncorrelated random effects against the alternative of $k+1$ uncorrelated random effects becomes

$$\sum_{m=0}^{1} \frac{1}{2} \binom{1}{m} \chi^2(m) \;=\; \frac{1}{2}\chi^2(0) + \frac{1}{2}\chi^2(1)$$

- The asymptotic null distribution for testing k uncorrelated random effects against the alternative of $k+2$ uncorrelated random effects becomes

$$\sum_{m=0}^{2} \frac{1}{4} \binom{2}{m} \chi^2(m) \;=\; \frac{1}{4}\chi^2(0) + \frac{1}{2}\chi^2(1) + \frac{1}{4}\chi^2(2)$$

- The asymptotic null distribution for testing k uncorrelated random effects against the alternative of $k+3$ uncorrelated random effects becomes

$$\sum_{m=0}^{3} \frac{1}{8} \binom{3}{m} \chi^2(m) \;=\; \frac{1}{8}\chi^2(0) + \frac{3}{8}\chi^2(1) + \frac{3}{8}\chi^2(2) + \frac{1}{8}\chi^2(3)$$

Display 8.1: Asymptotic null distributions for likelihood-ratio testing of variance components when random effects are uncorrelated

8.9 Crossed versus nested random effects revisited

The peak-expiratory-flow measurements are cross-classified by subject (17 individuals), method (Wright meter or Mini Wright meter), and occasion (first or second occasion for each method) according to a $17 \times 2 \times 2$ full factorial design. In such designs, it is natural to consider "main effects" of factors or categorical explanatory variables (here subjects, methods, and occasions), that is, effects that are constant across the categories of the other variables, as well as interactions between factors. If the main effects of several cross-classified factors are random, the model is said to include crossed random effects. Models with crossed random effects are the topic of chapter 9.

The three-level variance-components model considered above has a random main effect for only *one* of the factors, namely, subjects. There is another random effect for methods within subjects, or in other words, the method by subject interaction. This interaction (each of the 34 combinations of subjects and methods) is nested within subjects, so crossed random effects were not required.

The model does not include a main effect for methods and therefore assumes that the mean response over subjects and occasions is the same for both methods. We can relax this assumption by including a dummy variable x_j for the Mini Wright meter:

$$y_{ijk} = \beta_1 + \beta_2 x_j + \zeta_{jk}^{(2)} + \zeta_k^{(3)} + \epsilon_{ijk}$$

Occasion is ignored here, treating the two measurements for a given subject–method combination as exchangeable replicates.

This model can be fit by including `method` as a covariate in the fixed part of the `xtmixed` command:

```
. xtmixed w method || id: || method:, mle
Mixed-effects ML regression                     Number of obs      =        68
```

Group Variable	No. of Groups	Observations per Group Minimum	Average	Maximum
id	17	4	4.0	4
method	34	2	2.0	2

```
                                                Wald chi2(1)       =      0.60
Log likelihood = -344.99736                     Prob > chi2        =    0.4403
```

w	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
method	6.029412	7.812739	0.77	0.440	-9.283275	21.3421
_cons	447.8824	26.92329	16.64	0.000	395.1137	500.651

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
id: Identity				
sd(_cons)	108.6455	19.04646	77.05295	153.1915
method: Identity				
sd(_cons)	19.00386	4.789038	11.59675	31.14208
sd(Residual)	17.75859	2.153545	14.00184	22.52329

```
LR test vs. linear regression:       chi2(2) =   144.35   Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference.
```

The main effect of method is not significant at the 5% level ($z = 0.77$, $p = 0.44$). The estimates for this three-level random-intercept model were also presented under "RI" in table 8.1 on page 394.

Using ANOVA terminology, the above model includes main effects for methods and subjects and the method by subject interaction. Method is a fixed factor, whereas subject is a random factor. An interaction between a fixed and a random factor is automatically random. The model is called a two-way mixed-effects ANOVA model.

8.10 Does nutrition affect cognitive development of Kenyan children?

Whaley et al. (2003) describe a cluster-randomized intervention study from rural Kenya that was designed to investigate the impact of three different diets on the cognitive development of school children.

The primary dish consumed in the study area, the Embu district on the southeastern slopes of Mount Kenya, is githeri, a vegetable dish composed of maize, beans, vegetable oil, and some greens. Children begin regularly attending school around age 6, when they enter "Standard 1" (grade 1). The school year comprises three 3-month terms, with 1-month breaks between them (April, August, and December). In Standards 1 and 2, the school day lasts from 8 a.m. to 1 p.m. with a 30-minute playground break, and in Standards 3–8, school lasts until 4 p.m. with a 1-hour lunch break. Before the study, no meals were provided at any of the schools, and children infrequently brought a snack or lunch to school.

Twelve schools were selected for the study in 1998. Using a cluster-randomized design, these schools were randomly assigned to one of four nutrition interventions:

1. Githeri and meat (Meat group)
2. Githeri and milk (Milk group)
3. Githeri with additional oil (Calorie group)
4. No feeding (Control group)

All three supplements initially provided 240 kcal. After one year, the amount of supplement was increased to 313 kcal as the children grew. The study continued for 7 terms until the end of Standard 3, for a total of 21 months.

Cognitive assessments were carried out on all children at baseline and in terms 1, 2, 4, and 6. Here we will focus on Raven's colored progressive matrices assessment (Raven's score, for short), where children are presented with a matrix-like arrangement of symbols and are asked to complete the matrix by selecting the appropriate missing symbol from a group of symbols.

Variables in the dataset `kenya.dta` provided by Weiss (2005) include

- `id`: child identifier (j)
- `schoolid`: school identifier (k)
- `rn`: observation number (1, 2, 3, 4, 5) (i)
- `ravens`: Raven's score (Raven's colored progressive matrices assessment) (y_{ijk})
- `relyear`: time in years from baseline (t_{ijk})
- `treatment`: intervention group (1=meat; 2=milk; 3=calorie; 4=control)
- `age_at_time0`: age at baseline
- `gender`: gender of child (1=boy; 2=girl)

We read in the data using

```
. use http://www.stata-press.com/data/mlmus3/kenya
```

8.11 Describing and plotting three-level data

8.11.1 Data structure and missing data

Let us first investigate the missing-data patterns using `xtdescribe`. In some datasets, the level-2 identifier may not be unique across level-3 units, for example, children may be labeled from 1 to n_k for each school, where n_k is the number of children in school k. Although not necessary for the Kenya data, it is good practice to define a child identifier taking a unique value for each combination of `id` and `schoolid` (instead of relying on the values being unique already):

```
. egen child = group(id schoolid)
```

Now we look at missing-data patterns for the children:

```
. quietly xtset child rn
. xtdescribe if ravens<.
   child:  1, 2, ..., 546                                  n =        546
      rn:  1, 2, ..., 5                                    T =          5
           Delta(rn) = 1 unit
           Span(rn)  = 5 periods
           (child*rn uniquely identifies each observation)

Distribution of T_i:   min      5%     25%       50%       75%     95%     max
                         1       3       5         5         5       5       5

     Freq.  Percent    Cum.  |  Pattern
 ---------------------------+---------
       475    87.00   87.00  |  11111
        19     3.48   90.48  |  1111.
        12     2.20   92.67  |  11...
        11     2.01   94.69  |  111..
         8     1.47   96.15  |  1.111
         6     1.10   97.25  |  .1111
         5     0.92   98.17  |  1....
         2     0.37   98.53  |  1..11
         2     0.37   98.90  |  111.1
         6     1.10  100.00  |  (other patterns)
 ---------------------------+---------
       546   100.00          |  XXXXX
```

We see that 87% of children have complete data and that more than 8.6% (3.48% + 2.20%+2.01%+0.92%) of children have monotone missingness patterns—they drop out and do not return after missing an assessment.

We will now investigate how many children there are per school and what proportion of children per school have complete data. To do this, we first count the number of observations per child where the response variable is not missing:

```
. egen numobs2 = count(ravens), by(child)
```

We then define dummy variables `compl` for the child having complete data and `any` for the child having any data:

```
. generate compl = numobs2==5
. generate any = numobs2>0
```

Now we are ready to count the number of children with complete data and any data per school. We cannot simply add up the dummy variable `compl` within school because children with complete data would count five times. We therefore create a dummy variable, `pick_child`, taking the value one exactly once per child and zero otherwise and multiply `compl` and `any` by this variable before summing:

```
. egen pick_child = tag(child)
. egen numcomp3 = total(compl*pick_child), by(schoolid)
. egen numany3 = total(any*pick_child), by(schoolid)
```

We also calculate the proportion of children with complete data in each school:

```
. generate rate = numcomp3/numany3
```

We can now summarize these school-level variables by creating a dummy variable, `pick_school`, to pick out one observation per school:

```
. egen pick_school = tag(schoolid)
. summarize numany3 numcomp3 rate if pick_school==1
```

Variable	Obs	Mean	Std. Dev.	Min	Max
numany3	12	45.5	21.28807	12	91
numcomp3	12	39.58333	18.69593	9	80
rate	12	.8646263	.0560276	.75	.95

The number of children per school ranges from 12 to 91. Between 9 and 80 children per school have complete data, corresponding to a range of proportions of children with complete data from 0.75 to 0.95.

8.11.2 Level-1 variables

We have three kinds of variables—namely, level-1, level-2, and level-3 variables—that vary at the respective levels. `relyear` and `ravens` are level-1 (time-varying) variables, `age_at_time0` and `gender` are level-2 (child-specific) variables, and `treatment` is a level-3 (school-specific) variable. If there were a school-specific, time-varying variable, such as percentage of students with low income, this would typically be treated as level 1.

We can summarize the variability of time-varying variables within and between children, ignoring schools, using the `xtsum` command:

```
. quietly xtset child
. xtsum ravens relyear
```

Variable		Mean	Std. Dev.	Min	Max	Observations
ravens	overall	18.24904	2.984872	0	31	N = 2598
	between		1.946549	6	25.6	n = 546
	within		2.276076	7.999038	27.64904	T-bar = 4.75824
relyear	overall	.6496536	.7074833	-.23	2.01	N = 2598
	between		.1655664	-.15	1.4	n = 546
	within		.6975168	-.4403464	1.993654	T-bar = 4.75824

We see that the Raven's score varies nearly as much between children as within children and that the timing of the assessments varies between children.

To see how much these variables vary between schools, we can find the child means,

```
. egen mn_raven = mean(ravens), by(child)
. egen mn_relyr = mean(relyear), by(child)
```

and then use the `xtsum` command again, after declaring `schoolid` as the cluster identifier using `xtset`, as described below.

8.11.3 Level-2 variables

Before summarizing the child-level variables, we form a dummy variable for boys:

```
. quietly tabulate gender, generate(g)
. rename g1 boy
```

We now find the means and within- and between-school standard deviations of all child-level variables, being sure to use only one observation per child by specifying `if pick_child==1`.

```
. quietly xtset schoolid
. xtsum mn_raven mn_relyr boy age_at_time0 if pick_child==1
```

Variable		Mean	Std. Dev.	Min	Max	Observations
mn_raven	overall	18.25577	1.946549	6	25.6	N = 546
	between		.5474184	17.3875	19.33889	n = 12
	within		1.899147	6.270604	25.47102	T = 45.5
mn_relyr	overall	.6305443	.1655664	-.15	1.4	N = 546
	between		.0303738	.5888706	.6893792	n = 12
	within		.163019	-.1376712	1.402116	T = 45.5
boy	overall	.5201465	.5000521	0	1	N = 546
	between		.0929989	.3333333	.65	n = 12
	within		.4948453	-.1298535	1.186813	T = 45.5
age_at~0	overall	7.630406	1.414575	4.84	15.18	N = 542
	between		.3993327	7.017241	8.487359	n = 12
	within		1.356501	5.05585	14.42585	T = 45.1667

There is some between-school variability in the Raven's sore, but there is negligible between-school variability in the timing of assessments. From the `Min` and `Max` values for `boy`, we see that the percentage of boys per school varies between 33% and 65%.

8.11.4 Level-3 variables

We can summarize the level-3 variable, `treatments`, at the school level (treating school as the unit of analysis) by reporting the number of schools in each treatment group,

```
. tabulate treatment if pick_school==1
```

	Freq.	Percent	Cum.
meat	3	25.00	25.00
milk	3	25.00	50.00
calorie	3	25.00	75.00
control	3	25.00	100.00
Total	12	100.00	

or at the child level (treating child as the unit of analysis) by reporting the number of children in each treatment group:

```
. tabulate treatment if pick_child==1
```

	Freq.	Percent	Cum.
meat	131	23.99	23.99
milk	142	26.01	50.00
calorie	146	26.74	76.74
control	127	23.26	100.00
Total	546	100.00	

There are three schools per group with a total of 131 children in the meat group, 142 children in the milk group, 146 children in the calorie group, and 127 children in the control group.

For later use, we create dummy variables for the intervention groups and give them descriptive names:

```
. tabulate treatment, generate(treat)
```

	Freq.	Percent	Cum.
meat	655	23.99	23.99
milk	710	26.01	50.00
calorie	730	26.74	76.74
control	635	23.26	100.00
Total	2,730	100.00	

```
. rename treat1 meat
. rename treat2 milk
. rename treat3 calorie
```

8.11.5 Plotting growth trajectories

We now combine the ideas of spaghetti and trellis plots by displaying spaghetti plots for the children within panels for schools. It is important to first sort the data by `relyear` within child so that the `connect(ascending)` option can be used:

```
. sort schoolid id relyear
. twoway (line ravens relyear, connect(ascending)), by(schoolid, compact)
>        xtitle(Time in years) ytitle(Raven's score)
```

The graph is shown in figure 8.5.

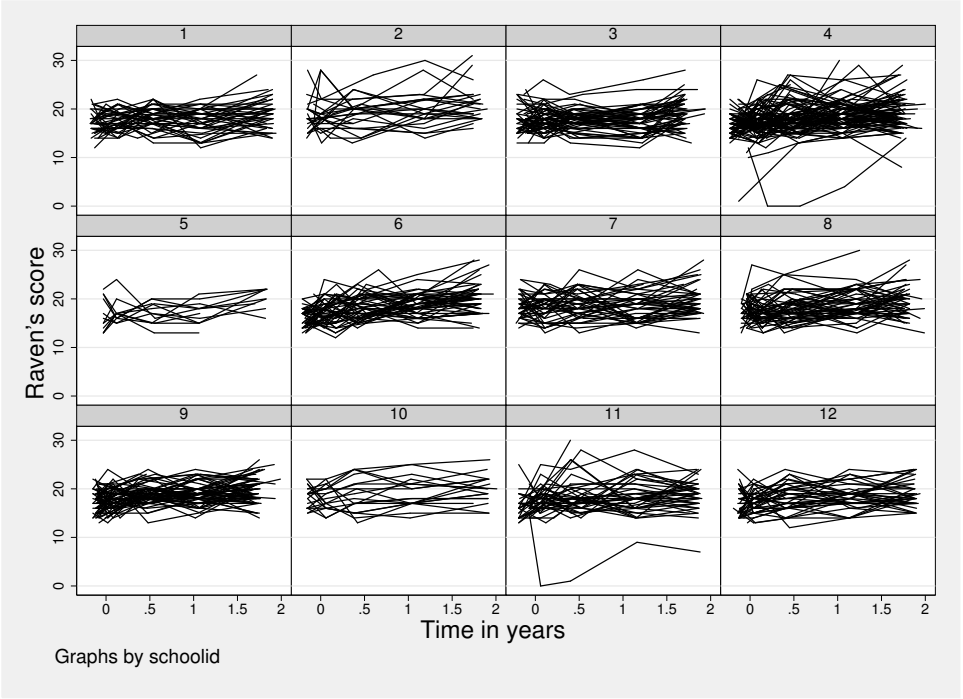


Figure 8.5: Trellis of spaghetti plots for schools in Kenyan nutrition study, showing observed growth trajectories

Schools 4 and 11 each have a child who scores very low at several occasions, and these children may merit further investigation.

8.12 Three-level random-intercept model

8.12.1 Model specification: Reduced form

For occasion i, child j, and school k, we will initially consider the three-level random-intercept model

$$\begin{aligned} y_{ijk} &= \beta_1 + \beta_2 w_{1k} + \beta_3 w_{2k} + \beta_4 w_{3k} + \beta_5 t_{ijk} + \beta_6 w_{1k} t_{ijk} + \beta_7 w_{2k} t_{ijk} + \beta_8 w_{3k} t_{ijk} \\ &\quad + \beta_9 x_{1jk} + \beta_{10} x_{2jk} + \zeta_{jk}^{(2)} + \zeta_k^{(3)} + \epsilon_{ijk} \end{aligned} \tag{8.1}$$

Here w_{1k}, w_{2k}, and w_{3k} are dummy variables for the three interventions meat, milk, and calorie, respectively. Note that these intervention variables are only indexed by k because the intervention was randomized at the school level. t_{ijk} is the time since baseline at occasion i for child jk, x_{1jk} is the child's age at baseline, and x_{2jk} is a dummy variable for being a boy. The fixed part of the model assumes that children's growth trajectories are linear with intervention-group-specific slopes of time.

We let all observed covariates in school k be denoted $\mathbf{X}_k$. It is assumed that the school-level random intercept $\zeta_k^{(3)}$ has zero mean and variance $\psi^{(3)}$, given the covariates $\mathbf{X}_k$; that the student-level random intercept $\zeta_{jk}^{(2)}$ has zero mean and variance $\psi^{(2)}$, given $\zeta_k^{(3)}$ and $\mathbf{X}_k$; and that the level-1 error term ϵ_{ijk} has zero mean and variance θ, given $\zeta_k^{(3)}$, $\zeta_{jk}^{(2)}$, and $\mathbf{X}_k$. The error terms in the model are assumed to be uncorrelated across levels.

8.12.2 Model specification: Three-stage formulation

The model can also be defined via a three-stage formulation using the notation of Raudenbush and Bryk (2002). The level-1 model for occasion i, child j, and school k is a linear regression on time and can be written as

$$y_{ijk} = \pi_{0jk} + \pi_{1jk} t_{ijk} + \epsilon_{ijk}$$

The intercept π_{0jk} and slope π_{1jk} in the level-1 model vary between children according to the following level-2 models:

$$\begin{aligned} \pi_{0jk} &= \beta_{00k} + \beta_{01} x_{1jk} + \beta_{02} x_{2jk} + r_{0jk} \\ \pi_{1jk} &= \beta_{10k} \end{aligned} \tag{8.2}$$

The intercepts in the level-2 models vary between schools according to the following level-3 models:

$$\begin{aligned} \beta_{00k} &= \gamma_{000} + \gamma_{001} w_{1k} + \gamma_{002} w_{2k} + \gamma_{003} w_{3k} + u_{0k} \\ \beta_{10k} &= \gamma_{100} + \gamma_{101} w_{1k} + \gamma_{102} w_{2k} + \gamma_{103} w_{3k} \end{aligned} \tag{8.3}$$

All Greek letters without i, j, or k subscripts are fixed parameters. u_{0k} is a level-3 random intercept, r_{0jk} is a level-2 random intercept, and ϵ_{ijk} is the level-1 residual as

before. We see that the slopes of time are determined by the treatment group dummy variables. There is no random slope at level 2 or level 3.

Substituting the level-3 models into the level-2 models, we obtain

$$\begin{aligned}\pi_{0jk} &= \gamma_{000} + \gamma_{001}w_{1k} + \gamma_{002}w_{2k} + \gamma_{003}w_{3k} + u_{0k} + \beta_{01}x_{1jk} + \beta_{02}x_{2jk} + r_{0jk}\\ \pi_{1jk} &= \gamma_{100} + \gamma_{101}w_{1k} + \gamma_{102}w_{2k} + \gamma_{103}w_{3k}\end{aligned}$$

and substituting the level-2 models into the level-1 model gives the reduced form

$$\begin{aligned}y_{ijk} &= (\gamma_{000} + \gamma_{001}w_{1k} + \gamma_{002}w_{2k} + \gamma_{003}w_{3k} + u_{0k} + \beta_{01}x_{1jk} + \beta_{02}x_{2jk} + r_{0jk})\\ &\quad + (\gamma_{100} + \gamma_{101}w_{1k} + \gamma_{102}w_{2k} + \gamma_{103}w_{3k})t_{ijk} + \epsilon_{ijk}\\ &= \gamma_{000} + \gamma_{001}w_{1k} + \gamma_{002}w_{2k} + \gamma_{003}w_{3k}\\ &\quad + \gamma_{100}t_{ijk} + \gamma_{101}w_{1k}t_{ijk} + \gamma_{102}w_{2k}t_{ijk} + \gamma_{103}w_{3k}t_{ijk}\\ &\quad + \beta_{01}x_{1jk} + \beta_{02}x_{2jk} + r_{0jk} + u_{0k} + \epsilon_{ijk}\end{aligned}$$

which is equivalent to the model in (8.1).

8.12.3 Estimation using xtmixed

Before fitting the three-level random-intercept model, we create the interactions between the intervention dummy variables and time:

```
. generate meat_year = meat*relyear
. generate milk_year = milk*relyear
. generate calorie_year = calorie*relyear
```

The three-level random-intercept model can now be fit using the following `xtmixed` command:

```
. xtmixed ravens meat milk calorie relyear meat_year milk_year calorie_year
> age_at_time0 boy || schoolid: || id:, mle
Mixed-effects ML regression                     Number of obs      =      2593
```

Group Variable	No. of Groups	Observations per Group Minimum	Average	Maximum
schoolid	12	57	216.1	434
id	542	1	4.8	5

```
                                                Wald chi2(9)       =    271.77
Log likelihood =  -6255.892                     Prob > chi2        =    0.0000
```

ravens	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
meat	-.255788	.3306285	-0.77	0.439	-.903808	.392232
milk	-.4792384	.3224394	-1.49	0.137	-1.111208	.1527312
calorie	-.3714558	.3290351	-1.13	0.259	-1.016353	.2734412
relyear	.9131069	.1406314	6.49	0.000	.6374745	1.188739
meat_year	.5111626	.1967277	2.60	0.009	.1255833	.8967418
milk_year	-.1057318	.1914511	-0.55	0.581	-.480969	.2695055
calorie_year	.122682	.193161	0.64	0.525	-.2559065	.5012705
age_at_time0	.1163285	.0614812	1.89	0.058	-.0041724	.2368295
boy	.5372871	.1657506	3.24	0.001	.2124219	.8621523
_cons	16.70638	.5077426	32.90	0.000	15.71122	17.70153

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
schoolid: Identity				
sd(_cons)	.2209702	.1334575	.0676458	.7218166
id: Identity				
sd(_cons)	1.532073	.0728596	1.395724	1.681742
sd(Residual)	2.412956	.0376427	2.340294	2.487874

```
LR test vs. linear regression:       chi2(2) =   306.40   Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference.
. estimates store mod1
```

From the first three coefficients, we see that there are no significant differences in the mean Raven's scores between the intervention groups at baseline, as would be expected in a well-executed randomized experiment. (All three coefficients could be tested simultaneously using `testparm`.) After controlling for the other variables, the mean slope of time in the control group is estimated as 0.91 units per year. The meat group grows an extra 0.51 units per year ($z = 2.60$, $p = 0.009$), but there is little evidence of a difference in growth between the other nutritional supplements and the control group. After controlling for treatment group, time, and gender, each extra year of age is associated with a mean increase in the Raven's score of 0.12 units, but this is not significant at the 5% level. Boys score on average 0.54 points higher than girls (z=3.24, $p = 0.001$) at a given time within a given intervention group and for a given age.

We can fit the model without explicitly creating dummy variables by using factor variables as follows:

```
xtmixed ravens ib4.treatment##c.relyear age_at_time0 boy || schoolid: || id:, mle
```

Because there are only 12 schools, it might be advisable to use REML for this application.

The estimates from the `xtmixed` output shown above are also reported under RI(2) & RI(3) in table 8.2.

Table 8.2: Maximum likelihood estimates for Kenyan nutrition data. Models with random intercept at both child and school levels [RI(2) & RI(3)], random coefficient at child level and random intercept at school level [RC(2) & RI(3)], and random coefficients at both child and school levels [RC(2) & RC(3)].

	RI(2) & RI(3)		RC(2) & RI(3)		RC(2) & RC(3)	
Parameter	Est	(SE)	Est	(SE)	Est	(SE)
Fixed part						
β_1 [_cons]	16.71	(0.51)	16.74	(0.51)	16.77	(0.52)
β_2 [meat]	−0.26	(0.33)	−0.24	(0.34)	−0.24	(0.37)
β_3 [milk]	−0.48	(0.32)	−0.48	(0.33)	−0.50	(0.37)
β_4 [calorie]	−0.37	(0.33)	−0.37	(0.34)	−0.37	(0.38)
β_5 [relyear]	0.91	(0.14)	0.92	(0.16)	0.92	(0.17)
β_6 [meat_year]	0.51	(0.20)	0.50	(0.22)	0.48	(0.24)
β_7 [milk_year]	−0.11	(0.19)	−0.12	(0.21)	−0.11	(0.23)
β_8 [calorie_year]	0.12	(0.19)	0.12	(0.21)	0.11	(0.24)
β_9 [age_at_time0]	0.12	(0.06)	0.11	(0.06)	0.11	(0.06)
β_{10} [boy]	0.54	(0.17)	0.49	(0.16)	0.49	(0.16)
Random part						
$\sqrt{\psi_{11}^{(2)}}$	1.53		1.46		1.45	
$\sqrt{\psi_{22}^{(2)}}$			0.86		0.86	
$\psi_{21}^{(2)}/\sqrt{\psi_{11}^{(2)}\psi_{22}^{(2)}}$			−0.00		0.01	
$\sqrt{\psi_{11}^{(3)}}$	0.22		0.25		0.32	
$\sqrt{\psi_{22}^{(3)}}$					0.11	
$\psi_{21}^{(3)}/\sqrt{\psi_{11}^{(3)}\psi_{22}^{(3)}}$					−1.00	
$\sqrt{\theta}$	2.41		2.32		2.32	
Log likelihood	−6,255.89		−6,241.34		−6,240.65	

8.13 Three-level random-coefficient models

8.13.1 Random coefficient at the child level

Within intervention groups, children may well vary in their individual rate of cognitive growth. Such variability can be modeled by adding the term $\zeta^{(2)}_{2jk}t_{ij}$ to the reduced form model (8.1) and renaming $\zeta^{(2)}_{jk}$ to $\zeta^{(2)}_{1jk}$, giving the random-coefficient model

$$\begin{aligned} y_{ijk} &= \beta_1 + \beta_2 w_{1k} + \beta_3 w_{2k} + \beta_4 w_{3k} + \beta_5 t_{ijk} + \beta_6 w_{1k} t_{ijk} + \beta_7 w_{2k} t_{ijk} + \beta_8 w_{3k} t_{ijk} \\ &\quad + \beta_9 x_{1jk} + \beta_{10} x_{2jk} + \zeta^{(2)}_{1jk} + \zeta^{(2)}_{2jk} t_{ij} + \zeta^{(3)}_{k} + \epsilon_{ijk} \end{aligned}$$

or by adding the term r_{1jk} to the level-2 model for π_{1jk} in the three-stage formulation.

Given the covariates $\mathbf{X}_k$, the random intercept $\zeta^{(2)}_{1jk}$ and random slope $\zeta^{(2)}_{2jk}$ at the child level have a bivariate distribution, assumed to have zero mean and covariance matrix

$$\mathbf{\Psi}^{(2)} = \begin{bmatrix} \psi^{(2)}_{11} & \psi^{(2)}_{12} \\ \psi^{(2)}_{21} & \psi^{(2)}_{22} \end{bmatrix} \equiv \begin{bmatrix} \mathrm{Var}(\zeta^{(2)}_{1jk}|\mathbf{X}_k, \zeta^{(3)}_k) & \mathrm{Cov}(\zeta^{(2)}_{1jk}, \zeta^{(2)}_{2jk}|\mathbf{X}_k, \zeta^{(3)}_k) \\ \mathrm{Cov}(\zeta^{(2)}_{2jk}, \zeta^{(2)}_{1jk}|\mathbf{X}_k, \zeta^{(3)}_k) & \mathrm{Var}(\zeta^{(2)}_{2jk}|\mathbf{X}_k, \zeta^{(3)}_k) \end{bmatrix}$$

where $\psi^{(2)}_{21} = \psi^{(2)}_{12}$. (You may want to refer back to section 4.4.1 on specification of two-level random-coefficient models.)

The `xtmixed` syntax for fitting a three-level random-coefficient model with a random coefficient at the child level for year since baseline is

```
. xtmixed ravens meat milk calorie relyear meat_year milk_year calorie_year
> age_at_time0 boy || schoolid: || id: relyear, covariance(unstructured) mle
Mixed-effects ML regression                     Number of obs      =      2593
```

Group Variable	No. of Groups	Observations per Group Minimum	Average	Maximum
schoolid	12	57	216.1	434
id	542	1	4.8	5

```
                                                Wald chi2(9)       =    220.66
Log likelihood = -6241.3378                     Prob > chi2        =    0.0000
```

ravens	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
meat	-.2371712	.3380466	-0.70	0.483	-.8997303	.425388
milk	-.4782935	.3303219	-1.45	0.148	-1.125712	.1691255
calorie	-.3686388	.3384154	-1.09	0.276	-1.031921	.2946432
relyear	.9235916	.156704	5.89	0.000	.6164574	1.230726
meat_year	.4990658	.2194377	2.27	0.023	.0689758	.9291558
milk_year	-.1155923	.2139539	-0.54	0.589	-.5349343	.3037497
calorie_year	.1169333	.2149049	0.54	0.586	-.3042726	.5381392
age_at_time0	.1146185	.0607949	1.89	0.059	-.0045373	.2337743
boy	.4902904	.1640913	2.99	0.003	.1686773	.8119034
_cons	16.74299	.5059629	33.09	0.000	15.75132	17.73466

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
schoolid: Identity				
sd(_cons)	.2546548	.1291915	.0942151	.6883089
id: Unstructured				
sd(relyear)	.864055	.11576	.6645129	1.123516
sd(_cons)	1.45822	.0936564	1.28574	1.653837
corr(relyear,_cons)	-.0010829	.1403704	-.2693884	.2673786
sd(Residual)	2.315432	.0419338	2.234685	2.399097

```
LR test vs. linear regression:       chi2(4) =   335.51   Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference.
. estimates store mod2
```

Here `relyear` has been added in the second random part to specify a child-level random slope for `relyear`. The `covariance(unstructured)` option was used to estimate the covariance matrix freely, that is, estimate $\psi_{11}^{(2)}$, $\psi_{21}^{(2)}$, and $\psi_{22}^{(2)}$ without constraints. (By default, `xtmixed` sets the covariance $\psi_{21}^{(2)}$ to zero.) The estimates from the above `xtmixed` command were also shown under RC(2) & RI(3) in table 8.2.

To test whether the random slope is needed, we formulate the hypotheses

$$H_0\text{: } \psi_{22}^{(2)} = 0 \qquad \text{against} \qquad H_a\text{: } \psi_{22}^{(2)} > 0$$

and perform a likelihood-ratio test using

```
. lrtest mod1 mod2
Likelihood-ratio test                                 LR chi2(2)  =     29.11
(Assumption: mod1 nested in mod2)                     Prob > chi2 =    0.0000
Note: The reported degrees of freedom assumes the null hypothesis is not on
      the boundary of the parameter space.  If this is not true, then the
      reported test is conservative.
```

Although conservative, the naïve p-value is tiny, so we can reject the null hypothesis. We do not know the asymptotic null distribution in this case, which would have been useful had the naïve test not been significant.

8.13.2 Random coefficient at the child and school levels

The previous model assumes that the school mean slopes of time do not vary around the treatment-group-specific means. We can relax this assumption by adding the term $\zeta_{2k}^{(3)} t_{ijk}$ to the reduced-form model (and renaming $\zeta_k^{(3)}$ to $\zeta_{1k}^{(3)}$), giving

$$\begin{aligned} y_{ijk} &= \beta_1 + \beta_2 w_{1k} + \beta_3 w_{2k} + \beta_4 w_{3k} + \beta_5 t_{ijk} + \beta_6 w_{1k} t_{ijk} + \beta_7 w_{2k} t_{ijk} + \beta_8 w_{3k} t_{ijk} \\ &\quad + \beta_9 x_{1jk} + \beta_{10} x_{2jk} + \zeta_{1jk}^{(2)} + \zeta_{1k}^{(3)} + (\zeta_{2jk}^{(2)} + \zeta_{2k}^{(3)}) t_{ij} + \epsilon_{ijk} \end{aligned}$$

or by adding the term u_{1k} to the level-3 model (8.3) for the school mean slope of time, to allow random slopes of time at the school level:

$$\beta_{10k} = \gamma_{100} + \gamma_{101} w_{1k} + \gamma_{102} w_{2k} + \gamma_{103} w_{3k} + u_{1k}$$

Given the covariates $\mathbf{X}_k$, the random intercept $\zeta_{1k}^{(3)}$ and random slope $\zeta_{2k}^{(3)}$ at the school level have a bivariate distribution, assumed to have zero mean and covariance matrix

$$\mathbf{\Psi}^{(3)} = \begin{bmatrix} \psi_{11}^{(3)} & \psi_{12}^{(3)} \\ \psi_{21}^{(3)} & \psi_{22}^{(3)} \end{bmatrix} \equiv \begin{bmatrix} \mathrm{Var}(\zeta_{1k}^{(3)}|\mathbf{X}_k) & \mathrm{Cov}(\zeta_{1k}^{(3)}, \zeta_{2k}^{(3)}|\mathbf{X}_k) \\ \mathrm{Cov}(\zeta_{2k}^{(3)}, \zeta_{1k}^{(3)}|\mathbf{X}_k) & \mathrm{Var}(\zeta_{2k}^{(3)}|\mathbf{X}_k) \end{bmatrix}$$

where $\psi_{21}^{(3)} = \psi_{12}^{(3)}$. Noting that `relyear` has a random slope in the random parts for schools and children and that the `covariance(unstructured)` option in `xtmixed` must be specified separately for each level. The three-level random-coefficient model with random coefficients at both the child and school levels can be fit using

```
. xtmixed ravens meat milk calorie relyear meat_year milk_year calorie_year
> age_at_time0 boy || schoolid: relyear, covariance(unstructured)
> || id: relyear, covariance(unstructured) mle
Mixed-effects ML regression                     Number of obs      =      2593
```

Group Variable	No. of Groups	Observations per Group Minimum	Average	Maximum
schoolid	12	57	216.1	434
id	542	1	4.8	5

```
                                                Wald chi2(9)       =    186.94
Log likelihood = -6240.6504                     Prob > chi2        =    0.0000
```

ravens	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
meat	-.2418509	.3729209	-0.65	0.517	-.9727624	.4890606
milk	-.5016431	.3655257	-1.37	0.170	-1.21806	.2147741
calorie	-.3713378	.3763629	-0.99	0.324	-1.108995	.3663199
relyear	.9186612	.1699896	5.40	0.000	.5854877	1.251835
meat_year	.4801711	.2380819	2.02	0.044	.0135392	.9468029
milk_year	-.106055	.2327757	-0.46	0.649	-.562287	.3501769
calorie_year	.1111154	.2359755	0.47	0.638	-.351388	.5736189
age_at_time0	.1127028	.0607339	1.86	0.063	-.0063335	.231739
boy	.4913901	.1639159	3.00	0.003	.1701209	.8126594
_cons	16.77486	.5180617	32.38	0.000	15.75948	17.79024

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
schoolid: Unstructured				
sd(relyear)	.1110955	.0944235	.0210007	.5877048
sd(_cons)	.3172716	.1371533	.135977	.7402816
corr(relyear,_cons)	-.9999998	.0002197	-1	1
id: Unstructured				
sd(relyear)	.8583323	.1162664	.6581957	1.119324
sd(_cons)	1.452461	.0933819	1.280497	1.647517
corr(relyear,_cons)	.0107735	.1427232	-.2626855	.2826305
sd(Residual)	2.31525	.041923	2.234523	2.398893

```
LR test vs. linear regression:       chi2(6) =   336.88   Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference.
```

These estimates were also shown under RC(2) & RC(3) in table 8.2.

Unfortunately, the correlation between the school-level random intercepts and slopes is estimated as -1 with a confidence interval from -1 to 1, essentially implying that the data provide no information on this correlation. The model appears to be too ambitious given the small number of schools, and we return to the previous model.

```
. estimates restore mod2
```

8.14 Residual diagnostics and predictions

The retained model includes random intercepts $\zeta_{1k}^{(3)}$ at the school level, random intercepts $\zeta_{1jk}^{(2)}$ and random slopes $\zeta_{2jk}^{(2)}$ at the child level, and level-1 residuals ϵ_{ijk}. We now predict all of these random terms to perform residual diagnostics, keeping in mind that the predictions are based on normality assumptions and will appear more normal than they are when normality is violated.

Empirical Bayes predictions or BLUPs $\widetilde{\zeta}_{1jk}^{(2)}$, $\widetilde{\zeta}_{2jk}^{(2)}$, and $\widetilde{\zeta}_{1k}^{(3)}$ for the random effects can be obtained using `predict` with the `reffects` option. Here it is important to remember that the highest-level random effects come first, and within a given level, the random intercept comes last (the `predict` command defines useful labels for the variables it creates). Denoting $\widetilde{\zeta}_{1k}^{(3)}$ as `ri3`, $\widetilde{\zeta}_{2jk}^{(2)}$ as `rc2`, and $\widetilde{\zeta}_{1jk}^{(2)}$ as `ri2`, the syntax is

```
. predict ri3 rc2 ri2, reffects
```

As always, the level-1 residuals are predicted using

```
. predict res, residuals
```

Because the random intercepts at the different levels and the level-1 residuals are all on the same scale, we plot the distributions on the same graph using box plots (the random slopes are on a different scale). However, we must be careful to use only one observation per school for the box plot of `ri3` and only one observation per student for the box plot of `ri2`. The easiest way of discarding the unnecessary observations is to replace them with missing values.

```
. replace ri3=. if pick_school!=1
. replace ri2 =. if rn!=1
. graph box ri3 ri2 res, ascategory box(1, bstyle(outline))
> yvaroptions(relabel(1 "School" 2 "Child" 3 "Occasion"))
> medline(lcolor(black))
```

The resulting graph in figure 8.6 reveals that there is much more variability within schools than between schools and that there appear to be some outlying children with very low intercepts (as we saw in figure 8.5).

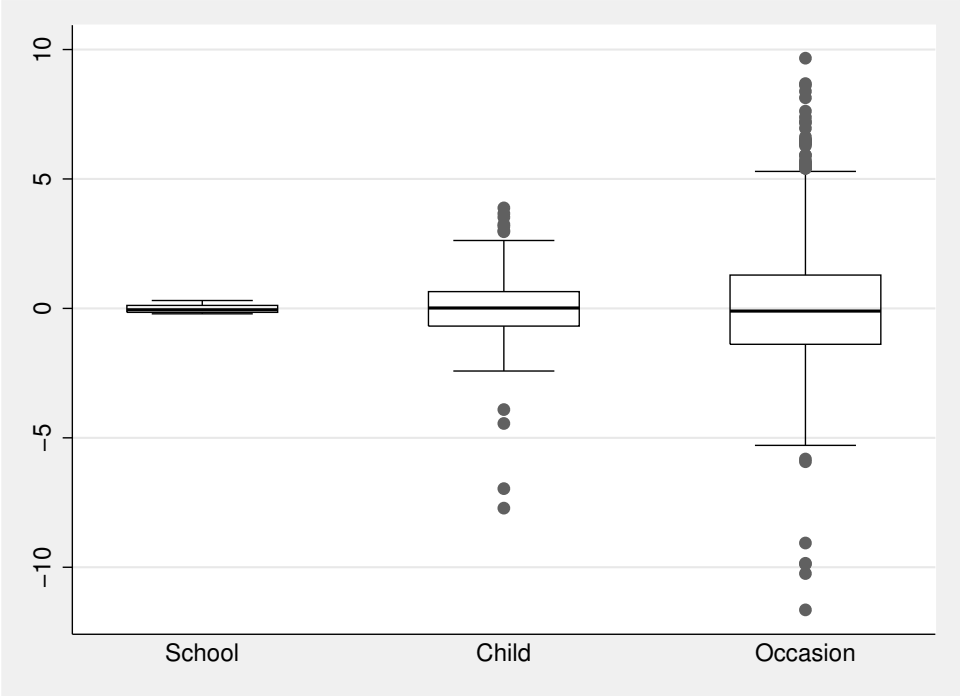


Figure 8.6: Box plots of empirical Bayes predictions for random intercepts at the school level $\widetilde{\zeta}_{1k}^{(3)}$, random intercepts at the child level $\widetilde{\zeta}_{1jk}^{(2)}$, and level-1 residuals $\widetilde{\epsilon}_{ijk}$ at the occasion level

A nice display of the bivariate distribution of the predicted child-level random intercepts and slopes, together with the univariate marginal distributions can be produced as follows (see page 205 for an explanation of the commands):

```
. scatter rc2 ri2 if rn==1, saving(yx, replace)
> xtitle("Random intercept") ytitle("Random slope")
. histogram rc2, freq horiz saving(hy, replace)
> yscale(alt) ytitle(" ") fxsize(35) normal
. histogram ri2, freq saving(hx, replace)
> xscale(alt) xtitle(" ") fysize(35) normal
. graph combine hx.gph yx.gph hy.gph, hole(2) imargin(0 0 0 0)
```

These commands produce the graph in figure 8.7.

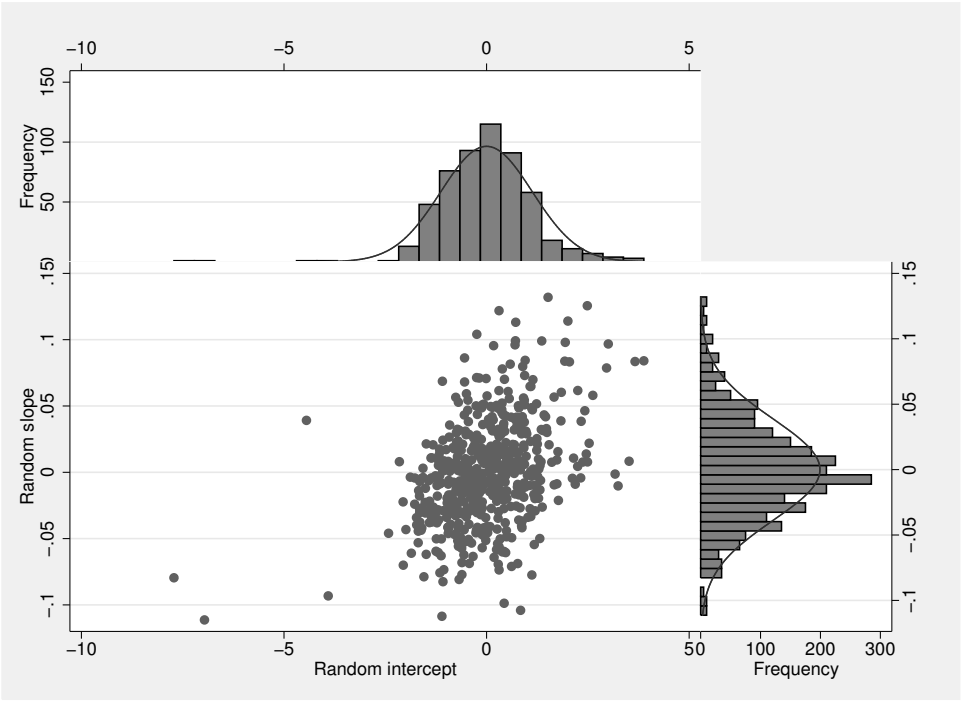


Figure 8.7: Bivariate and univariate distributions of empirical Bayes predictions for random intercepts $\widetilde{\zeta}^{(2)}_{1jk}$ and random slopes $\widetilde{\zeta}^{(2)}_{2jk}$ at the child level

We again see that there are some children with very low intercepts, whereas the slopes are more symmetrically distributed.

We can also plot the predicted child-specific growth trajectories in a trellis of spaghetti plots, analogous to the graph for the observed growth trajectories in figure 8.5. First, we use the `fitted` option in the `predict` command to obtain predicted growth trajectories,

```
. predict predtraj, fitted
```

and then we plot them using

```
. sort schoolid id relyear
. twoway (line predtraj relyear, connect(ascending)), by(schoolid, compact)
> xtitle(Time in years) ytitle(Raven's score)
```

The resulting graph is shown in figure 8.8.

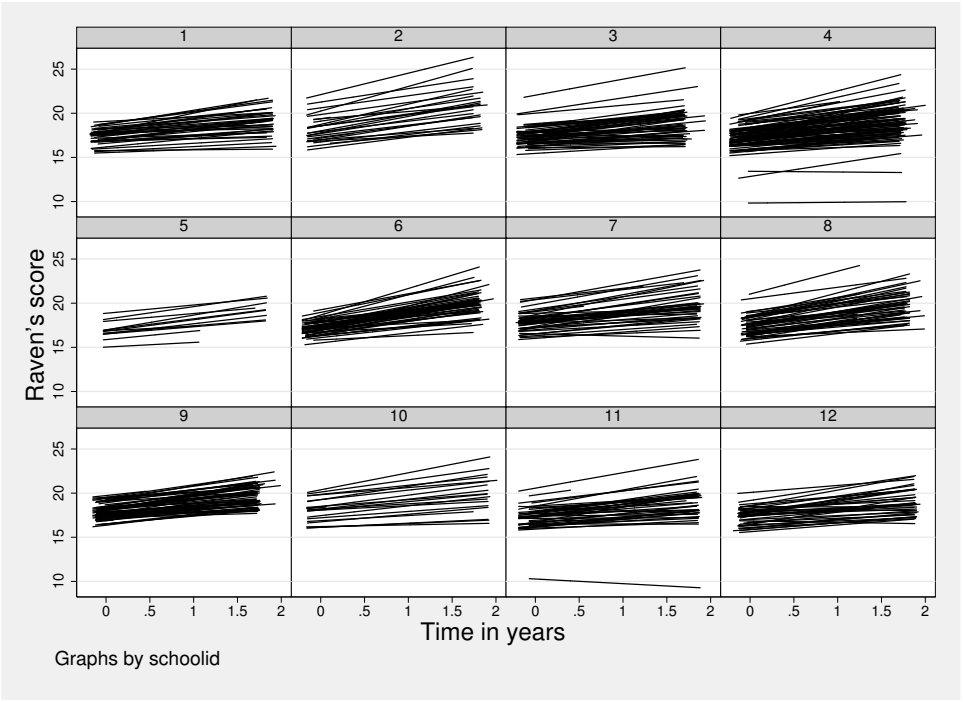


Figure 8.8: Trellis of spaghetti plots for schools in Kenyan nutrition study, showing predicted growth trajectories for children

To visualize the estimated treatment effects, it is useful to plot the model-implied mean Raven's scores as a function of time for the three intervention groups. To do this, we must first set the other covariates in the model, here `age_at_time0` (x_{1jk}) and `boy` (x_{2jk}), to constant values. We set age at baseline to its mean $\overline{x}_{1..}$, and we set the dummy variable for boys to 1 to obtain predictions for boys of average age at baseline.

$$\begin{aligned}\widehat{E}(y_{ijk}|w_{1k}, w_{2k}, w_{3k}, t_{ijk}, x_{1jk}=\overline{x}_{1..}, x_{2jk}=1) \;=\\ \widehat{\beta}_1 + \widehat{\beta}_2 w_{1k} + \widehat{\beta}_3 w_{2k} + \widehat{\beta}_4 w_{3k} + \widehat{\beta}_5 t_{ijk} + \widehat{\beta}_6 w_{1k} t_{ijk} + \widehat{\beta_7} w_{2k} t_{ijk}\\ + \widehat{\beta}_8 w_{3k} t_{ijk} + \widehat{\beta}_9 \overline{x}_{1..} + \widehat{\beta}_{10}\end{aligned}$$

To obtain the predictions using `predict`, we set the values of `age_at_time0` and `boy` using

```
. summarize age_at_time0 if rn==1
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
age_at_time0 |        542    7.630406    1.414575       4.84      15.18
. replace age_at_time0 = r(mean)
. replace boy = 1
```

and then use `predict` with the `xb` option:

```
. predict means, xb
. twoway (line means relyear if meat==1, sort lpatt(solid))
>        (line means relyear if milk==1, sort lpatt(dash))
>        (line means relyear if calorie==1, sort lpatt(shortdash))
>        (line means relyear if treatment==4, sort lpatt(longdash_dot)),
>        legend(order(1 "Meat" 2 "Milk" 3 "Calorie" 4 "Control"))
>        xtitle(Time in years) ytitle(Predicted mean Raven's score)
```

The graph in figure 8.9 shows that the estimated slope is considerably steeper for the meat group than for the other three intervention groups.

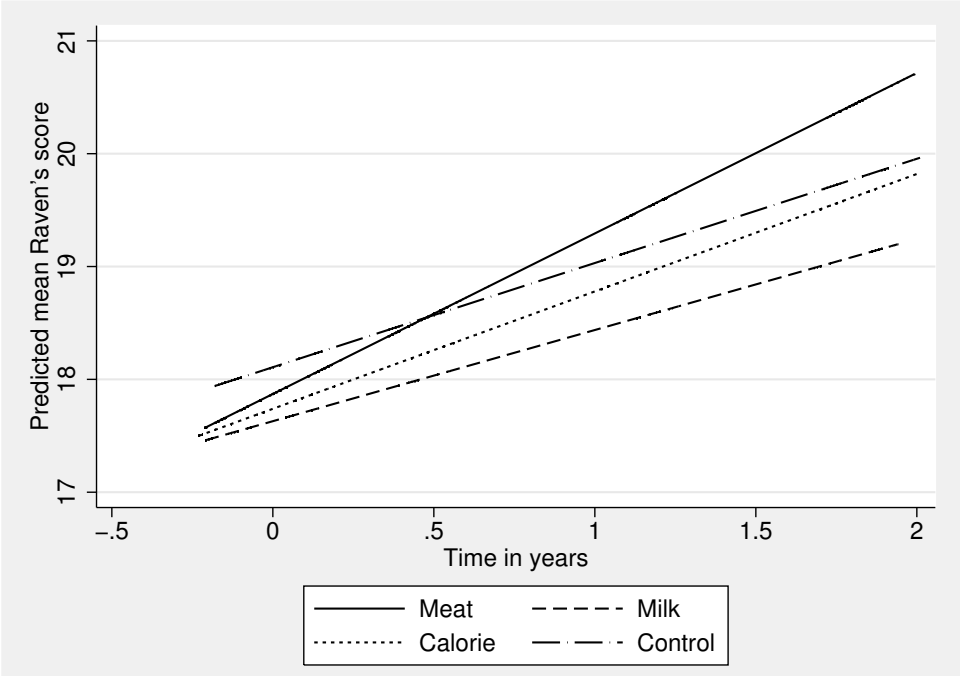


Figure 8.9: Predicted mean Raven's scores over time for the four intervention groups among boys whose age at baseline was average

8.15 Summary and further reading

We have introduced the idea of nested random effects for three-level datasets where there are two nested levels of clustering. A three-level random-intercept model includes error components for nested clusters to allow the total variance to be decomposed into the level-1 variance within clusters, the level-2 variance between clusters within superclusters, and the level-3 variance between superclusters. We discussed several intraclass correlations for this situation. We have seen that random slopes can be included to allow the effect of level-1 covariates to vary at level 2, at level 3, or at both levels. It is also possible to allow the effect of level-2 covariates to vary at level 3. Recall that a random coefficient should vary at a higher level than the associated covariate (unless used as a device for introducing heteroskedasticity). All of these ideas extend naturally to higher-level models (see exercise 8.8 for a four-level example).

The models discussed in this chapter can be extended by relaxing the homoskedasticity assumptions for the random effects (see section 7.5.2) or the level-1 residuals (see sections 6.4.2, 6.4.3, and 7.5.1). If the data are longitudinal, we may want to allow level-1 residuals to be correlated, for instance, with an AR(1) covariance structure, as discussed for two-level models in section 6.4.1.

Good references on linear multilevel models with several levels of nested random effects include Raudenbush and Bryk (2002, chap. 8), Goldstein (2011, chap. 3), and Snijders and Bosker (2012, sec. 4.9, 5.5). A review of linear two- and three-level models with an application to political science is given by Steenbergen and Jones (2002). Raudenbush (1989) discusses two types of multilevel longitudinal designs in education: repeated measurements on the same students nested in schools (see exercises 8.1 and 8.6) and repeated measurements for the same schools, but with changing cohorts of students (see exercise 8.5). Longitudinal data from economics and medicine are considered in exercises 8.3 and 8.4. Cross-sectional examples from education are considered in exercises 8.2 and 8.7.

As we have seen in the nutrition example, three-level data sometimes arise from randomized trials. The nutrition example is a cluster-randomized trial in which schools (level 3) were randomly assigned to treatments. In exercise 8.4, we consider a multisite hypertension study, where patients (level 2) are randomly assigned to treatments *within centers* (level 3). Similarly, in the Tennessee class-size experiment used in exercise 8.6, interventions were applied to classes *within schools*. Interestingly, the classes were not preexisting but were formed by randomly allocating both students and teachers to classes within schools. Some models not explicitly covered in this chapter that can be expressed as three-level models are introduced in exercises 8.9 (multivariate multilevel model) and 8.10 (biometrical genetic model for twin data).

8.16 Exercises

8.1 Math-achievement data Solutions

Raudenbush and Bryk (2002) and Raudenbush et al. (2004) discuss data from a longitudinal study of children's academic growth in the six primary school years. The data have a three-level structure with repeated observations on 1,721 students from 60 urban public primary schools.

The dataset `achievement.dta` has the following variables:

- Level 1 (occasion)
  - `math`: math test score derived from an item response model
  - `year`: year of study minus 3.5 (values -2.5, -1.5, -0.5, 0.5, 1.5, 2.5) (a_{1ijk})
  - `retained`: dummy variable for child being retained in grade (1: retained; 0: not retained)
- Level 2 (child)
  - `child`: child identifier
  - `female`: dummy variable for being female
  - `black`: dummy variable for being African American (X_{1jk})
  - `hispanic`: dummy variable for being Hispanic (X_{2jk})
- Level 3 (school)
  - `school`: school identifier
  - `size`: number of students enrolled in the school
  - `lowinc`: percentage of students from low-income families (W_{1k})
  - `mobility`: percentage of students moving during the course of a school year

Raudenbush et al. (2004) specify a three-level model in three stages. The level-1 model is

$$Y_{ijk} = \pi_{0jk} + \pi_{1jk}a_{1ijk} + e_{ijk}, \quad e_{ijk} \sim N(0, \sigma^2)$$

where Y_{ijk} is the jth child's math achievement at occasion i in school k and a_{1ijk} is `year` at that occasion. The level-2 models are

$$\pi_{pjk} = \beta_{p0k} + \beta_{p1}X_{1jk} + \beta_{p2}X_{2jk} + r_{pjk}, \quad p = 0, 1 \quad (r_{0jk}, r_{1jk})' \sim N(\mathbf{0}, \mathbf{T}_\pi)$$

where X_{1jk} is `black`, X_{2jk} is `hispanic`, and r_{pjk} is a random effect (intercept if $p = 0$, slope if $p = 1$) at level 2. The covariance matrix of the level-2 random effects is defined as

$$\mathbf{T}_\pi = \begin{bmatrix} \tau_{\pi 00} & \tau_{\pi 01} \\ \tau_{\pi 10} & \tau_{\pi 11} \end{bmatrix}, \quad \tau_{\pi 10} = \tau_{\pi 01}$$

Finally, the level-3 model is

$$\beta_{p0k} = \gamma_{p00} + \gamma_{p01}W_{1k} + u_{p0k}, \quad p = 0, 1 \quad u_{p0k} \sim N(0, T_\beta)$$

where W_{1k} is `lowinc` and u_{p0k} is a random intercept at level 3.

1. Substitute the level-3 models into the level-2 models and then the resulting level-2 models into the level-1 model. Rewrite the final reduced-form model using the notation of this book.
2. Fit the model using `xtmixed` and interpret the estimates.
3. Include some of the other covariates in the model and interpret the estimates.

8.2 Instructional-improvement data

West, Welch, and Galecki (2007) analyzed a dataset on first-grade students from the Study of Instructional Improvement by Hill, Rowan, and Ball (2005).

The question of interest is how teachers' experience, mathematics preparation, and mathematics content knowledge affect students' gain in mathematics achievement scores from kindergarten to first grade.

The variables in the dataset `instruction.dta` used here are

- Level 1 (students)
  - `childid`: student identifier
  - `mathgain`: gain in math achievement score from spring of kindergarten to spring of first grade
  - `mathkind`: match achievement score in spring of the kindergarten year
  - `girl`: dummy variable for being a girl
  - `minority`: dummy variable for being a minority student
  - `ses`: socioeconomic status
- Level 2 (class)
  - `classid`: class identifier
  - `yearstea`: first-grade teacher's years of teaching experience
  - `mathprep`: first-grade teacher's mathematics preparation (score based on number of mathematics content and methods courses)
  - `mathknow`: first-grade teacher's mathematics content knowledge, based on a 30-item scale with higher values indicating better knowledge
- Level 3 (school)
  - `schoolid`: school identifier
  - `housepov`: percentage of households in the neighborhood of the school below the poverty level

1. Treating `mathgain` as the response variable, write down the "unconditional" (without covariates) three-level random-intercept model for children nested in classes nested in schools, using
   a. the three-stage formulation
   b. the reduced form
2. Fit the model in Stata, obtain the estimated intraclass correlations, and interpret them.

3. For the three-stage formulation in step 1, write down an extended level-1 model that includes the four student-level variables, `mathkind`, `girl`, `minority`, and `ses`, as covariates. Similarly, write down an extended level-2 model by including the three class-level covariates, and an extended level-3 model by including the school-level covariate.
4. Fit the model from step 3. Interpret the estimated coefficients of the class-level covariates.
5. Fit an extended model that also includes the school means of `ses`, `minority`, and `mathkind`. Is there evidence that the within-school effects of these variables differ from the between-school effects?
6. Obtain empirical Bayes predictions of the random effects, and produce graphs to assess their distribution.

8.3 U.S. production data

In economics, a production function expresses the relationship between the output or production (the monetary value of all goods produced) of an economic unit (such as a country) and different inputs. A Cobb–Douglas production function expresses production P as a log-linear model of input, such as capital K and labor L,

$$P_i \;=\; AK_i^{\beta_2} L_i^{\beta_3} e^{\epsilon_i}$$

so that

$$\ln(P_i) \;=\; \ln(A) + \beta_2 \ln(K_i) + \beta_3 \ln(L_i) + \epsilon_i$$

Thus after taking logarithms of the output and all input variables, the production function can be estimated using linear regression. The research question concerns how public spending (on highways and streets, water and sewer facilities, and other buildings and structures) affects private production.

Baltagi, Song, and Jung (2001) analyzed data from Munnell (1990) on state productivity for 48 U.S. states from nine regions over the period 1970–1986. They estimate a Cobb–Douglas production function with error components for region and state.

The variables in `productivity.dta` are

- `state`: state identifier
- `region`: region identifier
- `year`: year 1970–1986
- `private`: logarithm of private capital stock
- `hwy`: logarithm of highway component of public stock
- `water`: logarithm of water component of public stock
- `other`: logarithm of building and other components of public stock
- `unemp`: state unemployment rate

1. Fit a three-level model for the logarithm of private capital stock, `private`, with covariates `hwy`, `water`, `other`, and `unemp` and with random intercepts for `state` and `region`. Use `xtmixed` with both the `mle` and the `reml` options.
2. Which components of public capital have a positive effect on private output?
3. Interpret the sizes of the estimated residual variance components. Also comment on any differences between the ML and the REML estimates.

See also exercise 9.3 for further analyses of these data.

8.4 Multicenter hypertension-trial data

Hall et al. (1991) describe a randomized double-blind multicenter trial of treatments for hypertension (high blood pressure). The data were made available by Brown and Prescott (2006).

Three hundred eleven patients from 29 centers met eligibility criteria. In the initial phase of the trial, the patients received a placebo treatment and were then reassessed for eligibility one week later (visit 2). The 288 patients who still met eligibility criteria were then randomized *within* each center to receive one of the three treatments (A=Carvedilol, B=Nifedipine, C=Atenolol). The patients were followed up every other week for four visits. Diastolic blood pressure (the pressure in the bloodstream when the heart fills with blood) was the primary endpoint (response) and will be considered here.

The variables in the dataset `bp.dta` that we will use here are

- `center`: center identifier
- `id`: patient identifier
- `time`: visit number 3, 4, 5, 6 (postrandomization)
- `bp`: diastolic blood pressure in mmHg
- `bp_base`: diastolic blood pressure during second visit, prior to randomization
- `treat`: treatment group A, B, C (a string variable)

1. Transform `time` so that it takes the value 0 at the first postrandomization visit (visit 3) and increases 2 units between visits (representing the number of weeks since first postrandomization visit).
2. Produce a trellis graph, with one panel per center, where each panel is a spaghetti plot of the patients' observed trajectories.
3. Fit a three-level random-intercept model for `bp` with random intercepts for patients and centers and with `bp_base`, `time`, and dummy variables for treatments B and C as covariates.
4. Use a significance level of 5% to consider the following additions to this model, keeping each significant addition in all subsequent models:
   a. a quadratic term for `time`
   b. interactions between the treatment dummies and `time`

c. a random slope of `time` at the patient level
d. a random slope of `time` at the center level

5. Write down and describe the chosen model, defining all the notation you are using, including subscripts and variances.
6. Interpret the estimated treatment effect.
7. Produce a graph similar to the graph in step 2 but with the predicted patient-specific growth trajectories instead of the observed trajectories.

8.5 School-effects data

The dataset considered here is a 50% random subset of data described in Nuttall et al. (1989) and Goldstein (1991) and is made available by the Centre for Multilevel Modelling at the University of Bristol.

Examination results are available for three successive cohorts of year 11 (age 16) students from 140 schools from the Inner London Education Authority in 1985, 1986, and 1987. Prior to entry to secondary school (at age 11), each child was assigned to one of three academic achievement bands, largely on the basis of a verbal reasoning test. Band 1 contains the highest 25%, band 2 contains the middle 50%, and band 3 contains the lowest 25%. The response variable is a score derived from grades obtained for ordinary level (O-level) and graduate certificate of secondary education (GCSE) exams taken at age 16.

The dataset is an example of the second type of longitudinal multilevel data discussed in Raudenbush (1989), where schools are followed over time, but at each time point a different cohort of students is considered (in a given grade). In contrast, the data in exercises 8.1 and 8.7 consider the same cohort of students over time as they progress through the grades. The present data can be used to assess the stability of school effects over time.

The variables in `schooleffects.dta` are

- `year`: year when test was taken (1: 1985; 2: 1986; 3: 1987), defining the cohort and calendar time (period)
- `school`: school identifier
- `score`: score, based on O-level and GSCE results
- `pfsm`: percentage of students in the school who are eligible for free school meals
- `pvr1`: percentage of students in the school in verbal reasoning band 1
- `female`: dummy variable for being female (1: female; 0: male)
- `vr`: verbal reasoning band of student (values 1, 2, 3)
- `ethnic`: ethnic group of student (11 groups; see value labels)
- `schgend`: school gender (1: mixed; 2: male; 3: female)
- `schden`: school denomination (1: no denomination; 2: Church of England; 3: Roman Catholic)

1. Goldstein (1991) considers a model for `score` with random intercepts for school (level 3) and cohort within school (level 2). Fit this model, also allowing the mean score to change linearly over calendar time/cohort (coded 0, 1, 2).
2. Raudenbush (1989) considers a model that is identical to the model in step 1 except that the random intercept for cohort within school is replaced by a school-level random slope of time (coded 0, 1, 2). Fit this model.
3. For the models in steps 1 and 2, write down the random part of the model for time 0, 1, and 2 (six expressions in total). Discuss how the models differ.
4. Extend the model from step 2 by adding a level-2 random effect for cohorts nested in schools (as in step 1).
   a. Write down the model.
   b. Fit the model.
   c. Interpret the estimates.
   d. Compare the model with the models in steps 1 and 2 using likelihood-ratio tests.
5. For the model from step 4b, produce a trellis graph of spaghetti plots for the predicted cohort and school-specific mean score against time, where the trellis panels are for combinations of `schgend` and `schden` (you can use the `by(schden schgen)` option). Describe the graph.

8.6 STAR data I

The Tennessee class-size reduction experiment, known as Project STAR (Student-Teacher Achievement Ratio), was a four-year experiment designed to evaluate the effect of small class sizes on learning. Three different class types were compared for kindergarten through third grade (K–3):

1. a small class size, with 13–17 students per class and no teacher's aide
2. a regular class size with 22–25 students per class and no teacher's aide
3. a regular class size with 22–25 students per class and a teacher's aide

Each of the 79 participating schools had at least one class of each type, and teachers of participating schools were randomly assigned to the classes within their schools. Students entering a participating school in kindergarten in 1985 or first grade in 1986 (kindergarten was optional) were also randomly assigned to the classes. In this exercise, we restrict analysis to the kindergarten year.

The data were made available by Heros Inc. and are documented in Finn et al. (2007). The variables in `star1.dta` that we will use here are

- `schid`: school identifier
- `class`: class identifier
- `stdntid`: student identifier
- `grade`: grade, coded 0 for kindergarten and 1, 2, 3 for grades 1, 2, and 3

- `tmaths`: total scale score for Stanford achievement test (SAT) in math (ranging from 0 to 1400)
- `classt`: class type, coded as shown above

1. Keep only the kindergarten data (grade 0).
2. Obtain the frequency distribution for the number of classes per school.
3. What are the minimum, mean, and maximum number of students per class for small and regular class sizes (not distinguishing between regular class sizes with and without an aide)?
4. Fit a three-level random-intercept model for the SAT math score, with random intercepts for classes and schools.
5. Add class type as an explanatory variable and discuss whether small class size appears to be beneficial. Also discuss the change in the estimated variance components if any.
6. The STAR study has been described by Frederick Mosteller as "one of the most important educational investigations ever carried out" (Mosteller 1995), presumably because both students and teachers were randomly assigned to classes within schools. However, Krueger (1999, 510) points out that independence between class size and other (possibly omitted) variables holds only within schools. There could be omitted school-level variables that are correlated with class size and student outcomes (that is, confounders). Repeat the analysis from step 5, but use fixed effects for schools instead of random effects to avoid school-level endogeneity or confounding. Do the conclusions regarding class size change?

8.7 STAR data II

In the previous exercise, analysis was restricted to the kindergarten year. Here we consider students' growth in math achievement from kindergarten through third grade. Students were assessed each year using the Stanford achievement test in math. Scale scores were derived from item response models to make them comparable across grades, though the test becomes more difficult over time.

As a result of mobility, school membership could change over time for some students. For these students, we found the school with the largest number of observations and resolved ties by a random choice of school. The corresponding school assignment is given in the variable `school`. For simplicity, we ignore class membership in this exercise.

Some of the variables we will use here are described in the previous exercise. The additional variables used here are

- `school`: school to which student belongs most often
- `frlnch`: percentage of students in school eligible for a free school lunch that grade

- `freelu`: student eligible for a free school lunch (1: yes; 2: no)
- `gender`: student's gender (1: male; 2: female)

1. What percentage of students change schools during the study? (You may want to use the `egen` function `sd()` to find the standard deviation of `schid` within students, keeping in mind that the standard deviation is not defined for students who were only observed once.)
2. Delete observations where `schid` differs from `school`.
3. Use `xtdescribe` to explore the patterns of missing values of `tmaths`.
4. Fit a three-level random-intercept model for `tmaths`, with random intercepts for students and schools.
5. Add grade as a covariate and allow the effect of grade to vary randomly between students and schools.
   a. Write down the model using a three-stage formulation and derive the reduced form.
   b. Fit the model.
   c. Interpret the estimates.
6. Add `classt`, `frlnch`, `freelu`, and `gender` as explanatory variables, using appropriate dummy variables for categorical variables.
7. Interpret the estimated coefficients.
8. Check whether there is any evidence that the mean annual growth in math scores differs between class types.

See also exercise 9.10 for further analyses of data from the STAR experiment.

8.8 Dairy-cow data

Dohoo et al. (2001) and Dohoo, Martin, and Stryhn (2010) analyzed data on dairy cows nested in herds and regions of Reunion Island. One outcome considered was the time interval between calving (giving birth to a calf) and first service (attempt to inseminate the cow again). This outcome was available for several lactations (calvings) per cow.

The variables in the dataset `dairy.dta` used here are

- `cow`: cow identifier
- `herd`: herd identifier
- `region`: geographic region
- `lncfs`: log of calving to first service interval (in log days)
- `fscr`: first service conception risk (dummy variable for cow becoming pregnant)
- `ai`: dummy variable for artificial insemination being used (versus natural) at first service
- `heifer`: dummy variable for being a young cow that has given birth only once

1. Fit a four-level random-intercept model with `lncfs` as the response variable and with random intercepts for cows, herds, and geographic regions. Do not include any covariates. Use restricted maximum likelihood (REML) estimation. There are only five geographic regions, so it is arguable that region should be treated as fixed.
2. Obtain the estimated intraclass correlations for 1) two observations for the same cow, 2) observations for two different cows from the same herd, and 3) observations for two different cows from different herds in the same region.
3. Use REML to fit a three-level model for lactations nested in cows nested in herds, including dummy variables for the five geographic regions and omitting the constant. Compare the estimates for this model with the estimates using a four-level model.

8.9 ❖ Exam-and-coursework data

In this exercise, we consider a so-called multivariate multilevel model—that is, a regression model with several response variables—where units are nested in clusters. A multivariate regression (also known as seemingly unrelated regressions) for single-level data was considered in exercise 6.5.

The data are on students in England who took the General Certificate of Secondary Education (GCSE) exam in science (at age 16) in 1989. In addition to a written exam, the students also completed coursework that included projects undertaken during the school year and graded by each student's teacher. Both the written exam and coursework component scores have been scaled so that the maximum score is 100. The students are nested in schools. The data are described in Rasbash et al. (2009) and Goldstein (2011, chap. 6) and made available by the Centre for Multilevel Modelling at the University of Bristol.

The variables in `coursework.dta` are

- `schid`: school identifier
- `stid`: student identifier
- `girl`: dummy variable for being a girl
- `written`: written exam score
- `coursework`: coursework score

The two component scores are expected to be correlated, possibly with different correlations at the student and school levels. Denoting the written exam score for student i in school j as w_{ij} and the corresponding coursework score as c_{ij}, an appropriate model, with a dummy variable g_{ij} for girl as a covariate, is therefore

$$\begin{aligned} w_{ij} &= \beta_{w1} + \beta_{w2} g_{ij} + \zeta_{wj} + \epsilon_{wij} \\ c_{ij} &= \beta_{c1} + \beta_{c2} g_{ij} + \zeta_{cj} + \epsilon_{cij} \end{aligned}$$

Here β_{w1} and β_{w2} are the intercept and slope of g_{ij} for the written exam, and β_{c1} and β_{c2} are the intercept and slope of g_{ij} for the coursework.

Given gender, the school-level random intercepts ζ_{wj} and ζ_{cj} are assumed to follow a bivariate normal distribution,

$$\begin{bmatrix} \zeta_{wj} \\ \zeta_{cj} \end{bmatrix} \sim N\left(\begin{bmatrix} 0 \\ 0 \end{bmatrix}, \begin{bmatrix} \psi_{ww} & \psi_{wc} \\ \psi_{wc} & \psi_{cc} \end{bmatrix}\right)$$

as do the level-1 errors,

$$\begin{bmatrix} \epsilon_{wij} \\ \epsilon_{cij} \end{bmatrix} \sim N\left(\begin{bmatrix} 0 \\ 0 \end{bmatrix}, \begin{bmatrix} \theta_{ww} & \theta_{wc} \\ \theta_{wc} & \theta_{cc} \end{bmatrix}\right)$$

The model can be fit using `xtmixed` by changing the data to long form, stacking the written exam and coursework exams into one variable. The data can then be thought of as three-level data with response variables (w_{ij} and c_{ij}) at level 1, students at level 2, and schools at level 3. We will use the notation y_{rjk}, with $y_{1jk} \equiv w_{ij}$ and $y_{2jk} \equiv c_{ij}$. To obtain different intercepts for the two response variables, we can use dummy variables w_r and c_r, where w_r is one when $r = 1$ and zero otherwise, whereas c_r is one when $r = 2$ and zero otherwise. The slopes β_{w2} and β_{c2} of g_{ij} correspond to the coefficients of the interactions $g_{ij}w_r$ and $g_{ij}c_r$, respectively.

The Stata dataset should look like this:

```
. sort schid stid variable
. list schid stid y variable w c girl_c girl_w in 1/6, sepby(stid) noobs
```

schid	stid	y	variable	w	c	girl_w	girl_c
20920	16	23	1	1	0	0	0
20920	16	.	2	0	1	0	0
20920	25	.	1	1	0	1	0
20920	25	71.2	2	0	1	0	1
20920	27	39	1	1	0	1	0
20920	27	76.8	2	0	1	0	1

There are two rows of data per student, the variable `y` contains the two responses, the variable `variable` keeps track of which response is which (denoted r above), `w` and `c` are dummy variables for the written exam and coursework scores, respectively, and `girl_w` and `girl_c` are interactions between these dummy variables and `girl`.

The random intercepts can be specified as random coefficients of the dummy variables `w` and `c` (with an unstructured covariance matrix). Finally, an unstructured covariance matrix for the level-1 residuals can be specified using the `residuals(unstructured, t(variable))` option, as shown in section 6.3.1.

1. Reshape the data to long form, creating the variable `variable` to keep track of which row of data corresponds to which response variable.

2. Missing responses are coded −1. Replace these with missing values (.) using the `mvdecode` command.
3. Create the dummy variables `w` and `c` and the interactions `girl_w` and `girl_c`.
4. Fit the model by ML using `xtmixed`.
5. Interpret the estimates.

8.10 ❖ Twin-neuroticism data

Here we consider the twin data used in exercise 2.3. The neuroticism scores for twins i and i' in the same twin-pair j are expected to be correlated because the twins share genes and aspects of the environment. A biometric model for the effects of genes and environment can be written as

$$y_{ij} \;=\; \mu + A_{ij} + D_{ij} + C_{ij} + \epsilon_{ij}$$

where A_{ij} are additive genetic effects, D_{ij} are dominance genetic effects, C_{ij} is a common environment effect, and ϵ_{ij} is a unique environment effect. The terms are uncorrelated with each other and have variances σ^2_A, σ^2_D, σ^2_C and σ^2_e, respectively. The genetic effects A_{ij} and D_{ij} are perfectly correlated between members of the same twin-pair for MZ (identical) twins and have correlations 1/2 and 1/4, respectively, for DZ (fraternal) twins. The shared environment effect C_{ij} is perfectly correlated for both types of twins, whereas ϵ_{ij} is uncorrelated for both types of twins. The full model is not identifiable using twin data, so the ACE or ADE models are usually fit (omitting either D_{ij} or C_{ij} from the model).

Rabe-Hesketh, Skrondal, and Gjessing (2008) show that the covariance structure implied by the biometrical model can be induced using the following three-level model:

$$y_{ikj} \;=\; \beta_1 + \zeta^{(2)}_{kj} + \zeta^{(3)}_{j} + \epsilon_{ikj} \tag{8.4}$$

where k is an artificially created identifier that equals the twin-pair identifier j for MZ twins and the person identifier i for DZ twins. The variance ψ_3 of $\zeta^{(3)}_j$ is then shared by both members of the twin-pair for both MZ and DZ twins, whereas the variance ψ_2 of $\zeta^{(2)}_{kj}$ is shared by members of the twin-pair only for MZ twins. The covariances are therefore

$$\mathrm{Cov}(y_{ij}, y_{i'j}) = \begin{cases} \psi_2 + \psi_3 = \sigma^2_A + \sigma^2_D + \sigma^2_C & \text{for MZ twins} \\ \psi_3 = \sigma^2_A/2 + \sigma^2_D/4 + \sigma^2_C & \text{for DZ twins} \end{cases}$$

For the ACE model ($\sigma^2_D = 0$), we have

$$\sigma^2_A = 2\psi_2 \qquad \sigma^2_C = \psi_3 - \psi_2 \qquad \sigma^2_e = \theta$$

and for the ADE model ($\sigma^2_C = 0$), we have

$$\sigma^2_A = 3\psi_3 - \psi_2 \qquad \sigma^2_D = 2(\psi_2 - \psi_3) \qquad \sigma^2_e = \theta$$

1. The data are in collapsed or aggregated form with `num2` representing the number of twin-pairs having a given pair of neuroticism scores. Expand the data using `expand num2`.

2. Create an identifier for twin-pairs (for example, using `generate pair = _n`) and reshape the data to long form, stacking the neuroticism scores into one variable.
3. Create the artificial identifier k and fit the model in (8.4).
4. Obtain the estimated variance components for the ACE and ADE models. Which model would you choose?

8.11 ❖ Peak-expiratory-flow data I

The three-level model for the peak-expiratory-flow data from Bland and Altman (1986) considered in this chapter can be written as

$$\begin{aligned} y_{ijk} &= \pi_{0jk} + \epsilon_{ijk} \\ \pi_{0jk} &= \underbrace{\gamma_{000} + u_{0k}}_{\beta_{0k}} + r_{0jk} \end{aligned}$$

where we have used the notation common in the three-stage formulation but with the level-3 model for β_{0k} substituted into the level-2 model for π_{0jk}. This model can be represented by the path diagram in the left panel of figure 8.10.

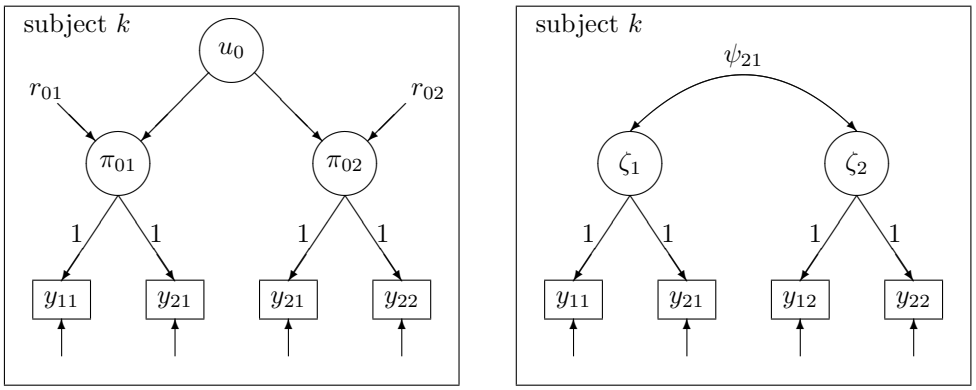


Figure 8.10: Path diagrams of equivalent models (left panel: three-stage formulation of three-level model; right panel: correlated random effects)

1. Express the correlation between π_{01k} and π_{02k} for the model represented in the left panel of figure 8.10 in terms of the variances $\psi^{(2)}$ at level 2 and $\psi^{(3)}$ at level 3.
2. The right panel in figure 8.10 represents a model with two method-specific correlated random intercepts, ζ_{1k} for method 1 and ζ_{2k} for method 2. Defining dummy variables d_{1j} for method 1 and d_{2j} for method 2, the model can be written as a two-level random-coefficient model:

$$y_{ijk} = \beta_1 + \zeta_{1k} d_{1j} + \zeta_{2k} d_{2j} + \epsilon_{ijk}$$

If the variances of the two random coefficients are constrained equal and if the covariance is positive, this model is equivalent to the previous three-level model. Verify this by fitting the above model by ML using `xtmixed`. You can use the `covariance(exchangeable)` option to constrain the variances of the random coefficients to be equal.

3. For the model in step 2, relax the assumption of equal variances of the random coefficients by using the `covariance(unstructured)` option. Compare this model with the model in step 2 using a likelihood-ratio test.
4. For the more complex model from step 3, obtain the estimated method-specific intraclass correlations, $\widehat{\rho}$(subject|method=1) and $\widehat{\rho}$(subject|method=2).
5. Extend the model further (still using `xtmixed`) by relaxing the assumption of equal measurement error variances θ. Is there any evidence that the measurement error variances differ between the methods? Again obtain the estimated method-specific intraclass correlations based on the more complex model.

8.12 ❖ Peak-expiratory-flow data II

This exercise is a useful transition to the next chapter, where we sometimes treat random intercepts for a factor as random coefficients of dummy variables for the levels of the factor.

For the peak-expiratory-flow data, we require a random intercept for method nested in subject. This can be achieved by having uncorrelated random coefficients at the subject level for a dummy variable d_{1j} for method 1 and d_{2j} for method 2. We also retain the random intercept at the subject level (now called ζ_{3k}):

$$y_{ijk} = \beta_1 + \zeta_{1k}d_{1j} + \zeta_{2k}d_{2j} + \zeta_{3k} + \epsilon_{ijk}$$

All three random effects should be mutually uncorrelated, but only the first two should have the same variance. This can be achieved by using two random parts for the same level: `|| id: d1 d2, covariance(identity) noconstant || id:`, where the `covariance(identity)` option specifies equal variances and no covariance for the random coefficients of `d1` and `d2` (the dummy variables) and the `noconstant` option suppresses the random intercept because this is already specified by the next equation, `|| id:`. Random effects in different random part specifications (separated by `||`) are assumed to be uncorrelated. Also note that the `noconstant` option is not necessary because `xtmixed` puts the constant only in the last equation for a given level by default.

Fit this model using `xtmixed`, and show that it is equivalent to the three-level random-intercept model specified using `|| id: || method:`.

9 Crossed random effects

9.1 Introduction

In the previous chapter, we discussed higher-level hierarchical models where units are classified by some factor (for instance, school) into top-level clusters. The units in each top-level cluster are then (sub)classified by a further factor (for instance, classroom) into clusters at a lower level, etc. The factors defining the classifications are nested in the sense that a lower-level cluster can only belong to *one* higher-level cluster (for instance, a classroom can only belong to one school).

We now discuss nonhierarchical models where units are *cross-classified* by two or more factors, with each unit potentially belonging to any combination of values of the different factors. If the *main* effects of these cross-classifications are represented by *random* effects, this leads to models with crossed random effects. Cross-classifications do of course frequently occur in the fixed part of the model where they can easily be handled by including dummy variables and interaction terms.

A prominent example of crossed data is students who are cross-classified by elementary schools and middle schools. Children from the same elementary school can go to different middle schools and children in the same middle school can come from different elementary schools. We would expect that the middle school attended by the child would have a main effect on, for instance, achievement in addition to the main effect of the elementary school attended. Usually, the factors elementary school and middle school are both treated as random. The random effects are then crossed, which produces a crossed random effects model. An example where Scottish primary schools are crossed with secondary schools is considered in section 9.4.

Longitudinal or panel data is another example of cross-classified data where the factor subject (or country or firm, etc.) is crossed with another factor, occasion (see section 9.2 for such an example). So far in this book, we have treated occasions as nested within subjects when considering longitudinal data. This means that the random part of the model has mean zero at each occasion across subjects. Occasion was represented in the random part by the level-1 error, taking a different value for each subject–occasion combination. There was hence no random main effect of occasion taking the same value across subjects. However, if all subjects are affected similarly by some events or characteristics associated with the occasions—such as weather conditions, strikes, new legislation, etc.—it seems reasonable to consider a random main effect of occasion. If the factors subject and occasion are both treated as random, the random effects are crossed and econometricians call the model a *two-way error-components model*. Such a model is considered in section 9.3.

9.2 How does investment depend on expected profit and capital stock?

Grunfeld (1958) and Boot and de Wit (1960), among others, analyzed investment data on 10 large American corporations collected annually from 1935 to 1954. This is a dataset with long panels as discussed in section 6.7.

The variables in the file `grunfeld.dta` provided by Baltagi (2008) are

- `fn`: firm identifier (i)
- `firmname`: firm name
- `yr`: year (j)
- `I`: annual gross investment (in \$1,000,000) defined as amount spent on plant and equipment plus maintenance and repairs (y_{ij})
- `F`: market value of firm (in \$1,000,000) defined as value of all shares plus book value of all debts outstanding at the beginning of the year (x_{2ij})
- `C`: real value of capital stock (in \$1,000,000) defined as the deviation of stock of plant and equipment from stock in 1933 (x_{3ij})

We read in the data using

```
. use http://www.stata-press.com/data/mlmus3/grunfeld
```

Grunfeld argued that the investment of firms depends on expected profit (measured as market value) and capital stock (see display 9.1 if you are interested in a brief summary of Grunfeld's investment theory). The theory implies an investment equation of the form

$$y_{ij} = \beta_1 + \beta_2 x_{2ij} + \beta_3 x_{3ij}$$

where we have denoted the gross investment `I` for firm i in year j as y_{ij}, the market value `F` as x_{2ij}, and the value of capital stock `C` as x_{3ij}.

Boot and de Wit (1960) summarize Grunfeld's (1958) investment theory as follows: Observed profits are rejected as an explanation of investment, and expected profits, measured as the market value of the firm $\texttt{F}(t)$ at time t, are used instead. The desired capital stock $C^*(t)$ is assumed to be a linear function of the market value:

$$C^*(t) \;=\; c_1 + c_2\texttt{F}(t)$$

The desired net investment is the difference between desired capital stock $C^*(t)$ and the existing capital stock $\texttt{C}(t)$: $C^*(t) - \texttt{C}(t)$. Assuming that a constant fraction q_1 of the desired net investment is made between t and $t+1$, the net investment for that year becomes

$$q_1\{C^*(t) - \texttt{C}(t)\} \;=\; q_1c_1 + q_1c_2\texttt{F}(t) - q_1\texttt{C}(t)$$

Assuming that replacement investment plus maintenance and repairs equals a constant fraction q_2 of the existing capital stock $\texttt{C}(t)$, the gross investment in the following year $\texttt{I}(t+1)$ becomes

$$\begin{aligned}\texttt{I}(t+1) &= q_1\{C^*(t) - \texttt{C}(t)\} + q_2\texttt{C}(t)\\ &= q_1c_1 + q_1c_2\texttt{F}(t) + (q_2 - q_1)\texttt{C}(t)\end{aligned}$$

Denoting the gross investment I for firm i in year j as y_{ij}, the market value F as x_{2ij}, and the value of capital stock C as x_{3ij}, the investment equation can finally be written as

$$y_{ij} \;=\; \beta_1 + \beta_2x_{2ij} + \beta_3x_{3ij}$$

where $\beta_1 \equiv q_1c_1$, $\beta_2 \equiv q_1c_2$, and $\beta_3 \equiv q_2 - q_1$. Both β_2 and β_3 are expected to be positive. However, the intercept β_1 has limited meaning because capital stock has been measured as a deviation from the stock in 1933.

Display 9.1: Brief summary of Grunfeld's (1958) investment theory

9.3 A two-way error-components model

9.3.1 Model specification

Because the investment behavior of corporations is surely not deterministic, statistical models including error terms have invariably been specified. Baltagi (2008) allows the effects of both firms and years on gross investment y_{ij} to vary by specifying the following two-way error-components model:

$$y_{ij} \;=\; \beta_1 + \beta_2x_{2ij} + \beta_3x_{3ij} + \zeta_{1i} + \zeta_{2j} + \epsilon_{ij} \tag{9.1}$$

Here x_{2ij} and x_{3ij} represent the market value and capital stock of firm i in year j. ζ_{1i} and ζ_{2j} are random intercepts for firms i and years j, respectively, and ϵ_{ij} is a residual error term.

Given the covariates x_{2ij} and x_{3ij}, the random intercepts have zero means and are uncorrelated with each other, ζ_{1i} has variance ψ_1 and is uncorrelated across firms, and

ζ_{2j} has variance ψ_2 and is uncorrelated across years. The random intercepts ζ_{1i} and ζ_{2j} are also uncorrelated with ϵ_{ij}. The residual ϵ_{ij} has zero mean and variance θ, given the covariates and random intercepts, and the residuals are uncorrelated across firms and years.

This model differs from the models considered so far because the two random intercepts represent factors that are crossed instead of nested. The random intercept for firm ζ_{1i} is shared across all years for a given firm i, whereas the random intercept for year ζ_{2j} is shared by all firms in a given year j. The residual error ϵ_{ij} comprises both the interaction between year and firm and any other effect specific to firm i in year j. An interaction between firm and year could be due to some events occurring in some years being more beneficial (or detrimental) to some firms than others.

9.3.2 Residual variances, covariances, and intraclass correlations

It follows from the assumptions that the variance for a response given the covariates becomes

$$\mathrm{Var}(y_{ij}|x_{2ij}, x_{3ij}) \;=\; \psi_1 + \psi_2 + \theta$$

Longitudinal correlations

Given the covariates, the covariance between responses for the same firm i at different years j and j' is

$$\mathrm{Cov}(y_{ij}, y_{ij'}|x_{2ij}, x_{3ij}, x_{2ij'}, x_{3ij'}) \;=\; \psi_1$$

As in section 8.5, this covariance can be derived by taking the expectations of the product of the random parts in y_{ij} and $y_{ij'}$. The only product term with a nonzero expectation under the model assumptions is the square of the random intercept for firms, whose expectation is $E(\zeta_{1i}^2) = \mathrm{Var}(\zeta_{1i}) \equiv \psi_1$. The corresponding longitudinal (between-year, within-firm) intraclass correlation is

$$\rho(\text{firm}) \equiv \mathrm{Cor}(y_{ij}, y_{ij'}|x_{2ij}, x_{3ij}, x_{2ij'}, x_{3ij'}) \;=\; \frac{\psi_1}{\psi_1 + \psi_2 + \theta}$$

Cross-sectional correlations

The covariance between responses for different firms i and i' in the same year j is

$$\mathrm{Cov}(y_{ij}, y_{i'j}|x_{2ij}, x_{3ij}, x_{2i'j}, x_{3i'j}) \;=\; \psi_2$$

This can be obtained by taking the expectations of the product of the random parts in y_{ij} and $y_{i'j}$, and here the only product term with a nonzero expectation is the square of the random intercept for year. The cross-sectional (between-firm, within-year) intraclass correlation becomes

$$\rho(\text{year}) \equiv \mathrm{Cor}(y_{ij}, y_{i'j}|x_{2ij}, x_{3ij}, x_{2i'j}, x_{3i'j}) \;=\; \frac{\psi_2}{\psi_1 + \psi_2 + \theta}$$

9.3.3 Estimation using xtmixed

The `xtmixed` command is primarily designed for multilevel models with nested random effects. To fit models with crossed effects, we therefore use the following trick described by Goldstein (1987):

- Consider the entire dataset as an artificial level-3 unit a within which both firms and years are nested.
- Treat either years or firms as level-2 units j, and specify a random intercept $u_{ja}^{(2)}$ for them. It is best to choose the factor with more levels, that is, years.
- For the other factor, here firm, specify a level-3 random intercept for each firm, $u_{pa}^{(3)}$, $(p = 1, \ldots, 10)$. This can be constructed by treating $u_{pa}^{(3)}$ as the random coefficient of the dummy variable d_{pi} for firm p, where

$$d_{pi} = \begin{cases} 1 & \text{if } p = i \\ 0 & \text{otherwise} \end{cases}$$

  The 10 random coefficients are then specified as having equal variance ψ_1 and being uncorrelated.

Here we have used the notation u for the random effects to avoid confusion between the different formulations. Model (9.1) can then be written as

$$\begin{aligned} y_{ija} &= \beta_1 + \beta_2 x_{2ij} + \beta_3 x_{3ij} + u_{ja}^{(2)} + \sum_p u_{pa}^{(3)} d_{pi} + \epsilon_{ija} \\ &= \beta_1 + \beta_2 x_{2ij} + \beta_3 x_{3ij} + \underbrace{u_{ja}^{(2)}}_{\zeta_{2j}} + \underbrace{u_{ia}^{(3)}}_{\zeta_{1i}} + \underbrace{\epsilon_{ija}}_{\epsilon_{ij}} \end{aligned}$$

where $u_{ja}^{(2)}$ and $u_{ia}^{(3)}$ are uncorrelated because they are specified at different levels.

The basic idea is to treat the 10 different realizations (or observations) of one random intercept $\zeta_i (i = 1, \ldots, 10)$ as realizations of 10 different random coefficients (or variables) $u_{ia}^{(3)}$ (similar to transforming data from long form to wide form where observations of one variable become different variables). Each random coefficient $u_{ia}^{(3)}$ takes on only one value for the entire dataset, and the dummy variable for firm i ensures that $u_{ia}^{(3)}$ contributes to the model only for firm i.

Recall that the firm identifier is `fn` and the year identifier is `yr`. Fortunately, `xtmixed` makes it easy to specify a random intercept $u_{pa}^{(3)}$ for each level of a factor (here each firm) or, as specified above, random coefficients for the corresponding dummy variables. The syntax `R.fn` in the random part accomplishes this and also automatically sets all variances equal and all correlations to zero as required. This covariance structure is called `identity` in `xtmixed` because the covariance matrix is proportional to the 10×10 identity matrix (a matrix with ones on the diagonal and zeros elsewhere). We also do

not need to create an artificial level-3 identifier because `xtmixed` accepts the cluster name `_all` for this purpose.

The first random part is therefore specified as `|| _all: R.fn`. Following this, we specify `|| yr:` to let year have a random intercept at level 2. The random effects for time and year are uncorrelated as required because they are specified in different random parts (separated by `||`).

We fit the two-way error-components model in `xtmixed` by maximum likelihood (ML) using

```
. xtmixed I F C || _all: R.fn || yr:, mle
Mixed-effects ML regression                     Number of obs      =       200
```

Group Variable	No. of Groups	Observations per Group Minimum	Average	Maximum
_all	1	200	200.0	200
yr	20	10	10.0	10

```
                                                Wald chi2(2)       =    661.06
Log likelihood = -1095.2485                     Prob > chi2        =    0.0000
```

I	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
F	.1099012	.010378	10.59	0.000	.0895607	.1302418
C	.3092288	.0172182	17.96	0.000	.2754818	.3429758
_cons	-58.27229	27.76304	-2.10	0.036	-112.6869	-3.857725

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
_all: Identity				
sd(R.fn)	80.4124	18.42495	51.32	125.9968
yr: Identity				
sd(_cons)	3.864611	15.26661	.0016771	8905.534
sd(Residual)	52.34725	2.903932	46.95415	58.3598

```
LR test vs. linear regression:       chi2(2) =   193.11   Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference
```

The market value (expected profit) and stock value (capital stock) of a firm both have positive effects on investment as expected. According to the fitted model, an increase in the market value of \$1,000,000 increases the mean investment by about \$110,000, controlling for stock value. An increase in the stock value of \$1,000,000 increases the mean investment by \$310,000, controlling for market value. The estimated residual standard deviation between firms is \$80.41 million, and the estimated residual standard deviation between years is only \$3.86 million. The remaining residual standard deviation, not due to additive effects of firms and years, is estimated as \$52.35 million. The estimates are also given under ML in table 9.1.

Table 9.1: Maximum likelihood (ML) and restricted maximum likelihood (REML) estimates of two-way error-components model for Grunfeld (1958) data

	ML		REML	
	Est	(SE)	Est	(SE)
Fixed part				
β_1	−58.27	(27.76)	−58.84	(29.51)
β_2 [F]	0.11	(0.01)	0.11	(0.01)
β_3 [C]	0.31	(0.02)	0.31	(0.02)
Random part				
$\sqrt{\psi_1}$ [Firm]	80.41		86.07	
$\sqrt{\psi_2}$ [Year]	3.86		5.40	
$\sqrt{\theta}$	52.35		52.47	
Log likelihood	−1,095.25		−1,097.90†	

†Restricted log likelihood

The reason for choosing year to be at level 3 and to have a random intercept for each firm at level 2 is to minimize the computational burden. With this formulation, the model has 10 random effects at level 3 (one for each firm) and 1 random effect at level 2. If we instead had chosen firm to be at level 2 and to have a separate random intercept for each year at level 3, we would have required 20 random effects at level 3 (one for each year) and 1 random effect at level 2. The syntax would be

```
xtmixed I F C || _all: R.yr || fn:, mle
```

Although more computationally demanding, this setup produces identical estimates to the command used above.

We have used the same estimation method (maximum likelihood) as for models with nested random effects, but it should be noted that asymptotics now rely on *both* the number of firms and the number of occasions going to infinity. Because we only have data on 10 firms over 20 years here, we cannot expect asymptotic results to hold and should treat them as approximate. For this reason, we do not test hypotheses regarding variance parameters for these data (see section 9.7.4 for such tests).

Another problem with a small number of clusters is that ML estimates of variance components are downward biased (see section 2.10.2). For balanced data, such as the Grunfeld (1958) investment data, restricted maximum likelihood (REML) yields unbiased estimates (if the estimates are allowed to be negative).

```
. xtmixed I F C || _all: R.fn || yr:, reml
Mixed-effects REML regression                   Number of obs      =       200
```

Group Variable	No. of Groups	Observations per Group Minimum	Average	Maximum
_all	1	200	200.0	200
yr	20	10	10.0	10

```
                                                Wald chi2(2)       =    643.60
Log restricted-likelihood = -1097.8951          Prob > chi2        =    0.0000
```

I	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
F	.1100654	.0106036	10.38	0.000	.0892828	.130848
C	.3106316	.0174474	17.80	0.000	.2764353	.344828
_cons	-58.83708	29.50687	-1.99	0.046	-116.6695	-1.00468

Random-effects Parameters		Estimate	Std. Err.	[95% Conf.	Interval]
_all: Identity	sd(R.fn)	86.06838	20.78351	53.61647	138.1621
yr: Identity	sd(_cons)	5.399614	11.48764	.0834521	349.3723
	sd(Residual)	52.46645	2.910242	47.0616	58.49202

```
LR test vs. linear regression:       chi2(2) =   196.43   Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference.
```

The estimates were also given under REML in table 9.1. We see that only the random-intercept standard deviations differ appreciably between REML and ML and are larger for REML as expected.

Based on the REML estimates, the residual longitudinal intraclass correlation within firms is estimated as

$$\widehat{\rho}(\text{firm}) \;=\; \frac{86.06838^2}{86.06838^2 + 5.399614^2 + 52.46645^2} = 0.73$$

and the residual cross-sectional intraclass correlation between firms within years is estimated as

$$\widehat{\rho}(\text{year}) \;=\; \frac{5.399614^2}{86.06838^2 + 5.399614^2 + 52.46645^2} = 0.003$$

Hence, there is a high correlation over years within firms and a negligible correlation over firms within years, given the covariates.

Instead of typing in the estimates, we can refer to them by the equation and column names, which we can find by displaying the matrix of estimates (or running `xtmixed` with the `estmetric` option):

```
. matrix list e(b)
e(b)[1,6]
             I:          I:          I:   lns1_1_1:   lns2_1_1:    lnsig_e:
             F           C       _cons       _cons       _cons       _cons
y1   .11006541   .31063164  -58.837081   4.4551421   1.6863275   3.9601739
```

The last three elements are the log-standard deviations of the random effects and level-1 residuals in the same order as given in the output. We can therefore obtain the estimated within-firm intraclass correlation using

```
. display exp(2*[lns1_1_1]_cons)/(exp(2*[lns1_1_1]_cons) + exp(2*[lns2_1_1]_cons)
> + exp(2*[lnsig_e]_cons))
.72698922
```

9.3.4 Prediction

Having fit the model using REML, it is easy to obtain various predictions. For instance, we can obtain empirical Bayes predictions or best linear unbiased predictions (BLUPs) $\widetilde{\zeta}_{1i}$ and $\widetilde{\zeta}_{2j}$ of the random effects of firm and year using `predict` with the `reffects` option,

```
. predict firm year, reffects
```

and list these predictions for four of the firms for the first three years:

```
. sort fn yr
. list fn firmname yr firm year if yr<1938&fn<5, sepby(fn) noobs
```

fn	firmname	yr	firm	year
1	General Motors	1935	-11.36264	3.290692
1	General Motors	1936	-11.36264	1.778602
1	General Motors	1937	-11.36264	.0498858
2	US Steel	1935	157.7599	3.290692
2	US Steel	1936	157.7599	1.778602
2	US Steel	1937	157.7599	.0498858
3	General Electric	1935	-173.6221	3.290692
3	General Electric	1936	-173.6221	1.778602
3	General Electric	1937	-173.6221	.0498858
4	Chrysler	1935	30.43414	3.290692
4	Chrysler	1936	30.43414	1.778602
4	Chrysler	1937	30.43414	.0498858

The predictions for the firms have all conveniently been placed into 1 variable, `firm`, not into 10 variables as might have been expected. We see that the prediction for firm 1 (General Motors) is -11.36 and the prediction for 1935 is 3.29. After controlling for market and stock value, General Motors was a firm with lower investment than the average across firms, and 1935 was a year with higher investment than the average over the 20-year interval.

We can visualize these effects by plotting the sum of the predicted random effects $\widetilde{\zeta}_{1i} + \widetilde{\zeta}_{2j}$ versus occasion j (`yr`) with a separate line for each firm i (`fn`):

```
. generate reffpart = firm + year
. twoway (line reffpart yr, connect(ascending))
> (scatter reffpart yr if yr==1954, msymbol(none) mlabel(firmnam) mlabpos(3)),
> xtitle(Year) ytitle(Predicted random effects of firm and year)
> xscale(range(1935 1958)) legend(off)
```

It is clear from the resulting figure 9.1 that the between-firm variability is much more considerable than the between-year variability.

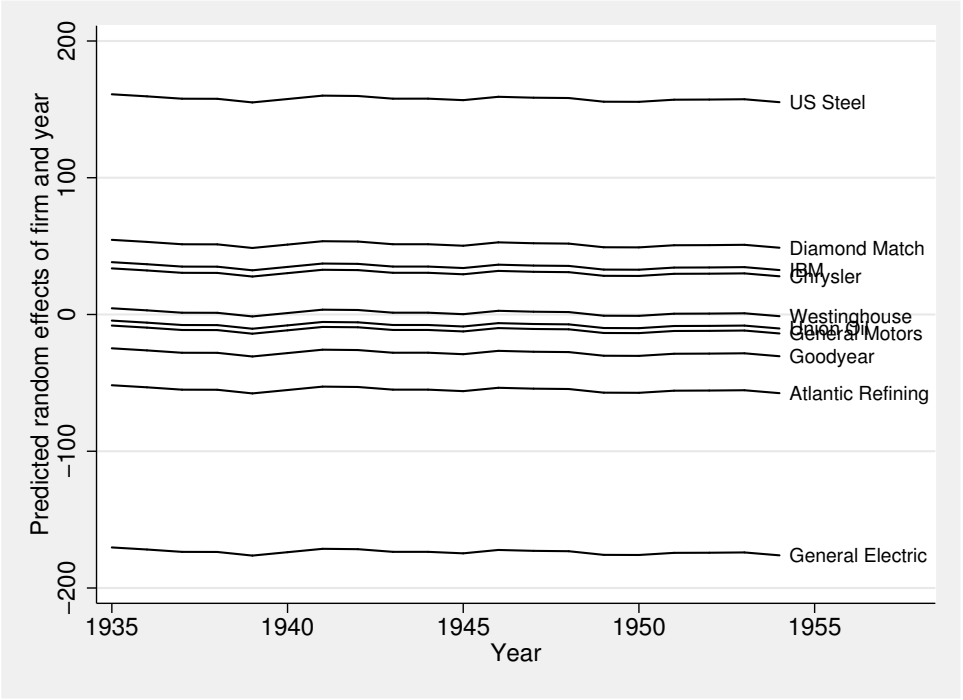


Figure 9.1: Sum of the predicted random effects $\widetilde{\zeta}_{1i} + \widetilde{\zeta}_{2j}$ versus time for 10 firms

The effect of year is hardly visible in figure 9.1 because it is negligible compared with the effect of firm. We therefore produce another graph just showing the effect of year on its own,

```
. twoway (line year yr if fn==1), xtitle(Year)
> ytitle(Predicted random effect for year)
```

which is given in figure 9.2. (Here we plotted the data for the first firm by using `if fn==1` but would have obtained an identical graph if we had picked another firm.)

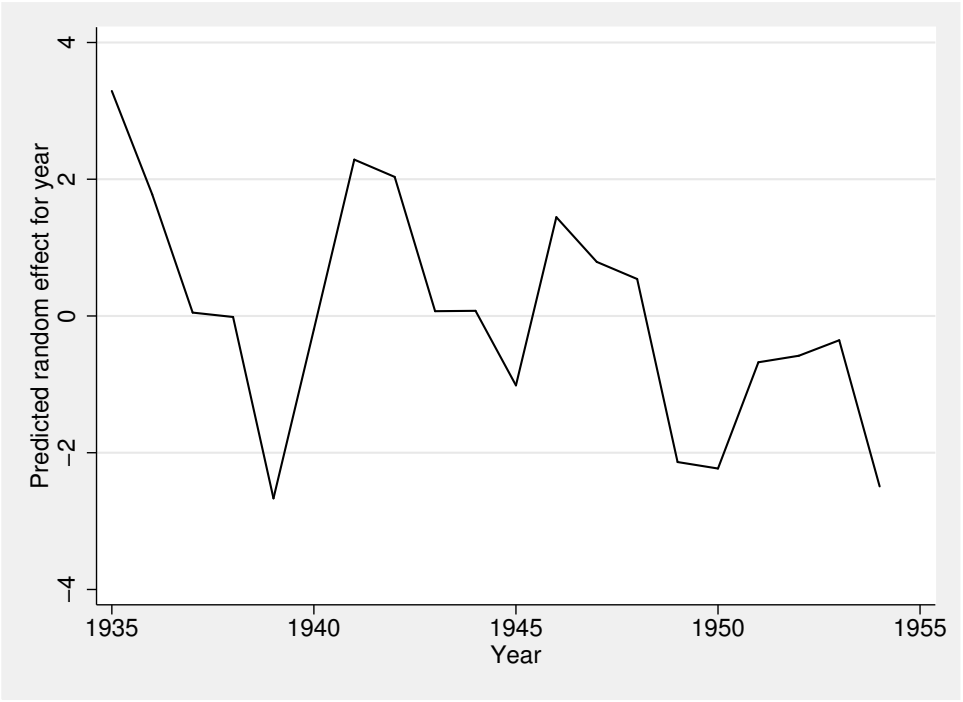


Figure 9.2: Predicted random effect of year $\widetilde{\zeta}_{2j}$

9.4 How much do primary and secondary schools affect attainment at age 16?

We now consider data described by Paterson (1991) on pupils (students) from Fife, Scotland, who are cross-classified by 148 primary schools (elementary schools) and 19 secondary schools (middle/high schools).

The dataset `fife.dta` is distributed with the MLwiN program (Rasbash et al. 2009) and has previously been analyzed by Goldstein (2011) and Rasbash (2005). The dataset has the following variables:

- `attain`: attainment score at age 16 [summary of passes in the Scottish Certificate of Education (SCE), a school exit examination] (y_{ijk})
- `pid`: identifier for primary school (up to age 12) (k)
- `sid`: identifier for secondary school (from age 12) (j)
- `vrq`: verbal reasoning score from test taken in the last year of primary school
- `sex`: gender (1: female; 0: male)

Here we investigate to what extent educational attainment at age 16 depends on the primary school attended up to age 12 and the secondary school attended thereafter.

We read in the data using

```
. use http://www.stata-press.com/data/mlmus3/fife, clear
```

9.5 Data structure

The structure of the Fife data is different than the Grunfeld investment data considered earlier in two regards: First, not every combination of primary and secondary school exists. Second, many combinations of primary and secondary school occur multiple times.

We first explore this crossed structure in more detail. For this, it is useful to define a dummy variable taking the value 1 for exactly one observation for each combination of the primary-school and secondary-school identifiers. The `egen` function `tag()` is designed for creating such dummy variables:

```
. egen pick_comb = tag(pid sid)
```

Now we can count the number of unique values of `sid` in each primary school (with identifier `pid`) using the `egen` function `total()`:

```
. egen numsid = total(pick_comb), by(pid)
```

We can list the unique secondary school identifiers for the first 10 primary schools using

```
. sort pid sid
. list pid sid numsid if pick_comb==1 & pid<10, sepby(pid) noobs
```

pid	sid	numsid
1	1	3
1	9	3
1	18	3
2	7	1
3	5	1
4	6	2
4	9	2
5	1	1
6	1	4
6	3	4
6	5	4
6	11	4
7	4	4
7	6	4
7	18	4
7	19	4
8	1	3
8	9	3
8	19	3
9	1	6
9	3	6
9	6	6
9	17	6
9	18	6
9	19	6

We see that, for instance, students in this sample who attended primary school 1 ended up in three (`numsid`=3) secondary schools, 1, 9, and 18.

To obtain the frequency distribution of `numsid`, the number of secondary schools per primary school, we must first define a dummy variable equal to 1 for one student per primary school (so we do not count primary schools more than once),

```
. egen pick_pid = tag(pid)
```

and can subsequently use the `tabulate` command:

```
. tabulate numsid if pick_pid
```

numsid	Freq.	Percent	Cum.
1	57	38.51	38.51
2	50	33.78	72.30
3	26	17.57	89.86
4	10	6.76	96.62
5	2	1.35	97.97
6	3	2.03	100.00
Total	148	100.00	

There are at most six secondary schools per primary school, and for about 90% of the primary schools there are at most three secondary schools per primary school.

Repeating the same commands as above, but with `sid` and `pid` interchanged, we obtain the frequency table of the number of primary schools per secondary school:

```
. egen numpid = total(pick_comb), by(sid)
. egen pick_sid = tag(sid)
. tabulate numpid if pick_sid==1
```

numpid	Freq.	Percent	Cum.
7	1	5.26	5.26
10	2	10.53	15.79
12	1	5.26	21.05
13	2	10.53	31.58
14	4	21.05	52.63
15	1	5.26	57.89
16	1	5.26	63.16
17	2	10.53	73.68
18	2	10.53	84.21
23	1	5.26	89.47
26	1	5.26	94.74
32	1	5.26	100.00
Total	19	100.00	

There are between 7 and 32 primary schools per secondary school, the median being between 13 and 14.

9.6 Additive crossed random-effects model

9.6.1 Specification

We first consider the following model for the attainment score y_{ijk} at age 16 for student i who went to secondary school j and primary school k:

$$y_{ijk} = \beta_1 + \zeta_{1j} + \zeta_{2k} + \epsilon_{ijk} \tag{9.2}$$

The random part of this model has exactly the same structure as in the investment application with additive (and uncorrelated) random effects ζ_{1j} and ζ_{2k} of the two cross-

classified factors, secondary school and primary school, respectively, plus a residual error term ϵ_{ijk}. The error components ζ_{1j} and ζ_{2i} have zero means and variances ψ_1 and ψ_2, respectively. Given ζ_{1j} and ζ_{2i}, the residual error ϵ_{ijk} has mean zero and variance θ.

9.6.2 Estimation using xtmixed

Because there are only 19 secondary schools compared with 148 primary schools, we use 19 random effects for the secondary schools at level 3 and treat primary schools as level-2 units.

The `xtmixed` command for fitting model (9.2) by ML is

```
. xtmixed attain || _all: R.sid || pid:, mle
Mixed-effects ML regression                     Number of obs      =      3435

------------------------------------------------------------------------------
                |     No. of       Observations per Group
 Group Variable |     Groups    Minimum    Average    Maximum
----------------+-------------------------------------------------------------
           _all |          1       3435     3435.0       3435
            pid |        148          1       23.2         72
------------------------------------------------------------------------------

                                                Wald chi2(0)       =          .
Log likelihood = -8574.5655                     Prob > chi2        =          .

------------------------------------------------------------------------------
      attain |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       _cons |    5.504009   .1749325    31.46   0.000     5.161148    5.846871
------------------------------------------------------------------------------

------------------------------------------------------------------------------
  Random-effects Parameters |   Estimate   Std. Err.     [95% Conf. Interval]
----------------------------+-------------------------------------------------
_all: Identity              |
                  sd(R.sid) |   .5900565   .1371156      .3741915    .9304505
----------------------------+-------------------------------------------------
pid: Identity               |
                sd(_cons)   |   1.060359   .0971078       .886135    1.268838
----------------------------+-------------------------------------------------
             sd(Residual)   |   2.848065   .0351956      2.779912     2.91789
------------------------------------------------------------------------------
LR test vs. linear regression:       chi2(2) =   278.13   Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference
. estimates store additive
```

The estimates are presented under "Additive" in table 9.2. We see that the estimated standard deviation $\sqrt{\widehat{\psi}_2}$ of the primary school random effect is 1.06, which is considerably larger than the estimated standard deviation $\sqrt{\widehat{\psi}_1}$ of the secondary school random effect, given by 0.59. Therefore, elementary schools appear to have greater effects or to be more variable in their effects on attainment than secondary schools. However, neither of these standard deviation estimates is very precise.

The estimated standard deviation $\sqrt{\widehat{\theta}}$ of ϵ_{ijk} is 2.85. This number reflects any interactions between primary and secondary schools (deviations of the means for the combinations of primary and secondary schools from the means implied by the additive effects) as well as variability within the groups of children belonging to the same combination of primary and secondary school.

9.7 Crossed random-effects model with random interaction

9.7.1 Model specification

For many combinations of primary and secondary school, we have several observations because more than one student attended that combination of schools. We can therefore include a random interaction term ζ_{3jk} between secondary schools j and primary schools k in the model

$$y_{ijk} = \beta_1 + \zeta_{1j} + \zeta_{2k} + \zeta_{3jk} + \epsilon_{ijk} \tag{9.3}$$

The interaction term takes on a different value for each combination of secondary and primary school to allow the assumption of additive (random) effects to be relaxed. For instance, some secondary schools may be more beneficial for students who attended particular elementary schools, perhaps because of similar instructional practices.

The random intercept ζ_{3jk} has zero mean and variance ψ_3, is uncorrelated with the other random terms (ζ_{1j}, ζ_{2k}, and ϵ_{ijk}), and is uncorrelated across combinations of primary and secondary school. The residual ϵ_{ijk} represents the deviation of an individual student's response from the mean for secondary school j and primary school k. For given random effects, ϵ_{ijk} has zero mean and variance θ.

Note that we could not include an interaction in the investment application because we had no replicates for any of the firm and year combinations, so the interaction would be completely confounded with the level-1 residual.

9.7.2 Intraclass correlations

We can consider several intraclass correlations for the crossed random-effects model that includes a random interaction. For students i and i' from the same primary school k but different secondary schools j and j', we obtain

$$\rho(\text{primary}) \equiv \text{Cor}(y_{ijk}, y_{i'j'k}) = \frac{\psi_2}{\psi_1 + \psi_2 + \psi_3 + \theta}$$

where $\psi_3 = 0$ if there is no interaction. For students from the same secondary school j but different primary schools k and k', the correlation is

$$\rho(\text{secondary}) \equiv \text{Cor}(y_{ijk}, y_{i'jk'}) = \frac{\psi_1}{\psi_1 + \psi_2 + \psi_3 + \theta}$$

Finally, for students from both the same secondary school j and the same primary school k, we have

$$\rho(\text{secondary},\text{primary}) \equiv \text{Cor}(y_{ijk}, y_{i'jk}) \;=\; \frac{\psi_1+\psi_2+\psi_3}{\psi_1+\psi_2+\psi_3+\theta}$$

We could also condition on secondary school and consider the intraclass correlation among children from the same secondary school due to being in the same primary school:

$$\rho(\text{primary}|\text{secondary}) \equiv \text{Cor}(y_{ijk}, y_{i'jk}|\zeta_{1j}) \;=\; \frac{\psi_2+\psi_3}{\psi_2+\psi_3+\theta}$$

where the between-secondary-school variance ψ_1 vanishes because secondary school is held constant. The analogous expression for the intraclass correlation due to secondary school for a given primary school is

$$\rho(\text{secondary}|\text{primary}) \equiv \text{Cor}(y_{ijk}, y_{i'jk}|\zeta_{2k}) = \frac{\psi_1+\psi_3}{\psi_1+\psi_3+\theta}$$

The covariances can be derived as in section 8.5 by taking the expectation of the product of the random parts. When conditioning on a particular random term, such as ζ_{2k}, this term is simply omitted from the random part (see also exercise 9.11).

9.7.3 Estimation using xtmixed

The crossed random-effects model with a random interaction (9.3) can be fit in `xtmixed` by augmenting the random-part specification of the previous command for the additive model (9.2) given by

```
xtmixed attain || _all: R.sid || pid:, mle
```

We require a random intercept taking on distinct values for each combination of primary and secondary school. We could achieve this by defining an identifier variable for the combinations using `egen` with the `group()` function,

```
. egen comb = group(sid pid)
```

and specifying a third random part as `|| comb:`. This random intercept would be treated as nested within `pid`, the cluster identifier for the previous equation.

A more convenient setup, not requiring the variable `comb`, is to specify the last equation as `|| sid:`. Because `sid` is treated as nested in `pid`, the cluster identifier in the preceding random part, the random intercept will take on a different value for each unique secondary school, `sid`, *within* each primary school, `pid`, that is, for each combination of primary and secondary school. The syntax becomes

```
. xtmixed attain || _all: R.sid || pid: || sid:, mle
Performing EM optimization:
Performing gradient-based optimization:
Computing standard errors:
Mixed-effects ML regression                     Number of obs      =      3435
```

Group Variable	No. of Groups	Observations per Group Minimum	Average	Maximum
_all	1	3435	3435.0	3435
pid	148	1	23.2	72
sid	303	1	11.3	72

```
                                                Wald chi2(0)       =         .
Log likelihood = -8573.9826                     Prob > chi2        =         .
```

attain	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
_cons	5.501309	.1690433	32.54	0.000	5.16999	5.832627

Random-effects Parameters		Estimate	Std. Err.	[95% Conf.	Interval]
_all: Identity	sd(R.sid)	.5595826	.1431873	.3388884	.9239993
pid: Identity	sd(_cons)	.9502642	.1547838	.690552	1.307652
sid: Identity	sd(_cons)	.4904358	.253612	.177007	1.3513
	sd(Residual)	2.84385	.0353697	2.775364	2.914025

```
LR test vs. linear regression:       chi2(3) =   279.29   Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference
. estimates store interaction
```

The estimates are presented under "Interaction" in table 9.2. We see that estimated standard deviations for the random effects of primary schools (with identifier `pid`) and secondary schools (with identifier `sid`) have decreased somewhat. The estimated standard deviation of the random interaction is of a similar magnitude to the secondary school standard deviation.

Table 9.2: Maximum likelihood estimates for crossed random-effects models for Fife data

	Additive		Interaction	
	Est	(SE)	Est	(SE)
Fixed part				
β_1	5.50	(0.17)	5.50	(0.17)
Random part				
$\sqrt{\psi_1}$ [Secondary]	0.59		0.56	
$\sqrt{\psi_2}$ [Primary]	1.06		0.95	
$\sqrt{\psi_3}$ [Primary×Secondary]			0.49	
$\sqrt{\theta}$	2.85		2.84	
Log likelihood	$-8,574.57$		$-8,573.98$	

The estimated intraclass correlations for the models with and without the random interaction are given in table 9.3, where we see that they generally do not change much after including the random interaction. The estimated intraclass correlation for students having attended the same primary school (but different secondary schools) is considerably higher than the correlation for students having attended the same secondary school (but different primary schools). Having attended the same primary school and secondary school increases the intraclass correlation somewhat compared with only having attended the same primary school. The estimated intraclass correlation due to having attended the same primary school given that a particular secondary school was attended is considerably higher than the correlation due to having attended the same secondary school given that a particular primary school was attended.

Table 9.3: Estimated intraclass correlations for Fife data

	Additive	Interaction
ρ(primary)	0.12	0.09
ρ(secondary)	0.04	0.03
ρ(secondary, primary)	0.15	0.15
ρ(primary|secondary)	0.12	0.12
ρ(secondary|primary)	0.04	0.06

9.7.4 Testing variance components

A natural question to ask at this point is whether the random effects are needed in the model. We therefore first consider the joint null hypothesis that all variance components ψ_1, ψ_2, and ψ_3 are zero against the alternative that at least one of them is greater than zero:

$$H_0\text{: } \psi_1 = \psi_2 = \psi_3 = 0 \qquad \text{against} \qquad H_a\text{: } \psi_1 > 0 \quad \text{or} \quad \psi_2 > 0 \quad \text{or} \quad \psi_3 > 0$$

A test statistic of 279.29 is given as `LR test vs. linear regression:` at the bottom of the `xtmixed` output for the model with random effects for primary schools, secondary schools, and their interaction. The asymptotic null distribution of the likelihood-ratio statistic is $1/8\,\chi^2(0) + 3/8\,\chi^2(1) + 3/8\,\chi^2(2) + 1/8\,\chi^2(3)$ (see display 8.1 on page 397). The p-value becomes

```
. display 3/8*chi2tail(1,279.29) + 3/8*chi2tail(2,279.29) + 1/8*chi2tail(3,279.29)
4.656e-61
```

and we therefore reject the null hypothesis that all variance components are zero.

Having rejected the null hypothesis that no random effects are needed, we can proceed by testing whether the random interaction term ζ_{3jk} is required (in addition to the additive random effects). In other words, we consider the null hypothesis that the variance component ψ_3 for the random interaction is zero against the one-sided alternative that it is greater than zero:

$$H_0\text{: } \psi_3 = 0 \qquad \text{against} \qquad H_a\text{: } \psi_3 > 0$$

A likelihood-ratio test can be performed by using the `lrtest` command:

```
. lrtest additive interaction
Likelihood-ratio test                                 LR chi2(1)  =      1.17
(Assumption: additive nested in interaction)          Prob > chi2 =    0.2802
Note: The reported degrees of freedom assumes the null hypothesis is not on
      the boundary of the parameter space.  If this is not true, then the
      reported test is conservative.
```

The asymptotic null distribution of the likelihood-ratio test statistic is $1/2\,\chi^2(0) + 1/2\,\chi^2(1)$, and the correct p-value can be obtained by simply dividing the naïve p-value reported in the output by two. Here the p-value becomes $0.28/2 = 0.14$, and the random interaction is hence not significant at the 5% level.

Assuming that there is no random interaction, we may want to test the joint null hypothesis that both additive variance components are zero against the alternative that at least one of the components is positive:

$$H_0\text{: } \psi_1 = \psi_2 = 0 \qquad \text{against} \qquad H_a\text{: } \psi_1 > 0 \quad \text{or} \quad \psi_2 > 0$$

The likelihood-ratio statistic is given as 278.13 under `LR test vs. linear regression:` in the output for the additive crossed random-effects model on page 447. In this case, the asymptotic null distribution of the likelihood-ratio test is $1/4\,\chi^2(0) + 1/2\,\chi^2(1) + 1/4\,\chi^2(2)$. The p-value becomes

```
. display 1/2*chi2tail(1,278.13) + 1/4*chi2tail(2,278.13)
1.102e-61
```

and the null hypothesis of no random effects of both primary and secondary school is therefore rejected.

We can also test the null hypothesis that the variance component for primary school ψ_2 is zero against the one-sided alternative that it is greater than zero:

$$H_0\text{: } \psi_2 = 0 \qquad \text{against} \qquad H_a\text{: } \psi_2 > 0$$

To perform a likelihood-ratio test of this hypothesis, we fit the model under H_0, where there is no random effect of primary school (only random effects of secondary school), and store the estimates:

```
. quietly xtmixed attain || sid:, mle
. estimates store secondary
. lrtest secondary additive
Likelihood-ratio test                                 LR chi2(1)  =    182.92
(Assumption: secondary nested in additive)            Prob > chi2 =    0.0000
Note: The reported degrees of freedom assumes the null hypothesis is not on
      the boundary of the parameter space.  If this is not true, then the
      reported test is conservative.
```

The asymptotic null distribution of the likelihood-ratio test statistic is $1/2\,\chi^2(0) + 1/2\,\chi^2(1)$. The correct p-value can be obtained by simply dividing the naïve p-value based on the $\chi^2(1)$ by two. We see that the null hypothesis of no random effect of primary school is rejected.

In an analogous manner, we can test the null hypothesis that the variance component for secondary school ψ_1 is zero against the one-sided alternative that it is greater than zero:

$$H_0\text{: } \psi_1 = 0 \qquad \text{against} \qquad H_a\text{: } \psi_1 > 0$$

In this case, we get a likelihood-ratio statistic of 22.82 (output not shown), leading to rejection of the null hypothesis.

The null distributions used for the above tests of variance components are asymptotic and rely on the number of primary and secondary schools being large. They might not be unreasonable in the current example where there are 148 primary schools and 19 secondary schools. However, for the Grunfeld (1958) investment data, the tests would have been based on data for only 10 firms and 20 years, and the true null distributions are likely to be quite different from the asymptotic distributions. We therefore did not test variance components in that application. Note that it is generally not necessary to perform an extensive sequence of tests for variance components, but we did so here to show how to test different kinds of hypotheses.

9.7.5 Some diagnostics

Because the hypothesis tests conducted above suggested that a random interaction was not required, we return to the crossed random-effects model without an interaction, (9.2):

```
. estimates restore additive
(results additive are active now)
```

We can obtain empirical Bayes predictions or best linear unbiased predictions of both the secondary and the primary school random effects. If the random effects and the level-1 residual are assumed to have normal distributions, these predictions should have normal distributions. (This is true only for linear models.) We now use `predict` to obtain these predictions to check for outliers and assess normality by using a normal Q–Q plot:

```
. predict secondary primary, reffects
. qnorm secondary if pick_sid, xtitle(Quantiles of normal distribution)
> ytitle(Quantiles of empirical Bayes predictions)
. qnorm primary if pick_pid, xtitle(Quantiles of normal distribution)
> ytitle(Quantiles of empirical Bayes predictions)
```

Here we used the previously defined dummy variable `pick_sid` to choose one observation per secondary school, and similarly for primary school. If this were not done, the `qnorm` command would compute the quantiles for the sample of *all* students, which could be different from the quantiles required if the number of students per school is not constant.

The graph of the predictions for secondary schools is given in figure 9.3, and the graph for primary schools is given in figure 9.4. The figures suggest that the predictions have distributions that are reasonably close to normal, although there appears to be an outlying secondary school.

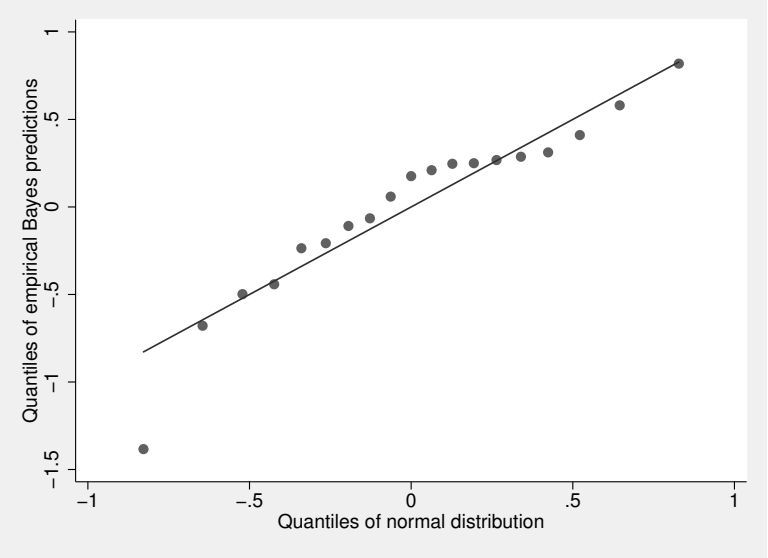


Figure 9.3: Normal Q–Q plot for secondary school predictions $\widetilde{\zeta}_{1j}$

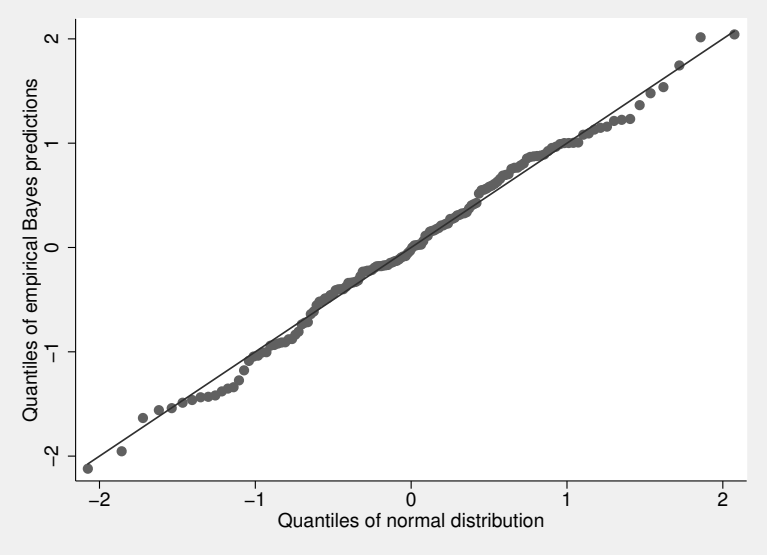


Figure 9.4: Normal Q–Q plot for primary school predictions $\widetilde{\zeta}_{2k}$

9.8 ❖ A trick requiring fewer random effects

We may have used more random effects than necessary for the primary and secondary school example. Imagine that both primary and secondary schools could be nested within regions. This would be the case if children attend both primary and secondary schools within the region in which they live and never move to a different region.

Suppose that no region has more than three secondary schools. In this case, we could arbitrarily number the secondary schools in each region from 1 to at most 3 in a variable, `sec`, and specify three corresponding random intercepts at the region level (with identifier `region`). The `xtmixed` syntax would be `|| region: R.sec`. Importantly, schools in different regions that happen to have the same value in `sec` would not have the same value of the corresponding random intercept because the intercept varies between regions. The random part for primary schools could then be specified as before, giving the `xtmixed` command (for the additive model):

```
xtmixed attain || region: R.sec || pid:, mle
```

This specification would require only three random intercepts at level 3 instead of 19.

In practice, there are no regions with insurpassable boundaries, but we could produce an identifier for a virtual level 3 within which both primary and secondary schools happen to be nested in the data. This approach becomes important if neither of the cross-classified factors has only a small number of levels and in the generalized linear mixed models discussed in volume 2 where computation may become prohibitive if there are many random effects.

The setup is shown in figure 9.5, where the students, shown as short vertical lines, can be viewed as nested in the primary schools, represented by vertical lines to their left. The students are also connected to the secondary schools to which they belong, shown as vertical lines to the right. The lines connecting students to their secondary school cross each other because primary and secondary schools are crossed. To the left of primary schools, we see the virtual level-3 units to which they belong, shown as even longer vertical lines. Both primary and secondary schools are nested within these virtual units. The random effect for primary school can be modeled by one random intercept, nested within the virtual level 3. For secondary school, the model requires 3 random coefficients of dummy variables d_{i1}, d_{i2}, and d_{i3} for the (at most) three secondary schools (numbered 1, 2, 3 in the figure) per virtual level-3 unit. The bullets show where these dummy variables take the value 1.

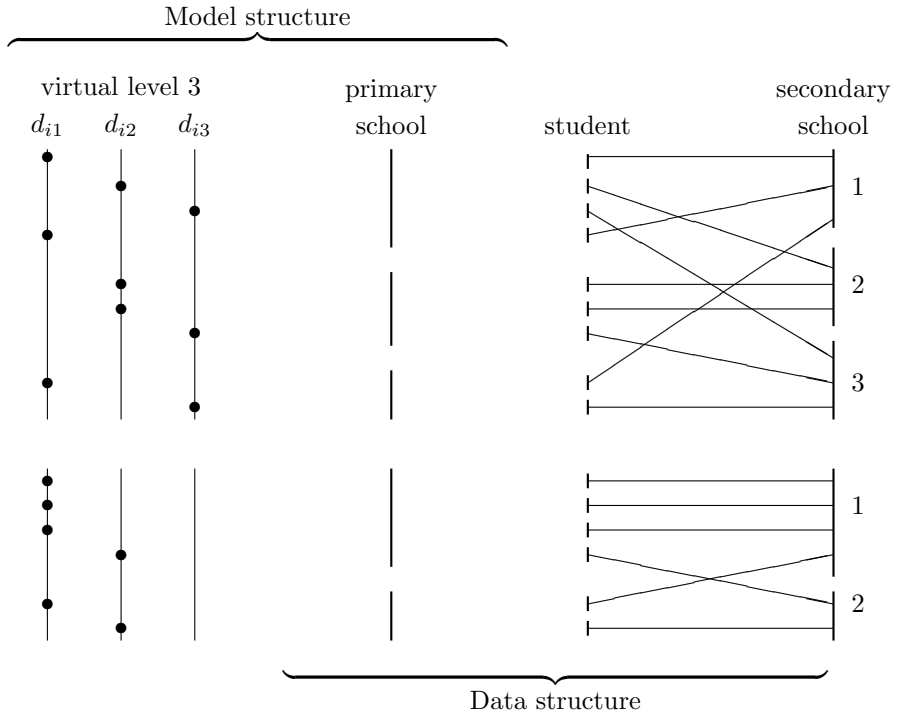


Figure 9.5: Model structure and data structure for students in primary schools crossed with secondary schools (*Source:* Skrondal and Rabe-Hesketh [2004a])

The virtual level-3 clustering variable can be produced using the command `supclust` developed by Ben Jann and available from the Statistical Software Component (SSC) archive maintained by Christopher F. (Kit) Baum. The command can be downloaded using

```
. ssc install supclust, replace
```

The syntax for generating a new variable, `region`, to serve as level-3 identifier is

```
. supclust pid sid, generate(region)
1 clusters in 3435 observations
```

Here one supercluster is found and thus the problem cannot be simplified. It is not possible to subdivide the sample into clusters within which both primary and secondary schools are nested.

To illustrate the trick, we will therefore delete primary and secondary school combinations that occur fewer than three times, which is also done in the MLwiN manual (Rasbash et al. 2009):

```
. egen num = count(attain), by(pid sid)
. drop if num<3
(168 observations deleted)
```

Now we will again try creating a virtual level-3 identifier:

```
. drop region
. supclust pid sid, gen(region)
6 clusters in 3267 observations
```

The command has identified six regions within which both `sid` and `pid` are nested. We create a new identifier for secondary schools, taking the values 1 to n_k within each region k:

```
. by region sid, sort: generate f = _n==1
. by region: generate sec = sum(f)
. table sec
```

sec	Freq.
1	1,020
2	769
3	267
4	292
5	467
6	99
7	249
8	104

There are at most 8 secondary schools per region, reducing the number of random effects required to 8 for secondary schools (compared with 19 previously) and 1 for primary schools.

In the `xtmixed` command, we simply replace `_all` with `region` and `sid` with `sec`:

```
. xtmixed attain || region: R.sec || pid:, mle
Mixed-effects ML regression                     Number of obs      =      3267
```

Group Variable	No. of Groups	Observations per Group Minimum	Average	Maximum
region	6	78	544.5	1330
pid	135	3	24.2	72

```
                                                Wald chi2(0)       =         .
Log likelihood = -8153.6587                     Prob > chi2        =         .
```

attain	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
_cons	5.581939	.1812378	30.80	0.000	5.22672	5.937159

Random-effects Parameters		Estimate	Std. Err.	[95% Conf.	Interval]
region: Identity	sd(R.sec)	.6196652	.1546558	.3799396	1.010647
pid: Identity	sd(_cons)	1.050124	.0982812	.8741311	1.261551
	sd(Residual)	2.84682	.0360606	2.777012	2.918382

```
LR test vs. linear regression:       chi2(2) =   263.22   Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference
```

The estimates are not identical to the previous estimates because we dropped a small proportion of the observations. We would not generally recommend dropping any observations but did so here to illustrate the trick.

9.9 Summary and further reading

In this chapter, we have discussed crossed random-effects models for data with two crossed clustering variables, or cross-classified random factors. We have described models with additive random effects of the factors, as well as a model including a random interaction between factors. The latter is identified only if there are several observations for at least some of the combinations of the categories of the factors.

Books on multilevel models with useful chapters on crossed random-effects models include Snijders and Bosker (2012, chap. 13), Raudenbush and Bryk (2002, chap. 12), and Goldstein (2011, chap. 12). Baltagi (2008, chap. 3) provides an econometric perspective. We also recommend the excellent articles and chapter by Raudenbush (1993), Browne, Goldstein, and Rasbash (2001), and Rasbash and Browne (2001).

We have considered two typical examples requiring crossed random effects: longitudinal or panel data with random occasion or time effects and data on individuals nested in two types of institutions. Further longitudinal exercises are considered in exercises 9.2, 9.3, and 9.9. For longitudinal data, time-series–cross-sectional analysis for long panels (discussed in section 6.7) can also be used to relax the assumption that units are uncorrelated at a given occasion (see exercise 9.9). The Fife data are revisited in exercise 9.1. Exercise 9.5 considers children nested in neighborhoods and schools, and exercise 9.6 uses data from an agricultural experiment.

Another typical example where several raters (the first random factor) rate each of several objects (the second random factor) is discussed in exercises 9.4 and 9.7. The latter exercise introduces some of the basic ideas of generalizability theory. Slightly more elaborate versions of models with crossed random effects are often applied to social-network data, where each individual may rate how much they like every other individual. The crossed factors are then the senders and the receivers of the ratings, where each person is both a sender and a receiver.

There were only two random factors in the examples considered in this chapter. In exercise 9.3, we consider a problem with three random factors: occasions, states, and regions. Although states are nested in regions, both states and regions are cross-classified with occasions. In exercise 9.8, state of birth and state of residence are crossed, and mothers are nested within the cross-classifications.

Models with crossed random effects must be distinguished from *multiple membership models*. Both types of models share the common feature that the classifications represented by random effects are not nested. In multiple membership models, a unit is a member of several clusters from the *same* classification with known weights designating the degree of membership. For instance, a student may have been taught by several teachers with weights representing the time spent with each teacher (see exercise 9.10). Browne, Goldstein, and Rasbash (2001), Rasbash and Browne (2001), and Goldstein (2011, chap. 13) discuss multiple membership models.

9.10 Exercises

9.1 Fife school data

Here we revisit the Fife school data analyzed in this chapter and described on page 443. In addition to the variables listed there, the dataset `fife.dta` contains a verbal reasoning score, `vrq`, which was considered a measure of ability by Paterson (1991).

1. Fit the model with the same random part as in (9.2) but with covariates `sex` and `vrq`. Use ML estimation.
2. Interpret the estimates, and discuss the change in the estimated variance components.

9.2 Airline cost data

Greene (2012) provides data on the annual total costs and output, fuel price, and load factor for six U.S. airlines over 15 years from 1970 to 1984. The data were provided to Greene by Professor Moshe Kim.

The variables in `airlines.dta` are

- `airline`: airline identifier
- `year`: year number (1–15)
- `cost`: total annual cost in U.S. $1,000
- `output`: annual output, in revenue passenger miles, index number
- `fuelprice`: fuel price
- `loadf`: load factor, the average capacity utilization of the fleet

Here the fuel price differs between airlines in a given year because different airlines use different mixes of types of planes and because there are regional differences in supply characteristics.

1. Write down a regression model for the log cost regressed on the log output, log fuel price, and load factor with random effects for airlines and years.
2. Fit the model using `xtmixed` with the `mle` and `reml` options.
3. Compare the estimates and explain why they differ.
4. Based on the REML estimates, interpret the effect of fuel price as an elasticity (see display 6.2).
5. Obtain empirical Bayes predictions of the random effects based on the REML estimates.
6. Plot the empirical Bayes predictions for the years against time.
7. Fit the model using fixed effects for years instead of random effects. Explain how and why the estimated coefficient of log fuel price changes compared with the model that treats year as random.

9.3 U.S. production data

The data are from Munnell (1990) and were described in exercise 8.3, where we considered a three-level model for state productivity.

1. Fit the three-level model described in exercise 8.3 using `xtmixed` with the `reml` option.
2. Add a random effect for year to this model. Choose the model specification in `xtmixed` that minimizes the number of random effects at a level. Fit the model by REML.
3. Compare the models using a likelihood-ratio test.
4. Interpret the variance-component estimates for the model in step 2.

9.4 Video-ratings data

The Vancouver Sedative Recovery Scale (VSRS) was developed to measure recovery from sedation following pediatric open heart surgery. Macnab et al. (1994) report a study where 16 ICU staff were trained by videotape instruction to use the VSRS. To determine whether videotaped instruction produced adequate skill, an interobserver reliability study was carried out.

In a balanced incomplete design, 16 staff each rated a different subset of 16 videotaped case examples using the VSRS so that each case was rated by six raters and each rater rated six cases. Two experts also rated all cases. The data, shown in table 9.4, were also analyzed by Dunn (2004).

Table 9.4: Rating data for 16 cases in incomplete block design

	Cases or Videos															
Raters	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1	.	.	.	6	.	.	.	0	18	.	12	.	14	.	.	19
2	.	.	.	5	.	4	.	.	13	13	.	0	.	.	16	.
3	.	.	20	.	13	1	.	0	15	.	.	.	.	15	.	.
4	9	.	.	.	.	.	22	.	19	18	.	.	14	14	.	.
5	11	0	21	.	.	.	.	.	19	.	10	.	.	.	19	.
6	.	1	.	.	13	.	22	.	16	.	.	0	.	.	.	22
7	12	0	.	0	.	1	22	0	.	.	.	.	.	.	.	.
8	.	1	19	5	14	.	.	.	.	15	.	.	14	.	.	.
9	.	.	.	9	16	.	15	.	.	.	10	.	.	12	19	.
10	10	.	17	7	.	.	.	.	.	.	.	0	.	13	.	20
11	.	0	.	.	.	.	.	0	.	.	.	0	13	16	22	.
12	.	.	20	.	.	.	20	0	.	12	10	0	.	.	.	.
13	6	.	.	.	15	.	.	0	.	17	.	.	.	.	19	22
14	8	.	.	.	16	1	.	.	.	.	11	0	15	.	.	.
15	.	.	21	.	.	1	18	.	.	.	.	.	16	.	21	22
16	.	0	.	.	.	1	.	.	.	18	15	.	.	10	.	21
17	10	0	21	8	18	4	16	0	18	16	10	0	16	12	19	20
18	10	0	21	5	19	7	18	0	16	15	12	0	14	14	20	21

Source: Macnab et al. (1994)

The long version of these data in `videos.dta` contains the following variables:

- `rater`: rater identifier (j)
- `video`: video (case example) identifier (i)
- `y`: VSRS score
- `novice`: dummy variable for rater being a novice (not an expert)

In generalizability theory, the design of this study can be viewed as a one-facet crossed design. Here the *objects of the measurement* are the cases shown in the videos, and these are crossed with raters, who can be thought of as *conditions* of a *facet* of the measurement.

We wish to generalize from this particular set of raters to a *universe* of raters, treating raters as a random sample of all *admissible* raters. Denoting cases or videos as i and raters as j, the model can be written as

$$y_{ij} = \beta + \zeta_{1i} + \zeta_{2j} + \epsilon_{ij}, \quad \psi_1 \equiv \text{Var}(\zeta_{1i}), \psi_2 \equiv \text{Var}(\zeta_{2j}), \theta \equiv \text{Var}(\epsilon_{ij})$$

Here ϵ_{ij} represents the sum of the case by rater interaction and any other sources of error. A good book on generalizability theory is Shavelson and Webb (1991).

1. Fit this model for the nonexperts using REML.
2. Interchange `rater` and `video` in your command for step 1 and compare the estimates.
3. If the intention is to use the VSRS score from one rater for an *absolute decision*, not just for the purpose of ranking cases rated by the same rater, the generalizability coefficient is defined as

$$\phi = \frac{\psi_1}{\psi_1 + \psi_2 + \theta}$$

   where $\psi_2+\theta$ represents the measurement error variance for absolute decisions. Obtain an estimate of this coefficient by plugging in the estimated variance components from step 1 or 2.
4. If the intention is to use the mean score from N_r raters for an absolute decision, the measurement error variance can be divided by N_r and the generalizability coefficient is defined as

$$\phi = \frac{\psi_1}{\psi_1 + (\psi_2 + \theta)/N_r}$$

   Estimate this generalizability coefficient for $N_r = 6$.

9.5 Neighborhood-effects data Solutions

We now consider the data from Garner and Raudenbush (1991), Raudenbush and Bryk (2002), and Raudenbush et al. (2004) previously analyzed in exercises 2.4 and 3.1. In exercise 2.4, we considered two separate models, one with a random intercept for schools and the other with a random intercept for neighborhoods. Here we will include both random intercepts in the same model.

The variables in `neighborhood.dta` are

- Student level
  - `attain`: a measure of educational attainment

  - `p7vrq`: primary seven (year 7 of primary school) verbal reasoning quotients
  - `p7read`: primary seven reading test scores
  - `dadocc`: father's occupation scaled on the Hope–Goldthorpe scale in conjunction with the Registrar General's social-class index (Willms 1986)
  - `dadunemp`: dummy variable for father being unemployed (1: unemployed; 0: not unemployed)
  - `daded`: dummy variable for father's schooling being past the age of 15
  - `momed`: dummy variable for mother's schooling being past the age of 15
  - `male`: dummy variable for student being male
- Neighborhood level
  - `neighid`: neighborhood identifier
  - `deprive`: social deprivation score, derived from poverty concentration, health, and housing stock of local community
- School level
  - `schid`: school identifier

1. Fit a model for student educational attainment without covariates but with random intercepts of neighborhood and school by ML.
2. Include a random interaction between neighborhood and school, and use a likelihood-ratio test to decide whether the interaction should be retained (use a 5% level of significance).
3. Include the neighborhood-level covariate `deprive`. Discuss both the estimated coefficient of `deprive` and the changes in the estimated standard deviations of the random effects due to including this covariate.
4. Remove the neighborhood-by-school random interaction (which is no longer significant at the 5% level) and include all student-level covariates. Interpret the estimated coefficients and the change in the estimated standard deviations.
5. For the final model, estimate the residual intraclass correlations due to being in
   a. the same neighborhood but not the same school
   b. the same school but not the same neighborhood
   c. both the same neighborhood and the same school
6. ❖ Use the `supclust` command to see if estimation can be simplified by defining a virtual level-3 identifier.

9.6 Nitrogen data

Littell et al. (2006) describe an experiment to evaluate the yield of two varieties of crop at five levels of nitrogen fertilization. The five levels of nitrogen were applied to 15 relatively large whole plots that formed a 3×5 grid. Because of substantial north–south and east–west gradients, the levels of nitrogen were applied in an incomplete Latin-square design, with each nitrogen level occurring in each row, but not in each column, as shown in table 9.5.

Table 9.5: Latin-square design for nitrogen fertilization experiment

	Col 1	Col 2	Col 3	Col 4	Col 5
Row 1	Nit 1	Nit 2	Nit 5	Nit 4	Nit 3
Row 2	Nit 2	Nit 1	Nit 3	Nit 5	Nit 4
Row 3	Nit 3	Nit 4	Nit 1	Nit 2	Nit 5

Each whole plot was split into two subplots to which the two crops were randomly assigned.

Letting i denote the subplots, j the rows, and k the columns in which the whole plots are arranged, a crossed random-effects model for crop yield y_{ijk} can be written as

$$y_{ijk} = \beta_1 + \zeta_{1j} + \zeta_{2k} + \zeta_{3jk} + \epsilon_{ijk}$$

where ζ_{1j} is the random effect of row, ζ_{2k} is the random effect of column, ζ_{3jk} is the random interaction between row and column, and ϵ_{ijk} is a residual error term. Note that the number of clusters is arguably too small for estimating variance components.

The variables in `nitrogen.dta` are

- `row`: row identifier (j)
- `col`: column identifier (k)
- `N`: nitrogen level (1, 2, 3, 4, 5)
- `G`: genotype or crop variety (1, 2)
- `y`: yield of the crop (y_{ijk})

1. Fit the model given above using REML. Interpret the estimated variance components.
2. Fit a model with the same random part as in step 1 but also including fixed effects of nitrogen level (treated as unordered), genotype, and their interaction.
3. Perform a Wald test for the nitrogen by genotype interaction. Omit the interaction terms if this test is not significant at the 5% level.
4. Interpret the estimated regression coefficients.

9.7 Olympic skating data

In the 1932 Lake Placid Winter Olympics, seven figure skating pairs were judged by seven judges using two different criteria (program and performance). The ratings are provided by Gelman and Hill (2007) and are shown in table 9.6, where the countries of origin of judges and pairs are also given as abbreviations for France, the United States, Hungary, Canada, Norway, Austria, Finland, and the United Kingdom.

Table 9.6: Ratings of seven skating pairs by seven judges using two criteria (program and performance) in the 1932 Winter Olympics

	Judge													
	1		2		3		4		5		6		7	
Pair	(Hun)		(Nor)		(Aus)		(Fin)		(Fra)		(UK)		(US)	
1 (Fra)	5.6	5.6	5.5	5.5	5.8	5.8	5.3	4.7	5.6	5.7	5.2	5.3	5.7	5.4
2 (US)	5.5	5.5	5.2	5.7	5.8	5.6	5.8	5.4	5.6	5.5	5.1	5.3	5.8	5.7
3 (Hun)	6.0	6.0	5.3	5.5	5.8	5.7	5.0	4.9	5.4	5.5	5.1	5.2	5.3	5.7
4 (Hun)	5.6	5.6	5.3	5.3	5.8	5.8	4.4	4.8	4.5	4.5	5.0	5.0	5.1	5.5
5 (Can)	5.4	4.8	4.5	4.8	5.8	5.5	4.0	4.4	5.5	4.6	4.8	4.8	5.5	5.2
6 (Can)	5.2	4.8	5.1	5.6	5.3	5.0	5.4	4.7	4.5	4.0	4.5	4.6	5.0	5.2
7 (US)	4.8	4.3	4.0	4.6	4.7	4.5	4.0	4.0	3.7	3.6	4.0	4.0	4.8	4.8

The data in `olympics.dta` contain one row for each combination of skating pair and judge with separate variables for the two criteria. The variables are

- `pair`: skating pair
- `judge`: judge
- `pcountry`: country of origin of pair
- `jcountry`: country of origin of judge
- `program`: rating for program (criterion 1)
- `performance`: rating for performance (criterion 2)

1. Write down a linear model for the program rating of judge j for pair k that includes a fixed overall intercept and random intercepts for judges and pairs. Interpret the random intercepts in the context of this example.
2. Fit the model from step 1 using REML.
3. Test whether both random intercepts are needed by comparing the model from step 1 with the two nested models having only one random intercept (using a 5% level of significance). Note, however, that the number of clusters is really too small to rely on these asymptotic tests.
4. Extend the model by constructing a dummy variable for judge and pair coming from the same country and including this as a covariate. Interpret the estimated regression coefficient and comment on its magnitude.
5. ❖ Consider joint models for program and performance ratings.
   a. Reshape the data to long form, stacking the ratings using the two criteria into one response variable, and produce a dummy variable for the criterion being performance.
   b. Fit the same model as in step 4 to the responses using both criteria.
   c. The model above makes these strong assumptions (among others):
      - The mean rating is the same for the two criteria after controlling for whether the pair and the judge are from the same country

- The ratings for the same skating pair from the same judge using two different criteria are conditionally independent given the covariate and the random intercepts for judges and pairs

Fit an extended model that relaxes these assumptions.

9.8 Smoking and birthweight data

We now consider the data from Abrevaya (2006) that were used in chapter 3. There we ignored the fact that mothers are nested in U.S. states of residence crossed with the states in which they were born. Here we consider the effects of the mother's state of residence and state of birth.

The variables in `smoking.dta` that we will use here are

- `momid`: mother identifier
- `birwt`: birthweight (in grams)
- `stateres`: mother's state of residence
- `mplbir`: mother's place (state) of birth
- `male`: dummy variable for child being male

1. Fit a model for birthweight with random effects for state of residence and state of birth and a fixed effect of `male`.
2. Fit the same model as in step 1 but also include a random interaction between state of residence and state of birth. Compare this model with the model from step 1 using a likelihood-ratio test. Use a 5% level of significance to decide which model to retain.
3. Fit the model from step 2 but with an additional random intercept for mothers. Mothers are nested within the combinations of state of residence and state of birth (mothers who moved between births could not be matched and were not included in the data). Compare this model with the model from step 2 using a likelihood-ratio test.
4. Interpret the parameter estimates for the model chosen in step 3.

9.9 Cigarette-consumption data

The dataset for this exercise concerns cigarette consumption from 1963 to 1992 in 48 U.S. states and is from Baltagi, Griffin, and Xiong (2000). In exercise 6.4, this long panel dataset was described and analyzed using the `xtpcse` and `xtgls` commands to accommodate cross-sectional dependence between states. Here we will consider a two-way error-components model instead.

1. The consumer price index is a weighted average of prices of a basket of consumer goods and services. In this dataset, `CPI` is 100 times the consumer price index in a given year divided by the consumer price index in 1983. Convert `price`, `pimin`, and `NDI` to 1983 U.S. dollars using the consumer price index. Such real prices and real income are adjusted for inflation over years. In the analyses below, you will use the natural logarithms of real prices and real disposable income.

2. Fit a model to the logarithm of the number of packs of cigarettes sold per person of smoking age with a random effect of state, a random effect of year, and the following covariates: the logarithm of real cigarette price, the logarithm of real disposable income, the logarithm of the real minimum price in adjoining states (a proxy for casual smuggling across states), and year (treated as continuous).
3. Calculate the estimated longitudinal within-state intraclass correlation and the estimated cross-sectional within-year intraclass correlation.
4. Extend the model by allowing the level-1 residuals to follow an AR(1) process over time.
5. Use a likelihood-ratio test to decide (at the 5% level) whether the AR(1) process is needed.
6. Can the random part of the model selected in step 5 be simplified?
7. ❖ Derive an expression for the longitudinal within-state correlation as a function of the time lag between occasions. What are the corresponding estimated lag-1 and lag-29 correlations?

9.10 ❖ STAR data

In this exercise, we consider multiple membership models for the STAR study used in exercises 8.6 and 8.7 and documented in Finn et al. (2007). We will analyze the dataset `star_mm.dta`, which was derived from `star1.dta`. The dataset contains only the second-grade data for the subset of children who were in the study from kindergarten through second grade; remained in the same school; have teacher information for kindergarten, first, and second grade; and have a reading score in second grade.

The variables in `star_mm.dta` we will analyze here are

- `schid` school identifier
- `reading`: total score for Stanford achievement test (SAT) in reading
- `wttr1-wttr30`: weight variables for multiple membership model
- `gr0wttr1-gr0wttr8` weight variables for kindergarten teacher
- `gr1wttr1-gr1wttr12` weight variables for grade 1 teacher
- `gr2wttr1-gr2wttr11` weight variables for grade 2 teacher

By second grade, the children have been taught reading for three years. It is possible that reading achievement depends on which teachers the child has had, in addition to which school the child is in. Each child has been taught by at most three teachers (and it turns out in this dataset, each teacher teaches only one grade so each child has been taught by three different teachers). We will let $j(ikg)$ denote the teacher j who taught child i in school k in grade g ($g = 0, 1, 2$ for kindergarten, first grade, second grade, respectively).

Then a multiple membership model can be written as

$$y_{ik} = \beta + \sum_{g=0}^{2} \frac{1}{3}\zeta^{(2)}_{j(ikg)} + \zeta^{(3)}_{k} + \epsilon_{ik}, \tag{9.4}$$

where $\frac{1}{3}\zeta^{(2)}_{j(ikg)}$ is the contribution of teacher $j(ikg)$ to the total effect of teachers on student ik's reading attainment, $\zeta^{(3)}_k$ is the effect of school k on reading, and ϵ_{ik} is a child-level residual. Each child is a member of at most three different teachers and each year of teaching contributes 1/3 to the overall teacher effect. The teacher random intercepts have variance $\psi^{(2)}$, and the school random intercepts have variance $\psi^{(3)}$. All random intercepts are mutually uncorrelated and uncorrelated across schools and teachers.

In order to fit the model in `xtmixed`, we label the teachers within each school from 1 to n_k, where in this dataset $n_k \leq 30$ in all schools. We define 30 school-level random coefficients $u^{(3)}_{aik}$, $a = 1, \ldots, 30$, for teachers, along with 30 weight variables w_{aik} taking the value 1/3 for child ik if the corresponding teacher ever taught that child and zero otherwise. The model can then be written as

$$y_{ik} = \beta + \sum_{a=1}^{30} w_{aik}u^{(3)}_{aik} + \zeta^{(3)}_{k} + \epsilon_{ik}$$

1. The required weight variables w_{aik} are called `wttr1` to `wttr30`. What should be the sum of these variables for each child? Verify that this is correct. Also list the data to make sure you understand the weight variables.
2. Fit the model in `xtmixed`. Keep in mind that the random coefficients $u^{(3)}_{aik}$ are uncorrelated with identity covariance structure and that you can specify two random parts for schools.
3. Interpret the estimates.
4. The model makes the strong assumption that the kindergarten, first-grade, and second-grade teachers all contribute equally to the child's reading in second grade. However, the teachers encountered the children at different stages of development, and the effect of previous teachers may fade over time. The weight variables `gr0wttr1`–`gr0wttr8`, `gr1wttr1`–`gr1wttr12`, and `gr2wttr1`–`gr2wttr11` are analogous to the weight variables used in step 1 except that they are specific to the kindergarten, grade 1, and grade 2 teachers, respectively (in this dataset, no teacher taught more than one grade, with grade identified by the third character of the variable names). There were at most 8 different kindergarten teachers, 12 different first-grade teachers, and 11 different second-grade teachers per school. For child ik, `gr0wttr1` takes the value 1/3 if the child was taught by the first kindergarten teacher of school k and zero otherwise, and analogously for the other teachers and grades.

a. Confirm that each set of variables takes the value 1/3 once for each child.
b. Fit a model identical to the multiple membership model in (9.4) except that $\zeta^{(2)}_{j(ikg)}$ has grade-specific variance $\psi^{(2)}_g$. This can be achieved by using eight random coefficients of `gr0wttr1`–`gr0wttr8` for kindergarten, and similarly for first and second grade, again keeping in mind that you can specify separate random parts to obtain different variances.
c. Interpret the estimates.
d. Compare the model with the model fit in step 2 using a likelihood-ratio test.
e. Can the selected model be simplified?

9.11 Different kinds of intraclass correlations

In this exercise, you will derive some of the intraclass correlations given in section 9.7.2.

1. Derive $\rho(\text{secondary})$.
2. Derive $\rho(\text{secondary}, \text{primary})$.
3. Derive $\rho(\text{primary}|\text{secondary})$.

A Useful Stata commands

Here we list commands and special options that are useful for handling multilevel and longitudinal data. These commands and options have all been illustrated in the book and are listed in the subject index.

Here we assume that the response variable is `y`, a covariate is `x`, and the cluster identifier is `cluster`. Sometimes we will assume that the data have three levels with repeated observations on subjects (identifier `subject`) nested in clusters and time variable `year`. We will not assume that `subject` takes on unique values across clusters, that is, subjects may be numbered from 1 within each cluster.

`by` — Repeat Stata command on subsets of the data

- Create a unit identifier, counting from 1 within each cluster (in ascending order of `x`) in two-level data:
  `by cluster (x), sort: generate` *varname* `= _n`
- As above, but counting from 1 within each subject in three-level data:
  `by cluster subject (x), sort: generate` *varname* `= _n`
- Create a lagged variable within the subjects:
  `by cluster subject (year), sort: ///`
  `generate` *varname2* `=` *varname1*`[_n-1]`
  See also Stata's time-series operator `L`, under `help tsvarlist`

`egen` — Extensions to `generate`

- Form cluster means:
  `egen` *varname2* `= mean(`*varname1*`), by(cluster)`
- Form cluster sizes:
  `egen` *varname2* `= count(`*varname1*`), by(cluster)`
- Construct variable taking the value 1 for one unit per cluster:
  `egen` *varname* `= tag(cluster)`
- Construct cluster identifier consisting of consecutive integers:
  `egen` *varname* `= group(cluster)`
- Construct unique subject identifier in three-level data:
  `egen` *varname* `= group(cluster subject)`

`graph twoway` — Two-way graphs

- Plot cluster-specific regression lines (spaghetti plot): After sorting by `cluster` and `x`, use `twoway line` with the `connect(ascending)` or `connect(L)` option (see also `xtline` command)

- Make a trellis graph of two-way plots for the individual clusters: Use the `twoway` command with the `by(cluster)` option; `by(cluster, compact, cols(5))` produces a compact trellis with graphs arranged in five columns

`merge` — Merge datasets

- Combine individual-level data `lev1.dta` (level-1 variables) with cluster-level data `lev2.dta` (level-2 variables). First sort both files by `cluster`
  - Read `lev2.dta` and use command
    `merge 1:m cluster using lev1.dta`
  - Read `lev1.dta` and use command
    `merge m:1 cluster using lev2.dta`

`reshape` — Convert data from wide to long form and vice versa

- Convert data from wide form (one line per cluster; variables `y1 y2 y3` are responses for units 1, 2, 3) to long form (multiple lines per cluster, with responses in different rows of one variable `y`), and new variable `occ` taking the values 1, 2, 3 to identify the values that were in the variables `y1 y2 y3`:
  `reshape long y, i(cluster) j(occ)`
- Convert data from long form to wide form:
  `reshape wide y, i(cluster) j(occ)`
- If variable names are `bygog f1gog f2gog` for base year, follow-up 1, and follow-up 2, respectively, use
  `reshape long @gog, i(cluster) j(occ) string`
  Here `@` is the position of the string variables that indicate the panel wave, and the `string` option is necessary when the panel wave labels are not numeric

`statsby` — Collect statistics for a command across a by-list

- Syntax: `statsby` *exp_list*`, by(`*varname*`):` *command*
- Save intercepts and slopes of least-squares regression fit to each cluster:
  `statsby b[_cons] b[x], by(cluster): regress y x, ///`
  `saving(estimates)`

`xtdescribe` — Describe missingness pattern of xt data

- Find missing-data pattern for balanced longitudinal data (assume every value of `year` that occurs for anyone should have occurred for everyone and `subject` takes a unique value for each subject):
  `xtset subject year`
  `xtdescribe if y<.`

`xtsum` — Summarize xt data

- Obtain within- and between-cluster standard deviations:
  `xtset cluster`
  `xtsum y x`

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Multilevel and Longitudinal Modeling Using Stata

Volume II: Categorical Responses, Counts, and Survival

Third Edition

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To my children Astrid and Inge
Anders Skrondal

To Simon
Sophia Rabe-Hesketh

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Models for categorical responses

10 Dichotomous or binary responses

10.1 Introduction

Dichotomous or binary responses are widespread. Examples include being dead or alive, agreeing or disagreeing with a statement, and succeeding or failing to accomplish something. The responses are usually coded as 1 or 0, where 1 can be interpreted as the answer "yes" and 0 as the answer "no" to some question. For instance, in section 10.2, we will consider the employment status of women where the question is whether the women are employed.

We start by briefly reviewing ordinary logistic and probit regression for dichotomous responses, formulating the models both as generalized linear models, as is common in statistics and biostatistics, and as latent-response models, which is common in econometrics and psychometrics. This prepares the foundation for a discussion of various approaches for clustered dichotomous data, with special emphasis on random-intercept models. In this setting, the crucial distinction between conditional or subject-specific effects and marginal or population-averaged effects is highlighted, and measures of dependence and heterogeneity are described.

We also discuss special features of statistical inference for random-intercept models with clustered dichotomous responses, including maximum likelihood estimation of model parameters, methods for assigning values to random effects, and how to obtain different kinds of predicted probabilities. This more technical material is provided here because the principles apply to all models discussed in this volume. However, you can skip it (sections 10.11 through 10.13) on first reading because it is not essential for understanding and interpreting the models.

Other approaches to clustered data with binary responses, such as fixed-intercept models (conditional maximum likelihood) and generalized estimating equations (GEE) are briefly discussed in section 10.14.

10.2 Single-level logit and probit regression models for dichotomous responses

In this section, we will introduce logit and probit models without random effects that are appropriate for datasets without any kind of clustering. For simplicity, we will start by considering just one covariate x_i for unit (for example, subject) i. The models can

be specified either as generalized linear models or as latent-response models. These two approaches and their relationship are described in sections 10.2.1 and 10.2.2.

10.2.1 Generalized linear model formulation

As in models for continuous responses, we are interested in the expectation (mean) of the response as a function of the covariate. The expectation of a binary (0 or 1) response is just the probability that the response is 1:

$$E(y_i|x_i) \;=\; \Pr(y_i = 1|x_i)$$

In linear regression, the conditional expectation of the response is modeled as a linear function $E(y_i|x_i) = \beta_1 + \beta_2 x_i$ of the covariate (see section 1.5). For dichotomous responses, this approach may be problematic because the probability must lie between 0 and 1, whereas regression lines increase (or decrease) indefinitely as the covariate increases (or decreases). Instead, a nonlinear function is specified in one of two ways:

$$\Pr(y_i = 1|x_i) \;=\; h(\beta_1 + \beta_2 x_i)$$

or

$$g\{\Pr(y_i = 1|x_i)\} \;=\; \beta_1 + \beta_2 x_i = \nu_i$$

where ν_i (pronounced "nu") is referred to as the *linear predictor*. These two formulations are equivalent if the function $h(\cdot)$ is the inverse of the function $g(\cdot)$. Here $g(\cdot)$ is known as the *link function* and $h(\cdot)$ as the *inverse link function*, sometimes written as $g^{-1}(\cdot)$. An appealing feature of generalized linear models is that they all involve a linear predictor resembling linear regression (without a residual error term). Therefore, we can handle categorical explanatory variables, interactions, and flexible curved relationships by using dummy variables, products of variables, and polynomials or splines, just as in linear regression.

Typical choices of link function for binary responses are the logit or probit links. In this section, we focus on the logit link, which is used for logistic regression, whereas both links are discussed in section 10.2.2. For the logit link, the model can be written as

$$\text{logit}\,\{\Pr(y_i = 1|x_i)\} \equiv \ln \underbrace{\left\{ \frac{\Pr(y_i = 1|x_i)}{1 - \Pr(y_i = 1|x_i)} \right\}}_{\text{Odds}(y_i=1|x_i)} \;=\; \beta_1 + \beta_2 x_i \qquad (10.1)$$

The fraction in parentheses in (10.1) represents the odds that $y_i = 1$ given x_i, the expected number of 1 responses per 0 response. The odds—or in other words, the expected number of successes per failure—is the standard way of representing the chances against winning in gambling. It follows from (10.1) that the logit model can alternatively be expressed as an exponential function for the odds:

$$\text{Odds}(y_i = 1|x_i) \;=\; \exp(\beta_1 + \beta_2 x_i)$$

Because the relationship between odds and probabilities is

$$\text{Odds} = \frac{\Pr}{1-\Pr} \qquad \text{and} \qquad \Pr = \frac{\text{Odds}}{1+\text{Odds}}$$

the probability that the response is 1 in the logit model is

$$\Pr(y_i = 1|x_i) \;=\; \text{logit}^{-1}(\beta_1 + \beta_2 x_i) \equiv \frac{\exp(\beta_1 + \beta_2 x_i)}{1 + \exp(\beta_1 + \beta_2 x_i)} \tag{10.2}$$

which is the inverse logit function (sometimes called logistic function) of the linear predictor.

We have introduced two components of a generalized linear model: the linear predictor and the link function. The third component is the distribution of the response given the covariates. Letting $\pi_i \equiv \Pr(y_i = 1|x_i)$, the distribution is specified as Bernoulli(π_i), or equivalently as binomial(1, π_i). There is no level-1 residual ϵ_i in (10.1), so the relationship between the probability and the covariate is deterministic. However, the responses are random because the covariate determines only the probability. Whether the response is 0 or 1 is the result of a Bernoulli trial. A Bernoulli trial can be thought of as tossing a biased coin with probability of heads equal to π_i. It follows from the Bernoulli distribution that the relationship between the conditional variance of the response and its conditional mean π_i, also known as the *variance function*, is $\text{Var}(y_i|x_i) = \pi_i(1-\pi_i)$. (Including a residual ϵ_i in the linear predictor of binary regression models would lead to a model that is at best weakly identified[1] unless the residual is shared between units in a cluster as in the multilevel models considered later in the chapter.)

The logit link is appealing because it produces a linear model for the log of the odds, implying a multiplicative model for the odds themselves. If we add one unit to x_i, we must add β_2 to the log odds or multiply the odds by $\exp(\beta_2)$. This can be seen by considering a 1-unit change in x_i from some value a to $a+1$. The corresponding change in the log odds is

$$\begin{aligned} \ln\{\text{Odds}(y_i = 1|x_i = a+1)\} \;-\; & \ln\{\text{Odds}(y_i = 1|x_i = a)\} \\ & = \{\beta_1 + \beta_2(a+1)\} - (\beta_1 + \beta_2 a) = \beta_2 \end{aligned}$$

Exponentiating both sides, we obtain the *odds ratio* (OR):

$$\begin{aligned} & \exp\left[\ln\{\text{Odds}(y_i = 1|x_i = a+1)\} \;-\; \ln\{\text{Odds}(y_i = 1|x_i = a)\}\right] \\ = \;& \frac{\text{Odds}(y_i = 1|x_i = a+1)}{\text{Odds}(y_i = 1|x_i = a)} \;=\; \frac{\Pr(y_i = 1|x_i = a+1)}{\Pr(y_i = 0|x_i = a+1)} \Big/ \frac{\Pr(y_i = 1|x_i = a)}{\Pr(y_i = 0|x_i = a)} \\ = \;& \exp(\beta_2) \end{aligned}$$

1. Formally, the model is identified by functional form. For instance, if x_i is continuous, the level-1 variance has a subtle effect on the shape of the relationship between $\Pr(y_i = 1|x_i)$ and x_i. With a probit link, single-level models with residuals are not identified.

Consider now the case where several covariates—for instance, x_{2i} and x_{3i}—are included in the model:

$$\text{logit}\left\{\Pr(y_i = 1|x_{2i}, x_{3i})\right\} = \beta_1 + \beta_2 x_{2i} + \beta_3 x_{3i}$$

In this case, $\exp(\beta_2)$ is interpreted as the odds ratio comparing $x_{2i} = a+1$ with $x_{2i} = a$ for given x_{3i} (controlling for x_{3i}), and $\exp(\beta_3)$ is the odds ratio comparing $x_{3i} = a + 1$ with $x_{3i} = a$ for given x_{2i}.

The predominant interpretation of the coefficients in logistic regression models is in terms of odds ratios, which is natural because the log odds is a *linear* function of the covariates. However, economists instead tend to interpret the coefficients in terms of marginal effects or partial effects on the response probability, which is a *nonlinear* function of the covariates. We relegate description of this approach to display 10.1, which may be skipped.

For a *continuous* covariate x_{2i}, economists often consider the partial derivative of the probability of success with respect to x_{2i}:

$$\Delta(x_{2i}|x_{3i}) \equiv \frac{\partial \Pr(y_i = 1|x_{2i}, x_{3i})}{\partial x_{2i}} = \beta_2 \frac{\exp(\beta_1 + \beta_2 x_{2i} + \beta_3 x_{3i})}{\{\exp(\beta_1 + \beta_2 x_i + \beta_3 x_{3i})\}^2}$$

A small change in x_{2i} hence produces a change of $\beta_2 \frac{\exp(\beta_1+\beta_2 x_{2i}+\beta_3 x_{3i})}{\{\exp(\beta_1+\beta_2 x_{2i}+\beta_3 x_{3i})\}^2}$ in $\Pr(y_i = 1|x_{2i}, x_{3i})$. Unlike in linear models, where the partial effect simply becomes β_2, the derivative of the nonlinear logistic function is not constant but depends on x_{2i} and x_{3i}.

For a *binary* covariate x_{3i}, economists consider the difference

$$\begin{aligned}\Delta(x_{3i}|x_{2i}) &\equiv \Pr(y_i = 1|x_{2i}, x_{3i} = 1) - \Pr(y_i = 1|x_{2i}, x_{3i} = 0) \\ &= \frac{\exp(\beta_1 + \beta_2 x_{2i} + \beta_3)}{1 + \exp(\beta_1 + \beta_2 x_{2i} + \beta_3)} - \frac{\exp(\beta_1 + \beta_2 x_{2i})}{1 + \exp(\beta_1 + \beta_2 x_{2i})}\end{aligned}$$

which, unlike linear models, depends on x_{2i}.

The partial effect at the average (PEA) is obtained by substituting the sample means $\overline{x}_{2\cdot} = \frac{1}{N}\sum_{i=1}^N x_{i2}$ and $\overline{x}_{3\cdot} = \frac{1}{N}\sum_{i=1}^N x_{i3}$ for x_{i2} and x_{i3}, respectively, in the above expressions. Note that for binary covariates, the sample means are proportions and subjects cannot be at the average (because the proportions are between 0 and 1).

The average partial effect (APE) overcomes this problem by taking the sample means of the individual partial effects, $\text{APE}(x_{2i}|x_{3i}) = \frac{1}{N}\sum_{i=1}^N \Delta(x_{2i}|x_{3i})$ and $\text{APE}(x_{3i}|x_{2i}) = \frac{1}{N}\sum_{i=1}^N \Delta(x_{3i}|x_{2i})$. Fortunately, the APE and PEA tend to be similar.

Display 10.1: Partial effects at the average (PEA) and average partial effects (APE) for the logistic regression model, $\text{logit}\left\{\Pr(y_i = 1|x_{2i}, x_{3i})\right\} = \beta_1 + \beta_2 x_{2i} + \beta_3 x_{3i}$, where x_{2i} is continuous and x_{3i} is binary.

To illustrate logistic regression, we will consider data on married women from the Canadian Women's Labor Force Participation Dataset used by Fox (1997). The dataset `womenlf.dta` contains women's employment status and two explanatory variables:

- `workstat`: employment status
  (0: not working; 1: employed part time; 2: employed full time)
- `husbinc`: husband's income in $1,000
- `chilpres`: child present in household (dummy variable)

The dataset can be retrieved by typing

```
. use http://www.stata-press.com/data/mlmus3/womenlf
```

Fox (1997) considered a multiple logistic regression model for a woman being employed (full or part time) versus not working with covariates `husbinc` and `chilpres`

$$\text{logit}\{\Pr(y_i=1|\mathbf{x}_i)\} \;=\; \beta_1 + \beta_2 x_{2i} + \beta_3 x_{3i}$$

where $y_i = 1$ denotes employment, $y_i = 0$ denotes not working, x_{2i} is `husbinc`, x_{3i} is `chilpres`, and $\mathbf{x}_i = (x_{2i}, x_{3i})'$ is a vector containing both covariates.

We first merge categories 1 and 2 (employed part time and full time) of `workstat` into a new category 1 for being employed,

```
. recode workstat 2=1
```

and then fit the model by maximum likelihood using Stata's `logit` command:

```
. logit workstat husbinc chilpres
Logistic regression                               Number of obs   =        263
                                                  LR chi2(2)      =      36.42
                                                  Prob > chi2     =     0.0000
Log likelihood = -159.86627                       Pseudo R2       =     0.1023

------------------------------------------------------------------------------
    workstat |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
     husbinc |  -.0423084   .0197801    -2.14   0.032    -.0810768   -.0035401
    chilpres |  -1.575648   .2922629    -5.39   0.000    -2.148473   -1.002824
       _cons |    1.33583   .3837632     3.48   0.000     .5836674    2.087992
------------------------------------------------------------------------------
```

The estimated coefficients are negative, so the estimated log odds of employment are lower if the husband earns more and if there is a child in the household. At the 5% significance level, we can reject the null hypotheses that the individual coefficients β_2 and β_3 are zero. The estimated coefficients and their estimated standard errors are also given in table 10.1.

Table 10.1: Maximum likelihood estimates for logistic regression model for women's labor force participation

	Est	(SE)	OR = exp(β)	(95% CI)
β_1 [_cons]	1.34	(0.38)		
β_2 [husbinc]	−0.04	(0.02)	0.96	(0.92, 1.00)
β_3 [chilpres]	−1.58	(0.29)	0.21	(0.12, 0.37)

Instead of considering changes in log odds, it is more informative to obtain odds ratios, the exponentiated regression coefficients. This can be achieved by using the `logit` command with the `or` option:

```
. logit workstat husbinc chilpres, or
Logistic regression                               Number of obs   =        263
                                                  LR chi2(2)      =      36.42
                                                  Prob > chi2     =     0.0000
Log likelihood = -159.86627                       Pseudo R2       =     0.1023

------------------------------------------------------------------------------
    workstat | Odds Ratio   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
     husbinc |   .9585741   .0189607    -2.14   0.032     .9221229    .9964662
    chilpres |   .2068734   .0604614    -5.39   0.000     .1166621    .3668421
       _cons |    3.80315    1.45951     3.48   0.000     1.792601    8.068699
------------------------------------------------------------------------------
```

Comparing women with and without a child at home, whose husbands have the same income, the odds of working are estimated to be about 5 ($\approx 1/0.2068734$) times as high for women who do not have a child at home as for women who do. Within these two groups of women, each \$1,000 increase in husband's income reduces the odds of working by an estimated 4% $\{-4\% = 100\%(0.9585741 - 1)\}$. Although this odds ratio looks less important than the one for `chilpres`, remember that we cannot directly compare the magnitude of the two odds ratios. The odds ratio for `chilpres` represents a comparison of two distinct groups of women, whereas the odds ratio for `husbinc` merely expresses the effect of a \$1,000 increase in the husband's income. A \$10,000 increase would be associated with an odds ratio of 0.66 ($= 0.958741^{10}$).

The exponentiated intercept, estimated as 3.80, represents the odds of working for women who do not have a child at home and whose husbands' income is 0. This is not an odds ratio as the column heading implies, but the odds when all covariates are zero. For this reason, the exponentiated intercept was omitted from the output in earlier releases of Stata (until Stata 12.0) when the `or` option was used. As for the intercept itself, the exponentiated intercept is interpretable only if zero is a meaningful value for all covariates.

In an attempt to make effects directly comparable and assess the relative importance of covariates, some researchers standardize all covariates to have standard deviation 1, thereby comparing the effects of a standard deviation change in each covariate. As

discussed in section 1.5, there are many problems with such an approach, one of them being the meaningless notion of a standard deviation change in a dummy variable, such as `chilpres`.

The standard errors of exponentiated estimated regression coefficients should generally not be used for confidence intervals or hypothesis tests. Instead, the 95% confidence intervals in the above output were computed by taking the exponentials of the confidence limits for the regression coefficients β:

$$\exp\{\widehat{\beta} \pm 1.96 \times \mathrm{SE}(\widehat{\beta})\}$$

In table 10.1, we therefore report estimated odds ratios with 95% confidence intervals instead of standard errors.

To visualize the model, we can produce a plot of the predicted probabilities versus `husbinc`, with separate curves for women with and without children at home. Plugging in maximum likelihood estimates for the parameters in (10.2), the predicted probability for woman i, often denoted $\widehat{\pi}_i$, is given by the inverse logit of the estimated linear predictor

$$\widehat{\pi}_i \equiv \widehat{\Pr}(y_i = 1|x_i) = \frac{\exp(\widehat{\beta}_1 + \widehat{\beta}_2 x_{2i} + \widehat{\beta}_3 x_{3i})}{1 + \exp(\widehat{\beta}_1 + \widehat{\beta}_2 x_{2i} + \widehat{\beta}_3 x_{3i})} = \mathrm{logit}^{-1}(\widehat{\beta}_1 + \widehat{\beta}_2 x_{2i} + \widehat{\beta}_3 x_{3i}) \tag{10.3}$$

and can be obtained for the women in the dataset by using the `predict` command with the `pr` option:

```
. predict prob, pr
```

We can now produce the graph of predicted probabilities, shown in figure 10.1, by using

```
. twoway (line prob husbinc if chilpres==0, sort)
> (line prob husbinc if chilpres==1, sort lpatt(dash)),
> legend(order(1 "No child" 2 "Child"))
> xtitle("Husband's income/$1000") ytitle("Probability that wife works")
```

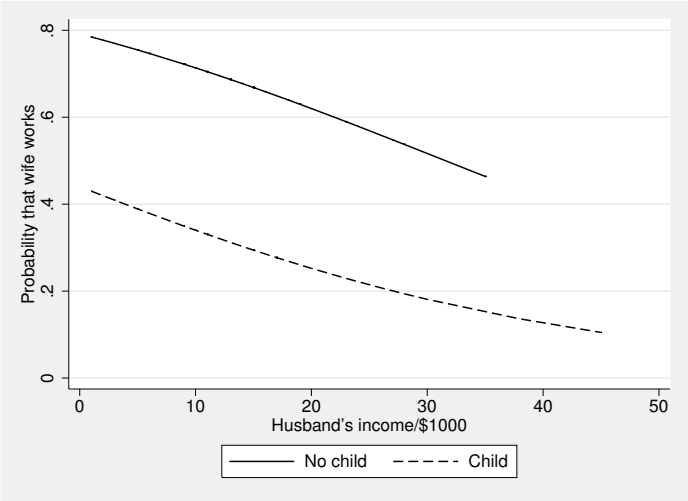


Figure 10.1: Predicted probability of working from logistic regression model (for range of `husbinc` in dataset)

The graph is similar to the graph of the predicted means from an analysis of covariance model (a linear regression model with a continuous and a dichotomous covariate; see section 1.7) except that the curves are not exactly straight. The curves have been plotted for the range of values of `husbinc` observed for the two groups of women, and for these ranges the predicted probabilities are nearly linear functions of `husbinc`.

To see what the inverse logit function looks like, we will now plot the predicted probabilities for a widely extended range of values of `husbinc` (including negative values, although this does not make sense). This could be accomplished by inventing additional observations with more extreme values of `husbinc` and then using the `predict` command again. More conveniently, we can also use Stata's useful `twoway` plot type, `function`:

```
. twoway (function y=invlogit(_b[husbinc]*x+_b[_cons]), range(-100 100))
> (function y=invlogit(_b[husbinc]*x+_b[chilpres]+_b[_cons]),
> range(-100 100) lpatt(dash)),
> xtitle("Husband's income/$1000") ytitle("Probability that wife works")
> legend(order(1 "No child" 2 "Child")) xline(1) xline(45)
```

The estimated regression coefficients are referred to as `_b[husbinc]`, `_b[chilpres]`, and `_b[_cons]`, and we have used Stata's `invlogit()` function to obtain the predicted probabilities given in (10.3). The resulting graph is shown in figure 10.2.

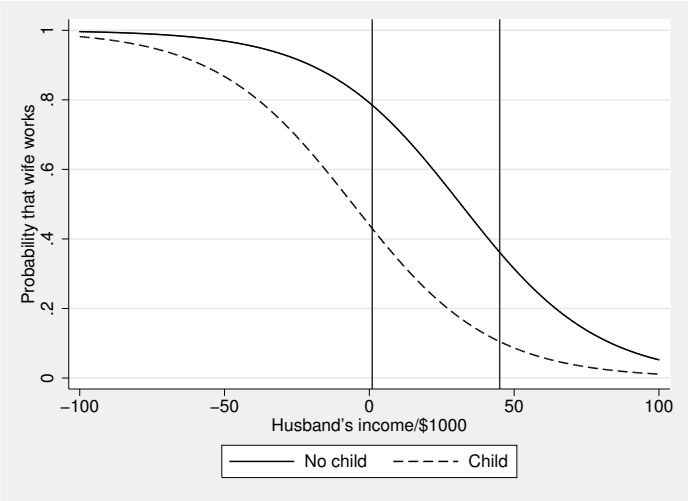


Figure 10.2: Predicted probability of working from logistic regression model (extrapolating beyond the range of `husbinc` in the data)

The range of `husbinc` actually observed in the data lies approximately between the two vertical lines. It would not be safe to rely on predicted probabilities extrapolated outside this range. The curves are approximately linear in the region where the linear predictor is close to zero (and the predicted probability is close to 0.5) and then flatten as the linear predictor becomes extreme. This flattening ensures that the predicted probabilities remain in the permitted interval from 0 to 1.

We can fit the same model by using the `glm` command for generalized linear models. The syntax is the same as that of the `logit` command except that we must specify the logit link function in the `link()` option and the binomial distribution in the `family()` option:

```
. glm workstat husbinc chilpres, link(logit) family(binomial)
Generalized linear models                         No. of obs      =       263
Optimization     : ML                             Residual df     =       260
                                                  Scale parameter =         1
Deviance         =  319.7325378                   (1/df) Deviance =  1.229741
Pearson          =  265.9615312                   (1/df) Pearson  =  1.022929
Variance function: V(u) = u*(1-u)                 [Bernoulli]
Link function    : g(u) = ln(u/(1-u))             [Logit]
                                                  AIC             =  1.238527
Log likelihood   = -159.8662689                   BIC             = -1129.028
```

workstat	Coef.	OIM Std. Err.	z	P>|z|	[95% Conf.	Interval]
husbinc	-.0423084	.0197801	-2.14	0.032	-.0810768	-.0035401
chilpres	-1.575648	.2922629	-5.39	0.000	-2.148473	-1.002824
_cons	1.33583	.3837634	3.48	0.000	.5836674	2.087992

To obtain estimated odds ratios, we use the `eform` option (for "exponentiated form"), and to fit a probit model, we simply change the `link(logit)` option to `link(probit)`.

10.2.2 Latent-response formulation

The logistic regression model and other models for dichotomous responses can also be viewed as latent-response models. Underlying the observed dichotomous response y_i (whether the woman works or not), we imagine that there is an unobserved or latent continuous response y_i^* representing the propensity to work or the excess utility of working as compared with not working. If this latent response is greater than 0, then the observed response is 1; otherwise, the observed response is 0:

$$y_i = \begin{cases} 1 & \text{if } y_i^* > 0 \\ 0 & \text{otherwise} \end{cases}$$

For simplicity, we will assume that there is one covariate x_i. A linear regression model is then specified for the latent response y_i^*

$$y_i^* = \beta_1 + \beta_2 x_i + \epsilon_i$$

where ϵ_i is a residual error term with $E(\epsilon_i|x_i) = 0$ and the error terms of different women i are independent.

The latent-response formulation has been used in various disciplines and applications. In genetics, where y_i is often a phenotype or qualitative trait, y_i^* is called a *liability*. For attitudes measured by agreement or disagreement with statements, the latent response can be thought of as a "sentiment" in favor of the statement. In economics, the latent response is often called an *index function*. In discrete-choice settings (see chapter 12), y_i^* is the *difference in utilities* between alternatives.

Figure 10.3 illustrates the relationship between the latent-response formulation, shown in the lower graph, and the generalized linear model formulation, shown in the

upper graph in terms of a curve for the conditional probability that $y_i = 1$. The regression line in the lower graph represents the conditional expectation of y_i^* given x_i as a function of x_i, and the density curves represent the conditional distributions of y_i^* given x_i. The dotted horizontal line at $y_i^* = 0$ represents the threshold, so $y_i = 1$ if y_i^* exceeds the threshold and $y_i = 0$ otherwise. Therefore, the areas under the parts of the density curves that lie above the dotted line, here shaded gray, represent the probabilities that $y_i = 1$ given x_i. For the value of x_i indicated by the vertical dotted line, the mean of y_i^* is 0; therefore, half the area under the density curve lies above the threshold, and the conditional probability that $y_i = 1$ equals 0.5 at that point.

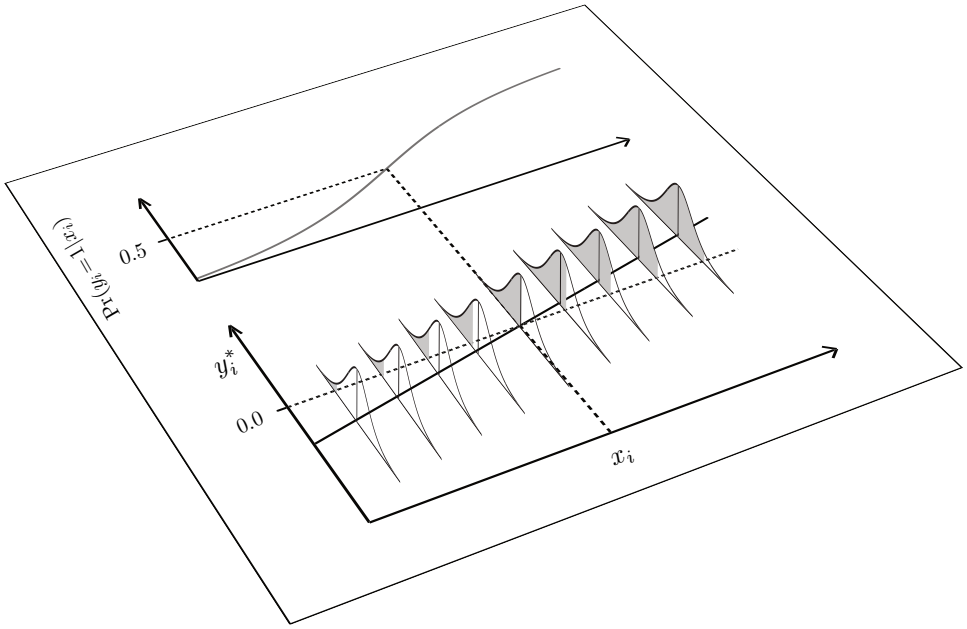


Figure 10.3: Illustration of equivalence of latent-response and generalized linear model formulations for logistic regression

We can derive the probability curve from the latent-response formulation as follows:

$$\begin{aligned}
\Pr(y_i = 1|x_i) &= \Pr(y_i^* > 0|x_i) = \Pr(\beta_1 + \beta_2 x_i + \epsilon_i > 0|x_i) \\
&= \Pr\{\epsilon_i > -(\beta_1 + \beta_2 x_i)|x_i\} = \Pr(-\epsilon_i \leq \beta_1 + \beta_2 x_i|x_i) \\
&= F(\beta_1 + \beta_2 x_i)
\end{aligned}$$

where $F(\cdot)$ is the cumulative density function of $-\epsilon_i$, or the area under the density curve for $-\epsilon_i$ from minus infinity to $\beta_1 + \beta_2 x_i$. If the distribution of ϵ_i is symmetric, the cumulative density function of $-\epsilon_i$ is the same as that of ϵ_i.

Logistic regression

In logistic regression, ϵ_i is assumed to have a standard logistic cumulative density function given x_i,

$$\Pr(\epsilon_i < \tau | x_i) = \frac{\exp(\tau)}{1+\exp(\tau)}$$

For this distribution, ϵ_i has mean zero and variance $\pi^2/3 \approx 3.29$ (note that π here represents the famous mathematical constant pronounced "pi", the circumference of a circle divided by its diameter).

Probit regression

When a latent-response formulation is used, it seems natural to assume that ϵ_i has a normal distribution given x_i, as is typically done in linear regression. If a standard (mean 0 and variance 1) normal distribution is assumed, the model becomes a probit model,

$$\Pr(y_i=1|x_i) = F(\beta_1+\beta_2 x_i) = \Phi(\beta_1+\beta_2 x_i) \tag{10.4}$$

Here $\Phi(\cdot)$ is the standard normal cumulative distribution function, the probability that a standard normally distributed random variable (here ϵ_i) is less than the argument. For example, when $\beta_1+\beta_2 x_i$ equals 1.96, $\Phi(\beta_1+\beta_2 x_i)$ equals 0.975. $\Phi(\cdot)$ is the inverse link function $h(\cdot)$, whereas the link function $g(\cdot)$ is $\Phi^{-1}(\cdot)$, the inverse standard normal cumulative distribution function, called the *probit link* function [the Stata function for $\Phi^{-1}(\cdot)$ is `invnormal()`].

To understand why a *standard* normal distribution is specified for ϵ_i, with the variance θ fixed at 1, consider the graph in figure 10.4. On the left, the standard deviation is 1, whereas the standard deviation on the right is 2. However, by doubling the slope of the regression line for y_i^* on the right (without changing the point where it intersects the threshold 0), we obtain the same curve for the probability that $y_i=1$. Because we can obtain equivalent models by increasing both the standard deviation and the slope by the same multiplicative factor, the model with a freely estimated standard deviation is not identified.

This lack of identification is also evident from inspecting the expression for the probability if the variance θ were not fixed at 1 [from (10.4)],

$$\Pr(y_i=1|x_i) = \Pr(\epsilon_i \le \beta_1+\beta_2 x_i) = \Pr\left(\frac{\epsilon_i}{\sqrt{\theta}} \le \frac{\beta_1+\beta_2 x_i}{\sqrt{\theta}}\right) = \Phi\left(\frac{\beta_1}{\sqrt{\theta}}+\frac{\beta_2}{\sqrt{\theta}}x_i\right)$$

where we see that multiplication of the regression coefficients by a constant can be counteracted by multiplying $\sqrt{\theta}$ by the same constant. This is the reason for fixing the standard deviation in probit models to 1 (see also exercise 10.10). The variance of ϵ_i in logistic regression is also fixed but to a larger value, $\pi^2/3$.

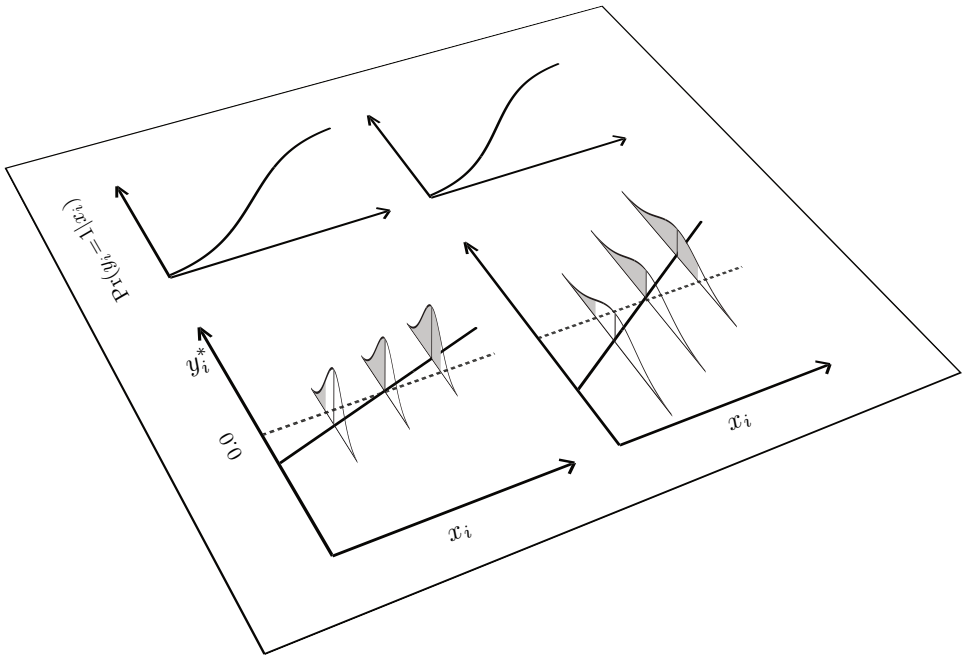


Figure 10.4: Illustration of equivalence between probit models with change in residual standard deviation counteracted by change in slope

A probit model can be fit to the women's employment data in Stata by using the `probit` command:

```
. probit workstat husbinc chilpres
Probit regression                                 Number of obs   =        263
                                                  LR chi2(2)      =      36.19
                                                  Prob > chi2     =     0.0000
Log likelihood = -159.97986                       Pseudo R2       =     0.1016

------------------------------------------------------------------------------
    workstat |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
    husbinc |  -.0242081   .0114252    -2.12   0.034    -.0466011    -.001815
    chilpres |  -.9706164   .1769051    -5.49   0.000    -1.317344   -.6238887
       _cons |   .7981507   .2240082     3.56   0.000     .3591028    1.237199
------------------------------------------------------------------------------
```

These estimates are closer to zero than those reported for the logit model in table 10.1 because the standard deviation of ϵ_i is 1 for the probit model and $\pi/\sqrt{3} \approx 1.81$ for the logit model. Therefore, as we have already seen in figure 10.4, the regression coefficients in logit models must be larger in absolute value to produce nearly the same curve for the conditional probability that $y_i = 1$. Here we say "nearly the same" because the shapes of the probit and logit curves are similar yet not identical. To visualize the

subtle difference in shape, we can plot the predicted probabilities for women without children at home from both the logit and probit models:

```
. twoway (function y=invlogit(1.3358-0.0423*x), range(-100 100))
> (function y=normal(0.7982-0.0242*x), range(-100 100) lpatt(dash)),
> xtitle("Husband's income/$1000") ytitle("Probability that wife works")
> legend(order(1 "Logit link" 2 "Probit link")) xline(1) xline(45)
```

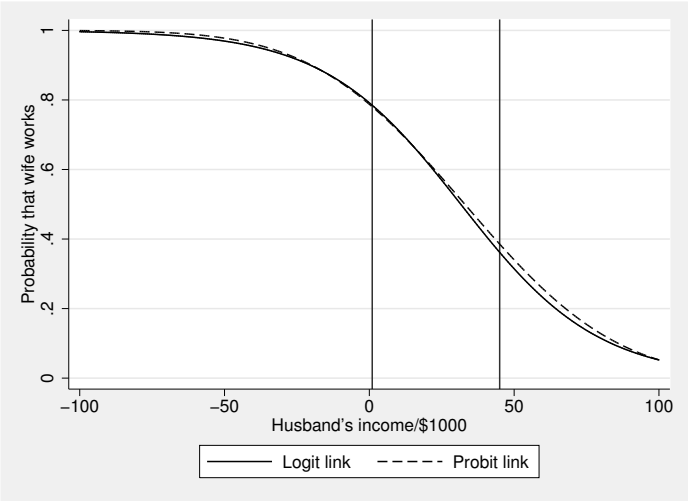


Figure 10.5: Predicted probabilities of working from logistic and probit regression models for women without children at home

Here the predictions from the models coincide nearly perfectly in the region where most of the data are concentrated and are very similar elsewhere. It is thus futile to attempt to empirically distinguish between the logit and probit links unless one has a huge sample.

Regression coefficients in probit models cannot be interpreted in terms of odds ratios as in logistic regression models. Instead, the coefficients can be interpreted as differences in the population means of the *latent response* y_i^*, controlling or adjusting for other covariates (the same kind of interpretation can also be made in logistic regression). Many people find interpretation based on latent responses less appealing than interpretation using odds ratios, because the latter refer to observed responses y_i. Alternatively, the coefficients can be interpreted in terms of average partial effects or partial effects at the average as shown for logit models[2] in display 10.1.

2. For probit models with continuous x_{2i} and binary x_{3i}, $\Delta(x_{2i}|x_{3i}) = \beta_2\,\phi(\beta_1 + \beta_2 x_{2i} + \beta_3 x_{3i})$, where $\phi(\cdot)$ is the density function of the standard normal distribution, and $\Delta(x_{3i}|x_{2i}) = \Phi(\beta_1 + \beta_2 x_{2i} + \beta_3) - \Phi(\beta_1 + \beta_2 x_{2i})$.

10.3 Which treatment is best for toenail infection?

Lesaffre and Spiessens (2001) analyzed data provided by De Backer et al. (1998) from a randomized, double-blind trial of treatments for toenail infection (dermatophyte onychomycosis). Toenail infection is common, with a prevalence of about 2% to 3% in the United States and a much higher prevalence among diabetics and the elderly. The infection is caused by a fungus, and not only disfigures the nails but also can cause physical pain and impair the ability to work.

In this clinical trial, 378 patients were randomly allocated into two oral antifungal treatments (250 mg/day terbinafine and 200 mg/day itraconazole) and evaluated at seven visits, at weeks 0, 4, 8, 12, 24, 36, and 48. One outcome is onycholysis, the degree of separation of the nail plate from the nail bed, which was dichotomized ("moderate or severe" versus "none or mild") and is available for 294 patients.

The dataset `toenail.dta` contains the following variables:

- `patient`: patient identifier
- `outcome`: onycholysis (separation of nail plate from nail bed) (0: none or mild; 1: moderate or severe)
- `treatment`: treatment group (0: itraconazole; 1: terbinafine)
- `visit`: visit number (1, 2, ..., 7)
- `month`: exact timing of visit in months

We read in the toenail data by typing

```
. use http://www.stata-press.com/data/mlmus3/toenail, clear
```

The main research question is whether the treatments differ in their efficacy. In other words, do patients receiving one treatment experience a greater decrease in their probability of having onycholysis than those receiving the other treatment?

10.4 Longitudinal data structure

Before investigating the research question, we should look at the longitudinal structure of the toenail data using, for instance, the `xtdescribe`, `xtsum`, and `xttab` commands, discussed in *Introduction to models for longitudinal and panel data (part III)*.

Here we illustrate the use of the `xtdescribe` command, which can be used for these data because the data were intended to be balanced with seven visits planned for the same set of weeks for each patient (although the exact timing of the visits varied between patients).

Before using `xtdescribe`, we `xtset` the data with `patient` as the cluster identifier and `visit` as the time variable:

```
. xtset patient visit
       panel variable:  patient (unbalanced)
        time variable:  visit, 1 to 7, but with gaps
                delta:  1 unit
```

The output states that the data are unbalanced and that there are gaps. [We would describe the time variable `visit` as balanced because the values are identical across patients apart from the gaps caused by missing data; see the introduction to models for longitudinal and panel data (part III in volume I).]

To explore the missing-data patterns, we use

```
. xtdescribe if outcome < .
 patient:  1, 2, ..., 383                                   n =        294
   visit:  1, 2, ..., 7                                     T =          7
           Delta(visit) = 1 unit
           Span(visit)  = 7 periods
           (patient*visit uniquely identifies each observation)

Distribution of T_i:   min      5%     25%       50%       75%     95%     max
                         1       3       7         7         7       7       7

     Freq.  Percent    Cum.  |  Pattern
------------------------------+---------
       224     76.19   76.19  |  1111111
        21      7.14   83.33  |  11111.1
        10      3.40   86.73  |  1111.11
         6      2.04   88.78  |  111....
         5      1.70   90.48  |  1......
         5      1.70   92.18  |  11111..
         4      1.36   93.54  |  1111...
         3      1.02   94.56  |  11.....
         3      1.02   95.58  |  111.111
        13      4.42  100.00  |  (other patterns)
------------------------------+---------
       294    100.00          |  XXXXXXX
```

We see that 224 patients have complete data (the pattern "`1111111`"), 21 patients missed the sixth visit ("`11111.1`"), 10 patients missed the fifth visit ("`1111.11`"), and most other patients dropped out at some point, never returning after missing a visit. The latter pattern is sometimes referred to as *monotone missingness*, in contrast with *intermittent missingness*, which follows no particular pattern.

As discussed in section 5.8, a nice feature of maximum likelihood estimation for incomplete data such as these is that all information is used. Thus not only patients who attended all visits but also patients with missing visits contribute information. If the model is correctly specified, maximum likelihood estimates are consistent when the responses are missing at random (MAR).

10.5 Proportions and fitted population-averaged or marginal probabilities

A useful graphical display of the data is a bar plot showing the proportion of patients with onycholysis at each visit by treatment group. The following Stata commands can be used to produce the graph shown in figure 10.6:

```
. label define tr 0 "Itraconazole" 1 "Terbinafine"
. label values treatment tr
. graph bar (mean) proportion = outcome, over(visit) by(treatment)
> ytitle(Proportion with onycholysis)
```

Here we defined value labels for `treatment` to make them appear on the graph.

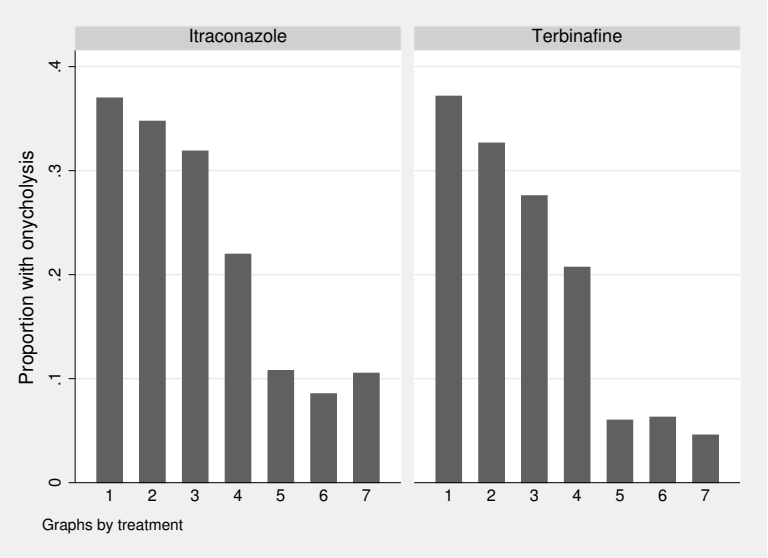


Figure 10.6: Bar plot of proportion of patients with toenail infection by visit and treatment group

We used the visit number `visit` to define the bars instead of the exact timing of the visit `month` because there would generally not be enough patients with the same timing to estimate the proportions reliably. An alternative display is a line graph, plotting the observed proportions at each visit against time. For this graph, it is better to use the average time associated with each visit for the x axis than to use visit number, because the visits were not equally spaced. Both the proportions and the average times for each visit in each treatment group can be obtained using the `egen` command with the `mean()` function:

```
. egen prop = mean(outcome), by(treatment visit)
. egen mn_month = mean(month), by(treatment visit)
. twoway line prop mn_month, by(treatment) sort
> xtitle(Time in months) ytitle(Proportion with onycholysis)
```

The resulting graph is shown in figure 10.7.

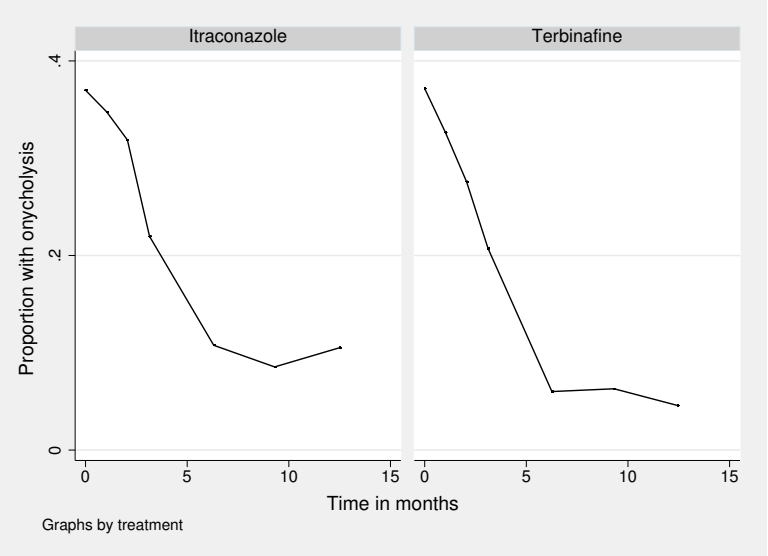


Figure 10.7: Line plot of proportion of patients with toenail infection by average time at visit and treatment group

The proportions shown in figure 10.7 represent the estimated average (or marginal) probabilities of onycholysis given the two covariates, time since randomization and treatment group. We are not attempting to estimate individual patients' personal probabilities, which may vary substantially, but are considering the population averages given the covariates.

Instead of estimating the probabilities for each combination of `visit` and `treatment`, we can attempt to obtain smooth curves of the estimated probability as a function of time. We then no longer have to group observations for the same visit number together—we can use the exact timing of the visits directly. One way to accomplish this is by using a logistic regression model with `month`, `treatment`, and their interaction as covariates. This model for the dichotomous outcome y_{ij} at visit i for patient j can be written as

$$\text{logit}\{\Pr(y_{ij}=1|\mathbf{x}_{ij})\} \;=\; \beta_1 + \beta_2 x_{2j} + \beta_3 x_{3ij} + \beta_4 x_{2j} x_{3ij} \tag{10.5}$$

where x_{2j} represents `treatment`, x_{3ij} represents `month`, and $\mathbf{x}_{ij} = (x_{2j}, x_{3ij})'$ is a vector containing both covariates. This model allows for a difference between groups at

baseline β_2, and linear changes in the log odds of onycholysis over time with slope β_3 in the itraconazole group and slope $\beta_3 + \beta_4$ in the terbinafine group. Therefore, β_4, the difference in the rate of improvement (on the log odds scale) between treatment groups, can be viewed as the treatment effect (terbinafine versus itraconazole).

This model makes the unrealistic assumption that the responses for a given patient are conditionally independent after controlling for the included covariates. We will relax this assumption in the next section. Here we can get satisfactory inferences for marginal effects by using robust standard errors for clustered data instead of using model-based standard errors. This approach is analogous to pooled OLS in linear models and corresponds to the generalized estimating equations approach discussed in section 6.6 with an independence working correlation structure (see 10.14.2 for an example with a different working correlation matrix).

We start by constructing an interaction term, `trt_month`, for `treatment` and `month`,

```
. generate trt_month = treatment*month
```

before fitting the model by maximum likelihood with robust standard errors:

```
. logit outcome treatment month trt_month, or vce(cluster patient)
Logistic regression                             Number of obs   =       1908
                                                Wald chi2(3)    =      64.30
                                                Prob > chi2     =     0.0000
Log pseudolikelihood = -908.00747               Pseudo R2       =     0.0830

------------------------------------------------------------------------------
             |               Robust
     outcome | Odds Ratio   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
   treatment |   .9994184   .2511294    -0.00   0.998     .6107468    1.635436
       month |   .8434052   .0246377    -5.83   0.000     .7964725    .8931034
   trt_month |    .934988   .0488105    -1.29   0.198     .8440528     1.03572
       _cons |   .5731389   .0982719    -3.25   0.001     .4095534    .8020642
------------------------------------------------------------------------------
```

Instead of creating a new variable for the interaction, we could have used factor-variables syntax as follows:

```
logit outcome i.treatment##c.month, or vce(cluster patient)
```

We will leave interpretation of estimates for later and first check how well predicted probabilities from the logistic regression model correspond to the observed proportions in figure 10.7. The predicted probabilities are obtained and plotted together with the observed proportions by using the following commands, which result in figure 10.8.

```
. predict prob, pr
. twoway (line prop mn_month, sort) (line prob month, sort lpatt(dash)),
> by(treatment) legend(order(1 "Observed proportions" 2 "Fitted probabilities"))
> xtitle(Time in months) ytitle(Probability of onycholysis)
```

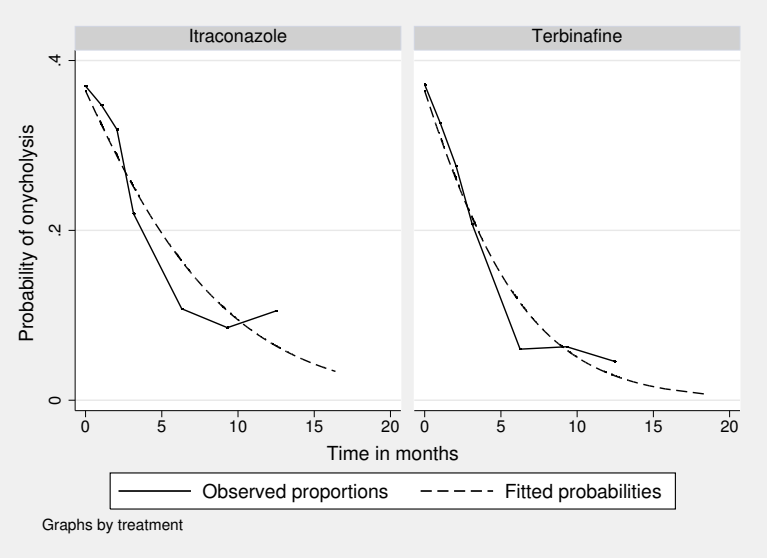


Figure 10.8: Proportions and fitted probabilities using ordinary logistic regression

The marginal probabilities predicted by the model fit the observed proportions reasonably well. However, we have treated the dependence among responses for the same patient as a nuisance by fitting an ordinary logistic regression model with robust standard errors for clustered data. We now add random effects to model the dependence and estimate the degree of dependence instead of treating it as a nuisance.

10.6 Random-intercept logistic regression

10.6.1 Model specification

Reduced-form specification

To relax the assumption of conditional independence among the responses for the same patient given the covariates, we can include a patient-specific random intercept ζ_j in the linear predictor to obtain a random-intercept logistic regression model

$$\text{logit}\{\Pr(y_{ij}=1|\mathbf{x}_{ij},\zeta_j)\} = \beta_1 + \beta_2 x_{2j} + \beta_3 x_{3ij} + \beta_4 x_{2j} x_{3ij} + \zeta_j \tag{10.6}$$

The random intercepts $\zeta_j \sim N(0,\psi)$ are assumed to be independent and identically distributed across patients j and independent of the covariates $\mathbf{x}_{ij}$. Given ζ_j and $\mathbf{x}_{ij}$, the responses y_{ij} for patient j at different occasions i are independently Bernoulli distributed. To write this down more formally, it is useful to define $\pi_{ij} \equiv \Pr(y_{ij}|\mathbf{x}_{ij},\zeta_j)$, giving

$$\begin{aligned} \text{logit}(\pi_{ij}) &= \beta_1 + \beta_2 x_{2j} + \beta_3 x_{3ij} + \beta_4 x_{2j} x_{3ij} + \zeta_j \\ y_{ij}|\pi_{ij} &\sim \text{Binomial}(1, \pi_{ij}) \end{aligned}$$

This is a simple example of a *generalized linear mixed model* (GLMM) because it is a generalized linear model with both fixed effects β_1 to β_4 and a random effect ζ_j. The model is also sometimes referred to as a hierarchical generalized linear model (HGLM) in contrast to a hierarchical linear model (HLM). The random intercept can be thought of as the combined effect of omitted patient-specific (time-constant) covariates that cause some patients to be more prone to onycholysis than others (more precisely, the component of this combined effect that is independent of the covariates in the model—not an issue if the covariates are exogenous). It is appealing to model this unobserved heterogeneity in the same way as observed heterogeneity by simply adding the random intercept to the linear predictor. As we will explain later, be aware that odds ratios obtained by exponentiating regression coefficients in this model must be interpreted conditionally on the random intercept and are therefore often referred to as conditional or subject-specific odds ratios.

Using the latent-response formulation, the model can equivalently be written as

$$y_{ij}^* = \beta_1 + \beta_2 x_{2j} + \beta_3 x_{3ij} + \beta_4 x_{2j} x_{3ij} + \zeta_j + \epsilon_{ij} \tag{10.7}$$

where $\zeta_j \sim N(0, \psi)$ and the ϵ_{ij} have standard logistic distributions. The binary responses y_{ij} are determined by the latent continuous responses via the threshold model

$$y_{ij} = \begin{cases} 1 & \text{if } y_{ij}^* > 0 \\ 0 & \text{otherwise} \end{cases}$$

Confusingly, logistic random-effects models are sometimes written as $y_{ij} = \pi_{ij} + e_{ij}$, where e_{ij} is a normally distributed level-1 residual with variance $\pi_{ij}(1 - \pi_{ij})$. This formulation is clearly incorrect because such a model does not produce binary responses (see Skrondal and Rabe-Hesketh [2007]).

In both formulations of the model (via a logit link or in terms of a latent response), it is assumed that the ζ_j are independent across patients and independent of the covariates $\mathbf{x}_{ij}$ at occasion i. It is also assumed that the covariates at other occasions do not affect the response probabilities given the random intercept (called strict exogeneity conditional on the random intercept). For the latent response formulation, the ϵ_{ij} are assumed to be independent across both occasions and patients, and independent of both ζ_j and $\mathbf{x}_{ij}$. In the generalized linear model formulation, the analogous assumptions are implicit in assuming that the responses are independently Bernoulli distributed (with probabilities determined by ζ_j and $\mathbf{x}_{ij}$).

In contrast to linear random effects models, consistent estimation in random-effects logistic regression requires that the random part of the model is correctly specified in

addition to the fixed part. Specifically, consistency formally requires (1) a correct linear predictor (such as including relevant interactions), (2) a correct link function, (3) correct specification of covariates having random coefficients, (4) conditional independence of responses given the random effects and covariates, (5) independence of the random effects and covariates (for causal inference), and (6) normally distributed random effects. Hence, the assumptions are stronger than those discussed for linear models in section 3.3.2. However, the normality assumption for the random intercepts seems to be rather innocuous in contrast to the assumption of independence between the random intercepts and covariates (Heagerty and Kurland 2001). As in standard logistic regression, the ML estimator is not necessarily unbiased in finite samples even if all the assumptions are true.

Two-stage formulation

Raudenbush and Bryk (2002) and others write two-level models in terms of a level-1 model and one or more level-2 models (see section 4.9). In generalized linear mixed models, the need to specify a link function and distribution leads to two further stages of model specification.

Using the notation and terminology of Raudenbush and Bryk (2002), the level-1 sampling model, link function, and structural model are written as

$$\begin{aligned} y_{ij} &\sim \text{Bernoulli}(\varphi_{ij}) \\ \text{logit}(\varphi_{ij}) &= \eta_{ij} \\ \eta_{ij} &= \beta_{0j} + \beta_{1j}x_{2j} + \beta_{2j}x_{3ij} + \beta_{3j}x_{2j}x_{3ij} \end{aligned}$$

respectively.

The level-2 model for the intercept β_{0j} is written as

$$\beta_{0j} = \gamma_{00} + u_{0j}$$

where γ_{00} is a fixed intercept and u_{0j} is a residual or random intercept. The level-2 models for the coefficients β_{1j}, β_{2j}, and β_{3j} have no residuals for a random-intercept model,

$$\beta_{pj} = \gamma_{p0}, \quad p = 1, 2, 3$$

Plugging the level-2 models into the level-1 structural model, we obtain

$$\begin{aligned} \eta_{ij} &= \gamma_{00} + u_{0j} + \gamma_{01}x_{2j} + \gamma_{02}x_{3ij} + \gamma_{03}x_{2j}x_{3ij} \\ &\equiv \beta_1 + \zeta_{0j} + \beta_2 x_{2j} + \beta_3 x_{3ij} + \beta_4 x_{2j}x_{3ij} \end{aligned}$$

Equivalent models can be specified using either the reduced-form formulation (used for instance by Stata) or the two-stage formulation (used in the HLM software of Raudenbush et al. 2004). However, in practice, model specification is to some extent influenced by the approach adopted as discussed in section 4.9.

10.7 Estimation of random-intercept logistic models

As of Stata 10, there are three commands for fitting random-intercept logistic models in Stata: `xtlogit`, `xtmelogit`, and `gllamm`. All three commands provide maximum likelihood estimation and use adaptive quadrature to approximate the integrals involved (see section 10.11.1 for more information). The commands have essentially the same syntax as their counterparts for linear models discussed in volume I. Specifically, `xtlogit` corresponds to `xtreg`, `xtmelogit` corresponds to `xtmixed`, and `gllamm` uses essentially the same syntax for linear, logistic, and other types of models.

All three commands are relatively slow because they use numerical integration, but for random-intercept models, `xtlogit` is much faster than `xtmelogit`, which is usually faster than `gllamm`. However, the rank ordering is reversed when it comes to the usefulness of the commands for predicting random effects and various types of probabilities as we will see in sections 10.12 and 10.13. Each command uses a default for the number of terms (called "integration points") used to approximate the integral, and there is no guarantee that a sufficient number of terms has been used to achieve reliable estimates. It is therefore the user's responsibility to make sure that the approximation is adequate by increasing the number of integration points until the results stabilize. The more terms are used, the more accurate the approximation at the cost of increased computation time.

We do not discuss random-coefficient logistic regression in this chapter, but such models can be fit with `xtmelogit` and `gllamm` (but not using `xtlogit`), using essentially the same syntax as for linear random-coefficient models discussed in section 4.5. Random-coefficient logistic regression using `gllamm` is demonstrated in chapters 11 (for ordinal responses) and 16 (for models with nested and crossed random effects) and using `xtmelogit` in chapter 16. The probit version of the random-intercept model is available in `gllamm` (see sections 11.10 through 11.12) and `xtprobit`, but random-coefficient probit models are available in `gllamm` only.

10.7.1 Using xtlogit

The `xtlogit` command for fitting the random-intercept model is analogous to the `xtreg` command for fitting the corresponding linear model. We first use the `xtset` command to specify the clustering variable. In the `xtlogit` command, we use the `intpoints(30)` option (`intpoints()` stands for "integration points") to ensure accurate estimates (see section 10.11.1):

```
. quietly xtset patient
. xtlogit outcome treatment month trt_month, intpoints(30)
Random-effects logistic regression              Number of obs      =      1908
Group variable: patient                         Number of groups   =       294
Random effects u_i ~ Gaussian                   Obs per group: min =         1
                                                               avg =       6.5
                                                               max =         7
                                                Wald chi2(3)       =    150.65
Log likelihood  = -625.38558                    Prob > chi2        =    0.0000
```

outcome	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
treatment	-.160608	.5796716	-0.28	0.782	-1.296744	.9755275
month	-.390956	.0443707	-8.81	0.000	-.4779209	-.3039911
trt_month	-.1367758	.0679947	-2.01	0.044	-.270043	-.0035085
_cons	-1.618795	.4303891	-3.76	0.000	-2.462342	-.7752477
/lnsig2u	2.775749	.1890237			2.405269	3.146228
sigma_u	4.006325	.3786451			3.328876	4.821641
rho	.8298976	.026684			.7710804	.8760322

```
Likelihood-ratio test of rho=0: chibar2(01) =   565.24 Prob >= chibar2 = 0.000
```

The estimated regression coefficients are given in the usual format. The value next to `sigma_u` represents the estimated residual standard deviation $\sqrt{\widehat{\psi}}$ of the random intercept and the value next to `rho` represents the estimated residual intraclass correlation of the latent responses (see section 10.9.1).

We can use the `or` option to obtain exponentiated regression coefficients, which are interpreted as conditional odds ratios here. Instead of refitting the model, we can simply change the way the results are displayed using the following short `xtlogit` command (known as "replaying the estimation results" in Stata parlance):

```
. xtlogit, or
Random-effects logistic regression              Number of obs      =      1908
Group variable: patient                         Number of groups   =       294
Random effects u_i ~ Gaussian                   Obs per group: min =         1
                                                               avg =       6.5
                                                               max =         7
                                                Wald chi2(3)       =    150.65
Log likelihood  = -625.38558                    Prob > chi2        =    0.0000
```

outcome	OR	Std. Err.	z	P>|z|	[95% Conf.	Interval]
treatment	.8516258	.4936633	-0.28	0.782	.2734207	2.652566
month	.6764099	.0300128	-8.81	0.000	.6200712	.7378675
trt_month	.8721658	.0593027	-2.01	0.044	.7633467	.9964976
_cons	.1981373	.0852762	-3.76	0.000	.0852351	.4605897
/lnsig2u	2.775749	.1890237			2.405269	3.146228
sigma_u	4.006325	.3786451			3.328876	4.821641
rho	.8298976	.026684			.7710804	.8760322

```
Likelihood-ratio test of rho=0: chibar2(01) =   565.24 Prob >= chibar2 = 0.000
```

The estimated odds ratios and their 95% confidence intervals are also given in table 10.2. We see that the estimated conditional odds (given ζ_j) for a subject in the itraconazole group are multiplied by 0.68 every month and the conditional odds for a subject in the terbinafine group are multiplied by 0.59 ($= 0.6764099 \times 0.8721658$) every month. In terms of percentage change in estimated odds, $100\%(\widehat{\text{OR}} - 1)$, the conditional odds decrease 32% [$-32\% = 100\%(0.6764099 - 1)$] per month in the itraconazole group and 41% [$-41\% = 100\%(0.6764099 \times 0.8721658 - 1)$] per month in the terbinafine group. (the difference between the kind of effects estimated in random-intercept logistic regression and ordinary logistic regression is discussed in section 10.8).

Table 10.2: Estimates for toenail data

	Marginal effects				Conditional effects			
	Ordinary logistic		GEE† logistic		Random int. logistic		Conditional logistic	
Parameter	OR	(95% CI)	OR	(95% CI)⋆	OR	(95% CI)	OR	(95% CI)
Fixed part								
$\exp(\beta_2)$ [`treatment`]	1.00	(0.74, 1.36)	1.01	(0.61, 1.68)	0.85	(0.27, 2.65)		
$\exp(\beta_3)$ [`month`]	0.84	(0.81, 0.88)	0.84	(0.79, 0.89)	0.68	(0.62, 0.74)	0.68	(0.62, 0.75)
$\exp(\beta_4)$ [`trt_month`]	0.93	(0.87, 1.01)	0.93	(0.83, 1.03)	0.87	(0.76, 1.00)	0.91	(0.78, 1.05)
Random part								
ψ					16.08			
ρ					0.83			
Log likelihood	−908.01				−625.39		−188.94•	

†Using exchangeable working correlation
⋆Based on the sandwich estimator
•Log conditional likelihood

10.7.2 Using xtmelogit

The syntax for `xtmelogit` is analogous to that for `xtmixed` except that we also specify the number of quadrature points, or integration points, using the `intpoints()` option

```
. xtmelogit outcome treatment month trt_month || patient:, intpoints(30)
Mixed-effects logistic regression               Number of obs      =      1908
Group variable: patient                         Number of groups   =       294
                                                Obs per group: min =         1
                                                               avg =       6.5
                                                               max =         7
Integration points =  30                        Wald chi2(3)       =    150.52
Log likelihood = -625.39709                     Prob > chi2        =    0.0000
```

outcome	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
treatment	-.1609377	.584208	-0.28	0.783	-1.305964	.984089
month	-.3910603	.0443957	-8.81	0.000	-.4780744	-.3040463
trt_month	-.1368073	.0680236	-2.01	0.044	-.270131	-.0034836
_cons	-1.618961	.4347772	-3.72	0.000	-2.471108	-.7668132

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
patient: Identity				
sd(_cons)	4.008164	.3813917	3.326216	4.829926

```
LR test vs. logistic regression: chibar2(01) =   565.22 Prob>=chibar2 = 0.0000
```

The results are similar but not identical to those from `xtlogit` because the commands use slightly different versions of adaptive quadrature (see section 10.11.1). Because the estimates took some time to obtain, we store them for later use within the same Stata session:

```
. estimates store xtmelogit
```

(The command `estimates save` can be used to save the estimates in a file for use in a future Stata session.)

Estimated odds ratios can be obtained using the `or` option. `xtmelogit` can also be used with one integration point, which is equivalent to using the Laplace approximation. See section 10.11.2 for the results obtained by using this less accurate but faster method for the toenail data.

10.7.3 Using gllamm

We now introduce the user-contributed command for multilevel and latent variable modeling, called `gllamm` (stands for generalized linear latent and mixed models) by Rabe-Hesketh, Skrondal, and Pickles (2002, 2005). See also http://www.gllamm.org where you can download the `gllamm` manual, the `gllamm` companion for this book, and find many other resources.

To check whether `gllamm` is installed on your computer, use the command

```
. which gllamm
```

If the message

```
command gllamm not found as either built-in or ado-file
```

appears, install `gllamm` (assuming that you have a net-aware Stata) by using the `ssc` command:

```
. ssc install gllamm
```

Occasionally, you should update `gllamm` by using `ssc` with the `replace` option:

```
. ssc install gllamm, replace
```

Using `gllamm` for the random-intercept logistic regression model requires that we specify a logit link and binomial distribution with the `link()` and `family()` options (exactly as for the `glm` command). We also use the `nip()` option (for the number of integration points) to request that 30 integration points be used. The cluster identifier is specified in the `i()` option:

```
. gllamm outcome treatment month trt_month, i(patient) link(logit) family(binomial)
> nip(30) adapt
number of level 1 units = 1908
number of level 2 units = 294

Condition Number = 23.0763

gllamm model

log likelihood = -625.38558
```

outcome	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
treatment	-.1608751	.5802054	-0.28	0.782	-1.298057	.9763066
month	-.3911055	.0443906	-8.81	0.000	-.4781096	-.3041015
trt_month	-.136829	.0680213	-2.01	0.044	-.2701484	-.0035097
_cons	-1.620364	.4322409	-3.75	0.000	-2.46754	-.7731873

```
Variances and covariances of random effects
------------------------------------------------------------------------------

***level 2 (patient)

    var(1): 16.084107 (3.0626224)
------------------------------------------------------------------------------
```

The estimates are again similar to those from `xtlogit` and `xtmelogit`. The estimated random-intercept variance is given next to `var(1)` instead of the random-intercept standard deviation reported by `xtlogit` and `xtmelogit`, unless the `variance` option is used for the latter. We store the `gllamm` estimates for later use:

```
. estimates store gllamm
```

We can use the `eform` option to obtain estimated odds ratios, or we can alternatively use the command

```
gllamm, eform
```

to replay the estimation results after having already fit the model. We can also use the `robust` option to obtain robust standard errors based on the sandwich estimator. At the time of writing this book, `gllamm` does not accept factor variables (`i.`, `c.`, and `#`) but does accept `i.` if the `gllamm` command is preceded by the prefix command `xi:`.

10.8 Subject-specific or conditional vs. population-averaged or marginal relationships

The estimated regression coefficients for the random-intercept logistic regression model are more extreme (more different from 0) than those for the ordinary logistic regression model (see table 10.2). Correspondingly, the estimated odds ratios are more extreme (more different from 1) than those for the ordinary logistic regression model. The reason for this discrepancy is that ordinary logistic regression fits overall *population-averaged* or *marginal* probabilities, whereas random-effects logistic regression fits *subject-specific* or *conditional* probabilities for the individual patients.

This important distinction can be seen in the way the two models are written in (10.5) and (10.6). Whereas the former is for the overall or population-averaged probability, conditioning only on covariates, the latter is for the subject-specific probability, given the subject-specific random intercept ζ_j and the covariates. Odds ratios derived from these models can be referred to as population-averaged (although the averaging is applied to the probabilities) or subject-specific odds ratios, respectively.

For instance, in the random-intercept logistic regression model, we can interpret the estimated subject-specific or conditional odds ratio of 0.68 for `month` (a covariate varying *within* patient) as the odds ratio for each patient in the itraconazole group: the odds for *a given patient* hence decreases by 32% per month. In contrast, the estimated population-averaged odds ratio of 0.84 for `month` means that the odds of having onycholysis *among the patients* in the itraconazole group decreases by 16% per month.

Considering instead the odds for `treatment` (a covariate only varying *between* patients) when `month` equals 1, the estimated subject-specific or conditional odds ratio is estimated as 0.74 (=0.85×0.87) and the odds are hence 26% lower for terbinafine than for itraconazole for each subject. However, because no patients are given both terbinafine and itraconazole, it might be best to interpret the odds ratio in terms of a comparison between two patients j and j' with the same value of the random intercept $\zeta_j = \zeta_{j'}$, one of whom is given terbinafine and the other itraconazole. The estimated population-averaged or marginal odds ratio of about 0.93 (=1.00×0.93) means that the odds are 7% lower for the group of patients given terbinafine compared with the group of patients given itraconazole.

When interpreting subject-specific or conditional odds ratios, keep in mind that these are not purely based on within-subject information and are hence not free from subject-level confounding. In fact, for between-subject covariates like treatment group above, there is no within-subject information in the data. Although the odds ratios are interpreted as effects keeping the subject-specific random intercepts ζ_j constant, these random intercepts are assumed to be independent of the covariates included in the model and hence do not represent effects of unobserved *confounders*, which are by definition correlated with the covariates. Unlike fixed-effects approaches, we are therefore not controlling for unobserved confounders. Both conditional and marginal effect estimates suffer from omitted-variable bias if subject-level or other confounders are not included in the model. See section 3.7.4 for a discussion of this issue in linear random-intercept models. Section 10.14.1 is on conditional logistic regression, the fixed-effects approach in logistic regression that controls for subject-level confounders.

The population-averaged probabilities implied by the random-intercept model can be obtained by averaging the subject-specific probabilities over the random-intercept distribution. Because the random intercepts are continuous, this averaging is accomplished by integration

$$\begin{aligned}
&\Pr(y_{ij}=1|x_{2j},x_{3ij}) \\
&= \int \Pr(y_{ij}=1|x_{2j},x_{3ij},\zeta_j)\phi(\zeta_j;0,\psi)\,d\zeta_j \\
&= \int \frac{\exp(\beta_1+\beta_2x_{2j}+\beta_3x_{3ij}+\beta_4x_{2j}x_{3ij}+\zeta_j)}{1+\exp(\beta_1+\beta_2x_{2j}+\beta_3x_{3ij}+\beta_4x_{2j}x_{3ij}+\zeta_j)}\,\phi(\zeta_j;0,\psi)\,d\zeta_j \\
&\neq \frac{\exp(\beta_1+\beta_2x_{2j}+\beta_3x_{3ij}+\beta_4x_{2j}x_{3ij})}{1+\exp(\beta_1+\beta_2x_{2j}+\beta_3x_{3ij}+\beta_4x_{2j}x_{3ij})} \qquad (10.8)
\end{aligned}$$

where $\phi(\zeta_j;0,\psi)$ is the normal density function with mean zero and variance ψ.

The difference between population-averaged and subject-specific effects is due to the average of a nonlinear function not being the same as the nonlinear function of the average. In the present context, the average of the inverse logit of the linear predictor, $\beta_1+\beta_2x_{2j}+\beta_3x_{3ij}+\beta_4x_{2j}x_{3ij}+\zeta_j$, is not the same as the inverse logit of the average of the linear predictor, which is $\beta_1+\beta_2x_{2j}+\beta_3x_{3ij}+\beta_4x_{2j}x_{3ij}$. We can see this by comparing the simple average of the logits of 1 and 2 with the logit of the average of 1 and 2:

```
. display (invlogit(1) + invlogit(2))/2
.80592783
. display invlogit((1+2)/1)
.95257413
```

We can also see this in figure 10.9. Here the individual, thin, dashed curves represent subject-specific logistic curves, each with a subject-specific (randomly drawn) intercept. These are inverse logit functions of the subject-specific linear predictors (here the linear predictors are simply $\beta_1+\beta_2x_{ij}+\zeta_j$). The thick, dashed curve is the inverse logit

function of the average of the linear predictor (with $\zeta_j = 0$) and this is not the same as the average of the logistic functions shown as a thick, solid curve.

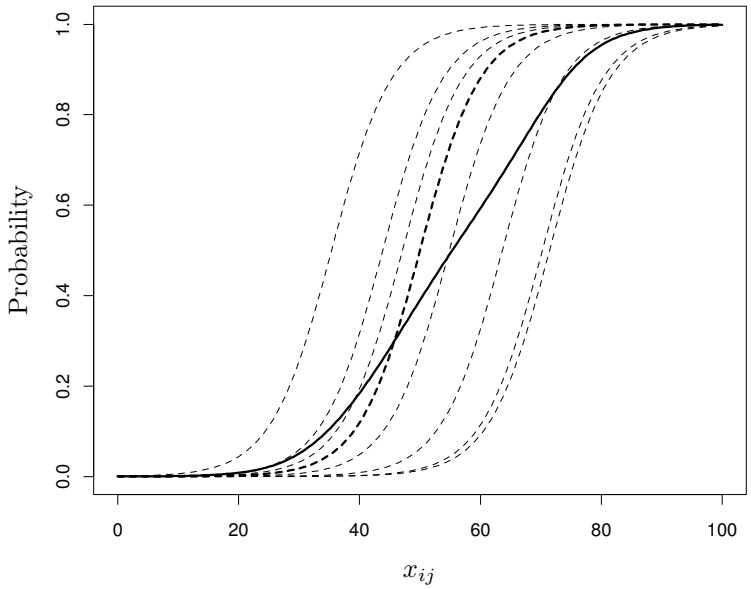


Figure 10.9: Subject-specific probabilities (thin, dashed curves), population-averaged probabilities (thick, solid curve), and population median probabilities (thick, dashed curve) for random-intercept logistic regression

The average curve has a different shape than the subject-specific curves. Specifically, the effect of x_{ij} on the average curve is smaller than the effect of x_{ij} on the subject-specific curves. However, the population median probability is the same as the subject-specific probability evaluated at the median of ζ_j ($\zeta_j = 0$), shown as the thick, dashed curve, because the inverse logit function is a strictly increasing function.

Another way of understanding why the subject-specific effects are more extreme than the population-averaged effects is by writing the random-intercept logistic regression model as a latent-response model:

$$y_{ij}^* = \beta_1 + \beta_2 x_{2j} + \beta_3 x_{3ij} + \beta_4 x_{2j} x_{3ij} + \underbrace{\zeta_j + \epsilon_{ij}}_{\xi_{ij}}$$

The total residual variance is

$$\mathrm{Var}(\xi_{ij}) = \psi + \pi^2/3$$

estimated as $\widehat{\psi} + \pi^2/3 = 16.08 + 3.29 = 19.37$, which is much greater than the residual variance of about 3.29 for an ordinary logistic regression model. As we have already seen in figure 10.4 for probit models, the slope in the model for y_i^* has to increase when the residual standard deviation increases to produce an equivalent curve for the marginal

probability that the observed response is 1. Therefore, the regression coefficients of the random-intercept model (representing subject-specific effects) must be larger in absolute value than those of the ordinary logistic regression model (representing population-averaged effects) to obtain a good fit of the model-implied marginal probabilities to the corresponding sample proportions (see exercise 10.10). In section 10.13, we will obtain predicted subject-specific and population-averaged probabilities for the toenail data.

Having described subject-specific and population-averaged probabilities or expectations of y_{ij}, for given covariate values, we now consider the corresponding variances. The subject-specific or conditional variance is

$$\mathrm{Var}(y_{ij}|\mathbf{x}_{ij},\zeta_j) \;=\; \Pr(y_{ij}=1|\mathbf{x}_{ij},\zeta_j)\{1-\Pr(y_{ij}=1|\mathbf{x}_{ij},\zeta_j)\}$$

and the population-averaged or marginal variance (obtained by integrating over ζ_j) is

$$\mathrm{Var}(y_{ij}|\mathbf{x}_{ij}) \;=\; \Pr(y_{ij}=1|\mathbf{x}_{ij})\{1-\Pr(y_{ij}=1|\mathbf{x}_{ij})\}$$

We see that the random-intercept variance ψ does not affect the relationship between the marginal variance and the marginal mean. This is in contrast to models for counts described in chapter 13, where a random intercept (with $\psi > 0$) produces so-called overdispersion, with a larger marginal variance for a given marginal mean than the model without a random intercept ($\psi = 0$). Contrary to widespread belief, overdispersion is impossible for dichotomous responses (Skrondal and Rabe-Hesketh 2007).

10.9 Measures of dependence and heterogeneity

10.9.1 Conditional or residual intraclass correlation of the latent responses

Returning to the latent-response formulation, the dependence among the dichotomous responses for the same subject (or the between-subject heterogeneity) can be quantified by the *conditional intraclass correlation* or *residual intraclass correlation* ρ of the latent responses y^*_{ij} given the covariates:

$$\rho \equiv \mathrm{Cor}(y^*_{ij},y^*_{i'j}|\mathbf{x}_{ij},\mathbf{x}_{i'j}) \;=\; \mathrm{Cor}(\xi_{ij},\xi_{i'j}) \;=\; \frac{\psi}{\psi+\pi^2/3}$$

Substituting the estimated variance $\widehat{\psi} = 16.08$, we obtain an estimated conditional intraclass correlation of 0.83, which is large even for longitudinal data. The estimated intraclass correlation is also reported next to `rho` by `xtlogit`.

For probit models, the expression for the residual intraclass correlation of the latent responses is as above with $\pi^2/3$ replaced by 1.

10.9.2 Median odds ratio

Larsen et al. (2000) and Larsen and Merlo (2005) suggest a measure of heterogeneity for random-intercept models with normally distributed random intercepts. They consider repeatedly sampling two subjects with the same covariate values and forming the odds ratio comparing the subject who has the larger random intercept with the other subject. For a given pair of subjects j and j', this odds ratio is given by $\exp(|\zeta_j - \zeta_{j'}|)$ and heterogeneity is expressed as the median of these odds ratios across repeated samples.

The median and other percentiles $a > 1$ can be obtained from the cumulative distribution function

$$\Pr\{\exp(|\zeta_j - \zeta_{j'}|) \leq a\} \;=\; \Pr\left\{\frac{|\zeta_j - \zeta_{j'}|}{\sqrt{2\psi}} \leq \frac{\ln(a)}{\sqrt{2\psi}}\right\} \;=\; 2\,\Phi\left\{\frac{\ln(a)}{\sqrt{2\psi}}\right\} - 1$$

If the cumulative probability is set to $1/2$, a is the median odds ratio, $\text{OR}_{\text{median}}$:

$$2\,\Phi\left\{\frac{\ln(\text{OR}_{\text{median}})}{\sqrt{2\psi}}\right\} - 1 \;=\; 1/2$$

Solving this equation gives

$$\text{OR}_{\text{median}} \;=\; \exp\{\sqrt{2\psi}\Phi^{-1}(3/4)\}$$

Plugging in the parameter estimates, we obtain $\widehat{\text{OR}}_{\text{median}}$:

```
. display exp(sqrt(2*16.084107)*invnormal(3/4))
45.855974
```

When two subjects are chosen at random at a given time point from the same treatment group, the odds ratio comparing the subject who has the larger odds with the subject who has the smaller odds will exceed 45.83 half the time, which is a very large odds ratio. For comparison, the estimated odds ratio comparing two subjects at 20 months who had the same value of the random intercept, but one of whom received itraconazole (`treatment`=0) and the other of whom received terbinafine (`treatment`=1), is about 18 $\{= 1/\exp(-0.1608751 + 20 \times -0.136829)\}$.

10.9.3 ❖ Measures of association for observed responses at median fixed part of the model

The reason why the degree of dependence is often expressed in terms of the residual intraclass correlation for the *latent* responses y^*_{ij} is that the intraclass correlation for the observed responses y_{ij} varies according to the values of the covariates.

One may nevertheless proceed by obtaining measures of association for specific values of the covariates. In particular, Rodríguez and Elo (2003) suggest obtaining the marginal association between the binary observed responses at the sample median value

of the estimated fixed part of the model, $\widehat{\beta}_1+\widehat{\beta}_2x_{2j}+\widehat{\beta}_3x_{3ij}+\widehat{\beta}_4x_{2j}x_{3ij}$. Marginal association here refers to the fact that the associations are based on marginal probabilities (averaged over the random-intercept distribution with the maximum likelihood estimate $\widehat{\psi}$ plugged in).

Rodríguez and Elo (2003) have written a program called `xtrho` that can be used after `xtlogit`, `xtprobit`, and `xtclog` to produce such marginal association measures and their confidence intervals. The program can be downloaded by issuing the command

```
. findit xtrho
```

clicking on `st0031`, and then clicking on `click here to install`. Having downloaded `xtrho`, we run it after refitting the random-intercept logistic model with `xtlogit`:

```
. quietly xtset patient
. quietly xtlogit outcome treatment month trt_month, re intpoints(30)
. xtrho
Measures of intra-class manifest association in random-effects logit
Evaluated at median linear predictor
Measure            |    Estimate     [95% Conf.Interval]
-------------------+-----------------------------------
Marginal prob.     |     .250812     .217334     .283389
Joint prob.        |     .178265     .139538     .217568
Odds ratio         |     22.9189     16.2512     32.6823
Pearson's r        |      .61392     .542645     .675887
Yule's Q           |     .916384     .884066     .940622
```

We see that for a patient whose fixed part of the linear predictor is equal to the sample median, the marginal probability of having onycholysis (a measure of toenail infection) at an occasion is estimated as 0.25 and the joint probability of having onycholysis at two occasions is estimated as 0.18. From the estimated joint probabilities for the responses 00, 10, 01, and 11 in the 2×2 table for two occasions (with linear predictor equal to the sample median), `xtrho` estimates various measures of association for onycholysis for two occasions, given that the fixed part of the linear predictor equals the sample median.

The estimated odds ratio of 22.92 means that the odds of onycholysis at one of the two occasions is almost 23 times as high for a patient who had onycholysis at the other occasion as for a patient with the same characteristics who did not have onycholysis at the other occasion. The estimated Pearson correlation of 0.61 for the observed responses is lower than the estimated residual correlation for the latent responses of 0.83, as would be expected from statistical theory. Squaring the Pearson correlation, we see that onycholysis at one occasion explains about 36% of the variation in onycholysis at the other occasion.

We can use the `detail` option to obtain the above measures of associations evaluated at sample percentiles other than the median. We can also use Rodríguez and Elo's (2003) `xtrhoi` command to obtain measures of associations for other values of the fixed part of the linear predictor and/or other values of the variance of the random-intercept distribution.

Note that `xtrho` and `xtrhoi` assume that the fixed part of the linear predictor is the same across occasions. However, in the toenail example, `month` must change between any two occasions within a patient, and the linear predictor is a function of `month`. Considering two occasions with `month` equal to 3 and 6, the odds ratio is estimated as 25.6 for patients in the control group and 29.4 for patients in the treatment group. A do-file that produces the 2×2 tables by using `gllamm` and `gllapred` with the `ll` option can be copied into the working directory with the command

```
copy http://www.stata-press.com/data/mlmus3/ch10table.do ch10table.do
```

10.10 Inference for random-intercept logistic models

10.10.1 Tests and confidence intervals for odds ratios

As discussed earlier, we can interpret the regression coefficient β as the difference in log odds associated with a unit change in the corresponding covariate, and we can interpret the exponentiated regression coefficient as an odds ratio, $\text{OR} = \exp(\beta)$. The relevant null hypothesis for odds ratios usually is H_0: $\text{OR} = 1$, and this corresponds directly to the null hypothesis that the corresponding regression coefficient is zero, H_0: $\beta = 0$.

Wald tests and z tests can be used for regression coefficients just as described in section 3.6.1 for linear models. Ninety-five percent Wald confidence intervals for individual regression coefficients are obtained using

$$\widehat{\beta} \pm z_{0.975}\,\widehat{\text{SE}}(\widehat{\beta})$$

where $z_{0.975} = 1.96$ is the 97.5th percentile of the standard normal distribution. The corresponding confidence interval for the odds ratio is obtained by exponentiating both limits of the confidence interval:

$$\exp\{\widehat{\beta} - z_{0.975}\,\widehat{\text{SE}}(\widehat{\beta})\} \quad \text{to} \quad \exp\{\widehat{\beta} + z_{0.975}\,\widehat{\text{SE}}(\widehat{\beta})\}$$

Wald tests for linear combinations of regression coefficients can be used to test the corresponding multiplicative relationships among odds for different covariate values. For instance, for the toenail data, we may want to obtain the odds ratio comparing the treatment groups after 20 months. The corresponding difference in log odds after 20 months is a linear combination of regression coefficients, namely, $\beta_2 + \beta_4 \times 20$ (see section 1.8 if this is not clear). We can test the null hypothesis that the difference in log odds is 0 and hence that the odds ratio is 1 by using the `lincom` command:

```
. lincom treatment + trt_month*20
 ( 1)  [outcome]treatment + 20*[outcome]trt_month = 0
```

outcome	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
(1)	-2.896123	1.309682	-2.21	0.027	-5.463053	-.3291935

If we require the corresponding odds ratio with a 95% confidence interval, we can use the `lincom` command with the `or` option:

```
. lincom treatment + trt_month*20, or
 ( 1)  [outcome]treatment + 20*[outcome]trt_month = 0
```

outcome	Odds Ratio	Std. Err.	z	P>|z|	[95% Conf.	Interval]
(1)	.0552369	.0723428	-2.21	0.027	.0042406	.7195038

After 20 months of treatment, the odds ratio comparing terbinafine (`treatment`=1) with itraconazole is estimated as 0.055. Such small numbers are difficult to interpret, so we can switch the groups around by taking the reciprocal of the odds ratio, 18 (= 1/0.055), which represents the odds ratio comparing itraconazole with terbinafine. Alternatively, we can always switch the comparison around by simply changing the sign of the corresponding difference in log odds in the `lincom` command:

```
lincom -(treatment + trt_month*20), or
```

If we had used factor-variable notation in the estimation command, using the syntax `i.treatment##c.month`, then the `lincom` command above would have to be replaced with

```
lincom -(1.treatment + 1.treatment#c.month*20), or
```

Multivariate Wald tests can be performed by using `testparm`. Wald tests and confidence intervals can be based on robust standard errors from the sandwich estimator. At the time of printing, robust standard errors can only be obtained using `gllamm` with the `robust` option.

Null hypotheses about individual regression coefficients or several regression coefficients can also be tested using likelihood-ratio tests. Although likelihood-ratio and Wald tests are asymptotically equivalent, the test statistics are not identical in finite samples. (See display 2.1 for the relationships between likelihood-ratio, Wald, and score tests.) If the statistics are very different, there may be a sparseness problem, for instance with mostly "1" responses or mostly "0" responses in one of the groups.

10.10.2 Tests of variance components

Both `xtlogit` and `xtmelogit` provide likelihood-ratio tests for the null hypothesis that the residual between-cluster variance ψ is zero in the last line of the output. The p-values are based on the correct asymptotic sampling distribution (not the naïve χ^2_1), as described for linear models in section 2.6.2. For the toenail data, the likelihood-ratio statistic is 565.2 giving $p < 0.001$, which suggests that a multilevel model is required.

10.11 Maximum likelihood estimation

10.11.1 ❖ Adaptive quadrature

The marginal likelihood is the joint probability of all observed responses given the observed covariates. For linear mixed models, this marginal likelihood can be evaluated and maximized relatively easily (see section 2.10). However, in generalized linear mixed models, the marginal likelihood does not have a closed form and must be evaluated by approximate methods.

To see this, we will now construct this marginal likelihood step by step for a random-intercept logistic regression model with one covariate x_j. The responses are conditionally independent given the random intercept ζ_j and the covariate x_j. Therefore, the joint probability of all the responses y_{ij} $(i = 1, \ldots, n_j)$ for cluster j given the random intercept and covariate is simply the product of the conditional probabilities of the individual responses:

$$\Pr(y_{1j}, \ldots, y_{n_j j}|x_j, \zeta_j) \;=\; \prod_{i=1}^{n_j} \Pr(y_{ij}|x_j, \zeta_j) \;=\; \prod_{i=1}^{n_j} \frac{\exp(\beta_1 + \beta_2 x_j + \zeta_j)^{y_{ij}}}{1 + \exp(\beta_1 + \beta_2 x_j + \zeta_j)}$$

In the last term

$$\frac{\exp(\beta_1 + \beta_2 x_j + \zeta_j)^{y_{ij}}}{1 + \exp(\beta_1 + \beta_2 x_j + \zeta_j)} \;=\; \begin{cases} \frac{\exp(\beta_1+\beta_2 x_j+\zeta_j)}{1+\exp(\beta_1+\beta_2 x_j+\zeta_j)} & \text{if } y_{ij} = 1 \\ \frac{1}{1+\exp(\beta_1+\beta_2 x_j+\zeta_j)} & \text{if } y_{ij} = 0 \end{cases}$$

as specified by the logistic regression model.

To obtain the marginal joint probability of the responses, not conditioning on the random intercept ζ_j (but still on the covariate x_j), we integrate out the random intercept

$$\Pr(y_{1j}, \ldots, y_{n_j j}|x_j) \;=\; \int \Pr(y_{1j}, \ldots, y_{n_j j}|x_j, \zeta_j)\, \phi(\zeta_j; 0, \psi)\, d\zeta_j \qquad (10.9)$$

where $\phi(\zeta_j, 0, \psi)$ is the normal density of ζ_j with mean 0 and variance ψ. Unfortunately, this integral does not have a closed-form expression.

The marginal likelihood is just the joint probability of all responses for all clusters. Because the clusters are mutually independent, this is given by the product of the marginal joint probabilities of the responses for the individual clusters

$$L(\beta_1, \beta_2, \psi) \;=\; \prod_{j=1}^{N} \Pr(y_{1j}, \ldots, y_{n_j j}|x_j)$$

This marginal likelihood is viewed as a function of the parameters β_1, β_2, and ψ (with the observed responses treated as given). The parameters are estimated by finding the values of β_1, β_2, and ψ that yield the largest likelihood. The search for the maximum is iterative, beginning with some initial guesses or starting values for the parameters and

updating these step by step until the maximum is reached, typically using a Newton–Raphson or expectation-maximization (EM) algorithm.

The integral over ζ_j in (10.9) can be approximated by a sum of R terms with e_r substituted for ζ_j and the normal density replaced by a weight w_r for the rth term, $r = 1, \ldots, R$,

$$\Pr(y_{1j}, \ldots, y_{n_j j}|x_j) \;\approx\; \sum_{r=1}^{R} \Pr(y_{1j}, \ldots, y_{n_j j}|x_j, \zeta_j = e_r)\, w_r$$

where e_r and w_r are called Gauss–Hermite quadrature locations and weights, respectively. This approximation can be viewed as replacing the continuous density of ζ_j with a discrete distribution with R possible values of ζ_j having probabilities $\Pr(\zeta_j = e_r)$. The Gauss–Hermite approximation is illustrated for $R = 5$ in figure 10.10. Obviously, the approximation improves when the number of points R increases.

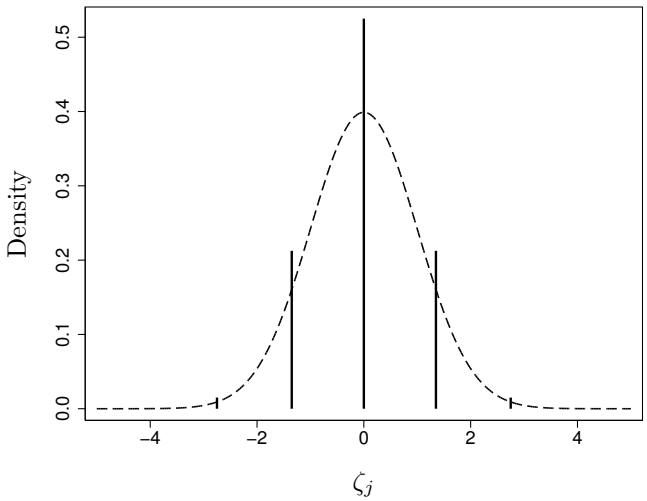


Figure 10.10: Gauss–Hermite quadrature: Approximating continuous density (dashed curve) by discrete distribution (bars)

The ordinary quadrature approximation described above can perform poorly if the function being integrated, called the *integrand*, has a sharp peak, as discussed in Rabe-Hesketh, Skrondal, and Pickles (2002, 2005). Sharp peaks can occur when the clusters are very large so that many functions (the individual response probabilities as functions of ζ_j) are multiplied to yield $\Pr(y_{1j}, \ldots, y_{n_j j}|x_j, \zeta_j)$. Similarly, if the responses are counts or continuous responses, even a few terms can result in a highly peaked function. Another potential problem is a high intraclass correlation. Here the functions being multiplied coincide with each other more closely because of the greater similarity of responses within clusters, yielding a sharper peak. In fact, the toenail data we have been analyzing, which has an estimated conditional intraclass correlation for the

latent responses of 0.83, poses real problems for estimation using ordinary quadrature, as pointed out by Lesaffre and Spiessens (2001).

The top panel in figure 10.11 shows the same five-point quadrature approximation and density of ζ_j as in figure 10.10. The solid curve is proportional to the integrand for a hypothetical cluster. Here the quadrature approximation works poorly because the peak falls between adjacent quadrature points.

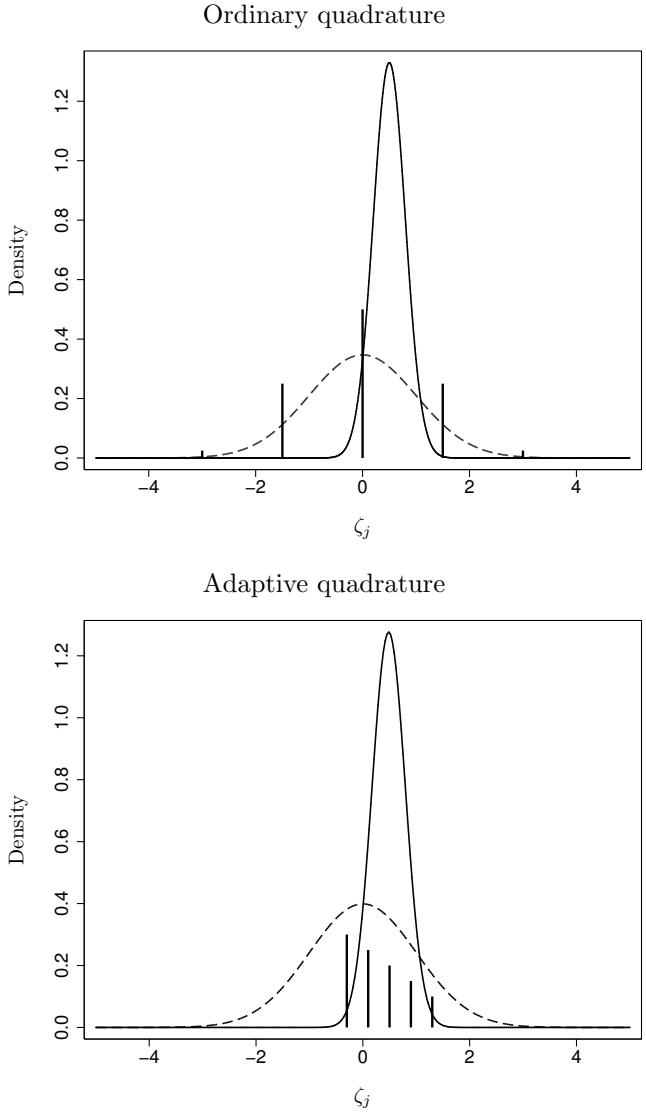


Figure 10.11: Density of ζ_j (dashed curve), normalized integrand (solid curve), and quadrature weights (bars) for ordinary quadrature and adaptive quadrature (*Source:* Rabe-Hesketh, Skrondal, and Pickles 2002)

The bottom panel of figure 10.11 shows an improved approximation, known as *adaptive quadrature*, where the locations are rescaled and translated,

$$e_{rj} = a_j + b_j e_r \tag{10.10}$$

to fall under the peak of the integrand, where a_j and b_j are cluster-specific constants. This transformation of the locations is accompanied by a transformation of the weights w_r that also depends on a_j and b_j. The method is called *adaptive* because the quadrature locations and weights are adapted to the data for the individual clusters.

To maximize the likelihood, we start with a set of initial or starting values of the parameters and then keep updating the parameters until the likelihood is maximized. The quantities a_j and b_j needed to evaluate the likelihood are functions of the parameters (as well as the data) and must therefore be updated or "readapted" when the parameters are updated.

There are two different implementations of adaptive quadrature in Stata that differ in the values used for a_j and b_j in (10.10). The method implemented in `gllamm`, which is the default method in `xtlogit` (as of Stata 10), uses the posterior mean of ζ_j for a_j and the posterior standard deviation for b_j. However, obtaining the posterior mean and standard deviation requires numerical integration so adaptive quadrature sometimes does not work when there are too few quadrature points (for example, fewer than five). Details of the algorithm are given in Rabe-Hesketh, Skrondal, and Pickles (2002, 2005) and Skrondal and Rabe-Hesketh (2004).

The method implemented in `xtmelogit`, and available in `xtlogit` with the option `intmethod(aghermite)`, uses the posterior mode of ζ_j for a_j and for b_j uses the standard deviation of the normal density that approximates the log posterior of ζ_j at the mode. An advantage of this approach is that it does not rely on numerical integration and can therefore be implemented even with one quadrature point. With one quadrature point, this version of adaptive quadrature becomes a Laplace approximation.

10.11.2 Some speed and accuracy considerations

As discussed in section 10.11.1, the likelihood involves integrals that are evaluated by numerical integration. The likelihood itself, as well as the maximum likelihood estimates, are therefore only approximate. The accuracy increases as the number of quadrature points increases, at the cost of increased computation time. We can assess whether the approximation is adequate in a given situation by repeating the analysis with a larger number of quadrature points. If we get essentially the same result, the lower number of quadrature points is likely to be adequate. Such checking should always be done before estimates are taken at face value. See section 16.4.1 for an example in `gllamm` and section 16.4.2 for an example in `xtmelogit`. For a given number of quadrature points, adaptive quadrature is more accurate than ordinary quadrature. Stata's commands therefore use adaptive quadrature by default, and we recommend using the `adapt` option in `gllamm`.

Because of numerical integration, estimation can be slow, especially if there are many random effects. The time it takes to fit a model is approximately proportional to the product of the number of quadrature points for all random effects (although this seems to be more true for `gllamm` than for `xtmelogit`). For example, if there are two random effects at level 2 (a random intercept and slope) and eight quadrature points are used for each random effect, the time will be approximately proportional to 64. Therefore, using four quadrature points for each random effect will take only about one-fourth (16/64) as long as using eight. The time is also approximately proportional to the number of observations and, for programs using numerical differentiation (`gllamm` and `xtmelogit`), to the square of the number of parameters. (For `xtlogit`, computation time increases less dramatically when the number of parameters increases because it uses analytical derivatives.)

For large problems, it may be advisable to estimate how long estimation will take before starting work on a project. In this case, we recommend fitting a similar model with fewer random effects, fewer parameters (for example, fewer covariates), or fewer observations, and then using the above approximate proportionality factors to estimate the time that will be required for the larger problem.

For random-intercept models, by far the fastest command is `xtlogit` (because it uses analytical derivatives). However, `xtlogit` cannot fit random-coefficient models or higher-level models introduced in chapter 16. For such models, `xtmelogit` or `gllamm` must be used. The quickest way of obtaining results here is using `xtmelogit` with one integration point, corresponding to the Laplace approximation. Although this method sometimes works well, it can produce severely biased estimates, especially if the clusters are small and the (true) random-intercept variance is large, as for the toenail data. For these data, we obtain the following:

```
. xtmelogit outcome treatment month trt_month || patient:, intpoints(1)
Mixed-effects logistic regression               Number of obs      =      1908
Group variable: patient                         Number of groups   =       294
                                                Obs per group: min =         1
                                                               avg =       6.5
                                                               max =         7
Integration points =   1                        Wald chi2(3)       =    131.96
Log likelihood = -627.80894                     Prob > chi2        =    0.0000
```

outcome	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
treatment	-.3070156	.6899551	-0.44	0.656	-1.659303	1.045272
month	-.4000908	.0470586	-8.50	0.000	-.492324	-.3078576
trt_month	-.1372594	.0695863	-1.97	0.049	-.2736459	-.0008728
_cons	-2.5233	.7882542	-3.20	0.001	-4.06825	-.9783501

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
patient: Identity				
sd(_cons)	4.570866	.7198949	3.356892	6.223858

```
LR test vs. logistic regression: chibar2(01) =   560.40 Prob>=chibar2 = 0.0000
Note: log-likelihood calculations are based on the Laplacian approximation.
```

We see that the estimated intercept and coefficient of `treatment` are very different from the estimates in section 10.7.1 using adaptive quadrature with 30 quadrature points. As mentioned in the previous section, `gllamm` cannot be used with only one quadrature point, and adaptive quadrature in `gllamm` typically requires at least five quadrature points.

Advice for speeding up estimation in gllamm

To speed up estimation in `gllamm`, we recommend using good starting values whenever they are available. For instance, when increasing the number of quadrature points or adding or dropping covariates, use the previous estimates as starting values. This can be done by using the `from()` option to specify a row matrix of starting values. This option should be combined with `skip` if the new model contains fewer parameters than supplied. You can also use the `copy` option if your parameters are supplied in the correct order yet are not necessarily labeled correctly. Use of these options is demonstrated in sections 11.7.2 and 16.4.1 and throughout this volume (see subject index).

The `from()` option can also be used with the `xtmelogit` command, together with the `refineopts(iterate(0))` option, to prevent `xtmelogit` from finding its own starting values (see section 16.4.2). However, the time saving is not as pronounced as in `gllamm`.

In `gllamm`, there are two other methods for speeding up estimation: collapsing the data and using spherical quadrature. These methods, which cannot be used for `xtlogit` or `xtmelogit`, are described in the following two paragraphs.

For some datasets and models, you can represent the data using fewer rows than there are observations, thus speeding up estimation. For example, if the response is dichotomous and we are using one dichotomous covariate in a two-level dataset, we can use one row of data for each combination of covariate and response (00, 01, 10, 11) for each cluster, leading to at most four rows per cluster. We can then specify a variable containing level-1 frequency weights equal to the number of observations, or level-1 units, in each cluster having each combination of the covariate and response values. Level-2 weights can be used if several clusters have the same level-2 covariates and the same number of level-1 units with the same response and level-1 covariate pattern. The `weight()` option in `gllamm` is designed for specifying frequency weights at the different levels. See exercise 10.7 for an example with level-1 weights, and see exercises 10.3 and 2.3 for examples with level-2 weights. In exercise 16.11, collapsing the data reduces computation time by about 99%. If the dataset is large, starting values could be obtained by fitting the model to a random sample of the data.

For models involving several random effects at the same level, such as two-level random-coefficient models with a random intercept and slope, the multivariate integral can be evaluated more efficiently using *spherical quadrature* instead of the default Cartesian-product quadrature. For the random intercept and slope example, Cartesian-product quadrature consists of evaluating the function being integrated on the rectangular grid of quadrature points consisting of all combinations of $\zeta_{1j} = e_1, \ldots, e_R$ and $\zeta_{2j} = e_1, \ldots, e_R$, giving R^2 terms. In contrast, spherical quadrature consists of evaluating ζ_{1j} and ζ_{2j} at values falling on concentric circles (spheres in more dimensions). The important point is that the same accuracy can now be achieved with fewer than R^2 points. For example, when $R = 8$, Cartesian-product quadrature requires 64 evaluations, while spherical quadrature requires only 44 evaluations, taking nearly 30% less time to achieve the same accuracy. Here accuracy is expressed in terms of the degree of the approximation given by $d = 2R-1$. For $R = 8$, $d = 15$. To use spherical quadrature, specify the `ip(m)` option in `gllamm` and give the degree d of the approximation by using the `nip(#)` option. Unfortunately, spherical integration is available only for certain combinations of numbers of dimensions (or numbers of random effects) and degrees of accuracy, d: For two dimensions, d can be 5, 7, 9, 11, or 15, and for more than two dimensions, d can be 5 or 7. See Rabe-Hesketh, Skrondal, and Pickles (2005) for more information.

10.12 Assigning values to random effects

Having estimated the model parameters (the β's and ψ), we may want to assign values to the random intercepts ζ_j for individual clusters j. The ζ_j are not model parameters, but as for linear models, we can treat the estimated parameters as known and then either estimate or predict ζ_j.

Such predictions are useful for making inferences for the clusters in the data, important examples being assessment of institutional performance (see section 4.8.5) or of abilities in item response theory (see exercise 10.4). The estimated or predicted values

of ζ_j should generally not be used for model diagnostics in random-intercept logistic regression because their distribution if the model is true is not known. In general, the values should also not be used to obtain cluster-specific predicted probabilities (see section 10.13.2).

10.12.1 Maximum "likelihood" estimation

As discussed for linear models in section 2.11.1, we can estimate the intercepts ζ_j by treating them as the only unknown parameters, after estimates have been plugged in for the model parameters:

$$\text{logit}\{\Pr(y_{ij}=1|\mathbf{x}_{ij},\zeta_j)\} = \underbrace{\text{offset}_{ij}}_{\widehat{\beta}_1+\widehat{\beta}_2 x_{2ij}+\cdots} + \zeta_j$$

This is a logistic regression model for cluster j with offset (a term with regression coefficient set to 1) given by the estimated fixed part of the linear predictor and with a cluster-specific intercept ζ_j.

We then maximize the corresponding likelihood for cluster j

$$\text{Likelihood}(y_{1j}, y_{2j}, \ldots, y_{n_j,j}|\mathbf{X}_j, \zeta_j)$$

with respect to ζ_j, where $\mathbf{X}_j$ is a matrix containing all covariates for cluster j. As explained in section 2.11.1, we put "likelihood" in quotes in the section heading because it differs from the marginal likelihood that is used to estimate the model parameters. Maximization can be accomplished by fitting logistic regression models to the individual clusters. First, obtain the offset from the `xtmelogit` estimates:

```
. estimates restore xtmelogit
(results xtmelogit are active now)
. predict offset, xb
```

Then use the `statsby` command to fit individual logistic regression models for each patient, specifying an offset:

```
. statsby mlest=_b[_cons], by(patient) saving(ml, replace): logit outcome,
> offset(offset)
(running logit on estimation sample)

      command:  logit outcome, offset(offset)
        mlest:  _b[_cons]
           by:  patient

Statsby groups
----+--- 1 ----+--- 2 ----+--- 3 ----+--- 4 ----+--- 5
......xx.......xx..xxx...x.x...xxxxx.xx...xxx.xxxx    50
xx.xxxxxxxxx.xxxx..xxxxxxxxx.x..xx..x.xxx.xxx.x...   100
xx.xxxxxxxxxx.xxx.x.x...x.xx.xxxxx.xx....xxx.x.xx   150
.x..x.xxxx..xxxxx.xx..xxxx..xxx.x.xxxxx.x.x.xxx...   200
.xxxxx.xx.xx..x.xxx...xx.x..xxxxx.x..x.x..x..xxxxx   250
x.xx.x..xxxxxx..x..x..xxx.x..xxxxxxxx.x.x...
```

Here we have saved the estimates under the variable name `mlest` in a file called `ml.dta` in the local directory. The `x`'s in the output indicate that the `logit` command did not converge for many clusters. For these clusters, the variable `mlest` is missing. This happens for clusters where all responses are 0 or all responses are 1 because the maximum likelihood estimate then is $-\infty$ and $+\infty$, respectively.

We now merge the estimates with the data for later use:

```
. sort patient
. merge m:1 patient using ml
. drop _merge
```

10.12.2 Empirical Bayes prediction

The ideas behind empirical Bayes prediction discussed in section 2.11.2 for linear variance-components models also apply to other generalized linear mixed models. Instead of basing inference completely on the likelihood of the responses for a cluster given the random intercept, we combine this information with the prior of the random intercept, which is just the density of the random intercept (a normal density with mean 0 and estimated variance $\widehat{\psi}$), to obtain the posterior density:

$$\text{Posterior}(\zeta_j|y_{1j},\ldots,y_{n_jj},\mathbf{X}_j) \;\propto\; \text{Prior}(\zeta_j)\times\text{Likelihood}(y_{1j},\ldots,y_{n_jj}|\mathbf{X}_j,\zeta_j)$$

The product on the right is proportional to, but not equal to, the posterior density. Obtaining the posterior density requires dividing this product by a normalizing constant that can only be obtained by numerical integration. Note that the model parameters are treated as known, and estimates are plugged into the expression for the posterior, giving what is sometimes called an estimated posterior distribution.

The estimated posterior density is no longer normal as for linear models, and hence its mode does not equal its mean. There are therefore two different types of predictions we could consider: the mean of the posterior and its mode. The first is undoubtedly the most common and is referred to as empirical Bayes prediction [sometimes called expected a posterior (EAP) prediction], whereas the second is referred to as empirical Bayes modal prediction [sometimes called modal a posterior (MAP) prediction].

The empirical Bayes prediction of the random intercept for a cluster j is the mean of the estimated posterior distribution of the random intercept. This can be obtained as

$$\widetilde{\zeta}_j = \int \zeta_j \, \text{Posterior}(\zeta_j | y_{1j}, \ldots, y_{n_j j}, \mathbf{X}_j) \, d\zeta_j$$

using numerical integration.

At the time of writing this book, the only Stata command that provides empirical Bayes predictions for generalized linear mixed models is the postestimation command `gllapred` for `gllamm` with the `u` option:

```
. estimates restore gllamm
. gllapred eb, u
```

The variable `ebm1` contains the empirical Bayes predictions. In the next section, we will produce a graph of these predictions, together with maximum likelihood estimates and empirical Bayes modal predictions.

The posterior standard deviations produced by `gllapred` in the variable `ebs1` represent the conditional standard deviations of the prediction errors, given the observed responses and treating the parameter estimates as known. The square of `ebs1` is also the conditional mean squared error of the prediction, conditional on the observed responses. As in section 2.11.3, we refer to this standard error as the *comparative standard error* because it can be used to make inferences regarding the random effects of individual clusters and to compare clusters.

We mentioned in section 2.11.3 that, for linear models, the posterior variance was the same as the unconditional mean squared error of prediction (MSEP). However, this is not true for generalized linear mixed models not having an identity link, such as the random-intercept logistic model discussed here.

There is also no longer an easy way to obtain the sampling standard deviation of the empirical Bayes predictions or diagnostic standard error (see section 2.11.3). The `ustd` option for standardized level-2 residuals therefore divides the empirical Bayes predictions by an approximation for this standard deviation, $\sqrt{\widehat{\psi} - \texttt{ebs1}^2}$ (see Skrondal and Rabe-Hesketh [2004, 231–232] or Skrondal and Rabe-Hesketh [2009] for details).

10.12.3 Empirical Bayes modal prediction

Instead of basing prediction of random effects on the mean of the posterior distribution, we can use the mode. Such empirical Bayes modal predictions are easy to obtain using the `predict` command with the `reffects` option after estimation using `xtmelogit`:

```
. estimates restore xtmelogit
. predict ebmodal, reffects
```

To see how the various methods compare, we now produce a graph of the empirical Bayes modal predictions (circles) and maximum likelihood estimates (triangles) ver-

sus the empirical Bayes predictions, connecting empirical Bayes modal predictions and maximum likelihood estimates with vertical lines.

```
. twoway (rspike mlest ebmodal ebm1 if visit==1)
> (scatter mlest  ebm1 if visit==1, msize(small) msym(th) mcol(black))
> (scatter ebmodal ebm1 if visit==1, msize(small) msym(oh) mcol(black))
> (function y=x, range(ebm1) lpatt(solid)),
> xtitle(Empirical Bayes prediction)
> legend(order(2 "Maximum likelihood" 3 "Empirical Bayes modal"))
```

The graph is given in figure 10.12.

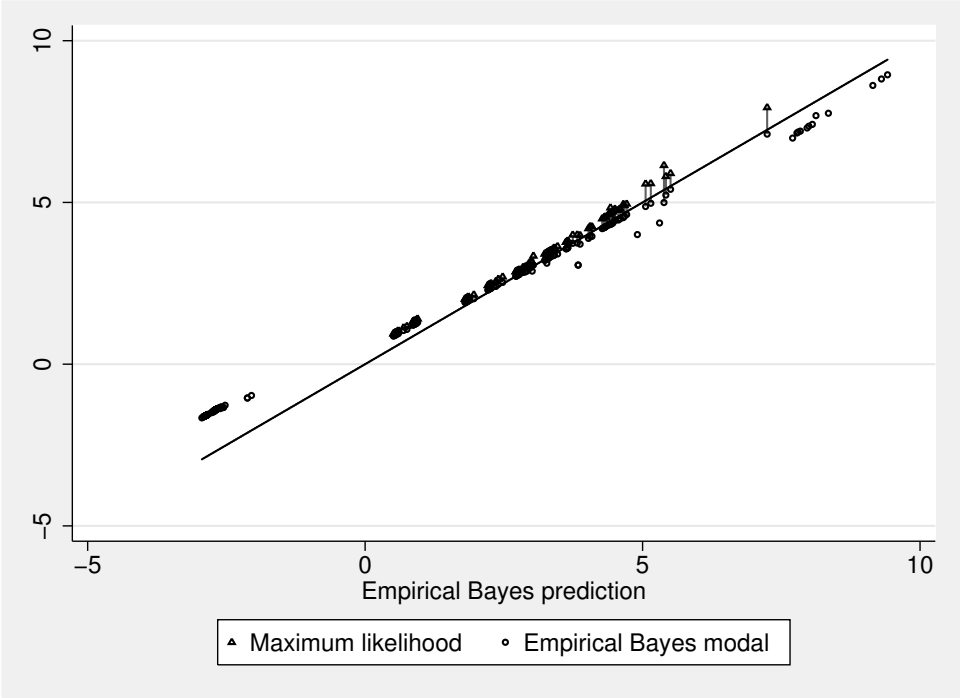


Figure 10.12: Empirical Bayes modal predictions (circles) and maximum likelihood estimates (triangles) versus empirical Bayes predictions

We see that the maximum likelihood predictions are missing when the empirical Bayes predictions are extreme (where the responses are all 0 or all 1) and that the empirical Bayes modal predictions tend to be quite close to the empirical Bayes predictions (close to the line).

We can also obtain standard errors for the random-effect predictions after estimation with `xtmelogit` by using the `predict` command with the `reses` (for "random-effects standard errors") option.

```
. predict se2, reses
```

These standard errors are the standard deviations of normal densities that approximate the posterior at the mode. They can be viewed as approximations of the posterior standard deviations provided by `gllapred`. Below we list the predictions and standard errors produced by `gllapred` (`ebm1` and `ebs1`) with those produced by `predict` after estimation with `xtmelogit` (`ebmodal` and `se2`), together with the number of 0 responses, `num0`, and the number of 1 responses, `num1`, for the first 16 patients:

```
. egen num0 = total(outcome==0), by(patient)
. egen num1 = total(outcome==1), by(patient)
. list patient num0 num1 ebm1 ebmodal ebs1 se2 if visit==1&patient<=12, noobs
```

patient	num0	num1	ebm1	ebmodal	ebs1	se2
1	4	3	3.7419957	3.736461	1.0534592	1.025574
2	4	2	1.8344596	1.934467	1.0192062	.9423445
3	6	1	.58899428	.9477552	1.3098199	1.131451
4	6	1	.60171957	.9552238	1.3148935	1.136338
6	4	3	3.2835777	3.253659	1.0118905	.9709948
7	4	3	3.4032244	3.367345	1.0307951	.9956154
9	7	0	-2.6807107	-1.399524	2.7073681	2.608825
10	7	0	-2.888319	-1.604741	2.6450981	2.503938
11	3	4	4.4649443	4.361801	1.0885138	1.072554
12	4	3	2.7279723	2.728881	.94173461	.8989795

We see that the predictions and standard errors agree reasonably well (except the extreme negative predictions). The standard errors are large when all responses are 0.

10.13 Different kinds of predicted probabilities

10.13.1 Predicted population-averaged or marginal probabilities

At the time of writing this book, population-averaged or marginal probabilities $\overline{\pi}(\mathbf{x}_{ij})$ can be predicted for random-intercept logistic regression models only by using `gllapred` after estimation using `gllamm`. This is done by evaluating the integral in (10.8) numerically for the estimated parameters and values of covariates in the data, that is, evaluating

$$\overline{\pi}(\mathbf{x}_{ij}) \equiv \int \widehat{\Pr}(y_{ij}=1|x_{2j},x_{3ij},\zeta_j)\phi(\zeta_j;0,\widehat{\psi})\,d\zeta_j$$

To obtain these predicted marginal probabilities using `gllapred`, specify the options `mu` (for the mean response, here a probability) and `marginal` (for integrating over the random-intercept distribution):

```
. estimates restore gllamm
. gllapred margprob, mu marginal
(mu will be stored in margprob)
```

We now compare predictions of population-averaged or marginal probabilities from the ordinary logit model (previously obtained under the variable name `prob`) and the random-intercept logit model, giving figure 10.13.

```
. twoway (line prob month, sort) (line margprob month, sort lpatt(dash)),
> by(treatment) legend(order(1 "Ordinary logit" 2 "Random-intercept logit"))
> xtitle(Time in months) ytitle(Fitted marginal probabilities of onycholysis)
```

The predictions are nearly identical. This is not surprising because marginal effects derived from generalized linear mixed models are close to true marginal effects even if the random-intercept distribution is misspecified (Heagerty and Kurland 2001).

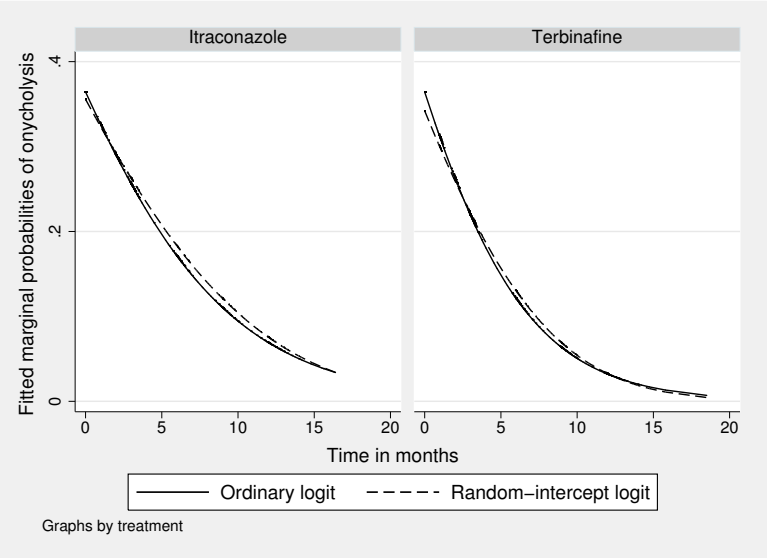


Figure 10.13: Fitted marginal probabilities using ordinary and random-intercept logistic regression

10.13.2 Predicted subject-specific probabilities

Predictions for hypothetical subjects: Conditional probabilities

Subject-specific or conditional predictions of $\widehat{\Pr}(y_{ij} = 1|x_{2j}, x_{3ij}, \zeta_j)$ for different values of ζ_j can be produced using `gllapred` with the `mu` and `us(`*varname*`)` options, where *varname*`1` is the name of the variable containing the value of the first (here the only) random effect. We now produce predicted probabilities for ζ_j equal to 0, -4, 4, -2, and 2:

```
. generate zeta1 = 0
. gllapred condprob0, mu us(zeta)
(mu will be stored in condprob0)
. generate lower1 = -4
. gllapred condprobm4, mu us(lower)
(mu will be stored in condprobm4)
. generate upper1 = 4
. gllapred condprob4, mu us(upper)
(mu will be stored in condprob4)
. replace lower1 = -2
(1908 real changes made)
. gllapred condprobm2, mu us(lower)
(mu will be stored in condprobm2)
. replace upper1 = 2
(1908 real changes made)
. gllapred condprob2, mu us(upper)
(mu will be stored in condprob2)
```

Plotting all of these conditional probabilities together with the observed proportions and marginal probabilities produces figure 10.14.

```
. twoway (line prop mn_month, sort)
> (line margprob month, sort lpatt(dash))
> (line condprob0 month, sort lpatt(shortdash_dot))
> (line condprob4 month, sort lpatt(shortdash))
> (line condprobm4 month, sort lpatt(shortdash))
> (line condprob2 month, sort lpatt(shortdash))
> (line condprobm2 month, sort lpatt(shortdash)),
> by(treatment)
> legend(order(1 "Observed proportion" 2 "Marginal probability"
>              3 "Median probability" 4 "Conditional probabilities"))
> xtitle(Time in months) ytitle(Probabilities of onycholysis)
```

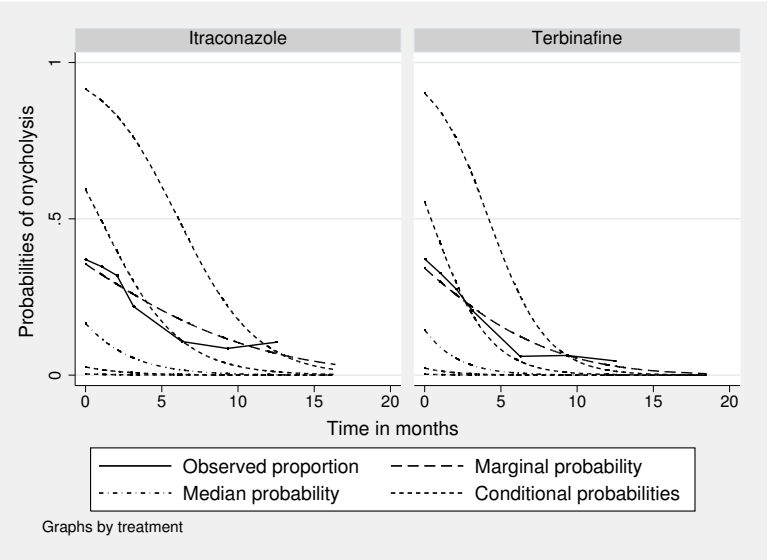


Figure 10.14: Conditional and marginal predicted probabilities for random-intercept logistic regression model

Clearly, the conditional curves have steeper downward slopes than does the marginal curve. The conditional curve represented by a dash-dot line is for $\zeta_j = 0$ and hence represents the population *median* curve.

Predictions for the subjects in the sample: Posterior mean probabilities

We may also want to predict the probability that $y_{ij} = 1$ for a given subject j. The predicted conditional probability, given the unknown random intercept ζ_j, is

$$\widehat{\Pr}(y_{ij} = 1|\mathbf{x}_{ij}, \zeta_j) = \frac{\exp(\widehat{\beta}_1 + \widehat{\beta}_2 x_{2j} + \widehat{\beta}_3 x_{3ij} + \widehat{\beta}_4 x_{2j} x_{3ij} + \zeta_j)}{1 + \exp(\widehat{\beta}_1 + \widehat{\beta}_2 x_{2j} + \widehat{\beta}_3 x_{3ij} + \widehat{\beta}_4 x_{2j} x_{3ij} + \zeta_j)}$$

Because our knowledge about ζ_j for subject j is represented by the posterior distribution, a good prediction $\widetilde{\pi}_j(\mathbf{x}_{ij})$ of the unconditional probability is obtained by integrating over the posterior distribution:

$$\begin{aligned} \widetilde{\pi}_j(\mathbf{x}_{ij}) &\equiv \int \widehat{\Pr}(y_{ij} = 1|\mathbf{x}_{ij}, \zeta_j) \times \text{Posterior}(\zeta_j|y_{1j}, \ldots, y_{n_j j}, \mathbf{X}_j)\, d\zeta_j \quad (10.11) \\ &\neq \widehat{\Pr}(y_{ij} = 1|\mathbf{x}_{ij}, \widetilde{\zeta}_j) \end{aligned}$$

This minimizes the mean squared error of prediction for known parameters. We cannot simply plug in the posterior mean of the random intercept $\widetilde{\zeta}_j$ for ζ_j in generalized linear

mixed models. The reason is that the mean of a given nonlinear function of ζ_j does not in general equal the same function evaluated at the mean of ζ_j.

The posterior means of the predicted probabilities as defined in (10.12) can be obtained using `gllapred` with the `mu` option (and not the `marginal` option) after estimation using `gllamm`:

```
. gllapred cmu, mu
(mu will be stored in cmu)
Non-adaptive log-likelihood: -625.52573
 -625.3853  -625.3856  -625.3856
log-likelihood:-625.38558
```

As of September 2008, `gllapred` can produce predicted posterior mean probabilities also for occasions where the response variable is missing. This is useful for making forecasts for a patient or for making predictions for visits where the patient did not attend the assessment. As we saw in section 10.4, such missing data occur frequently in the toenail data.

Listing `patient` and `visit` for patients 2 and 15,

```
. sort patient visit
. list patient visit if patient==2|patient==15, sepby(patient) noobs
```

patient	visit
2	1
2	2
2	3
2	4
2	5
2	6
15	1
15	2
15	3
15	4
15	5
15	7

we see that these patients each have one missing visit: visit 7 is missing for patient 2 and visit 6 is missing for patient 15. To make predictions for these visits, we must first create rows of data (or records) for these visits. A very convenient command to accomplish this is `fillin`:

```
. fillin patient visit
. list patient visit _fillin if patient==2|patient==15, sepby(patient) noobs
```

patient	visit	_fillin
2	1	0
2	2	0
2	3	0
2	4	0
2	5	0
2	6	0
2	7	1
15	1	0
15	2	0
15	3	0
15	4	0
15	5	0
15	6	1
15	7	0

`fillin` finds all values of `patient` that occur in the data and all values of `visit` and fills in all combinations of these values that do not already occur in the data, for example, patient 2 and visit 7. The command creates a new variable, `_fillin`, taking the value 1 for filled-in records and 0 for records that existed before. All variables have missing values for these new records except `patient`, `visit`, and `_fillin`.

Before we can make predictions, we must fill in values for the covariates: `treatment`, `month`, and the interaction `trt_month`. Note that, by filling in values for covariates, we are not imputing missing data but just specifying for which covariate values we would like to make predictions.

We start by filling in the appropriate values for `treatment`, taking into account that `treatment` is a time-constant variable.

```
. egen trt = mean(treatment), by(patient)
. replace treatment = trt if _fillin==1
```

We proceed by filling in the average time (month) associated with the visit number for the time-varying variable `month` by using

```
. drop mn_month
. egen mn_month = mean(month), by(treatment visit)
. replace month = mn_month if _fillin==1
```

Finally, we obtain the filled-in version of the interaction variable, `trt_month`, by multiplying the variables `treatment` and `month` that we have constructed:

```
. replace trt_month = treatment*month
```

It is important that the response variable, `outcome`, remains missing; the posterior distribution should only be based on the responses that were observed. We also cannot change the covariate values corresponding to these responses because that would change the posterior distribution.

We can now make predictions for the entire dataset by repeating the `gllapred` command (after deleting `cmu`) with the `fsample` (for "full sample") option:

```
. drop cmu
. gllapred cmu, mu fsample
(mu will be stored in cmu)
Non-adaptive log-likelihood: -625.52573
 -625.3853  -625.3856  -625.3856
log-likelihood:-625.38558
. list patient visit _fillin cmu if patient==2|patient==15, sepby(patient) noobs
```

patient	visit	_fillin	cmu
2	1	0	.54654227
2	2	0	.46888925
2	3	0	.3867953
2	4	0	.30986966
2	5	0	.12102271
2	6	0	.05282663
2	7	1	.01463992
15	1	0	.59144346
15	2	0	.47716226
15	3	0	.39755635
15	4	0	.30542907
15	5	0	.08992082
15	6	1	.01855957
15	7	0	.00015355

The predicted forecast probability for visit 7 for patient 2 hence is 0.015.

To look at some patient-specific posterior mean probability curves, we will produce trellis graphs of 16 randomly chosen patients from each treatment group. We will first randomly assign consecutive integer identifiers (1, 2, 3, etc.) to the patients in each group, in a new variable, `randomid`. We will then plot the data for patients with `randomid` 1 through 16 in each group.

To create the random identifier, we first generate a random number from the uniform distribution whenever `visit` is 1 (which happens once for each patient):

```
. set seed 1234421
. sort patient
. generate rand = runiform() if visit==1
```

Here use of the `set seed` and `sort` commands ensures that you get the same values of `randomid` as we do, because the same "seed" is used for the random-number generator. We now define a variable, `randid`, that represents the rank order of `rand` within treatment groups and is missing when `rand` is missing:

```
. by treatment (rand), sort: generate randid = _n if rand<.
```

`randid` is the required random identifier, but it is only available when `visit` is 1 and missing otherwise. We can fill in the missing values using

```
. egen randomid = mean(randid), by(patient)
```

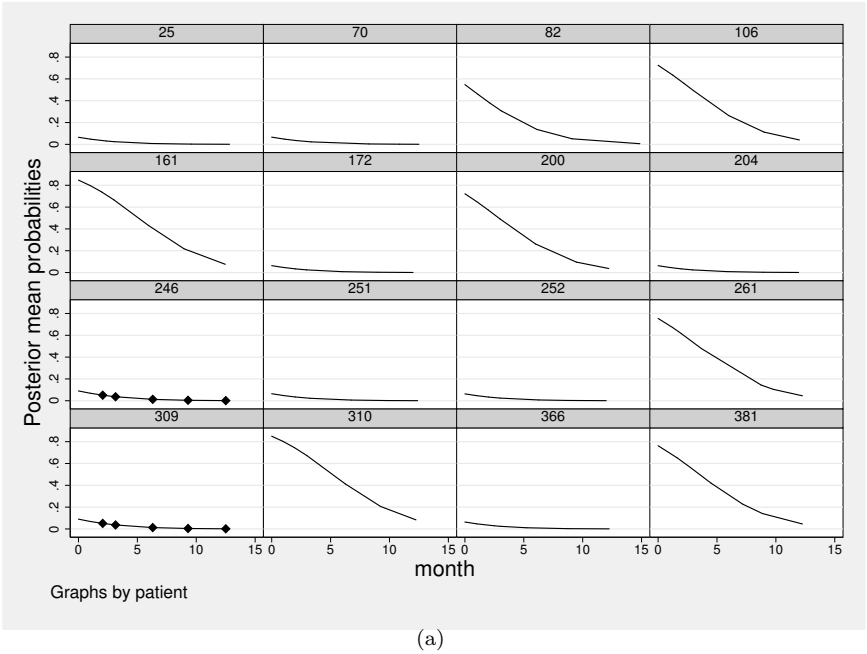
We are now ready to produce the trellis graphs:

```
. twoway (line cmu month, sort) (scatter cmu month if _fillin==1, mcol(black))
> if randomid<=16&treatment==0,  by(patient, compact legend(off)
> l1title("Posterior mean probabilities"))
```

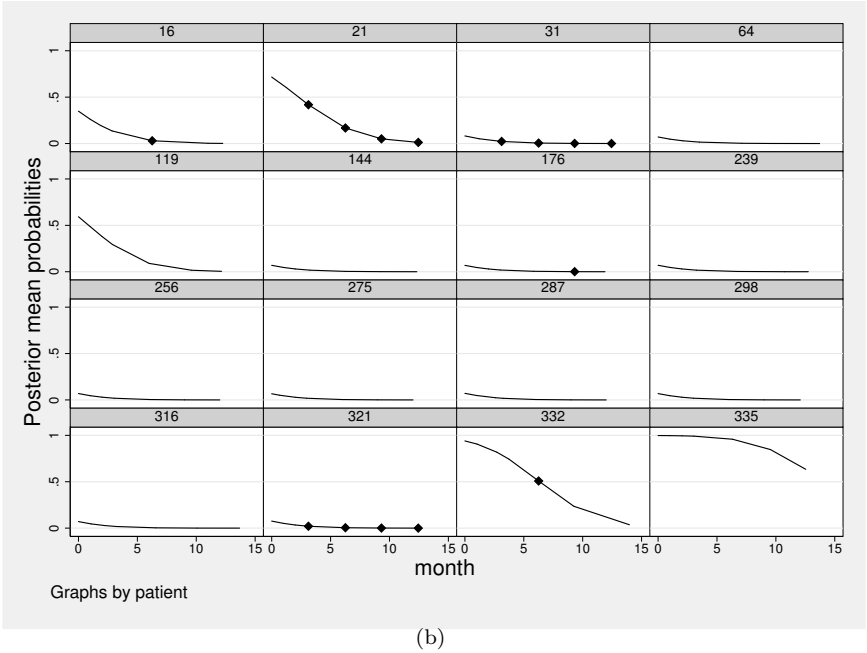
and

```
. twoway (line cmu month, sort) (scatter cmu month if _fillin==1, mcol(black))
> if randomid<=16&treatment==1,  by(patient, compact legend(off)
> l1title("Posterior mean probabilities"))
```

The graphs are shown in figure 10.15. We see that there is considerable variability in the probability trajectories of different patients within the same treatment group.



(a)



(b)

Figure 10.15: Posterior mean probabilities against time for 16 patients in the control group (a) and treatment group (b) with predictions for missing responses shown as diamonds

After estimation with `xtmelogit`, the `predict` command with the `mu` option gives the posterior mode of the predicted conditional probability $\widehat{\Pr}(y_{ij}|\mathbf{x}_{ij},\zeta_j)$ instead of the posterior mean. This is achieved by substituting the posterior mode of ζ_j into the expression for the conditional probability. [The mode of a strictly increasing function of ζ_j (here an inverse logit), is the same function evaluated at the mode of ζ_j.]

10.14 Other approaches to clustered dichotomous data

10.14.1 Conditional logistic regression

Instead of using random intercepts for clusters (patients in the toenail application), it would be tempting to use fixed intercepts by including a dummy variable for each patient (and omitting the overall intercept). This would be analogous to the fixed-effects estimator of within-patient effects discussed for linear models in section 3.7.2. However, in logistic regression, this approach would lead to inconsistent estimates of the within-patient effects unless n is large, due to what is known as the *incidental parameter problem*. Roughly speaking, this problem occurs because the number of cluster-specific intercepts (the incidental parameters) increases in tandem with the sample size (number of clusters), so that the usual asymptotic, or large-sample results, break down. Obviously, we also cannot eliminate the random intercepts in nonlinear models by simply cluster-mean-centering the responses and covariates, as in (3.12).

Instead, we can eliminate the patient-specific intercepts by constructing a likelihood that is conditional on the number of responses that take the value 1 (a sufficient statistic for the patient-specific intercept). This approach is demonstrated in display 12.2 in the chapter on nominal responses. In the linear case, assuming normality, ordinary least-squares estimation of the cluster-mean-centered model is equivalent to conditional maximum likelihood estimation. In logistic regression, conditional maximum likelihood estimation is more involved and is known as *conditional logistic regression*. Importantly, this method estimates conditional or subject-specific effects. When using conditional logistic regression, we can only estimate the effects of within-patient or time-varying covariates. Patient-specific covariates, such as `treatment`, cannot be included. However, interactions between patient-specific and time-varying variables, such as `treatment` by `month`, can be estimated.

Conditional logistic regression can be performed using Stata's `xtlogit` command with the `fe` option or using the `clogit` command (with the `or` option to obtain odds ratios):

```
. clogit outcome month trt_month, group(patient) or
note: multiple positive outcomes within groups encountered.
note: 179 groups (1141 obs) dropped because of all positive or
      all negative outcomes.
Conditional (fixed-effects) logistic regression   Number of obs   =        767
                                                  LR chi2(2)      =     290.97
                                                  Prob > chi2     =     0.0000
Log likelihood = -188.94377                       Pseudo R2       =     0.4350

------------------------------------------------------------------------------
     outcome | Odds Ratio   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       month |   .6827717   .0321547    -8.10   0.000     .6225707     .748794
   trt_month |   .9065404   .0667426    -1.33   0.183     .7847274    1.047262
------------------------------------------------------------------------------
```

The subject-specific or conditional odds ratio for the treatment effect (treatment by time interaction) is now estimated as 0.91 and is no longer significant at the 5% level. However, both this estimate and the estimate for `month`, also given in the last column of table 10.2 on page 526, are quite similar to the estimates for the random-intercept model.

The subject-specific or conditional odds ratios from conditional logistic regression represent within-effects, where patients serve as their own controls. As discussed in chapter 5, within-patient estimates cannot be confounded with omitted between-patient covariates and are hence less sensitive to model misspecification than estimates based on the random-intercept model (which makes the strong assumption that the patient-specific intercepts are independent of the covariates). A further advantage of conditional maximum likelihood estimation is that it does not make any assumptions regarding the distribution of the patient-specific effect. Therefore, it is reassuring that the conditional maximum likelihood estimates are fairly similar to the maximum likelihood estimates for the random-intercept model.

If the random-intercept model is correct, the latter estimator is more efficient and tends to yield smaller standard errors leading to smaller p-values, as we can see for the treatment by time interaction. Here the conditional logistic regression method is inefficient because, as noted in the output, 179 subjects whose responses were all 0 or all 1 cannot contribute to the analysis. This is because the conditional probabilities of these response patterns, conditioning on the total response across time, are 1 regardless of the covariates (for example, if the total is zero, all responses must be zero) and the conditional probabilities therefore do not provide any information on covariate effects.

The above model is sometimes referred to as the Chamberlain fixed-effects logit model in econometrics and is used for matched case–control studies in epidemiology. The same trick of conditioning is also used for the Rasch model in psychometrics and the conditional logit model for discrete choice and nominal responses (see section 12.2.2). Unfortunately, there is no counterpart to conditional logistic regression for probit models.

Note that dynamic models with subject-specific effects cannot be estimated consistently by simply including lagged responses in conditional logistic regression. Also,

subject-specific predictions are not possible in conditional logistic regression because no inferences are made regarding the subject-specific intercepts.

10.14.2 Generalized estimating equations (GEE)

Generalized estimating equations (GEE), first introduced in section 6.6, can be used to estimate marginal or population-averaged effects. Dependence among the responses of units in a given cluster is taken into account but treated as a nuisance, whereas this dependence is of central interest in multilevel modeling.

The basic idea of GEE is that an algorithm, known as reweighted iterated least squares, for maximum likelihood estimation of single-level generalized linear models requires only the mean structure (expectation of the response variable as a function of the covariates) and the variance function. The algorithm iterates between linearizing the model given current parameter estimates and then updating the parameters using weighted least squares, with weights determined by the variance function. In GEE, this iterative algorithm is extended to two-level data by assuming a within-cluster correlation structure, in addition to the mean structure and variance function, so that the weighted least-squares step becomes a generalized least-squares step (see section 3.10.1), and another step is required for updating the correlation matrix. GEE can be viewed as a special case of generalized methods of moments (GMM) estimation (implemented in Stata's `gmm` command).

In addition to specifying a model for the marginal relationship between the response variable and covariates, it is necessary to choose a structure for the correlations among the observed responses (conditional on covariates). The variance function follows from the Bernoulli distribution. The most common correlation structures are (see section 6.6 for some other correlation structures):

- Independence:
  Same as ordinary logistic regression
- Exchangeable:
  Same correlation for all pairs of units
- Autoregressive lag-1 [AR(1)]:
  Correlation declines exponentially with the time lag—only makes sense for longitudinal data and assumes constant time intervals between occasions (but allows gaps due to missing data).
- Unstructured:
  A different correlation for each pair of responses—only makes sense if units are not exchangeable within clusters, in the sense that the labels i attached to the units mean the same thing across clusters. For instance, it is meaningful in longitudinal data where units are occasions and the first occasion means the same thing across individuals, but not in data on students nested in schools where the numbering of students is arbitrary. In addition, each pair of unit labels i and i' must occur sufficiently often across clusters to estimate the pairwise correlations. Finally, the

number of unique unit labels, say, m, should not be too large because the number of parameters is $m(m-1)/2$.

The reason for specifying a correlation structure is that more efficient estimates (with smaller standard errors) are obtained if the specified correlation structure resembles the true dependence structure. Using ordinary logistic regression is equivalent to assuming an independence structure. GEE is therefore generally more efficient than ordinary logistic regression although the gain in precision can be meagre for balanced data (Lipsitz and Fitzmaurice 2009).

An important feature of GEE (and ordinary logistic regression) is that *marginal effects* can be consistently estimated, even if the dependence among units in clusters is not properly modeled. For this reason, correct specification of the correlation structure is downplayed by using the term "working correlations".

In GEE, the standard errors for the marginal effects are usually based on the robust sandwich estimator, which takes the dependence into account. Use of the sandwich estimator implicitly relies on there being many replications of the responses associated with each distinct combination of covariate values. Otherwise, the estimated standard errors can be biased downward. Furthermore, estimated standard errors based on the sandwich estimator can be very unreliable unless the number of clusters is large, so in this case model-based (nonrobust) standard errors may be preferable. See Lipsitz and Fitzmaurice (2009) for further discussion.

We now use GEE to estimate marginal odds ratios for the toenail data. We request an exchangeable correlation structure (the default) and robust standard errors by using `xtgee` with the `vce(robust)` and `eform` options:

```
. quietly xtset patient

. xtgee outcome treatment month trt_month, link(logit)
> family(binomial) corr(exchangeable) vce(robust) eform

GEE population-averaged model                   Number of obs      =      1908
Group variable:                     patient     Number of groups   =       294
Link:                                 logit     Obs per group: min =         1
Family:                            binomial                    avg =       6.5
Correlation:                   exchangeable                    max =         7
                                               Wald chi2(3)       =     63.44
Scale parameter:                           1   Prob > chi2        =    0.0000
                              (Std. Err. adjusted for clustering on patient)
```

outcome	Odds Ratio	Robust Std. Err.	z	P>|z|	[95% Conf.	Interval]
treatment	1.007207	.2618022	0.03	0.978	.6051549	1.676373
month	.8425856	.0253208	-5.70	0.000	.7943911	.893704
trt_month	.9252113	.0501514	-1.43	0.152	.8319576	1.028918
_cons	.5588229	.0963122	-3.38	0.001	.3986309	.7833889

These estimates are given under "GEE" in table 10.2 and can alternatively be obtained using `xtlogit` with the `pa` option.

We can display the fitted working correlation matrix by using `estat wcorrelation`:

```
. estat wcorrelation, format(%4.3f)
Estimated within-patient correlation matrix R:
```

	c1	c2	c3	c4	c5	c6	c7
r1	1.000						
r2	0.422	1.000					
r3	0.422	0.422	1.000				
r4	0.422	0.422	0.422	1.000			
r5	0.422	0.422	0.422	0.422	1.000		
r6	0.422	0.422	0.422	0.422	0.422	1.000	
r7	0.422	0.422	0.422	0.422	0.422	0.422	1.000

A problem with the exchangeable correlation structure is that the true marginal (over the random effects) correlation of the responses is in general not constant but varies according to values of the observed covariates. Using Pearson correlations for dichotomous responses is also somewhat peculiar because the odds ratio is the measure of association in logistic regression.

GEE is an *estimation method* that does not require the specification of a full statistical model. While the mean structure, variance function, and correlation structure are specified, it may not be possible to find a statistical model with such a structure. As we already pointed out, it may not be possible to specify a model for binary responses where the residual Pearson correlation matrix is exchangeable. For this reason, the approach is called an estimating equation approach rather than a modeling approach. This is in stark contrast to multilevel modeling, where statistical models are explicitly specified.

The fact that no full statistical model is specified has three important implications. First, there is no likelihood and therefore likelihood-ratio tests cannot be used. Instead, comparison of nested models typically proceeds by using Wald-tests. Unless the sample size is large, this approach may be problematic because it is known that these tests do not work as well as likelihood-ratio tests in ordinary logistic regression. Second, it is not possible to simulate or predict individual responses based on the estimates from GEE (see section 10.13.2 for prediction and forecasting based on multilevel models). Third, GEE does not share the useful property of ML that estimators are consistent when data are missing at random (MAR). Although GEE produces consistent estimates of marginal effects if the probability of responses being missing is covariate dependent [and for the special case of responses missing completely at random (MCAR)], it produces inconsistent estimates if the probability of a response being missing for a unit depends on observed responses for other units in the same cluster. Such missingness is likely to occur in longitudinal data where dropout could depend on a subjects' previous responses (see sections 5.8.1 and 13.12).

10.15 Summary and further reading

We have described various approaches to modeling clustered dichotomous data, focusing on random-intercept models for longitudinal data. Alternatives to multilevel modeling, such as conditional maximum likelihood estimation and generalized estimating equations, have also been briefly discussed. The important distinction between conditional or subject-specific effects and marginal or population-averaged effects has been emphasized.

We have described adaptive quadrature for maximum likelihood estimation and pointed out that you need to make sure that a sufficient number of quadrature points have been used for a given model and application. We have demonstrated the use of a variety of predictions, either cluster-specific predictions, based on empirical Bayes, or population-averaged predictions. Keep in mind that consistent estimation in logistic regression models with random effects in principle requires a completely correct model specification. Diagnostics for generalized linear mixed models are still being developed.

We did not cover random-coefficient models for binary responses in this chapter but have included two exercises (10.3 and 10.8), with solutions provided, involving these models. The issues discussed in chapter 4 regarding linear models with random coefficients are also relevant for other generalized linear mixed models. The syntax for random-coefficient logistic models is analogous to the syntax for linear random-coefficient models except that `xtmixed` is replaced with `xtmelogit` and `gllamm` is used with a different link function and distribution (the syntax for linear random-coefficient models in `gllamm` can be found in the `gllamm` companion). Three-level random-coefficient logistic models for binary responses are discussed in chapter 16. In chapter 11, `gllamm` will be used to fit random-coefficient ordinal logistic regression models; see section 11.7.2.

Dynamic or lagged-response models for binary responses have not been discussed. The reason is that such models, sometimes called transition models in this context, can suffer from similar kinds of endogeneity problems as those discussed for dynamic models with random intercepts in chapter 5 of volume I. However, these problems are not as straightforward to address for binary responses (but see Wooldridge [2005]).

We have discussed the most common link functions for dichotomous responses, namely, logit and probit links. A third link that is sometimes used is the complementary log-log link, which is introduced in section 14.6. Dichotomous responses are sometimes aggregated into counts, giving the number of successes y_i in n_i trials for unit i. In this situation, it is usually assumed that y_i has a binomial(n_i,π_i) distribution. `xtmelogit` can then be used as for dichotomous responses but with the `binomial()` option to specify the variable containing the values n_i. Similarly, `gllamm` can be used with the binomial distribution and any of the link functions together with the `denom()` option to specify the variable containing n_i.

Good introductions to single-level logistic regression include Collett (2003a), Long (1997), and Hosmer and Lemeshow (2000). Logistic and other types of regression using Stata are discussed by Long and Freese (2006), primarily with examples from social science, and by Vittinghoff et al. (2005), with examples from medicine.

Generalized linear mixed models are described in the books by McCulloch, Searle, and Neuhaus (2008), Skrondal and Rabe-Hesketh (2004), Molenberghs and Verbeke (2005), and Hedeker and Gibbons (2006). See also Goldstein (2011), Raudenbush and Bryk (2002), and volume 3 of the anthology by Skrondal and Rabe-Hesketh (2010). Several examples with dichotomous responses are discussed in Skrondal and Rabe-Hesketh (2004, chap. 9). Guo and Zhao (2000) is a good introductory paper on multilevel modeling of binary data with applications in social science. We also recommend the book chapter by Rabe-Hesketh and Skrondal (2009), the article by Agresti et al. (2000), and the encyclopedia entry by Hedeker (2005) for overviews of generalized linear mixed models. Detailed accounts of generalized estimating equations are given in Hardin and Hilbe (2003), Diggle et al. (2002), and Lipsitz and Fitzmaurice (2009).

Exercises 10.1, 10.2, 10.3, and 10.6 are on longitudinal or panel data. There are also exercises on cross-sectional datasets on students nested in schools (10.7 and 10.8), cows nested in herds (10.5), questions nested in respondents (10.4) and wine bottles nested in judges (10.9). Exercise 10.2 involves GEE, whereas exercises 10.4 and 10.6 involve conditional logistic regression. The latter exercise also asks you to perform a Hausman test. Exercises 10.3 and 10.8 consider random-coefficient models for dichotomous responses (solutions are provided for both exercises). Exercise 10.4 introduces the idea of item-response theory, and exercise 10.8 shows how `gllamm` can be used to fit multilevel models with survey weights.

10.16 Exercises

10.1 Toenail data

1. Fit the probit version of the random-intercept model in (10.6) with `gllamm`. How many quadrature points appear to be needed using adaptive quadrature?
2. Estimate the residual intraclass correlation for the latent responses.
3. Obtain empirical Bayes predictions using both the random-intercept logit and probit models and estimate the approximate constant of proportionality between these.
4. ❖ By considering the residual standard deviations of the latent response for the logit and probit models, work out what you think the constant of proportionality should be for the logit- and probit-based empirical Bayes predictions. How does this compare with the constant estimated in step 3?

10.2 Ohio wheeze data

In this exercise, we use data from the Six Cities Study (Ware et al. 1984), previously analyzed by Fitzmaurice (1998), among others. The dataset includes 537 children from Steubenville, Ohio, who were examined annually four times from age 7 to age 10 to ascertain their wheezing status. The smoking status of the mother was also determined at the beginning of the study to investigate whether maternal smoking increases the risk of wheezing in children. The mother's smoking status is treated as time constant, although it may have changed for some mothers over time.

The dataset `wheeze.dta` has the following variables:

- `id`: child identifier (j)
- `age`: number of years since ninth birthday (x_{2ij})
- `smoking`: mother smokes regularly (1: yes; 0: no) (x_{3j})
- `y`: wheeze status (1: yes; 0: no) (y_{ij})

1. Fit the following transition model considered by Fitzmaurice (1998):

$$\text{logit}\{\Pr(y_{ij}=1|\mathbf{x}_{ij}, y_{i-1,j})\} = \beta_1 + \beta_2 x_{2ij} + \beta_3 x_{3j} + \gamma y_{i-1,j}, \quad i = 2, 3, 4$$

   where x_{2ij} is `age` and x_{3j} is `smoking`. (The lagged responses can be obtained using `by id (age), sort: generate lag = y[_n-1]`. Alternatively, use the time-series operator `L.`; see table 5.3 on page 275.)
2. Fit the following random-intercept model considered by Fitzmaurice (1998):

$$\text{logit}\{\Pr(y_{ij}=1|\mathbf{x}_{ij}, \zeta_j)\} = \beta_1 + \beta_2 x_{2ij} + \beta_3 x_{3j} + \zeta_j, \quad i = 1, 2, 3, 4$$

   It is assumed that $\zeta_j \sim N(0, \psi)$, and that ζ_j is independent across children and independent of $\mathbf{x}_{ij}$.
3. Use GEE to fit the marginal model

$$\text{logit}\{\Pr(y_{ij}=1|\mathbf{x}_{ij})\} = \beta_1 + \beta_2 x_{2ij} + \beta_3 x_{3j}, \quad i = 1, 2, 3, 4$$

   specifying an unstructured correlation matrix (`xtset` the data using `xtset id age`). Try some other correlation structures and compare the fit (using `estat wcorrelation`) to the unstructured version.
4. Interpret the estimated effects of mother's smoking status for the models in steps 1, 2, and 3.

10.3 Vaginal-bleeding data Solutions

Fitzmaurice, Laird, and Ware (2011) analyzed data from a trial reported by Machin et al. (1988). Women were randomized to receive an injection of either 100 mg or 150 mg of the long-lasting injectable contraception depot medroxyprogesterone acetate (DMPA) at the start of the trial and at three successive 90-day

intervals. In addition, the women were followed up 90 days after the final injection. Throughout the study, each woman completed a menstrual diary that recorded any vaginal bleeding pattern disturbances. The diary data were used to determine whether a woman experienced amenorrhea, defined as the absence of menstrual bleeding for at least 80 consecutive days.

The response variable for each of the four 90-day intervals is whether the woman experienced amenorrhea during the interval. Data are available on 1,151 women for the first interval, but there was considerable dropout after that.

The dataset `amenorrhea.dta` has the following variables:

- `dose`: high dose (1: yes; 0: no)
- `y1`–`y4`: responses for time intervals 1–4 (1: amenorrhea; 0: no amenorrhea)
- `wt2`: number of women with the same dose level and response pattern

1. Produce an identifier variable for women, and reshape the data to long form, stacking the responses `y1`–`y4` into one variable and creating a new variable, `occasion`, taking the values 1–4 for each woman.
2. Fit the following model considered by Fitzmaurice, Laird, and Ware (2011):

$$\text{logit}\{\Pr(y_{ij}=1|x_j,t_{ij},\zeta_j)\} \;=\; \beta_1+\beta_2 t_{ij}+\beta_3 t_{ij}^2+\beta_4 x_j t_{ij}+\beta_5 x_j t_{ij}^2+\zeta_j$$

   where $t_{ij}=1,2,3,4$ is the time interval and x_j is `dose`. It is assumed that $\zeta_j \sim N(0,\psi)$, and that ζ_j is independent across women and independent of x_j and t_{ij}. Use `gllamm` with the `weight(wt)` option to specify that `wt2` are level-2 weights.
3. Write down the above model but with a random slope of t_{ij}, and fit the model. (See section 11.7.2 for an example of a random-coefficient model fit in `gllamm`.)
4. Interpret the estimated coefficients.
5. Plot marginal predicted probabilities as a function of time, separately for women in the two treatment groups.

10.4 Verbal-aggression data

De Boeck and Wilson (2004) discuss a dataset from Vansteelandt (2000) where 316 participants were asked to imagine the following four frustrating situations where either another or oneself is to blame:

1. Bus: A bus fails to stop for me (another to blame)
2. Train: I miss a train because a clerk gave me faulty information (another to blame)
3. Store: The grocery store closes just as I am about to enter (self to blame)
4. Operator: The operator disconnects me when I have used up my last 10 cents for a call (self to blame)

For each situation, the participant was asked if it was true (yes, perhaps, or no) that

1. I would (want to) curse
2. I would (want to) scold
3. I would (want to) shout

For each of the three behaviors above, the words "want to" were both included and omitted, yielding six statements with a 3×2 factorial design (3 behaviors in 2 modes) combined with the four situations. Thus there were 24 items in total.

The dataset `aggression.dta` contains the following variables:

- `person`: subject identifier
- `item`: item (or question) identifier
- `description`: item description (situation: bus/train/store/operator; behavior: curse/scold/shout; mode: do/want)
- `i1`–`i24`: dummy variables for the items, for example, `i5` equals 1 when `item` equals 5 and 0 otherwise
- `y`: ordinal response (0: no; 1: perhaps; 2: yes)
- Person characteristics:
  - `anger`: trait anger score (STAXI, Spielberger [1988]) (w_{1j})
  - `gender`: dummy variable for being male (1: male; 0: female) (w_{2j})
- Item characteristics:
  - `do_want`: dummy variable for mode being "do" (that is, omitting words "want to") versus "want" (x_{2ij})
  - `other_self`: dummy variable for others to blame versus self to blame (x_{3ij})
  - `blame`: variable equal to 0.5 for blaming behaviors curse and scold and -1 for shout (x_{4ij})
  - `express`: variable equal to 0.5 for expressive behaviors curse and shout and -1 for scold (x_{5ij})

1. Recode the ordinal response variable `y` so that either a "2" or a "1" for the original variable becomes a "1" for the recoded variable.
2. De Boeck and Wilson (2004, sec. 2.5) consider the following "explanatory item-response model" for the dichotomous response

$$\text{logit}\{\Pr(y_{ij}=1|\mathbf{x}_{ij},\zeta_j)\} = \beta_1 + \beta_2 x_{2ij} + \beta_3 x_{3ij} + \beta_4 x_{4ij} + \beta_5 x_{5ij} + \zeta_j$$

where $\zeta_j \sim N(0,\psi)$ can be interpreted as the latent trait "verbal aggressiveness". Fit this model using `xtlogit`, and interpret the estimated coefficients. In De Boeck and Wilson (2004), the first five terms have minus signs, so their estimated coefficients have the opposite sign.

3. De Boeck and Wilson (2004, sec. 2.6) extend the above model by including a latent regression, allowing verbal aggressiveness (now denoted η_j instead of ζ_j) to depend on the person characteristics w_{1j} and w_{2j}:

$$\text{logit}\{\Pr(y_{ij}=1|\mathbf{x}_{ij},\eta_j)\} = \beta_1 + \beta_2 x_{2ij} + \beta_3 x_{3ij} + \beta_4 x_{4ij} + \beta_5 x_{5ij} + \eta_j$$

$$\eta_j = \gamma_1 w_{1j} + \gamma_2 w_{2j} + \zeta_j$$

   Substitute the level-2 model for η_j into the level-1 model for the item responses, and fit the model using `xtlogit`.

4. Use `xtlogit` to fit the "descriptive item-response model", usually called a one-parameter logistic item response (IRT) model or *Rasch model*, considered by De Boeck and Wilson (2004, sec. 2.3):

$$\text{logit}\{\Pr(y_{ij}=1|d_{1i},\ldots,d_{24,i},\zeta_j)\} = \sum_{m=1}^{24} \beta_m d_{mi} + \zeta_j$$

   where d_{mi} is a dummy variable for item i, with $d_{mi} = 1$ if $m = i$ and 0 otherwise. In De Boeck and Wilson (2004), the first term has a minus sign, so their β_m coefficients have the opposite sign; see also their page 53.

5. The model above is known as a one-parameter item-response model because there is one parameter β_m for each item. The negative of these item-specific parameters $-\beta_m$ can be interpreted as "difficulties"; the larger $-\beta_m$, the larger the latent trait (here verbal aggressiveness, but often ability) has to be to yield a given probability (for example, 0.5) of a 1 response.

   Sort the items in increasing order of the estimated difficulties. For the least and most difficult items, look up the variable `description`, and discuss whether it makes sense that these items are particularly easy and hard to endorse (requiring little and a lot of verbal aggressiveness), respectively.

6. Replace the random intercepts ζ_j with fixed parameters α_j. Set the difficulty of the first item to zero for identification and fit the model by conditional maximum likelihood. Verify that differences between estimated difficulties for the items are similar as in step 4.

7. ❖ Fit the model in step 4 using `gllamm` or `xtmelogit` (this will take longer than `xtlogit`) and obtain empirical Bayes (also called EAP) or empirical Bayes modal (also called MAP) predictions (depending on whether you fit the model in `gllamm` or `xtmelogit`, respectively) and ML estimates of the latent trait. Also obtain standard errors (for ML, this means saving `_se[_cons]` in addition to `_b[_cons]` by adding `mlse = _se[_cons]` in the `statsby` command). Does there appear to be much shrinkage? Calculate the total score (sum of item responses) for each person and plot curves of the different kinds of standard errors with total score on the x axis. Comment on what you find.

See also exercise 11.2 for further analyses of these data.

10.5 Dairy-cow data

Dohoo et al. (2001) and Dohoo, Martin, and Stryhn (2010) analyzed data on dairy cows from Reunion Island. One outcome considered was the "risk" of conception at the first insemination attempt (first service) since the previous calving. This outcome was available for several lactations (calvings) per cow.

The variables in the dataset `dairy.dta` used here are

- `cow`: cow identifier
- `herd`: herd identifier
- `region`: geographic region
- `fscr`: first service conception risk (dummy variable for cow becoming pregnant)
- `lncfs`: log of time interval (in log days) between calving and first service (insemination attempt)
- `ai`: dummy variable for artificial insemination being used (versus natural) at first service
- `heifer`: dummy variable for being a young cow that has calved only once

1. Fit a two-level random-intercept logistic regression model for the response variable `fscr`, an indicator for conception at the first insemination attempt (first service). Include a random intercept for cow and the covariates `lncfs`, `ai`, and `heifer`. (Use either `xtlogit`, `xtmelogit`, or `gllamm`.)
2. Obtain estimated odds ratios with 95% confidence intervals for the covariates and interpret them.
3. Obtain the estimated residual intraclass correlation between the latent responses for two observations on the same cow. Is there much variability in the cows' fertility?
4. Obtain the estimated median odds ratio for two randomly chosen cows with the same covariates, comparing the cow that has the larger random intercept with the cow that has the smaller random intercept.

See also exercises 8.8 and 16.1.

10.6 Union membership data

Vella and Verbeek (1998) analyzed panel data on 545 young males taken from the U.S. National Longitudinal Survey (Youth Sample) for the period 1980–1987. In this exercise, we will focus on modeling whether the men were members of unions or not.

The dataset `wagepan.dta` was provided by Wooldridge (2010) and was previously used in exercise 3.6 and *Introduction to models for longitudinal and panel data (part III)*. The subset of variables considered here is

- `nr`: person identifier (j)
- `year`: 1980–1987 (i)
- `union`: dummy variable for being a member of a union (that is, wage being set in collective bargaining agreement) (y_{ij})
- `educ`: years of schooling (x_{2j})
- `black`: dummy variable for being black (x_{3j})
- `hisp`: dummy variable for being Hispanic (x_{4j})
- `exper`: labor market experience, defined as age$-6-$`educ` (x_{5ij})
- `married`: dummy variable for being married (x_{6ij})
- `rur`: dummy variable for living in a rural area (x_{7ij})
- `nrtheast`: dummy variable for living in Northeast (x_{8ij})
- `nrthcen`: dummy variable for living in Northern Central (x_{9ij})
- `south`: dummy variable for living in South ($x_{10,ij}$)

You can use the `describe` command to get a description of the other variables in the file.

1. Use maximum likelihood to fit the random-intercept logistic regression model

$$\text{logit}\{\Pr(y_{ij}=1|\mathbf{x}_{ij},\zeta_j)\} \;=\; \beta_1+\beta_2 x_{2j}+\cdots+\beta_{11}x_{10,ij}+\zeta_j$$

   where $\zeta_j \sim N(0,\psi)$, and ζ_j is assumed to be independent across persons and independent of $\mathbf{x}_{ij}$. Use `xtlogit` because it is considerably faster than the other commands here.
2. Interpret the estimated effects of the covariates from step 1 in terms of odds ratios, and report the estimated residual intraclass correlation of the latent responses.
3. Fit the marginal model

$$\text{logit}\{\Pr(y_{ij}=1|\mathbf{x}_{ij})\} \;=\; \beta_1+\beta_2 x_{2j}+\cdots+\beta_{11}x_{10,ij}$$

   using GEE with an exchangeable working correlation structure.
4. Interpret the estimated effects of the covariates from step 3 in terms of odds ratios, and compare these estimates with those from step 1. Why are the estimates different?
5. Explore the within and between variability of the response variable and covariates listed above. For which of the covariates is it impossible to estimate an effect using a fixed-effects approach? Are there any covariates whose effects you would expect to be imprecisely estimated when using a fixed-effects approach?
6. Use conditional maximum likelihood to fit the fixed-intercept logistic regression model

$$\text{logit}\{\Pr(y_{ij}=1|\mathbf{x}_{ij})\} \;=\; \beta_1+\beta_2 x_{2j}+\cdots+\beta_{11}x_{10,ij}+\alpha_j$$

where the α_j are unknown person-specific parameters.

7. Interpret the estimated effects of the covariates from step 6 in terms of odds ratios, and compare these estimates with those from step 1. Why are the estimates different?
8. Perform a Hausman test to assess the validity of the random-intercept model. What do you conclude?
9. Fit the probit versions of the random-intercept model from step 1 using `xtprobit`. Which type of model do you find easiest to interpret?

10.7 School retention in Thailand data

A national survey of primary education was conducted in Thailand in 1988. The data were previously analyzed by Raudenbush and Bhumirat (1992) and are distributed with the HLM software (Raudenbush et al. 2004). Here we will model the probability that a child repeats a grade any time during primary school.

The dataset `thailand.dta` has the following variables:

- `rep`: dummy variable for child having repeated a grade during primary school (y_{ij})
- `schoolid`: school identifier (j)
- `pped`: dummy variable for child having preprimary experience (x_{2ij})
- `male`: dummy variable for child being male (x_{3ij})
- `mses`: school mean socioeconomic status (SES) (x_{4j})
- `wt1`: number of children in the school having a given set of values of `rep`, `pped`, and `male` (level-1 frequency weights)

1. Fit the model

$$\text{logit}\{\Pr(y_{ij}=1|\mathbf{x}_{ij},\zeta_j)\} \;=\; \beta_1+\beta_2 x_{2ij}+\beta_3 x_{3ij}+\beta_4 x_{4j}+\zeta_j$$

where $\zeta_j \sim N(0,\psi)$, and ζ_j is independent across schools and independent of the covariates $\mathbf{x}_{ij}$. Use `gllamm` with the `weight(wt)` option to specify that each row in the data represents `wt1` children (level-1 units).
2. Obtain and interpret the estimated odds ratios and the estimated residual intraschool correlation of the latent responses.
3. Use `gllapred` to obtain empirical Bayes predictions of the probability of repeating a grade. These probabilities will be specific to the schools, as well as dependent on the student-level predictors.
   a. List the values of `male`, `pped`, `rep`, `wt1`, and the predicted probabilities for the school with `schoolid` equal to 10104. Explain why the predicted probabilities are greater than 0 although none of the children in the sample from that school have been retained. For comparison, list the same variables for the school with `schoolid` equal to 10105.

b. Produce box plots of the predicted probabilities for each school by `male` and `pped` (for instance, using `by(male)` and `over(pped)`). To ensure that each school contributes no more than four probabilities to the graph (one for each combination of the student-level covariates), use only responses where `rep` is 0 (that is, `if rep==0`). Do the schools appear to be variable in their retention probabilities?

10.8 PISA data

Solutions

Here we consider data from the 2000 Program for International Student Assessment (PISA) conducted by the Organization for Economic Cooperation and Development (OECD 2000) that are made available with permission from Mariann Lemke. The survey assessed educational attainment of 15-year-olds in 43 countries in various areas, with an emphasis on reading. Following Rabe-Hesketh and Skrondal (2006), we will analyze reading proficiency, treated as dichotomous (1: proficient; 0: not proficient), for the U.S. sample.

The variables in the dataset `pisaUSA2000.dta` are

- `id_school`: school identifier
- `pass_read`: dummy variable for being proficient in reading
- `female`: dummy variable for student being female
- `isei`: international socioeconomic index
- `high_school`: dummy variable for highest education level by either parent being high school
- `college`: dummy variable for highest education level by either parent being college
- `test_lang`: dummy variable for test language (English) being spoken at home
- `one_for`: dummy variable for one parent being foreign born
- `both_for`: dummy variable for both parents being foreign born
- `w_fstuwt`: student-level or level-1 survey weights
- `wnrschbq`: school-level or level-2 survey weights

1. Fit a logistic regression model with `pass_read` as the response variable and the variables `female` to `both_for` above as covariates and with a random intercept for schools using `gllamm`. (Use the default eight quadrature points.)
2. Fit the model from step 1 with the school mean of `isei` as an additional covariate. (Use the estimates from step 1 as starting values.)
3. Interpret the estimated coefficients of `isei` and school mean `isei` and comment on the change in the other parameter estimates due to adding school mean `isei`.
4. From the estimates in step 2, obtain an estimate of the between-school effect of socioeconomic status.
5. Obtain robust standard errors using the command `gllamm, robust`, and compare them with the model-based standard errors.

6. Add a random coefficient of `isei`, and compare the random-intercept and random-coefficient models using a likelihood-ratio test. Use the estimates from step 2 (or step 5) as starting values, adding zeros for the two additional parameters as shown in section 11.7.2.
7. ❖ In this survey, schools were sampled with unequal probabilities, π_j, and given that a school was sampled, students were sampled from the school with unequal probabilities $\pi_{i|j}$. The reciprocals of these probabilities are given as school- and student-level survey weights, `wnrschbg` ($w_j = 1/\pi_j$) and `w_fstuwt` ($w_{i|j} = 1/\pi_{i|j}$), respectively. As discussed in Rabe-Hesketh and Skrondal (2006), incorporating survey weights in multilevel models using a so-called *pseudolikelihood* approach can lead to biased estimates, particularly if the level-1 weights $w_{i|j}$ are different from 1 and if the cluster sizes are small. Neither of these issues arises here, so implement pseudomaximum likelihood estimation as follows:
   a. Rescale the student-level weights by dividing them by their cluster means [this is scaling method 2 in Rabe-Hesketh and Skrondal (2006)].
   b. Rename the level-2 weights and rescaled level-1 weights to `wt2` and `wt1`, respectively.
   c. Run the `gllamm` command from step 2 above with the additional option `pweight(wt)`. (Only the stub of the weight variables is specified; `gllamm` will look for the level-1 weights under `wt1` and the level-2 weights under `wt2`.) Use the estimates from step 2 as starting values.
   d. Compare the estimates with those from step 2. Robust standard errors are computed by `gllamm` because model-based standard errors are not appropriate with survey weights.

10.9 Wine-tasting data

Tutz and Hennevogl (1996) and Fahrmeir and Tutz (2001) analyzed data on the bitterness of white wines from Randall (1989).

The dataset `wine.dta` has the following variables:

- `bitter`: dummy variable for bottle being classified as bitter (y_{ij})
- `judge`: judge identifier (j)
- `temp`: temperature (low=1; high=0) x_{2ij}
- `contact`: skin contact when pressing the grapes (yes=1; no=0) x_{3ij}
- `repl`: replication

Interest concerns whether conditions that can be controlled while pressing the grapes, such as temperature and skin contact, influence the bitterness. For each combination of temperature and skin contact, two bottles of white wine were randomly chosen. The bitterness of each bottle was rated by the same nine judges, who were selected and trained for the ability to detect bitterness. Here we consider the binary response "bitter" or "nonbitter".

To allow the judgment of bitterness to vary between judges, a random-intercept logistic model is specified

$$\ln\left\{\frac{\Pr(y_{ij}=1|x_{2ij},x_{3ij},\zeta_j)}{\Pr(y_{ij}=0|x_{2ij},x_{3ij},\zeta_j)}\right\} = \beta_1+\beta_2 x_{2ij}+\beta_3 x_{3ij}+\zeta_j$$

where $\zeta_j \sim N(0,\psi)$. The random intercepts are assumed to be independent across judges and independent of the covariates x_{2ij} and x_{3ij}. Maximum likelihood estimates and estimated standard errors for the model are given in table 10.3 below.

Table 10.3: Maximum likelihood estimates for bitterness model

	Est	(SE)
Fixed part		
β_1	−1.50	(0.90)
β_2	4.26	(1.30)
β_3	2.63	(1.00)
Random part		
ψ	2.80	
Log likelihood	−25.86	

1. Interpret the estimated effects of the covariates as odds ratios.
2. State the expression for the residual intraclass correlation of the latent responses for the above model and estimate this intraclass correlation.
3. Consider two bottles characterized by the same covariates and judged by two randomly chosen judges. Estimate the median odds ratio comparing the judge who has the larger random intercept with the judge who has the smaller random intercept.
4. ❖ Based on the estimates given in table 10.3, provide an approximate estimate of ψ if a probit model is used instead of a logit model. Assume that the estimated residual intraclass correlation of the latent responses is the same as for the logit model.
5. ❖ Based on the estimates given in the table, provide approximate estimates for the marginal effects of x_{2ij} and x_{3ij} in an ordinary logistic regression model (without any random effects).

See also exercise 11.8 for further analysis of these data.

10.10 ❖ Random-intercept probit model

In a hypothetical study, an ordinary probit model was fit for students clustered in schools. The response was whether students gave the right answer to a question,

and the single covariate was socioeconomic status (SES). The intercept and regression coefficient of SES were estimated as $\widehat{\beta}_1 = 0.2$ and $\widehat{\beta}_2 = 1.6$, respectively. The analysis was then repeated, this time including a normally distributed random intercept for school with variance estimated as $\widehat{\psi} = 0.15$.

1. Using a latent-response formulation for the random-intercept probit model, derive the marginal probability that $y_{ij} = 1$ given SES. See page 512 and remember to replace ϵ_{ij} with $\zeta_j + \epsilon_{ij}$.
2. Obtain the values of the estimated school-specific regression coefficients for the random-intercept probit model.
3. Obtain the estimated residual intraclass correlation for the latent responses.

11 Ordinal responses

11.1 Introduction

An ordinal variable is a categorical variable with ordered categories. An example from sociology would be the response to an attitude statement such as "Murderers should be executed" in one of the ordered categories "disagree strongly", "disagree", "agree", or "agree strongly". Such questions asking about level of agreement with an attitude statement are called Likert-scale items. A medical example of an ordinal response is diagnosis of multiple sclerosis using the ordered categories "definitely not", "unlikely", "doubtful", "possible", "probable", and "certain". In education, level of proficiency ("below basic", "basic", "proficient", and "advanced") may be of interest.

In this chapter, we generalize the multilevel models for dichotomous responses that were discussed in the previous chapter to handle ordinal responses. Chapter 10 should therefore be read before embarking on this chapter. We start by introducing single-level cumulative logit and probit models for ordinal responses before extending these models to the multilevel and longitudinal setting by including random effects in the linear predictor.

Many of the issues that were discussed in the previous chapter—such as the distinction between conditional and marginal effects and the use of numerical integration for maximum likelihood estimation and empirical Bayes prediction—persist for multilevel modeling of ordinal responses. Indeed, the main difference between the logistic models considered in this and the previous chapter is that odds ratios must now be interpreted in terms of the odds of exceeding a given category.

11.2 Single-level cumulative models for ordinal responses

For simplicity, we start by introducing ordinal regression models for a single covariate x_i in the single-level case where units have index i. Just as for the dichotomous responses discussed in section 10.2, we can specify models for ordinal responses by using either a generalized linear model formulation or a latent-response formulation.

11.2.1 Generalized linear model formulation

Consider an ordinal response variable y_i with S ordinal categories denoted s ($s = 1, \ldots, S$). One way of specifying regression models for ordinal responses y_i is to let

the cumulative probability that a response is in a higher category than s, given a covariate x_i, be structured as

$$\Pr(y_i > s|x_i) \;=\; F(\beta_2 x_i - \kappa_s) \qquad s=1,\ldots,S-1 \tag{11.1}$$

where $F(\cdot)$ is a cumulative distribution function (CDF). $F(\cdot)$ is a standard normal CDF for the *ordinal probit model* and a logistic CDF for the *ordinal logit model*.

$F(\cdot)$ can be viewed as an inverse link function, denoted $h(\cdot)$ or $g^{-1}(\cdot)$, and the category-specific linear predictor ν_{is} is

$$\nu_{is} \;=\; \beta_2 x_i - \kappa_s$$

Here the κ_s are category-specific parameters, often called thresholds (the Greek letter κ is pronounced "kappa"). Notice that we have omitted the intercept β_1 because it is not identified if all the $S-1$ thresholds κ_s are free parameters (see section 11.2.4). The covariate effect β_2 is constant across categories, a property sometimes referred to as the *parallel-regressions assumption* because the linear predictors for different categories s are parallel.

It follows from the cumulative probabilities in (11.1) that the probability for a specific category s can be obtained as

$$\begin{aligned}\Pr(y_i = s|x_i) &= \Pr(y_i > s-1|x_i) - \Pr(y_i > s|x_i)\\ &= F(\beta_2 x_i - \kappa_{s-1}) - F(\beta_2 x_i - \kappa_s)\end{aligned}$$

For this reason, cumulative models for ordinal responses are sometimes called *difference models*.

Having specified the link function and linear predictor, the final ingredient for a generalized linear model is the conditional distribution of the responses. For ordinal responses, this is a multinomial distribution with category-specific probabilities, as given above. A simple example of a process following a multinomial distribution is rolling a fair die, where the probabilities for all categories $s=1,\ldots,6$ are equal to 1/6.

Cumulative models for ordinal responses differ from generalized linear models for other response types in one important way: the inverse-link function of the linear predictor $g^{-1}(\nu_{is})$ does not represent the expectation or mean of the response (given the covariates) but represents a cumulative probability. Perhaps for this reason, Stata's `glm` command cannot be used for these models; instead, these models are fit using the specialty commands `ologit` and `oprobit`.

11.2.2 Latent-response formulation

Cumulative models for ordinal responses can alternatively be viewed as linear regression models for latent (unobserved) continuous responses y_i^*,

$$y_i^* \;=\; \beta_2 x_i + \epsilon_i$$

where the conditional distribution of ϵ_i, given the observed covariate x_i, is standard normal for the ordinal probit model and standard logistic for the ordinal logit model.

Observed ordinal responses y_i are generated from the latent continuous responses y_i^* via a threshold model:

$$y_i = \begin{cases} 1 & \text{if} \quad y_i^* \leq \kappa_1 \\ 2 & \text{if} \quad \kappa_1 < y_i^* \leq \kappa_2 \\ \vdots & \vdots \quad \vdots \\ S & \text{if} \quad \kappa_{S-1} < y_i^* \end{cases}$$

This cutting up of the latent-response scale is shown for $S = 5$ categories in figure 11.1.

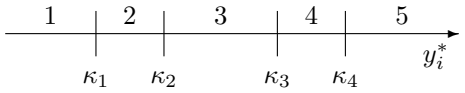


Figure 11.1: Illustration of threshold model for $S = 5$ categories

When there are no covariates and $y_i^* \sim N(0, 1)$, we obtain an ordinal probit model as shown for three categories ($S = 3$) in figure 11.2.

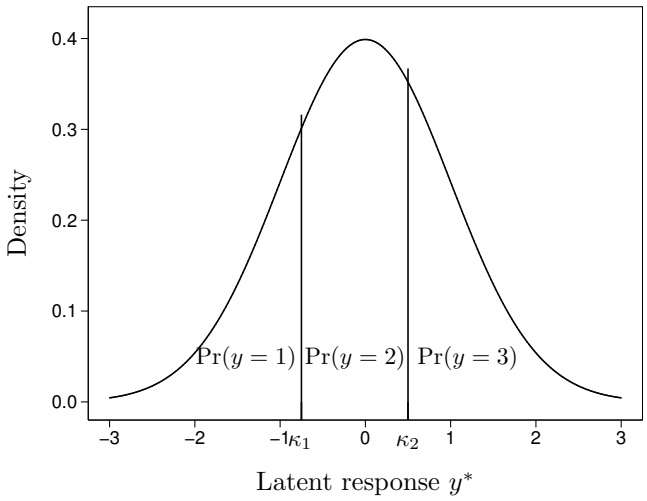


Figure 11.2: Illustration of three-category ordinal probit model without covariates

The observed response is 1 if the latent response y_i^* is less than κ_1 with corresponding probability $\Pr(y_i = 1)$ given by the area under the (standard) normal density to the left of κ_1. The response is 2 if y_i^* is larger than κ_1 but less than κ_2 with $\Pr(y_i = 2)$ given

by the area under the density between these thresholds. Finally, the response is 3 if y_i^* is larger than κ_2 with $\Pr(y_i=3)$ given by the area under the density to the right of κ_2. Similar graphs are also shown in figure 11.6.

The latent-response and generalized linear model formulations are equivalent for ordinal responses, just as previously shown for dichotomous responses in section 10.2.2. This can be seen by considering the cumulative probabilities in (11.1)

$$\begin{aligned}\Pr(y_i > s|x_i) &= \Pr(y_i^* > \kappa_s|x_i) = \Pr(\beta_2 x_i + \epsilon_i > \kappa_s|x_i) \\ &= \Pr(-\epsilon_i \leq \beta_2 x_i - \kappa_s|x_i) = F(\beta_2 x_i - \kappa_s)\end{aligned}$$

Figure 11.3 illustrates the equivalence of the formulations for an ordinal logit model with one covariate x_i. In the lower part of the figure, we present the (solid) regression line for the regression of a latent response y_i^* on a covariate x_i

$$E(y_i^*|x_i) = \beta_2 x_i$$

For selected values of x_i, we have plotted the conditional logistic densities of the latent responses y_i^*. The thresholds κ_1 and κ_2 are represented as dashed and dotted lines, respectively. For a given value of x_i, the probability of observing a category above 1 is given by the gray (combined light and dark) area under the corresponding logistic density above κ_1. The probability of a category above 2 is the dark gray area under the logistic density above κ_2. These probabilities are plotted in the upper part of the figure as dashed and dotted lines, respectively. The light gray area is the conditional probability that the response is 2. This probability increases as response 1 (white area) becomes less likely and decreases as response 3 (dark gray) becomes more likely.

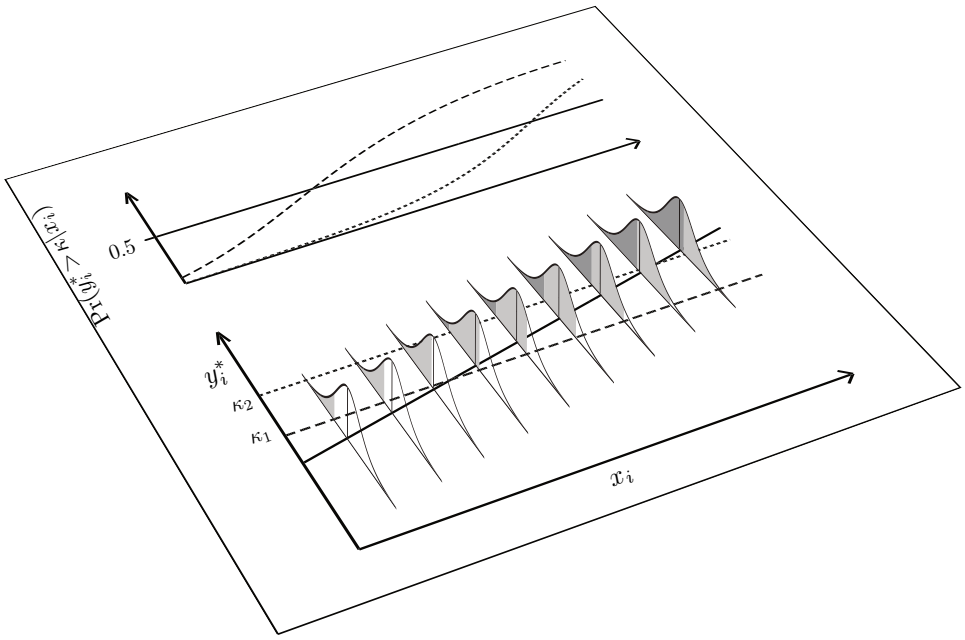


Figure 11.3: Illustration of equivalence of latent-response and generalized linear model formulation for ordinal logistic regression

The top panel of figure 11.4 shows the same cumulative probability curves as the upper part of figure 11.3:

$$\begin{aligned}\Pr(y_i>1|x_i) &= \Pr(y_i=2|x_i)+\Pr(y_i=3|x_i)\\ \Pr(y_i>2|x_i) &= \Pr(y_i=3|x_i)\end{aligned}$$

The corresponding probabilities of individual categories s are given by

$$\begin{aligned}\Pr(y_i=3|x_i) &= \Pr(y_i>2|x_i)\\ \Pr(y_i=2|x_i) &= \Pr(y_i>1|x_i)-\Pr(y_i>2|x_i)\\ \Pr(y_i=1|x_i) &= 1-\Pr(y_i>1|x_i)\end{aligned}$$

and are shown in the bottom panel of figure 11.4. The probabilities of the lowest and highest response categories 1 and S, which are categories 1 and 3 in the current example, are monotonic (strictly increasing or decreasing) functions of the covariates in cumulative models for ordinal responses. In contrast, the probability of an intermediate category is a unimodal or single-peaked function, as shown for $\Pr(y_i = 2|x_i)$ in the bottom panel (and as we saw when looking at the light gray area in figure 11.3).

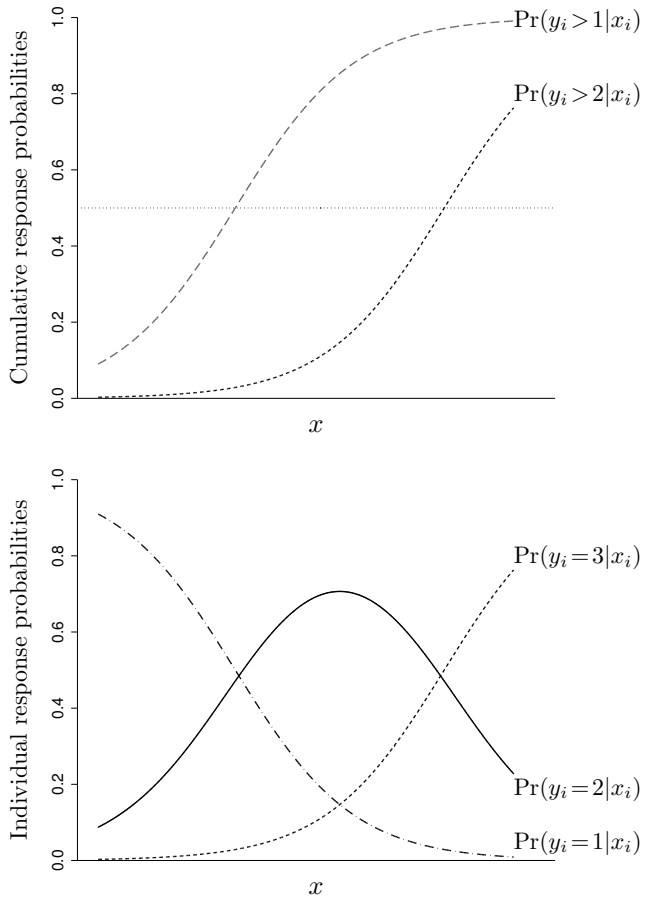


Figure 11.4: Illustration of cumulative and category-specific response probabilities

11.2.3 Proportional odds

If we specify a logit link or equivalently assume a standard logistic distribution for the residual ϵ_i in the latent-response model, the cumulative probabilities become

$$\Pr(y_i > s|x_i) \;=\; \frac{\exp(\beta_2 x_i - \kappa_s)}{1+\exp(\beta_2 x_i - \kappa_s)}$$

and the corresponding log odds are

$$\ln\left\{\frac{\Pr(y_i > s|x_i)}{1-\Pr(y_i > s|x_i)}\right\} \;=\; \beta_2 x_i - \kappa_s$$

It follows that the ratio of the odds that the response exceeds s for two covariate values, $x_i = a$ and $x_i = b$, becomes

$$\frac{\Pr(y_i > s|x_i = a)/\{1 - \Pr(y_i > s|x_i = a)\}}{\Pr(y_i > s|x_i = b)/\{1 - \Pr(y_i > s|x_i = b)\}} \;=\; \exp\{\beta_2(a-b)\} \;=\; \exp(\beta_2)^{(a-b)}$$

We see that for a unit increase in the covariate, $a - b = 1$, the odds ratio is $\exp(\beta_2)$. Indeed, for dummy variables the only possible increase is a unit increase from 0 to 1. In contrast, for a continuous covariate, we can also consider, for instance, a 10-unit increase. Then we must raise $\exp(\beta_2)$ to the 10th power because the model for the odds is multiplicative.

The category-specific parameter κ_s cancels out from the odds ratio, so the odds ratio is the same whatever category s is considered. For instance, for a four-category response, the odds ratio of being above 1 (that is, 2, 3, or 4) versus 1 is the same as the odds ratio of being above 2 (that is, 3 or 4) versus being at or below 2 (that is, 1 or 2). The corresponding odds are shown in the first two rows of figure 11.5 where the categories corresponding to 'success' (numerator of odds) are enclosed in thick frames and the categories corresponding to 'failure' (denominator of odds) are enclosed in thin frames. The third row corresponds to the odds of being above 3 (that is, 4) versus at or below 3 (that is, 1, 2, or 3). The odds themselves are not the same across the three rows but the *ratios* of the odds when a covariate increases by a unit are the same. This property, called *proportional odds*, makes it evident that these models are highly structured. It hence comes as no surprise that several models have been suggested that relax this property (see section 11.12).

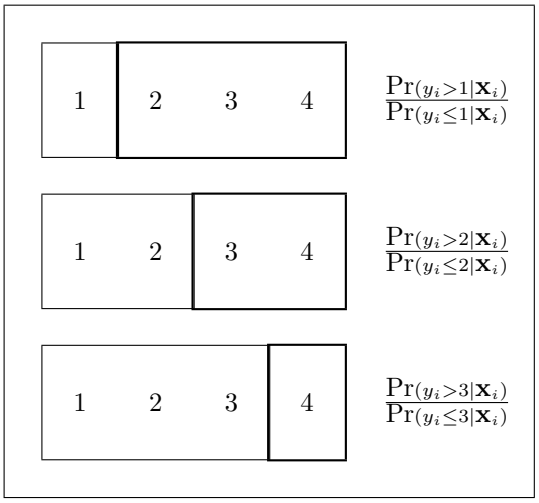


Figure 11.5: Relevant odds $\Pr(y_i > s|\mathbf{x}_i)/\Pr(y_i \leq s|\mathbf{x}_i)$ for $s = 1, 2, 3$ in a proportional odds model with four categories. Odds is a ratio of probabilities of events. Events included in numerator probability are in thick frames and events included in denominator probability are in thin frames [adapted from Brendan Halpin's web notes on "Models for ordered categories (ii)"].

If the proportional odds property holds, we can merge or collapse categories—or in the extreme case, dichotomize an ordinal variable—without changing the regression coefficient β_2. For instance, in the case of three categories, we could redefine the categories as $1 = \{2, 3\}$ and $0 = \{1\}$ and fit a binary logistic regression model. The interpretation of the odds ratios for this model would then correspond to one of the interpretations of the odds ratios for the original proportional odds model: the odds ratios for categories 2 or 3 versus 1. However, if the proportional odds assumption is violated, the estimates may be quite different.

11.2.4 ❖ Identification

Consider now for simplicity a model for y_i^* without covariates, but with an intercept β_1 and a variance parameter θ,

$$y_i^* \;=\; \beta_1 + \epsilon_i, \qquad \epsilon_i \sim N(0, \theta)$$

which can alternatively be written as

$$y_i^* \;\sim\; N(\beta_1, \theta)$$

It follows from this model that the probability of observing a category larger than s becomes

$$\Pr(y_i > s) \;=\; \Pr(y_i^* > \kappa_s) \;=\; \Pr\left(\frac{y_i^* - \beta_1}{\sqrt{\theta}} > \frac{\kappa_s - \beta_1}{\sqrt{\theta}}\right) \;=\; \Phi\left(\frac{\beta_1 - \kappa_s}{\sqrt{\theta}}\right)$$

where $\Phi(\cdot)$ is the cumulative standard normal density function.

We see from this expression that the cumulative probabilities $\Pr(y_i > s)$ do not change if we add some constant a to β_1 (or to the latent response y_i^*) and to all the thresholds κ_s, because the constant cancels out in the numerator $\beta_1 - \kappa_s$. Similarly, we see that the cumulative probabilities do not change if we multiply y_i^* by a constant b, so that β_1 and $\sqrt{\theta}$ are multiplied by b, as long as we also multiply κ_s by the same constant b, because we are in effect multiplying both the numerator and the denominator by the same constant. It follows that the location β_1 and scale $\sqrt{\theta}$ of the latent responses y_i^* are not identified if the thresholds are free parameters and thus cannot be estimated from the data.

This invariance is also illustrated in figure 11.6. It is evident from the left panel (top and bottom) that response probabilities are invariant to translation of the latent response y_i^*; the effect of adding 2 to y_i^* (or to the intercept β_1) can be counteracted by adding 2 to the thresholds κ_s. From the right panel (top and bottom), we see that the response probabilities are invariant to rescaling of y_i^*; the effect of multiplying y_i^* by 2 (or multiplying β_1 and $\sqrt{\theta}$ by 2) can be counteracted by multiplying the thresholds κ_s by 2. Thus the location and scale of the latent responses y_i^* are identified only relative to the location and spacing of the thresholds κ_s.

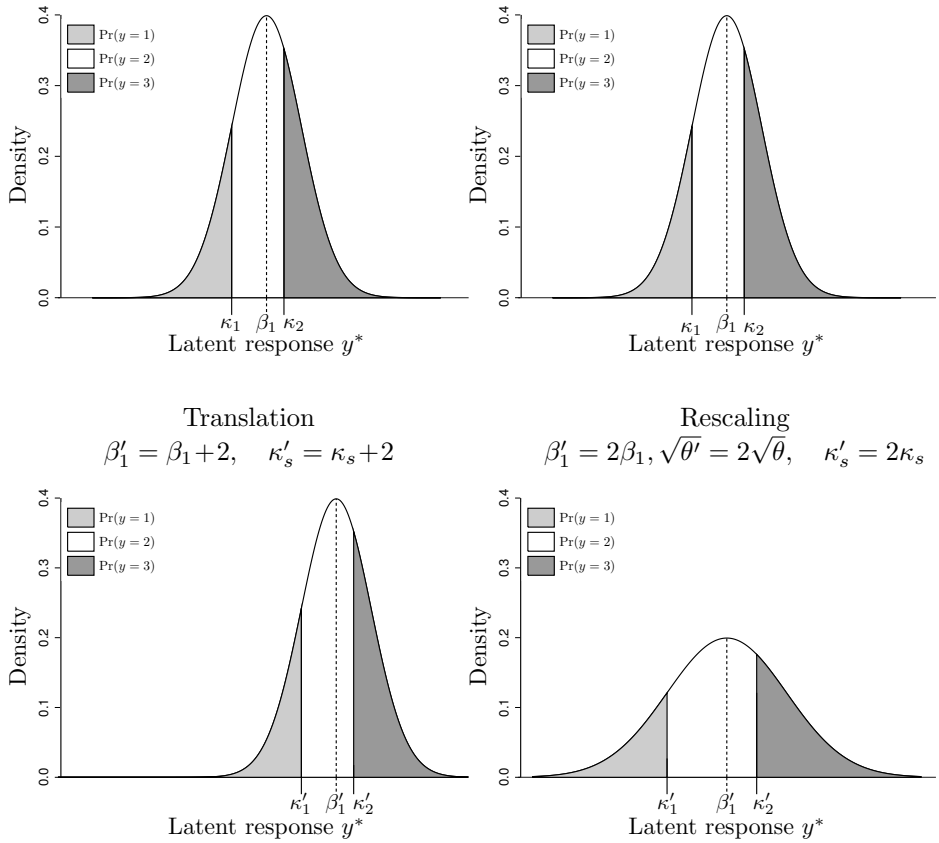


Figure 11.6: Illustration of scale and translation invariance in cumulative probit model

To identify ordinal regression models, the location of the latent response is usually fixed by setting the intercept β_1 to zero, which is what we have done so far in this chapter. The scale is usually fixed by setting $\theta = 1$ for probit models and $\theta = \pi^2/3$ for logit models. These two conventions are most common for ordinal models and are used by Stata's `ologit` and `oprobit` commands.

An alternative to fixing the location of y_i^* by setting $\beta_1 = 0$ is to fix the location of the thresholds, typically by setting $\kappa_1 = 0$ to identify the intercept β_1. This parameterization is common for dichotomous responses and is used in Stata's `logit`, `probit`, and `glm` commands. Less commonly, we could fix both the location and the scale of the thresholds by setting $\kappa_1 = 0$ and $\kappa_2 = 1$ so that both β_1 and θ can be estimated.

11.3 Are antipsychotic drugs effective for patients with schizophrenia?

Schizophrenia is a mental illness characterized by impairments in the perception or expression of reality, most commonly in terms of auditory hallucinations and paranoid or bizarre delusions. According to the U.S. National Institute of Mental Health (NIMH), the prevalence of schizophrenia is about 1% in the U.S. population aged 18 and older.

We now use data from the NIMH Schizophrenia Collaborative Study on treatment-related changes in overall severity of schizophrenia. The data have previously been analyzed by Gibbons and Hedeker (1994), Hedeker and Gibbons (1996, 2006), and Gibbons et al. (1988).

Patients were randomly assigned to receive one of four treatments: placebo (control), chlorpromazine, fluphenazine, or thioridazine. In the present analysis, we will not distinguish between the three antipsychotic drugs; instead, we call the combined group the treatment group. The outcome considered is "severity of illness" as measured by item 79 of the Inpatient Multidimensional Psychiatric Scale (IMPS) of Lorr and Klett (1966). The patients were examined weekly for up to six weeks.

The dataset `schiz.dta` has the following variables:

- `id`: patient identifier
- `week`: week of assessment since randomization (0, 1, ..., 6)
- `imps`: item 79 of IMPS (−9 represents missing)
- `treatment`: dummy variable for being in treatment group (1: treatment [drug]; 0: control)

We read in the schizophrenia data by typing

```
. use http://www.stata-press.com/data/mlmus3/schiz
```

Following Hedeker and Gibbons (1996), we recode item 79 of the IMPS into an ordinal severity of illness variable, `impso`, with four categories (1: normal or borderline mentally ill; 2: mildly or moderately ill; 3: markedly ill; 4: severely or among the most extremely ill). This can be accomplished using the `recode` command:

```
. generate impso = imps
. recode impso -9=. 1/2.4=1 2.5/4.4=2 4.5/5.4=3 5.5/7=4
```

11.4 Longitudinal data structure and graphs

Before we start modeling the severity of schizophrenia over time, let us look at the dataset, using both descriptive statistics and graphs. This may provide insights that can be used in subsequent model specification (see also *Introduction to models for longitudinal and panel data (part III)*).

11.4.1 Longitudinal data structure

We first `xtset` the data:

```
. xtset id week
       panel variable:  id (unbalanced)
        time variable:  week, 0 to 6, but with gaps
                delta:  1 unit
```

We then use the `xtdescribe` command to describe the participation pattern in the dataset:

```
. xtdescribe if impso<.
     id:  1103, 1104, ..., 9316                             n =        437
   week:  0, 1, ..., 6                                      T =          7
          Delta(week) = 1 unit
          Span(week)  = 7 periods
          (id*week uniquely identifies each observation)
Distribution of T_i:   min      5%     25%       50%       75%     95%     max
                         2       2       4         4         4       4       5
     Freq.  Percent    Cum. |  Pattern
------------------------------+---------
       308     70.48   70.48 |  11.1..1
        41      9.38   79.86 |  11.1...
        37      8.47   88.33 |  11.....
         8      1.83   90.16 |  11....1
         8      1.83   91.99 |  111....
         6      1.37   93.36 |  11.1.1.
         5      1.14   94.51 |  1..1..1
         5      1.14   95.65 |  11.11..
         3      0.69   96.34 |  .1.1..1
        16      3.66  100.00 |  (other patterns)
------------------------------+---------
       437    100.00          |  XXXXXXX
```

All patterns shown have missing assessments for at least three occasions. The predominant pattern, "`11.1..1`" (308 patients), has assessments only at weeks 0, 1, 3, and 6. We can tabulate the number of observations in each week for the treatment and control groups by using the `table` command:

```
. table week treatment, contents(count impso) col
```

week	treatment 0	1	Total
0	107	327	434
1	105	321	426
2	5	9	14
3	87	287	374
4	2	9	11
5	2	7	9
6	70	265	335

We see that few assessments took place in weeks 2, 4, and 5.

11.4.2 Plotting cumulative proportions

When considering cumulative models, it is natural to inspect the cumulative proportions in the dataset. We therefore calculate the proportions of patients having responses above 1, 2, and 3 at each occasion and by treatment group. These proportions can be calculated conveniently using Stata's `egen` command with the `mean()` function:

```
. egen propg1 = mean(impso>1), by(week treatment)
. egen propg2 = mean(impso>2), by(week treatment)
. egen propg3 = mean(impso>3), by(week treatment)
```

Because only a few assessments were made in weeks 2, 4, and 5, we will plot cumulative proportions only for weeks 0, 1, 3, and 6. To simplify later commands, we define a dummy variable, `nonrare`, for these weeks by using `egen` with the `anymatch()` function:

```
. egen nonrare = anymatch(week), values(0,1,3,6)
```

We then define a label for `treatment`,

```
. label define t 0 "Control" 1 "Treatment", modify
. label values treatment t
```

and produce a graph for the cumulative sample proportions against week,

```
. sort treatment id week
. twoway (line propg1 week, sort)
> (line propg2 week, sort lpatt(vshortdash))
> (line propg3 week, sort lpatt(dash)) if nonrare==1, by(treatment)
> legend(order(1 "Prop(y>1)" 2 "Prop(y>2)" 3 "Prop(y>3)")) xtitle("Week")
```

The resulting graph, shown in figure 11.7, suggests that antipsychotic drugs have a beneficial effect because the proportions in the higher, more severe categories decline more rapidly in the treatment group. We observe that the cumulative proportions also decline somewhat in the control group.

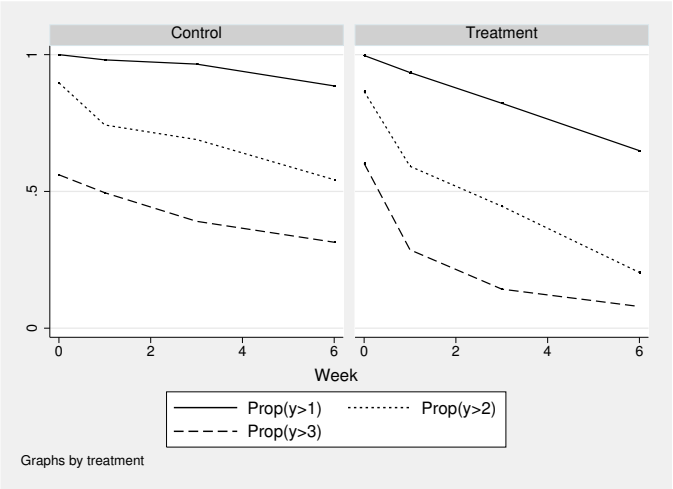


Figure 11.7: Cumulative sample proportions versus week

11.4.3 Plotting cumulative sample logits and transforming the time scale

In ordinal logistic regression, the cumulative log odds or logits, and not the cumulative probabilities, are specified as linear functions of covariates. Before specifying a model for the time trend, it is therefore useful to construct cumulative sample logits (logits of sample proportions),

```
. generate logodds1 = ln(propg1/(1-propg1))
. generate logodds2 = ln(propg2/(1-propg2))
. generate logodds3 = ln(propg3/(1-propg3))
```

and plot these against `week`, giving the graphs in figure 11.8.

```
. twoway (line logodds1 week, sort)
> (line logodds2 week, sort lpatt(vshortdash))
> (line logodds3 week, sort lpatt(dash)) if nonrare==1, by(treatment)
> legend(order(1 "Log Odds(y>1)" 2 "Log Odds(y>2)" 3 "Log Odds(y>3)"))
> xtitle("Week")
```

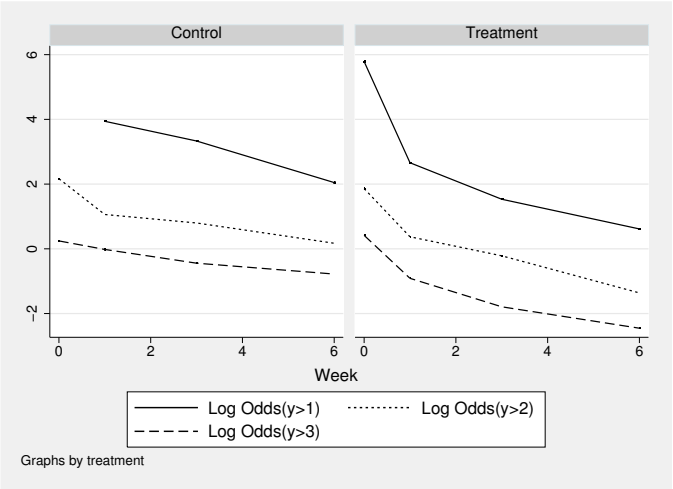


Figure 11.8: Cumulative sample logits versus week

The missing value for the log odds of being in categories above 1 in week 0 for the control group is due to the corresponding proportion being equal to 1 (see figure 11.7), giving an odds of ∞.

The cumulative sample logits in figure 11.8 would be poorly approximated by a linear function of `week` in the treatment group. One way to address this problem would be to depart from a linear trend for the cumulative logits and instead consider some polynomial function, such as a quadratic or cubic. Another approach, adopted by Hedeker and Gibbons (1996) and followed here, is to retain a linear trend for the logits but transform the time scale by taking the square root of `week`:

```
. generate weeksqrt = sqrt(week)
```

Plots for the cumulative sample logits against the transformed time variable, `weeksqrt`, are produced by the command

```
. twoway (line logodds1 weeksqrt, sort)
> (line logodds2 weeksqrt, sort lpatt(vshortdash))
> (line logodds3 weeksqrt, sort lpatt(dash)) if nonrare==1, by(treatment)
> legend(order(1 "Log Odds(y>1)" 2 "Log Odds(y>2)" 3 "Log Odds(y>3)"))
> xtitle("Square root of week")
```

and presented in figure 11.9.

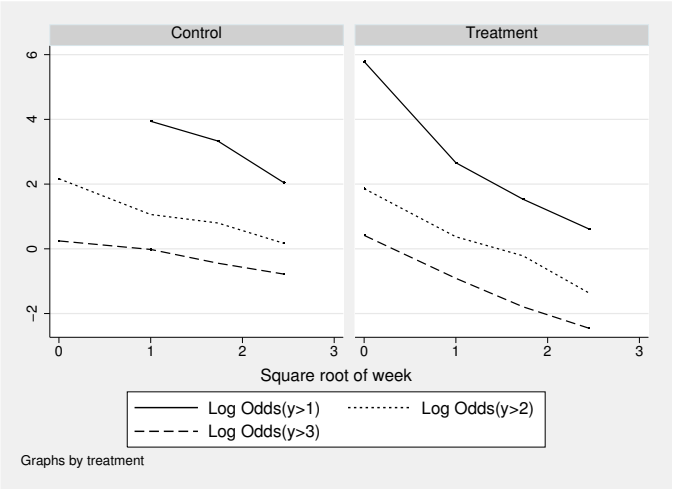


Figure 11.9: Cumulative sample logits versus square root of week

As desired, the curves generally appear to be more linear after the square-root transformation of time.

11.5 A single-level proportional odds model

We start modeling the schizophrenia data by fitting a single-level ordinal logistic regression model.

11.5.1 Model specification

Based on figure 11.9, it seems reasonable to assume a linear relationship between the cumulative logits and the square root of time, allowing the intercept and the slope to differ between the treatment and control groups,

$$\begin{aligned} \text{logit}\{\Pr(y_{ij} > s|x_{2ij}, x_{3j})\} &= \beta_2 x_{2ij} + \beta_3 x_{3j} + \beta_4 x_{2ij} x_{3j} - \kappa_s \\ &= (\beta_2 + \beta_4 x_{3j}) x_{2ij} + \beta_3 x_{3j} - \kappa_s \end{aligned} \tag{11.2}$$

where x_{2ij} represents `weeksqrt` and x_{3j} represents `treatment`. Here β_2 is the slope of transformed time for the control group, β_3 is the difference between treatment and control groups at week 0, and β_4 is the difference in the slopes of transformed time between treatment and control groups. From the figure, we would expect β_4 (which we can interpret as the treatment effect) to be negative and the corresponding odds ratio, given by $\exp(\beta_4)$, to be less than 1.

To interpret $\exp(\beta_4)$, consider the odds ratios for a unit increase in time x_{2ij} in the two treatment groups:

$$\exp(\beta_2 + \beta_4 x_{3j}) = \begin{cases} \exp(\beta_2) & \text{if } x_{3j} = 0 \quad \text{(control group)} \\ \exp(\beta_2)\exp(\beta_4) & \text{if } x_{3j} = 1 \quad \text{(treatment group)} \end{cases}$$

Thus $\exp(\beta_4)$ is the odds ratio for transformed time for the treatment group divided by the odds ratio for transformed time for the control group.

11.5.2 Estimation using Stata

We start by constructing an interaction term, `interact`, by taking the product of `weeksqrt` and `treatment`:

```
. generate interact = weeksqrt*treatment
```

The Stata commands for fitting the single-level proportional odds model (11.2) using the `ologit` command are

```
. ologit impso weeksqrt treatment interact, vce(cluster id) or
Ordered logistic regression                     Number of obs   =       1603
                                                Wald chi2(3)    =     440.17
                                                Prob > chi2     =     0.0000
Log pseudolikelihood = -1878.0969               Pseudo R2       =     0.1177
                                (Std. Err. adjusted for 437 clusters in id)
------------------------------------------------------------------------------
             |               Robust
       impso | Odds Ratio   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
   weeksqrt |   .5847056   .0591797    -5.30   0.000     .4794958    .7130004
  treatment |   .9993959   .2042595    -0.00   0.998     .6695244    1.491793
   interact |   .4719089   .0568135    -6.24   0.000     .3727189    .5974961
-------------+----------------------------------------------------------------
      /cut1 |  -3.807279   .1956796                     -4.190804   -3.423754
      /cut2 |  -1.760167   .1811041                     -2.115125    -1.40521
      /cut3 |  -.4221112   .1795596                     -.7740415   -.0701808
------------------------------------------------------------------------------
```

Here we have used the `vce(cluster id)` option to obtain robust standard errors (based on the sandwich estimator), taking into account the clustered nature of the data, and the `or` option to obtain estimated odds ratios $\exp(\widehat{\beta})$ with corresponding 95% confidence intervals. The output looks just like output from binary logistic regression, except for the additional estimates of the thresholds κ_1–κ_3, labeled `/cut1`–`/cut3`. Maximum likelihood estimates for the proportional odds model are presented under the heading "POM" in table 11.1.

Table 11.1: Maximum likelihood estimates and 95% CIs for proportional odds model (POM), random-intercept proportional odds model (RI-POM), and random-coefficient proportional odds model (RC-POM)

	POM		RI-POM		RC-POM	
	Est	(95% CI)†	Est	(95% CI)	Est	(95% CI)
Fixed part: Odds ratios						
$\exp(\beta_2)$ [`weeksqrt`]	0.58	(0.48, 0.71)	0.46	(0.36, 0.60)	0.41	(0.27, 0.63)
$\exp(\beta_3)$ [`treatment`]	1.00	(0.67, 1.49)	0.94	(0.51, 1.75)	1.06	(0.49, 2.28)
$\exp(\beta_4)$ [`interact`]	0.47	(0.37, 0.60)	0.30	(0.22, 0.40)	0.18	(0.11, 0.30)
Fixed part: Thresholds						
κ_1	−3.81		−5.86		−7.32	
κ_2	−1.76		−2.83		−3.42	
κ_3	−0.42		−0.71		−0.81	
Random part: Variances and covariance						
ψ_{11}			3.77		6.99	
ψ_{22}					2.01	
ψ_{21}					−1.51	
Log likelihood	−1,878.10		−1,701.38		−1,662.76	

†Based on the sandwich estimator

The odds ratios for this model represent marginal or population-averaged effects. All of these odds ratios are ratios of the odds of more severe versus less severe illness regardless of where we cut the ordinal scale to define more versus less. We see from table 11.1 that the odds ratio of more severe illness per unit of time (on the transformed scale) is estimated as 0.58 (95% CI from 0.48 to 0.71) for the control group. The corresponding odds ratio for the treatment group is estimated as $0.58 \times 0.47 = 0.28$. To obtain a confidence interval for the latter odds ratio, we can use the `lincom` command with the `or` (or `eform`) option:

```
. lincom weeksqrt+interact, or
 ( 1)  [impso]weeksqrt + [impso]interact = 0
```

impso	Odds Ratio	Std. Err.	z	P>|z|	[95% Conf.	Interval]
(1)	.2759278	.0179484	-19.80	0.000	.2428997	.3134469

The 95% confidence interval for the odds ratio per square root of week ranges from 0.24 to 0.31 in the treatment group.

We could have used factor-variable notation in the `ologit` and `lincom` commands, with the following syntax:

```
ologit impso i.treatment##c.weeksqrt, or
lincom c.weeksqrt+1.treatment#c.weeksqrt, or
```

We can easily assess the model fit by comparing model-implied probabilities with sample proportions. Model-implied probabilities for the individual response categories can be obtained by using the `predict` command with the `pr` option:

```
. predict prob1-prob4, pr
```

The corresponding cumulative probabilities of exceeding categories 3, 2, and 1 are obtained by the following commands:

```
. generate probg3 = prob4
. generate probg2 = prob3 + probg3
. generate probg1 = prob2 + probg2
```

We now plot these marginal probabilities together with the corresponding sample proportions against week:

```
. twoway (line propg1 week if nonrare==1, sort lpatt(solid))
> (line propg2 week if nonrare==1, sort lpatt(vshortdash))
> (line propg3 week if nonrare==1, sort lpatt(dash))
> (line probg1 week, sort lpatt(solid))
> (line probg2 week, sort lpatt(vshortdash))
> (line probg3 week, sort lpatt(dash)), by(treatment)
> legend(order(1 "Prob(y>1)" 2 "Prob(y>2)" 3 "Prob(y>3)")) xtitle("Week")
```

The resulting graphs, shown in figure 11.10, suggest that the sample proportions are well recovered by the model.

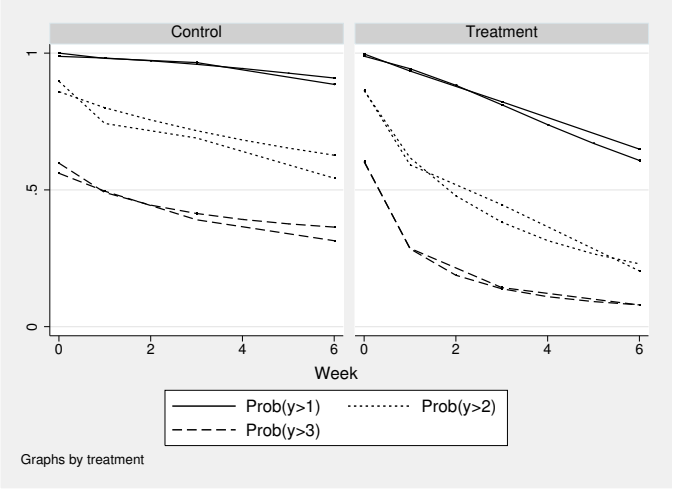


Figure 11.10: Cumulative sample proportions and predicted cumulative probabilities from ordinal logistic regression versus week

Fitting an ordinary proportional odds model and specifying robust standard errors for clustered data can be viewed as GEE (generalized estimating equations) with an independence working correlation matrix. The dependence is treated as a nuisance. (Stata's `xtgee` command cannot be used for ordinal responses.)

11.6 A random-intercept proportional odds model

11.6.1 Model specification

We now model the longitudinal dependence by including a patient-specific random intercept ζ_{1j} in the proportional odds model:

$$\text{logit}\{\Pr(y_{ij} > s|\mathbf{x}_{ij}, \zeta_{1j})\} = \beta_2 x_{2ij} + \beta_3 x_{3j} + \beta_4 x_{2j} x_{3ij} + \zeta_{1j} - \kappa_s \quad (11.3)$$

The overall level or intercept of the cumulative logits is ζ_{1j} and hence varies over patients j. As usual, we assume that the $\zeta_{1j} \sim N(0, \psi_{11})$ are independently distributed across patients and that ζ_{1j} is independent of the covariates $\mathbf{x}_{ij}$. (We denoted the random intercept ζ_{1j} instead of ζ_j and the variance ψ_{11} instead of ψ because we will add a random coefficient later.)

The model can alternatively be written in terms of a latent response y^*_{ij},

$$y^*_{ij} = \beta_2 x_{2ij} + \beta_3 x_{3j} + \beta_4 x_{2j} x_{3ij} + \zeta_{1j} + \epsilon_{ij}$$

where the ϵ_{ij} have standard logistic distributions, are independent across patients and occasions, and are independent of $\mathbf{x}_{ij}$. The ordinal severity of illness variable y_{ij} is related to the latent response via the threshold model:

$$y_{ij} = \begin{cases} 1 & \text{if} \quad y^*_{ij} \leq \kappa_1 \\ 2 & \text{if} \quad \kappa_1 < y^*_{ij} \leq \kappa_2 \\ 3 & \text{if} \quad \kappa_2 < y^*_{ij} \leq \kappa_3 \\ 4 & \text{if} \quad \kappa_3 < y^*_{ij} \end{cases}$$

11.6.2 Estimation using Stata

At the time of writing this book, there is no official Stata command for fitting multilevel models for ordinal responses, so we will use the user-written command `gllamm`. Ordinal logit and probit models can be fit in `gllamm` by using the `link(ologit)` and `link(oprobit)` options, respectively. To fit the random-intercept proportional odds model in (11.3), we use the following options: `i(id)` to specify that the responses are nested in patients with identifier `id`, `adapt` to request adaptive quadrature, and `eform` to obtain exponentiated estimates or odds ratios. The `gllamm` command is

```
. gllamm impso weeksqrt treatment interact, i(id) link(ologit) adapt eform
number of level 1 units = 1603
number of level 2 units = 437

Condition Number = 15.409532

gllamm model

log likelihood = -1701.3807
```

	exp(b)	Std. Err.	z	P>|z|	[95% Conf.	Interval]
impso						
weeksqrt	.4649524	.0608031	-5.86	0.000	.3598276	.6007898
treatment	.9439398	.2962805	-0.18	0.854	.5102372	1.74629
interact	.2993646	.0457031	-7.90	0.000	.2219474	.4037856
_cut11						
_cons	-5.858454	.331792	-17.66	0.000	-6.508754	-5.208153
_cut12						
_cons	-2.825669	.2900513	-9.74	0.000	-3.394159	-2.257179
_cut13						
_cons	-.7077079	.2750904	-2.57	0.010	-1.246875	-.1685405

```
Variances and covariances of random effects
------------------------------------------------------------------------------

***level 2 (id)

    var(1): 3.7733419 (.46496883)
------------------------------------------------------------------------------
. estimates store model1
```

The estimated odds ratios with 95% confidence intervals for the random-intercept proportional odds model were presented under "RI-POM" in table 11.1. As discussed in section 10.8 for binary responses, these estimates of conditional or subject-specific effects are further from 1 than the marginal or population-averaged counterparts from model (11.2). The subject-specific odds ratio of transformed time is estimated as 0.46 in the control group and as 0.14 ($= 0.46495 \times 0.29936$) in the treatment group.

11.6.3 Measures of dependence and heterogeneity

Residual intraclass correlation of latent responses

The random-intercept variance is estimated as $\widehat{\psi}_{11} = 3.773$, implying an estimated residual intraclass correlation for the latent responses y_{ij}^* of

$$\widehat{\rho} = \frac{\widehat{\psi}_{11}}{\widehat{\psi}_{11} + \pi^2/3} = \frac{3.773}{3.773 + \pi^2/3} = 0.53$$

Median odds ratio

The median odds ratio proposed by Larsen et al. (2000) and Larsen and Merlo (2005), and previously discussed in section 10.9.2, can be used as a measure of heterogeneity in ordinal random-intercept models.

The median odds ratio, $\text{OR}_{\text{median}}$, is given by

$$\text{OR}_{\text{median}} = \exp\{\sqrt{2\psi_{11}}\Phi^{-1}(3/4)\}$$

Plugging in $\widehat{\psi}_{11}$, we obtain $\widehat{\text{OR}}_{\text{median}}$:

```
. display exp(sqrt(2*3.7733416)*invnormal(3/4))
6.3783288
```

Hence, if two patients are chosen at random at a given time point from the same treatment group, the odds ratio comparing the subject with the larger odds to the subject with the smaller odds will exceed 6.38 half the time, which is a large odds ratio.

11.7 A random-coefficient proportional odds model

11.7.1 Model specification

To allow the slope of the time variable, `weeksqrt`, to vary randomly between patients within the two groups, we now include a random slope ζ_{2j} in addition to the random intercept ζ_{1j}:

$$\begin{aligned}\text{logit}\{\Pr(y_{ij} > s|\mathbf{x}_{ij}, \zeta_{1j}, \zeta_{2j})\} \\ &= \beta_2 x_{2ij} + \beta_3 x_{3j} + \beta_4 x_{2j} x_{3ij} + \zeta_{1j} + \zeta_{2j} x_{2ij} - \kappa_s \\ &= \zeta_{1j} + (\beta_2 + \zeta_{2j}) x_{2ij} + \beta_3 x_{3j} + \beta_4 x_{2j} x_{3ij} - \kappa_s \qquad (11.4)\end{aligned}$$

In this model, not only the intercept but also the slope $\beta_2 + \zeta_{2j}$ of `weeksqrt` (x_{2ij}) varies over patients j. We assume that the random intercept and slope have a bivariate normal distribution with zero mean and covariance matrix

$$\mathbf{\Psi} = \begin{bmatrix} \psi_{11} & \psi_{12} \\ \psi_{21} & \psi_{22} \end{bmatrix}, \qquad \psi_{21} = \psi_{12}$$

Both the random intercepts and the random slopes are assumed to be independent across patients and independent of the covariates $\mathbf{x}_{ij}$.

The random-coefficient proportional odds model can also be specified using a latent-response formulation, as shown for the random-intercept proportional odds model in section 11.6.1.

11.7.2 Estimation using gllamm

To fit the random-coefficient proportional odds model using `gllamm`, we must first define equations for the intercept and slope by using the `eq` command. We need one equation

for each random effect, specifying after the equation name and colon the variable that multiplies the random effect. For the random intercept, this variable is just 1, so we first create a variable, `cons`, equal to 1 and define an equation for the random intercept.

```
. generate cons = 1
. eq inter: cons
```

The random slope is multiplied by `weeksqrt`, and the corresponding equation is defined using

```
. eq slope: weeksqrt
```

We are now ready to fit the random-coefficient model using `gllamm` with the following options: `nrf(2)` to specify the number of random effects as 2 and `eqs()` to specify the equations defined above:

```
. gllamm impso weeksqrt treatment interact, i(id) nrf(2) eqs(inter slope)
> link(ologit) adapt eform
number of level 1 units = 1603
number of level 2 units = 437

Condition Number = 13.096305

gllamm model

log likelihood = -1662.76
```

impso	exp(b)	Std. Err.	z	P>|z|	[95% Conf.	Interval]
impso						
weeksqrt	.413742	.0901228	-4.05	0.000	.2699714	.6340762
treatment	1.058823	.4152368	0.15	0.884	.4909184	2.283693
interact	.1837951	.0463311	-6.72	0.000	.1121407	.3012346
_cut11						
_cons	-7.317879	.4733159	-15.46	0.000	-8.245561	-6.390197
_cut12						
_cons	-3.417252	.3869461	-8.83	0.000	-4.175652	-2.658851
_cut13						
_cons	-.8120713	.3526985	-2.30	0.021	-1.503348	-.1207948

```
Variances and covariances of random effects
------------------------------------------------------------------------------

***level 2 (id)

    var(1): 6.9861284 (1.3149731)
    cov(2,1): -1.5061266 (.53161343) cor(2,1): -.40212569

    var(2): 2.0079957 (.41890607)
------------------------------------------------------------------------------

. estimates store model2
```

Instead of fitting the model from scratch, it is often faster to use estimates for the random-intercept model as starting values for the random-coefficient model. To illustrate this, we first retrieve the random-intercept estimates,

```
. estimates restore model1
```

so that we can store the estimates in a matrix `a` by typing

```
. matrix a = e(b)
```

Although we could think of the parameter estimates as a vector, Stata stores them in a row matrix that we have accessed as `e(b)`. We can refer to the elements as, for instance, `a[1,3]` (for the third element). However, the random-coefficient model requires two additional parameters, which happen to be the last two parameters in the row matrix. We arbitrarily specify values 0.1 and 0 for these and correspondingly add these columns to row matrix `a`:

```
. matrix a = (a,.1,0)
```

We could then fit the random-coefficient model, using the `from(a)` and `copy` options to specify that the augmented matrix `a` contains the starting values in the correct order:

```
gllamm impso weeksqrt treatment interact, i(id) nrf(2) eqs(inter slope)
  link(ologit) adapt from(a) copy eform
```

We can compare the random-coefficient proportional odds model (11.4) with the random-intercept proportional odds model (11.3) by using a likelihood-ratio test:

```
. lrtest model1 model2
(log likelihoods of null models cannot be compared)
Likelihood-ratio test                                 LR chi2(2)  =     77.24
(Assumption: model1 nested in model2)                 Prob > chi2 =    0.0000
```

Although the test is conservative (because the null hypothesis is on the boundary of the parameter space; see section 2.6.2 for how to obtain the correct asymptotic p-value), we get a p-value that is close to zero. The random-intercept model is thus rejected in favor of the random-coefficient model.

The maximum likelihood estimates for the random-coefficient proportional odds model were presented under "RC-POM" in table 11.1. In this model, the patient-specific odds ratio per unit of time (in square root of week) is estimated as 0.41 in the control group and as 0.07 (=0.41375×0.183792) in the treatment group. The random-intercept variance is estimated as $\widehat{\psi}_{11} = 6.99$ and the random-slope variance as $\widehat{\psi}_{22} = 2.01$. The covariance between the random intercept and slope is estimated as $\widehat{\psi}_{21} = -1.51$, corresponding to a correlation of -0.40. This means that patients having severe schizophrenia at the onset of the study (`week`$=0$) tend to have a greater decline in severity than those with less severe schizophrenia in both the control and the treatment groups.

11.8 Different kinds of predicted probabilities

11.8.1 Predicted population-averaged or marginal probabilities

As shown for binary logistic regression models in section 10.13.1, we can obtain the population-averaged or marginal probabilities implied by the fitted random-coefficient proportional odds model by using `gllapred` with the `mu` and `marginal` options. Because there are several response categories in ordinal models, what `gllapred` actually provides are cumulative probabilities that the response is above category s,

$$\widehat{\Pr}(y_{ij} > s|\mathbf{x}_{ij})$$

The category s is specified in the `above()` option of `gllapred`:

```
. gllapred mprobg1, mu marginal above(1)
(mu will be stored in mprobg1)
. gllapred mprobg2, mu marginal above(2)
(mu will be stored in mprobg2)
. gllapred mprobg3, mu marginal above(3)
(mu will be stored in mprobg3)
```

These marginal cumulative probabilities can be plotted together with the cumulative sample proportions against `week` (we revert to `week` because we find it easier to interpret this natural time scale than `weeksqrt`).

```
. twoway (line propg1 week if nonrare==1, sort lpatt(solid))
> (line propg2 week if nonrare==1, sort lpatt(vshortdash))
> (line propg3 week if nonrare==1, sort lpatt(dash))
> (line mprobg1 week, sort lpatt(solid))
> (line mprobg2 week, sort lpatt(vshortdash))
> (line mprobg3 week, sort lpatt(dash)), by(treatment)
> legend(order(1 "Prob(y>1)" 2 "Prob(y>2)" 3 "Prob(y>3)")) xtitle("Week")
```

The resulting graphs are shown in figure 11.11.

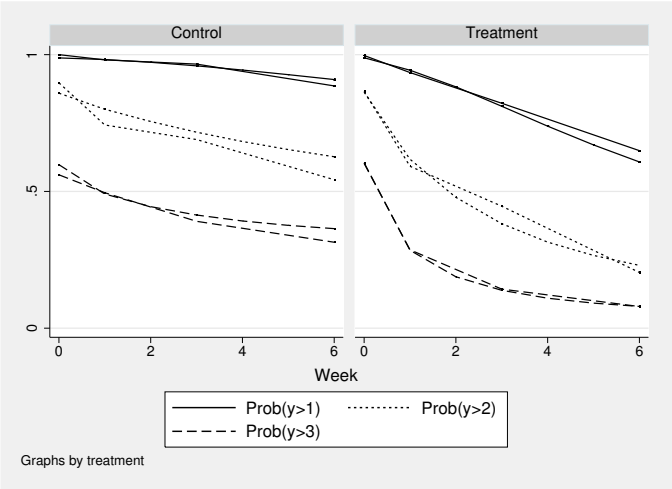


Figure 11.11: Cumulative sample proportions and cumulative predicted marginal probabilities from random-coefficient proportional odds model versus week

In addition to modeling the dependence of repeated measurements within patients, we see that the random-coefficient proportional odds model fits the cumulative proportions equally as well as the single-level proportional odds model in figure 11.10.

The corresponding marginal probabilities for the individual response categories s can be obtained using the relationship

$$\widehat{\Pr}(y_{ij} = s|\mathbf{x}_{ij}) \;=\; \widehat{\Pr}(y_{ij} > s-1|\mathbf{x}_{ij}) - \widehat{\Pr}(y_{ij} > s|\mathbf{x}_{ij})$$

where $\widehat{\Pr}(y_{ij} > 0|\mathbf{x}_{ij}) = 1$. The Stata commands for calculating these predicted probabilities are

```
. generate pr1 = 1 - mprobg1
. generate pr2 = mprobg1 - mprobg2
. generate pr3 = mprobg2 - mprobg3
. generate pr4 = mprobg3
```

Graphs of the marginal probabilities for each category against week are produced by the command

```
. twoway (line pr1 week, sort lpatt(solid))
> (line pr2 week, sort lpatt(vshortdash))
> (line pr3 week, sort lpatt(dash_dot))
> (line pr4 week, sort lpatt(dash)), by(treatment)
> legend(order(1 "Prob(y=1)" 2 "Prob(y=2)" 3 "Prob(y=3)" 4 "Prob(y=4)"))
> xtitle("Week")
```

giving the graph in figure 11.12.

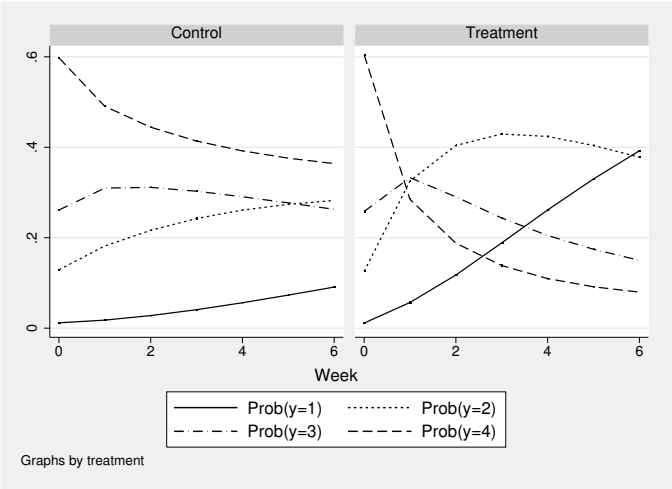


Figure 11.12: Marginal category probabilities from random-coefficient proportional odds model versus week

In the treatment group, the predicted marginal probability of being at most borderline ill (category 1) increases from nearly 0 to about 0.4, whereas the predicted marginal probability of being severely ill or among the most extremely ill (category 4) decreases from about 0.6 to about 0.1. These improvements are much less marked in the control group.

We could also make a graph that is similar to a stacked bar chart, but with a continuous x axis. In a stacked bar chart, the lowest bar represents $\Pr(y = 1)$, one bar up represents $\Pr(y = 2)$, etc., so the height of the top of the kth bar represents the sum of the probabilities up to and including k, $\Pr(y \leq k)$. We first calculate these heights:

```
. generate pr12 = 1 - mprobg2
. generate pr123 = 1 - mprobg3
. generate pr1234 = 1
```

Instead of making bars, we produce area graphs with the command

```
. twoway (area pr1 week, sort fintensity(inten10))
> (rarea pr12 pr1 week, sort fintensity(inten50))
> (rarea pr123 pr12 week, sort fintensity(inten70))
> (rarea pr1234 pr123 week, sort fintensity(inten90)), by(treatment)
> legend(order(1 "Prob(y=1)" 2 "Prob(y=2)" 3 "Prob(y=3)" 4 "Prob(y=4)"))
> xtitle("Week")
```

giving the graph shown in figure 11.13.

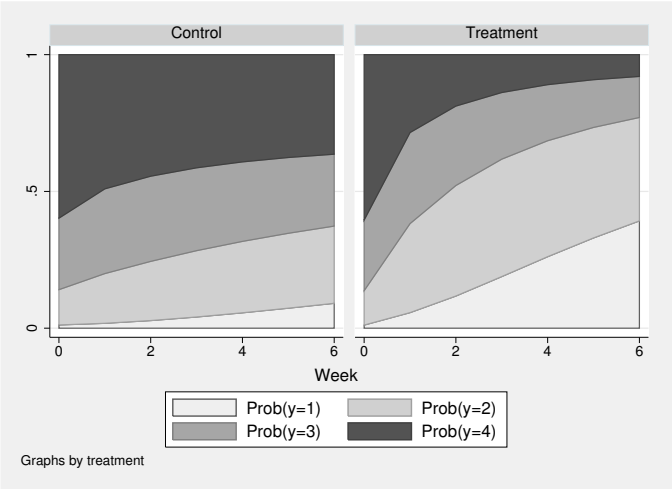


Figure 11.13: Area graph analogous to stacked bar chart for marginal predicted probabilities from random-coefficient proportional odds model

The combined area in the three lightest shades represents the marginal predicted probability that the severity is 3 (markedly ill) or less. The area for any given shade represents the probability that the severity is in the corresponding category. Perhaps the most striking feature is how much more the probability of the highest severity decreases over time in the treatment group compared with the control group.

11.8.2 Predicted subject-specific probabilities: Posterior mean

As shown for binary logistic regression in section 10.13.2, we can obtain empirical Bayes predictions of subject-specific probabilities for subjects in the sample. The corresponding posterior mean cumulative probabilities are

$$\widetilde{\Pr}(y_{ij} > s|\mathbf{x}_{ij}) \equiv \int \widehat{\Pr}(y_{ij} > s|\mathbf{x}_{ij}, \zeta_j) \times \text{Posterior}(\zeta_j|y_{1j}, \ldots, y_{n_j j}, \mathbf{X}_j)\, d\zeta_j$$

and the posterior mean category probabilities can be obtained as the differences

$$\widetilde{\Pr}(y_{ij} = s|\mathbf{x}_{ij}) = \widetilde{\Pr}(y_{ij} > s-1|\mathbf{x}_{ij}) - \widetilde{\Pr}(y_{ij} > s|\mathbf{x}_{ij})$$

with $\widetilde{\Pr}(y_{ij} > 0|\mathbf{x}_{ij}) = 1$.

To make predictions for weeks 0 through 6 for everyone even if the response variable was not observed, we first use the `fillin` command to produce rows of data for all combinations of the values of `id` and `week` that are missing (see also section 10.13.2):

```
. fillin id week
```

This produces missing values in the new rows of data for all variables except `id` and `week`. To make predictions, none of the variables used for estimation in `gllamm` can be missing except the response variable. We therefore replace the missing values, which occur whenever the dummy variable `_fillin` produced by the `fillin` command is 1:

```
. replace weeksqrt = sqrt(week) if _fillin==1
. egen trt = mean(treatment), by(id)
. replace treatment = trt if _fillin==1
(1456 real changes made)
. replace interact = weeksqrt*treatment if _fillin==1
(1456 real changes made)
. replace cons = 1 if _fillin==1
(1456 real changes made)
```

The posterior mean cumulative probabilities can now be obtained by using the `mu`, `above()`, and `fsample` options (but not the `marginal` option):

```
. gllapred pprobg1, mu above(1) fsample
(mu will be stored in pprobg1)
Non-adaptive log-likelihood:  -1662.1717
-1662.7601 -1662.7600 -1662.7600
log-likelihood:-1662.76
. gllapred pprobg2, mu above(2) fsample
(mu will be stored in pprobg2)
Non-adaptive log-likelihood:  -1662.1717
-1662.7601 -1662.7600 -1662.7600
log-likelihood:-1662.76
. gllapred pprobg3, mu above(3) fsample
(mu will be stored in pprobg3)
Non-adaptive log-likelihood:  -1662.1717
-1662.7601 -1662.7600 -1662.7600
log-likelihood:-1662.76
```

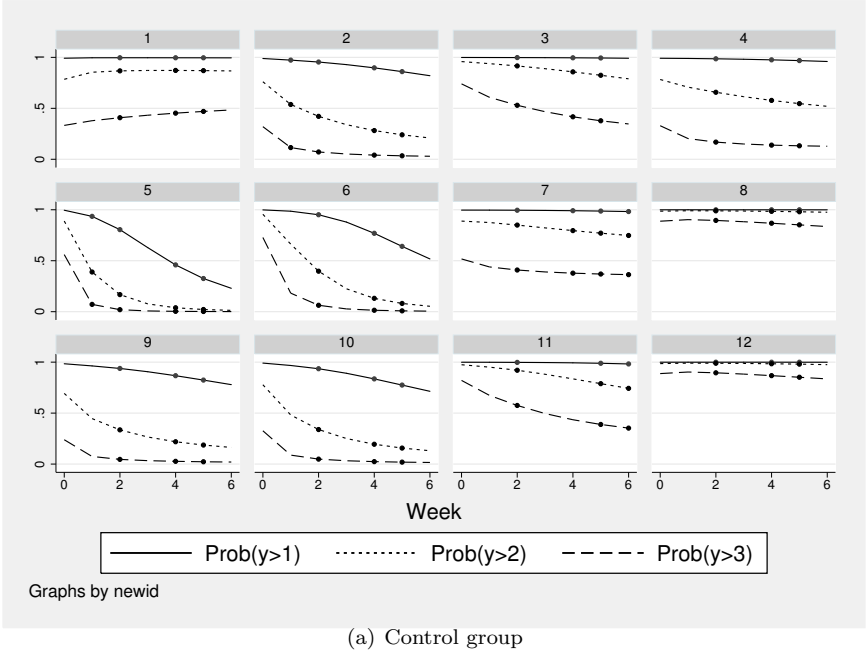
Before plotting the predictions, we define a new identifier, `newid`, that numbers patients within each group from 1:

```
. generate week0 = week==0
. sort treatment id week
. by treatment: generate newid = sum(week0)
```

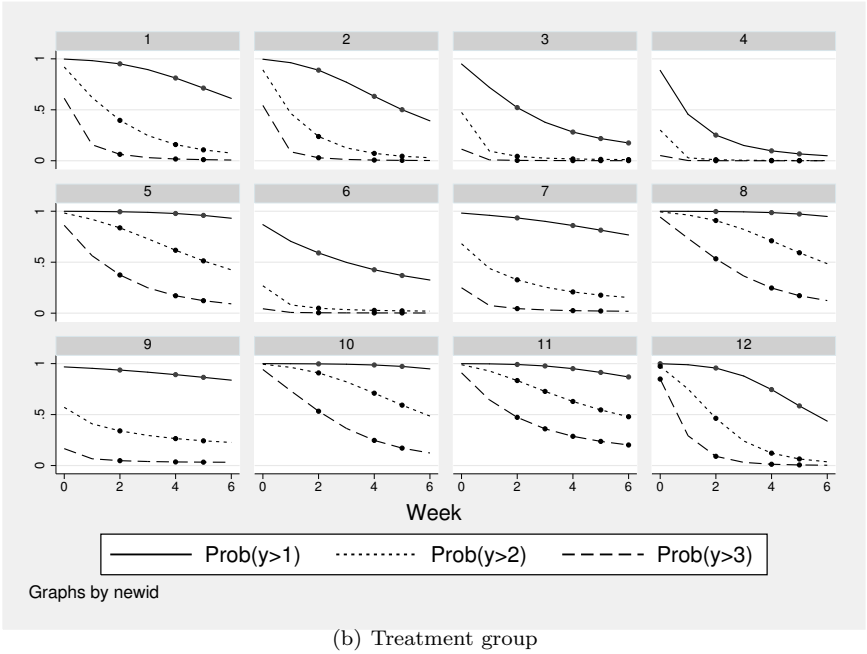
We now use this identifier to plot the curves for twelve subjects in each treatment group:

```
. twoway (line pprobg1 week, sort lpatt(solid))
> (line pprobg2 week, sort lpatt(vshortdash))
> (line pprobg3 week, sort lpatt(dash))
> (scatter pprobg1 week if _fillin==1, msym(o))
> (scatter pprobg2 week if _fillin==1, msym(o))
> (scatter pprobg3 week if _fillin==1, msym(o) mcol(black))
> if newid<13 & treatment==0, by(newid)
> legend(order(1 "Prob(y>1)" 2 "Prob(y>2)" 3 "Prob(y>3)") rows(1)) xtitle("Week")
. twoway (line pprobg1 week, sort lpatt(solid))
> (line pprobg2 week, sort lpatt(vshortdash))
> (line pprobg3 week, sort lpatt(dash))
> (scatter pprobg1 week if _fillin==1, msym(o))
> (scatter pprobg2 week if _fillin==1, msym(o))
> (scatter pprobg3 week if _fillin==1, msym(o) mcol(black))
> if newid<13 & treatment==1, by(newid)
> legend(order(1 "Prob(y>1)" 2 "Prob(y>2)" 3 "Prob(y>3)") rows(1)) xtitle("Week")
```

Here predictions for occasions where the response variable is missing are plotted as dots. The resulting graphs, shown in figure 11.14, illustrate the considerable variability in the course of schizophrenia over time between patients within the treatment groups.



(a) Control group



(b) Treatment group

Figure 11.14: Posterior mean cumulative probabilities for 12 patients in control group and 12 patients in treatment group versus week

11.9 Do experts differ in their grading of student essays?

We now consider data from Johnson and Albert (1999) on grades assigned to 198 essays by five experts. The grades are on a 10-point scale, with 10 being "excellent".

The variables in the dataset `essays.dta` used here are

- `essay`: identifier for essays (j)
- `grade`: grade on 10-point scale
- `grader`: identifier of expert grader (i)

We read in the data by typing

```
. use http://www.stata-press.com/data/mlmus3/essays, clear
```

The data can be considered as interrater reliability data. They are similar to the peak-expiratory-flow data considered in chapter 2 except that we have five experts instead of two methods and no replicate measurements for a given expert. However, the grades are on an ordinal scale instead of an interval scale.

It is useful to obtain a frequency table of the response:

```
. tabulate grade
```

grade	Freq.	Percent	Cum.
1	106	10.71	10.71
2	145	14.65	25.35
3	115	11.62	36.97
4	127	12.83	49.80
5	135	13.64	63.43
6	100	10.10	73.54
7	103	10.40	83.94
8	159	16.06	100.00
Total	990	100.00	

This output shows that the top grades of 9 and 10 were never used and that the remaining eight grades all occur at similar frequencies.

11.10 A random-intercept probit model with grader bias

11.10.1 Model specification

We consider a cumulative ordinal probit model with a random intercept, $\zeta_j \sim N(0, \psi)$. The initial model for the grade y_{ij} assigned by grader i to essay j is

$$\Pr(y_{ij} > s \,|\, \zeta_j) \;=\; \Phi(\zeta_j - \kappa_s)$$

where $\Phi(\cdot)$ is the standard normal cumulative density function.

This model can also be written using the latent-response formulation, with the latent-response model and the threshold model specified as

$$y^*_{ij} = \zeta_j + \epsilon_{ij}, \qquad \zeta_j \sim N(0,\psi), \quad \epsilon_{ij}|\zeta_j \sim N(0,\theta) \tag{11.5}$$

$$y_{ij} = s \qquad \text{if } \kappa_{s-1} < y^*_{ij} \leq \kappa_s, \quad s = 1,\ldots,S \tag{11.6}$$

respectively. When the threshold model is written in this compact form, we must also state that $\kappa_0 = -\infty$ and $\kappa_S = \infty$. This is a classical test-theory model for y^*_{ij}, where ζ_j represents the truth and ϵ_{ij} represents measurement error. The model assumes that all graders i measure the same truth ζ_j with the same measurement error variance θ and assign grades using the same thresholds κ_s ($s=1,\ldots,S-1$).

At the least, we should allow for grader bias by including grader-specific intercepts β_i. However, one of the intercepts must be set to zero to identify all thresholds. Retaining the threshold model (11.6), we extend the latent-response model (11.5) to

$$y^*_{ij} = \zeta_j + \beta_2 x_{2i} + \beta_3 x_{3i} + \beta_4 x_{4i} + \beta_5 x_{5i} + \epsilon_{ij} \tag{11.7}$$

where $\mathbf{x}_i = (x_{2i}, x_{3i}, x_{4i}, x_{5i})'$ are dummy variables for graders 2–5. The corresponding regression coefficients (β_2, β_3, β_4, and β_5) represent how much more generous or lenient graders 2–5 are than the first grader.

11.10.2 Estimation using gllamm

We start by creating dummy variables for the graders (called `grad1`–`grad5`) by typing

```
. quietly tabulate grader, generate(grad)
```

The random-intercept probit model with grader-specific bias can then be fit by maximum likelihood using `gllamm` with the `link(oprobit)` option:

```
. gllamm grade grad2-grad5, i(essay) link(oprobit) adapt
number of level 1 units = 990
number of level 2 units = 198
log likelihood = -1808.0929
```

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
grade						
grad2	-1.127551	.1123199	-10.04	0.000	-1.347694	-.9074085
grad3	-.6301196	.1102999	-5.71	0.000	-.8463033	-.4139358
grad4	-.673948	.1087182	-6.20	0.000	-.8870318	-.4608642
grad5	-1.283113	.1128503	-11.37	0.000	-1.504295	-1.06193
_cut11						
_cons	-2.760615	.145463	-18.98	0.000	-3.045717	-2.475512
_cut12						
_cons	-1.831267	.1308097	-14.00	0.000	-2.087649	-1.574885
_cut13						
_cons	-1.275763	.1246812	-10.23	0.000	-1.520133	-1.031392
_cut14						
_cons	-.7281207	.1203823	-6.05	0.000	-.9640658	-.4921757
_cut15						
_cons	-.1590002	.1183832	-1.34	0.179	-.3910269	.0730266
_cut16						
_cons	.3013533	.118667	2.54	0.011	.0687702	.5339364
_cut17						
_cons	.8585616	.1224719	7.01	0.000	.6185211	1.098602

```
Variances and covariances of random effects
------------------------------------------------------------------------------

***level 2 (essay)
    var(1): 1.4066991 (.18918365)
------------------------------------------------------------------------------
. estimates store model1
```

We see that grader 1 is the most generous because the estimated coefficients of the dummies for graders 2–5 are all negative. These graders are all significantly more stringent than grader 1 at, say, the 5% level.

11.11 ❖ Including grader-specific measurement error variances

11.11.1 Model specification

Although the above model accommodates grader bias, it is relatively restrictive because it still assumes that all graders i have the same measurement error variance θ. We

can relax this homoskedasticity assumption by retaining the previous models (11.6) and (11.7) except that we now also allow each grader to have a grader-specific residual variance or measurement error variance θ_i:

$$\epsilon_{ij}|\mathbf{x}_i, \zeta_j \;\sim\; N(0, \theta_i)$$

In `gllamm`, this can be accomplished by specifying a linear model for the log standard deviation of the measurement errors:

$$\ln(\sqrt{\theta_i}) = \ln(\theta_i)/2 \;=\; \delta_2 x_{2i} + \delta_3 x_{3i} + \delta_4 x_{4i} + \delta_5 x_{5i} \tag{11.8}$$

In this model for level-1 heteroskedasticity, we have again omitted the dummy variable for the first grader, which amounts to setting the standard deviation of the measurement error for this grader to 1 because $\exp(0) = 1$. A constraint like this is necessary to identify the model because all thresholds κ_s $(s = 1, \ldots, S)$ are freely estimated (see section 11.2.4). In terms of the above parameterization, the measurement error variance θ_i for grader i (apart from grader 1) becomes $\exp(2\delta_i)$.

In this model, each grader has his or her own mean and variance,

$$y^*_{ij}|\zeta_j \sim N(\zeta_j + \beta_i, \theta_i), \quad \beta_1 = 0$$

but applies the same thresholds to the latent responses to generate the observed ratings. The cumulative probabilities are

$$\begin{aligned}\Pr(y_{ij} > s \,|\, \zeta_j) \;=\; \Pr(y^*_{ij} > \kappa_s \,|\, \zeta_j) \;&=\; \Pr\left(\frac{y^*_{ij} - \zeta_j - \beta_i}{\sqrt{\theta_i}} > \frac{\kappa_s - \zeta_j - \beta_i}{\sqrt{\theta_i}}\right) \\ &=\; \Phi\left(\frac{\zeta_j + \beta_i - \kappa_s}{\sqrt{\theta_i}}\right)\end{aligned}$$

This model can be thought of as a generalized linear model with a *scaled probit link*, where the scale parameter $\sqrt{\theta_i}$ differs between graders, i.

11.11.2 Estimation using gllamm

To specify model (11.8) for the log standard deviations of the measurement errors in `gllamm`, we need to first define a corresponding equation:

```
. eq het: grad2-grad5
```

(`gllamm` will not add an intercept to this equation for heteroskedasticity). Then we pass this equation on to `gllamm` using the `s()` option, change the link to `soprobit` (for scaled ordinal probit), and use the previous estimates as starting values:

```
. matrix a = e(b)
. gllamm grade grad2-grad5, i(essay) link(soprobit) s(het) from(a) adapt
number of level 1 units = 990
number of level 2 units = 198

log likelihood = -1767.6284
```

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
grade						
grad2	-1.372239	.1625285	-8.44	0.000	-1.690789	-1.053689
grad3	-.6924764	.183522	-3.77	0.000	-1.052173	-.33278
grad4	-.8134375	.1183584	-6.87	0.000	-1.045416	-.5814594
grad5	-1.552205	.1632283	-9.51	0.000	-1.872127	-1.232284
_cut11						
_cons	-3.443449	.3145287	-10.95	0.000	-4.059914	-2.826984
_cut12						
_cons	-2.248858	.2234508	-10.06	0.000	-2.686814	-1.810902
_cut13						
_cons	-1.547513	.1784254	-8.67	0.000	-1.897221	-1.197806
_cut14						
_cons	-.8606409	.1468759	-5.86	0.000	-1.148512	-.5727694
_cut15						
_cons	-.1507223	.1338984	-1.13	0.260	-.4131584	.1117138
_cut16						
_cons	.420217	.1403799	2.99	0.003	.1450775	.6953565
_cut17						
_cons	1.120534	.1679034	6.67	0.000	.7914498	1.449619

```
Variance at level 1
------------------------------------------------------------------------------

    equation for log standard deviation:

    grad2: .24143083 (.11558242)
    grad3: .72935227 (.1063642)
    grad4: -.09545464 (.13094183)
    grad5: .04306859 (.12477309)

Variances and covariances of random effects
------------------------------------------------------------------------------

***level 2 (essay)

    var(1): 2.0587449 (.41200888)
------------------------------------------------------------------------------
```

We see that grader 3 has the largest estimated measurement error variance of $\exp(0.729)^2 = 4.30$.

We can use a likelihood-ratio test to test the null hypothesis that the measurement error variances are identical for the graders, H_0: $\theta_i = \theta$, against the alternative that the measurement error variances are different for at least two graders:

```
. estimates store model2
. lrtest model1 model2
Likelihood-ratio test                                 LR chi2(4)  =     80.93
(Assumption: model1 nested in model2)                 Prob > chi2 =    0.0000
```

There is strong evidence to suggest that the graders differ in their measurement error variances.

11.12 ❖ Including grader-specific thresholds

11.12.1 Model specification

Model (11.7), which allows for grader bias by including grader-specific intercepts β_i, can equivalently be specified by omitting the β_i from the latent regression model and instead defining grader-specific thresholds

$$\kappa_{si} \;=\; \kappa_s - \beta_i$$

Here all the thresholds of a given grader are translated relative to the thresholds of another grader.

A final model extension would be to allow different graders to apply a different set of thresholds that are not just shifted or translated by a constant between graders:

$$\kappa_{si} \;=\; \alpha_{s1} + \alpha_{s2}x_{2i} + \cdots + \alpha_{s5}x_{5i} \tag{11.9}$$

The model now becomes

$$\Pr(y_{ij} > s \,|\, \zeta_j) \;=\; \Phi\left(\frac{\zeta_j - \kappa_{si}}{\sqrt{\theta_i}}\right) = \Phi\left(\frac{\zeta_j}{\sqrt{\theta_i}} - \frac{\kappa_{si}}{\sqrt{\theta_i}}\right)$$

Here $\sqrt{\theta_i}$ is identified because it determines the effect of ζ_j on the response probabilities for the individual raters. In fact, $1/\sqrt{\theta_i}$ can be interpreted as a discrimination parameter or factor loading, and the model is equivalent to a specific item-response model (see exercise 11.2) called Samejima's graded-response model (see Embretson and Reise [2000] for a discussion of this model). Because the thresholds are free parameters, dividing them by $\sqrt{\theta_i}$ does not modify the threshold model (the ratios $\kappa_{si}/\sqrt{\theta_i}$ can take the same set of values as the original thresholds κ_{si}).

11.12.2 Estimation using gllamm

In `gllamm`, we can specify model (11.9) for the thresholds by first defining an equation:

```
. eq thr: grad2-grad5
```

The intercept α_{s1} will be added by `gllamm` to the equation for the thresholds and does not need to be specified. This equation is then passed to `gllamm` using the `thresh()` option (beware that it takes a long time to fit the model).

```
. gllamm grade, i(essay) link(soprobit) s(het) thresh(thr) from(a) adapt skip
number of level 1 units = 990
number of level 2 units = 198

log likelihood = -1746.814
```

grade	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
_cut11						
grad2	1.728073	.2924749	5.91	0.000	1.154833	2.301314
grad3	1.061355	.3765653	2.82	0.005	.3233002	1.799409
grad4	.6380823	.3413275	1.87	0.062	-.0309073	1.307072
grad5	1.277385	.3128488	4.08	0.000	.6642124	1.890557
_cons	-3.170991	.3363843	-9.43	0.000	-3.830292	-2.51169
_cut12						
grad2	1.654293	.2124865	7.79	0.000	1.237827	2.070759
grad3	1.237556	.2612418	4.74	0.000	.7255312	1.74958
grad4	.9826652	.2164376	4.54	0.000	.5584553	1.406875
grad5	1.53219	.21934	6.99	0.000	1.102292	1.962089
_cons	-2.269541	.240086	-9.45	0.000	-2.740101	-1.798981
_cut13						
grad2	1.668863	.1944094	8.58	0.000	1.287828	2.049899
grad3	1.088168	.2214152	4.91	0.000	.6542024	1.522134
grad4	.8398826	.1800113	4.67	0.000	.4870669	1.192698
grad5	1.738926	.2082086	8.35	0.000	1.330847	2.147009
_cons	-1.658147	.192857	-8.60	0.000	-2.03614	-1.280162
_cut14						
grad2	1.236493	.1748537	7.07	0.000	.8937858	1.5792
grad3	.7111893	.1962876	3.62	0.000	.3264727	1.095906
grad4	.8942423	.1603884	5.58	0.000	.5798868	1.208598
grad5	1.601494	.2126157	7.53	0.000	1.184775	2.018213
_cons	-.8794996	.156047	-5.64	0.000	-1.185346	-.573653
_cut15						
grad2	1.054329	.1857238	5.68	0.000	.6903165	1.418341
grad3	.4492806	.1922589	2.34	0.019	.07246	.8261011
grad4	.8514869	.1742843	4.89	0.000	.509896	1.193078
grad5	1.664346	.2603403	6.39	0.000	1.154089	2.174604
_cons	-.1793809	.1425642	-1.26	0.208	-.4588016	.1000399
_cut16						
grad2	.8328646	.2000713	4.16	0.000	.440732	1.224997
grad3	.3282962	.2088497	1.57	0.116	-.0810417	.7376341
grad4	.7664851	.1991761	3.85	0.000	.3761071	1.156863
grad5	1.409385	.2812254	5.01	0.000	.8581937	1.960577
_cons	.4440509	.1446484	3.07	0.002	.1605452	.7275565
_cut17						
grad2	.466475	.2244542	2.08	0.038	.0265529	.9063971
grad3	.1412568	.2524279	0.56	0.576	-.3534927	.6360063
grad4	.5492535	.2395074	2.29	0.022	.0798276	1.018679
grad5	1.233665	.3404629	3.62	0.000	.5663696	1.90096
_cons	1.233925	.1691786	7.29	0.000	.9023413	1.565509

```
Variance at level 1
------------------------------------------------------------------------------

    equation for log standard deviation:

    grad2: -.20109559 (.16420779)
    grad3: .45238552 (.15515942)
    grad4: -.13881034 (.1708705)
    grad5: .03002795 (.16735946)

Variances and covariances of random effects
------------------------------------------------------------------------------

***level 2 (essay)

    var(1): 1.676465 (.40806705)
------------------------------------------------------------------------------
```

Here the coefficient `[_cut16]_cons` is the estimate of $\kappa_{61} = \alpha_{61}$, the sixth threshold for grader 1, whereas `[_cut16]grad2` is the estimate of α_{62}, the difference between the sixth thresholds for graders 2 and 1.

A likelihood-ratio test again suggests that the more elaborate model is preferred:

```
. estimates store model3
. lrtest model2 model3
Likelihood-ratio test                                 LR chi2(24) =     41.63
(Assumption: model2 nested in model3)                 Prob > chi2 =    0.0142
```

However, it may not be necessary to relax the parallel-regressions assumption for all graders. For instance, we can consider the null hypothesis that all thresholds for grader 2 are simply translated by a constant relative to those of grader 1:

$$H_0\text{: } \alpha_{12} = \alpha_{22} = \cdots = \alpha_{72}$$

A multivariate Wald test of this null hypothesis can be performed using the `test` command,

```
. test [_cut11=_cut12=_cut13=_cut14=_cut15=_cut16=_cut17]: grad2
 ( 1)  [_cut11]grad2 - [_cut12]grad2 = 0
 ( 2)  [_cut11]grad2 - [_cut13]grad2 = 0
 ( 3)  [_cut11]grad2 - [_cut14]grad2 = 0
 ( 4)  [_cut11]grad2 - [_cut15]grad2 = 0
 ( 5)  [_cut11]grad2 - [_cut16]grad2 = 0
 ( 6)  [_cut11]grad2 - [_cut17]grad2 = 0
           chi2(  6) =   25.60
         Prob > chi2 =    0.0003
```

and similarly for other pairs of graders, keeping in mind that we may have to correct for multiple testing (for instance, using the Bonferroni method by dividing the significance level of each test by the number of tests).

The `thresh()` option can be used more generally to relax the parallel-regressions assumption of constant covariate effects across categories s. As explained in section 11.2.3,

this assumption corresponds to the proportional odds assumption in ordinal logit models. To relax the parallel-regressions assumption for a covariate x_{2i}, we can simply move it to the threshold model (11.9) to estimate $S-1$ threshold parameters α_{s2} ($s=1,\ldots,S-1$) instead of one regression parameter β_2. We cannot estimate both β_2 and the α_{s2} because such a model would not be identified.

Maximum likelihood estimates for the sequence of models developed in this section are given in table 11.2, using the notation for the final model. For "Model 1", the measurement error variances are set to 1, and the thresholds of all graders are set to be equal; that is, in models (11.8) and (11.9), the constraints

$$\delta_i = 0 \quad \text{and} \quad \alpha_{si} = 0, \quad i = 2,3,4,5$$

are in place, but the intercepts β_i for raters 2–5 are free parameters. "Model 2" is the same except that the constraints for the δ_i are relaxed. In "Model 1" and "Model 2", $\alpha_{s1} \equiv \kappa_s$. Finally, in "Model 3" the constraints for both the δ_i and the α_{si} are relaxed, but the intercepts are set to zero: $\beta_i = 0$.

To facilitate comparison of estimates between models, we also report estimates of the "reduced-form" thresholds:

$$\frac{\kappa_{si}}{\sqrt{\theta_i}} = \begin{cases} \frac{\alpha_{s1}-\beta_i}{\exp(\delta_i)} & \text{for } i=1 \\ \frac{\alpha_{s1}+\alpha_{si}-\beta_i}{\exp(\delta_i)} & \text{for } i>1 \end{cases}$$

Table 11.2: Maximum likelihood estimates for essay grading data (for models 1 and 2, $\alpha_{s1} \equiv \kappa_s$)

	Model 1					Model 2					Model 3				
Grader i	1	2	3	4	5	1	2	3	4	5	1	2	3	4	5
β_i	0	−1.1	−0.6	−0.7	−1.3	0	−1.4	−0.7	−0.8	−1.6	0	0	0	0	0
α_{1i}	−2.8	0	0	0	0	−3.4	0	0	0	0	−3.2	1.7	1.1	0.6	1.3
α_{2i}	−1.8	0	0	0	0	−2.2	0	0	0	0	−2.3	1.7	1.2	1.0	1.5
α_{3i}	−1.3	0	0	0	0	−1.5	0	0	0	0	−1.7	1.7	1.1	0.8	1.7
α_{4i}	−0.7	0	0	0	0	−0.9	0	0	0	0	−0.9	1.2	0.7	0.9	1.6
α_{5i}	−0.2	0	0	0	0	−0.2	0	0	0	0	−0.2	1.1	0.4	0.9	1.7
α_{6i}	0.3	0	0	0	0	0.4	0	0	0	0	0.4	0.8	0.3	0.8	1.4
α_{7i}	0.9	0	0	0	0	1.1	0	0	0	0	1.2	0.5	0.1	0.5	1.2
δ_i	0	0	0	0	0	0	0.2	0.7	−0.1	0.0	0	−0.2	0.5	−0.1	0.0
$\frac{\alpha_{1i}-\beta_i}{\exp(\delta_i)}$	−2.8	−1.6	−2.1	−2.1	−1.5	−3.4	−1.6	−1.3	−2.9	−1.8	−3.2	−1.8	−1.3	−2.9	−1.8
$\frac{\alpha_{1i}+\alpha_{2i}-\beta_i}{\exp(\delta_i)}$	−1.8	−0.7	−1.2	−1.2	−0.5	−2.4	−0.7	−0.8	−1.6	−0.7	−2.3	−0.8	−0.7	−1.5	−0.7
$\frac{\alpha_{1i}+\alpha_{3i}-\beta_i}{\exp(\delta_i)}$	−1.3	−0.1	−0.6	−0.6	0.0	−1.5	−0.1	−0.4	−0.8	0.0	−1.7	0.0	−0.4	−0.9	0.0
$\frac{\alpha_{1i}+\alpha_{4i}-\beta_i}{\exp(\delta_i)}$	−0.7	0.4	−0.1	−0.1	0.6	−0.9	0.4	−0.1	−0.1	0.7	−0.9	0.4	−0.1	0.0	0.7
$\frac{\alpha_{1i}+\alpha_{5i}-\beta_i}{\exp(\delta_i)}$	−0.2	1.0	0.5	0.5	1.1	−0.2	1.0	0.3	0.7	1.3	−0.2	1.1	0.2	0.8	1.4
$\frac{\alpha_{1i}+\alpha_{6i}-\beta_i}{\exp(\delta_i)}$	0.3	1.4	0.9	1.0	1.6	0.4	1.4	0.5	1.4	1.9	0.4	1.6	0.5	1.4	1.8
$\frac{\alpha_{1i}+\alpha_{7i}-\beta_i}{\exp(\delta_i)}$	0.9	2.0	1.5	1.5	2.1	1.1	2.0	0.9	2.1	2.6	1.2	2.1	0.9	2.0	2.4
ψ			1.41					2.06					1.68		
Log likelihood			−1808.09					−1767.63					−1746.81		

11.13 ❖ Other link functions

In this chapter, we have considered cumulative logit and probit models for ordinal responses. In both models, the link function (logit or probit) is applied to the probability of being above a given category s. The linear predictor then includes a category-specific intercept $-\kappa_s$ but the coefficients of covariates are assumed constant across categories. With two covariates and no random effects, the linear predictor for category s can be written as

$$\nu_{is} = \beta_2 x_{2i} + \beta_3 x_{3i} - \kappa_s \tag{11.10}$$

This parallel-regressions assumption (that only the intercept differs between categories) translates into the proportional odds assumption if a logit link is used.

Cumulative complementary log-log model

In addition to logit and probit links, we could also apply a complementary log-log link to the probability of being above category s. The link function can be written as

$$\ln[-\ln\{1 - \Pr(y > s)\}]$$

(where we have omitted the i subscript and the conditioning on covariates, as we will do whenever possible in this section). Cumulative complementary log-log link models can be written as latent-response models if $-\epsilon_i$ has a Gumbel or type I extreme value distribution with variance $\pi^2/6$. This distribution is not symmetric, so unlike the logit and probit counterparts, reversing the ordinal scale will change the log likelihood and not simply reverse the sign of the regression coefficients. An appealing property of all cumulative models is that the interpretation of the regression coefficients does not change when groups of adjacent categories are merged. Without random effects, the model can be fit by using the user-contributed command `oglm` (Williams 2010), and with or without random effects using `gllamm` with the `link(ocll)` option. See sections 14.6 and 14.7 for more information on the complementary log-log link function but for binary responses.

Continuation-ratio logit model

In addition to cumulative logit models, there are several other models for ordinal data based on the logit link. In a continuation-ratio logit model, the linear predictor in (11.10) is set equal to the log odds of stopping at a given category s, given that the individual reached at least category s,

$$\begin{aligned} \ln\{\text{Odds}(y = s|y \geq s)\} &= \text{logit}\{\Pr(y = s|y \geq s)\} \\ &= \ln\left\{\frac{\Pr(y = s|y \geq s)}{\Pr(y \neq s|y \geq s)}\right\} = \ln\left\{\frac{\Pr(y = s)}{\Pr(y > s)}\right\} \end{aligned} \tag{11.11}$$

This model is often used for discrete-time survival (see chapter 14), such as the number of semesters until completion of a degree. Then $\Pr(y = s|y \geq s)$, the probability

of completing the degree in semester s given that the student has studied at least s semesters, is called a discrete-time hazard. If a student has not yet completed a degree during the observation period, his or her response is said to be right-censored, and this is easily handled with the continuation-ratio logit link.

If a complementary log-log link is specified for $\Pr(y = s|y \geq s)$ instead of a logit link, the model is equivalent to an interval-censored survival model where the underlying continuous survival time follows a proportional hazards model (see section 14.6).

The model can also be used for any sequential process where a given category can be reached only after reaching the previous category, such as educational attainment ("no high school", "high school", "some college", "college degree"), or stages of development or disease, such as cancer stages (0, I, II, III, and IV). See exercise 14.8 for an example.

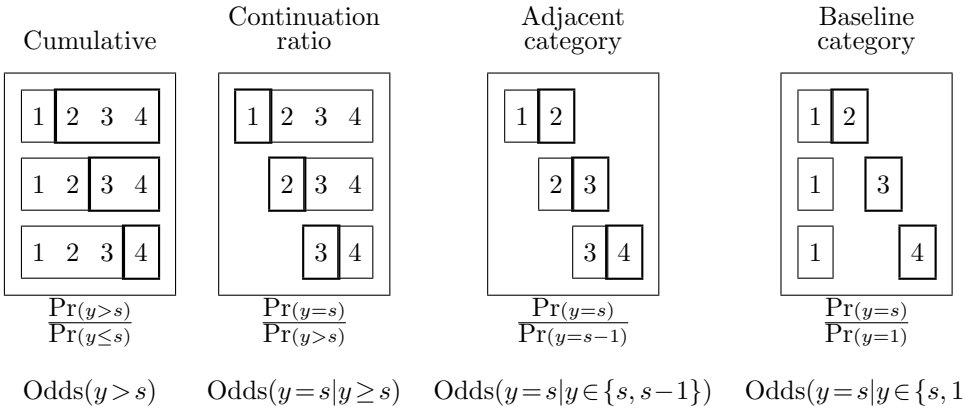


Figure 11.15: Relevant odds for different logit link models for ordinal responses. Events corresponding to "success" are in thick frames, and events corresponding to "failure" are in thin frames—when not all categories are shown, the odds are conditional on the response being in one of the categories shown [adapted from Brendan Halpin's web notes on "Models for ordered categories (ii)"].

The odds involved in the continuation-ratio logit model with four categories are shown in the second column of figure 11.15. The odds are defined as the ratio of two probabilities, as shown in (11.11). The numerator probability is $\Pr(y = s)$, so category s is enclosed in a thick frame for $s = 1, 2, 3$. The corresponding denominator probability is $\Pr(y > s)$, so categories above s are enclosed in a thin frame. The odds are conditional on y being equal to one of the categories that is displayed.

Adjacent-category logit model

Another logit model for ordinal responses is the adjacent-category logit model. Here the linear predictor is equated with

$$\ln\{\text{Odds}(y=s|y\in\{s,s-1\})\}=\text{logit}\{\Pr(y=s|y\in\{s,s-1\})\}=\ln\left\{\frac{\Pr(y=s)}{\Pr(y=s-1)}\right\}$$

A diagram illustrating this model is given in the third row of figure 11.15 for four categories. We see that the probability that $y=s$ (thick frame) is divided by the probability that $y=s-1$ (thin frame) and that the odds should be interpreted as conditional on y being equal to either s or $s-1$. Again, a parallel-regressions assumption is made by constraining the regression coefficients of covariates to be the same for all s. Zheng and Rabe-Hesketh (2007) show how adjacent-category logit models can be fit in `gllamm` with the `link(mlogit)` option.

As discussed for cumulative logit models in section 11.12, the parallel-regressions assumption made by all models discussed so far can be relaxed for some covariates.

Baseline-category logit and stereotype models

The final model displayed in figure 11.15 is the baseline category logit model. In this model, the odds for category s is the ratio of the probability of that category divided by the probability of the baseline category, here category $s=1$. In this model, it is not assumed that covariates have the same coefficient for each category s. With two covariates, the model can be written as

$$\ln\left\{\frac{\Pr(y_i=s|x_i)}{\Pr(y_i=1|x_i)}\right\} \;=\; \beta_1^{[s]}+\beta_2^{[s]}x_{2i}+\beta_3^{[s]}x_{3i}$$

This looks like $s-1$ binary logistic regression models for subsets of the data comprising the category of interest and the baseline category (but some efficiency is gained by fitting the model to all data jointly). Because the model does not impose any constraints on the coefficients, it can be used for nominal or unordered categorical responses (see chapter 12). Baseline category logit models, often simply called multinomial logit models, can be fit in `mlogit` without random effects and in `gllamm` with the `link(mlogit)` option with or without random effects (see chapter 12).

An ordinal version of the multinomial logit model is the stereotype model where category-specific regression coefficients are constrained as follows:

$$\beta_2^{[s]}=\alpha^{[s]}\beta_2 \qquad \beta_3^{[s]}=\alpha^{[s]}\beta_3$$

The ratios of regression coefficients $\beta_k^{[s]}/\beta_k^{[s']}=\alpha^{[s]}/\alpha^{[s\prime]}$ for all pairs of categories s and s' are then the same for all covariates x_{ki}. If the relationship between covariates and the response variable is ordinal, $\alpha^{[1]}\geq\alpha^{[2]}\geq\cdots\geq\alpha^{[S]}$. The Stata command `slogit` can be used to fit stereotype models without random effects, but at the time of writing this book we are not aware of any Stata command for stereotype models with random effects.

11.14 Summary and further reading

We started by introducing cumulative models for ordinal responses, with special emphasis on the proportional odds model. Both the generalized linear and the latent-response formulations of the model were outlined, and the problem of identification in ordinal regression models was discussed. Finally, we discussed various extensions to cumulative models for ordinal responses. The most important is relaxing the parallel-regressions or proportional odds assumption in cumulative models, as shown in (11.9), using the `thresh()` option in `gllamm` (see also exercise 11.7, for which solutions are available).

Cumulative models are sometimes applied to discrete-time duration or survival data. However, this is appropriate only if there is no left- or right-censoring or if the model is extended to handle censoring (see Rabe-Hesketh, Yang, and Pickles [2001b] and Skrondal and Rabe-Hesketh [2004, sec. 12.3]), which is possible using composite links in `gllamm`. More common approaches to modeling discrete-time survival data are discussed in chapter 14.

Other models for ordinal responses were briefly described in section 11.13, and some of these will be discussed in detail in chapters 12 and 14 on nominal or unordered categorical responses and discrete-time survival, respectively. For introductions to these models (mostly without random effects), see for instance, Fahrmeir and Tutz (2001), Agresti (2002, 2010), Long (1997, chap. 5), and Greenland (1994).

Generalized estimating equations (GEE) can be used for ordinal responses, but this is currently not implemented in Stata. However, GEE with an independence structure is easily implemented by fitting an ordinary cumulative logit model and using robust standard errors for clustered data. It is unfortunately not possible to use conditional maximum likelihood estimation for ordinal models with fixed cluster-specific intercepts, in contrast to the dichotomous case.

Useful books discussing random-effects models for ordinal responses include Agresti (2010), Hedeker and Gibbons (2006), and Johnson and Albert (1999), the latter adopting a Bayesian approach. We also recommend the book chapter by Rabe-Hesketh and Skrondal (2009), the encyclopedia entry by Hedeker (2005), and the review article by Agresti and Natarajan (2001). Skrondal and Rabe-Hesketh (2004, chap. 10) analyze several datasets with ordinal responses by using various approaches, including growth-curve modeling.

The exercises of this chapter are based on longitudinal data on children's respiratory status (exercise 11.1), children's recovery after surgery (exercise 11.7), and adults' attitudes to abortion (exercise 11.5); repeated measures data on verbal aggression (exercise 11.2), essay grades (exercise 11.4), and wine assessments by different raters (exercise 11.8); data from a cluster-randomized trial of classroom interventions to prevent smoking (exercise 11.3); cross-sectional data on first graders' math proficiency (exercise 11.9); and on married spouse's closeness to each other (exercise 11.6). Exercise 11.7, for which solutions are provided, involves relaxing the proportional odds assumption.

11.15 Exercises

11.1 Respiratory-illness data

Koch et al. (1990) analyzed data from a clinical trial comparing two treatments for respiratory illness. In each of two centers, eligible patients were randomized to active treatment or placebo. The respiratory status was determined prior to randomization and during four visits after randomization. The dichotomized response was analyzed by Davis (1991) and Everitt and Pickles (2004), among others. Here we analyze the original ordinal response.

The dataset `respiratory.dta` has the following variables:

- `center`: center (1 or 2)
- `patient`: patient identifier
- `drug`: treatment group (1: active treatment; 0: placebo)
- `male`: dummy variable for patient being male
- `age`: age of patient in years
- `bl`: respiratory status at baseline (0: terrible; 1: poor; 2: fair; 3: good; 4: excellent)
- `v1` to `v4`: respiratory status at visits 1–4 (0: terrible; 1: poor; 2: fair; 3: good; 4: excellent)

1. Reshape the data by stacking the responses for visits 1–4 into a single variable.
2. Fit a proportional odds model with `drug`, `male`, `age`, and `bl` as covariates and a random intercept for patients.
3. Check whether there is a linear trend for the logits over time (after controlling for the patient-specific covariates) and whether the slope differs between treatment groups.
4. For your chosen model, plot the model-implied posterior mean cumulative probabilities over time for some of the patients.

11.2 Verbal-aggression data

Consider the data in `aggression.dta` from Vansteelandt (2000) and De Boeck and Wilson (2004), described in exercise 10.4. Use five-point adaptive quadrature to speed up estimation, which will be slow.

1. Fit the following explanatory item-response model for the original ordinal response y_{ij} (0: no; 1: perhaps; 2: yes):

$$\text{logit}\{\Pr(y_{ij} > s|\mathbf{x}_{ij}, \zeta_j)\} = \beta_2 x_{2ij} + \beta_3 x_{3ij} + \beta_4 x_{4ij} + \beta_5 x_{5ij} + \zeta_j - \kappa_s$$

where $s = 0, 1$ and $\zeta_j \sim N(0, \psi)$ can be interpreted as the latent trait "verbal aggressiveness". Item-response models with cumulative logit or probit links for ordinal data are called graded-response models. Interpret the estimated coefficients.

2. Now extend the above model by including a latent regression, allowing verbal aggressiveness (now denoted η_j instead of ζ_j) to depend on the personal characteristics w_{1j} and w_{2j}:

$$\text{logit}\{\Pr(y_{ij} > s|\mathbf{x}_{ij}, \eta_j)\} = \beta_2 x_{2ij} + \beta_3 x_{3ij} + \beta_4 x_{4ij} + \beta_5 x_{5ij} + \eta_j - \kappa_s$$

$$\eta_j = \gamma_1 w_{1j} + \gamma_2 w_{2j} + \zeta_j$$

   Substitute the level-2 model for η_j into the level-1 model for the item responses, and fit the resulting model.

3. ❖ Relax the proportional odds assumption for x_{2ij} (*do* versus *want*). Interpret the estimates, and perform a likelihood-ratio test to assess whether there is any evidence that the proportional odds assumption is violated for this variable.

11.3 Smoking-intervention data

Gibbons and Hedeker (1994) and Hedeker and Gibbons (2006) analyzed data from a subset of the Television School and Family Smoking Prevention and Cessation Project (TVSFP) (see Flay et al. [1988]).

Schools were randomized to one of four conditions defined by different combinations of two factors: 1) TV, a media (television) intervention (1: present; 0: absent), and 2) CC, a social-resistance classroom curriculum (1: present; 0: absent). The outcome measure is the tobacco and health knowledge scale (THKS) score, defined as the number of correct answers to seven items on tobacco and health knowledge. This variable has been collapsed into four ordinal categories.

Students are nested in classes, which are nested in schools. We consider two-level models in this exercise but will revisit the data for three-level modeling in exercise 16.4.

The dataset `tvsfpors.dta` has the following variables:

- `school`: school identifier
- `class`: class identifier
- `thk`: ordinal THKS score postintervention (four categories)
- `prethk`: ordinal THKS score preintervention (four categories)
- `cc`: social-resistance classroom curriculum (dummy variable)
- `tv`: television intervention (dummy variable)

1. Investigate how tobacco and health knowledge is influenced by the interventions by fitting a two-level, random-intercept proportional odds model with students nested in schools. Include the covariates `cc`, `tv`, and their interaction, and control for `prethk`.
   a. Obtain estimated odds ratios for the interventions and interpret these.
   b. Calculate the estimated residual intraclass correlation for the latent responses underlying the observed ordinal response.

2. Fit a two-level, random-intercept proportional odds model with students nested in classes (instead of schools).
   a. Obtain estimated odds ratios for the interventions and interpret these.
   b. Calculate the estimated residual intraclass correlation for the latent responses underlying the observed ordinal response.
   c. Does class or school appear to induce more dependence among students?

See also exercise 16.4 for further analyses of these data.

11.4 Essay-grading data

Here we consider the dataset from Johnson and Albert (1999) that was analyzed in section 11.9.

The dataset `essays.dta` has the following variables:

- `essay`: identifier for essays
- `grade`: grade on 10-point scale
- `grader`: identifier of expert grader
- `wordlength`: average word length
- `sqrtwords`: square root of the number of words in the essay
- `commas`: number of commas $\times$ 100 divided by number of words
- `errors`: percentage of spelling errors
- `prepos`: percentage of prepositions
- `sentlength`: average sentence length

1. For simplicity, collapse the variable `grade` into four categories: {1,2}, {3,4}, {5,6}, and {7,8,9,10}. Fit an ordinal probit model without covariates and with a random intercept for essays. Obtain the estimated intraclass correlation for the latent responses.
2. Include dummy variables for graders 2–5 to allow some graders to be more generous in their grading than others. Does this model fit better?
3. Include the six essay characteristics as further covariates. Interpret the estimated coefficients.
4. Extend the model to investigate whether the graders differ in the importance they attach to the length of the essay (`sqrtwords`). Discuss your findings.

11.5 Attitudes-to-abortion data

Wiggins et al. (1990) analyzed data from the British Social Attitudes (BSA) survey. All adults aged 18 or over and living in private households in Britain were eligible to participate. A multistage sample was drawn, and in this dataset we have identifiers for districts that were drawn at stage 2. Respondents were sampled in stage 3. A subset of the respondents in the 1983 survey were followed up each year until 1986. Here we analyze the subset of respondents with complete

data at all four waves that can be downloaded from the webpage of the Centre for Multilevel Modelling at the University of Bristol.

The respondents were asked for each of seven circumstances whether abortion should be allowed by law. The circumstances included "The woman decides on her own that she does not wish to have the child" and "The woman became pregnant as a result of rape". The variables in the dataset `abortion.dta` are

- `district`: district identifier
- `person`: subject identifier
- `year`: year (1–4)
- `score`: number of items (circumstances) where respondents answered "yes" to the question if abortion should be allowed by law (0–7)
- `male`: dummy variable for being male
- `age`: age in years
- `religion`: religion (1: catholic; 2: protestant; 3: other; 4: none)
- `party`: party chosen (1: conservative; 2: labour; 3: liberal; 4: other; 5: none)
- `class`: self-assessed social class (1: middle class; 2: upper working class; 3: lower working class)

1. Recode the variable `score` to merge the relatively rare responses 0, 1, and 2 into one category.
2. Fit an ordinal logistic regression model with the recoded `score` variable as the response and with `male`, `age`, and dummy variables for `religion` and `year` as covariates. Use the `vce(cluster person)` option to obtain appropriate standard errors. Obtain odds ratios and interpret them.
3. Now include a normally distributed random intercept for subjects in the above model. You can use the `nip(5)` option to speed up estimation and get relatively accurate estimates.
   a. Is there any evidence for residual between-subject variability in attitudes to abortion?
   b. Compare the estimated odds ratios for this model with the odds ratios for the model not including a random intercept. Explain why they differ the way they do.
   c. Obtain the estimated residual intraclass correlation for the latent responses.
   d. The model does not take the clustering of subjects within districts into account. The `cluster()` option can be used to obtain standard errors based on the sandwich estimator that take clustering into account. Either include the `cluster(district)` option in the `gllamm` command when fitting the model or fit the model without this option, and then issue the command

```
gllamm, cluster(district)
```

11.6 Marriage data

Kenny, Kashy, and Cook (2006) analyzed data from Acitelli (1997) on 148 married couples. Both husbands and wives were asked to rate their closeness to their spouse, their commitment to the marriage, and their satisfaction with the marriage. The length of the marriage at the time of data collection was also recorded.

The variables in the dataset `marriage.dta` are

- `couple`: couple identifier
- `husband`: dummy variable for being the husband
- `close`: closeness, rated from 1 to 4 (from less close to closer)
- `commit`: commitment, rated from 1 to 4
- `satis`: satisfaction, rated from 1 to 4
- `lmarr`: length of marriage in years

1. Fit an ordinal probit model for the variable `close` for both spouses including a random intercept for couples and a dummy variable for the wife. Assume that husbands and wives have the same threshold parameters.
2. Obtain the estimated residual intraclass correlation for the latent responses.
3. Investigate whether length of marriage has an impact on closeness, allowing for different regression coefficients for husbands and wives.
   a. Write down the model using the latent-response formulation.
   b. Fit the model.
4. Interpret the estimated odds ratios.
5. State the following null hypotheses in terms of the model parameters and conduct hypothesis testing (with two-sided alternatives) using Stata:
   a. The coefficient of length of marriage is zero for husbands.
   b. The coefficient of length of marriage is zero for wives.
   c. The coefficients of length of marriage are zero both for husbands and wives (jointly).
   d. The coefficients of length of marriage are equal for husbands and wives.
6. ❖ In the model from step 3, relax the assumption that the residual variance in the latent-response formulation is the same for husbands and wives (see section 11.11 on using the `s()` option in `gllamm`). Use a likelihood-ratio test to compare this model with the model from step 3.

11.7 Recovery after surgery data Solutions

Davis (1991, 2002) analyzed data from a clinical trial comparing the effects of different dosages of anesthetic on postsurgical recovery. Sixty young children undergoing outpatient surgery were randomly assigned to four groups of size 15, receiving 15, 20, 25, and 30 milligrams of anesthetic per kilogram of body weight. Recovery was assessed upon admission to the recovery room (0 minutes) and 5,

15, and 30 minutes after admission to the recovery room. The recovery score was an ordinal variable with categories 1 (least favorable) through 6 (most favorable).

The variables in `recovery.dta` are

- `dosage`: dosage of anesthetic in milligram per kilogram bodyweight
- `id`: subject identifier, taking values 1–15 in each dosage group
- `age`: age of child in months
- `duration`: duration of surgery in minutes
- `score1`, `score2`, `score3`, `score4`: recovery scores 0, 5, 15, and 30 minutes after admission to the recovery room

1. Reshape the data to long form, stacking the recovery scores at the four occasions into a single variable and generating an identifier, `occ`, for the four occasions. (You can specify several variables in the `i()` option of the `reshape` command if one variable does not uniquely identify the individuals.) Recode the recovery score to four categories (to simplify some of the commands below) by merging {0,1}, {2,3}, and {4,5} and calling the new categories 1, 2, 3, and 4.
2. Construct a variable, `time`, taking the values 0, 5, 15, and 30 at the four occasions. Fit a random-intercept proportional odds model with dummy variables for the dosage groups, `age`, `duration`, and `time` as covariates. (Make sure there are 60 level-2 clusters.)
3. Compare the model from step 2 with a model including `dosage` as a continuous covariate instead of the dummy variables for dosage groups, using a likelihood-ratio test at the 5% significance level.
4. Extend the model chosen in step 3 to include an interaction between `dosage` and `time`. Test the interaction using a Wald test at the 5% level of significance.
5. For the model selected in step 4, interpret the estimated odds ratios and random-intercept variance.
6. ❖ Extend the model selected in step 4 by relaxing the proportional odds assumption for dosage (see section 11.12 on using the `thresh()` option in `gllamm` to relax proportional odds). Test whether the odds are proportional by using a likelihood-ratio test.
7. For age equal to 37 months, duration equal to 80 minutes, and time in recovery room equal to 15 minutes, produce a graph of predicted marginal probabilities similar to figure 11.13 for the model selected in step 6 or for the model selected in step 4. Also produce a stacked bar chart, treating dosage group as categorical.

11.8 Wine-tasting data

In exercise 10.9, data on judges' bitterness ratings of white wines were analyzed. There we considered a binary response, `bitter`, taking on the values 1: bitter and

0: nonbitter. In this exercise, we will also analyze the original ordinal variable, `bitterness`. Judges were asked to indicate the intensity of bitterness by making a mark on a horizontal line marked "none" at one end and "intense" at the other. The categories were derived by dividing the line into five intervals of equal length and assigning the values 1–5 according to the interval in which the mark was located.

The following model will be used to analyze `bitterness`:

$$\ln\left\{\frac{\Pr(y_{ij}>s|x_{2ij},x_{3ij},\zeta_j)}{\Pr(y_{ij}\leq s|x_{2ij},x_{3ij},\zeta_j)}\right\} = \beta_2 x_{2ij} + \beta_3 x_{3ij} + \zeta_j - \kappa_s$$

where x_{2ij} is the temperature, `temp`, and x_{3ij} is a dummy variable, `contact`, for skin contact. It is assumed that $\zeta_j \sim N(0,\psi)$ is independent across judges and independent of x_{2ij} and x_{3ij}.

1. Fit the random-intercept proportional odds model given above and store the estimates.
2. Interpret the estimates.
3. Fit a random-intercept binary logistic regression model with response variable `bitter` that has the same linear predictor as above with $-\kappa_s$ replaced by β_1.
4. Comment on how the estimates from step 3 compare with those for the proportional odds model in step 1.
5. Obtain predicted marginal probabilities that the bitterness ratings are above 3 for the models in steps 1 and 3 (`bitter` is an indicator for `bitterness` being above 3) and use graphs to compare the predictions.

11.9 Early childhood math proficiency data

Here we analyze data from the Early Childhood Longitudinal Study—kindergarten cohort (ECLS-K), made available by O'Connell and McCoach (2008) and analyzed by O'Connell et al. (2008). In the ECLS-K, a random sample of kindergarten children was drawn from a random sample of U.S. schools in 1998 and followed up into eighth grade.

Here we consider the mathematics proficiency for a subsample of the children as they neared the end of first grade. Specifically, the children were native English speakers, were not repeating first grade, and had not been retained in kindergarten. Furthermore, only schools with complete information on school-level variables and with at least five children in the sample were selected. Finally, students with missing data on student-level variables of interest were dropped.

The response variable is math proficiency conceptualized as the highest developmental milestone reached by the child. Five clusters of four test items each were used to assess learning milestones in mathematics. Getting any three items within a cluster correct was viewed as passing the milestone, and it was verified that children who pass a given milestone have also mastered all the previous milestones (only 5% of response patterns did not fit this hierarchical structure). The milestones are (Rock and Pollack 2002)

1 Number and shape: identifying some one-digit numerals, recognizing geometric shapes, and one-to-one counting of up to ten objects.

2 Relative size: reading all single-digit numerals, counting beyond ten, recognizing a sequence of patterns, and using nonstandard units of length to compare objects.

3 Ordinary number sequence: reading two-digit numerals, recognizing the next number in a sequence, identifying the ordinal position of an object, and solving a simple word problem.

4 Addition/subtraction: solving simple addition and subtraction problems.

5 Multiplication/division: solving simple multiplication and division problems and recognizing more complex number patterns.

Mathematics proficiency was rated 0 if the child did not pass proficiency level 1, and 1–5 according to the highest proficiency level passed.

There are two datasets: `ecls_child.dta` contains the student-level data, whereas `ecls_school.dta` contains the school-level data. The variables in these datasets that we will use here are the following:

- `ecls_child.dta`
  - `s4_id`: school identifier (string variable)
  - `profmath`: proficiency level (0 to 5)
  - `numrisks`: number of risk factors out of the following four: living in a single parent household, living in a family that receives welfare payments or food stamps, having a mother with less than a high school education, and having parents whose primary language is not English
- `ecls_school.dta`
  - `s4_id`: school identifier (string variable)
  - `nbhoodcl`: neighborhood climate, a composite of the principal's perception of six specific problems in the vicinity of the school, including extent of litter, drug activity, gang activity, crime, violence, and existence of vacant lots or homes
  - `pubpriv2`: dummy variable for school being private (1: private, 0: public)

1. Use the `merge` command to combine the two datasets.
2. Create a numeric school identifier from the string variable `s4_id`.
3. Summarize the student-level and school-level variables, treating school as the unit of analysis when summarizing school-level variables (see section 3.2.1).
4. Following O'Connell et al. (2008), fit a proportional odds model to the math proficiency data with `numrisks`, `nbhoodcl`, and `pubpriv2` as covariates. Because `profmath` takes the value 0 for only nine children, merge the lowest two categories before fitting the model.
5. Interpret the estimates.

6. Obtain predicted marginal probabilities of proficiency being 4 or 5 for all possible combinations of `numrisks` and `pubpriv2` when `nbhoodcl` takes the value 0. Plot the predicted probabilities versus `numrisks` with separate lines for public and private schools.

See also exercise 14.8, where we consider continuation-ratio logit models for these data.

12 Nominal responses and discrete choice

12.1 Introduction

A nominal variable is a categorical variable with categories that do not have a unique ordering. An example from biomedicine is blood type with categories "O", "A", "B", and "AB". A classical example from economics is the choice of travel mode from the set of alternatives "plane", "train", "bus", and "car". In marketing, the purchasing behavior of consumers is important, for instance, the brand of yogurt that is bought among the alternatives "Yoplait", "Dannon", and "Weight Watchers". In political science, a central nominal variable is the political party voted for in an election, such as "Labour", "Conservatives", or "Liberal Democrats" in the United Kingdom. The last three examples all concern individuals' choices from a discrete set of alternatives or, in other words, *discrete choices*. While it may be possible to order the categories of nominal variables according to some criterion, there is not one unique ordering as for ordinal variables.

Sometimes variables have partially ordered categories, such as Likert-scale items for attitude measurement with a "don't know" category, labeled, for instance, as "disagree strongly", "disagree", "agree", "agree strongly", and "don't know". These kinds of responses are often treated as ordinal, with "don't know" ordered between "disagree" and "agree". However, this may not be appropriate because lack of knowledge does not necessarily imply a neutral attitude. It might instead be preferable to treat such partially ordered responses as nominal.

In this chapter, we generalize the multilevel models for dichotomous responses discussed in chapter 10 to handle nominal responses and discrete choices. Many of the issues discussed in that chapter persist for multilevel modeling of nominal responses. The main difference between the logistic models considered here and those discussed in the chapter on dichotomous responses is that several odds ratios involving different pairs of categories must now be considered.

Models for nominal responses can include covariates characterizing the subjects (or units), the alternatives (or categories), or the combination of subjects and alternatives. For example, for choice of mobile (or cell) phone, the age of the customer characterizes the subject, the price characterizes the alternative, and whether any friends have the phone characterizes the subject and alternative combination.

It is common to distinguish between two kinds of logistic models for nominal responses. Multinomial logit models are for subject-specific covariates only and are popular, for instance, in biostatistics. In contrast, conditional logit models traditionally use covariates that vary between alternatives and possibly between subjects as well and are popular, for instance, in economics. As we will see later, the multinomial logit model can actually be viewed as a special case of the conditional logit model. Both types of models can be specified either directly, writing down the expression for the probability that the response falls in a particular category, or via a utility-maximization formulation where the category with the highest utility or attractiveness is chosen. The utility-maximization formulation was developed in psychometrics and econometrics, and the term "discrete choice" is often used in economics.

We start by describing single-level models for nominal responses, using the direct formulation to introduce multinomial logit models and conditional logit models before discussing the utility-maximization formulation of these models. We then extend these models to the multilevel and longitudinal setting by including random effects in the linear predictor.

12.2 Single-level models for nominal responses

In this section, we consider a nominal response variable y_i with S unordered categories denoted $s = 1, \ldots, S$. Regression models for nominal responses are often called "multinomial" because the conditional distribution of the response given the covariates is a multinomial distribution for the S possible categories of the response. The multinomial distribution was also used for ordinal responses in the previous chapter, and the special case of the binomial distribution (where $S = 2$) was used in chapter 10.

We first discuss multinomial logit models for covariates that vary only over subjects i but do not vary over response categories or alternatives s. Thereafter, we describe conditional logit models for covariates that vary between alternatives or response categories s and possibly between subjects i.

12.2.1 Multinomial logit models

Recall the binary logistic regression model (10.2) for a single covariate x_i that we discussed in chapter 10. There we only specified $\Pr(y_i = 1|x_i)$ because $\Pr(y_i = 0|x_i) = 1 - \Pr(y_i = 1|x_i)$, but these probabilities can be written as

$$\begin{aligned} \Pr(y_i = 0|x_i) &= \frac{1}{1 + \exp(\beta_1 + \beta_2 x_i)} \\ \Pr(y_i = 1|x_i) &= \frac{\exp(\beta_1 + \beta_2 x_i)}{1 + \exp(\beta_1 + \beta_2 x_i)} \end{aligned}$$

The denominator for the two probabilities above is the sum of the numerators, guaranteeing that the probabilities sum to one.

For the case of $S = 3$ categories (typically coded 1, 2, and 3 in this context), a natural extension would be to model the probabilities that $y_i = 1$, $y_i = 2$, and $y_i = 3$ as

$$\begin{aligned}
\Pr(y_i = 1|x_i) &= \frac{1}{1 + \exp(\beta_1^{[2]} + \beta_2^{[2]} x_i) + \exp(\beta_1^{[3]} + \beta_2^{[3]} x_i)} \\
\Pr(y_i = 2|x_i) &= \frac{\exp(\beta_1^{[2]} + \beta_2^{[2]} x_i)}{1 + \exp(\beta_1^{[2]} + \beta_2^{[2]} x_i) + \exp(\beta_1^{[3]} + \beta_2^{[3]} x_i)} \\
\Pr(y_i = 3|x_i) &= \frac{\exp(\beta_1^{[3]} + \beta_2^{[3]} x_i)}{1 + \exp(\beta_1^{[2]} + \beta_2^{[2]} x_i) + \exp(\beta_1^{[3]} + \beta_2^{[3]} x_i)}
\end{aligned} \tag{12.1}$$

In the binary case, we needed only one intercept and one coefficient, but for three categories, two intercepts and two coefficients are required. We use the superscript [2] for the intercept and coefficient that enter the numerator for category $s = 2$, and we use the superscript [3] for the intercept and coefficient that enter the numerator for category $s = 3$. Again to ensure that the probabilities sum to one, the denominator is equal to the sum of the numerators.

Another way of expressing the three-category model is by defining additional parameters $\beta_1^{[1]}$ and $\beta_2^{[1]}$ for category 1 and setting them to zero, giving the general expression

$$\begin{aligned}
\Pr(y_i = s|x_i) &= \frac{\exp(\beta_1^{[s]} + \beta_2^{[s]} x_i)}{\exp(\beta_1^{[1]} + \beta_2^{[1]} x_i) + \exp(\beta_1^{[2]} + \beta_2^{[2]} x_i) + \exp(\beta_1^{[3]} + \beta_2^{[3]} x_i)} \\
&= \frac{\exp(\beta_1^{[s]} + \beta_2^{[s]} x_i)}{\sum_{c=1}^{3} \exp(\beta_1^{[c]} + \beta_2^{[c]} x_i)}
\end{aligned}$$

In the sum in the denominator, the index c takes the values 1, 2, and 3 to produce the three required terms. The probabilities are the same as in equation (12.1) because $\exp(\beta_1^{[1]} + \beta_2^{[1]} x_i) = \exp(0 + 0x_i) = 1$.

Following the same reasoning, we can consider the general case of S categories where the probability that the response is category s becomes

$$\Pr(y_i = s|x_i) = \frac{\exp(\beta_1^{[s]} + \beta_2^{[s]} x_i)}{\sum_{c=1}^{S} \exp(\beta_1^{[c]} + \beta_2^{[c]} x_i)}, \qquad s = 1, \ldots, S \tag{12.2}$$

Because the coding of the categories is arbitrary, we can designate any category r as *baseline category* or *base outcome* by setting the intercept and coefficients for that category to zero; $\beta_1^{[r]} = 0$ and $\beta_2^{[r]} = 0$. However, in practice, we will often have a preference regarding which category we find it most natural to compare the others with.

Category probabilities from (12.2) are shown in figure 12.1 for $S = 4$ categories (for some made-up values for the coefficients).

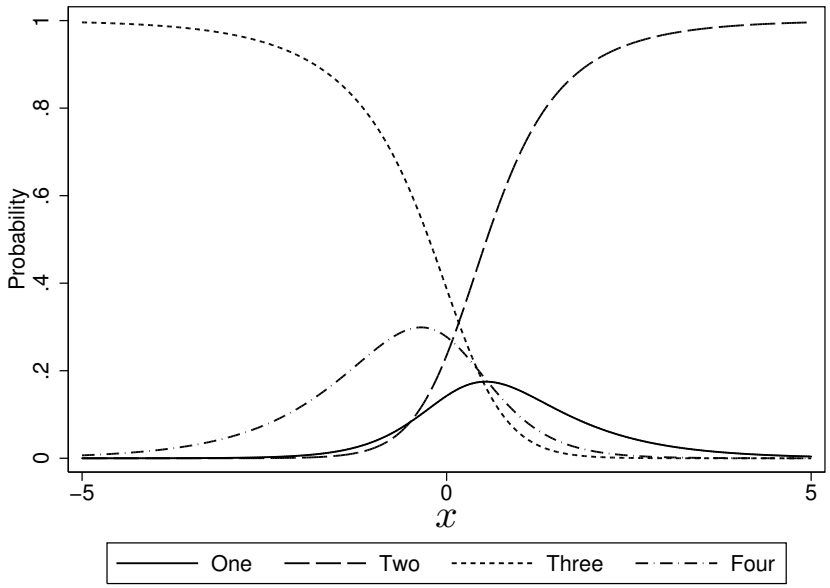


Figure 12.1: Illustration of category probabilities for multinomial logit model with four categories

When there are three or more categories, there will always be one monotonically increasing curve, and one monotonically decreasing curve; the other curve(s) are unimodal with upper and lower tails approaching zero as x becomes extreme. These features of the category probabilities may not be apparent for the range of x observed in a given dataset.

The model can alternatively be expressed as

$$\ln \overbrace{\left\{\frac{\Pr(y_i=s|x_i)}{\Pr(y_i=r|x_i)}\right\}}^{\text{Odds}(y_i=s \text{ vs. } y_i=r|x_i)}$$

$$= \ln\left[\left\{\frac{\exp(\beta_1^{[s]}+\beta_2^{[s]}x_i)}{\sum_{c=1}^{S}\exp(\beta_1^{[c]}+\beta_2^{[c]}x_i)}\right\} \Big/ \left\{\frac{\exp(\beta_1^{[r]}+\beta_2^{[r]}x_i)}{\sum_{c=1}^{S}\exp(\beta_1^{[c]}+\beta_2^{[c]}x_i)}\right\}\right]$$

$$= \ln[\exp\{(\beta_1^{[s]} - \underbrace{\beta_1^{[r]}}_{=0}) + (\beta_2^{[s]} - \underbrace{\beta_2^{[r]}}_{=0})x_i\}] = \beta_1^{[s]} + \beta_2^{[s]}x_i$$

The coefficients represent log odds-ratios for the odds of each category versus the baseline category, and the model is therefore also called a *baseline category logit model*. The relevant odds for a four-alternative example, $S = 4$, where $r = 1$ is chosen as base outcome are shown in figure 12.2

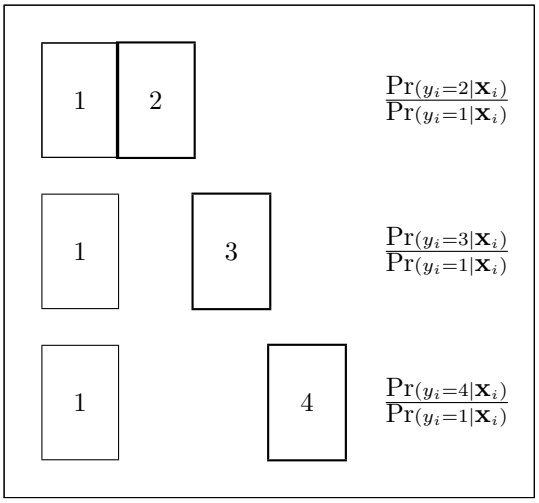


Figure 12.2: Relevant odds $\Pr(y_i = s|\mathbf{x}_i)/\Pr(y_i = 1|\mathbf{x}_i)$ for $(s = 2, 3, 4)$ in a baseline category logit model with four categories. Odds is the ratio of probabilities of events; events included in the numerator probability are in thick frames, and events included in the denominator probability are in thin frames [adapted from Brendan Halpin's web notes on "Models for ordered categories (ii)"].

A one-unit increase in the covariate x_i from some value a to $a + 1$ corresponds to the odds ratio $\text{OR}_{s:r}$ for category s versus the base outcome r.

$$\text{OR}_{s:r} \equiv \frac{\text{Odds}(y_i = s \text{ vs. } y_i = r|x_i = a + 1)}{\text{Odds}(y_i = s \text{ vs. } y_i = r|x_i = a)} = \frac{\exp(\beta_1^{[s]} + \beta_2^{[s]}(a + 1))}{\exp(\beta_1^{[s]} + \beta_2^{[s]}a)} = \exp(\beta_2^{[s]})$$

The odds ratio for category s versus a category other than the base outcome r, say, category t, can simply be obtained as

$$\text{OR}_{s:t} = \exp(\beta_2^{[s]})/\exp(\beta_2^{[t]}) = \exp(\beta_2^{[s]} - \beta_2^{[t]})$$

because

$$\frac{\Pr(y_i = s|x_i)}{\Pr(y_i = t|x_i)} = \frac{\Pr(y_i = s|x_i)}{\Pr(y_i = r|x_i)} \Big/ \frac{\Pr(y_i = t|x_i)}{\Pr(y_i = r|x_i)}$$

To illustrate regression modeling with a nominal response, we will use data from Greene (2012) on choice of transport between Melbourne and Sydney in Australia. The dataset `travel1.dta` contains the travelers' chosen mode of transport and two explanatory variables:

- `traveler`: identifier for traveler
- `alt`: chosen mode of transport
  (1: Air; 2: Train; 3: Bus; 4: Car)
- `Hinc`: household income of traveler in Australian \$1,000 (x_{2i})
- `Psize`: number of people traveling together (x_{3i})

We first read in the dataset,

```
. use http://www.stata-press.com/data/mlmus3/travel1
```

before listing the variables for the first 10 travelers:

```
. list traveler alt Hinc Psize in 1/10, noobs clean
   traveler   alt   Hinc   Psize
          1     4     35       1
          2     4     30       2
          3     4     40       1
          4     4     70       3
          5     4     45       2
          6     2     20       1
          7     1     45       1
          8     4     12       1
          9     4     40       1
         10     4     70       2
```

We see that eight of these individuals drive (alternative or category 4 is car), traveler 6 uses the train, and traveler 7 flies. Note that the covariates `Hinc` and `Psize` are characteristics of the travelers, not specific to the mode of transport for a traveler (a covariate that could depend on the mode of transport would be the cost of travel).

The response variable has four unordered categories $s = 1, \ldots, 4$, and we will use Car (category 4) as the base outcome r henceforth, because we want the parameters to refer to comparisons with this alternative. We specify the following multinomial logit model:

$$\Pr(y_i = s|x_{2i}, x_{3i}) \;=\; \frac{\exp(\beta_1^{[s]} + \beta_2^{[s]} x_{2i} + \beta_3^{[s]} x_{3i})}{\sum_{c=1}^{4} \exp(\beta_1^{[c]} + \beta_2^{[c]} x_{2i} + \beta_3^{[c]} x_{3i})}, \qquad s = 1, \ldots, 4$$

where $\beta_1^{[4]} = \beta_2^{[4]} = \beta_3^{[4]} = 0$.

The model can be fit by maximum likelihood using the `mlogit` command (for "multinomial logit"). We use the `baseoutcome(4)` option to designate Car as the base outcome (Stata otherwise uses the most frequent category, in this case Train, as base outcome).

```
. mlogit alt Hinc Psize, baseoutcome(4)
Multinomial logistic regression                 Number of obs   =        210
                                                LR chi2(6)      =      60.84
                                                Prob > chi2     =     0.0000
Log likelihood = -253.34085                     Pseudo R2       =     0.1072

------------------------------------------------------------------------------
         alt |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
1            |
        Hinc |   .0035438   .0103047     0.34   0.731    -.0166531    .0237407
       Psize |  -.6005541   .1992005    -3.01   0.003    -.9909798   -.2101284
       _cons |   .9434923    .549847     1.72   0.086    -.1341881    2.021173
-------------+----------------------------------------------------------------
2            |
        Hinc |  -.0573078   .0118416    -4.84   0.000    -.0805169   -.0340987
       Psize |  -.3098126   .1955598    -1.58   0.113    -.6931028    .0734775
       _cons |   2.493848   .5357211     4.66   0.000     1.443854    3.543842
-------------+----------------------------------------------------------------
3            |
        Hinc |  -.0303253   .0132228    -2.29   0.022    -.0562415    -.004409
       Psize |   -.940414   .3244532    -2.90   0.004    -1.576331   -.3044974
       _cons |   1.977971    .671715     2.94   0.003     .6614334    3.294508
-------------+----------------------------------------------------------------
4            |  (base outcome)
------------------------------------------------------------------------------
```

For each category of the response, apart from the base outcome, the output gives the estimated intercept $\widehat{\beta}_1^{[s]}$ and coefficients $\widehat{\beta}_2^{[s]}$ and $\widehat{\beta}_3^{[s]}$. It also shows the estimated standard errors; Wald statistics `z` with corresponding p-values, `P>|z|`; and 95% confidence intervals for the parameters. In the top panel where `alt` is `1`, estimates are given for alternative 1, Air versus the base outcome 4, which is Car. In the panel labeled `2`, estimates for Train versus Car are given, and the panel labeled `3` contains estimates for Bus versus Car. The final panel, labeled `4` for the base outcome (which the other alternatives are compared with), is empty. The estimated coefficients and their standard errors are also given under "Only traveler-specific covariates" in table 12.1.

Table 12.1: Estimates for nominal regression models for choice of transport

	Multinomial logit				Conditional logit							
	Only traveler-specific covariates				Only alternative-specific covar.				Both traveler & alt.-specific covar.			
	Est	(SE)	OR	(95% CI)	Est	(SE)	OR	(95% CI)	Est	(SE)	OR	(95% CI)
Traveler-specific covariates												
Air												
$\beta_1^{[1]}$ [_cons]	0.94	(0.55)							7.87	(0.99)		
$\beta_2^{[1]}$ [Hinc]	0.00	(0.01)	1.00	(0.98, 1.02)					0.00	(0.01)	1.00	(0.98, 1.03)
$\beta_3^{[1]}$ [Psize]	−0.60	(0.55)	0.55	(0.37, 0.81)					−1.03	(0.27)	0.36	(0.21, 0.60)
Train												
$\beta_1^{[2]}$ [_cons]	2.49	(0.54)							5.56	(0.70)		
$\beta_2^{[2]}$ [Hinc]	−0.06	(0.01)	0.94	(0.92, 0.97)					−0.06	(0.01)	0.95	(0.92, 0.97)
$\beta_3^{[2]}$ [Psize]	−0.31	(0.20)	0.73	(0.50, 1.08)					−0.30	(0.23)	1.35	(0.87, 2.11)
Bus												
$\beta_1^{[3]}$ [_cons]	1.98	(0.67)							4.43	(0.78)		
$\beta_2^{[3]}$ [Hinc]	−0.03	(0.01)	0.97	(0.95, 1.00)					−0.02	(0.02)	0.98	(0.95, 1.01)
$\beta_3^{[3]}$ [Psize]	−0.94	(0.32)	0.39	(0.21, 0.74)					−0.03	(0.33)	0.97	(0.50, 1.87)
Alternative-specific covariates												
β_2 [CC]					-0.01	(0.00)	0.99	(0.98,1.00)	-0.02	(0.01)	0.98	(0.97,0.99)
β_3 [Ttime]					-0.01	(0.00)	0.99	(0.98,0.99)	-0.10	(0.11)	0.90	(0.88,0.92)
Log likelihood			−253.34				−270.11†				−177.45†	

†Log conditional likelihood

Rather than considering changes in log odds, most people find it more informative to interpret odds ratios, comparing the odds for an alternative versus the base outcome (here Car) for a unit difference in a covariate. We use "odds" to refer to the probability of a category s divided by the probability of another category r. Strictly speaking, it is the conditional odds given that the category is r or s. In contrast, Stata's definition of "odds" is the probability of a category s divided by the probability of the complement (all other categories than s), and what we have called "odds ratios" (ORs) are referred to as "relative-risk ratios" (RRRs). Display 12.1 shows that the odds ratios can be interpreted as relative-risk ratios (this can be skipped if you like).

$$\overbrace{\frac{\text{Odds}(y_i = s \text{ vs. } y_i = r | x_i = a+1)}{\text{Odds}(y_i = s \text{ vs. } y_i = r | x_i = a)}}^{\text{Odds ratio used in this book}} = \frac{\Pr(y_i = s|x_i = a+1)/\Pr(y_i = r|x_i = a+1)}{\Pr(y_i = s|x_i = a)/\Pr(y_i = r|x_i = a)}$$

$$= \underbrace{\frac{\text{Risk ratio}(y_i = s|x_i = a+1 \text{ vs. } x_i = a)}{\text{Risk ratio}(y_i = r|x_i = a+1 \text{ vs. } x_i = a)}}_{\text{Stata's relative-risk ratio}} = \frac{\Pr(y_i = s|x_i = a+1)/\Pr(y_i = s|x_i = a)}{\Pr(y_i = r|x_i = a+1)/\Pr(y_i = r|x_i = a)}$$

Display 12.1: Odds ratio used in this book equals Stata's relative-risk ratio

Estimated odds ratios can be obtained by using the `mlogit` command but now with the `rrr` option (for "relative-risk ratio"). We also define value labels for `alt` to make them appear in the output instead of the numerical values of `alt`:

```
. label define modelabels 1 "Air" 2 "Train" 3 "Bus" 4 "Car"
. label values alt modelabels
```

We fit the model using `mlogit`:

```
. mlogit alt Hinc Psize, baseoutcome(4) rrr
Multinomial logistic regression                 Number of obs   =        210
                                                LR chi2(6)      =      60.84
                                                Prob > chi2     =     0.0000
Log likelihood = -253.34085                     Pseudo R2       =     0.1072

------------------------------------------------------------------------------
         alt |        RRR   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
Air          |
        Hinc |    1.00355   .0103413     0.34   0.731     .9834848    1.024025
       Psize |    .5485076    .109263    -3.01   0.003     .3712128    .8104802
       _cons |    2.568937   1.412523     1.72   0.086     .8744256    7.547171
-------------+----------------------------------------------------------------
Train        |
        Hinc |    .9443033   .0111821    -4.84   0.000     .9226393    .9664761
       Psize |    .7335844   .1434596    -1.58   0.113     .5000222    1.076244
       _cons |    12.10778   6.486392     4.66   0.000     4.236994     34.5996
-------------+----------------------------------------------------------------
Bus          |
        Hinc |    .9701299   .0128279    -2.29   0.022     .9453108    .9956007
       Psize |    .3904662    .126688    -2.90   0.004     .2067323    .7374939
       _cons |     7.22806   4.855196     2.94   0.003     1.937568    26.96414
-------------+----------------------------------------------------------------
Car          |  (base outcome)
------------------------------------------------------------------------------
```

These estimated odds ratios with their 95% confidence intervals were also reported in table 12.1 under "Only traveler-specific covariates". It is often useful to express odds ratios as percentage changes using $100\%(\text{OR} - 1)$. We see that household income does not appear to affect the odds of traveling by air compared with going by car (the base outcome) because the estimated odds ratio of 1.004 is practically 1 with a 95% confidence interval including 1, controlling for the number of people traveling together. However, for given a number of travelers, the odds of taking the train compared with driving is reduced by an estimated 6% [$-6\% = 100\%(0.9443033-1)$] per \$1,000 increase in income, and the odds of taking the bus compared with driving is reduced by an estimated 3% [$-3\% = 100\%(0.9701299 - 1)$] per \$1,000. According to the fitted model, increasing the number of people traveling together reduces the odds of flying, taking the train, and taking the bus versus driving considerably, for given household income. Specifically, the odds of flying compared with driving is reduced by an estimated 45% [$-45\% = 100\%(0.5485076 - 1)$], the odds of taking the train compared with driving is reduced by an estimated 27% [$-27\% = 100\%(0.7335844 - 1)$], and the odds of taking the bus compared with driving is reduced by an estimated 61% [$-61\% = 100\%(0.3904662 - 1)$] per person traveling.

12.2.2 Conditional logit models

In conditional logit models, there are covariates that characterize the alternatives instead of characterizing the units as in multinomial logit models. The covariates are often called the attributes of the different alternatives. An example would be the cost of traveling

by Air, Train, Bus, or Car. A change in an attribute, such as cost, is assumed to have the *same* effect β for all alternatives, so there are no alternative-specific coefficients for attributes. This makes it possible to make predictions of the marginal probability (for example, market share) for a hypothetical alternative (for example, product), because we can use the estimated β to obtain predictions for hypothetical alternatives that are not in the data.

Much of the theory and practice of conditional logit modeling was developed by the econometrician Daniel McFadden to forecast usage of the Bay Area Rapid Transit (BART) system, a subway (underground) system in the San Francisco Bay area of the U.S.A., before it was open for service.

Classical conditional logit models

We first consider the classical conditional logit models for a single covariate or attribute $x_i^{[s]}$ that varies between alternatives or response categories s and possibly between units i. In contrast to the multinomial logit model discussed in section 12.2.1, where the covariate x_i had alternative-specific effects $\beta^{[s]}$, the covariate $x_i^{[s]}$ has a coefficient β that does not vary over alternatives s. Moreover, there are no covariates x_i included that vary only over units and there are no alternative-specific intercepts $\beta^{[s]}$.

The standard model for such data is the *conditional logit model*:

$$\Pr(y_i = s|x_i^{[1]}, \ldots, x_i^{[S]}) \;=\; \frac{\exp(\beta x_i^{[s]})}{\sum_{c=1}^{S} \exp(\beta x_i^{[c]})} \tag{12.3}$$

The probabilities have the same form as (12.2) except that the regression parameter β does not vary over alternatives while the covariate does. Because β is constant across alternatives, there is no base outcome as in the multinomial logit model.

It follows from the conditional logit model that the log of the odds of choosing alternative s versus t is

$$\begin{aligned} \ln\left\{\frac{\Pr(y_i = s|x_i^{[1]}, \ldots, x_i^{[S]})}{\Pr(y_i = t|x_i^{[1]}, \ldots, x_i^{[S]})}\right\} &= \ln\left\{\frac{\exp(\beta x_i^{[s]})/\sum_{c=1}^{S}\exp(\beta x_i^{[c]})}{\exp(\beta x_i^{[t]})/\sum_{c=1}^{S}\exp(\beta x_i^{[c]})}\right\} \\ &= \beta(x_i^{[s]} - x_i^{[t]}) \end{aligned} \tag{12.4}$$

and depends only on the difference in the attribute for these alternatives, for instance, the difference in the cost of traveling by Air and Train. We see that only parameters for attributes that vary over alternatives $x_i^{[s]}$ can be estimated in (12.3), because the parameters would cancel out for covariates x_i that vary only over units, $\beta(x_i - x_i) = 0$.

A one-unit increase in the difference of the attribute for two alternatives s and t from $x_i^{[s]} - x_i^{[t]} = a$ to $x_i^{[s]} - x_i^{[t]} = a + 1$ corresponds to the odds ratio

$$\text{OR} \;\equiv\; \frac{\text{Odds}(y_i = s \text{ vs. } y_i = t|x_i^{[s]} - x_i^{[t]} = a + 1)}{\text{Odds}(y_i = s \text{ vs. } y_i = t|x_i^{[s]} - x_i^{[t]} = a)} \;=\; \frac{\exp\{\beta(a+1)\}}{\exp\{\beta(a)\}} \;=\; \exp(\beta)$$

The exponential of the regression coefficient, $\exp(\beta)$, can actually be interpreted in three different ways. First, as shown above, it represents the ratio of the odds of alternative s versus t per unit increase in the difference $x_i^{[s]} - x_i^{[t]}$ in the attribute, for example, the price difference. Second, if $x_i^{[t]}$ stays constant, $\exp(\beta)$ is the odds ratio comparing s with t per unit change in the attribute $x_i^{[s]}$. Third, $\exp(\beta)$ is the ratio of the odds of choosing an alternative s versus choosing *any* of the other alternatives per unit increase in $x_i^{[s]}$ when the attributes of all other alternatives remain the same. To see this, we note that

$$\ln\left\{\frac{\Pr(y_i = s|x_i^{[1]},\ldots,x_i^{[S]})}{\sum_{t\neq s}\Pr(y_i = t|x_i^{[1]},\ldots,x_i^{[S]})}\right\} = \beta(x_i^{[s]} - \sum_{t\neq s} x_i^{[t]})$$

so that $\exp(\beta)$ is the odds ratio per unit increase in the difference $x_i^{[s]} - \sum_{t\neq s} x_i^{[t]}$. As pointed out earlier, only the third interpretation would be consistent with Stata's use of the term "odds ratio".

The conditional logit model (12.3) is often used for making predictions regarding marginal (not conditional on the attributes $x_i^{[s]}$) probabilities $\Pr(y_i^{[s]})$ for nominal responses. It is particularly useful for forecasting the market share for a new alternative or product $S+1$. Such predictions can be accomplished by specifying the attributes $\mathbf{x}^{[S+1]}$ of the new product, such as the price, keeping the attributes for the existing alternatives at their sample values, and using the fitted conditional logit model to obtain predicted probabilities for the new product for each unit,

$$\widehat{\Pr}(y_i = S+1|x_i^{[1]},\ldots,x_i^{[S]},x_i^{[S+1]}) = \frac{\exp(\widehat{\beta}x_i^{[S+1]})}{\sum_{c=1}^{S+1}\exp(\widehat{\beta}x_i^{[c]})}$$

The market share can then be estimated as the marginal or mean probability of choosing the new product in the sample (of size N),

$$\widehat{\Pr}(y_i = S+1) = \frac{1}{N}\sum_{i=1}^{N}\widehat{\Pr}(y_i = S+1|x_i^{[1]},\ldots,x_i^{[S]},x_i^{[S+1]})$$

A potential problem with using conditional logit models for prediction is the independence of irrelevant alternatives (IIA) property of these models, an issue that will be discussed in section 12.3.

To illustrate conditional logit modeling, we use the dataset `travel2.dta`, which contains a different set of covariates for the same Australian travelers as before. Here we consider the following variables:

- `traveler`: identifier for traveler
- `alt`: mode of transport
  (1: Air; 2: Train; 3: Bus; 4: Car)
- `Choice`: dummy variable for chosen alternative for traveler
- `GC`: generalized cost in Australian $ ($x_{2i}^{[s]}$), defined as
  (in-vehicle cost) + (time spent traveling) × (wagelike measure)
- `Ttime`: time spent in terminal in minutes ($x_{3i}^{[s]}$)

We read in the data by typing

```
. use http://www.stata-press.com/data/mlmus3/travel2
```

In contrast to the dataset used in the previous section, `travel2.dta` is "expanded" in the sense that it contains a row (record) for each possible alternative for each traveler, in this case, four records per traveler.

We take a look at the variables for the first two travelers contained in the first eight records of the dataset:

```
. list traveler alt Choice GC Ttime in 1/8, sepby(traveler) noobs
```

traveler	alt	Choice	GC	Ttime
1	1	0	70	69
1	2	0	71	34
1	3	0	70	35
1	4	1	30	0
2	1	0	68	64
2	2	0	84	44
2	3	0	85	53
2	4	1	50	0

The variable `alt` no longer represents the alternative being chosen, as it did in the dataset `travel1.dta`, but instead represents all alternatives s ($s = 1, 2, 3, 4$) a traveler i could choose among. For each traveler, the binary variable `Choice` is 1 for the alternative chosen and 0 for the three alternatives not chosen. Also note that there are not four real responses per traveler because only one alternative is chosen by each traveler and there is hence only one piece of information per traveler. As observed earlier when inspecting the travel data, the first two travelers both chose to drive (`Choice` is 1 when `alt` is 4 for Car). The covariates `GC` and `Ttime` vary over mode of transport for each traveler and between travelers for a given mode of transport. For travelers 1 and 2, we see that the cost, `GC`, happens to be lowest for the chosen alternative. `Ttime` takes on the value 0 for Car because there is no waiting time in a terminal when driving.

An expanded dataset not only makes it straightforward to include variables that vary over alternatives but also allows different travelers to choose from different alternative sets. For instance, if air traffic controllers had been on strike when traveler 2 made his

trip, the alternative Air would no longer be available to him and line 5 could have been deleted from the dataset.

We now consider estimation of the conditional logit model (12.3). We use $v_i^{[s]}$ to denote the binary choice indicator `Choice` for alternative s for traveler i. Note that this notation departs from the usual convention of placing all indices in the subscript, here i and s, that identify the rows in the data. Similarly, the value of a covariate x for alternative s and traveler i is denoted $x_i^{[s]}$.

It would be tempting to use a *binary* logistic regression model for the probability that $v_i^{[s]} = 1$. However, such a model would be misspecified because it falsely assumes that the responses $v_i^{[s]}$ are independent given the covariates. The $v_i^{[s]}$ are clearly dependent because a 1 can occur only once for each traveler. So if we know that a traveler is driving, there is a zero probability of traveling by any other mode.

In the expanded dataset with one record per alternative, the conditional logit model actually represents the conditional probability that the choice indicator takes the value 1 for the chosen alternative s, *given* that exactly one alternative is chosen by the traveler, $\sum_{c=1}^{S} v_i^{[c]} = 1$,

$$\Pr(v_i^{[s]} = 1 | x_i^{[1]}, \ldots, x_i^{[S]}, \textstyle\sum_{c=1}^{S} v_i^{[c]} = 1) \;=\; \frac{\exp(\beta x_i^{[s]})}{\sum_{c=1}^{S} \exp(\beta x_i^{[c]})} \;=\; \Pr(y_i = s | x_i^{[1]}, \ldots, x_i^{[S]}) \tag{12.5}$$

The conditioning on the sum of indicators being 1 is the reason why the model is called a *conditional* logit model. To avoid conditioning on $\sum_{c=1}^{S} v_i^{[c]} = 1$ in all expressions, we write the probability in terms of $y_i = s$ as shown after the second equality, although the response variable is really the binary choice indicator $v_i^{[s]}$. A proof of the first equality in (12.5) is presented in display 12.2 (feel free to skip it).

Imagine making an independent decision for each alternative whether to choose that alternative (without any restriction on the number of alternatives that can be chosen). In this case, a binary logistic regression model would be appropriate for the probability that alternative s is chosen, $v_i^{[s]} = 1$:

$$\Pr(v_i^{[s]} = 1 | x_i^{[s]}) = \frac{\exp(\beta x_i^{[s]})}{1 + \exp(\beta x_i^{[s]})}$$

However, when exactly *one* alternative must be chosen, the sum of the choice indicators $v_i^{[s]}$ must be one. We must therefore consider the conditional probability of choosing alternative s, given that $\sum_{c=1}^{S} v_i^{[c]} = 1$. It follows that (suppressing the conditioning on $x_i^{[1]}, \ldots, x_i^{[S]}$)

1. The probability that $v_i^{[s]} = 1$ and the other choice indicators for unit i are zero is

$$\Pr(v_i^{[s]} = 1, \textstyle\sum_{c=1}^{S} v_i^{[c]} = 1) \;=\; \frac{\exp(\beta x_i^{[s]})}{\prod_{c=1}^{S}\{1 + \exp(\beta x_i^{[c]})\}}$$

   For instance, for $S = 4$ the probability that $v_i^{[1]} = 0$, $v_i^{[2]} = 1$, $v_i^{[3]} = 0$, and $v_i^{[4]} = 0$ is

$$\begin{aligned}\frac{1}{1 + \exp(\beta x_i^{[1]})} \times \frac{\exp(\beta x_i^{[2]})}{1 + \exp(\beta x_i^{[2]})} \times \frac{1}{1 + \exp(\beta x_i^{[3]})} \times \frac{1}{1 + \exp(\beta x_i^{[4]})} \\ = \frac{\exp(\beta x_i^{[2]})}{\prod_{c=1}^{4}\{1 + \exp(\beta x_i^{[c]})\}}\end{aligned}$$

2. The probability that the indicator variable is 1 for exactly one alternative for unit i, $\sum_{c=1}^{S} v_i^{[c]} = 1$, is the sum of the probabilities of all the S ways this can be accomplished,

$$\begin{aligned}\Pr(\textstyle\sum_{c=1}^{S} v_i^{[c]} = 1) &= \frac{\exp(\beta x_i^{[1]})}{\prod_{c=1}^{S}[1 + \exp(\beta x_i^{[c]})]} + \cdots + \frac{\exp(\beta x_i^{[S]})}{\prod_{c=1}^{S}[1 + \exp(\beta x_i^{[c]})]} \\ &= \frac{\sum_{c=1}^{S} \exp(\beta x_i^{[c]})}{\prod_{c=1}^{S}[1 + \exp(\beta x_i^{[c]})]}\end{aligned}$$

3. The required conditional probability that alternative s is chosen by unit i, given that only one alternative is chosen, becomes

$$\Pr(v_i^{[s]} = 1 | \textstyle\sum_{c=1}^{S} v_i^{[c]} = 1) \;=\; \frac{\Pr(v_i^{[s]} = 1, \sum_{c=1}^{S} v_i^{[c]} = 1)}{\Pr(\sum_{c=1}^{S} v_i^{[c]} = 1)} \;=\; \frac{\exp(\beta x_i^{[s]})}{\sum_{c=1}^{S} \exp(\beta x_i^{[c]})}$$

Display 12.2: Conditional probability of choosing an alternative s given that exactly one alternative is chosen

Returning to the travel-choice application, we specify the following conditional logit model for the alternatives Air, Train, Bus, and Car:

$$\Pr(y_i = s|\mathbf{x}_i^{[1]}, \ldots, \mathbf{x}_i^{[4]}) = \frac{\exp(\beta_2 x_{2i}^{[s]} + \beta_3 x_{3i}^{[s]})}{\sum_{c=1}^{4} \exp(\beta_2 x_{2i}^{[c]} + \beta_3 x_{3i}^{[c]})}, \qquad s = 1, 2, 3, 4 \tag{12.6}$$

where $\mathbf{x}_i^{[s]} = (x_{2i}^{[s]}, x_{3i}^{[s]})'$ is the vector of attributes, `GC` and `Ttime`, for mode or alternative s.

We now fit the model by conditional maximum likelihood using the `clogit` command (for "conditional logit") that we have previously used for the fixed-effects approach to clustered dichotomous responses in section 10.14.1. Here we use the `group(traveler)` option to specify that `traveler` is the unit identifier (so `Choice` takes the value 1 once for each unique value of `traveler`)

```
. clogit Choice GC Ttime, group(traveler)
Conditional (fixed-effects) logistic regression   Number of obs   =        840
                                                  LR chi2(2)      =      42.03
                                                  Prob > chi2     =     0.0000
Log likelihood = -270.10821                       Pseudo R2       =     0.0722

------------------------------------------------------------------------------
      Choice |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
          GC |  -.0106331   .0034624    -3.07   0.002    -.0174192    -.003847
       Ttime |   -.012981   .0028943    -4.49   0.000    -.0186537   -.0073083
------------------------------------------------------------------------------
```

These estimates were reported in table 12.1 under "Only alternative-specific covariates".

Estimated odds ratios with associated 95% confidence intervals are produced by including the `or` option in the `clogit` command,

```
. clogit Choice GC Ttime, group(traveler) or
Conditional (fixed-effects) logistic regression   Number of obs   =        840
                                                  LR chi2(2)      =      42.03
                                                  Prob > chi2     =     0.0000
Log likelihood = -270.10821                       Pseudo R2       =     0.0722

------------------------------------------------------------------------------
      Choice | Odds Ratio   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
          GC |   .9894232   .0034257    -3.07   0.002     .9827316    .9961604
       Ttime |   .9871029   .0028569    -4.49   0.000     .9815192    .9927183
------------------------------------------------------------------------------
```

and were also reported under "Only alternative-specific covariates" in table 12.1.

According to the fitted model a \$10 increase in the generalized cost for any of the alternatives would decrease the odds of that alternative being chosen by an estimated 10% [$-10\% = 100\%\{\exp(10 \times -0.0106331) - 1\}$], keeping the cost of the other alternatives constant. Increasing terminal time by 10 minutes for a particular mode of transport would decrease the odds of traveling with that alternative by an estimated 12% [$-12\% = 100\%\{\exp(10 \times -0.012981) - 1\}$]. Inversely, decreasing terminal time by

10 minutes would increase the odds of traveling with that alternative by an estimated 14% [$= 100\%\{\exp(-10 \times -0.012981) - 1\}$].

Conditional logit models also including covariates that vary only over units

We now consider two additional variables from `travel2.dta` that vary only over travelers i:

- `Hinc`: household income in Australian $1,000 ($x_{2i}$)
- `Psize`: number of people traveling together (x_{3i})

As discussed for the multinomial logit model in section 12.2.1, covariates like x_{2i} that do not vary between alternatives must have alternative-specific coefficients $\beta_2^{[s]}$ because a term like $\beta_2 x_{2i}$ would cancel out of the expression for the probability. With data in expanded form, as here, where s denotes a row in the data, we can include alternative-specific coefficients by using dummy variables for the alternatives. Let $d_1^{[s]}$ be a dummy variable for the first alternative, taking the value 1 if $s = 1$ and 0 otherwise. We need dummy variables $d_1^{[s]}$, $d_2^{[s]}$, and $d_3^{[s]}$ for each alternative apart from the fourth (Car), which is the base outcome. The required term $\beta_2^{[s]} x_{2i}$ is then obtained using

$$\beta_2^{[s]} x_{2i} = \beta_2^{[1]} d_1^{[s]} x_{2i} + \beta_2^{[2]} d_2^{[s]} x_{2i} + \beta_2^{[3]} d_3^{[s]} x_{2i}$$

Only one dummy variable—namely, the dummy variable $d_2^{[s]}$ for alternative 2—takes the value 1 and hence picks out the appropriate coefficient $\beta_2^{[s]}$. We will also include alternative-specific intercepts by using the same dummy variables.

To write down the model compactly, we use the notation $V_i^{[s]}$ for the linear predictor in the numerator of the probability,

$$\Pr(y_i = s | x_{2i}, x_{3i}, \mathbf{x}_{ij}^{[1]}, \ldots, \mathbf{x}_{ij}^{[4]}) \;=\; \frac{\exp(V_i^{[s]})}{\sum_{c=1}^{4} \exp(V_i^{[c]})}$$

We can now specify the form of the linear predictor as

$$\begin{aligned} V_i^{[s]} \;=\; & \beta_1^{[1]} d_1^{[s]} + \beta_1^{[2]} d_2^{[s]} + \beta_1^{[3]} d_3^{[s]} \\ & + \beta_2^{[1]} d_1^{[s]} x_{2i} + \beta_2^{[2]} d_2^{[s]} x_{2i} + \beta_2^{[3]} d_3^{[s]} x_{2i} + \beta_3^{[1]} d_1^{[s]} x_{3i} + \beta_3^{[2]} d_2^{[s]} x_{3i} + \beta_3^{[3]} d_3^{[s]} x_{3i} \\ & + \beta_4 x_{4i}^{[s]} + \beta_5 x_{5i}^{[s]} \end{aligned}$$

The model includes alternative-specific intercepts ($\beta_1^{[1]}$, $\beta_1^{[2]}$, and $\beta_1^{[3]}$), alternative-specific coefficients for `Hinc` ($\beta_2^{[1]}$, $\beta_2^{[2]}$, and $\beta_2^{[3]}$) and `Psize` ($\beta_3^{[1]}$, $\beta_3^{[2]}$, and $\beta_3^{[3]}$), and coefficients β_4 and β_5 for `GC` and `Ttime`.

Before estimation using `clogit`, we construct dummy variables for the alternatives $d_i^{[s]}$,

```
. tabulate alt, gen(a)
```

and give the dummy variables more descriptive names

```
. rename a1 air
. rename a2 train
. rename a3 bus
. rename a4 car
```

We construct interactions between the dummy variables (apart from the dummy for the base outcome) and the traveler-specific covariates:

```
. generate airXhinc = air*Hinc
. generate trainXhinc = train*Hinc
. generate busXhinc = bus*Hinc
. generate airXpsize = air*Psize
. generate trainXpsize = train*Psize
. generate busXpsize = bus*Psize
```

If there are many covariates, it is faster to use a `foreach` loop, as follows:

```
foreach var of varlist Hinc Psize {
   generate airX‘var’ = air*‘var’
   generate trainX‘var’ = train*‘var’
   generate busX‘var’ = bus*‘var’
}
```

The coefficients of these interactions correspond to the alternative-specific coefficients $\beta_2^{[s]}$ and $\beta_3^{[s]}$ of the covariates `Hinc` and `Psize`. Specifically, the coefficient for `airXhinc` is $\beta_2^{[1]}$, the coefficient for `trainXhinc` is $\beta_2^{[2]}$, and the coefficient for `airXhinc` is $\beta_2^{[3]}$. Likewise, the coefficient for `airXpsize` is $\beta_3^{[1]}$, the coefficient for `trainXpsize` is $\beta_3^{[2]}$, and the coefficient for `airXpsize` is $\beta_3^{[3]}$.

We can now fit the model by conditional maximum likelihood using `clogit`:

```
. clogit Choice airXhinc airXpsize air trainXhinc trainXpsize train
> busXhinc busXpsize bus GC Ttime, group(traveler)
Conditional (fixed-effects) logistic regression   Number of obs   =        840
                                                  LR chi2(11)     =     227.34
                                                  Prob > chi2     =     0.0000
Log likelihood =  -177.4541                       Pseudo R2       =     0.3904

------------------------------------------------------------------------------
      Choice |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
    airXhinc |    .004071   .0127247     0.32   0.749    -.0208689     .029011
   airXpsize |  -1.027423   .2656569    -3.87   0.000    -1.548101   -.5067448
         air |   7.873608   .9868475     7.98   0.000     5.939423    9.807794
  trainXhinc |  -.0551849   .0144824    -3.81   0.000    -.0835698      -.0268
 trainXpsize |   .3023954   .2256155     1.34   0.180    -.1398029    .7445937
       train |   5.559205   .6991387     7.95   0.000     4.188918    6.929492
    busXhinc |  -.0233237   .0162973    -1.43   0.152    -.0552658    .0086185
   busXpsize |  -.0300096   .3339774    -0.09   0.928    -.6845933     .624574
         bus |   4.433192   .7783339     5.70   0.000     2.907685    5.958698
          GC |   -.019685   .0054015    -3.64   0.000    -.0302717   -.0090983
       Ttime |  -.1015659   .0112306    -9.04   0.000    -.1235776   -.0795543
------------------------------------------------------------------------------
```

These estimates, as well as estimated odds ratios with associated 95% confidence intervals produced by including the `or` option, were reported in table 12.1 on page 636 under "Both traveler and alternative-specific covariates".

According to this model, a $10 increase in the generalized cost for any of the alternatives would decrease the odds of that alternative being chosen by an estimated 18% [$-18\% = 100\%\{\exp(10 \times -0.019685) - 1\}$], keeping the cost of the other alternatives as well as `Ttime`, `Hinc`, and `Psize` constant. Increasing terminal time by 10 minutes for a particular mode of transport would decrease the odds of traveling with that alternative by an estimated 64% [$-64\% = 100\%\{\exp(10 \times -0.1015659) - 1\}$], keeping the other covariates constant. A $1,000 increase in household income would hardly change the odds of flying [$0.4\% = 100\%\{\exp(0.004071) - 1\}$], decrease the odds of taking the train by 5% [$5\% = 100\%\{\exp(-0.0551849) - 1\}$], and decrease the odds of taking the bus by 2% [$2\% = 100\%\{\exp(-0.0233237) - 1\}$], keeping the other covariates constant. An extra person in the traveling party would reduce the odds of flying by 64% [$64\% = 100\%\{\exp(-1.027423) - 1\}$], increase the odds of taking the train by 35% [$35\% = 100\%\{\exp(0.3023954) - 1\}$], and decrease the odds of taking the bus by 3% [$3\% = 100\%\{\exp(-0.0300096) - 1\}$], keeping the other covariates constant.

We could alternatively have used the `asclogit` command (for "alternative-specific conditional logit"), which does not require explicit construction of the interactions. However, the setup for `clogit` is similar to the one that we will use for models involving random effects estimated by `gllamm` later in this chapter.

In `asclogit`, we specify the unit identifier by using the `case()` option, the covariates having alternative-specific coefficients by using the `casevars()` option, the variable labeling the alternatives by using the `alternatives()` option, and the base outcome

by using the `basealternative()` option. Alternative-specific covariates are listed after the response variable. In the present setting, the `asclogit` command is

```
. asclogit Choice GC Ttime, case(traveler) casevars(Hinc Psize)
> alternatives(alt) basealternative(4)
Alternative-specific conditional logit          Number of obs      =       840
Case variable: traveler                         Number of cases    =       210
Alternative variable: alt                       Alts per case: min =         4
                                                               avg =       4.0
                                                               max =         4
                                                  Wald chi2(8)     =    112.25
Log likelihood =  -177.4541                       Prob > chi2      =    0.0000
```

Choice	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
alt						
GC	-.019685	.0054015	-3.64	0.000	-.0302717	-.0090983
Ttime	-.1015659	.0112306	-9.04	0.000	-.1235776	-.0795543
1						
Hinc	.004071	.0127247	0.32	0.749	-.0208689	.029011
Psize	-1.027423	.2656569	-3.87	0.000	-1.548101	-.5067448
_cons	7.873608	.9868475	7.98	0.000	5.939423	9.807794
2						
Hinc	-.0551849	.0144824	-3.81	0.000	-.0835698	-.0268
Psize	.3023954	.2256155	1.34	0.180	-.1398029	.7445937
_cons	5.559205	.6991387	7.95	0.000	4.188918	6.929492
3						
Hinc	-.0233237	.0162973	-1.43	0.152	-.0552658	.0086185
Psize	-.0300096	.3339774	-0.09	0.928	-.6845933	.624574
_cons	4.433192	.7783339	5.70	0.000	2.907685	5.958698
4	(base alternative)					

We see that the estimates are identical to those produced by `clogit` with the appropriate interactions included.

12.3 Independence from irrelevant alternatives

An important feature of multinomial logit and conditional logit models is so-called independence of irrelevant alternatives (IIA). This means that the odds comparing an alternative s to another alternative t only depends on the characteristics of these two alternatives and *not* on any third alternative u. This is evident for the conditional logit model, where we see from expression (12.4) that the odds are

$$\frac{\Pr(y_i = s|x_i^{[1]}, \ldots, x_i^{[S]})}{\Pr(y_i = t|x_i^{[1]}, \ldots, x_i^{[S]})} = \exp\{\beta(x_i^{[s]} - x_i^{[t]})\} \tag{12.7}$$

which clearly depends only on the attributes of alternatives s and t. The odds also remain the same if an alternative is removed from or added to the alternative set because this affects the denominators of both probabilities equally; see (12.4).

The notion of IIA was proposed in decision theory, where it was considered to be a required property of appropriately specified choice probabilities. Indeed, the conditional logit model was originally derived by Luce (1959) from IIA, viewing IIA as a desirable axiom.

Although IIA may be realistic in some choice situations, it is clearly inappropriate in others. A famous example is the red-bus–blue-bus problem of McFadden (1974). Consider a commuter who can travel to work either by car or by taking a blue bus, and for simplicity assume that the probability of each of these alternatives is 1/2, giving an odds of 1. Now suppose that a red bus is introduced and that the commuter finds the two bus alternatives (which differ only in color) to be equally attractive. The probability of taking the red bus hence equals the probability of taking the blue bus. However, as shown above, the odds of choosing the blue bus compared with the car remains 1 in the conditional logit model, implying that each of the three alternatives is equally likely, with probabilities 1/3. It is clearly counterintuitive that the probability of driving decreases from 1/2 to 1/3 due to the introduction of the red bus. In reality, we would expect the probability of taking a bus to be split evenly at 1/4 between the old (blue) bus and the new (red) bus, keeping the probability of driving equal to 1/2 and increasing the odds of car versus blue bus from 1 to 2.

The utility-maximization formulation discussed in the next section is convenient for relaxing the IIA assumption.

12.4 Utility-maximization formulation

Instead of writing down multinomial logit and conditional logit models directly in terms of the probability of a category s, we can alternatively derive and motivate these models from a rational-choice perspective.

Consider the utility or "attractiveness" $U_i^{[s]}$ associated with alternative or category s for a subject i. The rational choice for subject i is then to choose the alternative for which his or her utility is the highest. In other words, alternative s is chosen by subject i if the utility of this alternative is greater than the utility of any other alternative t:

$$U_i^{[s]} > U_i^{[t]} \quad \text{for all } t \neq s$$

We then let the utilities be linear functions of subject-specific covariates x_i and alternative-specific covariates $x_i^{[s]}$,

$$U_i^{[s]} = \underbrace{\beta_1^{[s]} + \beta_2^{[s]} x_i + \beta_3 x_i^{[s]}}_{V_i^{[s]}} + \epsilon_i^{[s]}$$

where $\epsilon_i^{[s]}$ is an error term that varies over both alternatives and subjects, and

$$V_i^{[s]} \equiv \beta_1^{[s]} + \beta_2^{[s]} x_i + \beta_3 x_i^{[s]}$$

represents the fixed part of the utility and is equal to the linear predictor of model (12.6). This provides an appealing interpretation of the coefficients in regression models for nominal responses as linear effects of covariates on utilities.

For the case of three alternatives, 1, 2, and 3, it follows that the probability of choosing an alternative—say, alternative 2—given the covariates, becomes

$$\begin{aligned}
\Pr(y_i = 2|x_i, x_i^{[1]}, x_i^{[2]}, x_i^{[3]}) &= \Pr(U_i^{[2]} > U_i^{[1]},\ U_i^{[2]} > U_i^{[3]}) \\
&= \Pr(U_i^{[2]} - U_i^{[1]} > 0,\ U_i^{[2]} - U_i^{[3]} > 0) \\
&= \Pr\left(\epsilon_i^{[2]} - \epsilon_i^{[1]} > V_i^{[2]} - V_i^{[1]},\ \epsilon_i^{[2]} - \epsilon_i^{[3]} > V_i^{[2]} - V_i^{[3]}\right)
\end{aligned}$$

where

$$V_i^{[2]} - V_i^{[1]} = \beta_1^{[2]} - \beta_1^{[1]} + (\beta_2^{[2]} - \beta_2^{[1]})x_i + \beta_3(x_i^{[2]} - x_i^{[1]})$$

and

$$V_i^{[2]} - V_i^{[3]} = \beta_1^{[2]} - \beta_1^{[3]} + (\beta_2^{[2]} - \beta_2^{[3]})x_i + \beta_3(x_i^{[2]} - x_i^{[3]})$$

There are analogous expressions for $\Pr(y_i = 1|x_i, x_i^{[1]}, x_i^{[2]}, x_i^{[3]})$ and $\Pr(y_i = 3|x_i, x_i^{[1]}, x_i^{[2]}, x_i^{[3]})$.

We can identify the regression coefficients β_3 for alternative-specific covariates but only identify the differences between intercepts $\beta_1^{[2]} - \beta_1^{[1]}$ and $\beta_1^{[2]} - \beta_1^{[3]}$, and differences between regression coefficients for subject-specific covariates $\beta_2^{[2]} - \beta_2^{[1]}$ and $\beta_2^{[2]} - \beta_2^{[3]}$. However, the intercepts and coefficients for subject-specific covariates become identified once we fix the intercepts and coefficients for a base or reference category—say, category 1—to zero; $\beta_1^{[1]} = 0$ and $\beta_2^{[1]} = 0$.

If the error terms $\epsilon_i^{[s]}$ have independent Gumbel or standard extreme value type I distributions (with expectation equal to Euler's constant of about 0.577 and variance of $\pi^2/6$), the differences $\epsilon_i^{[s]} - \epsilon_i^{[t]}$ have standard logistic distributions (with expectation 0 and variance $\pi^2/3$). It can be shown that the resulting choice probability is given by the *conditional logit model* (12.3). Conversely, this particular utility-maximization formulation follows from the expression for the probabilities in (12.3).

Seen from the utility-maximization perspective, IIA can be relaxed by letting the utilities of different alternatives be dependent. The more similar the alternatives are, the more correlated their utilities would be expected to be. Indeed, in the red-bus–blue-bus example, the utilities for the two almost identical types of bus would be almost perfectly correlated. In the multilevel setting, correlation among utilities can be introduced by including random effects in multinomial logit and conditional logit models. This is the topic of the rest of the chapter.

12.5 Does marketing affect choice of yogurt?

Although Americans on average eat only about 7 pounds of yogurt a year compared with about 49 pounds in France, yogurt sales in the U.S. have grown by nearly 10% annually for the past three decades, unlike most other grocery products. It hence comes as no surprise that marketing is viewed as crucial by the competitors in the yogurt market.

In the rest of this chapter, we show how conditional logit models—in particular, multilevel conditional logit models that include various kinds of random effects—can be used to investigate how marketing variables affect the brand choice of yogurt. To this end, we use panel data on choice of brand of yogurt by 100 households in Springfield, Missouri, U.S.A. from the marketing research firm A. C. Nielsen.

The data were collected by optical scanners at supermarket checkouts over a period of about two years and contain information on brand purchases, store environment variables (for example, prices of brands), the marketing environment (for example, newspaper feature advertisements), and the value of any coupons used by the panel members (that is, households). Each participant was provided with an identification card to present at the time of purchase, and all purchases were scanned under the corresponding identification number. These data provide a reasonably complete record of the households' purchases over time.

The data considered here were confined to purchases of either the six-ounce size of Yoplait or Weight Watchers or the comparable eight-ounce size of Dannon (known by its original name, Danone, in Europe) or Hiland. Between 4 and 185 purchases per household were recorded (mean 24), giving a total of 2,412 purchases. The market shares for Yoplait, Dannon, Weight Watchers, and Hiland in these data were 34%, 40%, 23%, and 3%, respectively.

This dataset was previously analyzed by Jain, Vilcassim, and Chintagunta (1994) and Chen and Kuo (2001), and provided by Lynn Kuo. The variables are

- `house`: identifier for household (j)
- `occ`: purchasing occasion (i)
- `brand`: brand (1: Yoplait; 2: Dannon; 3: Hiland; 4: Weight Watchers)
- `choice`: dummy variable for the chosen brand
- `feature`: dummy variable for newspaper feature advertisement for brand ($x_{2i}^{[s]}$)
- `price`: price of brand in U.S.$/oz ($x_{3i}^{[s]}$). For the brand purchased, the price is the actual price (shelf price net of value of coupons redeemed); for all other brands, the price is the shelf price.

The dataset `yogurt.dta`, which is in expanded form, is read in by typing

```
. use http://www.stata-press.com/data/mlmus3/yogurt, clear
```

Because the market share of Hiland was only 3%, we will consider only those purchasing occasions where either Yoplait, Dannon, or Weight Watchers was chosen. We therefore drop Hiland from all choice sets,

```
. drop if brand==3
(2412 observations deleted)
```

and drop all choice sets where Hiland was chosen (that is, where `choice` takes the value 0 for all three brands that now remain in the data),

```
. egen sum = total(choice), by(house occ)
. drop if sum==0
(213 observations deleted)
```

We then recode the value of Weight Watchers from 4 to 3 so that `brand` takes the values 1: Yoplait, 2: Dannon, and 3: Weight Watchers:

```
. recode brand(4=3)
(brand: 2341 changes made)
. label define b 1 "Yoplait" 2 "Dannon" 3 "WeightW", modify
. label values brand b
```

We construct the variable `set`, which numbers the purchasing occasions or choice sets where Yoplait, Dannon, or Weight Watchers was chosen:

```
. egen set = group(house occ)
```

The variable `price` is measured in U.S.$/oz in the dataset. However, it is more convenient to interpret price coefficients in terms of cent/oz, and we therefore construct a new price variable, `pricec`, and drop the old one:

```
. generate pricec = price*100
. drop price
```

We can now list the variables for household number 24:

```
. sort house occ
. list if house==24, sepby(occ) noobs
```

house	occ	brand	choice	feature	sum	set	pricec
24	1	Yoplait	0	0	1	602	11
24	1	Dannon	1	0	1	602	7.4
24	1	WeightW	0	0	1	602	7.900001
24	2	Yoplait	0	0	1	603	11
24	2	Dannon	1	0	1	603	8.1
24	2	WeightW	0	0	1	603	7.900001
24	3	Yoplait	0	0	1	604	11
24	3	Dannon	1	1	1	604	8.1
24	3	WeightW	0	0	1	604	7.900001
24	4	Yoplait	0	0	1	605	10.3
24	4	Dannon	1	0	1	605	8.1
24	4	WeightW	0	0	1	605	7.900001
24	5	Yoplait	1	0	1	606	10.3
24	5	Dannon	0	0	1	606	9.8
24	5	WeightW	0	0	1	606	7.900001
24	6	Yoplait	0	0	1	607	10.8
24	6	Dannon	1	1	1	607	8.1
24	6	WeightW	0	0	1	607	8.6
24	7	Yoplait	0	0	1	608	11.5
24	7	Dannon	1	0	1	608	8.1
24	7	WeightW	0	0	1	608	8.6

There are three possible choices of yogurt at each purchasing occasion for a household, and the choice set at each occasion is hence of size 3. We see that household 24 makes seven purchases of yogurt during the study period, buying Dannon at all occasions except the fifth, where Yoplait was bought. For this household, the only newspaper feature advertisements coinciding with purchasing occasions were for Dannon at occasions 3 and 6. The prices for the competing brands differ at each occasion and change over time for a given brand.

This dataset contains only covariates that vary over alternatives. There are no covariates that are constant across alternatives at a given occasion for a given household (such as income).

12.6 Single-level conditional logit models

We start by fitting standard conditional logit models to the yogurt data, letting i be the index for occasions, j the index for households (the clusters in this application), and as before letting s designate the choice.

12.6.1 Conditional logit models with alternative-specific intercepts

Following Jain, Vilcassim, and Chintagunta (1994) and Chen and Kuo (2001), we first consider a conditional logit model, using the marketing variables `feature` and `pricec` as covariates.

The probability that alternative s is chosen by household j at the ith purchasing occasion is modeled as

$$\Pr(y_{ij}=s|\mathbf{x}_{ij}^{[1]},\mathbf{x}_{ij}^{[2]},\mathbf{x}_{ij}^{[3]}) \;=\; \frac{\exp(\beta_1^{[1]}d_1^{[s]}+\beta_1^{[3]}d_3^{[s]}+\beta_2 x_{2ij}^{[s]}+\beta_3 x_{3ij}^{[s]})}{\sum_{c=1}^{3}\exp(\beta_1^{[1]}d_1^{[c]}+\beta_1^{[3]}d_3^{[c]}+\beta_2 x_{2ij}^{[c]}+\beta_3 x_{3ij}^{[c]})},\quad s=1,2,3 \tag{12.8}$$

where $\mathbf{x}_{ij}^{[s]}=(x_{2ij}^{[s]},x_{3ij}^{[s]})'$ is the vector of covariates, `feature` and `pricec`, for brand s. In contrast to the classical conditional logit model (12.3) specified on page 639, alternative-specific intercepts $\beta_1^{[s]}$ are included in this model by using dummy variables $d_1^{[s]}$ and $d_3^{[s]}$ for alternatives 1 and 3 (Yoplait and Weight Watchers) with alternative 2 (Dannon) as base outcome.

The model is equivalent to a linear model for the utility $U_{ij}^{[s]}$ of alternative s for household j at the ith purchasing occasion,

$$U_{ij}^{[s]} \;=\; \beta_1^{[1]}d_1^{[s]}+\beta_1^{[3]}d_3^{[s]}+\beta_2 x_{2ij}^{[s]}+\beta_3 x_{3ij}^{[s]}+\epsilon_{ij}^{[s]}$$

where the $\epsilon_{ij}^{[s]}$ have Gumbel distributions (with variance $\pi^2/6$) that are independent over alternatives, occasions, and households. In this formulation, alternative 1 (Yoplait) is chosen by household j at occasion i if its utility is higher than the utilities of alternatives 2 (Dannon) and 3 (Weight Watchers); $U_{ij}^{[1]}>U_{ij}^{[2]}$ and $U_{ij}^{[1]}>U_{ij}^{[3]}$. Similarly, alternative 2 is chosen if $U_{ij}^{[2]}>U_{ij}^{[1]}$ and $U_{ij}^{[2]}>U_{ij}^{[3]}$, and alternative 3 is chosen if $U_{ij}^{[3]}>U_{ij}^{[1]}$ and $U_{ij}^{[3]}>U_{ij}^{[2]}$ (see also section 12.4).

Before fitting this model using `clogit`, we construct dummy variables for the alternatives,

```
. tabulate brand, generate(br)
```

brand	Freq.	Percent	Cum.
Yoplait	2,341	33.33	33.33
Dannon	2,341	33.33	66.67
WeightW	2,341	33.33	100.00
Total	7,023	100.00	

and rename these:

```
. rename br1 Yoplait
. rename br2 Dannon
. rename br3 WeightW
```

We can then use `clogit` to obtain the estimates for the conditional logit model noting that Dannon is base outcome because the alternative-specific covariate `Dannon` is omitted:

```
. clogit choice Yoplait WeightW feature pricec, group(set) vce(cluster house)
Conditional (fixed-effects) logistic regression   Number of obs   =       7023
                                                  Wald chi2(4)    =      61.11
                                                  Prob > chi2     =     0.0000
Log pseudolikelihood = -2356.6791                 Pseudo R2       =     0.0837
                                (Std. Err. adjusted for 100 clusters in house)
------------------------------------------------------------------------------
             |               Robust
      choice |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
     Yoplait |   .7463574   .2757005     2.71   0.007     .2059945     1.28672
     WeightW |  -.6393524   .4462032    -1.43   0.152    -1.513895    .2351897
     feature |   .3047969   .1651837     1.85   0.065    -.0189571    .6285509
      pricec |  -.3676407   .0552442    -6.65   0.000    -.4759174    -.259364
------------------------------------------------------------------------------
```

These estimated coefficients have marginal or population-averaged interpretations, as discussed for dichotomous responses in chapter 10. Because we have used `clogit` with the `vce(cluster house)` option, the estimated standard errors, test-statistics, and confidence intervals for the marginal effects are "robust", taking the dependence of purchases across occasions within households into account.

The first two coefficients represent the estimated log odds of buying the corresponding brand versus Dannon when the covariates `feature` and `pricec` are zero. According to the estimates for `feature` and `pricec`, the use of newspaper feature advertising for a brand increases the odds of buying that brand by an estimated 36% [$36\% = 100\% \times \{\exp(0.3047969) - 1\}$], keeping the prices of the brands constant and for given advertising of the other brands. The estimated coefficient of `pricec` corresponds to an odds ratio of $\exp(-0.3676407) = 0.6923659$. It follows that increasing the price of a brand by 1 cent per oz (corresponding to an 8 cent increase for an 8 oz yogurt) reduces the odds of buying that brand by an estimated 31% [$-31\% = 100\% \times (0.6923659 - 1)$], controlling for the prices of other brands and feature advertising.

As a precursor for our treatment of multilevel modeling of these data, we also estimate the conditional logit model using `gllamm`:

```
. gllamm brand Yoplait WeightW feature pricec, i(house) link(mlogit)
> expanded(set choice o) noconstant cluster(house) robust init
number of level 1 units = 7023

Condition Number = 9.5142813

gllamm model

log likelihood = -2356.6791

Robust standard errors for clustered data: cluster(house)
```

brand	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
Yoplait	.7463572	.2757004	2.71	0.007	.2059943	1.28672
WeightW	-.6393524	.4462032	-1.43	0.152	-1.513895	.2351897
feature	.3047968	.1651837	1.85	0.065	-.0189572	.6285508
pricec	-.3676406	.0552442	-6.65	0.000	-.4759173	-.2593639

We store the estimates for later use under the name `condlogit`:

```
. estimates store condlogit
```

We see that the estimates for the conditional logit model from `gllamm` are practically identical to those produced by `clogit`.

The part of the `gllamm` command preceding the options is the same as for the `clogit` command used above except that the response variable is `brand` instead of `choice`. However, the options (given after the comma) are different. The option `i(house)` designates household as a cluster variable, but estimation proceeds without considering any random effects here because the `init` option (for initial values) is also given. The option `link(mlogit)` specifies a multinomial logit link, and the `expanded(set choice o)` option means that the data are in the form required by the `clogit` command (with three records per purchase), where

- `set` is the identifier for the alternative set
- `choice` is the indicator for the response category or chosen alternative
- `o` means that one set of coefficients should be estimated for the covariates (`m` would mean that a separate set would be estimated for each alternative as in the multinomial logit model)

The options `cluster(house)` and `robust` produce robust standard errors, taking the clustering of purchasing occasions within household into account.

We can obtain estimated odds ratios with associated 95% confidence intervals by replaying the results, without reestimation of the model, with the `eform` option (for exponentiated form):

```
. gllamm, eform
number of level 1 units = 7023

Condition Number = 9.5142813

gllamm model

log likelihood = -2356.6791
```

brand	exp(b)	Std. Err.	z	P>|z|	[95% Conf.	Interval]
Yoplait	2.109302	.1750415	8.99	0.000	1.792674	2.481854
WeightW	.527634	.0287251	-11.74	0.000	.4742335	.5870476
feature	1.356349	.1725318	2.40	0.017	1.057051	1.740392
pricec	.692366	.0175438	-14.51	0.000	.6588206	.7276193

The estimated coefficients and their robust standard errors as well as corresponding odds ratios with 95% confidence intervals are practically identical to the results from `clogit` and are reported under "Conditional logit" in table 12.2.

Table 12.2: Estimates for nominal regression models for choice of yogurt

	Single-level				Multilevel							
	Conditional logit				Random alt.-specific intercepts				Random coefficients			
	Est	(SE*)	OR	(95% CI*)	Est	(SE)	OR	(95% CI)	Est	(SE)	OR	(95% CI)
Fixed intercepts												
$\beta_1^{[1]}$ [`Yoplait`]	0.75	(0.28)			0.88	(0.54)			0.99	(0.10)		
$\beta_1^{[2]}$ [`Dannon`]	0				0				0			
$\beta_1^{[3]}$ [`WeightW`]	−0.64	(0.45)			−2.55	(0.67)			−0.66	(0.06)		
Fixed coefficients												
β_2 [`feature`]	0.30	(0.17)	1.36	(1.06, 1.74)	0.81	(0.22)	2.24	(1.47, 3.43)	0.79	(0.31)	2.21	(1.21, 4.02)
β_3 [`pricec`]	−0.37	(0.06)	0.69	(0.66, 0.73)	−0.46	(0.05)	0.63	(0.58, 0.69)	−0.53	(0.08)	0.59	(0.50, 0.69)
Random intercepts												
$\psi^{[1]}$ [`Yoplait`]					15.01	(3.62)						
$\psi^{[2]}$ [`Dannon`]					0							
$\psi^{[3]}$ [`WeightW`]					17.69	(4.61)						
$\psi^{[21]}$					0							
$\psi^{[31]}$					10.28	(3.34)						
$\psi^{[32]}$					0							
Random coefficients												
ψ_2 [`feature`]									0.50	(0.10)		
ψ_3 [`pricec`]									3.24	(1.19)		
ψ_{32}									0.54	(0.27)		
Log likelihood		−2356.68†				−1009.54				−1891.28		

*Robust standard errors accommodating clustering of purchasing occasions within households
†Log conditional likelihood

12.7 Multilevel conditional logit models

In the yogurt application, we have panel data with purchasing occasions i nested in households j. Hence, the assumption of conditional logit models that brand choice is independent over time for households, given newspaper feature advertising and prices, is unrealistic. To accommodate longitudinal dependence, we introduce household-specific random effects. The random effects represent unobserved heterogeneity, such as taste variation in households' preferences for yogurt or household-specific effects of the marketing variables. In contrast to the marginal models discussed in section 12.6, all coefficients in this section have conditional or household-specific interpretations.

12.7.1 Preference heterogeneity: Brand-specific random intercepts

Let $\zeta_{1j}^{[s]}$ be an alternative-specific random intercept for brand s that varies randomly over households j. These intercepts represent the households' unobserved heterogeneity or taste variation for the different brands and have variances denoted $\psi^{[s]}$. In marketing, this kind of heterogeneity is often called *preference heterogeneity*.

As for fixed alternative-specific intercepts, we must designate a base outcome to ensure identification. We continue to use Dannon ($s = 2$) as base category, for which we set $\zeta_{1j}^{[2]} = 0$ or equivalently fix its variance to zero, $\psi^{[2]} = 0$.

The conditional probability of choosing brand s ($s = 1, \ldots, 3$), given the covariates $\mathbf{x}_{ij}^{[s]}$ and the random alternative-specific intercepts $\zeta_{1j}^{[s]}$, is specified as

$$\begin{aligned} &\Pr(y_{ij} = s|\mathbf{x}_{ij}^{[1]}, \mathbf{x}_{ij}^{[2]}, \mathbf{x}_{ij}^{[3]}, \zeta_{1j}^{[1]}, \zeta_{1j}^{[3]}) \\ = &\frac{\exp\left\{(\beta_1^{[1]} + \zeta_{1j}^{[1]})d_1^{[s]} + (\beta_1^{[3]} + \zeta_{1j}^{[3]})d_3^{[s]} + \beta_2 x_{2ij}^{[s]} + \beta_3 x_{3ij}^{[s]}\right\}}{\sum_{c=1}^{3} \exp\left\{(\beta_1^{[1]} + \zeta_{1j}^{[1]})d_1^{[c]} + (\beta_1^{[3]} + \zeta_{1j}^{[3]})d_3^{[c]} + \beta_2 x_{2ij}^{[c]} + \beta_3 x_{3ij}^{[c]}\right\}} \end{aligned} \tag{12.9}$$

Here $\beta_1^{[s]} + \zeta_{1j}^{[s]}$ is the total alternative-specific intercept for brand s, composed of the sum of a fixed alternative-specific intercept $\beta_1^{[s]}$ and a random deviation $\zeta_{1j}^{[s]}$ for household j.

Given the covariates and the random intercepts, the above model is equivalent to a linear model for the utility $U_{ij}^{[s]}$ of alternative s for household j at the ith purchasing occasion:

$$U_{ij}^{[s]} = (\beta_1^{[1]} + \zeta_{1j}^{[1]})d_1^{[s]} + (\beta_1^{[3]} + \zeta_{1j}^{[3]})d_3^{[s]} + \beta_2 x_{2ij}^{[s]} + \beta_3 x_{3ij}^{[s]} + \epsilon_{ij}^{[s]}$$

Here the $\epsilon_{ij}^{[s]}$ have Gumbel distributions (with variance $\pi^2/6$) that are independent over alternatives, occasions, and households.

Compared with the ordinary conditional logit model with alternative-specific intercepts, discussed in section 12.6.1, the new feature of the model is the random alternative-specific intercepts $\zeta_{1j}^{[s]}$ that are shared for different purchasing occasions of a household.

Importantly, the utilities are no longer independent as they were in section 12.4, and the assumption of independence of irrelevant alternatives (IIA) discussed in section 12.3 is hence relaxed.

The covariances $\psi^{[st]}$ between the random intercepts for any pair of alternatives s and t are free parameters except for the covariances involving the intercept for Dannon ($s = 2$) that are all zero because $\zeta_{1j}^{[2]}$ does not vary.

A normal distribution is then specified for the vector of alternative-specific random intercepts,

$$\begin{bmatrix} \zeta_{1j}^{[1]} \\ \zeta_{1j}^{[3]} \end{bmatrix} \sim N\left(\begin{bmatrix} 0 \\ 0 \end{bmatrix}, \begin{bmatrix} \psi^{[1]} & \\ \psi^{[31]} & \psi^{[3]} \end{bmatrix}\right)$$

where the random intercepts are assumed to be independent of the observed covariates for all alternatives ($\mathbf{x}_{ij}^{[1]}$, $\mathbf{x}_{ij}^{[2]}$, and $\mathbf{x}_{ij}^{[3]}$).

The correlations between the utility differences implied by the model are shown in display 12.3 (this can be skipped if you like).

Given the covariates, it follows from model (12.9) that the correlation between the utility differences $u_{ij}^{[1]} - u_{ij}^{[2]}$ and $u_{ij}^{[3]} - u_{ij}^{[2]}$ (where the base category 2 is involved in both differences) becomes

$$\text{Cor}\{(u_{ij}^{[1]} - u_{ij}^{[2]}), (u_{ij}^{[3]} - u_{ij}^{[2]}) \,|\, \mathbf{x}_{ij}^{[1]}, \mathbf{x}_{ij}^{[2]}, \mathbf{x}_{ij}^{[3]}\} = \frac{\psi^{[31]} + \pi^2/6}{\sqrt{\psi^{[1]} + \pi^2/3}\sqrt{\psi^{[3]} + \pi^2/3}}$$

where $\pi^2/3$ is the variance of the difference between two independent Gumbel distributions with variances $\pi^2/6$. The expression for the correlation between utility differences such as $u_{ij}^{[2]} - u_{ij}^{[1]}$ and $u_{ij}^{[3]} - u_{ij}^{[1]}$ (where the base category 2 is involved in only one of the differences) is more convoluted:

$$\text{Cor}\{(u_{ij}^{[2]} - u_{ij}^{[1]}), (u_{ij}^{[3]} - u_{ij}^{[1]}) \,|\, \mathbf{x}_{ij}^{[1]}, \mathbf{x}_{ij}^{[2]}, \mathbf{x}_{ij}^{[3]}\} = \frac{\psi^{[1]} - \psi^{[31]} + \pi^2/6}{\sqrt{\psi^{[1]} + \pi^2/3}\sqrt{\psi^{[1]} + \psi^{[3]} - 2\psi^{[31]} + \pi^2/3}}$$

Similarly, the correlation between $u_{ij}^{[1]} - u_{ij}^{[3]}$ and $u_{ij}^{[2]} - u_{ij}^{[3]}$ is

$$\text{Cor}\{(u_{ij}^{[1]} - u_{ij}^{[3]}), (u_{ij}^{[2]} - u_{ij}^{[3]}) \,|\, \mathbf{x}_{ij}^{[1]}, \mathbf{x}_{ij}^{[2]}, \mathbf{x}_{ij}^{[3]}\} = \frac{\psi^{[1]} - \psi^{[31]} + \pi^2/6}{\sqrt{\psi^{[1]} + \psi^{[3]} - 2\psi^{[31]} + \pi^2/3}\sqrt{\psi^{[3]} + \pi^2/3}}$$

Conditional on both covariates and random intercepts, the correlations between all utility differences (from base category) become $\frac{\pi^2/6}{\sqrt{\pi^2/3}\sqrt{\pi^2/3}} = 0.5$. It also follows that utility *differences* (from base category) have a correlation of 0.5 even if the utilities themselves are uncorrelated. Correlated utilities therefore correspond to correlations among utility differences (from base category) that are different from 0.5.

Display 12.3: Correlations between utility differences in conditional logit model with alternative-specific random intercepts

Before using `gllamm` to fit the model, we use the `eq` command to specify the variables that multiply the random effects. Here the alternative-specific intercepts for Yoplait and Dannon are multiplied by the corresponding dummy variables $d_1^{[s]}$ and $d_3^{[s]}$:

```
. eq Yo: Yoplait
. eq We: WeightW
```

The names `Yo` and `We` are arbitrary; they were chosen to be short but descriptive.

We can then fit the model by maximum likelihood using the following `gllamm` command with the equation names given in the `eqs()` option:

```
. gllamm brand Yoplait WeightW feature pricec, i(house) link(mlogit)
> expanded(set choice o) noconstant nrf(2) eqs(Yo We) adapt
number of level 1 units = 7023
number of level 2 units = 100

Condition Number = 18.432026

gllamm model

log likelihood = -1009.5358
```

brand	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
Yoplait	.8782923	.5437034	1.62	0.106	-.1873469	1.943931
WeightW	-2.549511	.6673952	-3.82	0.000	-3.857582	-1.241441
feature	.8085093	.2160702	3.74	0.000	.3850194	1.231999
pricec	-.4606993	.0450446	-10.23	0.000	-.5489851	-.3724136

```
Variances and covariances of random effects
------------------------------------------------------------------------------


***level 2 (house)

    var(1): 15.007983 (3.6153107)
    cov(2,1): 10.282717 (3.341922) cor(2,1): .63115183

    var(2): 17.685843 (4.6099075)
------------------------------------------------------------------------------
. estimates store rint
```

This `gllamm` command adds some new options to the one used earlier. Specifically, `nrf(2)` stands for two random effects, and `eqs(Yo We)` is used to specify that the variables defined above with the `eq` commands have random coefficients (in this case, a bivariate normal distribution is assumed for the alternative-specific intercepts).

We can use a likelihood-ratio test to compare the fitted model (12.9) with the standard conditional logit model (12.8) that did not include random alternative-specific intercepts. This can be accomplished using the command

```
. lrtest rint condlogit
Likelihood-ratio test                                 LR chi2(3)  =   2694.29
(Assumption: condlogit nested in rint)                Prob > chi2 =    0.0000
```

The asymptotic null distribution is not simply chi-squared with 3 degrees of freedom (for two variances and one covariance) in this case because the null hypothesis is on the border of the parameter space (because variances cannot be negative). As mentioned in section 4.6, we do not know the distribution for testing the null hypothesis that several variances are zero if the corresponding random effects are correlated. Although the naïve p-value is too large, it is still less than 0.05, so we know that we can reject the standard conditional logit model in favor of the conditional logit model with random alternative-specific intercepts at the 5% significance level.

Estimated variances and covariances of the random alternative-specific intercepts are given under `Variances and covariances of random effects` in the output. The index for these parameters runs from 1 to 2 (because there are two random intercepts) and hence differs from the one used in our model specification (where the base outcome is 2). Hence, 1 refers to Yoplait as before, but 2 now refers to Weight Watchers.

The estimated coefficients in the upper part of the output represent conditional or household-specific effects on the log odds for the brands compared with the base outcome Dannon. Because odds ratios are usually preferred for interpretation, we obtain estimated odds ratios with confidence intervals without refitting the model as

```
. gllamm, eform
number of level 1 units = 7023
number of level 2 units = 100

Condition Number = 18.432026

gllamm model

log likelihood = -1009.5358
```

brand	exp(b)	Std. Err.	z	P>|z|	[95% Conf.	Interval]
Yoplait	2.406786	1.308578	1.62	0.106	.8291561	6.986163
WeightW	.0781198	.0521368	-3.82	0.000	.021119	.2889676
feature	2.244559	.4849824	3.74	0.000	1.469643	3.428076
pricec	.6308423	.028416	-10.23	0.000	.5775356	.6890692

(*Estimates for random part not shown*)

The estimated coefficients and their standard errors as well as corresponding odds ratios with 95% confidence intervals were reported under "Random alt.-specific intercepts" in table 12.2 on page 658. The estimated coefficient of `feature` corresponds to a household-specific odds ratio of $\exp(0.8085093) = 2.244559$. According to the model, the use of newspaper feature advertising for a brand hence increases the odds of buying that brand by an estimated 124% [$124\% = 100\% \times (2.244559 - 1)$] for a given household, keeping the prices of the brands and the advertising of the other brands constant.

The estimated coefficient of `pricec` corresponds to a household-specific odds ratio of $\exp(-0.4606993) = 0.6308423$. It follows that increasing the price of a brand by 1 cent per oz (corresponding to an 8 cent increase for an 8 oz yogurt) reduces the odds of buying that brand by an estimated 37% [$-37\% = 100\% \times (0.6308423 - 1)$] for a given household, controlling for the prices of other brands and feature advertising.

Comparing these conditional or household-specific estimates for the odds ratios with the marginal or population-averaged estimates presented for the conditional logit model under "Single-level" in the table, we see that the latter are closer to 1 as expected. For instance, the estimated odds ratio for feature advertising is about 1.36 for the conditional logit model and 2.24 for the model with random alternative-specific intercepts.

12.7.2 Response heterogeneity: Marketing variables with random coefficients

It may very well be that the effects of the marketing variables vary over households. For instance, some households may be more or less susceptible to newspaper feature advertisements than others and more or less sensitive to changes in the prices of the yogurt brands.

We now consider a model where the coefficients for the marketing variables are allowed to vary randomly over households j but not over alternatives s. In contrast to the previous model, the alternative-specific intercepts are treated as fixed. The coefficients of `feature` are $\beta_2 + \zeta_{2j}$, where ζ_{2j} is a random deviation from the fixed effect β_2 for households j, and the coefficients of `pricec` become $\beta_3 + \zeta_{3j}$, where ζ_{3j} vary randomly over households. In marketing, this kind of heterogeneity in the effects of covariates is often called *response heterogeneity*.

The following model is specified for the conditional probability that brand s is chosen, given the covariates $\mathbf{x}_{ij}^{[s]}$ and the random coefficients ζ_{2j} and ζ_{3j}:

$$\begin{aligned} &\Pr(y_{ij}=s|\mathbf{x}_{ij}^{[1]},\mathbf{x}_{ij}^{[2]},\mathbf{x}_{ij}^{[3]},\zeta_{2j},\zeta_{3j}) \\ &= \frac{\exp\left\{\beta_1^{[1]}d_1^{[s]} + \beta_1^{[3]}d_3^{[s]} + (\beta_2+\zeta_{2j})x_{2ij}^{[s]} + (\beta_3+\zeta_{3j})x_{3ij}^{[s]}\right\}}{\sum_{c=1}^{3}\exp\left\{\beta_1^{[1]}d_1^{[c]} + \beta_1^{[3]}d_3^{[c]} + (\beta_2+\zeta_{2j})x_{2ij}^{[c]} + (\beta_3+\zeta_{3j})x_{3ij}^{[c]}\right\}} \end{aligned} \tag{12.10}$$

Given the covariates and the random coefficients, this model is equivalent to a linear model for the utility $U_{ij}^{[s]}$ of alternative s for household j at the ith purchasing occasion,

$$U_{ij}^{[s]} = \beta_1^{[1]}d_1^{[s]} + \beta_1^{[3]}d_3^{[s]} + (\beta_2+\zeta_{2j})x_{2ij}^{[s]} + (\beta_3+\zeta_{3j})x_{3ij}^{[s]} + \epsilon_{ij}^{[s]}$$

where the $\epsilon_{ij}^{[s]}$ have Gumbel distributions that are independent over alternatives, occasions, and households. Because the random coefficients ζ_{2j} and ζ_{3j} are shared for different purchasing occasions of a household, the utilities are no longer independent, and the assumption of IIA is relaxed.

It is assumed that the random coefficients have a bivariate normal distribution,

$$\begin{bmatrix} \zeta_{2j} \\ \zeta_{3j} \end{bmatrix} \sim N\left(\begin{bmatrix} 0 \\ 0 \end{bmatrix}, \begin{bmatrix} \psi_2 & \\ \psi_{32} & \psi_3 \end{bmatrix}\right)$$

and that the random coefficients are independent of the observed covariates $\mathbf{x}_{ij}^{[1]}$, $\mathbf{x}_{ij}^{[2]}$, and $\mathbf{x}_{ij}^{[3]}$.

Let us now estimate (12.10) using `gllamm`. To specify random coefficients of the marketing variables, we first define equations by using the `eq` commands:

```
. eq pr: pricec
. eq fea: feature
```

The only changes that must be made to the previous `gllamm` command are to specify different equations in `eqs()` to let the two marketing variables have random coefficients.

```
. gllamm brand Yoplait WeightW feature pricec,
> i(house) link(mlogit) expanded(set choice o) noconstant nrf(2) eqs(pr fea) adapt
number of level 1 units = 7023
number of level 2 units = 100

Condition Number = 6.6305969

gllamm model

log likelihood = -1891.2796
```

brand	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
Yoplait	.9850251	.0998629	9.86	0.000	.7892974	1.180753
WeightW	-.6631998	.0573897	-11.56	0.000	-.7756817	-.550718
feature	.792219	.3051963	2.60	0.009	.1940452	1.390393
pricec	-.5337412	.0841761	-6.34	0.000	-.6987233	-.3687592

```
Variances and covariances of random effects
------------------------------------------------------------------------------

***level 2 (house)

    var(1): .49884763 (.09903316)
    cov(2,1): .54118847 (.26753215) cor(2,1): .42572259

    var(2): 3.2394835 (1.1857948)
------------------------------------------------------------------------------
. estimates store rcoeff
```

We can again use a likelihood-ratio test to compare model (12.10) with the standard conditional logit model (12.8) by using the commands

```
. lrtest rcoeff condlogit
Likelihood-ratio test                                 LR chi2(3)  =    930.80
(Assumption: condlogit nested in rcoeff)              Prob > chi2 =    0.0000
```

Again the asymptotic null distribution is not simply a chi-squared with 3 degrees of freedom (for two variances and one covariance) because the variances cannot be negative. The naïve p-value is less than 0.05 and we know that it is too large, so we can reject the standard conditional logit model in favor of the conditional logit model with random coefficients at the 5% significance level.

As before, we can obtain estimated odds ratios with confidence intervals without refitting the model by using

```
. gllamm, eform
number of level 1 units = 7023
number of level 2 units = 100

Condition Number = 6.6305969

gllamm model

log likelihood = -1891.2796
```

brand	exp(b)	Std. Err.	z	P>|z|	[95% Conf.	Interval]
Yoplait	2.677879	.2674208	9.86	0.000	2.201849	3.256825
WeightW	.5152001	.0295672	-11.56	0.000	.4603898	.5765357
feature	2.208291	.6739624	2.60	0.009	1.214151	4.016428
pricec	.586407	.0493614	-6.34	0.000	.4972197	.6915919

(*Estimates for random part not shown*)

The estimated coefficients and their standard errors as well as corresponding odds ratios with 95% confidence intervals were reported under "Random coefficients" in table 12.2 on page 658. According to the random-coefficient model, the use of newspaper feature advertising for a brand increases the odds of buying that brand by an estimated 121% [$121\% = 100\% \times (2.208291 - 1)$] for a given household, keeping the prices of the brands and the advertising of the other brands constant. Increasing the price of a brand by 1 cent per oz reduces the odds of buying that brand by an estimated 41% [$-41\% = 100\% \times (0.586407 - 1)$] for a given household, controlling for the prices of other brands and feature advertising. We see that the estimated household-specific effects of `feature` and `pricec` are quite similar to those reported for the model with alternative-specific random intercepts. Comparing the estimated conditional or household-specific effects of the marketing variables with their marginal or population-averaged counterparts, we again see that the latter are closer to 1, as would be expected.

Based on the estimated random-coefficient model, the 95% range of the household-specific odds ratios for `feature` can be obtained as (see section 4.7)

```
. display exp(.792219 - 1.96*sqrt(.49884762))
.55315764
. display exp(.792219 + 1.96*sqrt(.49884762))
8.8158413
```

We see that the 95% range from 0.55 to 8.82 includes 1, so the household-specific effect of feature advertising is not necessarily positive. Analogously, the 95% range of the household-specific odds ratios for `pricec` can be obtained as

```
. display exp(-.5337412 - 1.96*sqrt(1.1857948))
.06938618
. display exp(-.5337412 + 1.96*sqrt(1.1857948))
4.9559319
```

The 95% range from 0.07 to 4.96 is wide and also includes 1. The correlation between the two random coefficients is estimated as 0.43.

12.7.3 ❖ Preference and response heterogeneity

A final model to consider combines the models fit in the two previous sections by including both preference heterogeneity (brand-specific random intercepts $\zeta_{1j}^{[1]}$ and $\zeta_{1j}^{[3]}$) and response heterogeneity (random coefficients ζ_{2j} and ζ_{3j} for the marketing variables). Hence, the two random-effects models that we have previously discussed in this chapter are both nested in this model.

The conditional probability of choosing brand s ($s = 1, \ldots, 3$), given the covariates, the random alternative-specific intercepts, and the random coefficients, is specified as

$$\begin{aligned}&\Pr(y_{ij} = s|\mathbf{x}_{ij}^{[1]}, \mathbf{x}_{ij}^{[2]}, \mathbf{x}_{ij}^{[3]}, \zeta_{1j}^{[1]}, \zeta_{1j}^{[3]}, \zeta_{2j}, \zeta_{3j}) \\ = &\frac{\exp\left\{(\beta_1^{[1]} + \zeta_{1j}^{[1]})d_1^{[s]} + (\beta_1^{[3]} + \zeta_{1j}^{[3]})d_3^{[s]} + (\beta_2 + \zeta_{2j})x_{2ij}^{[s]} + (\beta_3 + \zeta_{3j})x_{3ij}^{[s]}\right\}}{\sum_{c=1}^{3}\exp\left\{(\beta_1^{[1]} + \zeta_{1j}^{[1]})d_1^{[c]} + (\beta_1^{[3]} + \zeta_{1j}^{[3]})d_3^{[c]} + (\beta_2 + \zeta_{2j})x_{2ij}^{[c]} + (\beta_3 + \zeta_{3j})x_{3ij}^{[c]}\right\}}\end{aligned}$$

Given the covariates and the random coefficients, the corresponding model for the utility $U_{ij}^{[s]}$ is

$$U_{ij}^{[s]} = (\beta_1^{[1]} + \zeta_{1j}^{[1]})d_1^{[s]} + (\beta_1^{[3]} + \zeta_{1j}^{[3]})d_3^{[s]} + (\beta_2 + \zeta_{2j})x_{2ij}^{[s]} + (\beta_3 + \zeta_{3j})x_{3ij}^{[s]} + \epsilon_{ij}^{[s]}$$

where the $\epsilon_{ij}^{[s]}$ have independent Gumbel distributions.

As before, we assume that the random effects have a multivariate normal distribution:

$$\begin{bmatrix} \zeta_{1j}^{[1]} \\ \zeta_{1j}^{[3]} \\ \zeta_{2j} \\ \zeta_{3j} \end{bmatrix} \sim N\left(\begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}, \begin{bmatrix} \psi^{[1]} & & & \\ \psi^{[31]} & \psi^{[3]} & & \\ \psi_2^{[1]} & \psi_2^{[3]} & \psi_2 & \\ \psi_3^{[1]} & \psi_3^{[3]} & \psi_{32} & \psi_3 \end{bmatrix}\right)$$

The random effects are assumed to be independent from the observed covariates $\mathbf{x}_{ij}^{[1]}$, $\mathbf{x}_{ij}^{[2]}$, and $\mathbf{x}_{ij}^{[3]}$.

Estimation using gllamm

The model including both preference and response heterogeneity has a complicated random part with four random effects and altogether 10 variance and covariance parameters. Fitting this model by maximum likelihood is very computationally challenging using `gllamm`. Unless you have a powerful computer as well as a patient personality, our best advice is "don't try this at home!" (it can take a couple of days using a laptop).

For the four random effects of the model (two for the alternative-specific intercepts and two for the marketing variables), we define the following equations for `gllamm`:

```
. eq Yo: Yoplait
. eq We: WeightW
. eq pr: pricec
. eq fea: feature
```

We fit the model by maximum likelihood in `gllamm` using eight-point (the default) adaptive quadrature:

```
. gllamm brand Yoplait WeightW feature pricec, i(house) link(mlogit)
> expanded(set choice o) noconstant eqs(Yo We pr fea) nrf(4) adapt
number of level 1 units = 7023
number of level 2 units = 100

Condition Number = 11.388455

gllamm model

log likelihood = -986.19516
```

brand	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
Yoplait	1.27877	.5334415	2.40	0.011	.2332441	2.324296
WeightW	-2.765252	.6674995	-4.14	0.000	-4.073527	-1.456977
feature	1.179442	.3337126	3.53	0.000	.5253771	1.833506
pricec	-.642399	.0943309	-6.81	0.000	-.8272841	-.4575139

```
Variances and covariances of random effects
------------------------------------------------------------------------------

***level 2 (house)

    var(1): 14.80929 (4.206074)
    cov(2,1): 9.9720435 (3.5426805) cor(2,1): .57027494

    var(2): 20.647407 (5.429534)
    cov(3,1): .1715578 (.47452189) cor(3,1): .09051308
    cov(3,2): .65328064 (.53710655) cor(3,2): .29190063

    var(3): .24258503 (.10729907)
    cov(4,1): 2.2522654 (1.8464909) cor(4,1): .83550404
    cov(4,2): .58244816 (1.5580014) cor(4,2): .18298716
    cov(4,3): -.14708314 (.16674517) cor(4,3): -.42631144

    var(4): .49069066 (.60326651)
------------------------------------------------------------------------------
```

Estimated odds ratios with confidence intervals for the model are obtained as

```
. gllamm, eform
number of level 1 units = 7023
number of level 2 units = 100

Condition Number = 11.388455

gllamm model

log likelihood = -986.19516
```

brand	exp(b)	Std. Err.	z	P>|z|	[95% Conf.	Interval]
Yoplait	3.592219	1.916239	2.40	0.017	1.26269	10.21949
WeightW	.0629603	.0420259	-4.14	0.000	.0170173	.2329394
feature	3.252558	1.085419	3.53	0.000	1.691096	6.255783
pricec	.526029	.0496208	-6.81	0.000	.4372352	.632855

(*Estimates for random part not shown*)

Regarding the estimates for the fixed part of the model, we see that the estimates for the alternative-specific intercepts of 1.28 and −2.77 are fairly similar to those reported for the model with just preference heterogeneity (see "Random alt.-specific intercepts" in table 12.2 on page 658). The fixed coefficients of `feature` and `pricec` are estimated as 1.18 and −0.64, respectively, corresponding to odds ratios of 3.25 and 0.53. Compared with the estimates for the special cases of this model shown under "Multilevel" in table 12.2, the household-specific odds ratio of feature advertising is considerably larger and the household-specific effect of price somewhat lower in this model.

We see that the estimated variances of the alternative-specific random intercepts of 14.81 and 20.65, and the estimated covariance between the intercepts of 9.97, are quite close to the corresponding estimates for the model with just preference heterogeneity (see "Random alt.-specific intercepts" in table 12.2). In contrast, the estimated variances of the random coefficients of `feature` and `pricec` of 0.24 and 0.49, and the estimated covariance between the coefficients of −0.15, are very different from those for the model with only response heterogeneity (see "Random coefficients" in table 12.2).

Estimation using mixlogit

Because maximum likelihood estimation using adaptive quadrature in `gllamm` takes a very long time for discrete-choice models with many random effects, it is worthwhile considering alternative approaches to estimation.

A popular approach for discrete choice models is *simulated maximum likelihood* (SML), where the required integration is performed by simulation instead of numerical integration. The simulations are performed by drawing quasi-random numbers in a clever way, using what are called Halton draws, to reduce the number of draws required to obtain a given Monte Carlo error. We refer to Train (2009) for the theory and practice of simulated maximum likelihood for discrete-choice models.

To fit the model with preference and response heterogeneity by simulated maximum likelihood in Stata, we will use the user-contributed program `mixlogit` by Hole (2007), which can be downloaded by using the command

```
. ssc install mixlogit, replace
```

(it is a good idea to obtain the latest version, which is faster than the original). The `mixlogit` command fits *mixed logit models* or, in other words, logit models with random effects such as those used in this chapter. `mixlogit` also has a `mixlpred` postestimation command for predicting choice probabilities.

The model can be fit by using the following `mixlogit` command:

```
. mixlogit choice, group(set) id(house) rand(Yoplait WeightW feature pricec) corr
Mixed logit model                               Number of obs   =       7023
                                                LR chi2(10)     =    2720.01
Log likelihood = -996.67586                     Prob > chi2     =     0.0000
```

choice	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
Yoplait	1.619169	.2246412	7.21	0.000	1.17888	2.059457
WeightW	-2.050162	.3352067	-6.12	0.000	-2.707155	-1.393169
feature	1.336173	.2879728	4.64	0.000	.7717566	1.900589
pricec	-.6084425	.0655207	-9.29	0.000	-.7368607	-.4800242
/l11	2.956528	.3831274	7.72	0.000	2.205612	3.707444
/l21	2.261802	.3130134	7.23	0.000	1.648307	2.875297
/l31	.4597804	.3384704	1.36	0.174	-.2036094	1.12317
/l41	.1973935	.0852472	2.32	0.021	.030312	.364475
/l22	5.769872	.4939714	11.68	0.000	4.801706	6.738038
/l32	-.5196223	.3845178	-1.35	0.177	-1.273263	.2340187
/l42	.3530624	.0678431	5.20	0.000	.2200923	.4860326
/l33	.8147397	.3559046	2.29	0.022	.1171796	1.5123
/l43	-.4663116	.0562559	-8.29	0.000	-.5765711	-.356052
/l44	-.042378	.0441377	-0.96	0.337	-.1288862	.0441303

In `mixlogit`, `choice` is the response variable. The `group()` option is used to specify the purchasing occasions or choice sets, the `id()` option to specify the cluster variable, and the `rand()` option to specify the covariates that have random coefficients. A covariate designated to have a random coefficient is automatically given a fixed effect in `mixlogit` and is therefore not included in the specification of the fixed part of the model (this is the reason that no covariates are included after `choice` because all covariates have random coefficients in this case). The `corr` option specifies that we want to fit a model where the random effects are correlated and the `nrep()` option can be used to determine the number of Halton draws used (the default is 50). We refer to Hole (2007) for more information regarding the syntax of `mixlogit`.

`mixlogit` reports the estimated Cholesky decomposition of the covariance matrix of the random effects. To obtain the desired estimated variances and covariances of the random effects, we use the postestimation command `mixlcov`:

```
. mixlcov
```

choice	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
v11	8.741058	2.265455	3.86	0.000	4.30085	13.18127
v21	6.687082	1.612455	4.15	0.000	3.526729	9.847435
v31	1.359354	1.047854	1.30	0.195	-.6944015	3.41309
v41	.5835993	.2153143	2.71	0.007	.1615911	1.005608
v22	38.40717	6.144645	6.25	0.000	26.36389	50.45046
v32	-1.958222	2.28916	-0.86	0.392	-6.444892	2.528449
v42	2.48359	.5644682	4.40	0.000	1.377253	3.589927
v33	1.145206	.7358702	1.56	0.120	-.2970729	2.587485
v43	-.472624	.2328278	-2.03	0.042	-.9289581	-.0162899
v44	.3828596	.0916587	4.18	0.000	.2032119	.5625074

Fitting the model is very fast in `mixlogit` with the default of 50 Halton draws, but we see that the estimates and the log likelihood are dramatically different from those produced by `gllamm`. The log likelihood is -986.20 in `gllamm` and -996.68 in `mixlogit`. The estimates for the fixed alternative-specific intercepts are 1.62 and -2.05 compared with 1.28 and -2.77, for `mixlogit` and `gllamm`, respectively, and the fixed coefficients of `feature` and `pricec` are estimated as 1.34 and -0.61 compared with 1.18 and -0.64. Regarding the random part of the model, we see that the variances of the alternative-specific random intercepts are estimated as 8.74 and 38.41 by `mixlogit` compared with 14.81 and 20.65 by `gllamm`, and the variance of the random coefficients of `feature` and `pricec` are estimated as 1.15 and 0.38 compared with 0.24 and 0.49.

As would be expected, the more Halton draws you use, the more reliable the estimates should become because Monte Carlo error is reduced at the cost of computation time. It is sometimes suggested that 50 Halton draws may suffice for model selection and 500 draws for the final model (Hole 2007). However, Hensher, Rose, and Greene (2005) point out that the number of draws required depends on the complexity of the model, such as the number of random effects and whether these are correlated. They also recommend refitting the models with an increasing number of Halton draws and monitoring the stability of the estimates to make sure that the results are reliable (anal-

ogous to the approach for assessing adequacy of the quadrature approximation). For the model considered in this section with four correlated random effects, we found that as many as 5,000 or 10,000 Halton draws may be required to give reliable results, which is very different from the default of just 50 Halton draws in `mixlogit`.

The following `mixlogit` command fits the model with preference and response heterogeneity using 10,000 Halton draws (this will take a long time):

```
. mixlogit choice,
> group(set) id(house) rand(Yoplait WeightW feature pricec) corr nrep(10000)
Mixed logit model                                 Number of obs   =       7023
                                                  LR chi2(10)     =    2742.32
Log likelihood = -985.51663                       Prob > chi2     =     0.0000
```

choice	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
Yoplait	1.056259	.4436564	2.38	0.017	.1867085	1.92581
WeightW	-2.730497	.5927365	-4.61	0.000	-3.89224	-1.568755
feature	1.152327	.3262482	3.53	0.000	.5128918	1.791761
pricec	-.6352615	.092048	-6.90	0.000	-.8156723	-.4548508
/l11	3.911001	.5862744	6.67	0.000	2.761924	5.060078
/l21	2.724117	.8150612	3.34	0.001	1.126627	4.321608
/l31	.5800756	.4833779	1.20	0.230	-.3673277	1.527479
/l41	.0642829	.1315759	0.49	0.625	-.1936012	.322167
/l22	3.961898	.5530667	7.16	0.000	2.877907	5.045889
/l32	-.2746034	.3283181	-0.84	0.403	-.918095	.3688882
/l42	.1107349	.093737	1.18	0.237	-.0729862	.2944561
/l33	.4247641	.3889848	1.09	0.275	-.3376321	1.18716
/l43	-.3219568	.0718756	-4.48	0.000	-.4628304	-.1810831
/l44	.3022503	.1211518	2.49	0.013	.0647971	.5397034

We use `mixlcov` to obtain the estimated variances and covariances of the random effects (`mixlcov` with the `sd` option reports the estimated standard deviations of the random effects instead of the covariance matrix):

```
. mixlcov
```

choice	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
v11	15.29593	4.58584	3.34	0.001	6.307848	24.28401
v21	10.65403	4.201682	2.54	0.011	2.418879	18.88917
v31	2.268676	1.954882	1.16	0.246	-1.562822	6.100175
v41	2514104	.5072169	0.50	0.620	-.7427165	1.245537
v22	23.11745	5.38359	4.29	0.000	12.56581	33.66909
v32	.4922433	1.743574	0.28	0.778	-2.925099	3.909585
v42	.6138345	.4404169	1.39	0.163	-.2493667	1.477036
v33	.5923193	.6826357	0.87	0.386	-.745622	1.930261
v43	-.1298749	.1450726	-0.90	0.371	-.414212	.1544621
v44	.2114059	.0832908	2.54	0.011	.0481589	.3746529

The estimates from `mixlogit` based on 10,000 Halton draws are quite similar to those produced by `gllamm` with eight-point adaptive quadrature.

Simulated maximum likelihood is certainly an interesting alternative to maximum likelihood using adaptive quadrature when there are many random effects. However, we recommend that caution is exercised when using `mixlogit` to ensure that enough Halton draws are used to obtain reliable estimates. The number of draws should be increased until the difference in estimates is small. In summary, it is worth heeding the words of caution from Train (2009, 230):

> "The use of Halton draws and other quasi-random numbers in simulation-based estimation is fairly new and not completely understood."

12.8 Prediction of random effects and response probabilities

We illustrate prediction of random effects and response probabilities by returning to the model with response heterogeneity discussed in section 12.7.2. The model included fixed alternative-specific intercepts and random coefficients for `feature` and `pricec`.

We begin by restoring the `gllamm` estimates for this model:

```
. estimates restore rcoeff
```

For each household, we can obtain empirical Bayes predictions $\widetilde{\zeta}_{2j}$ and $\widetilde{\zeta}_{3j}$ of the random coefficients of `pricec` and `feature`, respectively, by using `gllapred` with the `u` option,

```
. gllapred eb, u
(means and standard deviations will be stored in ebm1 ebs1 ebm2 ebs2)
```

and empirical Bayes predictions of the household-specific coefficients $\widehat{\beta}_2+\widetilde{\zeta}_{2j}$ and $\widehat{\beta}_3+\widetilde{\zeta}_{3j}$ as

```
. generate eb_pricec = ebm1 + _b[pricec]
. generate eb_feature = ebm2 + _b[feature]
```

We can then plot the predicted household-specific coefficients,

```
. egen pickone = tag(house)
. twoway scatter eb_pricec eb_feature if pickone==1, mlabel(house)
> xtitle(EB prediction of feature coefficient)
> ytitle(EB prediction of price coefficient)
```

giving the graph in figure 12.3. The predicted coefficients of `feature` are mostly positive, whereas the predicted coefficients of `pricec` are mostly negative, as expected. However, some households appear to behave strangely. For instance, household 55 seems to like high prices and household 97 appears to be less likely to choose a brand when it has been advertised than when it has not been advertised. These predictions could of course also be due to chance or omitted covariates.

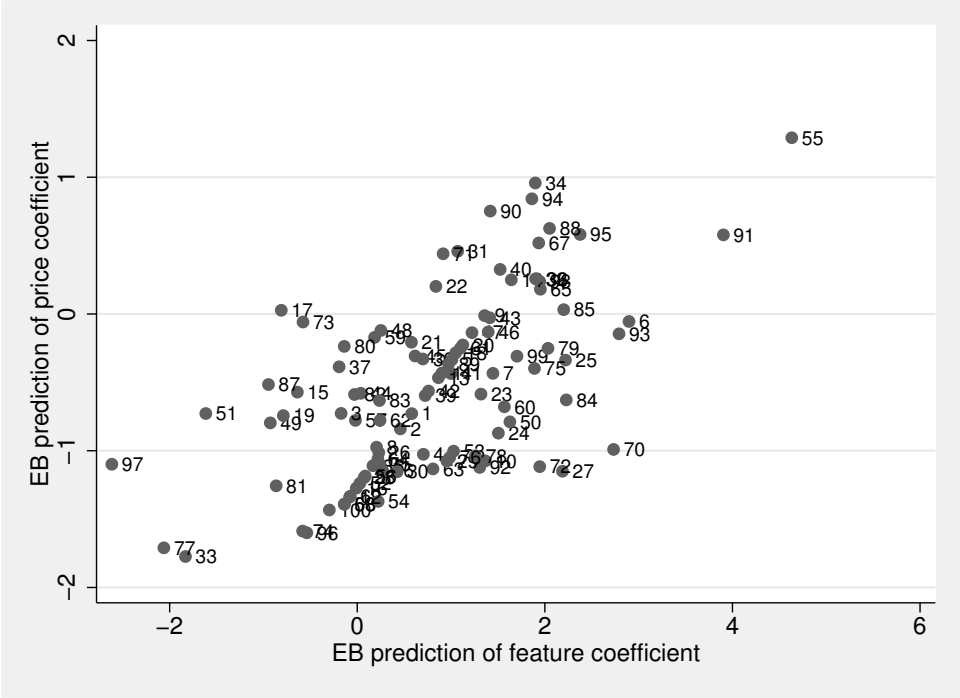


Figure 12.3: Empirical Bayes (EB) predictions of household-specific coefficients of `pricec` and `feature`

Another way of aiding our understanding of the response heterogeneity is by plotting the brand choice probabilities for individual households against covariates. We consider the case where there is no feature advertising (`feature`=0) and where the price of Weight Watchers and Dannon is held constant at 8 cents/oz, whereas the price of Yoplait varies from 0.5 cent/oz to 20 cents/oz (approximately the range in the data). To obtain posterior mean probabilities for particular households, we need to create new rows of data for these households (prediction data), with covariates equal to the desired values. By setting the response variable to missing for invented data, we make sure that they do not affect the posterior distribution of the random effects (see section 10.13.2).

We first save the data and create a new dataset for the prediction data and then append the original data. For the predictions, we start by creating data for one household, initially 40 rows of data, with `pricec` increasing in steps of 0.5 cents/oz from 0.5 to 20:

```
. save temp, replace
(note: file temp.dta not found)
file temp.dta saved
. drop _all
. set obs 40
obs was 0, now 40
. generate pricec =  _n*.5
```

We then expand the data to alternative sets comprising the three brands. The variable `set` should be unique for each alternative set for a given household, and we hence use values greater than 3,000 to be sure that these values do not already occur in the data:

```
. generate set = 3000 + _n
. expand 3
(80 observations created)
```

At this point, we create all the variables used in the original `gllamm` command so that `gllapred` can make the required predictions. In addition to the variable `pricec`, which should vary for Yoplait but be constant at 8 cents/oz for the other brands, we create a variable, `yopprice`, for the price of Yoplait (constant within the alternative sets) to use for making the graph later:

```
. by set, sort: generate brand=_n
. generate yopprice = pricec
. replace pricec = 8 if brand > 1
(78 real changes made)
. generate feature = 0
. tabulate brand, generate(br)
```

brand	Freq.	Percent	Cum.
1	40	33.33	33.33
2	40	33.33	66.67
3	40	33.33	100.00
Total	120	100.00	

```
. rename br1 Yoplait
. rename br2 Dannon
. rename br3 WeightW
. generate choice = Dannon
```

The `choice` variable is arbitrary but needs to be equal to 1 once per choice set in the prediction data. Here it was arbitrarily set equal to `Dannon`.

Predictions will be made for six households, namely, household 33, 15, 7, 48, 6, and 55. These households were deliberately selected to vary considerably in their household-specific coefficient of `pricec` by inspecting figure 12.3. We need to create identical prediction data for each of these households, which is easily accomplished using the `expand` command:

```
. expand 6
(600 observations created)
. by set brand, sort: generate house=_n
. recode house 1=33 2=15 3=7 4=48 5=6 6=55
(house: 720 changes made)
```

The response variable is set to missing as explained above, and the original data (`temp.dta`) are appended to the prediction data:

```
. replace brand = .
(720 real changes made, 720 to missing)
. append using temp
(label b already defined)
```

To keep track of which subset of the data is prediction data, we generate a dummy variable, `preddata`:

```
. generate preddata = brand ==.
```

We are now ready to obtain posterior mean purchasing probabilities by using the `gllapred` command with the `mu` option to specify that we want predicted probabilities (because the `marginal` option is not used, we obtain the default posterior mean probabilities instead of marginal probabilities) and the `fsample` option to obtain predictions for observations that are not in the estimation sample:

```
. gllapred probs, mu fsample
(mu will be stored in probs)
```

The posterior mean probabilities for the six selected households can then be plotted using

```
. egen select = anymatch(house), values(33 15 7 48 6 55)
. twoway (line probs yopprice if Yoplait==1, sort)
> (line probs yopprice if WeightW==1, sort lpatt(longdash))
> (line probs yopprice if Dannon==1, sort lpatt(shortdash))
> if feature==0&select==1&preddata==1,
> by(house) legend(order(1 "Yoplait" 2 "WeightW" 3 "Dannon") rows(1))
> xtitle(Price of Yoplait in cents/oz) ytitle(Probability of purchase)
```

and the resulting graph is shown in figure 12.4.

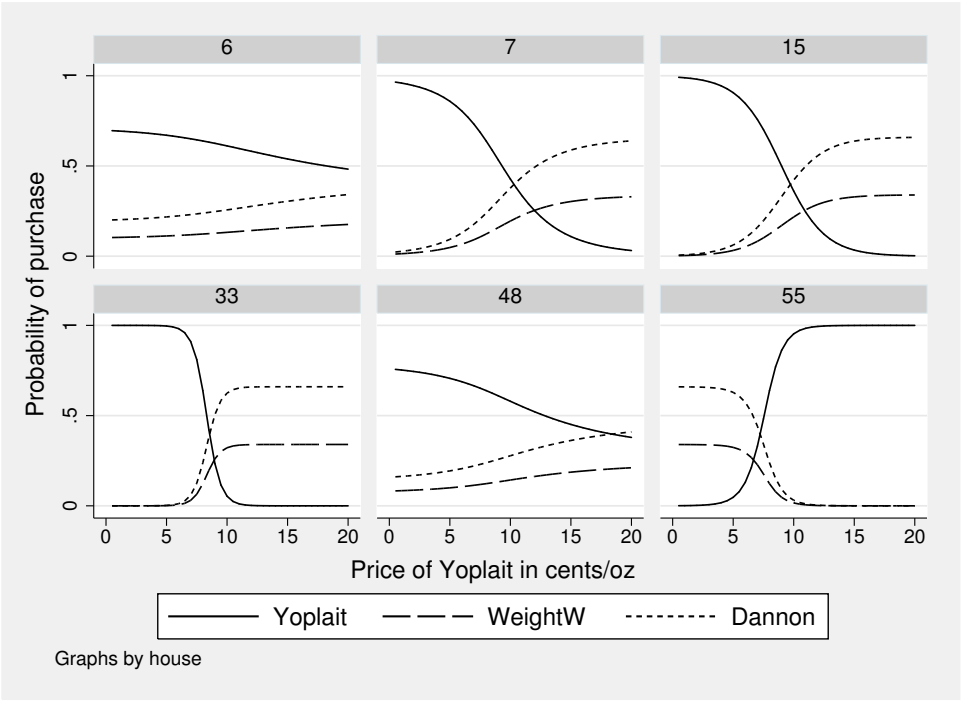


Figure 12.4: Posterior mean choice probabilities versus price in cents/oz of Yoplait for six households. Based on conditional logit model with response heterogeneity when there is no feature advertising and when the price of Weight Watchers and Dannon is held constant at 8c/oz.

Households 7, 15, and 33 had large negative empirical Bayes predictions of the household-specific coefficient of `pricec`, and this strong price sensitivity is apparent in the figure where the solid curve for the probability of purchasing Yoplait decreases rapidly. Households 6 and 48 are less price sensitive. Household 55, which had an extremely large empirical Bayes prediction of the household-specific coefficient of `pricec`, appears to find Yoplait more attractive (compared with the other brands) when it is more expensive (keeping the price of the other brands constant).

12.9 Summary and further reading

We have introduced the most commonly used models for nominal responses or discrete choices: the multinomial logit model and the conditional logit model. The models can be derived from a utility-maximization perspective that makes them attractive for applications involving choices made by individuals. The multinomial logit and conditional logit models possess a property called independence of irrelevant alternatives (IIA) which is often deemed to be unrealistic in practice. IIA is relaxed in the multilevel versions of

the models that we have described in this chapter. We will return to the multinomial logit model in section 14.2.5, where it is used for discrete-time survival modeling of multiple competing events.

We have not discussed multinomial probit models in this chapter. In these models, the error terms $\epsilon_{ij}^{[s]}$ in the utility-maximization formulation have normal distributions instead of the Gumbel distributions assumed for logit models. Stata's `mprobit` program fits multinomial probit models with independent $\epsilon_{ij}^{[s]}$ by maximum likelihood using ordinary quadrature. The `asmprobit` (for "alternative-specific multinomial probit") program also fits multinomial probit models where the $\epsilon_{ij}^{[s]}$ are correlated or heteroskedastic (different covariance structures can be specified) and alternative-specific covariates can be included. Estimation proceeds by maximum simulated likelihood using the Geweke–Hajivassiliou–Keane (GHK) algorithm. We have also not considered models for rankings in this chapter. The Stata program `rologit` can be used to fit such models without random effects, and `gllamm` can be used for models including random effects (and other kinds of latent variables); see chapter 9 of the `gllamm` manual (Rabe-Hesketh et al. 2004).

For a readable introduction to models for nominal responses (without random effects), we refer the reader to Long (1997, chap. 6). The book by Train (2009) is an excellent introduction to modeling nominal responses or discrete choices, both with and without random effects, with an emphasis on simulation-based inference. We also recommend the papers by Skrondal and Rabe-Hesketh (2003a) and Skrondal and Rabe-Hesketh (2003c), the latter paper being quite demanding, and the book chapter by Hedeker (2008).

The exercises involve choices of cars (exercise 12.2) and electricity suppliers (exercise 12.6) in conjoint experiments, purchases of saltine crackers (exercise 12.1), type of housing found for homeless people (exercise 12.3), type of contraception used by Bangladeshi women (exercise 12.5), and parties voted for in British national elections (exercise 12.4).

12.10 Exercises

12.1 Buying crackers data

Jain, Vilcassim, and Chintagunta (1994) analyzed data on 2,509 purchases of saltine crackers by 100 households. The method of data collection was the same as for the yogurt data described in section 12.5, via optical scanners and identification cards. There were three major national brands: Sunshine, Keebler, and Nabisco. Local brands were grouped together as "Private" labels.

The variables in the dataset `crackers.dta` are

- `id`: identifier for household
- `occ`: purchasing occasion

- `brand`: brands
  (1: Sunshine; 2: Keebler; 3: Nabisco; 4: Private)
- `choice`: dummy variable for the chosen brand
- `feature`: dummy variable for newspaper feature advertisement
- `display`: dummy variable for brand being on special end-of-aisle or middle-of-aisle display
- `price`: price in U.S.$/oz at occasion. For the brand purchased, the price is the actual price (shelf price net of value of coupons redeemed) and for all other brands it is the shelf price.

1. Create a unique identifier for each combination of `id` and `occ`. Also create dummy variables for the brands, treating Private as the reference category.
2. Use `clogit` to fit a conditional logit model with the covariates `feature`, `display`, and `price` and dummies for the brands Sunshine, Keebler, and Nabisco.
3. Interpret the estimates.
4. Fit the same model using `gllamm`.
5. Include a random coefficient for `feature` only, and compare this model with the model from step 4 by using a likelihood-ratio test.
6. Include a random coefficient for `display` only, and compare this model with the model from step 4 by using a likelihood-ratio test.
7. Include a random coefficient for `price` only, and compare this model with the model from step 4 by using a likelihood-ratio test.
8. Comment on the findings.

12.2 Hybrid car data

We consider a subset of the hybrid car data described by Train and Sonnier (2005). The data are provided with Kenneth Train's matlab program for mixed logit estimation by maximum simulated likelihood.

Each survey respondent was presented with 15 choice situations in each of which they were asked to choose one among three hypothetical cars. The cars were described in terms of several attributes including price and fuel type: gasoline (petrol), electric, and hybrid (gasoline–electric) cars. Such data are referred to as stated preference data in contrast to revealed preference data where the purchasing behavior is observed. An advantage of stated preference data is that the attributes can be varied in so-called conjoint designs to obtain the required information on the importance and trade-offs of attributes in making decisions. It is also possible to include alternatives that do not exist yet, such as a new subway. However, a problem with stated preference data is that the choices have no real implications for the respondent and are therefore fundamentally different from real purchasing decisions.

Random-digit dialing was used to contact potential respondents throughout the state of California, U.S.A. Those intending to buy a new vehicle within the next

three years were asked to participate in the study. If they were willing to participate, they were sent a packet of materials, including information sheets that described the new vehicles and the choice experiments. The respondents were later called to go over the information and obtain their choices and demographic details.

The variables in the dataset `hybrid.dta` are

- `id`: identifier for respondent
- `situation`: choice situation (unique identifier for each respondent–situation combination)
- `chosen`: dummy variable for choosing the alternative
- `price`: price in U.S.$10,000
- `electric`: dummy variable for electric car
- `hybrid`: dummy variable for hybrid car
- `cost`: running cost in U.S.$ per month
- `range`: number of miles between refueling/recharging
- `highperf`: dummy variable for high-performance car (top speed 120 miles per hour, 8 seconds to reach 60 miles per hour)
- `medperf`: dummy variable for medium-performance car (top speed 100 miles per hour, 12 seconds to reach 60 miles per hour)
  (The low category had a top speed of 80 miles per hour and 16 seconds to reach 60 miles per hour.)

1. Use the `clogit` command to fit a model with `chosen` as the response variable and `price`, `cost`, `range`, `electric`, `hybrid`, `highperf`, and `medperf` as explanatory variables (one coefficient per covariate).
2. Interpret the estimates.
3. Fit the same model in `gllamm`. Note that `gllamm` requires an identifier for the alternatives as response variable, but here each choice set has a different set of hypothetical alternatives characterized by the attributes. You can arbitrarily label the four alternatives for each situation from 1 to 4.
4. Extend the model to include correlated random coefficients for `hybrid` and `electric`, and fit the model using `gllamm`. Use `ip(m)` and `nip(11)` for degree-11 spherical quadrature to speed up estimation (this will take some time to run).

12.3 Housing the homeless data

The McKinney Homeless Research Project study (Hough et al. 1997; Hurlburt, Wood, and Hough 1996) was conducted in San Diego, California, to evaluate an intervention that aimed to provide independent housing for severely mentally ill homeless people. The intervention was a program of federal assistance to provide subsidized housing for low-income families and individuals, known as Section 8. Eligibility for the study was restricted to individuals diagnosed with severe and

persistent mental illness who were either homeless or at high risk of becoming homeless at the start of the study. Study participants were randomly assigned to one of two levels of access to independent housing using Section 8 certificates. They were followed up at 6, 12, and 24 months to determine their housing status (streets or shelters, community housing, or independent housing). The data are provided with the book by Hedeker and Gibbons (2006) and with the `supermix` software.

The variables in the dataset `homeless.dta` are

- `id`: person identifier
- `time`: occasion (0, 1, 2, 3), corresponding to 0, 6, 12, and 24 months, respectively
- `housing`: housing status (0: Streets or shelters; 1: Community housing; 2: Independent housing)
- `section8`: dummy variable for Section 8 group (1: Yes; 0: No)

1. Explore the missing-data patterns.
2. Create dummy variables for the three postrandomization time points and interactions between the time dummies and the treatment (Section 8) dummy.
3. Use `mlogit` to fit a multinomial logit model for `housing`, treating streets or shelters as the base outcome, with the treatment, the three time dummies, and the three time by treatment interactions as covariates.
4. Expand the data and fit the model from step 3 in `gllamm`.
5. Fit the model with two correlated alternative-specific random intercepts (use five-point adaptive quadrature—this will take a while).
6. Interpret the estimates.

12.4 British election data Solutions

Skrondal and Rabe-Hesketh (2003c, 2004) modeled data from the 1987–1992 panel of the British Election Study (Heath et al. 1993) and were given permission by Anthony Heath to make the data available. In the 1987 and 1992 panel waves, respondents were asked to state which party they had voted for in the British general elections earlier the same year. The three major political parties were Conservative, Labour, and Liberal (Alliance), and votes for other parties were treated as missing.

The variables in the dataset `elections.dta` are

- `serialno`: identifier for respondent
- `occ`: unique identifier for each combination of `serialno` and panel wave
- `party`: political party (1: Conservative; 2: Labour; 3: Liberal)
- `rank`: rank ordering of parties, where first ranking is party actually voted for

- `lrdist`: the distance between a voter's position on the left–right political dimension and the mean position of the party voted for. The mean positions of the parties over voters were used to avoid rationalization problems (Brody and Page 1972). The placements were constructed from four scales, where respondents located themselves and each of the parties on an 11-point scale anchored by two contrasting statements (priority should be unemployment versus inflation, increase government services versus cut taxation, nationalization versus privatization, more effort to redistribute wealth versus less effort).
- `yr87`: dummy variable for the 1987 national elections
- `yr92`: dummy variable for the 1992 national elections
- `male`: dummy for the voter being male
- `age`: age of the voter in 10-year units
- `manual`: dummy variable for father of voter being a manual worker
- `inflation`: rating of perceived inflation since the last election on a five-point scale

1. Create a variable, `chosen`, equal to 1 for the party voted for (`rank` equal to 1) and 0 for the other parties.
2. Standardize `lrdist` and `inflation` to have mean 0 and variance 1. Produce all the dummy variables and interactions necessary to fit a conditional logistic regression model (using `clogit`) for `chosen`, with the following covariates: the standardized versions of `lrdist` and `inflation`, and the dummy variables `yr87`, `yr92`, `male`, and `manual`. All variables except the standardized version of `lrdist` should have party-specific coefficients.
3. Fit the model using `clogit` and `gllamm`, using Conservatives as the base outcome.
4. Extend the model to include a person-level random slope for `lrdist`, and fit the extended model in `gllamm`.
5. Write down the model and interpret the estimates.
6. Instead of including a random slope for `lrdist`, include correlated person-level random intercepts for Labour and Liberal. Use the options `ip(m)` and `nip(15)` to use degree-15 spherical quadrature. This problem will take quite a long time to run.

See also exercise 16.8 for three-level modeling of these data.

12.5 Contraceptive method data

Here we analyze a subsample of the Bangladesh Fertility Survey (Huq and Cleland 1990) that was previously analyzed by Amin, Diamond, and Steele (1998) and made available with the MLwiN software (Rasbash et al. 2009).

The variables in the dataset `contraceptive.dta` that will be considered here are

- `woman`: woman identifier

- `district`: district identifier
- `method`: contraceptive method (1: sterilization; 2: modern reversible method; 3: traditional method; 4: not using contraception)
- `children`: number of living children at the time of the survey
- `urban`: dummy variable for living in an urban area (1: urban; 0: rural)
- `educ`: level of education (1: none; 2: lower primary; 3: upper primary; 4: secondary or higher)
- `hindu`: dummy variable for being Hindu (1: Hindu; 0: Muslim)
- `d_lit`: proportion of women in district who are literate
- `d_pray`: proportion of Muslim women in district who pray every day

1. Produce dummy variables, `one` and `twoplus`, for having one child and two or more children, respectively. Produce a dummy variable, `educat`, for having any education. Drop women who use the traditional method (to keep the model simpler and make it faster to estimate), and recode `method` so that it takes the values 1, 2, and 3 for sterilization, modern reversible method, and no contraception, respectively.
2. Use `mlogit` to fit a multinomial logit model with `method` as response variable and `one`, `twoplus`, `urban`, `educat`, `hindu`, `d_lit`, and `d_pray` as covariates.
3. Expand the data and fit the same model as in step 2 using `gllamm`.
4. Fit a two-level model that includes the same covariates as in steps 2 and 3. Include correlated district-level random intercepts for sterilization and the modern method. To speed up estimation in `gllamm`, use the options `ip(m)` and `nip(7)` for degree-7 spherical quadrature.
5. Interpret the estimates.

12.6 Electricity supplier data

Here we will analyze stated preference data on choice of electricity supplier originally used by Revelt and Train (2000). The data were made available by Kenneth Train and also accompanies Hole (2007). A sample of residential electricity customers were presented with up to 12 experiments. Each experiment consisted of choosing among four hypothetical electricity suppliers that differed in terms of the characteristics described in the variable list below. (See exercise 12.2 for a brief discussion of stated preference data.)

The variables in the dataset `electricity.dta` are

- `price`: price in cents per kilowatt-hour (kWh), 0 if time-of-day or seasonal rates
- `contract`: contract length in years (prices are guaranteed for duration of contract and customer pays penalty for switching suppliers during contract period; 0 means either side can stop the agreement at any time)
- `local`: dummy variable for company being local
- `known`: dummy variable for company being well known

- `tod`: dummy variable for time-of-day rates (11 cents per kWh between 8 a.m. and 8 p.m., and 5 cents per kWh from 8 p.m. to 8 a.m.)
- `seasonal`: dummy variable for seasonal rates (10 cents per kWh in the summer, 8 cents per kWh in the winter, and 6 cents per kWh in the spring and fall)

1. Fit a conditional logit model using `clogit` with `price`, `contract`, `local`, `known`, `tod`, and `seasonal` as explanatory variables that have constant coefficients.
2. Fit the same model using `gllamm`. This requires an identifier of the alternatives as response variable. In this example, a variable that arbitrarily labels the four alternatives for each experiment from 1 to 4 can be used.
3. Extend the model by including a random coefficient of `local`, and fit the model using `gllamm`.
4. Use a likelihood-ratio test at the 5% level of significance to compare the models in steps 2 and 3.
5. Extend the model further by including another random coefficient for `known`. Use `ip(m)` and `nip(11)` to speed up estimation.
6. Compare the models in steps 3 and 5 using a likelihood-ratio test at the 5% level of significance.
7. Interpret the estimates for the chosen model.

Part VI

Models for counts

13 Counts

13.1 Introduction

An important outcome in many investigations is a count of how many times some event has occurred. For instance, we could count the number of epileptic seizures in a week for a patient, the number of patents awarded to a company in a 5-year period, or the number of murders in a year in a city. Counts are nonnegative, integer-valued responses, taking on values 0, 1, 2, ...

In this chapter, we will discuss Poisson models for counts. After introducing single-level Poisson regression models, we describe multilevel Poisson regression models, which include random effects to model dependence and unobserved heterogeneity. Some new issues that arise in modeling counts, such as using offsets and dealing with overdispersion, will be considered. We also briefly describe negative binomial models for count data, as well as fixed-effects models and generalized estimating equations.

Two applications are considered: longitudinal modeling of number of doctor visits and small area estimation or disease mapping of lip cancer incidence. On first reading, it might be a good idea to concentrate on the first application.

13.2 What are counts?

13.2.1 Counts versus proportions

In this chapter, we consider counts of events that could in principle occur any time during a time interval (or anywhere within a spatial region). For instance, von Bortkiewicz (1898) observed 14 corps of the Prussian army from 1875 to 1894 and counted the number of deaths from horse kicks (see the logo on the spine of this book). Other examples of such counts are the number of times a person visits a doctor during a year, the number of times a person blinks in an hour, and the number of violent fights occurring in a school during a week. The term *count* without further qualification usually implies this type of count. As we discuss in section 13.3, a Poisson distribution is often appropriate in this case.

Another type of count is a count of events or *successes* that can only occur at a predetermined number of *trials*. The count y is then less than or equal to the number of trials n, and the response can be expressed as a sample proportion $p = y/n$. For instance, when counting the number of retired people in a city block at a given point in time,

each of n inhabitants is either retired (success) or not (failure), and the count cannot exceed n. A meaningful summary then is the proportion of the city block's population that is retired. An appropriate distribution for the corresponding count is often the binomial distribution for n trials. If there are covariates, the same models as those for dichotomous responses are used, such as the logit or probit model. The only difference is that a binomial denominator n_i must be specified for each unit i. In `xtmelogit`, the `binomial()` option can be used to specify a variable containing the values n_i; in `gllamm`, the `denom()` option does this. For low probabilities of success and large n_i, the binomial distribution is well approximated by the Poisson distribution. We do not consider proportions further in this chapter.

13.2.2 Counts as aggregated event-history data

Counts can be thought of as aggregated versions or summaries of more detailed data on the occurrences of some kind of event. For instance, when considering the number of crimes, we usually aggregate over spatial regions and time intervals instead of retaining the original information on the locations and timings of the individual crimes. The size of spatial regions and time intervals determines the resolution at which we can investigate spatial and temporal variation. When counts are broken down by time intervals, the analysis can be referred to as survival analysis, a common model being the piecewise exponential model we will discuss in chapter 15.

Covariate information can be considered by aggregating within categories of categorical covariates, for example, producing separate counts of crimes for each type of victim classified by race and gender. If spatial and temporal variation are also of interest, we could obtain counts by region, time interval, race, and gender so that the observations are just cells of a contingency table. In this case, the observations for analysis are not units in the usual sense. As we will see in the next section, in Poisson regression it does not matter how aggregated the data are as long as we do not aggregate over covariate values. For a given set of covariate values, there can be several counts or one count equal to the sum of the counts. The parameter estimates will be the same in either case.

However, some of the variables defining the cells may be viewed as defining units or clusters that could be characterized by unobserved covariates and hence modeled by including random effects. In the crime example, regions or neighborhoods might be considered as such clusters. As we will see in section 13.10, it is possible to include random intercepts, say, for regions, even if the data have been aggregated to one count per region. Although such aggregated data provide no information on the dependence among counts within regions (because there is only one count per region), they do provide information on the random-intercept variance via the phenomenon known as overdispersion, to be discussed later.

13.3 Single-level Poisson models for counts

It is often assumed that events occur independently of each other and at a constant *incidence rate* λ (pronounced "lambda"), defined as the instantaneous probability of a new event per time interval. It follows that the number of events y occurring in a time interval of length t has a Poisson distribution

$$\Pr(y;\mu) \;=\; \frac{\exp(-\mu)\mu^y}{y!}$$

where μ is the expectation of y and is given by

$$\mu \;=\; \lambda t$$

The incidence rate λ is also often called the *intensity*, and the time interval t is sometimes referred to as the *exposure*.

If we observe two independent counts y_1 and y_2 during two successive time intervals of length t, and if the incidence rate λ is the same for both intervals, we can either add the counts together, thus obtaining an interval of length $2t$, or consider the counts separately. A convenient property of the Poisson distribution is that both approaches yield the same likelihood, up to a multiplicative constant.

$$\begin{aligned}
\Pr(y_1;\mu{=}\lambda t)\Pr(y_2;\mu{=}\lambda t) &= \frac{\exp(-\lambda t)(\lambda t)^{y_1}}{y_1!}\frac{\exp(-\lambda t)(\lambda t)^{y_2}}{y_2!} \\
&= \frac{\exp(-\lambda 2t)(\lambda t)^{y_1+y_2}}{y_1!\,y_2!} \\
&= \frac{\exp(-\lambda 2t)(\lambda 2t)^{y_1+y_2}}{(y_1+y_2)!} \times \frac{(y_1+y_2)!}{2^{y_1+y_2}y_1!\,y_2!} \\
&\propto \Pr(y_1+y_2;\mu{=}\lambda 2t) \qquad (13.1)
\end{aligned}$$

The multiplicative constant does not affect parameter estimation because it does not depend on the parameters. Therefore, no information regarding λ is lost by aggregating the data. We must, however, keep track of the exposure by using offsets, as discussed below.

When counts are observed for different units or subjects i characterized by covariates, the expectation μ_i is usually modeled using a log-linear model. For one covariate x_i, a multiplicative regression model for the expected counts is specified as

$$\mu_i \equiv E(y_i|x_i) \;=\; \exp(\beta_1+\beta_2 x_i) \;=\; \exp(\beta_1)\times\exp(\beta_2 x_i) \qquad (13.2)$$

where we note that the exponential function precludes negative expected counts. The model can alternatively be written as an additive log-linear model:

$$\ln(\mu_i) \;=\; \beta_1+\beta_2 x_i$$

If we think of this as a generalized linear model, the link function $g(\cdot)$ is just the natural logarithm, and the inverse link function $h(\cdot){\equiv}g^{-1}(\cdot)$ is the exponential.

A nice feature of the log link is that if the exposure time t is the same for all persons, then the exponentiated coefficient $\exp(\beta_2)$ can be interpreted as the *incidence-rate ratio* (IRR) for a unit increase in x_i. This can be seen by substituting $\mu_i = \lambda_i t$ in (13.2):

$$\lambda_i t \;=\; \exp(\beta_1 + \beta_2 x_i) \;=\; \exp(\beta_1)\exp(\beta_2 x_i)$$

Then the ratio for two persons i and i' with covariate values x_i and $x_{i'}$ becomes

$$\frac{\lambda_i}{\lambda_{i'}} \;=\; \frac{\lambda_i t}{\lambda_{i'} t} \;=\; \frac{\exp(\beta_1)\exp(\beta_2 x_i)}{\exp(\beta_1)\exp(\beta_2 x_{i'})} \;=\; \exp\{\beta_2(x_i - x_{i'})\} \;=\; \exp(\beta_2)^{(x_i - x_{i'})}$$

When the covariate increases by 1 unit, $x_i - x_{i'} = 1$, the ratio of the incidence rates, $\lambda_i/\lambda_{i'}$, or incidence-rate ratio is hence $\exp(\beta_2)$.

The log-linear model for the expectation is combined with the assumption that conditional on the covariate x_i, the count y_i has a Poisson distribution with mean μ_i:

$$\Pr(y_i|x_i) \;=\; \frac{\exp(-\mu_i)\mu_i^{y_i}}{y_i!}$$

If different persons have different exposures t_i, the natural logarithm of the exposure must be included as an *offset*, a covariate with regression coefficient set to 1:

$$\lambda_i t_i \;=\; \exp\{\beta_1 + \beta_2 x_i + \underbrace{\ln(t_i)}_{\text{offset}}\} \;=\; \exp(\beta_1)\exp(\beta_2 x_i) t_i$$

Then the incidence rate becomes

$$\lambda_i \;=\; \exp(\beta_1)\exp(\beta_2 x_i)$$

so $\exp(\beta_2)$ still represents the incidence-rate ratio, $\lambda_i/\lambda_{i'}$, when $x_i - x_{i'} = 1$.

Following the logic of (13.1), it is clear that we can sum the counts for all persons sharing the same covariate value and let i denote the corresponding group of persons. If we also sum the corresponding exposures, we obtain the same maximum likelihood estimates of the parameters β_1 and β_2 using the aggregated data as using the unit-level data.

For the Poisson distribution, the conditional variance of the counts, given the covariate, equals the conditional expectation

$$\mathrm{Var}(y_i|x_i) \;=\; \mu_i \tag{13.3}$$

As mentioned in section 10.2.1, such a relationship between the variance and the mean is called a variance function. In practice, the conditional sample variance is often larger or smaller than the mean; phenomena known as *overdispersion* or *underdispersion*, respectively. Overdispersion could be due to variability in the incidence rates λ_i that is not fully accounted for by the included covariates and is more common than underdispersion. Underdispersion could be due to a regularity in the events being counted, such as buses arriving in approximately 20-minute intervals. In this case, the number of buses counted in, say, 2-hour intervals would vary less than that expected for the Poisson distribution. We will return to overdispersion in section 13.9.

13.4 Did the German health-care reform reduce the number of doctor visits?

Government expenditures on health care surged in Germany in the 80s and 90s. To reduce the expenditure, a major health-care reform took place in 1997. The reform raised the copayments for prescription drugs by up to 200% and imposed upper limits on reimbursement of physicians by the state insurance. Given the large share of gross domestic product (GDP) spent on health, it is of interest to investigate whether the reform was a success in the sense that the number of doctor visits decreased after the reform.

To address this research question, Winkelmann (2004) analyzed data from the German Socio-Economic Panel (SOEP Group 2001) that can be downloaded from the *Journal of Applied Econometrics Data Archive*. We will consider a subset of his data, comprised of women working full time in the 1996 panel wave preceding the reform and the 1998 panel wave following the reform.

The dataset `drvisits.dta` has the following variables:

- `id`: person identifier (j)
- `numvisit`: self-reported number of visits to a doctor during the 3 months before the interview (y_{ij})
- `reform`: dummy variable for interview being during the year after the reform versus the year before the reform (x_{2i})
- `age`: age in years (x_{3ij})
- `educ`: education in years (x_{4ij})
- `married`: dummy variable for being married (x_{5ij})
- `badh`: dummy variable for self-reported current health being classified as "very poor" or "poor" (versus "very good", "good", or "fair") (x_{6ij})
- `loginc`: logarithm of household income (in 1995 German Marks, based on OECD weights for household members) (x_{7ij})

We read in the German health-care data by typing

```
. use http://www.stata-press.com/data/mlmus3/drvisits
```

13.5 Longitudinal data structure

As pointed out in *Introduction to models for longitudinal and panel data (part III)*, it is useful to describe longitudinal data before statistical modeling. We start by exploring the participation patterns for the two panel waves by using the `xtdescribe` command:

```
. quietly xtset id reform
. xtdescribe if numvisit<.
      id:  3, 4, ..., 9189                                 n =       1518
  reform:  0, 1, ..., 1                                    T =          2
           Delta(reform) = 1 unit
           Span(reform)  = 2 periods
           (id*reform uniquely identifies each observation)
Distribution of T_i:   min      5%     25%       50%       75%     95%     max
                         1       1       1         1         2       2       2
     Freq.  Percent    Cum. |  Pattern
-----------------------------+---------
       709    46.71   46.71 |  11
       418    27.54   74.24 |  .1
       391    25.76  100.00 |  1.
-----------------------------+---------
      1518   100.00          |  XX
```

Fewer than half the persons provide responses for both occasions (having the pattern "11"). Some of the missing data is due to attrition (dropout) and nonresponse, and some is due to younger people entering and older people leaving the sample because the sample is restricted to those aged between 20 and 60 years at any point in time (a *rotating panel*). We could also summarize the variables using `xtsum`.

13.6 Single-level Poisson regression

Before including random effects to model longitudinal dependence, we consider ordinary Poisson regression for the number of doctor visits.

13.6.1 Model specification

The expected number of visits μ_{ij} at occasion i for person j is specified as a log-linear model,

$$\ln(\mu_{ij}) \;=\; \nu_{ij} = \beta_1 + \beta_2 x_{2i} + \cdots + \beta_7 x_{7ij}$$

or equivalently as an exponential model for the expected number of visits:

$$\mu_{ij} \;=\; \exp(\nu_{ij})$$

The number of doctor visits y_{ij} is assumed to have a Poisson distribution with expectation μ_{ij}, given the covariates. We do not have to include an offset because doctor visits were counted for the same interval, namely, 3 months, for all persons at both occasions. The exponentiated regression coefficients can therefore be interpreted as rate ratios or as ratios of expected counts for any length of interval we like to think about.

13.6.2 Estimation using Stata

We first fit the Poisson regression model with the `poisson` command, using the `irr` option (for "incidence-rate ratio") to obtain exponentiated estimates. We specify the `vce(cluster id)` option to produce standard errors based on the sandwich estimator taking clustering into account, and we store the estimates for later use:

```
. poisson numvisit reform age educ married badh loginc summer, irr vce(cluster id)
Poisson regression                                Number of obs   =       2227
                                                  Wald chi2(7)    =     248.40
                                                  Prob > chi2     =     0.0000
Log pseudolikelihood = -5942.6924                 Pseudo R2       =     0.1073
                                  (Std. Err. adjusted for 1518 clusters in id)
------------------------------------------------------------------------------
             |               Robust
    numvisit |        IRR   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      reform |   .8689523    .048284    -2.53   0.011     .7792885    .9689328
         age |   1.004371   .0033158     1.32   0.186     .9978928     1.01089
        educ |   .9894036   .0115247    -0.91   0.360     .9670715    1.012251
     married |   1.042542   .0722475     0.60   0.548     .9101354    1.194212
        badh |   3.105111   .2642862    13.31   0.000     2.628019    3.668814
      loginc |   1.160559    .091528     1.89   0.059     .9943449    1.354558
      summer |   1.010269   .0939635     0.11   0.913     .8419145    1.212288
       _cons |   .6617582   .3796245    -0.72   0.472     .2149803    2.037042
------------------------------------------------------------------------------
. estimates store ordinary
```

We can alternatively view the Poisson regression model as a generalized linear model and use the `glm` command with the `family(poisson)`, `link(log)`, and `vce(cluster id)` options. (The log link is the default link for the Poisson distribution, so the `link()` option could be omitted.) To facilitate interpretation, we use the `eform` option to get exponentiated regression coefficients that represent incidence-rate ratios:

```
. glm numvisit reform age educ married badh loginc summer,
> family(poisson) link(log) vce(cluster id) eform
Generalized linear models                         No. of obs      =      2227
Optimization     : ML                             Residual df     =      2219
                                                  Scale parameter =         1
Deviance         =  7419.853221                   (1/df) Deviance =  3.343782
Pearson          =  9688.740471                   (1/df) Pearson  =  4.366264
Variance function: V(u) = u                       [Poisson]
Link function    : g(u) = ln(u)                   [Log]
                                                  AIC             =  5.344133
Log pseudolikelihood =  -5942.69244               BIC             =  -9685.11
                                (Std. Err. adjusted for 1518 clusters in id)
```

numvisit	IRR	Robust Std. Err.	z	P>|z|	[95% Conf.	Interval]
reform	.8689523	.048284	-2.53	0.011	.7792885	.9689328
age	1.004371	.0033158	1.32	0.186	.9978928	1.01089
educ	.9894036	.0115247	-0.91	0.360	.9670715	1.012251
married	1.042542	.0722475	0.60	0.548	.9101354	1.194212
badh	3.105111	.2642862	13.31	0.000	2.628019	3.668814
loginc	1.160559	.091528	1.89	0.059	.9943449	1.354558
summer	1.010269	.0939635	0.11	0.913	.8419145	1.212288
_cons	.6617582	.3796245	-0.72	0.472	.2149803	2.037042

The estimates from `poisson` and `glm` are identical, as would be expected, and are displayed under the heading "Poisson" in table 13.1. The confidence intervals are based on the sandwich estimator taking the dependence of the repeated counts (given the covariates) into account. The estimated incidence-rate ratio for `reform` is 0.87, implying a 13% reduction in the number of doctor visits per time unit (such as month or year) between 1996 and 1998 for given covariate values.

The variable `reform` changes from 0 in 1996 to 1 in 1998 for everyone, so it is completely confounded with any other changes that may have occurred in Germany in that time period (secular trends). A superior design for causal inference would be to have a control group that does not experience the treatment at the second occasion, in which case a difference-in-difference approach such as that described in exercise 5.3 could be used (including treatment group, time, and time $\times$ treatment group in the model, where treatment group is a time-constant covariate for ever receiving the treatment). It should therefore be kept in mind that when we talk about the effect of reform, we mean this casually and not necessarily causally.

Table 13.1: Estimates for different kinds of Poisson regression: Ordinary, GEE, random-intercept (RI), and fixed-intercept (FI)

	Marginal effects				Conditional effects			
	Poisson		GEE* Poisson		RI Poisson		FI§ Poisson	
	Est	(95% CI)†	Est	(95% CI)†	Est	(95% CI)	Est	(95% CI)
Fixed part								
Incidence-rate ratios								
$\exp(\beta_2)$ [`reform`]	0.87	(0.78, 0.97)	0.88	(0.80, 0.98)	0.95	(0.90, 1.02)	1.02	(0.95, 1.09)
$\exp(\beta_3)$ [`age`]	1.00	(1.00, 1.01)	1.01	(1.00, 1.01)	1.01	(1.00, 1.01)		
$\exp(\beta_4)$ [`educ`]	0.99	(0.97, 1.01)	0.99	(0.97, 1.01)	1.01	(0.98, 1.03)	0.98	(0.71, 1.36)
$\exp(\beta_5)$ [`married`]	1.04	(0.91, 1.19)	1.04	(0.90, 1.19)	1.08	(0.97, 1.20)	1.05	(0.84, 1.30)
$\exp(\beta_6)$ [`badh`]	3.11	(2.63, 3.67)	3.02	(2.54, 3.58)	2.47	(2.19, 2.78)	1.77	(1.51, 2.08)
$\exp(\beta_7)$ [`loginc`]	1.16	(0.99, 1.35)	1.15	(0.98, 1.34)	1.10	(0.96, 1.25)	0.97	(0.77, 1.21)
$\exp(\beta_8)$ [`summer`]	1.01	(0.84, 1.21)	0.97	(0.82, 1.16)	0.87	(0.76, 0.98)	0.81	(0.69, 0.95)
Random part								
$\sqrt{\psi_{11}}$					0.90			
Log likelihood	−5,942.69				−4,643.36		−2,903.51•	

*Using exchangeable working correlation
†Based on the sandwich estimator
§`age` omitted from model because within-effects of `reform` and `age` are perfectly confounded
•Log conditional likelihood

13.7 Random-intercept Poisson regression

We now explicitly model the dependence between the number of doctor visits before the reform y_{1j} and the number of visits after the reform y_{2j} for a person j, given included covariates.

13.7.1 Model specification

One way to model the dependence within persons is to include a person-specific random intercept ζ_{1j} in the Poisson regression model:

$$\begin{aligned}\mu_{ij} \equiv E(y_{ij}|\mathbf{x}_{ij},\zeta_{1j}) &= \exp(\beta_1+\beta_2 x_{2i}+\cdots+\beta_7 x_{7ij}+\zeta_{1j}) \\ &= \exp\{(\beta_1+\zeta_{1j})+\beta_2 x_{2i}+\cdots+\beta_7 x_{7ij}\} \\ &= \exp(\zeta_{1j})\exp(\beta_1+\beta_2 x_{2i}+\cdots+\beta_7 x_{7ij})\end{aligned}$$

It is assumed that $\zeta_{1j}|\mathbf{x}_{ij} \sim N(0,\psi_{11})$, which implies that ζ_{1j} and $\mathbf{x}_{ij}$ are independent, and it is assumed that ζ_{1j} are independent across persons j. The exponential of the random intercept, $\exp(\zeta_{1j})$, is sometimes called a *frailty*. The number of visits y_{1j} and y_{2j} for a person j at the two occasions are specified as conditionally independent given the random intercept ζ_{1j} (and the covariates $\mathbf{x}_{1j}$ and $\mathbf{x}_{2j}$).

As always in random-effects models, the regression coefficients have conditional or cluster-specific interpretations. In the present application, the clusters are persons, so the coefficients represent person-specific effects. Interestingly, we can also interpret the coefficients as marginal or population-averaged effects because the relationship between the marginal expectation of the count (given $\mathbf{x}_{ij}$ but averaged over ζ_{1j}) and the covariates is

$$\mu_{ij}^M = \exp\{(\beta_1+\psi_{11}/2)+\beta_2 x_{2i}+\cdots+\beta_7 x_{7ij}\}$$

The intercept is the only parameter that is not the same in the marginal and conditional models [in general the marginal intercept is $E\{\exp(\beta_1+\zeta_{1j})\}$, which becomes $\exp(\beta_1+\psi_{11}/2)$ for a normally distributed random intercept]. For random-coefficient models, the fixed coefficients of the covariates that have random coefficients are also not the same in conditional and marginal models (see section 13.8).

Because marginal and conditional effects coincide for random-intercept Poisson regression models, in contrast to random-intercept logistic regression, consistent estimation of regression parameters (apart from the intercept) does not hinge on the correct choice of random-intercept distribution. What is required is correct specification of the mean structure and lack of correlation between the random intercept and the covariates.

The marginal or population-averaged variance (given $\mathbf{x}_{ij}$ but averaged over ζ_{1j}) is

$$\mathrm{Var}(y_{ij}|\mathbf{x}_{ij}) = \mu_{ij}^M + (\mu_{ij}^M)^2\{\exp(\psi_{11})-1\} \tag{13.4}$$

If $\psi_{11} > 0$, this variance is greater than the marginal mean. Therefore, the variance–mean relationship for Poisson models in (13.3) is relaxed, and the variance is greater than that implied by a Poisson model, producing overdispersion.

13.7.2 Measures of dependence and heterogeneity

The intraclass correlation between the counts y_{1j} and y_{2j} at the two occasions depends on the values of the observed covariates (and the exposure if this is included as an offset in the linear predictor) and therefore cannot be used as a simple measure of dependence. In contrast to logit, probit, or complementary log-log models for dichotomous and ordinal responses, Poisson models cannot be formulated in terms of latent responses underlying the observed responses. Thus we cannot define an intraclass correlation in terms of latent responses as shown in section 10.9.1 for dichotomous responses.

Stryhn et al. (2006) show that the conditional (given the covariates) intraclass correlation of the counts y_{ij} and $y_{i'j}$ for two units within the same cluster that have a common fixed part of the linear predictor $\mathbf{x}'\boldsymbol{\beta} \equiv \beta_1 + \beta_2 x_2 + \cdots + \beta_7 x_7$, is given by

$$\rho = \frac{\exp(2\mathbf{x}'\boldsymbol{\beta} + 2\psi) - \exp(2\mathbf{x}'\boldsymbol{\beta} + \psi)}{\exp(2\mathbf{x}'\boldsymbol{\beta} + 2\psi) - \exp(2\mathbf{x}'\boldsymbol{\beta} + \psi) + \exp(\mathbf{x}'\boldsymbol{\beta} + \psi/2)}$$

and hence depends on the covariates in a quite complex manner.

As a measure of heterogeneity, we can consider randomly drawing pairs of persons j and j' with the same covariate values and forming the incidence-rate ratio, or ratio of expected counts for the same exposure, comparing the person who has the larger random intercept with the person who has the smaller random intercept, given by $\exp(|\zeta_j - \zeta_{j'}|)$. Following the derivation in section 10.9.2, the median incidence-rate ratio is given by

$$\text{IRR}_{\text{median}} = \exp\left\{\sqrt{2\psi_{11}}\Phi^{-1}(3/4)\right\}$$

13.7.3 Estimation using Stata

Random-intercept Poisson models can be fit using `xtpoisson`, `xtmepoisson`, and `gllamm`. All three programs use numerical integration, as discussed in section 10.11.1. The details of implementation and speed considerations (see section 10.11.2) are the same as those for logistic models, with `xtpoisson` corresponding to `xtlogit` and `xtmepoisson` to `xtmelogit`. The predictions available for each of the commands also correspond to their logistic counterparts described in section 10.12.

Using xtpoisson

The syntax for `xtpoisson` is similar to that for `xtlogit`, but we must specify the `normal` option because `xtpoisson` otherwise assumes a gamma distribution for the frailty $\exp(\zeta_{1j})$, as briefly described in section 13.9.2. The command for fitting the random-intercept model therefore is

```
. quietly xtset id
. xtpoisson numvisit reform age educ married badh loginc summer, normal irr
Random-effects Poisson regression               Number of obs      =      2227
Group variable: id                              Number of groups   =      1518
Random effects u_i ~ Gaussian                   Obs per group: min =         1
                                                               avg =       1.5
                                                               max =         2
                                                Wald chi2(7)       =    253.16
Log likelihood  = -4643.3608                    Prob > chi2        =    0.0000
```

numvisit	IRR	Std. Err.	z	P>|z|	[95% Conf.	Interval]
reform	.9547597	.0310874	-1.42	0.155	.895733	1.017676
age	1.006003	.0028278	2.13	0.033	1.000475	1.01156
educ	1.008656	.0127767	0.68	0.496	.9839221	1.034011
married	1.077904	.0595749	1.36	0.175	.9672414	1.201228
badh	2.466573	.1519255	14.66	0.000	2.186076	2.783061
loginc	1.097455	.0747067	1.37	0.172	.9603805	1.254095
summer	.8672783	.0562749	-2.19	0.028	.763707	.9848956
_cons	.5159176	.2645129	-1.29	0.197	.1888714	1.409271
/lnsig2u	-.2016963	.0611823	-3.30	0.001	-.3216115	-.0817812
sigma_u	.9040703	.0276566			.8514575	.9599341

```
Likelihood-ratio test of sigma_u=0: chibar2(01) =  2598.66 Pr>=chibar2 = 0.000
```

According to this model, the estimated effect of `reform` is to reduce the incidence rate, and therefore the expected number of visits in a given period, by about 5% (controlling for the other variables), but this is not significant at the 5% level. Each extra year of age is associated with an estimated 0.6% increase in the incidence rate; the incidence-rate ratio for a 10-year increase in age is estimated as $1.006^{10} = 1.06$, corresponding to a 6% increase, for given values of the other covariates. The estimates also suggest that being in bad health more than doubles the incidence rate and that the incidence rate decreases by 13% in the summer, controlling for the other variables. The other coefficients are not significant at the 5% level. The estimates were also reported under the heading "RI Poisson" in table 13.1.

From the last line of output, we see that we can reject the null hypothesis that the random-intercept variance is zero, $\psi_{11} = 0$, with a likelihood-ratio statistic of 2,598.66 and $p < 0.001$. (As discussed in section 2.6.2, the `chibar2(01)` notation indicates that the p-value reported in the output takes into account that the null hypothesis is on the border of parameter space.)

The median incidence-rate ratio is estimated as

```
. display exp(sqrt(2)*.90407*invnormal(3/4))
2.3687622
```

Half the time, the ratio of the expected number of visits (in a given period) for two randomly chosen persons with the same covariate values, comparing the one who has the larger expected value with the other one, will exceed 2.37. We could avoid having

to say "comparing the one who has the larger expected value with the other one" by saying the following: Half the time, the ratio of the expected number of visits will lie in the range from 0.42 (= 1/2.37) to 2.37, and the other half the time, the ratio will lie outside that range.

Using xtmepoisson

The syntax for `xtmepoisson` is exactly as that for `xtmelogit` except that we use the `irr` option to get exponentiated regression coefficients instead of the `or` option. We fit the model and store the estimates using the following commands:

```
. xtmepoisson numvisit reform age educ married badh loginc summer || id:, irr
Mixed-effects Poisson regression                Number of obs      =      2227
Group variable: id                              Number of groups   =      1518
                                                Obs per group: min =         1
                                                               avg =       1.5
                                                               max =         2
Integration points =   7                        Wald chi2(7)       =    253.06
Log likelihood = -4643.2823                     Prob > chi2        =    0.0000
```

numvisit	IRR	Std. Err.	z	P>|z|	[95% Conf.	Interval]
reform	.9547758	.0310889	-1.42	0.155	.8957463	1.017695
age	1.006003	.0028283	2.13	0.033	1.000475	1.011562
educ	1.008659	.0127792	0.68	0.496	.9839206	1.034019
married	1.077902	.059584	1.36	0.175	.9672229	1.201245
badh	2.466399	.1519349	14.65	0.000	2.185887	2.782909
loginc	1.09743	.0747155	1.37	0.172	.96034	1.254089
summer	.8672584	.0562778	-2.19	0.028	.7636823	.9848822
_cons	.5159046	.264545	-1.29	0.197	.1888388	1.409443

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
id: Identity				
sd(_cons)	.9043832	.0276826	.8517217	.9603006

```
LR test vs. Poisson regression:  chibar2(01) =  2598.82 Prob>=chibar2 = 0.0000
. estimates store xtri
```

The estimates are nearly identical to those produced by `xtpoisson`.

We could also fit the model more quickly by using one quadrature point, giving the Laplace method. This method works well in this example, but as discussed in section 10.11.2 we do not recommend it in general because the estimates can be poor.

Using gllamm

The random-intercept Poisson model can be fit as follows using `gllamm`:

```
. generate cons = 1
. eq ri: cons
. gllamm numvisit reform age educ married badh loginc summer,
> family(poisson) link(log) i(id) eqs(ri) eform adapt
number of level 1 units = 2227
number of level 2 units = 1518

Condition Number = 723.77605

gllamm model

log likelihood = -4643.3427
```

numvisit	exp(b)	Std. Err.	z	P>|z|	[95% Conf.	Interval]
reform	.9547481	.0310831	-1.42	0.155	.8957293	1.017656
age	1.006002	.0028266	2.13	0.033	1.000477	1.011557
educ	1.008646	.0127702	0.68	0.497	.9839247	1.033988
married	1.077896	.059554	1.36	0.175	.9672696	1.201174
badh	2.466857	.15192	14.66	0.000	2.186367	2.78333
loginc	1.097486	.0746823	1.37	0.172	.9604527	1.25407
summer	.8673159	.0562616	-2.19	0.028	.7637672	.9849033
_cons	.5157228	.2643128	-1.29	0.196	.188872	1.408203

```
Variances and covariances of random effects
------------------------------------------------------------------------------

***level 2 (id)

    var(1): .81691979 (.04972777)
------------------------------------------------------------------------------
. estimates store glri
```

Here we specified an equation, `ri`, for the random intercept by using the `eqs()` option. This is not necessary because `gllamm` would include a random intercept by default. However, defining the intercept explicitly from the start makes it easier to use estimates from this model as starting values for random-coefficient models because the parameter matrix will have the correct column labels.

The estimates are close to those by using `xtlogit` and `xtmepoisson`, including the random-intercept standard deviation, estimated by `gllamm` as

```
. display sqrt(.81691979)
.90383615
```

We could also obtain robust standard errors using the command

```
gllamm, robust eform
```

There is no likelihood-ratio test for the random-intercept variance in the `gllamm` output, but we can perform this test ourselves by comparing the random-intercept model (with estimates stored under `glri`) with the ordinary Poisson model (with estimates stored under `ordinary`):

```
. lrtest ordinary glri, force
Likelihood-ratio test                                 LR chi2(1)  =   2598.70
(Assumption: ordinary nested in glri)                 Prob > chi2 =    0.0000
```

We used the `force` option to force Stata to perform the test, which is necessary because the two models being compared were fit using different commands. We must divide the p-value by 2, as discussed in section 2.6.2, which makes no difference to the conclusion here that the random-intercept variance is highly significant.

13.8 Random-coefficient Poisson regression

13.8.1 Model specification

The random-intercept Poisson regression model accommodates dependence among the repeated counts. However, it assumes that the effect of the health-care reform is the same for all persons. In this section, we relax this assumption by introducing an additional person-level random coefficient ζ_{2j} for `reform` (x_{2i}):

$$\begin{aligned}\ln(\mu_{ij}) &= \beta_1 + \beta_2 x_{2i} + \cdots + \beta_7 x_{7ij} + \zeta_{1j} + \zeta_{2j} x_{2ij} \\ &= (\beta_1 + \zeta_{1j}) + (\beta_2 + \zeta_{2j}) x_{2i} + \cdots + \beta_7 x_{7ij}\end{aligned}$$

The above specification allows the effect of the health-care reform $\beta_2 + \zeta_{2j}$ to vary over persons j. We assume that, given the covariates $\mathbf{x}_{ij}$, the random intercept and random coefficient have a bivariate normal distribution with zero means and covariance matrix

$$\mathbf{\Psi} = \begin{bmatrix} \psi_{11} & \psi_{12} \\ \psi_{21} & \psi_{22} \end{bmatrix}, \qquad \psi_{21} = \psi_{12}$$

The correlation between the random intercept and random coefficient becomes

$$\rho_{21} = \frac{\psi_{21}}{\sqrt{\psi_{11}\psi_{22}}}$$

It follows from the normality assumption for the random effects, given the covariates, and the homoskedasticity assumptions above, that the random effects are independent of the covariates.

The marginal expected count is given by

$$\begin{aligned}E(y_{ij}|\mathbf{x}_{ij}) &= \exp\{\beta_1 + \beta_2 x_{2i} + \cdots + \beta_7 x_{7ij} + (\psi_{11} + 2\psi_{21} x_{2i} + \psi_{22} x_{2i}^2)/2\} \\ &= \exp\{\beta_1 + \psi_{11}/2 + \beta_2 x_{2i} + \psi_{21} x_{2i} + (\psi_{22}/2) x_{2i}^2 + \cdots + \beta_7 x_{7ij}\} \\ &= \exp\{\beta_1 + \psi_{11}/2 + (\beta_2 + \psi_{21} + \psi_{22}/2) x_{2i} + \cdots + \beta_7 x_{7ij}\}\end{aligned}$$

where the last equality holds only if x_{2i} is a dummy variable, because $x_{2i} = x_{2i}^2$ in this case.

Hence, the multiplicative effect of the reform on the *marginal* expected count now no longer equals $\exp(\beta_2)$ as in the random-intercept model but $\exp(\beta_2 + \psi_{21} + \psi_{22}/2)$. In general, the marginal expected count is given by the exponential of the sum of the linear predictor and half the variance of the random part of the model. Unfortunately, this variance is usually not a linear function of the variable x_{2ij} having a random coefficient (except when x_{2i} is a dummy variable), so the variable no longer has a simple multiplicative effect on the marginal expectation.

13.8.2 Estimation using Stata

Using xtmepoisson

`xtpoisson` cannot be used for random-coefficient models. The syntax for random-coefficient models in `xtmepoisson` is the same as that for `xtmixed` or `xtmelogit`, apart from the `irr` option that is used to obtain exponentiated regression coefficients:

```
. xtmepoisson numvisit reform age educ married badh loginc summer ||
> id: reform, covariance(unstructured) irr
Mixed-effects Poisson regression               Number of obs      =      2227
Group variable: id                             Number of groups   =      1518
                                               Obs per group: min =         1
                                                              avg =       1.5
                                                              max =         2
Integration points =   7                       Wald chi2(7)       =    241.11
Log likelihood = -4513.7299                    Prob > chi2        =    0.0000
```

numvisit	IRR	Std. Err.	z	P>|z|	[95% Conf.	Interval]
reform	.9022792	.0483866	-1.92	0.055	.812257	1.002278
age	1.003456	.0028317	1.22	0.222	.997921	1.009021
educ	1.008894	.0128121	0.70	0.486	.9840931	1.034321
married	1.086874	.064118	1.41	0.158	.9681982	1.220097
badh	3.028323	.2322948	14.44	0.000	2.605606	3.519619
loginc	1.135636	.0866487	1.67	0.096	.9778964	1.31882
summer	.9140246	.0741941	-1.11	0.268	.7795846	1.071649
_cons	.4060731	.2305667	-1.59	0.112	.1334429	1.2357

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
id: Unstructured				
sd(reform)	.9303105	.0561786	.8264687	1.047199
sd(_cons)	.9541108	.0357016	.8866412	1.026714
corr(reform,_cons)	-.4908242	.0506047	-.583535	-.3854839

```
LR test vs. Poisson regression:      chi2(3) =  2857.93   Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference.
```

We store the estimates,

```
. estimates store xtrc
```

for use in the likelihood-ratio test below.

The random-intercept Poisson regression model is nested in the random-coefficient model (with $\psi_{22}=\psi_{21}=0$). We can therefore perform a likelihood-ratio test using

```
. lrtest xtri xtrc
Likelihood-ratio test                                 LR chi2(2)  =    259.10
(Assumption: xtri nested in xtrc)                     Prob > chi2 =    0.0000
Note: The reported degrees of freedom assumes the null hypothesis is not on the
      boundary of the parameter space.  If this is not true, then the reported
      test is conservative.
```

As discussed in section 4.6, the asymptotic null distribution for this test is $1/2\chi^2_1+1/2\chi^2_2$, and we conclude that the random-intercept Poisson model is rejected in favor of the random-coefficient Poisson model.

Maximum likelihood estimates for the random-coefficient Poisson model are reported under "RC Poisson" in table 13.2, where we for comparison also report estimates for the random-intercept Poisson model.

Table 13.2: Estimates for different kinds of random-effects Poisson regression: random-intercept (RI) and random-coefficient (RC) models

	RI Poisson		RC Poisson	
	Est	(95% CI)	Est	(95% CI)
Fixed part				
Incidence-rate ratios				
$\exp(\beta_2)$ [reform]	0.95	(0.90, 1.02)	0.90	(0.81, 1.00)
$\exp(\beta_3)$ [age]	1.01	(1.00, 1.01)	1.00	(1.00, 1.01)
$\exp(\beta_4)$ [educ]	1.01	(0.98, 1.03)	1.01	(0.98, 1.03)
$\exp(\beta_5)$ [married]	1.08	(0.97, 1.20)	1.09	(0.97, 1.22)
$\exp(\beta_6)$ [badh]	2.47	(2.19, 2.78)	3.03	(2.61, 3.52)
$\exp(\beta_7)$ [loginc]	1.10	(0.96, 1.25)	1.14	(0.98, 1.32)
$\exp(\beta_8)$ [summer]	0.87	(0.76, 0.98)	0.91	(0.78, 1.07)
Random part				
$\sqrt{\psi_{11}}$	0.90		0.95	
$\sqrt{\psi_{22}}$			0.93	
$\rho_{21}=\psi_{21}/(\sqrt{\psi_{11}}\sqrt{\psi_{22}})$			−0.49	
Log likelihood	−4,643.36		−4,513.73	

Using gllamm

We now fit the random-coefficient Poisson regression model in `gllamm`, using the estimates from the random-intercept model (stored under `glri`) as starting values:

```
. estimates restore glri
. matrix a = e(b)
. eq rc: reform
. gllamm numvisit reform age educ married badh loginc summer,
> family(poisson) link(log) i(id) nrf(2) eqs(ri rc) from(a) eform adapt
number of level 1 units = 2227
number of level 2 units = 1518

Condition Number = 812.85865

gllamm model

log likelihood = -4513.8005
```

numvisit	exp(b)	Std. Err.	z	P>|z|	[95% Conf.	Interval]
reform	.9023139	.048376	-1.92	0.055	.8123103	1.00229
age	1.003457	.0028304	1.22	0.221	.9979246	1.00902
educ	1.008889	.0128058	0.70	0.486	.9841002	1.034303
married	1.086858	.0640872	1.41	0.158	.9682361	1.220013
badh	3.02813	.2322062	14.45	0.000	2.605564	3.519226
loginc	1.13564	.0866072	1.67	0.095	.9779701	1.318731
summer	.9140484	.0741615	-1.11	0.268	.7796627	1.071597
_cons	.406047	.2304432	-1.59	0.112	.1335043	1.234973

```
Variances and covariances of random effects
------------------------------------------------------------------------------

***level 2 (id)

    var(1): .90914636 (.06767417)
    cov(2,1): -.43462184 (.07121035) cor(2,1): -.49034787

    var(2): .8641332 (.10415944)
------------------------------------------------------------------------------
```

We store the estimates for later use:

```
. estimates store glrc
```

It was not necessary to add two new elements to the matrix of starting values for the two new parameters being estimated (as we did in section 11.7.2). This is because the column labels of the matrix `a` let `gllamm` know which parameters are supplied, and `gllamm` sets the starting values of the other parameters to zero. By specifying the same equation `ri` for the random intercept in both models, we ensure that `gllamm` recognizes the previous estimate of the (square root of the) random-intercept variance as the starting value for that parameter in the random-coefficient model.

Robust standard errors and confidence intervals can be obtained using

```
gllamm, robust eform
```

13.8.3 Interpretation of estimates

The estimated incidence-rate ratios have changed somewhat compared with the random-intercept Poisson model. Note in particular that the estimated incidence-rate ratio for `reform` now implies a 10% reduction in the expected number of visits per year *for a given person* and is nearly significant at the 5% level.

Instead of thinking of this model as a random-coefficient model, we could view it as a model with a random intercept ζ_{1j} for 1996 and a random intercept $\zeta_{1j}+\zeta_{2j}$ for 1998, because x_{2i} is 0 in 1996 and 1 in 1998. In 1996, the random-intercept variance is

$$\mathrm{Var}(\zeta_{1j}|\mathbf{x}_{1j}) \;=\; \psi_{11}$$

which is estimated as 0.91. In 1998, the variance is

$$\mathrm{Var}(\zeta_{1j}+\zeta_{2j}|\mathbf{x}_{2j}) \;=\; \psi_{11}+\psi_{22}+2\psi_{21}$$

and is estimated as 0.90. The covariance between the intercepts is

$$\mathrm{Cov}(\zeta_{1j},\zeta_{1j}+\zeta_{2j}|\mathbf{x}_{1j},\mathbf{x}_{2j}) \;=\; \psi_{11}+\psi_{21}$$

which is estimated as 0.48.

In contrast, the conventional random-intercept model (13.4) with the same random intercept ζ_{1j} in 1996 and 1998 had a single parameter ψ_{11} representing both the random-intercept variance at the two occasions as well as the covariance across time. Assuming that this parameter "tries" to produce variances and covariance close to the estimated values using the more flexible model, it is not surprising that the estimate $\widehat{\psi}_{11}=0.82$ is between 0.91 and 0.48.

The reason we can identify the three parameters of the random part is that the variance parameters for 1996 and 1998 determine the relationship between marginal mean and marginal variance (given the covariates) at these two time points, as shown in (13.4), and the covariance parameter affects the correlation between the counts. In the random-intercept model, all three properties were determined by one parameter, whereas the random-coefficient model uses separate parameters for overdispersion at the two time points and for dependence across time.

As discussed in section 4.10, an analogous *linear* random-coefficient model with only two time points is not identified because it includes a fourth parameter, the level-1 variance θ, in the random part. The analogous random-coefficient logistic or probit model for dichotomous responses is also not identified because random intercepts have no effect on the marginal variance–mean relationship in these models (see section 10.8).

13.9 Overdispersion in single-level models

We now temporarily return to single-level models to discuss models for overdispersion in the absence of clustering. Subsequently, we allow for overdispersion at level 1 in two-level models in section 13.10.

The assumption of the Poisson model that the variance of the count is equal to the expectation (given the covariates) is often violated. The most common violation is overdispersion or extra-Poisson variability, meaning that the variance is larger than the expectation. Overdispersion could be due to unobserved covariates that vary between the units of observation. For this to be meaningful, the "cases" or records of data must correspond to units, such as persons, occasions, houses, or schools, that could potentially be characterized by omitted covariates. If the data have been aggregated over units or disaggregated within units, the methods described here are not appropriate.

In this section, we consider methods for dealing with overdispersion in single-level models as a preparation for the next section, where we discuss overdispersion in two-level models. We therefore ignore clustering for simplicity, but note that this is inappropriate for the health-care reform data. We will use model-based standard errors so that the impact of modeling overdispersion on standard errors can be seen, but these standard errors are not correct because clustering is ignored.

13.9.1 Normally distributed random intercept

As discussed in section 13.7.1, random intercepts induce overdispersion. Even when we do not have clustered data, random intercepts can therefore be included to model overdispersion. The model and its implied marginal mean and variance are exactly as those for two-level models except that the random intercept varies between the level-1 units and hence does not produce any dependence among groups of observations.

The model can be written as

$$\ln(\mu_{ij}) \;=\; \beta_1 + \beta_2 x_{2i} + \cdots + \beta_7 x_{7ij} + \zeta_{ij}^{(1)} \tag{13.5}$$

where $\zeta_{ij}^{(1)}|\mathbf{x}_{ij} \sim N(0, \psi^{(1)})$ and we have included a (1) superscript to denote that the random intercept varies at level 1 (and not at level 2 or higher as elsewhere in this book).

The marginal expectation becomes

$$\mu_{ij}^M \equiv E(y_{ij}|\mathbf{x}_{ij}) \;=\; \exp(\underbrace{\beta_1 + \psi^{(1)}/2}_{\beta_1^M} + \beta_2 x_{2i} + \cdots + \beta_7 x_{7ij}) \tag{13.6}$$

and the marginal variance is

$$\mathrm{Var}(y_{ij}|\mathbf{x}_{ij}) \;=\; \mu_{ij}^M + (\mu_{ij}^M)^2\{\exp(\psi^{(1)}) - 1\} \tag{13.7}$$

which is larger than the marginal expectation μ_{ij}^M if $\psi^{(1)} > 0$.

To fit the model with a normally distributed random intercept at level 1, we first generate an identifier, `obs`, for the level-1 observations,

```
. generate obs = _n
```

and then specify `obs` as the "clustering" variable in the `xtpoisson` command:

```
. quietly xtset obs
. xtpoisson numvisit reform age educ married badh loginc summer, normal irr
Random-effects Poisson regression               Number of obs      =      2227
Group variable: obs                             Number of groups   =      2227
Random effects u_i ~ Gaussian                   Obs per group: min =         1
                                                               avg =       1.0
                                                               max =         1
                                                Wald chi2(7)       =    272.60
Log likelihood  = -4546.8881                    Prob > chi2        =    0.0000
```

numvisit	IRR	Std. Err.	z	P>|z|	[95% Conf.	Interval]
reform	.881623	.0466248	-2.38	0.017	.7948166	.97791
age	1.002419	.0026053	0.93	0.353	.9973256	1.007538
educ	1.005101	.0117969	0.43	0.665	.9822433	1.02849
married	1.084023	.0602281	1.45	0.146	.9721784	1.208735
badh	3.203538	.2429967	15.35	0.000	2.760985	3.717027
loginc	1.151836	.0840599	1.94	0.053	.9983224	1.328956
summer	.9576537	.0786351	-0.53	0.598	.8152943	1.124871
_cons	.3949809	.2143587	-1.71	0.087	.13634	1.144271
/lnsig2u	-.1143904	.0548408	-2.09	0.037	-.2218765	-.0069043
sigma_u	.9444097	.0258961			.894994	.9965538

```
Likelihood-ratio test of sigma_u=0: chibar2(01) =  2791.61 Pr>=chibar2 = 0.000
```

We see from the estimated standard deviation of the level-1 random intercept of 0.94 and the highly significant likelihood-ratio test that there is evidence for overdispersion. The factor $\exp(\psi^{(1)})-1$, that multiplies the squared marginal expectation to obtain the additive overdispersion component [see expression (13.7)], is estimated as about 1.44.

Another consequence of including a random intercept, in addition to overdispersion, is that it produces a larger marginal probability of zeros than the ordinary Poisson model. Thus the problem of excess zeros often observed in count data is addressed to some extent. So-called zero-inflated Poisson (ZIP) models are tailor-made to address this problem, but these models will not be discussed here.

13.9.2 Negative binomial models

As previously mentioned, the random-intercept model with a normally distributed random intercept does not have a closed-form likelihood and is hence fit using numerical integration. An appealing and computationally more efficient approach is to alter the model specification so that a closed-form likelihood is achieved. This can be accom-

plished by specifying a gamma distribution either for the exponentiated random intercept $\exp(\zeta_j)$ (NB2) or for the cluster-specific mean μ_{ij} (NB1), yielding two different kinds of negative binomial models.

Mean dispersion or NB2

The *mean dispersion* or NB2 version of the negative binomial model can be written as a random-intercept model as in (13.5), but instead of assuming a normal distribution for the level-1 random intercept $\zeta_{ij}^{(1)}$, we assume a gamma distribution for the frailty $\exp(\zeta_{ij}^{(1)})$ with mean 1 and variance α (pronounced "alpha"). The gamma distribution is then said to have scale parameter α and shape parameter $1/\alpha$.

It follows from this specification that the marginal mean is

$$\mu_{ij}^M \equiv E(y_{ij}|\mathbf{x}_{ij}) \;=\; \exp(\beta_1 + \beta_2 x_{2i} + \cdots + \beta_7 x_{7ij}) \tag{13.8}$$

and that the marginal variance has the same quadratic form as (13.7), with

$$\mathrm{Var}(y_{ij}|\mathbf{x}_{ij}) \;=\; \mu_{ij}^M + (\mu_{ij}^M)^2\alpha$$

so that α corresponds to $\exp(\psi^{(1)})-1$ in (13.7).

This model can be fit using the `nbreg` command with the `dispersion(mean)` option:

```
. nbreg numvisit reform age educ married badh loginc summer,
> irr dispersion(mean)
Negative binomial regression                    Number of obs   =       2227
                                                LR chi2(7)      =     303.15
Dispersion     = mean                           Prob > chi2     =     0.0000
Log likelihood = -4562.0459                     Pseudo R2       =     0.0322

------------------------------------------------------------------------------
    numvisit |        IRR   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      reform |   .8734045   .0447241    -2.64   0.008     .7900022    .9656119
         age |   1.004806   .0024754     1.95   0.052     .9999656    1.009669
        educ |   .9971352   .0115579    -0.25   0.805     .9747375    1.020047
     married |   1.081049    .057606     1.46   0.144     .9738393    1.200062
        badh |   3.118932   .2335543    15.19   0.000     2.693181    3.611987
      loginc |   1.142179    .081637     1.86   0.063     .9928749    1.313934
      summer |   .9424437    .074725    -0.75   0.455     .8067981    1.100895
       _cons |   .6648993   .3553603    -0.76   0.445     .2332518    1.895339
-------------+----------------------------------------------------------------
    /lnalpha |   .0007291   .0475403                     -.0924481    .0939064
-------------+----------------------------------------------------------------
       alpha |   1.000729    .047575                      .9116965    1.098457
------------------------------------------------------------------------------
Likelihood-ratio test of alpha=0:  chibar2(01) = 2761.29 Prob>=chibar2 = 0.000
```

The same estimates can be obtained using `xtpoisson`, as shown in section 13.9.1 but without the `normal` option. We see that α is estimated as practically 1, which is considerably lower than the corresponding factor $\exp(\psi^{(1)}) - 1$ from Poisson regression with a normally distributed random intercept at level 1, which is estimated as about 1.44.

Constant dispersion or NB1

The *constant dispersion* or NB1 version of the negative binomial model cannot be derived from a random-intercept model but is instead obtained by assuming that the person-specific expected count μ_{ij} has a gamma distribution with expectation $\exp(\beta_1+\beta_2 x_{2i}+\cdots+\beta_7 x_{7ij})$ and variance $\exp(\beta_1+\beta_2 x_{2i}+\cdots+\beta_7 x_{7ij})\delta$.

From this specification, it follows that the count y_{ij} has the same expectation as the NB2 version of the model in (13.8) but the variance function now is

$$\mathrm{Var}(y_{ij}|\mathbf{x}_{ij}) \;=\; \mu_{ij}^{M}(1+\delta)$$

Unlike the random-intercept models, the variance for the constant-dispersion negative binomial model is a constant multiple of the expectation. This model can be fit using the `nbreg` command with the `dispersion(constant)` option:

```
. nbreg numvisit reform age educ married badh loginc summer,
> irr dispersion(constant)
Negative binomial regression                    Number of obs   =       2227
                                                LR chi2(7)      =     226.58
Dispersion     = constant                       Prob > chi2     =     0.0000
Log likelihood = -4600.3276                     Pseudo R2       =     0.0240

------------------------------------------------------------------------------
    numvisit |        IRR   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      reform |   .9002629   .0401958    -2.35   0.019     .8248293    .9825952
         age |   1.001107   .0022372     0.50   0.621     .9967317    1.005501
        educ |   1.007226   .0097883     0.74   0.459     .9882232    1.026595
     married |   1.038237   .0490102     0.79   0.427     .9464885    1.138879
        badh |   2.596117    .148113    16.72   0.000     2.321462    2.903265
      loginc |   1.131328   .0685746     2.04   0.042     1.004601    1.274041
      summer |    1.00864   .0693101     0.13   0.900     .8815455    1.154058
       _cons |   .7705889   .3470568    -0.58   0.563      .318757    1.862884
-------------+----------------------------------------------------------------
    /lndelta |   .9885984   .0532775                      .8841765     1.09302
-------------+----------------------------------------------------------------
       delta |   2.687465   .1431814                      2.42099    2.983271
------------------------------------------------------------------------------
Likelihood-ratio test of delta=0:  chibar2(01) = 2684.73 Prob>=chibar2 = 0.000
```

We see that δ is estimated as 2.69, and the multiplicative overdispersion term $1+\delta$ is hence estimated as 3.69.

13.9.3 Quasilikelihood

Generalized linear models are often fit using an algorithm called iteratively reweighted least squares that depends only on the expectation and variance of the response as a function of the covariates (although the log likelihood is used to monitor convergence). In the quasilikelihood approach, this same algorithm (or set of estimating equations) is used with a variance-expectation relationship (or variance function) of our choice, even when there is no statistical model that implies such a relationship. For the expectation, we retain the expression from the conventional Poisson regression model,

$$\ln(\mu_{ij}) \;=\; \beta_1 + \beta_2 x_{2i} + \cdots + \beta_7 x_{7ij}$$

However, for the variance we relax the assumption inherent in the Poisson distribution that it is equal to the expectation by introducing the proportionality parameter ϕ (pronounced "phi")

$$\mathrm{Var}(y_{ij}|\mathbf{x}_{ij}) \;=\; \phi\mu_{ij}$$

This variance function has the same form as that for the negative binomial model type NB1, whereas random-intercept models have variances that are quadratic functions of the mean.

The estimates of the regression parameters are the same as the maximum likelihood estimates for an ordinary Poisson model, and the proportionality parameter ϕ is estimated by a simple moment estimator, most commonly by the Pearson chi-squared statistic divided by the residual degrees of freedom. The scale parameter affects the standard errors only; they are multiplied by $\sqrt{\widehat{\phi}}$.

We can use the `glm` command with the `scale()` option to obtain maximum quasi-likelihood estimates. Here we use the `scale(x2)` option to estimate the proportionality parameter by the Pearson chi-squared statistic divided by the residual degrees of freedom:

```
. glm numvisit reform age educ married badh loginc summer,
> family(poisson) link(log) eform scale(x2)
Generalized linear models                         No. of obs      =      2227
Optimization     : ML                             Residual df     =      2219
                                                  Scale parameter =         1
Deviance         =  7419.853221                   (1/df) Deviance =  3.343782
Pearson          =  9688.740471                   (1/df) Pearson  =  4.366264
Variance function: V(u) = u                       [Poisson]
Link function    : g(u) = ln(u)                   [Log]
                                                  AIC             =  5.344133
Log likelihood   =  -5942.69244                   BIC             =  -9685.11
------------------------------------------------------------------------------
             |                 OIM
    numvisit |        IRR   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      reform |   .8689523   .0482622    -2.53   0.011     .7793268    .9688851
         age |   1.004371   .0027347     1.60   0.109     .9990249    1.009745
        educ |   .9894036   .0124256    -0.85   0.396     .9653472    1.014059
     married |   1.042542   .0607123     0.72   0.474     .9300882    1.168593
        badh |   3.105111   .1966385    17.89   0.000     2.742665    3.515454
      loginc |   1.160559   .0874758     1.98   0.048     1.001173     1.34532
      summer |   1.010269   .0853037     0.12   0.904     .8561784    1.192091
       _cons |   .6617582   .3721437    -0.73   0.463     .2197967    1.992405
------------------------------------------------------------------------------
(Standard errors scaled using square root of Pearson X2-based dispersion.)
```

We see from the output next to `(1/df) Pearson` that the proportionality parameter is estimated as $\widehat{\phi} = 4.37$, which can be compared with the corresponding parameter for the negative binomial model of type NB1, $1 + \widehat{\delta} = 3.69$. It follows that the estimated

model-based standard errors for the naïve Poisson model that does not accommodate overdispersion would be $1/\sqrt{\widehat{\phi}} = 0.48$ times the estimated standard errors from the quasilikelihood approach. This can also be seen by fitting the model with model-based standard errors by using the `glm` command above (without the `scale(x2)` option) or the `poisson` command (output not shown).

Because the quasilikelihood method changes only the standard errors, an alternative but similar approach is to use the sandwich estimator for the standard errors by specifying the `vce(robust)` option in the `glm` command.

13.10 Level-1 overdispersion in two-level models

We now return to two-level Poisson regression models with random effects. As seen in (13.4), we would expect that including a random intercept ζ_{1j} at level 2 has, at least to some degree, addressed the problem of overdispersion. However, as discussed in section 13.8.3, the model uses a single parameter to induce both overdispersion for the level-1 units and dependence among level-1 units in the same cluster.

Sometimes there may be additional overdispersion at level 1 not accounted for by the random effect at level 2. For instance, in the health-care reform data, there may be unobserved heterogeneity between occasions within persons, such as medical problems (representing unobserved time-varying covariates) that can lead to several extra doctor visits within the same 3-month period. After conditioning on the person-level random effect, the counts at the occasions are then overdispersed.

The most natural approach to handling level-1 overdispersion in a two-level model is by including a level-1 random intercept in addition to the level-2 random effect(s). The model then becomes a three-level model, with random effects at two nested levels, as discussed in chapter 8 (see exercise 16.6).

Hausman, Hall, and Griliches (1984) suggested another approach. Their model, which can be fit using Stata's `xtnbreg` command, has a closed-form likelihood and is specified as follows. The conditional expectation μ_{ij} is assumed to have a gamma distribution with mean $\exp(\beta_1 + \beta_2 x_{2i} + \cdots + \beta_7 x_{7ij})\delta_j$ and variance $\exp(\beta_1 + \beta_2 x_{2i} + \cdots + \beta_7 x_{7ij})\delta_j^2$. For a cluster j with a given δ_j, the conditional expectation of the count becomes

$$\begin{aligned} E(y_{ij}|\mathbf{x}_{ij}, \delta_j) &= \exp(\beta_1 + \beta_2 x_{2i} + \cdots + \beta_7 x_{7ij})\delta_j \\ &= \exp\{(\beta_1 + \ln\delta_j) + \beta_2 x_{2i} + \cdots + \beta_7 x_{7ij}\} \end{aligned} \tag{13.9}$$

and the conditional variance becomes

$$\mathrm{Var}(y_{ij}|\mathbf{x}_{ij}, \delta_j) = E(y_{ij}|\mathbf{x}_{ij}, \delta_j)(1 + \delta_j) \tag{13.10}$$

The counts for the level-1 units in cluster j therefore have a cluster-specific intercept $\beta_1 + \ln\delta_j$ and are subject to multiplicative overdispersion (of the NB1 form) with a cluster-specific overdispersion factor $(1 + \delta_j)$. It is then assumed that $1/(1 + \delta_j)$ has a beta distribution. The syntax for fitting this model is

```
xtset id
xtnbreg numvisit reform age educ married badh loginc summer, irr
```

A weakness of this model is that the person-specific intercept and level-1 overdispersion factor are both determined by the same parameter δ_j. It is therefore not possible to have heterogeneity at level 2 without having overdispersion at level 1 or vice versa. A consequence is that although the single-level Poisson model is a special case of the single-level negative binomial model (with $\delta = 0$ for NB1 and $\alpha = 0$ for NB2), the two-level Poisson model is not a special case of the two-level negative binomial model. Another problem with the model is that the parameters of the beta distribution are difficult to interpret. We therefore do not recommend using this model.

Perhaps the simplest approach to handling overdispersion at level 1 in a two-level random-intercept Poisson model is to use the sandwich estimator for the standard errors. At the time of writing this book, the only command that can provide these standard errors is `gllamm` with the `robust` option. After restoring the random-intercept model estimates,

```
. estimates restore glri
```

we can simply issue the command

```
. gllamm, robust eform

number of level 1 units = 2227
number of level 2 units = 1518

Condition Number = 723.77605

gllamm model

log likelihood = -4643.3427

Robust standard errors
```

numvisit	exp(b)	Std. Err.	z	P>|z|	[95% Conf.	Interval]
reform	.9547481	.0503036	-0.88	0.379	.8610748	1.058612
age	1.006002	.0031322	1.92	0.055	.9998817	1.01216
educ	1.008646	.0127823	0.68	0.497	.9839016	1.034012
married	1.077896	.0708484	1.14	0.254	.9476075	1.226097
badh	2.466857	.2880487	7.73	0.000	1.962236	3.101249
loginc	1.097486	.095603	1.07	0.286	.9252306	1.301811
summer	.8673159	.0722128	-1.71	0.087	.7367263	1.021053
_cons	.5157228	.3259741	-1.05	0.295	.1494154	1.780071

```
Variances and covariances of random effects
------------------------------------------------------------------------------

***level 2 (id)

    var(1): .81691979 (.0523264)
------------------------------------------------------------------------------
```

We see that the robust confidence intervals are somewhat wider than those based on model-based standard errors.

13.11 Other approaches to two-level count data

13.11.1 Conditional Poisson regression

Instead of using random intercepts ζ_{1j} for persons, we could instead treat the intercepts as fixed parameters α_j. An advantage of such a fixed-effects approach is that it does not make any assumptions regarding the person-specific intercepts. The estimated regression coefficients represent within effects, where persons serve as their own controls. A disadvantage is that effects of variables that do not vary within persons, such as gender, cannot be estimated.

As discussed for fixed-intercept logistic regression in section 10.14.1, we can eliminate the person-specific intercepts by constructing a likelihood that is conditional on the sum of the counts for each person, a sufficient statistic for the person-specific intercept. Only persons having observations in both years contribute to the conditional likelihood analysis; in the current application, this means that we lose the information from as many as 809 persons. We also lose the information from 95 persons who had zero doctor visits at both occasions (conditional on the sum being 0, the probability that both counts are 0 is 1, regardless of the parameter values. Hence, these observations do not provide information on the parameters).

Recall that within-person effects are estimated in the fixed-intercept approach. Attempting to fit the fixed-intercept Poisson regression model by conditional maximum likelihood using `xtpoisson` with the `fe` option,

```
xtset id
xtpoisson numvisit reform age educ married badh loginc summer, fe irr
```

fails. The reason is that the within-person variation in the covariates `reform` and `age` is perfectly confounded, in the sense that `reform` changes from 0 to 1 for all persons from 1996 to 1998 and `age` increases by 2 years for all persons from 1996 to 1998. It follows that the effects of `reform` and `age` are not separately identified in the fixed-intercept approach. In contrast, these effects are separately identified in ordinary Poisson regression and random-effects Poisson regression because `age` also varies *between* patients. This issue is similar to that discussed for different time scales in the fixed-effects approach to continuous longitudinal data in section 5.4.

Because of the confounding of the within effects of `reform` and `age`, we need to omit one of these covariates from the model; we omit `age`. This means that the estimated within effect of `reform` represents the combined within effects of `reform` and `age`. After omitting `age`, we can fit the fixed-intercept Poisson regression model by using the `fe` option:

```
. quietly xtset id

. xtpoisson numvisit reform educ married badh loginc summer, fe irr
note: 809 groups (809 obs) dropped because of only one obs per group
note: 95 groups (190 obs) dropped because of all zero outcomes
Conditional fixed-effects Poisson regression    Number of obs      =      1228
Group variable: id                              Number of groups   =       614
                                                Obs per group: min =         2
                                                               avg =       2.0
                                                               max =         2
                                                Wald chi2(6)       =     57.97
Log likelihood  =  -1080.974                    Prob > chi2        =    0.0000
```

numvisit	IRR	Std. Err.	z	P>|z|	[95% Conf.	Interval]
reform	1.015137	.0359576	0.42	0.671	.9470517	1.088116
educ	.9839241	.1610757	-0.10	0.921	.7138608	1.356156
married	1.045286	.1181487	0.39	0.695	.8375752	1.304507
badh	1.772883	.1450189	7.00	0.000	1.510265	2.081167
loginc	.9680603	.1119556	-0.28	0.779	.7717229	1.214349
summer	.8079478	.0676067	-2.55	0.011	.6857365	.9519396

The estimates were reported together with estimates from other models in table 13.1 on page 695. The nonsignificant point estimate of 1.02 for the IRR suggests that the German health-care reform did not affect the number of doctor visits. However, the estimated effect of `reform` from the fixed-intercept Poisson regression model should be interpreted with extra caution, as discussed above.

We can alternatively fit fixed-intercept Poisson models by maximum likelihood (instead of conditional maximum likelihood) if we include dummy variables for persons j. This method would be analogous to the fixed-effects estimator of within-person effects discussed for linear models in section 3.7.2. In contrast to logistic regression, maximum likelihood estimation of Poisson regression models with log links that include person dummies yields consistent estimates of the within-person effects (identical to the conditional maximum likelihood estimates), even when the cluster sizes are small as in the German health-care data. To replicate the estimates above from `fe`, we use the `poisson` command for maximum likelihood estimation and use `i.id` to include dummy variables for all persons (apart from one, who is represented by the intercept). Because a very large number of parameters is estimated, we need to increase the matrix size allowed in Stata by using the `set matsize` command before fitting the model. For Stata/MP and Stata/SE, the command to type is

```
set matsize 2000
```

For Stata/IC and Small Stata, this example cannot be run because of size limits.

```
. poisson numvisit reform educ married badh loginc summer i.id, irr
Poisson regression                                Number of obs   =       2227
                                                  LR chi2(1523)   =    7507.36
                                                  Prob > chi2     =     0.0000
Log likelihood = -2903.5113                       Pseudo R2       =     0.5639
```

numvisit	IRR	Std. Err.	z	P>|z|	[95% Conf.	Interval]
reform	1.015137	.0359576	0.42	0.671	.9470518	1.088116
educ	.9839241	.1610757	-0.10	0.921	.7138608	1.356156
married	1.045286	.1181487	0.39	0.695	.8375752	1.304507
badh	1.772883	.1450189	7.00	0.000	1.510265	2.081167
loginc	.9680603	.1119556	-0.28	0.779	.7717229	1.214349
summer	.8079478	.0676067	-2.55	0.011	.6857365	.9519396

(*Estimates for the very large number of person dummies not shown*)

We see that the estimates are identical to those produced by `xtpoisson`. However, this approach is somewhat impractical when there are many clusters as here because a large number of parameters must be estimated.

13.11.2 Conditional negative binomial regression

Hausman, Hall, and Griliches (1984) proposed a conditional negative binomial model where the parameter δ_j in (13.9) and (13.10) is treated as fixed. However, while the fixed-effects Poisson model does not allow for overdispersion, the fixed-effects negative binomial model does not allow for lack of overdispersion. Another oddity of the fixed-effects negative binomial model is that effects of cluster-specific covariates can be estimated (in contrast to other fixed-effects models) because their inclusion affects the variance function. See also Allison and Waterman (2002).

The syntax for fitting this model in Stata is

```
xtnbreg numvisit reform age educ married badh loginc summer, fe irr
```

13.11.3 Generalized estimating equations

We now consider a multivariate extension of the quasilikelihood approach discussed in section 13.9.3 called generalized estimating equations (GEE). GEE can be used to estimate *marginal effects*, just as in ordinary Poisson regression but taking the dependence among units nested in clusters into account. The ideas are the same as discussed for dichotomous responses in section 10.14.2.

GEE estimates using the default exchangeable correlation structure but with robust sandwich-based standard errors are obtained using

```
. quietly xtset id

. xtgee numvisit reform age educ married badh loginc summer,
> family(poisson) link(log) vce(robust) eform

GEE population-averaged model                   Number of obs      =      2227
Group variable:                           id    Number of groups   =      1518
Link:                                    log    Obs per group: min =         1
Family:                              Poisson                   avg =       1.5
Correlation:                 exchangeable                      max =         2
                                               Wald chi2(7)       =    235.37
Scale parameter:                          1    Prob > chi2        =    0.0000
                                  (Std. Err. adjusted for clustering on id)
```

numvisit	IRR	Robust Std. Err.	z	P>|z|	[95% Conf.	Interval]
reform	.8849813	.0467574	-2.31	0.021	.7979238	.9815371
age	1.005253	.0033549	1.57	0.116	.9986986	1.01185
educ	.9906936	.0117057	-0.79	0.429	.9680144	1.013904
married	1.038283	.072958	0.53	0.593	.904698	1.191593
badh	3.020459	.264062	12.64	0.000	2.544821	3.584997
loginc	1.150186	.0914521	1.76	0.078	.9842114	1.34415
summer	.9741462	.0862448	-0.30	0.767	.8189626	1.158735
_cons	.6818911	.3926379	-0.66	0.506	.2205906	2.107867

These estimates were reported under the heading "GEE Poisson" in table 13.1.

We display the fitted working correlation matrix using `estat wcorrelation`,

```
. estat wcorrelation
Estimated within-id correlation matrix R:
```

	c1	c2
r1	1	
r2	.2135204	1

and see that the correlation between the Pearson residuals at the two occasions is estimated as 0.21.

13.12 Estimating marginal and conditional effects when responses are missing at random

From the discussion in section 13.7.1, we would expect the estimated conditional effects using random-intercept Poisson models to be similar to the estimated marginal effects using ordinary Poisson regression or GEE (apart from the intercept). However, it is evident from table 13.1 that the estimates are quite different.

This discrepancy is probably due to the extremely unbalanced nature of the data. As discussed for linear models in section 5.8.1, if the responses are missing at random (missingness does not depend on unobserved responses, given the observed responses and covariates) and if the probability of a response being missing at an occasion depends on the observed response at the other occasion, then maximum likelihood estimation of

the correct model gives consistent parameter estimates. However, maximum likelihood estimation of an incorrect model, such as Poisson regression that ignores within-person dependence, gives inconsistent estimates. GEE is also not consistent if the probability of a response being missing at an occasion depends on the observed response at another occasion after controlling for covariates. It is often claimed that GEE requires data to be missing completely at random (MCAR) for consistency, but missingness can actually depend on the covariates.

❖ Simulation

We now simulate complete data from a random-intercept Poisson model (with parameter values equal to those we have estimated for the data) and produce data that are missing at random (MAR) by letting the probability of being missing at the second occasion depend on the observed response at the first occasion. We then compare estimates from GEE using an exchangeable correlation structure with maximum likelihood estimates for ordinary and random-intercept Poisson models. This simulation is similar to the one described in section 5.8.1 (see also exercise 6.6).

We can use the postestimation command `gllasim` for `gllamm` to simulate responses from the model just fit in `gllamm`. To create missing data according to a process of our choice, we must first simulate complete data. To accomplish this, we must first ensure that each person has two rows of data, one for 1996 and one for 1998. (see also section 10.13.2 where we used `fillin` to produce balanced data). We create a variable, `num`, containing the number of rows of data per person by typing

```
. egen num = count(numvisit), by(id)
```

For those with one row only, we want to expand the data by 2, and for those with two rows, we do not want to expand the data, which is equivalent to expanding them by a factor of 1.

```
. generate mult = 3 - num
. expand mult
(809 observations created)
```

We now generate an occasion identifier, `occ`, equal to `reform` for those who already have complete data and equal to 0 and 1 for arbitrarily chosen rows otherwise.

```
. by id (reform), sort: generate occ = _n - 1
```

To keep track of which responses were actually missing in the original data, we create the dummy variable `missing`:

```
. generate missing = (occ!=reform & num==1)
```

People with `num` equal to 1 originally had only one observation. If the observation was from 1996, `reform` takes on the value 0 twice in the expanded data (because the `expand` command just clones all variables) whereas `occ` is 0 and 1, so the 1998 observation is flagged as missing. For someone with missing data for 1996, reform is 1 twice, and the

1996 response is flagged as missing. Now we replace responses where `missing` equals 1 with missing values:

```
. replace numvisit = . if missing==1
(809 real changes made, 809 to missing)
```

For persons with missing data, the variable `reform` takes on the same value at both occasions. We rectify this by replacing the value of `reform` at the occasion when the response was missing with `occ`:

```
. replace reform = occ if missing==1
(809 real changes made)
```

We are now ready to simulate new responses `y`. To ensure that the results can be replicated, we first sort the data and then set the random-number seed to an arbitrary number:

```
. sort id reform
. set seed 1211
```

We then retrieve the `gllamm` estimates for the random-intercept Poisson model and use the `gllasim` command with the `fsample` option to simulate responses for the full sample, not just the estimation sample

```
. estimates restore glri
. gllasim y, fsample
(simulated responses will be stored in y)
```

For those who visited the doctor at least twice in 1996, we replace the response for 1998 with a missing value with a probability of 0.9:

```
. by id (reform), sort: generate drop = (y[1]>2 & runiform()<.9)
. replace y = . if drop==1 & reform==1
(466 real changes made, 466 to missing)
```

Because the responses are missing at random (MAR), maximum likelihood estimation of the model that generated the data should yield consistent estimates.

```
. quietly xtset id
. xtpoisson y reform age educ married badh loginc summer, normal irr
Random-effects Poisson regression               Number of obs      =      2570
Group variable: id                              Number of groups   =      1518
Random effects u_i ~ Gaussian                   Obs per group: min =         1
                                                               avg =       1.7
                                                               max =         2
                                                Wald chi2(7)       =    213.48
Log likelihood  = -4840.7573                    Prob > chi2        =    0.0000
```

y	IRR	Std. Err.	z	P>|z|	[95% Conf.	Interval]
reform	1.029429	.036059	0.83	0.408	.9611257	1.102586
age	1.006054	.0028652	2.12	0.034	1.000453	1.011685
educ	1.020096	.0126798	1.60	0.109	.9955447	1.045254
married	1.151819	.0669211	2.43	0.015	1.027849	1.290742
badh	2.660478	.2005024	12.98	0.000	2.295146	3.083962
loginc	1.04616	.0756244	0.62	0.532	.9079598	1.205395
summer	.8274459	.0645118	-2.43	0.015	.7101919	.9640588
_cons	.6261601	.3363712	-0.87	0.383	.2184856	1.794519
/lnsig2u	-.1261919	.0571691	-2.21	0.027	-.2382412	-.0141425
sigma_u	.9388534	.0268367			.8877007	.9929537

```
Likelihood-ratio test of sigma_u=0: chibar2(01) =  2871.89 Pr>=chibar2 = 0.000
```

We see that the estimates above are close to the "true" parameter values, which are the estimates for the original data.

However, ordinary Poisson regression produces quite different estimates:

```
. poisson y reform age educ married badh loginc summer, irr
Poisson regression                              Number of obs   =       2570
                                                LR chi2(7)      =    1426.49
                                                Prob > chi2     =     0.0000
Log likelihood = -6276.7036                     Pseudo R2       =     0.1020
```

y	IRR	Std. Err.	z	P>|z|	[95% Conf.	Interval]
reform	.6131784	.0177075	-16.94	0.000	.5794363	.6488855
age	1.004305	.0012989	3.32	0.001	1.001763	1.006854
educ	1.01852	.0057876	3.23	0.001	1.007239	1.029926
married	1.128861	.031214	4.38	0.000	1.069311	1.191727
badh	2.719263	.0854277	31.84	0.000	2.556879	2.891961
loginc	1.108184	.0392507	2.90	0.004	1.033863	1.187847
summer	.8433938	.0343386	-4.18	0.000	.7787066	.9134545
_cons	.6891216	.1810127	-1.42	0.156	.4118218	1.153141

Specifically, the intervention now looks effective because those who visited the doctor frequently in 1998 were more likely to drop out, and because of the within-person dependence between responses, it is these same people who tended to visit the doctor frequently in 1996. Consequently, the mean number of doctor visits in 1998 is un-

derestimated by ordinary Poisson regression. In contrast, the random-intercept model "knows" about the within-person dependence and hence makes the correct adjustment.

Interestingly, generalized estimating equations (GEE) does not work well in this case although we allow for within-person dependence by specifying an exchangeable correlation structure:

```
. quietly xtset id
. xtgee y reform age educ married badh loginc summer, family(poisson)
> link(log) vce(robust) eform
GEE population-averaged model                   Number of obs      =      2570
Group variable:                           id    Number of groups   =      1518
Link:                                    log    Obs per group: min =         1
Family:                              Poisson                   avg =       1.7
Correlation:                    exchangeable                   max =         2
                                               Wald chi2(7)       =    242.22
Scale parameter:                          1    Prob > chi2        =    0.0000
                                  (Std. Err. adjusted for clustering on id)
```

y	IRR	Robust Std. Err.	z	P>|z|	[95% Conf.	Interval]
reform	.7609233	.0251568	-8.26	0.000	.7131804	.8118624
age	1.004157	.0030258	1.38	0.169	.9982446	1.010105
educ	1.017779	.0134357	1.33	0.182	.9917829	1.044456
married	1.131598	.0699859	2.00	0.046	1.002416	1.277428
badh	2.718051	.2167291	12.54	0.000	2.324799	3.177824
loginc	1.119422	.0891531	1.42	0.157	.9576402	1.308535
summer	.8264793	.0788856	-2.00	0.046	.6854672	.9964999
_cons	.646465	.3697563	-0.76	0.446	.2107105	1.98337

13.13 Which Scottish counties have a high risk of lip cancer?

We now consider models for disease mapping or small-area estimation. Clayton and Kaldor (1987) presented and analyzed data on lip cancer for each of 56 Scottish counties over the period 1975–1980. These data have also been analyzed by Breslow and Clayton (1993) and Leyland (2001) among many others.

The dataset `lips.dta` has the following variables:

- `county`: county identifier (1 to 56)
- `o`: observed number of lip cancer cases
- `e`: expected number of lip cancer cases
- `x`: percentage of population working in agriculture, fishing, or forestry

The expected number of lip cancer cases is based on the age-specific lip cancer rates for the whole of Scotland and the age distribution of the counties. We read in the lip cancer data by typing

```
. use http://www.stata-press.com/data/mlmus3/lips, clear
```

13.14 Standardized mortality ratios

The standardized mortality ratio (SMR) for a county is defined as the ratio of the incidence rate to that expected if the age-specific incidence rates were equal to those of a reference population (for example, Breslow and Day [1987]), here the whole of Scotland. The crude estimate of the SMR for county j is obtained using

$$\widehat{\text{SMR}}_j = \frac{o_j}{e_j}$$

where o_j is the observed number of cases and e_j is the expected number of cases.

We first calculate the crude SMRs as percentages for the lip cancer data:

```
. generate smr = 100*o/e
```

The number of observed and expected lip cancer cases, and crude SMRs for the 56 counties are presented in table 13.3. The crude SMRs are also shown in the map in figure 13.1. When the SMR exceeds 100, the county has more cases than would be expected given the age distribution.

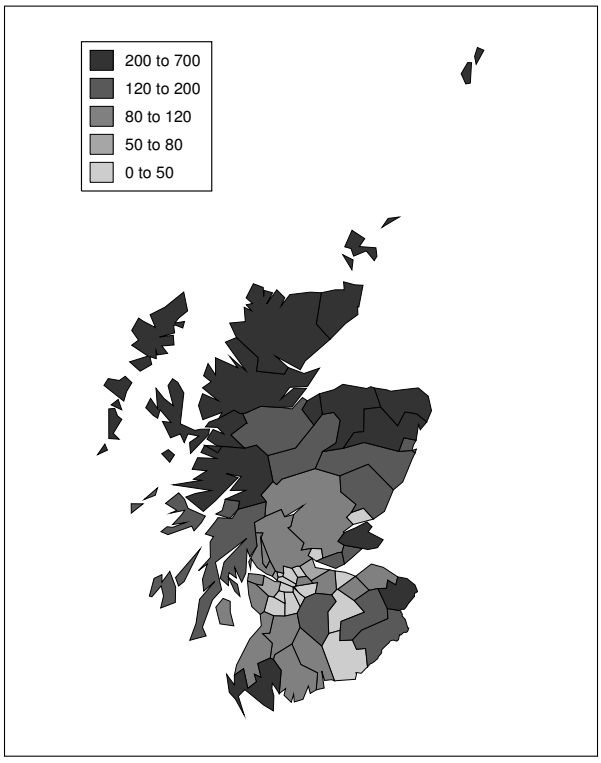


Figure 13.1: Map of crude SMR as percentage (*Source:* Skrondal and Rabe-Hesketh 2004)

Table 13.3: Observed and expected numbers of lip cancer cases and various SMR estimates (in percentages) for Scottish counties

		Obs	Exp	Crude	Predicted SMRs	
County	#	o_j	e_j	SMRs	Norm.	NPMLE
Skye. Lochalsh	1	9	1.4	652.2	470.7	342.6
Banf. Buchan	2	39	8.7	450.3	421.8	362.4
Caithness	3	11	3.0	361.8	309.4	327.1
Berwickshire	4	9	2.5	355.7	295.2	321.6
Ross. Cromarty	5	15	4.3	352.1	308.5	327.6
Orkney	6	8	2.4	333.3	272.0	311.1
Moray	7	26	8.1	320.6	299.9	322.2
Shetland	8	7	2.3	304.3	247.8	292.5
Lochaber	9	6	2.0	303.0	239.0	280.1
Gordon	10	20	6.6	301.7	279.1	319.9
W. Isles	11	13	4.4	295.5	262.5	315.5
Sutherland	12	5	1.8	279.3	219.2	254.3
Nairn	13	3	1.1	277.8	198.4	222.7
Wigtown	14	8	3.3	241.7	210.9	249.6
NE. Fife	15	17	7.8	216.8	204.6	245.3
Kincardine	16	9	4.6	197.8	178.9	171.4
Badenoch	17	2	1.1	186.9	151.9	163.2
Ettrick	18	7	4.2	167.5	154.7	136.7
Inverness	19	9	5.5	162.7	154.2	128.4
Roxburgh	20	7	4.4	157.7	149.1	130.3
Angus	21	16	10.5	153.0	147.8	117.1
Aberdeen	22	31	22.7	136.7	135.0	116.4
Argyll. Bute	23	11	8.8	125.4	123.3	116.4
Clydesdale	24	7	5.6	124.6	122.9	116.7
Kirkcaldy	25	19	15.5	122.8	121.6	116.4
Dunfermline	26	15	12.5	120.1	119.1	116.3
Nithsdale	27	7	6.0	115.9	116.3	115.5
E. Lothian	28	10	9.0	111.6	111.4	115.9
Perth. Kinross	29	16	14.4	111.3	111.1	116.3
W. Lothian	30	11	10.2	107.8	108.5	115.9
Cumnock-Doon	31	5	4.8	105.3	107.2	111.5
Stewartry	32	3	2.9	104.2	109.1	109.4
Midlothian	33	7	7.0	99.6	102.7	113.1
Stirling	34	8	8.5	93.8	97.3	112.9
Kyle. Carrick	35	11	12.3	89.3	92.2	114.1
Inverclyde	36	9	10.1	89.1	92.6	112.4
Cunninghame	37	11	12.7	86.8	89.7	113.3
Monklands	38	8	9.4	85.6	89.4	109.4
Dumbarton	39	6	7.2	83.3	89.4	104.9
Clydebank	40	4	5.3	75.9	85.7	94.5

Table 13.3: Observed and expected numbers of lip cancer cases and various SMR estimates (in percentages) for Scottish counties (cont.)

		Obs	Exp	Crude	Predicted SMRs	
County	#	o_j	e_j	SMRs	Norm.	NPMLE
Renfrew	41	10	18.8	53.3	59.1	40.6
Falkirk	42	8	15.8	50.7	57.9	40.9
Clackmannan	43	2	4.3	46.3	68.8	65.5
Motherwell	44	6	14.6	41.0	50.7	37.5
Edinburgh	45	19	50.7	37.5	40.8	36.2
Kilmarnock	46	3	8.2	36.6	53.2	42.2
E. Kilbride	47	2	5.6	35.8	57.9	49.7
Hamilton	48	3	9.3	32.1	48.5	38.8
Glasgow	49	28	88.7	31.6	33.8	36.2
Dundee	50	6	19.6	30.6	39.8	36.2
Cumbernauld	51	1	3.4	29.1	63.1	57.8
Bearsden	52	1	3.6	27.6	61.1	55.4
Eastwood	53	1	5.7	17.4	46.4	40.6
Strathkelvin	54	1	7.0	14.2	40.8	37.8
Tweeddale	55	0	4.2	0.0	43.2	40.8
Annandale	56	0	1.8	0.0	64.9	60.6

Source: Clayton and Kaldor (1987)

13.15 Random-intercept Poisson regression

An important limitation of crude SMRs is that estimates for counties with small populations are very imprecise. This problem can be addressed by using random-intercept Poisson models in conjunction with empirical Bayes prediction. The resulting SMRs are shrunken toward the overall SMR, thereby borrowing strength from other counties (see section 2.11.2).

Although we only have one observation per county, we can introduce a county-level random intercept to model overdispersion, as discussed in section 13.9.

13.15.1 Model specification

We consider a random-intercept Poisson regression model where the observed number of lip cancer cases in county j is assumed to have a Poisson distribution with mean μ_j,

$$\ln(\mu_j) \;=\; \ln(e_j) + \beta_1 + \zeta_j$$

Here $\zeta_j \sim N(0, \psi)$ is a random intercept representing unobserved heterogeneity between counties and $\ln(e_j)$ is an offset, a covariate with regression coefficient set to 1. The purpose of the offset is to ensure that $\beta_1 + \zeta_j$ can be interpreted as a model-based county-specific log SMR. This interpretation becomes clear by subtracting the offset from both sides of the equation:

$$\ln(\mu_j) - \ln(e_j) \;=\; \ln(\underbrace{\mu_j/e_j}_{\text{SMR}_j}) \;=\; \beta_1 + \zeta_j$$

13.15.2 Estimation using gllamm

We will use `gllamm` for estimation because this is the only command that can provide the required posterior expectations of the standardized mortality ratios at the time of writing this book.[1] We first generate a variable for the offset,

```
. generate lne = ln(e)
```

and then we pass this variable to `gllamm` using the `offset()` option. We also specify a Poisson distribution and log link using the `family()` and `link()` options, respectively:

```
. gllamm o, i(county) offset(lne) family(poisson) link(log) adapt
number of level 1 units = 56
number of level 2 units = 56

gllamm model

log likelihood = -181.32392
```

o	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
_cons	.080211	.1167416	0.69	0.492	-.1485983	.3090204
lne	1	(offset)				

```
Variances and covariances of random effects
------------------------------------------------------------------------------

***level 2 (county)

    var(1): .58432672 (.14721754)
------------------------------------------------------------------------------
```

The maximum likelihood estimates for the random-intercept model are given in table 13.4 under "Normal ML". We could also include the percentage of the population in county j working in agriculture, fishing, or forestry as a county-level covariate; see exercise 13.6.

1. `xtmepoisson` could be used to obtain posterior modes of ζ_j and hence posterior modes of SMRs.

Table 13.4: Estimates for random-intercept models for Scottish lip cancer data

	Normal ML		NPMLE ($C=4$)	
	Est	(SE)	Est	(SE)
β_1 [_cons]	0.08	(0.12)	0.08	(0.12)
ψ	0.58		0.63†	
Log likelihood	−181.32		−174.39	

†Derived from discrete distribution

13.15.3 Prediction of standardized mortality ratios

We now consider predictions of the SMRs using empirical Bayes(see also section 10.13.2). Specifically, we would like to estimate the posterior expectation of the SMR,

$$\widetilde{\text{SMR}}_j = \int \exp(\widehat{\beta}_1 + \zeta_j)\ \text{Posterior}(\zeta_j|o_j, e_j)\ d\zeta_j \tag{13.11}$$

It may be tempting to obtain the predicted SMRs by simply plugging in the estimate $\widehat{\beta}_1$ and the predicted random intercept $\widetilde{\zeta}_j$ in the exponential function. However, this would be incorrect because the expectation of a nonlinear function of a random variable is not equal to the nonlinear function of the expectation of the random variable.

Empirical Bayes predictions of the SMRs can be obtained using `gllapred` with the `mu` option to get posterior means on the scale of the response and the `nooffset` option to omit the offset $\ln(e_j)$ from the linear predictor,

```
. gllapred mu, mu nooffset
. generate thet = 100*mu
```

where `thet` are the predicted SMRs in percent. We then list these predicted SMRs for the first 10 counties:

```
. sort county
. list county thet in 1/10, clean noobs
    county       thet
         1   470.7203
         2   421.7975
         3   309.4238
         4   295.1885
         5   308.5293
         6   272.0485
         7   299.8875
         8   247.8383
         9   238.9533
        10   279.1406
```

These empirical Bayes predictions were given under "Norm." in table 13.3 and are displayed as a map in figure 13.2. The maps in figures 13.1 and 13.2 were drawn using Stata, and an annotated do-file to create the maps can be obtained by typing

```
copy http://www.stata-press.com/data/mlmus3/scotmaps.do scotmaps.do
```

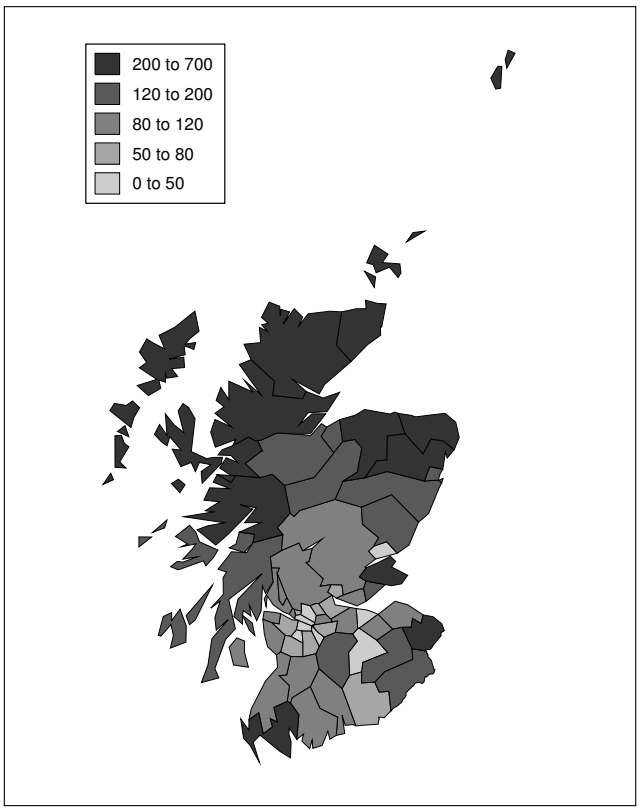


Figure 13.2: Map of SMRs assuming normally distributed random intercept (no covariate) (*Source:* Skrondal and Rabe-Hesketh 2004)

We can plot the empirical Bayes predictions against the crude SMRs by typing

```
. twoway (scatter thet smr, msymbol(none) mlabpos(0) mlabel(county))
> (function y=x, range(0 600)), xline(108) yline(108)
> xtitle(Crude SMR) ytitle(Empirical Bayes SMR) legend(off)
```

The $y = x$ line has been superimposed, as well as lines $x = 108$ and $y = 108$, representing the SMR in percent, $100 \times \exp(\widehat{\beta}_1)$, when ζ_j equals its mean 0 (these are median SMRs). The resulting graph is given in figure 13.3. Shrinkage is apparent because counties with particularly high crude SMRs lie below the $y = x$ line (have predictions lower than the crude SMR) and counties with particularly low crude SMRs lie above the $y = x$ line.

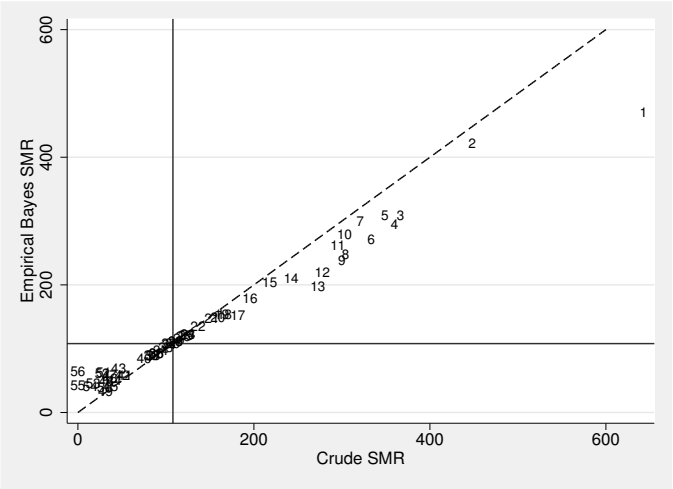


Figure 13.3: Empirical Bayes SMRs versus crude SMRs

13.16 ❖ Nonparametric maximum likelihood estimation

13.16.1 Specification

Instead of assuming that the random intercept ζ_j is normally distributed, we can relax this assumption using nonparametric maximum likelihood estimation (NPMLE).

It can been shown that the nonparametric estimator of the random-intercept distribution is discrete with locations $\zeta_j = e_c$ and probabilities π_c $(c=1,\ldots,C)$, where the number of locations C with nonzero probabilities is determined to make the likelihood as large as possible.

Obviously, the probabilities must add to one:

$$\pi_1 + \cdots + \pi_C \;=\; 1 \tag{13.12}$$

The discrete distribution of ζ_j can be parameterized so that it has zero mean,

$$\pi_1 e_1 + \cdots + \pi_C e_C \;=\; 0 \tag{13.13}$$

which has the advantage that we need not omit the intercept β_1 from the model:

$$\ln(\mu_j) \;=\; \ln(e_j) + \beta_1 + \zeta_j$$

13.16.2 Estimation using gllamm

To obtain the nonparametric maximum likelihood estimates, we must use the maximum possible number of locations so that it is not possible to achieve a larger likelihood by introducing more locations.

This maximum number can be determined using the following iterative approach. First, we fit the model with a given number of locations C, for instance, $C=2$. Keeping all the parameters equal to the resulting maximum likelihood estimates, we introduce another point with a small probability π_{C+1} and evaluate the likelihood for a large number of different locations for this point, for example, by setting $e_{C+1} = -5 + l/100$, $(l=1,\ldots,1000)$. If the likelihood increases for any of these locations, we have evidence that another point is required. The model is then refit with $C+1$ points, and we repeat the search for a location at which introducing a new point increases the likelihood. These cycles are repeated until the search does not identify any more locations.

For the Scottish lip cancer data, we start with $C=2$ locations and maximize the likelihood with respect to β_1, e_1, and π_1, with e_2 and π_2 determined by the constraints in (13.12) and (13.13). This is accomplished in `gllamm` using the `ip(f)` and `nip(2)` options.

```
. gllamm o, i(county) offset(lne) family(poisson) link(log) ip(f) nip(2)
number of level 1 units = 56
number of level 2 units = 56

Condition Number = 9.5651502

gllamm model

log likelihood = -205.40139
```

o	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
_cons	.0314632	.1037764	0.30	0.762	-.1719348	.2348612
lne	1	(offset)				

```
Probabilities and locations of random effects
------------------------------------------------------------------------------

***level 2 (county)

    loc1: -.85205, .54307
  var(1): .46272368
    prob: 0.3893, 0.6107
------------------------------------------------------------------------------
```

We see that the locations are estimated as $\widehat{e}_1 = -0.85$ and $\widehat{e}_2 = 0.54$ with estimated probabilities $\widehat{\pi}_1 = 0.39$ and $\widehat{\pi}_2 = 0.61$. The variance of this discrete distribution,

$$\widehat{\mathrm{Var}}(\zeta_j) \;=\; \widehat{\pi}_1\widehat{e}_1^2 + \widehat{\pi}_2\widehat{e}_2^2$$

is given as 0.46 next to `var(1)`.

We now gradually increase the number of locations until the likelihood cannot be increased any further. For $C=3$ locations, we use the `nip(3)` option and the previous estimates for $C=2$ as starting values. We also use the `gateaux()` option (for the *Gâteaux derivative* or directional derivative) to specify the smallest and largest locations to be considered in the search, as well as the number of equally spaced steps to take within these limits. Finally, we must also supply the previous log likelihood using the `lf0()` option, which requires as its first argument the number of parameters in the previous model. It is convenient to obtain the parameter estimates, log likelihood, and number of parameters in the previous model as follows:

```
. matrix a = e(b)
. local ll = e(ll)
. local k = e(k)
. gllamm o, i(county) offset(lne) family(poisson) link(log) ip(f) nip(3)
> gateaux(-5 5 100) from(a) lf0(`k' `ll')
.....................................................................
> ......................
maximum gateaux derivative is 6.872835

number of level 1 units = 56
number of level 2 units = 56

Condition Number = 9.2086581


gllamm model                                    Number of obs   =         56
                                                LR chi2(2)      =      61.92
Log likelihood = -174.44216                     Prob > chi2     =     0.0000
------------------------------------------------------------------------------
           o |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       _cons |    .0860003   .1189174     0.72   0.470    -.1470736    .3190742
         lne |           1  (offset)
------------------------------------------------------------------------------


Probabilities and locations of random effects
------------------------------------------------------------------------------

***level 2 (county)

    loc1: -1.1012, 1.1149, .07126
  var(1): .63591774
    prob: 0.2753, 0.241, 0.4836
------------------------------------------------------------------------------
```

To increase the number of locations to $C=4$, we use the same commands and options as before except that we change the `nip()` option from `nip(3)` to `nip(4)`:

```
. matrix a = e(b)
. local ll = e(ll)
. local k = e(k)
```

```
. gllamm o, i(county) offset(lne) family(poisson) link(log) ip(f) nip(4)
> gateaux(-5 5 100) from(a) lf0(‘k’ ‘ll’)
.....................................................................
> .....................
maximum gateaux derivative is .00020442

number of level 1 units = 56
number of level 2 units = 56

Condition Number = 72.542683


gllamm model                                        Number of obs   =         56
                                                    LR chi2(2)      =       0.11
Log likelihood = -174.38535                         Prob > chi2     =     0.9448
------------------------------------------------------------------------------
           o |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       _cons |   .0847742   .1188573     0.71   0.476    -.1481819    .3177303
         lne |           1  (offset)
------------------------------------------------------------------------------


Probabilities and locations of random effects
------------------------------------------------------------------------------


***level 2 (county)

    loc1: -1.1002, 1.0426, 1.2628, .06676
  var(1): .6339741
    prob: 0.2749, 0.1847, 0.0617, 0.4788
------------------------------------------------------------------------------
```

For $C=5$, we obtain

```
. matrix a = e(b)
. local ll = e(ll)
. local k = e(k)
. gllamm o, i(county) offset(lne) family(poisson) link(log) nip(5) ip(f)
> gateaux(-5 5 100) from(a) lf0(‘k’ ‘ll’)
.....................................................................
> .....................
maximum gateaux derivative is -.00005128
maximum gateaux derivative less than 0.00001
```

The output suggests that the likelihood cannot be increased by including a fifth point. However, we have only tried 100 locations. To make sure that there is no location at which the likelihood can be increased, we also used the option `gateaux(-5 5 1000)`, but the maximum Gâteaux derivative was still negative.

We therefore conclude that nonparametric maximum likelihood estimation (NPMLE) has $C=4$ locations. The nonparametric maximum likelihood estimates were shown in table 13.4 under “NPMLE”. The estimates from NPMLE are similar to those obtained by assuming normality.

To visualize the discrete distribution, we can access the matrices of location and log-probability estimates stored by `gllamm` by using

```
. matrix locs = e(zlc2)'
. matrix lp = e(zps2)'
```

Here the apostrophe in `e(zlc2)'` transposes the row matrix to a column matrix that can be stored as a variable in the dataset by using `svmat`:

```
. svmat locs
. svmat lp
```

We then transform the estimated log probabilities to probabilities and the log-incidence rates e_c to SMRs by using

```
. generate p = exp(lp1)
. generate smrloc = 100*exp(_b[_cons] + locs1)
```

Finally, we produce a graph of the discrete distribution:

```
. twoway (dropline p smrloc), xtitle(Location) ytitle(Probability)
```

The graph is shown in figure 13.4.

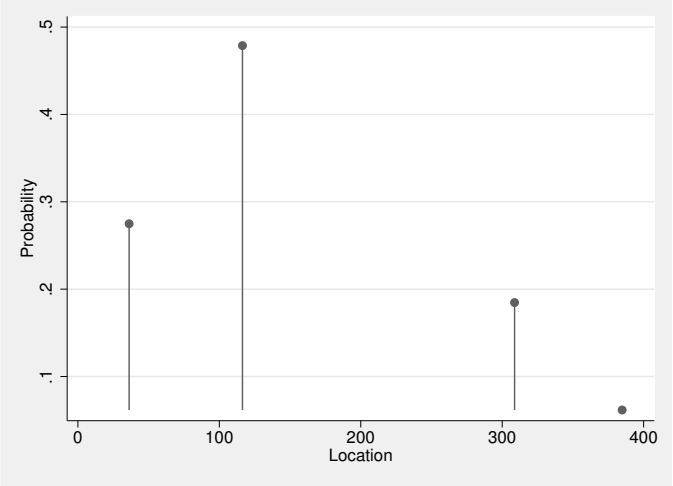


Figure 13.4: Lip cancer in Scotland: SMRs (locations) and probabilities for nonparametric maximum likelihood estimate of random-intercept distribution

13.16.3 Prediction

Empirical Bayes predictions of the SMRs based on nonparametric maximum likelihood estimation can be obtained as

```
. gllapred mu2, mu nooffset
. generate thet2 = 100*mu2
```

where `thet2` are the predicted SMRs in percentages. We list these predicted SMRs for the first 10 counties together with predictions based on the normality assumption for the random intercept `thet`:

```
. sort county
. list county thet thet2 in 1/10, clean noobs
    county       thet      thet2
         1   470.7203   342.6493
         2   421.7975   362.4183
         3   309.4238   327.1122
         4   295.1885   321.6138
         5   308.5293   327.5669
         6   272.0485    311.061
         7   299.8875   322.2489
         8   247.8383   292.5375
         9   238.9533   280.1219
        10   279.1406   319.8951
```

Predicted SMRs based on nonparametric maximum likelihood estimation (NPMLE) for all Scottish counties were reported under "NPMLE" in table 13.3.

13.17 Summary and further reading

In this chapter, we have discussed Poisson regression modeling of count data. Multilevel Poisson regression models with random effects were fit to longitudinal data on number of doctor visits in Germany and small-area estimation or disease mapping of standardized mortality ratios (SMRs) for lip cancer in Scotland.

We have outlined the motivation and some of the basic properties of the Poisson distribution, such as the equality of the expectation and variance. Different approaches for handling overdispersion in Poisson regression were considered such as quasilikelihood, robust standard errors, and the introduction of a level-1 random intercept. We have introduced random effects at the cluster level to accommodate within-cluster dependence, which must be tackled, for instance, when modeling longitudinal or panel data of counts. Both random-intercept and random-coefficient models were considered. Other approaches to modeling clustered count data were briefly considered, such as conditional maximum likelihood, GEE, and NPMLE where the distributional assumption for the random intercept is relaxed (see also Rabe-Hesketh, Pickles, and Skrondal [2003]).

Most of the issues discussed for prediction of random effects for dichotomous responses persist for counts, such as the choice between using the mean or the mode of the posterior distribution. We also experience shrinkage in empirical Bayes prediction

as before. In small-area estimation or disease mapping, inclusion of random effects is beneficial for "borrowing strength" from other counties in predicting SMRs. Empirical Bayes predictions for disease mapping can be improved by modeling spatial dependence (see Skrondal and Rabe-Hesketh, [2004, sec 11.4]), which results in an even smoother disease map.

Poisson regression is often used to model survival or durations in continuous time. If events occur according to a Poisson process, the durations between events have an exponential distribution, and piecewise exponential survival models can be fit via Poisson regression, as described in section 15.4.1. Chapter 15 uses Poisson and random-effects Poisson regression throughout.

Extensive treatments of methods for count data are given by Cameron and Trivedi (1998) and Winkelmann (2008), both of which also discuss some models for clustered data. A brief introduction to single-level regression models for counts is provided by Long (1997, chap. 8), and Hilbe (2011) is devoted to the negative binomial model. Use of Poisson regression for disease mapping is described in Lawson et al. (1999) and Lawson, Browne, and Vidal Rodeiro (2003).

The exercises cover a wide range of applications in various disciplines. Poisson regression models with random intercepts are used in exercise 13.1 on a longitudinal randomized controlled clinical trial of treatments for epilepsy, exercise 13.2 on a randomized crossover trial investigating the effects of an artificial sweetener on the number of headaches, exercise 13.3 on the number of police stops and ethnicity in New York precincts, exercise 13.4 on panel data to investigate the effects of research and development expenditures on the number of patents awarded to firms, exercise 13.5 on days absent from school among aboriginal and white Australian children, and exercise 13.7 on skin cancer mortality in the European Economic Community. Exercises 13.1, 13.2, and 13.3 also include random-coefficient models. Many of the exercises consider empirical Bayes prediction of random effects and the use of offsets to take varying exposure into account. Exercise 13.5 is on modeling overdispersion in single-level data and exercise 13.5 is on including cluster-specific covariates in small-area estimation and disease mapping. Exercise 13.2 includes a comparison of random-effects and fixed-effects approaches.

13.18 Exercises

13.1 Epileptic-fit data Solutions

We now consider the famous longitudinal epilepsy data used by Thall and Vail (1990), also analyzed in the seminal paper by Breslow and Clayton (1993). The data come from a randomized controlled trial comparing the drug progabide for the treatment of epilepsy with a placebo. The outcomes are counts of epileptic seizures during the 2 weeks before each of four clinic visits.

The dataset `epilep.dta` has the following variables:

- `subj`: subject identifier (j)
- `y`: count of epileptic seizures over 2-week period (y_{ij})
- `visit`: visit time (z_{ij}) coded -0.3, -0.1, 0.1, 0.3
- `treat`: treatment group (x_{2j}) (1: progabide; 0: placebo)
- `lbas`: logarithm of quarter of number of seizures in 8 weeks preceding entry to trial (x_{3j})
- `lbas_trt`: interaction between `lbas` and `treat` (x_{4j})
- `lage`: logarithm of age (x_{5j})
- `v4`: dummy variable for fourth visit (x_{6ij})

The covariates `lbas`, `lbas_trt`, `lage`, and `v4` have all been mean centered, which will affect only the intercept β_1 in the models below.

1. Model II in Breslow and Clayton is a log-linear (Poisson regression) model with covariates `lbas`, `treat`, `lbas_trt`, `lage`, and `v4` and a normally distributed random intercept for subjects. Fit this model using `gllamm`.
2. Breslow and Clayton also considered a random-coefficient model (Model IV) using the variable `visit` instead of `v4`. The effect of `visit` z_{ij} varies randomly between subjects. The model can be written as

$$\log(\mu_{ij}) = \beta_1 + \beta_2 x_{2j} + \cdots + \beta_5 x_{5j} + \beta_6 z_{ij} + \zeta_{1j} + \zeta_{2j} z_{ij}$$

   where the subject-specific random intercept ζ_{1j} and slope ζ_{2j} have a bivariate normal distribution, given the covariates. Fit this model using `gllamm`.
3. Plot the posterior mean counts versus time for 12 patients in each treatment group.

13.2 Headache data

Here we consider data that were originally presented, described, and analyzed by McKnight and van den Eeden (1993), a subset of which were also analyzed by Hedeker (1999). A multiple-period, two-treatment, double-blind crossover trial was conducted to investigate if aspartame, an artificial sweetener, causes headaches.

The basic idea of a crossover trial is to administer both the active treatment and the placebo to each subject, hence letting the subjects serve as their own controls. Different sequences of the treatments are assigned so that period effects can be controlled for. Typically, treatment periods are separated by a washout period in an attempt to preclude carryover effects from treatment assignment in one period to the response in a following period. We refer to Jones and Kenward (2003) and Senn (2002) for detailed treatments of the design and analysis of crossover trials.

Twenty-seven patients were randomized to different sequences of aspartame (A) and placebo (P). Each sequence was preceded by a 7-day placebo run-in period

followed by four treatment periods of 7 days each. Each treatment period was separated by a washout day. Both aspartame, given at a dose of 30mg/kg/day, and placebo were administered in capsules in three doses per day. The four possible orderings of treatments after the run-in period were APAP, APPA, PAPA, and PAAP. Before beginning treatment, each subject was asked how certain he or she was of experiencing headaches after ingesting aspartame.

The dataset `headache.dta` has the following variables:

- `id`: subject identifier
- `y`: number of headaches in week i for subject j, for some subjects counted over fewer than 7 days
- `days`: number of days for which headaches were counted (t_{ij})
- `aspartame`: dummy variable for aspartame versus placebo (x_{1ij})
- `belief`: dummy variable taking the value 1 for patients who were very sure that aspartame caused him or her headaches (before treatment) and 0 otherwise (x_{2j})
- `sequence`: the sequence of treatments administered over the four treatment periods
- `period`: taking the value 1 for the run-in period and 2–5 for the four treatment periods

1. Fit the random-intercept model given below using `xtmepoisson`,

$$\begin{aligned} \log(\mu_{ij}) &= \underbrace{\ln(t_{ij})}_{\text{Offset}} + \tau_i + \beta_2 x_{1ij} + \zeta_{1j} \\ \mu_{ij} &= t_{ij} \underbrace{\exp(\tau_i + \beta_2 x_{1ij} + \zeta_{1j})}_{\text{Rate}} \end{aligned}$$

   where $\ln(t_{ij})$, the logarithm of `days`, is an offset; τ_i is a period-specific parameter; and $\zeta_{1j}|x_{ij} \sim N(0, \psi_{11})$. Interpret the estimated coefficients.
2. Extend the model to investigate whether the effect of `aspartame` depends on the prior beliefs regarding its effect (at the 5% level). Interpret your results.
3. Extend the retained model from step 2 to investigate whether there is a carryover effect of `aspartame` (again at the 5% level). Make sure that the lagged treatment takes the value 0 in period 1 for all subjects (assuming that none of the subjects used the drug in the period preceding the run-in period).
4. In the discussion section of McKnight and van den Eeden (1993), the authors highlight that a limitation of their approach is that the treatment effect is not allowed to be subject specific. Extending the model retained in step 3, investigate whether the treatment effect varies randomly between subjects.
5. Fit the selected model using `gllamm` and produce a graph showing the empirical Bayes predictions of the headache rate per day for each patient (except patient 26, who never took aspartame) versus treatment. To plot the graph, it is helpful to pick out one observation for each combination of `id` and `aspartame`

(using the `egen` function `tag()`) and to use the `connect(ascending)` option in the `twoway` command.

6. Fit the fixed-effects version of the model from step 2. Comment on any differences in the parameter estimates.

13.3 Police stops data

Gelman and Hill (2007) analyzed data on the number of times the police stopped individuals for questioning or searching on the streets of New York City. In particular, Gelman and Hill wanted to investigate whether ethnic minorities were stopped disproportionately often compared with whites. They used data collected by the police over a 15-month period in 1998–1999 in which the stops were classified by ethnicity, type of suspected crime, and the precinct (area) in which it occurred. Only the three largest ethnic groups (black, Hispanic, and white) are included here.

It could be argued that it would be reasonable if the police stopped individuals from the different ethnic groups in proportion to their population size or in proportion to the number of crimes they have committed in the past. As a proxy for the latter, Gelman and Hill (2007) use the number of arrests in 1997.

The rows in the data in `police.dta` correspond to each possible combination of ethnicity, type of crime, and precinct. The dataset contains the following variables:

- `eth`: ethnicity (1: black; 2: Hispanic; 3: white)
- `crime`: type of crime (1: violent crimes; 2: weapons offenses; 3: property crimes; 4: drug crimes)
- `precinct`: New York City precinct (1–75)
- `stops`: number of police stops over 15-month period in 1998–1999
- `arrests`: number of arrests in New York City in 1997
- `pop`: population size of each ethnic group in the precinct
- `prblack`: proportion of precinct population that is black
- `prhisp`: proportion of precinct population that is Hispanic

These data, provided with Gelman and Hill (2007), have had some noise added to protect confidentiality. In this exercise, we will analyze the data on violent crimes only, so you can delete the data on the other types of crimes.

1. For stops because of suspected violent crimes, fit a Poisson model with the number of police stops as the response variable, dummies for the ethnic minority groups (blacks and Hispanics) as explanatory variables, and with

   a. `pop` as an exposure
   b. `arrests` as an exposure

   Use robust standard errors that take the clustering within precincts into account. Interpret the estimated incidence-rate ratios for the two types of exposure, and comment on the difference.

2. Fit the model from step 1 with `arrests` as the exposure but also including `prblack` and `prhisp` as further covariates.
3. Compare the estimated incidence-rate ratios for the minority groups between the model considered in step 2 and a model that uses fixed effects for precincts instead of the covariates `prblack` and `prhisp`. Does there appear to be much precinct-level confounding in step 2?
4. Fit the model from step 2 but also include a normally distributed random intercept for precincts. Use `xtmepoisson`.
5. For the model in step 4, calculate the estimated median incidence-rate ratio, comparing the precinct that has the larger random intercept with the precinct that has the smaller random intercept for two randomly chosen precincts having the same covariate values. Interpret this estimate.
6. ❖ Extend the model from step 4 further by including random coefficients for the ethnic minority dummy variables, specifying a trivariate normal distribution for the random intercept and slopes with a freely estimated covariance matrix.
   a. Write down the model using a two-stage formulation as discussed in section 4.9.
   b. Fit the model using `xtmepoisson` (this will take a long time).
   c. Obtain empirical Bayes modal predictions of the intercepts and slopes, and plot them using a scatterplot matrix.

13.4 Patent data

Hall, Griliches, and Hausman (1986) analyzed panel data on the number of patents awarded to 346 firms between 1975 and 1979. In particular, they considered the effect of research and development (R&D) expenditures in the current and previous years. The dataset has been analyzed many times. Good discussions can be found in Cameron and Trivedi (1998; 2005), who made the data available on the web page for their 1998 book.

The variables in the dataset `patents.dta` that we will use here are

- `cusip`: Compustat's (Committee on Uniform Security Identification Procedures) identifying number for firm (j)
- `year`: year (i) (1–5)
- `pat`: number of patents applied for during the year that were eventually granted (y_{ij})
- `scisect`: dummy variable for firm being in the scientific sector
- `logk`: logarithm of the book value of capital in 1972
- `logr`: logarithm of R&D spending during the year (in 1972 dollars) [$\ln(r_{ij})$]
- `logr1`, `logr2`, ..., `logr5`: lagged `logr` variable 1 year, 2 years, ..., 5 years ago [$\ln(r_{i-1,j})$, $\ln(r_{i-2,j})$, ..., $\ln(r_{i-5,j})$]

Consider the following model, which allows the expected number of patents successfully applied for by firm j in year i to depend on the logarithms of R&D expenditure for the current and previous 5 years:

$$\ln(\mu_{ij}) = \alpha + \beta_0 \ln(r_{ij}) + \beta_1 \ln(r_{i-1,j}) + \cdots + \beta_5 \ln(r_{i-5,j}) \tag{13.14}$$

We can consider the effect of multiplying the expenditures for all years for a given firm by a constant a:

$$\ln(\mu_{ij}^a) = \alpha + \beta_0 \ln(ar_{ij}) + \beta_1 \ln(ar_{i-1,j}) + \cdots + \beta_5 \ln(ar_{i-5,j})$$

Taking derivatives with respect to a (using the chain rule), we find that

$$\begin{aligned} \frac{\partial \ln(\mu_{ij}^a)}{\partial a} = \frac{1}{\mu_{ij}^a} \frac{\partial \mu_{ij}^a}{\partial a} &= \beta_0 \frac{r_{ij}}{ar_{ij}} + \beta_1 \frac{r_{i-1,j}}{ar_{i-1,j}} + \cdots + \beta_5 \frac{r_{i-5,j}}{ar_{i-5,j}} \\ &= \frac{1}{a}(\beta_0 + \beta_1 + \cdots + \beta_5) \end{aligned}$$

so that the *elasticity* is (see also display 6.2)

$$\left(\frac{\partial \mu_{ij}^a}{\partial a}\right)\left(\frac{a}{\mu_{ij}^a}\right) = \frac{\partial \mu_{ij}^a}{\mu_{ij}^a} \Big/ \frac{\partial a}{a} = \beta_0 + \beta_1 + \cdots + \beta_5$$

The sum of the coefficients therefore represents the relative or percentage change in the expected number of patents per percentage change in total expenditures over the last 5 years (a given percentage change in a amounts to the same percentage change in ax).

1. Fit a Poisson model with the mean modeled as shown in (13.14) but also include a normally distributed random intercept for firm j and four dummy variables for years 2 to 5. Use `gllamm` with the `robust` option to obtain reasonable inferences even if there is overdispersion at level 1.
2. Use `lincom` to obtain the sum of the estimated coefficients of the contemporaneous and lagged log expenditures (the elasticity) and its 95% confidence interval. Also use the `test` or `lincom` command to test the null hypothesis that the elasticity is 1 at the 5% level of significance. Comment on your finding.
3. Repeat the above analysis (steps 1 and 2) also controlling for `logk`, a measure of the size of the firm, and `scisect`, a dummy variable for the firm being in the scientific sector.

13.5 School-absenteeism data

These data come from a sociological study by Quine (1973) and have previously been analyzed by Aitkin (1978). The sample included Australian aboriginal and white children from four age groups (final year in primary school and first 3 years in secondary school) who were classified as slow or average learners. The number

of days absent from school during the school year was recorded for each child (children who had suffered a serious illness during the year were excluded).

The dataset `absenteeism.dta` has the following variables:

- `id`: child identifier
- `days`: number of days absent from school in one year
- `aborig`: dummy variable for child being aboriginal (versus white)
- `girl`: dummy variable for child being a girl
- `age`: age group (1: last year in primary school; 2: first year in secondary school; 3: second year in secondary school; 4: third year in secondary school)
- `slow`: dummy variable for child being a slow learner (1: slow; 0: average)

1. Use the `glm` command to fit an ordinary Poisson model with `aborig`, `girl`, dummy variables for age groups 2 to 4, and `slow` as covariates.
2. Repeat the analysis but this time use quasilikelihood estimation to include an overdispersion parameter ϕ. How have the estimates and standard errors changed?
3. Fit a negative binomial model of type NB1 and compare the estimated overdispersion factor with that estimated in step 2.
4. Use `xtpoisson` to include a normally distributed random intercept for children.
5. Write down the model of step 4, and interpret the estimates.

13.6 Lip-cancer data

1. Extend the model considered in section 13.15 by including `x`, the percentage of the population working in agriculture, fishing, or forestry, as a covariate.
   a. Write down the model and state all assumptions.
   b. Fit the model using `gllamm`.
   c. Interpret the exponentiated estimated coefficient of `x`.
2. Obtain the predicted standardized mortality ratios (SMRs) for this model.

13.7 Skin-cancer data

Langford and Lewis (1998) analyzed data from the Atlas of Cancer Mortality in the European Economic Community (Smans, Muir, and Boyle 1993). Malignant-melanoma (skin cancer) mortalities were defined as deaths recorded and certified by a medical practitioner as ICD-8 172 (ICD is an abbreviation of International Classification of Diseases). The data were collected between 1971 and 1980, although for the United Kingdom, Ireland, Germany, Italy, and The Netherlands, data were only available from 1975–1976 onward and are aggregated over the period of data collection. Because incidence was generally rising during this period, it is important to include nation as a variable in the analysis.

The geographical resolution of the data, referred to here as counties, was European Economic Community (EEC) levels II or III (identified by EEC statistical services).

For example, these units are counties in England and Wales, départements in France and Regierungsbezirke in (West) Germany. Regions are the EEC level-I areas.

The main research question is how malignant melanoma (skin cancer) is associated with ultraviolet (UV) radiation exposure.

Seven variables are included in the dataset `skincancer.dta`:

- `nation`: nation identifier (labeled)
  1. Belgium
  2. W. Germany
  3. Denmark
  4. France
  5. UK
  6. Italy
  7. Ireland
  8. Luxembourg
  9. Netherlands
- `region`: region identifier (EEC level-I areas)
- `county`: county identifier (EEC level-II and level-III areas)
- `deaths`: number of male deaths due to malignant melanoma (skin cancer) during 1971–1980 (1976–1980 for some countries)
- `expected`: expected number of male deaths due to malignant melanoma during 1971–1980 (1976–1980 for some countries), calculated from crude rates for all countries combined
- `uv`: epidemiological index of UV dose reaching the earth's surface in each county (see Langford and Lewis [1998]), mean centered

1. Fit a Poisson model for the number of male deaths from skin cancer using the log expected number of male deaths as an offset, dummy variables for the nations as covariates, and a normally distributed random intercept for counties. Use `gllamm`.
2. Write down the model, and interpret the estimates.
3. Refit the model including `uv` and squared `uv` as further covariates.
4. Obtain predictions of the fixed part of the linear predictor without the offset (using the `xb` and `nooffset` options), and plot these against `uv` by nation. Interpret the graph.
5. For the model in step 3, obtain empirical Bayes predictions of the SMR for each county (as a percentage). Summarize the SMRs by nation.

See also exercise 16.7 for a four-level model for these data.

Part VII

Models for survival or duration data

Introduction to models for survival or duration data (part VII)

In this part, we consider survival data, also referred to as failure-time, time-to-event, event-history, or duration data. Examples include time between surgery and death, duration in first employment, time to failure of light bulbs, and time to dropout from school.

The variable of main interest in survival analysis is the time from some event, such as the beginning of employment, to another event, such as unemployment. A unit or subject is said to become *at risk* of (or be eligible for) the event of interest after the initial event has occurred. Alternatively, we can view the response variable as the duration spent in origin state (employment) until transition to the destination state (unemployment). A state is called *absorbing* if it is impossible to leave the state, a canonical example being death.

Special methods are needed for survival data mainly because of right-censoring, where the time of the event is not known exactly for some subjects because the event has not happened by the end of the observation period. Left-truncation can also occur, where subjects are not included in the study if the event happened before the beginning of the study. A nice feature of survival analysis is that time-varying covariates can be included.

Defining analysis time: The origin

When analyzing the time to an event, perhaps the most important consideration is the origin of the time scale, the point in time when the clock starts ticking and the subject becomes at risk of experiencing the event. For instance, in studies of breast cancer mortality, time from birth until death from breast cancer may be less meaningful than time from menarche (onset of menstruation) since the risk of breast cancer before menarche is negligible. For divorce, the relevant duration may be time since marriage or perhaps the time since cohabitation, because the process leading to break-up may well begin when the couple starts living together. In general mortality studies, the origin is usually not conception, but birth, or in perinatal mortality, the origin is foetal viability (22 weeks of gestation) and death up to 7 days after birth is considered. Perinatal mortality can obviously have very different causes than death after infancy.

The origin may differ from the start of observation, depending on the research design. We use the term *analysis time* for the time scale that takes the value 0 at the origin, which is consistent with Stata's terminology. In clinical trials, the origin is typically the time at which treatment and placebo are administered, and the time at which patients become at risk coincides with the start of the observation period. In observational studies, such as epidemiological cohort studies, analysis time will often be age. For this reason, there is often delayed entry, where subjects have already been at risk before they enter the study. In Stata's `stset` command for defining survival data, the `origin()` option is used to specify the origin (when subjects become at risk), whereas the `enter()` option is used to specify the start of the observation period. When the entry time is later than the origin, we have delayed entry.

In some studies, several time scales may be relevant, for instance, both the age (time since birth) and the time from onset of exposure to a risk factor. In this case, one time scale is chosen as analysis time and the other time scales can be used as time-varying covariates.

Defining the event: Competing events and censoring

Another important consideration is the definition of the event itself. For instance, when studying teacher turnover, the event could be leaving the school, and right-censoring occurs if the teacher is still employed by the same school at the end of the observation period or is lost to follow-up. An important assumption in standard survival analysis is *independent censoring*, which means that the censoring time is independent of the survival time given the covariates in the model.

Unfortunately, it is not always obvious how to define the event. Teachers could leave the school because of dismissal, retirement, change of career, or change of school, among other reasons. We could define the event as exiting employment at the school regardless of the reason. However, by doing so, we implicitly assume that effects of covariates do not depend on the reason for exiting, and this may be unrealistic. Alternatively, we could define the event as change of school or change of career. The other reasons (for example, dismissal and retirement) can be thought of as competing events because their occurrence precludes occurrence of the event of interest. Analysis of the times to several events is called competing-risk analysis, and the models are called competing-risk or multistate models. If the survival times of the different events are not conditionally independent given the covariates, joint modeling is complex and requires unverifiable assumptions. Under conditional independence and in the case of continuous time, each event can be analyzed separately, treating all other events as censoring. In the discrete-time case, it is not possible to analyze the events separately, but joint modeling is straightforward.

Different kinds of censoring and truncation

The left panel of figure VII.1 shows the event histories of several hypothetical units or subjects in terms of calendar time. The lines start when the subjects become at risk of experiencing the event of interest (the origin). For most subjects, the line ends when the event occurs, as indicated by a •. The vertical lines represent the beginning and end of the observation period, from the recruitment of subjects into the study until the end of the study. The right panel of the figure shows the same event histories as the left panel but now the time axis represents *analysis time* with origin defined as the onset of risk. On the analysis time scale, the time when the event occurs is the survival time or duration. Here B and E represent the beginning and end of the time spent in the study, in terms of analysis time.

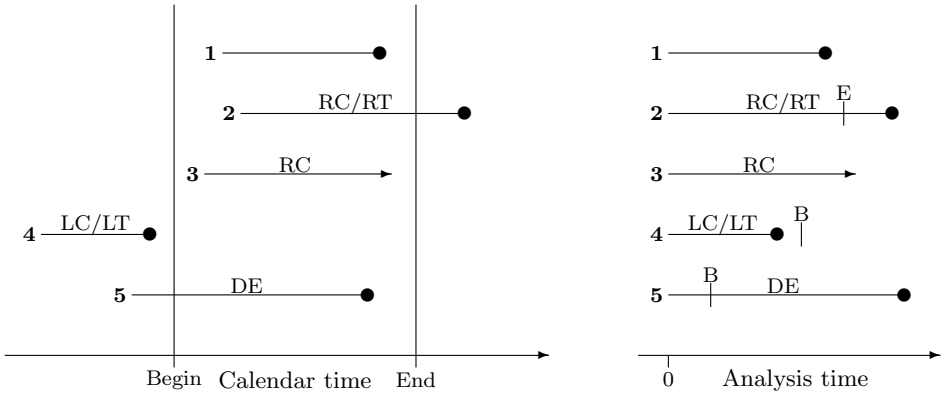


Figure VII.1: Illustration of different types of censoring and truncation in calendar time (left panel) and analysis time (right panel). Dots represent events and arrowheads represent censoring.

Subject 1, represented by the top line in the figure, is ideal in the sense that he becomes at risk within the observation period and experiences the event within the observation period, so the survival time is known.

When *censoring* occurs, the survival time is not exactly known. In one form of right-censoring (RC), often called generalized type I censoring, the event does not occur before the end of the observation period, and all we know is that the survival time exceeds the time between becoming at risk and the end of the observation period (situation 2 in the figure). Another form of right-censoring occurs when the subject stops being at risk of the event under investigation before the end of the observation period; for instance, he may experience a competing event such as dying from a disease other than the one under investigation or he may drop out of the study. For this type of censoring, the time the subject ceases to be at risk is indicated by an arrowhead (situation 3). It is usually assumed that censoring is noninformative in the sense that the survival times for the competing events are conditionally independent of the survival time of interest, given the covariates (also known as *independent censoring*).

When all that is known is that the event occurred before observation began (situation 4), the survival time is called left-censored (LC). For example, the event of interest may be onset of drug use, but all we may know at the start of observation is that a person has used drugs but not when he or she started this practice. Left-censoring is less common than right-censoring because in most studies observation begins when subjects become at risk for the event or those who have already experienced the event are not eligible for inclusion in the study.

In *current status data*, each subject is either left- or right-censored. For instance, surveys sometimes ask individuals whether they have had their sexual debut, producing a left-censored response at their current age if the answer is yes and a right-censored response if the answer is no.

When we only know that the event occurred within a time interval, but not precisely when it occurred, we say that the time is *interval-censored*. For instance, time of HIV infection may be known only to lie between the dates of a negative and positive HIV test, employment status may be known only at each wave of a panel survey, and age at first marriage may be rounded to years. Interval-censoring is also sometimes referred to as grouping and the resulting data as grouped-time survival data if the censoring limits are the same for all subjects.

Truncation occurs when a subject is not included in the study because of the timing of his or her event. *Left-truncation* (LT) occurs when subjects are excluded from the study because the event of interest occurred *before* observation began (situation 4). This can happen only if subjects become at risk before observation begins (situations 4 and 5 in the figure). Situation 5, where the subject enters the study after having already been at risk for a period, is called *delayed entry* (DE). Delayed entry and left-truncation are common in epidemiological cohort studies where only disease-free individuals are typically followed up, thus including subjects who have already been at risk and excluding subjects who developed the disease before observation began. We will discuss delayed entry and left-truncation in more detail in section 14.2.6.

Right-truncation (RT) occurs when a subject is excluded from the study because his event happened *after* the end of the observation period (situation 2). This can happen in retrospective studies, for instance, when investigating the incubation period of AIDS in patients who have developed the disease. Any person who has yet to experience the event is then not included in the study because he is not known to be at risk.

In chapters 14 and 15, we discuss methods that are suitable when left-truncation and right-censoring occur, but we assume that there is no left-censoring or right-truncation. As discussed in the *Discrete- versus continuous-time survival data* section of this introduction, interval-censoring can also be handled and is indeed one of the reasons why discrete-time methods may be appropriate, rather than continuous-time methods.

Time-varying covariates and different time scales

A special feature of survival data is *time-varying covariates*—covariates that can change between the time a person becomes at risk and experiences the event. For instance, if the event is reoffending after release from prison, employment status could be a time-varying covariate. A person's risk of reoffending could be lower during periods of employment than during periods of unemployment. Any aspect of the covariate history might be of interest, such as ever being employed after release from prison, the number of times employed, or the proportion of time or length of time employed. All of these aspects are time varying as the employment history unfolds.

In epidemiology, the risk of lung cancer among underground miners may be affected by exposure to radioactive radon gas, and therefore, the cumulative radon exposure (if regular measurements have been taken) or the length of employment as a miner, are potential time-varying covariates.

As discussed in *Introduction to models for longitudinal and panel data (part III)*, several different time scales can be of interest. The survival time itself is an age-like time scale because it is the time since the subject-specific event of becoming at risk (which is birth in studies of longevity). Period (current calendar time) and cohort (calendar time when becoming at risk) may also be of interest. Unless all subjects became at risk at the same calendar time, one of these time scales can be included, and period would be a time-varying covariate. The subject-specific timing of other events may also be of interest. For instance, if analysis time is age, time since start of employment as a miner (or exposure to other risk factors) could be included. Similarly, if the origin is time of surgery, age could be included as a time-varying covariate, or alternatively, age at the time of surgery could be included as a time-constant covariate.

Discrete- versus continuous-time survival data

It is useful to distinguish between discrete-time survival data and continuous-time survival data.

In *continuous-time survival data*, the exact survival and censoring times are recorded in relatively fine time units. Methods for continuous time can then be used, some of which assume that all survival times are unique and that there are no pairs of individuals with identical or *tied* survival times. We will discuss modeling of continuous-time survival data in chapter 15.

In chapter 14, we will consider *discrete-time survival data* characterized by relatively few possible survival (or censoring) times with many subjects sharing the same survival time. Discrete-time data can result from interval-censoring, where the event occurs in continuous time but we only know the time interval within which it occurred. In this case, we assume that the beginning and end of each interval is the same for all subjects in analysis time. Alternatively, the time scale is sometimes inherently or intrinsically discrete, examples being the number of menstrual cycles to conception and the number of elections to a change of government.

Multilevel and recurrent-event survival data

In one type of multilevel survival data, the subjects experience an event (for instance, death) that is *absorbing* (can only occur once), and subjects are nested in clusters, such as hospitals. An alternative type of multilevel survival data, sometimes called multivariate survival data, multiple spell data, or multiepisode data, arises if subjects can experience multiple events, either events of different types or the same event repeatedly. The latter type of data are called *recurrent-event* data. Several decisions must be made when analyzing such multiple-event data. For instance, is a subject at risk of the kth event before experiencing the $(k-1)$th event? Does the risk of an event depend on whether other events have already occurred? The answers to these questions determine the definition of analysis time and other aspects of the analysis. These issues for recurrent-event data are discussed in section 15.12 of the chapter on continuous-time survival. The same issues apply to discrete-time survival.

14 Discrete-time survival

14.1 Introduction

As discussed in *Introduction to models for survival or duration data (part VII)*, in discrete-time survival data there are just a few possible survival times shared by many subjects. This can be due to *interval-censoring*, where an event actually occurs in continuous time but the researcher only knows the time interval within which the event occurred. For instance, employment status may be known only at panel waves in longitudinal surveys. Another form of interval censoring is using coarse time-scales, for instance, expressing time to events in years. Alternatively, time scales can be *inherently or intrinsically discrete*. Examples include the number of menstrual cycles to conception and the number of elections to a change of government.

Discrete-time survival models are specified in terms of the discrete-time *hazard*, defined as the conditional probability of the event occurring at a time point given that it has not already occurred. A convenient feature of these survival models is that they become models for dichotomous responses when the data have been expanded to so-called person–period data. Standard logit and probit models can then be used, as well as complementary log-log models that have not been introduced yet. It is a good idea to read chapter 10 before embarking on this chapter.

We discuss multilevel discrete-time survival models where random effects, often called *frailties* in this context, are included to handle unobserved heterogeneity between clusters and within-cluster dependence. Discrete-time frailty models are applied to data on time from birth to death (or censoring) for different children nested in mothers.

14.2 Single-level models for discrete-time survival data

14.2.1 Discrete-time hazard and discrete-time survival

We now consider data used by Long, Allison, and McGinnis (1993) and provided with the book by Allison (1995). Three hundred one male biochemists who received their doctorates in 1956 or 1963 and were assistant professors at research universities in the United States some time in their careers were followed up for 10 years from the beginning of their assistant professorships.

The event of interest is promotion to associate professor, which usually corresponds to receiving tenure (a permanent position). Promotions typically take effect at a specific

date of the year, making the survival time to promotion inherently discrete. Censoring occurs when assistant professors leave their research university for a job outside academia or for a position at a college or university in which teaching is the primary mission. If some of these transitions occur because of concerns about not being able to pass tenure, the survival and censoring times are not independent given the covariates and censoring becomes informative, unless these concerns are captured by the covariates in the model. Here we assume independent censoring.

The promotions data can be read in by typing

```
. use http://www.stata-press.com/data/mlmus3/promotion
```

Initially, we will not include covariates and only use the following variables:

- `id`: person identifier
- `dur`: number of years from beginning of assistant professorship to promotion or censoring
- `event`: dummy variable for promotion to associate professor (1: promoted; 0: censored)

We will use the notation T for the time in years to promotion, which can take on integer values $t = 1, 2, \ldots, 10$. If the variable `event` equals 1, we know that T equals `dur`, and if `event` equals 0, we know that T is greater than `dur`.

Discrete-time survival models are specified in terms of the *discrete-time hazard*, defined as the conditional probability that the event occurs at time t, given that it has not yet occurred:

$$h_t \equiv \Pr(T = t | T > t - 1) = \Pr(T = t | T \geq t)$$

Stata's `ltable` command for life tables provides us with all the information we need to estimate these hazards:

```
. ltable dur event, noadjust
```

Interval		Beg. Total	Deaths	Lost	Survival	Std. Error	[95% Conf.	Int.]
1	2	301	1	1	0.9967	0.0033	0.9767	0.9995
2	3	299	1	6	0.9933	0.0047	0.9737	0.9983
3	4	292	17	12	0.9355	0.0143	0.9008	0.9584
4	5	263	42	10	0.7861	0.0243	0.7337	0.8294
5	6	211	53	9	0.5887	0.0297	0.5280	0.6442
6	7	149	46	7	0.4069	0.0303	0.3473	0.4656
7	8	96	31	6	0.2755	0.0282	0.2217	0.3319
8	9	59	15	2	0.2055	0.0262	0.1567	0.2590
9	10	42	7	6	0.1712	0.0248	0.1258	0.2227
10	11	29	4	25	0.1476	0.0241	0.1043	0.1981

(See section 14.4 for an explanation of the `noadjust` option.)

We see that there are 301 individuals at the beginning of the first year, one of whom gets promoted (somewhat inappropriately for this particular application denoted as `Deaths` in the output) and one of whom is censored (`Lost`). The estimated hazard for this interval is $\widehat{h}_1 = 1/301 = 0.0033$. At the beginning of year 2, there are 299 individuals left in the sample who have not yet experienced the event (301 minus 1 promoted minus 1 censored) and are hence *at risk*. One of these individuals gets promoted in year 2, so $\widehat{h}_2 = 1/299 = 0.0033$. For the following years, we have $\widehat{h}_3 = 17/292 = 0.0582$, $\widehat{h}_4 = 42/263 = 0.1597$, $\widehat{h}_5 = 53/211 = 0.2512$, $\widehat{h}_6 = 46/149 = 0.3087$, $\widehat{h}_7 = 31/96 = 0.3229$, $\widehat{h}_8 = 15/59 = 0.2542$, $\widehat{h}_9 = 7/42 = 0.1667$, and $\widehat{h}_{10} = 4/29 = 0.1379$. The individuals who are at risk at a given interval and contribute to the denominator for the estimated hazard are called the *risk set* for that interval.

We can obtain these estimated hazards directly using the `ltable` command with the `hazard` and `noadjust` options:

```
. ltable dur event, hazard noadjust
```

Interval		Beg. Total	Cum. Failure	Std. Error	Hazard	Std. Error	[95% Conf.	Int.]
1	2	301	0.0033	0.0033	0.0033	0.0033	0.0001	0.0123
2	3	299	0.0067	0.0047	0.0033	0.0033	0.0001	0.0123
3	4	292	0.0645	0.0143	0.0582	0.0141	0.0339	0.0890
4	5	263	0.2139	0.0243	0.1597	0.0246	0.1151	0.2115
5	6	211	0.4113	0.0297	0.2512	0.0345	0.1882	0.3232
6	7	149	0.5931	0.0303	0.3087	0.0455	0.2260	0.4041
7	8	96	0.7245	0.0282	0.3229	0.0580	0.2194	0.4461
8	9	59	0.7945	0.0262	0.2542	0.0656	0.1423	0.3981
9	10	42	0.8288	0.0248	0.1667	0.0630	0.0670	0.3109
10	11	29	0.8524	0.0241	0.1379	0.0690	0.0376	0.3023

We see that the estimated hazard reaches a maximum in year 7 and then declines; those who have not been promoted by the end of year 9 have only a 14% chance of being promoted in year 10. Perhaps some of these assistant professors will never be promoted.

The discrete-time survival function is the probability of not experiencing the event by time t,

$$S_t \equiv \Pr(T > t)$$

For $t = 1$, this is simply 1 minus the probability that the event occurs at time 1 (given that it has not yet occurred, which is impossible), $S_1 = (1 - h_1)$. For $t = 2$, S_2 is the probability that the event did not occur at time 1 and that it did not occur at time 2, given that it did not occur at time 1, and can be expressed as $S_2 = \Pr(T > 2) = \Pr(T > 2|T > 1)\Pr(T > 1) = (1 - h_2)(1 - h_1)$. In general, we have

$$S_t \;=\; \prod_{s=1}^{t}(1 - h_s) \tag{14.1}$$

Substituting the estimated hazards gives the estimated survival function given under `Survival` in the output of the `ltable` command when the `hazard` option was not

used, as shown on page 750. The cumulative failure function $1 - S_t$ is given under `Cum. Failure` in the output of the `ltable` command with the `hazard` option. The `ltable` command provides estimated standard errors for the survival function, the cumulative failure function, and the hazard function.

14.2.2 Data expansion for discrete-time survival analysis

By expanding the data appropriately and defining a binary variable, `y`, taking the values 0 and 1, we can obtain the estimated hazards as the proportions of 1s observed each year. As we will see later, this data expansion is necessary for conducting the most common type of discrete-time survival analysis.

Consider the first two individuals in the data:

```
. list id dur event if id<3, noobs
```

id	dur	event
1	10	0
2	4	1

The person with `id`=1 was censored at $t = 10$ because `event` takes the value 0 when `dur` is 10. This person therefore represents 1 of the 301 individuals at risk in year 1 (that is, is part of the risk set in year 1), 1 of the 299 individuals at risk in year 2, and so forth up to and including year 10. In the expanded dataset, this person should contribute one observation for each of the 10 years, with `y` equal to zero, so that the observation contributes to the denominator but not to the numerator of the estimated hazard. Similarly, the person with `id`=2 should be represented by four observations, for years 1–4, because the professor experiences the event at $t = 4$. For the first 3 years, `y` should be 0. For the fourth year, `y` should be 1 because the event occurs that year, and the observation should contribute to the numerator as well as the denominator of the estimated hazard. After having experienced the event, the professor no longer belongs to the risk set for promotion and therefore does not contribute more than four observations.

In general, each person should be represented by a row of data for each year the person was at risk. We therefore expand the data to obtain `dur` rows per person:

```
. expand dur
```

We then create a new variable, `year`, that labels the years,

```
. by id, sort: generate year = _n
```

and list the expanded data for the first two individuals:

```
. list id dur year event if id<3, sepby(id) noobs
```

id	dur	year	event
1	10	1	0
1	10	2	0
1	10	3	0
1	10	4	0
1	10	5	0
1	10	6	0
1	10	7	0
1	10	8	0
1	10	9	0
1	10	10	0
2	4	1	1
2	4	2	1
2	4	3	1
2	4	4	1

The response variable y should be 1 if a promotion occurs for the person that year and 0 otherwise.

```
. generate y = 0
. replace y = event if year==dur
```

The expansion of the data for the first two professors is also shown in figure 14.1.

Original data

id	dur	event
1	10	0
2	4	1

$\longrightarrow$

Person–year data

id	year	y
1	1	0
1	2	0
1	3	0
1	4	0
1	5	0
1	6	0
1	7	0
1	8	0
1	9	0
1	10	0
2	1	0
2	2	0
2	3	0
2	4	1

Figure 14.1: Expansion of original data to person–year data for first two assistant professors (first one right-censored in year 10, second one promoted in year 4)

The data are now in person–year or person–period form, where each year of observation for each assistant professor has one record or observation for each period he or she is at risk of being promoted.

14.2.3 Estimation via regression models for dichotomous responses

We can obtain the sample hazards or estimated hazards $\widehat{h}_t$ for each year t by finding the proportion of 1s each year, for instance, using the `tabulate` command:

```
. tabulate year y, row
```

Key
frequency *row percentage*

year	y 0	1	Total
1	300	1	301
	99.67	0.33	100.00
2	298	1	299
	99.67	0.33	100.00
3	275	17	292
	94.18	5.82	100.00
4	221	42	263
	84.03	15.97	100.00
5	158	53	211
	74.88	25.12	100.00
6	103	46	149
	69.13	30.87	100.00
7	65	31	96
	67.71	32.29	100.00
8	44	15	59
	74.58	25.42	100.00
9	35	7	42
	83.33	16.67	100.00
10	25	4	29
	86.21	13.79	100.00
Total	1,524	217	1,741
	87.54	12.46	100.00

The penultimate column in the output above gives the estimated hazards as percentages, and these agree with the estimated hazards on page 751 produced by the `ltable` command.

Alternatively, we can obtain estimated hazards as predicted probabilities by using a logistic regression model where the covariates are dummy variables for each year,

$$\text{logit}\{\Pr(y_{si}=1|\mathbf{d}_{si})\} \;=\; \alpha_1+\alpha_2 d_{2si}+\cdots+\alpha_{10}d_{10,si}$$

Here y_{si} is an indicator for the event occurring at time s for person i; d_{2si}, ..., $d_{10,si}$ are dummy variables for years 2–10; and $\mathbf{d}_{si}=(d_{2si},\ldots,d_{10,si})'$ is a vector containing all the dummy variables for professor i.

The Stata command to fit this model by maximum likelihood is

```
. logit y i.year
Logistic regression                               Number of obs   =       1741
                                                  LR chi2(9)      =     251.17
                                                  Prob > chi2     =     0.0000
Log likelihood = -529.15641                       Pseudo R2       =     0.1918

------------------------------------------------------------------------------
           y |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
        year |
          2  |    .006689   1.416576     0.00   0.996    -2.76975    2.783128
          3  |   2.920224   1.032372     2.83   0.005    .8968116    4.943637
          4  |   4.043289    1.01571     3.98   0.000    2.052533    6.034045
          5  |   4.611479   1.014165     4.55   0.000    2.623753    6.599205
          6  |   4.897695   1.017242     4.81   0.000    2.903937    6.891452
          7  |   4.963382   1.025171     4.84   0.000    2.954084     6.97268
          8  |   4.627643   1.045336     4.43   0.000    2.578822    6.676463
          9  |   4.094344   1.083864     3.78   0.000    1.970009    6.218679
         10  |   3.871201   1.137248     3.40   0.001    1.642236    6.100166
             |
       _cons |  -5.703782   1.001665    -5.69   0.000    -7.66701   -3.740555
------------------------------------------------------------------------------
```

where the `i.` preceding the covariate `year` produces dummy variables for `year` and includes them in the model, omitting the dummy variable for year 1. Predicted probabilities, which here correspond to estimated discrete-time hazards, can be obtained using the `predict` command with the `pr` option:

```
. predict haz, pr
```

Finally, we list the estimated hazards, the time-specific event indicator y_{is} and the variable `event`, for the years where each of the first two assistant professors in the dataset are at risk of promotion:

```
. list id year haz y event if id<3, sepby(id) noobs
```

id	year	haz	y	event
1	1	.0033223	0	0
1	2	.0033445	0	0
1	3	.0582192	0	0
1	4	.1596958	0	0
1	5	.2511848	0	0
1	6	.3087248	0	0
1	7	.3229167	0	0
1	8	.2542373	0	0
1	9	.1666667	0	0
1	10	.137931	0	0
2	1	.0033223	0	1
2	2	.0033445	0	1
2	3	.0582192	0	1
2	4	.1596958	1	1

The estimated hazards are identical to those obtained using the `ltable` command. We could use any other link function, such as the probit link or the complementary log-log link introduced in section 14.6, to obtain the same predicted hazards.

We can plot the discrete-time hazards by selecting an assistant professor who has observations for all periods, such as professor 1 (the same results would be obtained here if we picked another professor), and using the `twoway` command,

```
. twoway (line haz year if id==1, connect(stairstep)), legend(off)
> xtitle(Year) ytitle(Discrete-time hazard)
```

which produces the graph in figure 14.2.

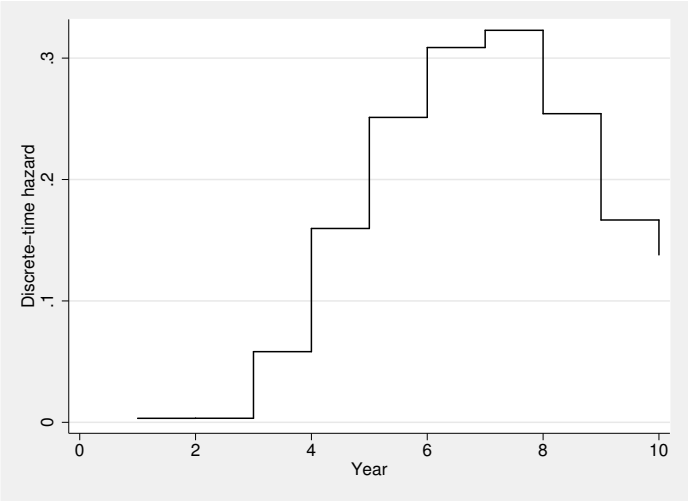


Figure 14.2: Discrete-time hazard (conditional probability of promotion given that promotion has not yet occurred)

Here we have used the `connect(stairstep)` option to plot a step function (but you can omit this option).

The likelihood from the binary regression models based on the expanded data is just the required likelihood for discrete-time survival data, and the resulting predicted hazards are maximum likelihood estimates. To see this, consider the required likelihood contribution for a person who was censored at time t, which is just the corresponding probability $S_{ti} \equiv \Pr(T_i > t)$. From (14.1), this probability is given by

$$S_{ti} = \prod_{s=1}^{t}(1 - h_{si})$$

where h_{si} is the discrete-time hazard at time s for person i. In the expanded dataset, someone who is censored at time t is represented by a row of data for $s = 1, 2, \ldots, t$ with $\mathtt{y} = 0$. The corresponding likelihood contributions from binary regression are the model-implied probabilities of the observed responses, $\Pr(y_{si} = 0) = (1 - h_s)$, and these are simply multiplied together because the observations are taken as independent, giving the required likelihood contribution for discrete-time survival.

For an assistant professor who was promoted at time t, the likelihood contribution should be

$$\begin{aligned}\Pr(T_i = t) &= \Pr(T_i = t|T_i > t-1)\Pr(T_i > t-1) \\ &= h_{ti}\prod_{s=1}^{t-1}(1 - h_{si})\end{aligned}$$

Such a person is represented by a row of data for $s = 1, 2, \ldots, t$ with y equal to zero for $s \leq t-1$ and y equal to 1 for $s = t$. The likelihood contribution from binary regression is therefore $\Pr(y_{1i} = 0) \times \cdots \times \Pr(y_{t-1,i} = 0) \times \Pr(y_{ti} = 1)$ as required.

We can interpret the logistic regression model as a linear model for the logit of the discrete-time hazard,

$$\text{logit}\{\Pr(y_{si} = 1|\mathbf{d}_{si})\} = \alpha_1 + \alpha_2 d_{2si} + \cdots + \alpha_{10} d_{10,si} = \text{logit}\{\underbrace{\Pr(T_i = s|T_i \geq s, \mathbf{d}_{si})}_{h_{si}}\}$$

No functional form is imposed on the relationship between discrete-time hazard and year because dummy variables are used for years 2–10 (the intercept represents year 1).

14.2.4 Including covariates

Although it is interesting to investigate how the population-averaged or marginal hazard evolves over time, the main purpose of survival analysis is usually to estimate the effects of covariates on the hazard. Here regression models become useful.

Time-constant covariates

The following time-constant or person-specific covariates are available:

- `undgrad`: selectivity of undergraduate institution (scored from 1–7) (x_{2i})
- `phdmed`: dummy variable for having a PhD from a medical school (1: yes; 0: no) (x_{3i})
- `phdprest`: a measure of prestige of the PhD institution (ranges from 0.92 to 4.62) (x_{4i})

We specify a logistic regression for the expanded data with these three covariates added to the dummy variables for years 2–10,

$$\text{logit}\{\Pr(y_{si} = 1|\mathbf{d}_{si}, \mathbf{x}_i)\} = \alpha_1 + \alpha_2 d_{2si} + \cdots + \alpha_{10} d_{10,si} + \beta_2 x_{2i} + \beta_3 x_{3i} + \beta_4 x_{4i}$$

where $\mathbf{x}_i = (x_{2i}, x_{3i}, x_{4i})'$ is the vector of covariates. The first part of the linear predictor, from α_1 to $\alpha_{10} d_{10,si}$ determines the so-called *baseline hazard*, the hazard when the covariates $\mathbf{x}_i$ are all zero. The model could be described as semiparametric because no assumptions are made regarding the functional form for the baseline hazard, whereas the effects of covariates are assumed to be linear and additive on the logit scale.

We can fit this model by using the `logit` command:

```
. logit y i.year undgrad phdmed phdprest
Logistic regression                             Number of obs   =       1741
                                                LR chi2(12)     =     260.79
                                                Prob > chi2     =     0.0000
Log likelihood = -524.34273                     Pseudo R2       =     0.1992

------------------------------------------------------------------------------
           y |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
        year |
          2  |   .0063043   1.416703     0.00   0.996    -2.770383    2.782991
          3  |   2.923036   1.032552     2.83   0.005      .899272    4.946801
          4  |   4.051509   1.015925     3.99   0.000     2.060334    6.042685
          5  |   4.619307    1.01441     4.55   0.000     2.631099    6.607514
          6  |   4.924625   1.017614     4.84   0.000     2.930139    6.919111
          7  |   4.992068   1.025703     4.87   0.000     2.981728    7.002409
          8  |    4.69053   1.046322     4.48   0.000     2.639776    6.741284
          9  |   4.167769   1.085192     3.84   0.000     2.040833    6.294706
         10  |   3.964635   1.139095     3.48   0.001      1.73205    6.197219
             |
     undgrad |   .1576609     .06007     2.62   0.009      .039926    .2753959
      phdmed |  -.0950034   .1665181    -0.57   0.568    -.4213728    .2313661
    phdprest |   .0650372   .0854488     0.76   0.447    -.1024394    .2325138
       _cons |   -6.67189   1.081551    -6.17   0.000    -8.791692   -4.552088
------------------------------------------------------------------------------
```

This model assumes that the difference in log odds between individuals with different covariates is constant over time. For instance, the predicted log odds of individuals 1 and 4 (both of whom have 10 observations and who differ in all three covariates) can be obtained and plotted by typing

```
. predict lo, xb
. twoway (line lo year if id==1, connect(stairstep) lpatt(solid))
> (line lo year if id==4, connect(stairstep) lpatt(dash)),
> legend(off) xtitle(Year) ytitle(Log odds)
```

giving the graph in figure 14.3.

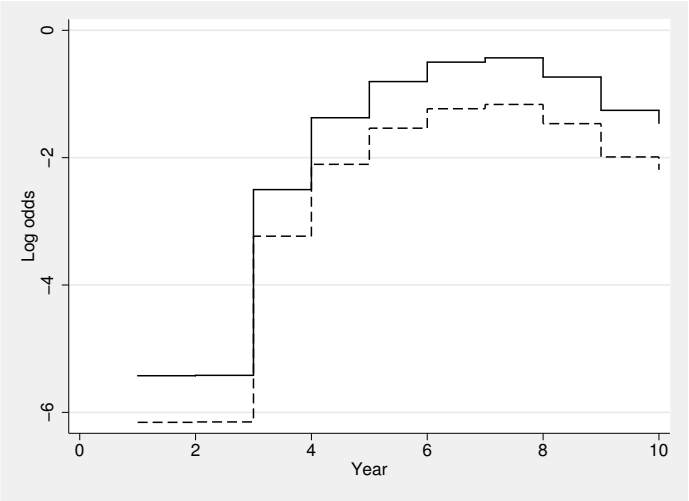


Figure 14.3: Predicted log odds of promotion given that promotion has not yet occurred for professors 1 (solid) and 4 (dashed)

A constant difference in the log odds corresponds to a constant ratio of the odds. For this reason, the model is often called a *proportional odds model*, not to be confused with the ordinal logistic regression model of the same name discussed in chapter 11. We will see in section 14.6 how time-varying covariates can be used to relax the proportionality assumption.

The model is also referred to as a *continuation-ratio logit* model or sequential logit model because the logit can be written as

$$\begin{aligned}
\text{logit}\{\Pr(T_i = s|T_i \geq s, \mathbf{d}_i, \mathbf{x}_i)\} &= \underbrace{\ln\left\{\frac{\Pr(T_i = s|T_i \geq s, \mathbf{d}_i, \mathbf{x}_i)}{\Pr(T_i > s|T_i \geq s, \mathbf{d}_i, \mathbf{x}_i)}\right\}}_{\text{Odds}(T_i=s|T_i\geq s, \mathbf{d}_i, \mathbf{x}_i)} \\
&= \ln\left\{\frac{\Pr(T_i = s, T_i \geq s, \mathbf{d}_i, \mathbf{x}_i)/\Pr(T_i \geq s, \mathbf{d}_i, \mathbf{x}_i)}{\Pr(T_i > s, T_i \geq s, \mathbf{d}_i, \mathbf{x}_i)/\Pr(T_i \geq s, \mathbf{d}_i, \mathbf{x}_i)}\right\} \\
&= \ln\left\{\frac{\Pr(T_i = s, T_i \geq s, \mathbf{d}_i, \mathbf{x}_i)}{\Pr(T_i > s, T_i \geq s, \mathbf{d}_i, \mathbf{x}_i)}\right\} \\
&= \ln\left\{\frac{\Pr(T_i = s|\mathbf{d}_i, \mathbf{x}_i)}{\Pr(T_i > s|\mathbf{d}_i, \mathbf{x}_i)}\right\}
\end{aligned}$$

which is the log of the odds (or ratio of probabilities) of stopping at time s versus continuing beyond time s. This becomes a model for the odds of continuing versus stopping if we replace 0 with 1 and 1 with 0 in the response variable (see exercises 14.5

and 14.8). The relevant continuation-ratio odds for a four-interval example, $S = 4$, is shown in figure 14.4.

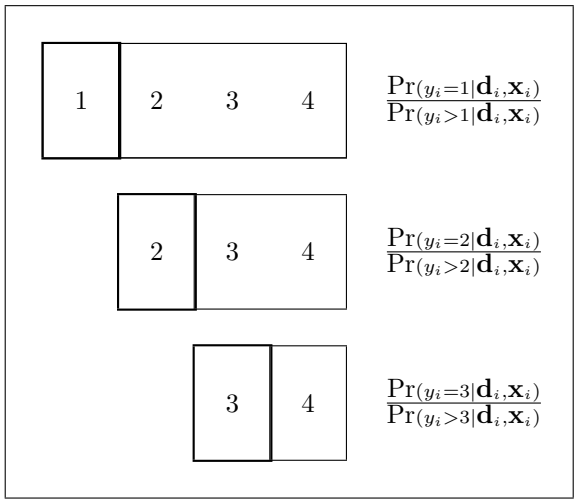


Figure 14.4: Relevant odds $\Pr(y_i = s|\mathbf{d}_i, \mathbf{x}_i)/\Pr(y_i > s|\mathbf{d}_i, \mathbf{x}_i)$ for $(s = 1, 2, 3)$ in a continuation-ratio logit model with four time intervals. Odds is ratio of probabilities of events; events included in numerator probability are in thick frames and events included in denominator probability are in thin frames. [This diagram is very similar to those in Brendan Halpin's web notes on "Models for ordered categories (ii)".]

We can obtain the estimated odds ratios associated with the three covariates by using the `or` option with the `logit` command or by exponentiating the coefficients. For `undergrad`, the odds ratio is estimated as $\exp(0.157) = 1.17$, implying that the odds of being promoted in any given year (given that promotion has not already occurred) increase 17% for every unit increase in the selectivity of the undergraduate institution, controlling for the other covariates.

Log-odds curves are not easy to interpret, and usually survival curves are presented instead. The estimated hazards $\widehat{h}_{si}$ can be obtained from the log odds `lo` by using the `invlogit()` function. To get the cumulative products in (14.1) for each person, we use the `sum()` function combined with the `by` prefix and apply this to the logarithms, using the relationship

$$\widehat{S}_{ti} \;=\; \prod_{s=1}^{t}(1-\widehat{h}_{si}) \;=\; \exp\left\{\sum_{s=1}^{t}\ln(1-\widehat{h}_{si})\right\}$$

```
. generate ln_one_m_haz = ln(1-invlogit(lo))
. by id (year), sort: generate ln_surv = sum(ln_one_m_haz)
. generate surv = exp(ln_surv)
. twoway (line surv year if id==1, connect(stairstep) lpatt(solid))
> (line surv year if id==4, connect(stairstep) lpatt(dash)),
> legend(off) xtitle(Year) ytitle(Survival)
```

The graph is given in figure 14.5.

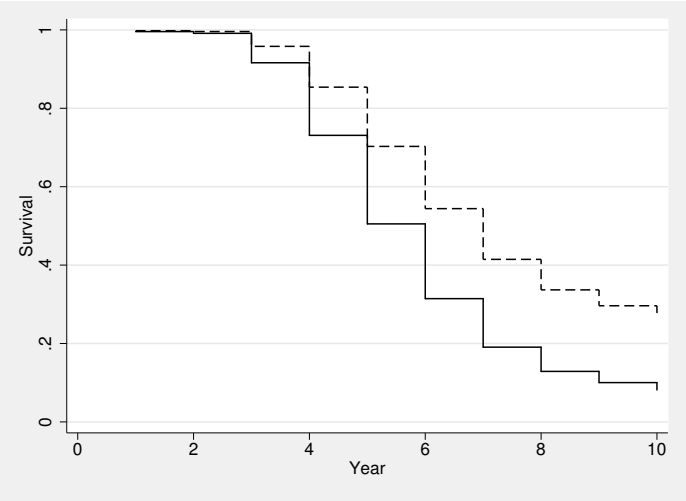


Figure 14.5: Predicted probability of remaining an assistant professor for professors 1 (solid) and 4 (dashed)

We see that professors with the covariate values of professor 1 (`undgrad` = 7, `phdmed` = 0, and `phdprest` = 2.21) have a 50% chance of being promoted by year 5.

Time-varying covariates

The dataset contains four types of time-varying information: the cumulative number of papers published each year, the cumulative number of citations each year to all papers previously published, whether the employer is the same as at the start of the assistant professorship, and the prestige of the current employer. This information is coded in the following variables:

- `art1`–`art10`: the cumulative number of articles published in each of the 10 years
- `cit1`–`cit10`: the cumulative number of citations to all previous articles in each of the 10 years
- `jobtime`: number of years until change of employer from start of assistant professorship, coded as missing for those who did not change employer

- `prest1`: a measure of prestige of the assistant professor's first employing institution (ranges from 0.65 to 4.6)
- `prest2`: prestige of the assistant professor's second employing institution, coded as missing for those who did not change employers (no one had more than two employers)

Because the data are in person–year form with one observation for each year each person is at risk, it is straightforward to include time-varying covariates by creating variables that take on the appropriate values for each person in each year. For the first two variables above, this is most easily achieved by reading in the data in their original form (with one row per person),

```
. use http://www.stata-press.com/data/mlmus3/promotion, clear
```

and using the `reshape` command to produce person–year data:

```
. reshape long art cit, i(id) j(year)
(note: j = 1 2 3 4 5 6 7 8 9 10)
Data                               wide   ->   long
-----------------------------------------------------------------------------
Number of obs.                      301   ->    3010
Number of variables                  29   ->      12
j variable (10 values)                    ->   year
xij variables:
                    art1 art2 ... art10   ->   art
                    cit1 cit2 ... cit10   ->   cit
-----------------------------------------------------------------------------
```

We can then list the data:

```
. list id year art cit dur event if id<3, sepby(id) noobs
```

id	year	art	cit	dur	event
1	1	0	0	10	0
1	2	0	0	10	0
1	3	2	1	10	0
1	4	2	1	10	0
1	5	2	1	10	0
1	6	2	1	10	0
1	7	2	1	10	0
1	8	2	1	10	0
1	9	2	1	10	0
1	10	2	1	10	0
2	1	8	27	4	1
2	2	10	44	4	1
2	3	14	57	4	1
2	4	18	63	4	1
2	5	.	.	4	1
2	6	.	.	4	1
2	7	.	.	4	1
2	8	.	.	4	1
2	9	.	.	4	1
2	10	.	.	4	1

We see that the first assistant professor stopped publishing after year 3, was cited only once in 10 years, and did not get promoted within 10 years, whereas the second professor published 18 papers and had 63 citations by the fourth year when he or she got promoted.

The `reshape` command has produced 10 rows of data for each person although only `dur` rows are required. We therefore delete the excess rows of data and create the variables `year` and `y` as before:

```
. drop if year>dur
(1269 observations deleted)
. generate y = 0
. replace y = event if year==dur
(217 real changes made)
```

The time-varying covariates `art` and `cit` are now ready for inclusion in the model. Following Allison (1995), we will use the prestige of the current employer as the third time-varying covariate. We generate a new variable, `prestige`, which initially equals `prest1` for everyone and then changes to `prest2` for those who changed employers in the year given in `jobtime`:

```
. generate prestige = prest1
. replace prestige = prest2 if year>=jobtime
(181 real changes made)
```

The variable `jobtime` is missing for those who never changed employers. Because Stata interprets missing values as very large numbers, the logical expression `year>=jobtime` is never true for those who did not change employers, and therefore `prestige` remains equal to `prest1` for those individuals as required. The data for the first two assistant professors are given in table 14.1.

Table 14.1: Expanded data with time-constant and time-varying covariates for first two assistant professors

		Covariates						Response
		Time-constant			Time-varying			
`id`	`year`	`undgrad`	`phdmed`	`phdprest`	`art`	`cit`	`prestige`	`y`
i	s	x_{2i}	x_{3i}	x_{4i}	x_{5si}	x_{6si}	x_{7si}	y_{si}
1	1	7	0	2.21	0	0	2.36	0
1	2	7	0	2.21	0	0	2.36	0
1	3	7	0	2.21	2	1	2.36	0
1	4	7	0	2.21	2	1	2.36	0
1	5	7	0	2.21	2	1	2.36	0
1	6	7	0	2.21	2	1	2.36	0
1	7	7	0	2.21	2	1	2.36	0
1	8	7	0	2.21	2	1	2.36	0
1	9	7	0	2.21	2	1	2.36	0
1	10	7	0	2.21	2	1	2.36	0
2	1	6	0	2.21	8	27	1.84	0
2	2	6	0	2.21	10	44	1.84	0
2	3	6	0	2.21	14	57	2.88	0
2	4	6	0	2.21	18	63	2.88	1

As in figure 14.1, the expanded data has 10 records for the first assistant professor and 4 records for the second. For the first professor, the response y_{si} is equal to 0 throughout the 10 years ($s = 1, \ldots, 10$); for the second professor, the response is 0 for the first 3 years ($s = 1, 2, 3$) and then 1 in year $s = 4$. There are three time-constant covariates, `undgrad`, `phdmed`, and `phdprest` (x_{2i}, x_{3i}, and x_{4i}), and three time-varying covariates, `art`, `cit`, and `prestige` (x_{5si}, x_{6si}, and x_{7si}).

Using expanded data of the above form, we can fit a logistic discrete-time hazards model including both time-constant and time-varying covariates,

$$\begin{aligned}\text{logit}\{\Pr(y_{si} = 1|\mathbf{d}_{si}, \mathbf{x}_{si})\} &= \alpha_1 + \alpha_2 d_{2si} + \cdots + \alpha_{10} d_{10,si} \\ &\quad + \beta_2 x_{2i} + \beta_3 x_{3i} + \beta_4 x_{4i} + \beta_5 x_{5si} + \beta_6 x_{6si} + \beta_7 x_{7si}\end{aligned}$$

where $\mathbf{x}_{si} = (x_{2i}, x_{3i}, x_{4i}, x_{5si}, x_{6si}, x_{7si})'$.

This model can be fit using the command

```
. logit y i.year undgrad phdmed phdprest art cit prestige, or
Logistic regression                               Number of obs   =       1741
                                                  LR chi2(15)     =     303.80
                                                  Prob > chi2     =     0.0000
Log likelihood = -502.83976                       Pseudo R2       =     0.2320

------------------------------------------------------------------------------
           y | Odds Ratio   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
        year |
          2  |   .9126348    1.29337    -0.06   0.949      .056753    14.67591
          3  |   15.10083   15.61356     2.63   0.009     1.990204    114.5787
          4  |   44.34795   45.12593     3.73   0.000     6.035867    325.8423
          5  |   73.16483    74.3748     4.22   0.000     9.977552    536.5136
          6  |   93.20208   95.14476     4.44   0.000     12.60323    689.2383
          7  |   97.98613    100.932     4.45   0.000     13.01284    737.8311
          8  |   69.18332   72.81854     4.03   0.000      8.79172    544.4137
          9  |    37.2479   40.90447     3.29   0.001     4.328515     320.527
         10  |   32.10152   36.91194     3.02   0.003     3.371095    305.6892
             |
     undgrad |    1.21355   .0767456     3.06   0.002      1.07208    1.373688
      phdmed |   .7916123   .1357166    -1.36   0.173     .5656917    1.107759
    phdprest |   1.022572   .0951069     0.24   0.810     .8521685    1.227049
         art |   1.076152   .0194367     4.06   0.000     1.038723    1.114929
         cit |   1.000092   .0013031     0.07   0.944      .997541    1.002649
    prestige |   .7816668   .0887699    -2.17   0.030     .6256841     .976536
       _cons |   .0017972   .0019711    -5.76   0.000     .0002094    .0154221
------------------------------------------------------------------------------
```

The maximum likelihood estimates of the odds ratios for this model are also presented in table 14.2.

Table 14.2: Maximum likelihood estimates for logistic discrete-time hazards model for promotions of assistant professors

	Odds ratio	(95% CI)
$\exp(\alpha_2)$ [`year 2`]	0.91	(0.1, 14.7)
$\exp(\alpha_3)$ [`year 3`]	15.10	(2.0, 114.6)
$\exp(\alpha_4)$ [`year 4`]	44.35	(6.0, 325.8)
$\exp(\alpha_5)$ [`year 5`]	73.17	(10.0, 536.5)
$\exp(\alpha_6)$ [`year 6`]	93.20	(12.6, 689.3)
$\exp(\alpha_7)$ [`year 7`]	97.99	(13.0, 737.8)
$\exp(\alpha_8)$ [`year 8`]	69.18	(8.8, 544.4)
$\exp(\alpha_9)$ [`year 9`]	37.25	(4.3, 320.5)
$\exp(\alpha_{10})$ [`year 10`]	32.10	(3.4, 305.7)
$\exp(\beta_2)$ [`undgrad`]	1.21	(1.1, 1.4)
$\exp(\beta_3)$ [`phdmed`]	0.79	(0.6, 1.1)
$\exp(\beta_4)$ [`phdprest`]	1.02	(0.9, 1.2)
$\exp(\beta_5)$ [`art`]	1.08	(1.0, 1.1)
$\exp(\beta_6)$ [`cit`]	1.00	(1.0, 1.0)
$\exp(\beta_7)$ [`prestige`]	0.78	(0.6, 1.0)
Log likelihood	−502.84	

At the 5% level, only the odds ratios for `undergrad`, `art`, and `prestige` are significant. As might be expected, a more selective undergraduate institution and more published articles are associated with a greater odds of promotion (given that promotion has not yet occurred), whereas being employed at a more prestigious institution is associated with a decreased odds of promotion. Regarding the coefficients of the dummy variables, their exponentials represent the odds ratio of promotion in a given year (given that promotion did not occur earlier) compared with year 1, when $\mathbf{x}_{si} = \mathbf{0}$. So, for instance, the odds of promotion are 98 times as great in year 7 as they are in year 1 when all covariates take the value zero. The reason for these large odds ratios and wide confidence intervals is that the estimated odds of promotion in year 1 (reported in the output next to `_cons`) are merely 0.0018 and poorly estimated. It would perhaps be better to use a different year as reference category.

It is also interesting to consider a parametric form for the discrete-time baseline hazard as a function of time instead of using dummy variables. Allison (1995) specifies a polynomial relationship for these data (see also exercise 14.1).

14.2.5 Multiple absorbing events and competing risks

There are sometimes multiple types of absorbing events or, in other words, multiple modes of failure. A classical example is different causes of death in mortality studies.

In the promotions data, we might, for instance, distinguish between two types of events that could be experienced by an assistant professor: 1) promotion at the first university he works at and 2) leaving the first university before being promoted there. A separate discrete-time hazard can then be defined for each type of absorbing event. This situation is referred to as *competing risks* because the events are competing in the sense that a person experiencing one of the events is removed from the risk sets of all other events.

Discrete-time hazard modeling for multiple absorbing events can proceed in a similar manner as for single events with the difference that the responses in the expanded data are nominal (with different categories of events) and no longer binary. The data are expanded so that professors have a 0 for every year where neither event happened and a 1 or 2 for the year where the professor is promoted or leaves the university, respectively. We can then fit a logistic discrete-time hazards model for multiple absorbing events by using the multinomial logit model for nominal responses discussed in section 12.2.1.

We start by rereading in the promotions data:

```
. use http://www.stata-press.com/data/mlmus3/promotion, clear
```

We then define the two events with dummy variables `event1` and `event2` for being promoted and leaving, respectively. The first type of event is defined by using

```
. generate event1 = 0
. replace event1 = 1 if dur<jobtime & event==1
(163 real changes made)
```

This produces a 1 if a promotion was experienced (`event==1`) *and* the promotion occurred before leaving the first university (`dur<jobtime`), and a 0 otherwise. We see that 163 of the professors are promoted at the first university they work at. The second kind of event is defined by using

```
. generate event2 = 0
. replace event2 = 1 if dur>=jobtime
(74 real changes made)
```

producing a 1 if the assistant professor leaves his first university before having been promoted (`dur>=jobtime`) and a 0 otherwise. It is assumed here that a professor who is promoted in the same year as he leaves his first university is promoted at his new university. We see that 74 of the professors leave their first university without having been promoted there. For this event, we also need to redefine the time to event, which is now the time of leaving the first university (`jobtime`):

```
. replace dur = jobtime if event2==1
(31 real changes made)
```

Repeating the commands we previously used for single-event data, we expand the original data to person–year data,

```
. reshape long art cit, i(id) j(year)
(note: j = 1 2 3 4 5 6 7 8 9 10)
Data                               wide   ->   long
-----------------------------------------------------------------------------
Number of obs.                      301   ->    3010
Number of variables                  31   ->      14
j variable (10 values)                    ->   year
xij variables:
                    art1 art2 ... art10   ->   art
                    cit1 cit2 ... cit10   ->   cit
-----------------------------------------------------------------------------
```

and get rid of redundant rows in the data:

```
. drop if year>dur
(1376 observations deleted)
```

We can then list some of the person–year data for three of the assistant professors, including both `event1` and `event2`:

```
. list id year jobtime dur event1 event2 if id==1|id==2|id==161, sepby(id) noobs
```

id	year	jobtime	dur	event1	event2
1	1	.	10	0	0
1	2	.	10	0	0
1	3	.	10	0	0
1	4	.	10	0	0
1	5	.	10	0	0
1	6	.	10	0	0
1	7	.	10	0	0
1	8	.	10	0	0
1	9	.	10	0	0
1	10	.	10	0	0
2	1	3	3	0	1
2	2	3	3	0	1
2	3	3	3	0	1
161	1	.	2	1	0
161	2	.	2	1	0

We see that the first professor experienced neither of the events over the 10-year observation period. In contrast, the second professor experienced the second event, leaving the first university he was employed at in year 3 without having been promoted there (he was, however, promoted at his new university in year 4, as can be seen in table 14.1). Professor 161 was promoted in year 2 at her original university.

In preparation for modeling multiple types of events, we then define a nominal variable, `yy`, taking the value 0 until an event is experienced, 1 if the professor is promoted at his first university, and 2 if the professor is leaving without having been promoted:

```
. generate yy = 0
. replace yy = 1 if year==dur & event1==1
(163 real changes made)
. replace yy = 2 if year==dur & event2==1
(74 real changes made)
```

We define value labels for the nominal response:

```
. label define eventlabel 1 "promfirst" 2 "leave"
. label values yy eventlabel
```

The data for the three professors now look like this:

```
. list id year jobtime dur event1 event2 yy if id==1|id==2|id==161,
> sepby(id) noobs
```

id	year	jobtime	dur	event1	event2	yy
1	1	.	10	0	0	0
1	2	.	10	0	0	0
1	3	.	10	0	0	0
1	4	.	10	0	0	0
1	5	.	10	0	0	0
1	6	.	10	0	0	0
1	7	.	10	0	0	0
1	8	.	10	0	0	0
1	9	.	10	0	0	0
1	10	.	10	0	0	0
2	1	3	3	0	1	0
2	2	3	3	0	1	0
2	3	3	3	0	1	leave
161	1	.	2	1	0	0
161	2	.	2	1	0	promfirst

We are now ready to fit a logistic discrete-time hazard model for multiple absorbing events. The same covariates are used as previously for the single-event case (we use `prest1` instead of `prestige` because it is the prestige of the first institution that matters here). Letting the superscripts $^{[1]}$ and $^{[2]}$ denote the two types of events, we specify a model with separate baseline hazards for each type of event:

$$\begin{aligned}\ln\left\{\frac{\Pr(y_{si}=1|\mathbf{d}_{si},\mathbf{x}_{si})}{\Pr(y_{si}=0|\mathbf{d}_{si},\mathbf{x}_{si})}\right\} &= \alpha_1^{[1]}+\alpha_2^{[1]}d_{2si}+\cdots+\alpha_{10}^{[1]}d_{10,si}\\ &\quad+\beta_2^{[1]}x_{2i}+\beta_3^{[1]}x_{3i}+\beta_4^{[1]}x_{4i}\\ &\quad+\beta_5^{[1]}x_{5si}+\beta_6^{[1]}x_{6si}+\beta_7^{[1]}x_{7si}\end{aligned}$$

$$\begin{aligned}\ln\left\{\frac{\Pr(y_{si}=2|\mathbf{d}_{si},\mathbf{x}_{si})}{\Pr(y_{si}=0|\mathbf{d}_{si},\mathbf{x}_{si})}\right\} &= \alpha_1^{[2]}+\alpha_2^{[2]}d_{2si}+\cdots+\alpha_{10}^{[2]}d_{10,si}\\ &\quad+\beta_2^{[2]}x_{2i}+\beta_3^{[2]}x_{3i}+\beta_4^{[2]}x_{4i}\\ &\quad+\beta_5^{[2]}x_{5si}+\beta_6^{[2]}x_{6si}+\beta_7^{[2]}x_{7si}\end{aligned}$$

This model is identical to the multinomial logit model for nominal responses discussed in section 12.2.1.

We can use `mlogit` with the `rrr` option to fit the model by maximum likelihood and obtain estimated odds ratios. We specify `ib6.year` to use year 6 as reference category for the categorical variable `year` (instead of the default year 1).

```
. mlogit yy ib6.year undgrad phdmed phdprest art cit prest1, rrr
Multinomial logistic regression                 Number of obs   =       1634
                                                LR chi2(30)     =     304.51
                                                Prob > chi2     =     0.0000
Log likelihood = -671.38843                     Pseudo R2       =     0.1849
```

yy	RRR	Std. Err.	z	P>|z|	[95% Conf.	Interval]
0	(base outcome)					
promfirst						
year						
1	.0128989	.0132414	-4.24	0.000	.0017248	.0964621
2	.0122117	.0125222	-4.30	0.000	.0016366	.0911208
3	.1534968	.056125	-5.13	0.000	.074966	.3142931
4	.5828765	.1631651	-1.93	0.054	.3367433	1.008914
5	.8152931	.2278044	-0.73	0.465	.4714939	1.409781
7	1.341087	.4405855	0.89	0.372	.7043897	2.553296
8	.5111122	.2438342	-1.41	0.159	.200649	1.301954
9	.4703872	.2643801	-1.34	0.180	.156329	1.415375
10	.2883422	.2297488	-1.56	0.119	.0604892	1.374481
undgrad	1.144861	.0832787	1.86	0.063	.992739	1.320292
phdmed	.8185376	.1616294	-1.01	0.311	.5558523	1.205363
phdprest	.9981063	.1047621	-0.02	0.986	.8125198	1.226082
art	1.073669	.0213433	3.58	0.000	1.032641	1.116327
cit	.9999352	.0014397	-0.05	0.964	.9971174	1.002761
prest1	.7938277	.1035595	-1.77	0.077	.6147265	1.02511
_cons	.1967245	.10549	-3.03	0.002	.0687728	.5627301
leave						
year						
1	1.02e-07	.0000599	-0.03	0.978	0	.
2	.249396	.1322296	-2.62	0.009	.0882233	.705011
3	.7734526	.3347741	-0.59	0.553	.3311368	1.806591
4	.5758507	.2730709	-1.16	0.244	.227335	1.458658
5	.7946052	.3772739	-0.48	0.628	.3133328	2.015102
7	1.639593	.8569544	0.95	0.344	.5886331	4.566963
8	.897801	.6303747	-0.15	0.878	.2267381	3.554969
9	1.633939	1.067844	0.75	0.452	.4538807	5.882065
10	1.241043	1.041922	0.26	0.797	.2394185	6.433038
undgrad	1.226955	.1219456	2.06	0.040	1.009785	1.490832
phdmed	.5137594	.1324057	-2.58	0.010	.3100193	.8513944
phdprest	.8188393	.1205438	-1.36	0.175	.6136076	1.092714
art	1.011262	.0306538	0.37	0.712	.9529311	1.073163
cit	1.001728	.0020015	0.86	0.388	.9978124	1.005658
prest1	1.264341	.2231535	1.33	0.184	.8946	1.786897
_cons	.0412265	.031836	-4.13	0.000	.0090753	.1872807

The estimated odds ratios for being promoted at the first university (given in the upper panel of the output under `promfirst`) are generally not that different from those previously reported for promotion at any research university in the single-event case. Regarding the estimated odds ratios for leaving without having been promoted (given in the lower panel under `leave`), a one-unit increase in the selectivity of the undergraduate institution corresponds to an increase in the odds of leaving by about 23%, whereas having a PhD from a medical school reduces the odds by 49%, controlling for other covariates. None of the other adjusted odds ratios are significantly different from 1 at the 5% level.

14.2.6 Handling left-truncated data

In the promotion data, all individuals were sampled at the beginning of their assistant professorships, that is, when they became at risk for promotion to associate professor. Such a sampling design, where the start of the observation period coincides with the time individuals become at risk, is sometimes called *sampling the inflow* (here the inflow to the state of assistant professor). This design is typical in experimental studies where, for instance, duration to death following surgery is investigated. When sampling the inflow, the start of observation is also the origin of analysis time.

However, in observational studies, we often have more complex sample designs where the times individuals become at risk do not necessarily coincide with the start of the observation period. *Delayed entry* means that individuals become at risk before entering the study. In such a design, *left-truncation* occurs if those who have experienced the event are not included in the study. For instance, when investigating the duration of unemployment, a *stock sample* includes individuals from the stock of unemployed at a given time and their times to employment (or censoring) are recorded. Those not unemployed at the start of observation are not eligible for the study, and the sample is in this sense truncated. If we analyze unemployment durations among those selected into the sample, without any correction, we are likely to underestimate the hazard of employment in the general population. The sampling is said to be *length biased* because the probability of selection at a given point in time depends on the time spent at risk.

In truncated samples, we require the conditional hazard of survival, given that the subject is selected into the study. Consider an individual who we know has already been at risk for a time t_b when he enters the study. This situation was illustrated by case 5 in the right panel of the figure on page 745, where B denotes the beginning of the study. Because the individual would not have been included in the study if the event had occurred at a time $t \leq t_b$, we must condition on the fact that $t > t_b$. The likelihood contribution for this person if he is right-censored at time $t > t_b$ therefore becomes

$$\Pr(T_i > t | T_i > t_b) = \frac{\Pr(T_i > t, T_i > t_b)}{\Pr(T_i > t_b)} = \frac{\prod_{s=1}^{t}(1-h_{si})}{\prod_{s=1}^{t_b}(1-h_{si})} = \prod_{s=t_b+1}^{t}(1-h_{si})$$

and the likelihood contribution if he experiences the event at time $t > t_b$ is

$$\Pr(T_i = t|T_i > t_b) \;=\; \frac{\Pr(T_i = t, T_i > t_b)}{\Pr(T_i > t_b)} \;=\; \frac{h_{ti}\prod_{s=1}^{t-1}(1-h_{si})}{\prod_{s=1}^{t_b}(1-h_{si})} \;=\; h_{ti}\prod_{s=t_b+1}^{t-1}(1-h_{si})$$

The correct likelihood contribution under delayed entry is thus simply obtained by letting the individual start contributing observations from entering the study at $t_b + 1$ and discarding the preceding periods, $t = 1, \ldots, t_b$. For instance, if professor 10 had already completed 3 years as assistant professor when he entered the study, we would simply delete the data for years 1–3 for him and let his initial hazard in the study at year 4 be $h_{4,10}$.

The above correction cannot be used if the time at risk before entering the study t_b is unknown. Fortunately, bias can be avoided here by simply discarding subjects with late entry; however, this can incur a substantial loss in efficiency.

Different kinds of sampling designs for survival analysis are discussed in, for instance, Lancaster (1990), Hamerle (1991), Guo (1993), Jenkins (1995), and Klein and Moeschberger (2003).

14.3 How does birth history affect child mortality?

Pebley and Stupp (1987) and Guo and Rodríguez (1992) analyzed data on child mortality in Guatemala. The data come from a retrospective survey conducted in 1974–76 by the Instituto Nutrición de Centroamérica y Panamá (UNCAP) and the think tank RAND, and have been made available by Germán Rodríguez.

Most of the data come from a female life history survey that covered all women aged 15–49 who lived in six villages and towns. The survey questionnaire asked about the complete birth history, maternal education, and related subjects. The data include all children except multiple births (twins or triplets), stepchildren, and children born more than 15 years before the survey. Observations with missing socioeconomic data or inconsistent dates of events have been deleted.

The outcome of interest is the children's length of life. Because most of the mothers have several children, this is an example of multilevel or clustered survival data. The variables we will use here are

- `kidid`: child identifier (i)
- `momid`: mother identifier (j)
- `time`: time in months from birth to death or censoring
- `death`: dummy variable for death (1: death; 0: censoring)
- `mage`: mother's age at time of birth of child
- `border`: birth order of child

- `p0014`, `p1523`, `p2435`, `p36up`: dummy variables for time between birth of index child and birth of previous child being 0–14, 15–23, 24–35, and 36 or more months, respectively (the reference category is no previous birth)
- `pdead`: dummy variable for previous child having died before conception of the index child
- `f0011` and `f1223`: dummy variables for next child being born within 0–11 and 12–23 months after the birth of the index child, respectively, and before the death of the index child (the reference category is no subsequent birth within 23 months and before the death of the index child)

We read in the data by typing

```
. use http://www.stata-press.com/data/mlmus3/mortality, clear
```

14.4 Data expansion

Pebley and Stupp (1987) treat these data as continuous-time survival data and use a piecewise exponential model (see section 15.4.1 and exercise 15.5) with constant hazards in the intervals <1, 1–5, 6–11, 12–23, and >23 months. Here we will treat these same intervals as discrete-time intervals and use discrete-time survival models. When the exact timing is known, the piecewise exponential model described in section 15.4.1 may be more appropriate because it takes into account that individuals were at risk for only parts of the time interval within which they either died or were censored. In contrast, discrete-time survival analysis treats these individuals as being at risk for the entire interval, an issue we will return to shortly. On the other hand, the piecewise exponential model assumes that the hazard is constant throughout each interval, whereas discrete-time models make no such assumption.

First, we use the `egen` function `cut()` to categorize the variable `time`, and then we use the `table` command to make sure that we have done this correctly:

```
. egen discrete = cut(time), at(0 1 6 12 24 61) icodes
. table discrete, contents(min time max time)
```

discrete	min(time)	max(time)
0	.25	.25
1	1	5
2	6	11
3	12	23
4	24	60

The variable `discrete` takes on consecutive integer values from 0 to 4 because we used the `icodes` option in the `egen` command. However, for the data expansion to work, we require that `discrete` starts from 1, so we add 1:

```
. replace discrete = discrete + 1
```

Before expanding the data, we summarize them in a life table using the `ltable` command so that we can check that our data expansion is correct:

```
. ltable discrete death, noadjust
```

Interval		Beg. Total	Deaths	Lost	Survival	Std. Error	[95% Conf.	Int.]
1	2	3120	109	9	0.9651	0.0033	0.9580	0.9710
2	3	3002	92	94	0.9355	0.0044	0.9263	0.9436
3	4	2816	66	126	0.9136	0.0051	0.9031	0.9230
4	5	2624	94	238	0.8808	0.0059	0.8687	0.8919
5	6	2292	42	2250	0.8647	0.0063	0.8518	0.8765

Returning to the issue of how to deal with individuals who died or were censored within an interval, `ltable` with the `noadjust` option treats these individuals as being at risk during the entire interval (assuming that the event and censoring take place at the end of the interval). This gives estimated hazards of $\widehat{h}_1 = 109/3120 = 0.0349$ and so on. The data expansion method described in section 14.2.2 yields these same estimates. If time is truly discrete, this is the correct method for estimating the hazards.

However, if time is treated as interval-censored as it is here, we do not know when during the first interval the $109 + 9 = 118$ individuals died or were censored. To allow for partial contributions to the risk set for those who were censored or died during the interval, the *actuarial adjustment* consists of excluding half the 118 individuals from the denominator, giving $\widehat{h}_1 = 109/(3120 - 118/2) = 0.0356$. This can be motivated by assuming that the hazard of removal from the risk set follows a uniform distribution over the interval. The estimated hazards from the actuarial method are provided by `ltable` without the `noadjust` option. In this dataset, the adjustment makes a considerable difference in the last interval where 2,250 individuals were censored.

We expand the data and produce a table for comparison with the life table above:

```
. expand discrete
(10734 observations created)
. by kidid, sort: generate interval = _n
. generate y = 0
. replace y = death if interval == discrete
(403 real changes made)
```

```
. tabulate interval y, row
```

Key
frequency *row percentage*

interval	y 0	1	Total
1	3,011 96.51	109 3.49	3,120 100.00
2	2,910 96.94	92 3.06	3,002 100.00
3	2,750 97.66	66 2.34	2,816 100.00
4	2,530 96.42	94 3.58	2,624 100.00
5	2,250 98.17	42 1.83	2,292 100.00
Total	13,451 97.09	403 2.91	13,854 100.00

The row totals and numbers of 1s agree with the `Beg. Total` and `Deaths` in the life table, so we can trust our data expansion.

14.5 ❖ Proportional hazards and interval-censoring

The most popular methods for modeling covariate effects for continuous-time survival data (discussed in detail in section 15.4) assume that the continuous-time hazards are proportional,

$$h(z|\mathbf{x}_{ij}) \;=\; h_0(z)\exp(\beta_2 x_{2ij} + \cdots + \beta_p x_{pij})$$

where $h(z|\mathbf{x}_{ij})$ is the continuous-time hazard function for subject i in cluster j at time z and $h_0(z)$ is the *baseline hazard function* (the hazard when $x_{2ij} = \cdots = x_{pij} = 0$). It follows that continuous-time hazards are proportional in the sense that the hazard ratio

$$\frac{h(z|\mathbf{x}_{ij})}{h(z|\mathbf{x}_{i'j'})} \;=\; \exp\{\beta_2(x_{2ij} - x_{2i'j'}) + \cdots + \beta_p(x_{pi} - x_{pi'j'})\}$$

does not depend on time. We see that an exponentiated coefficient, say, $\exp(\beta_2)$, represents the *hazard ratio* for a one-unit change in x_{2ij}, controlling for the other covariates.

It can be shown (see display 15.3 in the next chapter) that the proportionality assumption translates to the following relationship for the survival function,

$$S(z|\mathbf{x}_{ij}) \equiv \Pr(Z_{ij} > z|\mathbf{x}_{ij}) \;=\; S_0(z)^{\exp(\beta_2 x_{2ij} + \cdots + \beta_p x_{pij})}$$

where Z_{ij} is the continuous survival time for subject i in cluster j and $S_0(z)$ is the *baseline survival function*, the survival function when the covariates are all zero.

If the survival times are interval-censored, so we only observe integer values $T_{ij} = t$ if $z_{t-1} < Z_{ij} \leq z_t$ $(t=1,2,\ldots)$, then the discrete-time hazard is given by

$$\begin{aligned} h_{tij} \equiv \Pr(T_{ij} = t | \mathbf{x}_{ij}, T_{ij} > t-1) &= \frac{\Pr(Z_{ij} > z_{t-1}|\mathbf{x}_{ij}) - \Pr(Z_{ij} > z_t|\mathbf{x}_{ij})}{\Pr(Z_{ij} > z_{t-1}|\mathbf{x}_{ij})} \\ &= 1 - \frac{S(z_t|\mathbf{x}_{ij})}{S(z_{t-1}|\mathbf{x}_{ij})} \end{aligned}$$

It follows that

$$1 - h_{tij} = \frac{S(z_t|\mathbf{x}_{ij})}{S(z_{t-1}|\mathbf{x}_{ij})} = \left\{ \frac{S_0(z_t)}{S_0(z_{t-1})} \right\}^{\exp(\beta_2 x_{2ij} + \cdots + \beta_p x_{pij})}$$

and

$$\ln(1 - h_{tij}) = \exp(\beta_2 x_{2ij} + \cdots + \beta_p x_{pij}) \{\ln S_0(z_t) - \ln S_0(z_{t-1})\}$$

The right-hand side is negative, so we reverse the signs and then take the logarithms and obtain

$$\ln\{-\ln(1 - h_{tij})\} = \beta_2 x_{2ij} + \cdots + \beta_p x_{pij} + \underbrace{\ln\{\ln S_0(z_{t-1}) - \ln S_0(z_t)\}}_{\alpha_t}$$

This model, which is linear in the covariates, contains the same regression parameters as the continuous-time proportional-hazards model and contains time-specific constants α_t. The model is a generalized linear model with a complementary log-log link $g(h_{tij}) = \ln\{-\ln(1 - h_{tij})\}$.

By estimating the parameters α_t freely for each time point t, we are making no assumption regarding the shape of the baseline survival function $S_0(z_t)$ or the corresponding baseline hazard function within the time intervals $z_{t-1} < Z_{ij} \leq z_t$. This is in contrast to the piecewise exponential model discussed in section 15.4.1, which assumes constant baseline hazards within time intervals.

14.6 Complementary log-log models

We will use the complementary log-log link here instead of the logit link because, as shown in section 14.5, this link function follows if a proportional hazards model holds in continuous time and the survival times are interval-censored. Hence, for child i of mother j, we consider the complementary log-log discrete-time survival model,

$$\text{cloglog}(h_{sij}) \equiv \ln\{-\ln(1 - h_{sij})\} = \alpha_1 d_{1sij} + \cdots + \alpha_5 d_{5sij}$$

where we have included one dummy variable for each period but no constant (instead of a constant and dummy variables for all but the first period as in section 14.2). The model can alternatively be written as

$$h_{sij} = \text{cloglog}^{-1}(\alpha_1 d_{1sij} + \cdots + \alpha_5 d_{5sij}) \equiv 1 - \exp\{-\exp(\alpha_1 d_{1sij} + \cdots + \alpha_5 d_{5sij})\}$$

As mentioned in section 14.5, the exponentiated regression coefficients can be interpreted as hazard ratios in continuous time.

Unlike probit and logit models that are symmetric with

$$\text{probit}(h_{sij}) \;=\; \Phi^{-1}(h_{sij}) = -\Phi^{-1}(1-h_{sij})$$

$$\text{logit}(h_{sij}) \;=\; -\text{logit}(1-h_{sij})$$

the complementary log-log link is not symmetric,

$$\text{cloglog}(h_{sij}) \;\neq\; -\text{cloglog}(1-h_{sij})$$

This means that switching the 0s and 1s in the response variable will not merely reverse the sign of the estimated coefficients as for logit and probit models. It is worth noting that the complementary log-log and logit models are very similar when the time intervals are small.

By using dummy variables for the time intervals, we are not making any assumption regarding the shape of the discrete-time hazard function, and in the model without further covariates, we will get the same hazard estimates whatever link we use.

We construct the dummies for the time intervals,

```
. quietly tabulate interval, generate(int)
```

and use the `cloglog` command to fit a model with a complementary log-log link,

```
. cloglog y int1-int5, noconstant
Complementary log-log regression                Number of obs     =      13854
                                                Zero outcomes     =      13451
                                                Nonzero outcomes  =        403
                                                Wald chi2(5)      =    4943.80
Log likelihood = -1811.6791                     Prob > chi2       =     0.0000
------------------------------------------------------------------------------
           y |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
        int1 |  -3.336513   .0957877   -34.83   0.000    -3.524253   -3.148772
        int2 |  -3.469723   .1042614   -33.28   0.000    -3.674072   -3.265374
        int3 |  -3.741583   .1230944   -30.40   0.000    -3.982844   -3.500323
        int4 |  -3.310976   .1031478   -32.10   0.000    -3.513142   -3.108809
        int5 |  -3.990277   .1543055   -25.86   0.000    -4.292711   -3.687844
------------------------------------------------------------------------------
```

We can estimate the hazards for the children in each time interval by typing

```
. predict haz, pr
```

and list the estimated hazards (which are the same for all children) for child 101 by typing

```
. sort kidid interval
. list kidid interval haz if kidid==101, noobs
```

kidid	interval	haz
101	1	.0349359
101	2	.03064624
101	3	.0234375
101	4	.03582317
101	5	.01832461

The marginal (over the covariates) hazard function estimated above is of some interest, but we are more interested in the relationships between covariates and the death hazard. Understanding these relationships might provide insight into the etiology of child mortality and could potentially guide targeted interventions to reduce mortality.

Mother's age at birth is known to be a risk factor for child mortality. We thus allow for linear and quadratic functions of age by including the covariates `mage` (x_{2ij}) and `mage2` (x_{3ij}), with the latter variable constructed as

```
. generate mage2 = mage^2
```

Because birth order (often called *parity* in epidemiology) is a known risk factor, we also include `border` (x_{4ij}).

The other covariates relate to the timing of other births in the family. As discussed by Pebley and Stupp (1987), birth spacing may be important for several reasons; for instance, several children of similar ages may compete for scarce resources (food, clothing, and parental time). We therefore include dummy variables for the time intervals between the births of the index child and the previous child: `p0014` (x_{5ij}), `p1523` (x_{6ij}), `p2435` (x_{7ij}), and `p36up` (x_{8ij}).

However, Pebley and Stupp point out that there may be a spurious relationship between the previous birth interval and the death of the index child if the previous birth interval is shortened by the previous child's death and if the risks of dying are correlated between children in the same family. For this reason, the survival status of the previous child, `pdead` (x_{9ij}), is included as a covariate.

Also, the birth interval to the next child may be shortened by the index child's death. Therefore, the dummy variables `f0011` and `f1223` for the next birth interval being 0–11 months and 12–23 months, respectively, have been set to zero if the index child died within the corresponding time intervals. The birth of a subsequent child can affect the index child only after it has occurred, for a short birth interval (0–11 months) when the index child is at least 12 months old (interval 4 onward) and for a long birth interval (12–23 months) when the index child is at least 24 months old (interval 5). We therefore follow Guo and Rodríguez (1992) in defining the time-varying dummy variables `comp12` ($x_{10,sij}$), `comp24e` ($x_{11,sij}$), and `comp24l` ($x_{12,sij}$) for competition with the subsequent child when the index child is 12–23 months old (interval 4) and over 24 months old (interval 5), differentiating in the latter interval between competition with children born earlier and later.

```
. generate comp12 = f0011*(interval==4)
. generate comp24e = f0011*(interval==5)
. generate comp24l = f1223*(interval==5)
```

We now include all the above covariates in the complementary log-log model:

$$\ln\{-\ln(1-h_{sij})\} \;=\; \alpha_1 d_{1sij} + \cdots + \alpha_5 d_{5sij} + \beta_2 x_{2ij} + \cdots + \beta_{12} x_{12,sij}$$

Estimates with robust standard errors for clustered data can be obtained using

```
. cloglog y int1-int5 mage mage2 border p0014 p1523 p2435 p36up pdead
> comp12 comp24e comp24l, noconstant eform vce(cluster momid)
Complementary log-log regression                Number of obs     =      13854
                                                Zero outcomes     =      13451
                                                Nonzero outcomes  =        403
                                                Wald chi2(16)     =    4512.16
Log pseudolikelihood = -1784.1899               Prob > chi2       =     0.0000
                                (Std. Err. adjusted for 851 clusters in momid)
------------------------------------------------------------------------------
             |               Robust
           y |     exp(b)   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
        int1 |   .2318333     .17652    -1.92   0.055      .052127    1.031071
        int2 |   .2042155   .1572742    -2.06   0.039     .0451383    .9239144
        int3 |   .1560266    .121621    -2.38   0.017     .0338607    .7189539
        int4 |   .2300307     .17649    -1.92   0.055     .0511335    1.034824
        int5 |   .1221787   .0922591    -2.78   0.005     .0278125    .5367243
       mage  |   .8617077   .0499925    -2.57   0.010     .7690897    .9654793
      mage2  |   1.002562   .0010004     2.56   0.010     1.000603    1.004525
      border |   1.063391   .0364623     1.79   0.073     .9942743    1.137311
      p0014  |    1.73225   .3591742     2.65   0.008     1.153766    2.600779
      p1523  |   .8764676   .1549602    -0.75   0.456     .6197873     1.23945
      p2435  |   .7697006   .1391446    -1.45   0.148     .5400621    1.096983
      p36up  |   .6681857   .1366279    -1.97   0.049     .4475556    .9975793
      pdead  |   1.118051    .178947     0.70   0.486     .8170047    1.530026
     comp12  |   4.909925   2.279635     3.43   0.001     1.976375    12.19777
    comp24e  |   4.436945   3.158989     2.09   0.036     1.099135    17.91089
    comp24l  |   .8476108   .3038621    -0.46   0.645     .4198045    1.711378
------------------------------------------------------------------------------
```

We see that mother's age at birth (`mage` and `mage2`), being born within 14 months of the previous child (`p0014`), and getting a new sibling within the first 11 months of life (`comp12` and `comp24e`) have statistically significant coefficients at the 5% level. For example, the estimated hazard of death increases 73% if the index child was born within 14 months of the previous child, controlling for the other covariates. Having a new sibling within the first 11 months of life increases the estimated hazard 4.91-fold at age 12 to 23 months and 4.44-fold at age 24–60 months, controlling for the other covariates. It appears that competition with children born shortly before, but even more so shortly after, the index child is an important risk factor. The estimates are also given under "No random intercept" in table 14.3. The exponentiated coefficients of the dummy variables (not given in the table) do not represent hazard ratios here because the overall constant was omitted.

Table 14.3: Maximum likelihood estimates for complementary log-log models with and without random intercept for Guatemalan child mortality data

	No random intercept		Random intercept	
	Hazard ratio	(95% CI)*	Hazard ratio	(95% CI)
Fixed part				
$\exp(\beta_2)$ [mage]	0.86	(0.77, 0.97)	0.86	(0.76, 0.96)
$\exp(\beta_3)$ [mage2]	1.00	(1.00, 1.00)	1.00	(1.00, 1.00)
$\exp(\beta_4)$ [border]	1.06	(0.99, 1.14)	1.06	(0.99, 1.14)
$\exp(\beta_5)$ [p0014]	1.73	(1.15, 2.60)	1.79	(1.17, 2.74)
$\exp(\beta_6)$ [p1523]	0.88	(0.62, 1.24)	0.90	(0.62, 1.30)
$\exp(\beta_7)$ [p2435]	0.77	(0.54, 1.10)	0.79	(0.55, 1.15)
$\exp(\beta_8)$ [p36up]	0.67	(0.45, 1.00)	0.68	(0.45, 1.03)
$\exp(\beta_9)$ [pdead]	1.12	(0.82, 1.53)	0.95	(0.67, 1.35)
$\exp(\beta_{10})$ [comp12]	4.91	(1.98, 12.20)	4.94	(1.98, 12.34)
$\exp(\beta_{11})$ [comp24e]	4.44	(1.10, 17.91)	4.53	(1.07, 19.17)
$\exp(\beta_{12})$ [comp24l]	0.85	(0.42, 1.71)	0.85	(0.41, 1.73)
Random part				
$\sqrt{\psi}$			0.43	
Log likelihood	$-1,784.19$		$-1,782.70$	

*Using robust standard errors for clustered data

14.7 A random-intercept complementary log-log model

14.7.1 Model specification

To accommodate dependence among the survival times of different children of the same woman, after conditioning on the observed covariates, we include a random intercept ζ_j for mother j in the complementary log-log model,

$$\ln\{-\ln(1-h_{sij})\} = \alpha_1 d_{1sij} + \cdots + \alpha_5 d_{5sij} + \beta_2 x_{2ij} + \cdots + \beta_{12} x_{12,sij} + \zeta_j$$

where $\zeta_j \sim N(0, \psi)$ and the random intercept is independent from the covariates.

The model can also be written in terms of a continuous latent response,

$$y^*_{sij} = \alpha_1 d_{1sij} + \cdots + \alpha_5 d_{5sij} + \beta_2 x_{2ij} + \cdots + \beta_{12} x_{12,sij} + \zeta_j + \epsilon_{sij}$$

where ϵ_{sij} has a standard extreme-value type-1 or Gumbel distribution, given the covariates and the random intercept ζ_j. The standard Gumbel distribution has a mean of

about 0.577 (called Euler's constant) and a variance of $\pi^2/6$, and is asymmetric. Recall that such a Gumbel distribution was also used for the multinomial and conditional logit models discussed in chapter 12. It is assumed that the ϵ_{sij} are mutually independent and independent of ζ_j and the covariates. The latent response y^*_{sij} determines the observed binary response y_{sij} via the threshold model

$$y_{sij} = \begin{cases} 1 & \text{if } y^*_{sij} > 0 \\ 0 & \text{otherwise} \end{cases}$$

The exponentiated random intercept, $\exp(\zeta_j)$, is called a *shared frailty* because it is a mother-specific disposition or *frailty* that is shared among children nested in a mother. Frailties are sometimes also included in single-level survival models, a practice that we do not generally recommend because such models are often not well identified.

14.7.2 Estimation using Stata

Two commands are available for fitting the random-intercept complementary log-log model: `xtcloglog` and `gllamm` with the `link(cll)` option. Whereas `xtcloglog` can be used only for a two-level random-intercept model, `gllamm` can also be used for random-coefficient and higher-level models. However, `xtcloglog` is considerably faster than `gllamm`.

The syntax for `xtcloglog` is analogous to that for `xtlogit`:

```
. quietly xtset momid

. xtcloglog y int1-int5 mage mage2 border p0014 p1523 p2435 p36up pdead
> comp12 comp24e comp24l, noconstant eform

Random-effects complementary log-log model      Number of obs      =     13854
Group variable: momid                           Number of groups   =       851

Random effects u_i ~ Gaussian                   Obs per group: min =         1
                                                               avg =      16.3
                                                               max =        40

                                                Wald chi2(16)      =   2582.92
Log likelihood  = -1782.7021                    Prob > chi2        =    0.0000
```

y	exp(b)	Std. Err.	z	P>|z|	[95% Conf.	Interval]
int1	.2333078	.1806049	-1.88	0.060	.0511693	1.063774
int2	.2071299	.1606492	-2.03	0.042	.0452954	.9471781
int3	.1591151	.1239453	-2.36	0.018	.0345664	.7324346
int4	.2358834	.1833431	-1.86	0.063	.0514151	1.082191
int5	.1261628	.0998945	-2.61	0.009	.0267275	.5955317
mage	.8559014	.0513772	-2.59	0.010	.7609018	.9627618
mage2	1.00268	.0010671	2.52	0.012	1.000591	1.004774
border	1.059005	.0375963	1.61	0.106	.9878226	1.135316
p0014	1.790715	.3899374	2.68	0.007	1.168619	2.743974
p1523	.8967051	.1696206	-0.58	0.564	.6189227	1.299161
p2435	.7923456	.1489941	-1.24	0.216	.5480915	1.14545
p36up	.6810089	.1444591	-1.81	0.070	.449357	1.032082
pdead	.948696	.1702308	-0.29	0.769	.6674064	1.34854
comp12	4.941595	2.307624	3.42	0.001	1.978671	12.3413
comp24e	4.534147	3.335828	2.05	0.040	1.072151	19.17499
comp24l	.8459522	.3100246	-0.46	0.648	.4124748	1.734979
/lnsig2u	-1.672034	.6326815			-2.912067	-.4320015
sigma_u	.4334333	.1371126			.2331592	.8057347
rho	.1025014	.0582035			.0319916	.2829852

```
Likelihood-ratio test of rho=0: chibar2(01) =     2.98 Prob >= chibar2 = 0.042
```

The estimated subject-specific or conditional hazard ratios and their corresponding 95% confidence intervals were also shown under "Random intercept" in table 14.3.

The estimated residual correlation among the latent responses for two children of the same mother is only

$$\widehat{\rho} = \frac{\widehat{\psi}}{\widehat{\psi} + \pi^2/6} = \frac{0.433^2}{0.433^2 + \pi^2/6} = 0.10$$

(given as `rho` in the output), suggesting that there is not much dependence among the survival times for children of the same mother after controlling for the observed covariates.

Because of the small within-mother correlation, the estimated hazard ratios are close to those from the model without a random intercept. Not surprisingly, we see from the output that the test of the null hypothesis of zero between-mother variance, H_0: $\psi = 0$,

is barely significant at the 5% level. However, `pdead`, a dummy variable for the previous child having died before conception of the index child is included in the model, so some of the dependence among the siblings is captured by the fixed part of the model.

Another way of assessing the degree of unobserved heterogeneity is in terms of the median hazard ratio. Imagine randomly drawing children with the same covariate values but having different mothers j and j'. The hazard ratio comparing the child whose mother has the larger random intercept with the other child is given by $\exp(|\zeta_j - \zeta_{j'}|)$. Following the derivation in section 10.9.2, the median hazard ratio is given by

$$\text{HR}_{\text{median}} = \exp\left\{\sqrt{2\psi}\Phi^{-1}(3/4)\right\}$$

Plugging in the parameter estimates, we obtain $\widehat{\text{HR}}_{\text{median}}$:

```
. display exp(sqrt(2*.433433^2)*invnormal(3/4))
1.5120099
```

When two children with the same covariate values but different mothers are randomly sampled, the hazard ratio comparing the child who has the larger hazard with the child who has the smaller hazard will exceed 1.51 in 50% of the samples, which is of moderate magnitude compared with the estimated hazard ratios for some of the covariates.

14.8 ❖ Population-averaged or marginal vs. subject-specific or conditional survival probabilities

We now consider the model-implied subject-specific or conditional survival probabilities, given that $\zeta_j = 0$, as well as the corresponding population-averaged or marginal survival probabilities, integrating over the random-intercept distribution.

The predicted conditional or mother-specific survival probabilities for $\zeta_j = 0$ are given by

$$S^C_{tij} = \prod_{s=1}^{t}\{1 - \text{cloglog}^{-1}(\widehat{\alpha}_1 d_{1sij} + \cdots + \widehat{\beta}_{12}x_{12,sij} + \underbrace{0}_{\zeta_j})\}$$

and the predicted marginal or population-averaged survival probabilities are given by

$$S^M_{tij} = \int\left[\prod_{s=1}^{t}\{1 - \text{cloglog}^{-1}(\widehat{\alpha}_1 d_{1sij} + \cdots + \widehat{\beta}_{12}x_{12,sij} + \zeta_j)\}\right]\phi(\zeta_j; 0, \widehat{\psi})\, d\zeta_j$$

The product inside the square brackets is the probability that a child with given covariates and a given value of the random intercept ζ_j survives past time t. Integrating this over the random-intercept distribution gives the corresponding survival probability, averaged over all children with the same covariate values. As explained in section 10.8, marginal probabilities are different from conditional probabilities evaluated at the population mean of the random intercept. Indeed, the marginal survival curve need not

correspond to any subject-specific survival curve because at each point in time it represents the average over the selected population of subjects who are still at risk at that time.

For a mother with one child in the data who was censored at time t, the contribution to the marginal likelihood has exactly the same form as S^M_{tij}. By constructing an appropriate prediction dataset, we can therefore obtain S^M_{tij} by calculating the marginal likelihood contributions using `gllapred` with the `ll` option, but first we must fit the model using `gllamm`:

```
. gllamm y int1-int5 mage mage2 border p0014 p1523 p2435 p36up pdead
> comp12 comp24e comp24l, noconstant eform i(momid) link(cll) family(binomial)
> adapt

number of level 1 units = 13854
number of level 2 units = 851

Condition Number = 27451.829

gllamm model

log likelihood = -1782.702
```

y	exp(b)	Std. Err.	z	P>|z|	[95% Conf.	Interval]
int1	.2333055	.1806242	-1.88	0.060	.0511597	1.063951
int2	.2071278	.1606663	-2.03	0.042	.0452869	.947336
int3	.1591135	.1239584	-2.36	0.018	.03456	.7325563
int4	.2358809	.1833625	-1.86	0.063	.0514054	1.082371
int5	.1261616	.0999049	-2.61	0.009	.0267225	.5956308
mage	.8559022	.0513834	-2.59	0.010	.7608919	.9627761
mage2	1.00268	.0010672	2.51	0.012	1.000591	1.004774
border	1.059005	.0375963	1.61	0.106	.9878227	1.135317
p0014	1.790712	.3899412	2.68	0.007	1.168611	2.743983
p1523	.8967037	.1696228	-0.58	0.564	.6189185	1.299165
p2435	.7923441	.1489964	-1.24	0.216	.548087	1.145455
p36up	.6810076	.1444607	-1.81	0.070	.4493538	1.032085
pdead	.9487002	.1702355	-0.29	0.769	.6674039	1.348557
comp12	4.941589	2.307621	3.42	0.001	1.978668	12.34128
comp24e	4.534112	3.335808	2.05	0.040	1.07214	19.17489
comp24l	.8459486	.310024	-0.46	0.648	.4124724	1.734974

```
Variances and covariances of random effects
------------------------------------------------------------------------------

***level 2 (momid)

    var(1): .18785803 (.11886731)
------------------------------------------------------------------------------
```

Now we will produce a small prediction dataset from the data for child 101 because this child has a row of data for each interval (we will not save the data first, but sometimes this may be a good idea):

```
. keep if kidid==101
```

It is required that `y` be zero for each interval, which is already true. We can change the covariates to whatever values we want and then save the data under the name `junk.dta`

```
. replace pdead = 0
. replace p2435 = 0
. save junk, replace
```

We now replicate the data five times for this child, creating unique identifiers 1–5 in `kidid` for the replications. To obtain S_{tij}^{M} for $t = 1, \ldots, 5$, we let child 1 have data for interval 1 only (corresponding to censoring at $t = 1$), child 2 for intervals 1 and 2, etc. The likelihood contributions for children 1–5 will then correspond to the marginal survival probabilities for times 1–5, respectively.

We first produce data for the five children by appending the data for child 101 to itself four times, changing `kidid` appropriately each time,

```
. replace kidid = 1
. append using junk
. replace kidid = 2 if kidid==101
. append using junk
. replace kidid = 3 if kidid==101
. append using junk
. replace kidid = 4 if kidid==101
. append using junk
. replace kidid = 5 if kidid==101
```

and then delete the unnecessary rows of data:

```
. drop if interval > kidid
```

The data now look like the following:

```
. sort kidid interval
. list kidid interval y, sepby(kidid) noobs
```

kidid	interval	y
1	1	0
2	1	0
2	2	0
3	1	0
3	2	0
3	3	0
4	1	0
4	2	0
4	3	0
4	4	0
5	1	0
5	2	0
5	3	0
5	4	0
5	5	0

For the log-likelihood contributions to correspond to $\ln S_{tij}^{M}$, we must have one child per mother (otherwise we would get joint survival probabilities for all children):

```
. replace momid = kidid
```

The log-likelihood contributions are obtained using `gllapred` with the `ll` option, and with the `fsample` option to get predictions for the full sample (not just the estimation sample but everyone in the data):

```
. gllapred loglik, ll fsample
```

The population-averaged or marginal survival probabilities S_{tij}^{M}, called `msurv`, are then obtained by exponentiation:

```
. generate msurv = exp(loglik)
```

The mother-specific or conditional hazards can be obtained by defining a variable, `zeta1`, for the random-intercept values and then using the `mu` (and not `marginal`) option, together with the `us(zeta)` option:

```
. generate zeta1 = 0
. gllapred chaz, mu us(zeta) fsample
(mu will be stored in chaz)
```

To get the corresponding conditional survival probabilities S_{tij}^{C}, we use commands similar to those on page 762:

```
. generate ln1mchaz = ln(1-chaz)
. by kidid (interval), sort: generate sln1mchaz = sum(ln1mchaz)
. generate csurv = exp(sln1mchaz)
```

We can now plot the survival probabilities as a function of `interval`:

```
. twoway (line msurv interval if kidid==interval, sort lpatt(solid))
> (line csurv interval if kidid==5, sort lpatt(dash)),
> legend(order(1 "marginal" 2 "conditional"))
> ytitle(Survival probability)
```

This command produces figure 14.6.

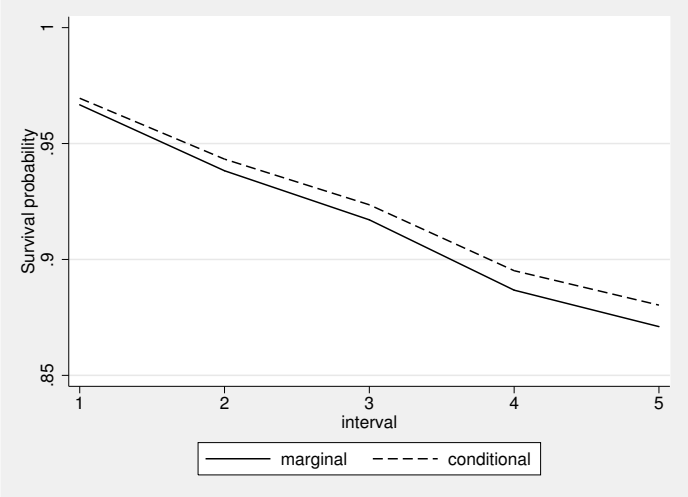


Figure 14.6: Predicted subject-specific or conditional survival functions and population-averaged or marginal survival functions

We see that the conditional and marginal survival curves are similar because of the relatively small random-intercept variance.

14.9 Summary and further reading

We have demonstrated how discrete-time survival analysis can proceed by using standard models for dichotomous responses once the data have been expanded appropriately. Using a logit link gives the continuation-ratio logit model in which the conditional odds of the event occurring given that it has not yet occurred are proportional. Using a complementary log-log link corresponds to proportional hazards in continuous time. In both models, proportionality can be relaxed by constructing appropriate time-varying covariates by multiplying the covariates with dummy variables for time intervals (or other functions of time); see also exercises 14.4, 14.5, and 14.6.

Discrete-time survival analysis can also be performed using versions of the cumulative model for ordinal responses discussed in chapter 11 that allow for right-censoring. These models are sometimes called grouped continuous models, whereas the models discussed in this chapter are called continuation-ratio models. A major drawback of the ordinal approach is that time-varying covariates cannot be handled.

Good introductory books on survival analysis in general include Collett (2003b) and Hosmer, Lemeshow, and May (2008) for medicine and Allison (1984, 1995), Singer and Willett (2003), and Box-Steffensmeier and Jones (2004) for social science. Useful introductory articles on single-level discrete-time survival modeling include Allison (1982) and Singer and Willett (1993).

To accommodate clustered or multilevel survival data, we can include random effects in discrete-time survival models. Here we have included a random intercept, the exponential of which is usually called a *frailty* in the survival context. Random coefficients could of course also be included in the same manner as demonstrated in other chapters of the book, using `xtmelogit` or `gllamm`.

Multilevel discrete-time survival models are discussed for instance in the papers by Hedeker, Siddiqui, and Hu (2000), Barber et al. (2000), Rabe-Hesketh, Yang, and Pickles (2001b), and Grilli (2005). Models with discrete random effects, and many other issues in survival analysis, are discussed in the book by Vermunt (1997).

There are three exercises on single-level discrete-time survival analysis: exercise 14.1 based on the promotions data used in this chapter, exercise 14.2 on teacher turnover, and exercise 14.3 on the time to first sexual intercourse. Exercises on multilevel discrete-time survival analysis are based on the child mortality data used in this chapter (exercise 14.4), survey data on the length of schooling among brothers (exercise 14.5), a randomized trial on time to onset of blindness in patients with diabetic retinopathy (exercise 14.6), and a cluster-randomized intervention to reduce the risk of onset of smoking (exercise 14.7). Exercise 14.8 on early math proficiency is not about survival but uses the continuation-ratio logit model for the cognitive milestone reached.

14.10 Exercises

14.1 Assistant professor promotions data

In this exercise, we revisit the dataset `promotion.dta` on promotion to associate professor that was used to introduce discrete-time survival modeling.

1. Fit the logistic regression model considered on page 766.
2. Modify the model from step 1 by using a low-order polynomial of time instead of dummy variables for time. Start with a linear relationship and include successively higher-order terms until the highest-order term is not significant at the 5% level.
3. Produce graphs of the model-implied discrete-time hazards for professors 1 and 4 using the models from steps 1 and 2.

4. Fit the model from step 1 but with a complementary log-log link instead of a logit link.
5. Interpret the estimated exponentiated regression coefficients from step 4 for `undgrad` and `art`.
6. For individuals 1 and 4, plot the model-implied survival functions for the models with a logit link (from step 1) and a complementary log-log link (from step 4). Compare the curves for the two different models for the same individual.

14.2 Teacher turnover data

Here we consider data from Singer (1993) made available by Singer and Willett (2003). The careers of 3,941 special educators newly hired in Michigan public schools between 1972 and 1978 were tracked for 13 years. The outcome of interest is the number of years the teachers worked at the school, from the date they were hired until they left the school.

The variables in the dataset `teachers.dta` are

- `id`: teacher identifier
- `t`: number of years teacher worked at the school, that is, time to leaving school (no censoring) or end of study (censoring)
- `censor`: censoring indicator, equal to 1 if censored and 0 otherwise

1. Expand the data to person–years.
2. Obtain predicted hazards using a regression model of your choice with dummy variables for the periods.
3. Calculate and plot the predicted survival function over time.
4. Fit a continuation-ratio logit discrete-time survival model with a polynomial in time. What order of the polynomial seems to be required?
5. Produce a graph of the model-implied survival functions for the models in steps 2 and 4.

14.3 First sexual intercourse data

We now analyze the age at first intercourse data from Capaldi, Crosby, and Stoolmiller (1996) that is supplied with the book by Singer and Willett (2003). One hundred eighty at-risk boys (who had not had intercourse before) were followed from grades 6–12 and the date of first intercourse was recorded.

The variables in `firstsex.dta` are

- `id`: boy identifier (j)
- `time`: grade (school-year) in which either intercourse occurred (no censoring) or the boy dropped out of the study (censoring). Children are about 6 years old in first grade, so their approximate age in a given grade is the grade plus 5 years.

- `censor`: censoring indicator, equal to 1 if censored and 0 otherwise
- `pt`: a dummy variable for parental transition having occurred before seventh grade (0: lived with both parents; 1: experienced one or more parental transitions)
- `pas`: parental antisocial behavior when the boy was in fourth grade (based on arrests and driver license suspensions, drug-use, subscales 2 and 9 of the Minnesota Multiphasic Personality Inventory, and the mother's age at birth)

1. Expand the data to person–years, remembering that boys in this study could not experience the event before grade 7 (an example of a stock sample; see section 14.2.6).
2. Fit a logistic regression model with a dummy variable for each grade and `pt` as the only covariate, and interpret the exponentiated estimated regression coefficient of `pt`.
3. Plot the predicted survival functions separately for boys who have and have not had parental transitions (variable `pt`).
4. Extend the model by including `pas` as a further covariate, and interpret the exponentiated estimated coefficients of `pt` and `pas`.
5. Is there evidence for an interaction between `pas` and `pt`?

14.4 Child mortality data

Consider some further analyses of the child mortality data from Pebley and Stupp (1987) and Guo and Rodríguez (1992).

In addition to the variables listed in section 14.3, the following variables are included in `mortality.dta`:

- `sex`: sex of child (0: female; 1: male)
- `home`: dummy variable for child being born at home (1: home; 0: clinic or hospital)
- `edyears`: mother's years of education
- `income`: family annual income in quetzales in 1974–1975; the quetzal was pegged to the U.S.$ with a fixed exchange rate of 1 quetzal = 1 U.S.$. Missing responses are coded as −9.

1. Repeat the analyses presented in section 14.7.2.
2. Add the variables given above to the analysis.
3. Interpret the estimated hazard ratios for these new variables.
4. Relax the proportional-hazards assumption for home birth. Specifically, include an interaction between the first time interval and home birth to test whether home birth has a greater effect on the hazard of death shortly after, or during, birth than later on.

14.5 Brothers' school transition data

Mare (1994) analyzed data from the 1973 Occupational Changes in a Generation II survey (OCG) to investigate the relationship between the educational attainment of fathers and their sons. He selected male respondents who had at least one brother and considered the years of schooling of the respondent, his oldest brother, and his father.

The variables in `brothers.dta` are

- `id`: family identifier
- `brother`: brother identifier (0: respondent; 1: respondent's brother)
- `time`: length of schooling (1: <12 years; 2: 12 years; 3: ≥13 years)
- `feduc`: length of schooling for father (1: 0–8 years; 2: 9–11 years; 3: 12 years; 4: 13–15 years; 5: ≥16 years)
- `freq`: number of families

The data are in collapsed form, with `freq` indicating the number of families having the given levels of education for the respondent, his brother, and his father.

1. Expand the data so that there is one row of data for the transition to the 12th year of schooling for every subject and another row of data for the transition to the 13th year of schooling for those brothers who had 13 years or more of schooling. Define a variable, `transition`, equal to 1 and 2 for the two transitions and a dummy variable, `event`, equal to 1 if the transition occurred and 0 otherwise. This is just the expansion to person–period data discussed in this chapter except that the response variable is now a dummy variable for continuing in education ("censoring"), not for leaving.
2. For the respondents (and not their brothers), fit a continuation-ratio logit model with dummy variables `tr1` and `tr2` for the two transitions and dummy variables `ed2` to `ed5` for father's education levels 2 to 5. Use `freq` as frequency weights (see `help weights`).
3. Now relax the proportional odds assumption by allowing the effect of father's education to be different for the first and second transitions. Use a likelihood-ratio test (at the 5% level) to choose the more appropriate model.
4. Fit the model selected in step 2 for both brothers, assuming that the covariate effects are the same for both brothers, and including a random intercept for families. Use `gllamm`, specifying `freq` as level-2 weights by first renaming `freq` to `wt2` and then using the `gllamm` option `weight(wt)`.
5. Interpret the parameter estimates for the random-intercept model.

14.6 Blindness data

Diabetic retinopathy is a complication associated with diabetes mellitus and is a major cause of visual loss. Huster, Brookmeyer, and Self (1989) describe data from the Diabetic Retinopathy Study (DRS) conducted in 1971 to investigate the

effectiveness of laser photocoagulation in delaying the onset of blindness in patients with diabetic retinopathy. One eye of each patient was randomly selected for treatment, and patients were assessed at 4-month intervals. The endpoint used to assess the treatment effect was the occurrence of visual acuity less than 5/200 at two consecutive assessments. The data considered by Huster, Brookmeyer, and Self (1989) and provided by Ross and Moore (1999) are a 50% sample of the high-risk patients as defined by DRS criteria. Following Ross and Moore (1999), we treat the data as discrete-time survival data using the intervals [6,10), [10,14), . . . , [50,54), [54,58), [58,66), [66,83).

The variables in `blindness.dta` are

- `id`: patient identifier
- `eye`: eye identifier
- `treat`: dummy variable for eye being treated by photocoagulation
- `time`: onset of blindness in months
- `discrete`: discrete-time intervals 1: [6,10); 2: [10,14); . . .; 12: [50,54); 13: [54,58); 14: [58,66); 15: [66,83)
- `censor`: dummy variable for blindness occurring
- `late`: dummy variable for late onset, or adult diabetes (onset at age 20 or later)

1. Expand the data to eye periods, with periods defined by the variable `discrete`.
2. Fit a continuation-ratio logit discrete-time survival model with dummy variables for time intervals; `treat`, `late`, and their interaction as covariates; and a random intercept for patients.
3. Test the proportional odds assumption for `treat` by including an interaction between `treat` and a new variable, `midp`, defined as the middle of the discrete-time intervals. (Hint: Except for the last two intervals, `midp` = 4 + 4*`discrete`.)
4. ❖ For the selected model, plot the model-implied marginal survival functions for the two eyes for patients with late onset diabetes.

See also exercise 15.6 for continuous-time analysis of these data.

14.7 Cigarette data Solutions

Hedeker, Siddiqui, and Hu (2000) analyzed data from a subset of the Television School and Family Smoking Prevention and Cessation Project (TVSFP; see Flay et al. [1988]). The data are supplied with the SuperMix program (Hedeker et al. 2008).

In 1986, schools in Los Angeles were randomized to one of four conditions given by different combinations of two factors: (1) TV: a media (television) intervention (1: present; 0: absent) and (2) CC: a social-resistance classroom curriculum

(1: present; 0: absent). The intervention took place when the students were in seventh grade (when the children were about 12 years old). The students were assessed pre- and postintervention in 1986 and again a year later and two years later. At each of the four time points, the students were asked: "Have you ever smoked a cigarette?" To estimate the effect of the intervention, only those who answered "no" to the question before the intervention were included in the study. The first time the students answered "yes" after the intervention will be the event of interest in this exercise.

In addition to the clustering of students in classes, the classes are clustered in schools. We will consider two-level models in this exercise but will revisit the data for three-level modeling in exercise 16.5.

The variables in `cigarette.dta` are

- `school`: school identifier
- `class`: class identifier
- `time`: postintervention time point (1: 7th grade; 2: 8th grade; 3: 9th grade)
- `event`: dummy variable for student responding "yes" to the question about smoking
- `cc`: social-resistance classroom curriculum (dummy variable)
- `tv`: television intervention (dummy variable)

1. Expand the data to person–period data.
2. Estimate the discrete-time model that assumes the continuous-time hazards to be proportional. Include `cc`, `tv`, and their interaction as explanatory variables and specify a random intercept for classes. Use dummy variables for periods.
3. Interpret the exponentials of the estimated regression coefficients.
4. Obtain the estimated residual intraclass correlation of the latent responses.

See also exercise 16.5 for three-level models of these data.

14.8 Early childhood math proficiency data

In this exercise, we analyze the data described in exercise 11.9. There are two datasets: `ecls_child.dta` contains the student-level data and `ecls_school.dta` contains the school-level data.

As described in exercise 11.9, the response variable, math proficiency, is the highest of five developmental milestones reached, where it is assumed that a given milestone can be reached only after reaching the previous milestone. Although these data are not survival data, it makes sense to fit a continuation-ratio logit model because children are assumed to progress through the stages sequentially. However, instead of modeling the odds of stopping at a given milestone given that it has been reached, as in discrete-time survival, it makes more sense to model the odds of progressing to the next milestone given that the milestone has been

reached. The data expansion will be the same as discussed in this chapter, but the response variable will be 1 for every milestone where the child did *not* stop (analogous to censoring) and 0 for the highest milestone the child reached (analogous to death). Because 5 is the highest level that can be reached, everyone with data for that level in the expanded dataset will have a 0 response. In the expanded data, there should therefore not be a row of data for level 5.

The first three steps of the exercise below are identical to the first three steps of exercise 11.9.

1. Use the `merge` command to combine the two datasets.
2. Create a numeric school identifier from the string variable `s4_id`.
3. Summarize the student-level and school-level variables, treating school as the unit of analysis when summarizing school-level variables.
4. Fit a continuation-ratio logit model to the math proficiency data with `numrisks`, `nbhoodcl`, and `pubpriv2` as covariates. Because `profmath` takes the value 0 for only nine children, merge the lowest two categories before fitting the model. See text above for how to expand the data and define the response variable.
5. Interpret the estimates.

15 Continuous-time survival

15.1 Introduction

In this chapter, we consider continuous survival data or duration data where an event (such as death) can occur at any instant in continuous time and survival times can be viewed as recorded on a continuous scale. In contrast, survival data are viewed as discrete when the event can occur only at specific time points (as in the number of menstrual cycles until conception) or when the time units are coarse (as in the number of semesters until dropout from university). In theory, a continuous scale implies that there is a zero probability of ties, where several units have identical survival times. In practice, the survival times are of course rounded, for instance, to seconds, hours, or days, depending on the application. However, the time units must be sufficiently small for the probability of ties to be small. If ties are common, the data are typically treated as discrete-time survival data and the methods discussed in the previous chapter are used.

Basic features of survival data, such as censoring, truncation, delayed entry, and time-varying covariates, were discussed in the *Introduction to models for survival or duration data (part VII)*. We assume that you have read this introduction before embarking on this chapter.

15.2 What makes marriages fail?

We will use data from the 1968–1990 waves of the Panel Study of Income Dynamics (PSID) to introduce survival modeling. The PSID is the world's longest running household panel survey, starting in 1968 with a sample of approximately 5,500 U.S. individuals and their families. The household members and their children were followed up even if they moved out of the original household. New households formed by sample members were also followed and interviewed in the same way as the original households. The sample members were surveyed annually.

The dataset is from the aML manual (Lillard and Panis 2003) and is part of the data used by Lillard and Panis (1996) that included all respondents who survived and remained in the panel through 1984. In 1985, the PSID collected special retrospective marital and fertility histories of both the household heads and their spouses and continually updated the information since then. This information was available on 95% of the sample. For the remaining respondents, Lillard and Panis (1996) constructed marriage

histories using 1968–1990 panel information, including more highly detailed questions in 1968 (for the male head) and 1976 (for the wife).

The variable of main interest for us is the duration of the respondents' first marriage until divorce or censoring. Censoring can occur because individuals drop out of the study, because of death of a spouse, or because the first marriage is intact at the last interview. If divorced, the respondents were asked in which month of which year they were divorced. However, in some cases, the recall was less precise and the variables `lower` and `upper` provide the lower and upper bounds of the time interval in which divorce occurred. For right-censored durations, the lower and upper time bounds are identical. To produce a continuous time variable when the bounds were different, we simulated random numbers from uniform distributions on the intervals.

The sample includes only individuals who were married at least once. The unit of analysis is the couple, but this need not be a couple that is cohabiting at any of the panel waves. For divorcees, the couple would be themselves and their spouse from their first marriage.

The file `divorce.dta` contains the following variables for 3,371 couples:

- `id`: identification number for couple
- `lower`: lower bound for time from wedding to divorce in years
- `upper`: upper bound for time from wedding to divorce in years
- `dur`: time from wedding to divorce or censoring in years; made continuous if `lower` $\neq$ `upper` by simulating from a uniform distribution on [`lower`,`upper`)
- `divorce`: dummy variable for marriage ending in divorce (1: divorce; 0: censored)
- `hiseduc`: husband's education in years of schooling
- `hereduc`: wife's education in years of schooling
- `heblack`: dummy variable for husband being black (1: black; 0: nonblack)
- `sheblack`: dummy variable for wife being black (1: black; 0: nonblack)
- `agediff`: age difference between husband and wife in years (positive value means husband is older)

We start by reading in the divorce data:

```
. use http://www.stata-press.com/data/mlmus3/divorce
```

Following Lillard and Panis (2003), we then construct several dummy variables that will be used as covariates: `mixrace` for marriage being between spouses of different races,

```
. generate mixrace = (heblack & !sheblack) | (sheblack & !heblack)
```

`hedropout` for husband having less than 12 years of education,

```
. generate hedropout = hiseduc<12
```

`hecollege` for husband having 16 years or more of education,

```
. generate hecollege = hiseduc>=16 if hiseduc<.
```

`heolder` for husband being 10 years or more older than his wife,

```
. generate heolder = agediff > 10 if agediff<.
```

and `sheolder` for wife being 10 years or more older than her husband,

```
. generate sheolder = agediff< -10
```

15.3 Hazards and survival

We assume that the events are *absorbing* in the sense that once an event has occurred for a unit, the unit is no longer at risk for this event. For instance, after break up of a first marriage, the first marriage can no longer break up (although subsequent marriages can of course break up).

The time or duration from becoming at risk of experiencing the event is called the *survival time* and is denoted t. The survival time t may be regarded as a realization of a continuous random variable T with a cumulative density function $F(t)$ and probability density function $f(t)$. In the divorce dataset, the observed time from the first wedding to divorce for a particular couple i is denoted t_i (its value is unknown when `divorce`=0).

The start of the observation period coincides with the time of becoming at risk of divorce (time of wedding) because respondents report the wedding and divorce dates of their first marriage retrospectively. If, instead of considering the break up of the first marriage, the survey had focused on break up of the marriage that couples were in at the first panel wave in 1968, we would have delayed entry. This means that all couples who married before 1968 have been at risk of divorce before entering the study. Couples who divorced before 1968 would not have been included in the dataset (unless they have remarried). As discussed in section 14.2.6, such a design is known to suffer from length-biased sampling.

An obvious quantity of interest in survival analysis is the probability of surviving to time t or beyond, the *survival function* $S(t)$, which is given by

$$S(t) \equiv \Pr(T \geq t) \;=\; 1 - F(t) \tag{15.1}$$

where $F(\cdot)$ is a cumulative density function.

A further function of interest for survival data is the *hazard function*, *intensity function*, or *incidence rate* $h(t)$. This represents the instantaneous risk of the event per unit of time, given that the event has not yet occurred.

To obtain a formal definition of the hazard, consider an event occurring in a time interval from t to $t + \Delta$ (where Δ is positive), that is, $t \leq T < t + \Delta$. If we want the probability of the event occurring in the interval among those still at risk of experiencing the event, we must condition on the event not yet having occurred at time t, that is,

$T \geq t$. The conditional probability of the event occurring in the time interval given that the event has not yet occurred is $\Pr(t \leq T < t + \Delta | T \geq t)$. The hazard is this probability divided by the length of the time interval Δ when the time interval becomes tiny:

$$h(t) \equiv \lim_{\Delta \to 0} \left\{ \frac{\Pr(t \leq T < t + \Delta | T \geq t)}{\Delta} \right\} \tag{15.2}$$

Note that the hazard is a *rate*, expressed in units of 1 over time, for example, per second or per month.

The hazard function (15.2) can alternatively be expressed as the density function $f(t)$ divided by the survival function $S(t)$:

$$h(t) = \frac{f(t)}{S(t)}$$

The survival function (15.1) can alternatively be expressed as

$$S(t) = \exp\{-H(t)\} = \exp\{-\underbrace{\int_0^t h(u)\,\mathrm{d}u}_{H(t)}\} \tag{15.3}$$

where $H(t)$ is the *integrated hazard function* or *cumulative hazard function*. Display 15.1 derives these relationships, but we invite you to skip these derivations because they involve calculus and are somewhat more technical than most of the book.

1. Demonstrating that $h(t) = f(t)/S(t)$:

   Because $\Pr(A|B) = \Pr(A, B)/\Pr(B)$, we obtain

   $$\Pr(t \le T < t + \Delta | T \ge t) \;=\; \frac{\Pr(t \le T < t + \Delta, T \ge t)}{\Pr(T \ge t)} = \frac{\Pr(t \le T < t + \Delta)}{\Pr(T \ge t)}$$

   Using the definitions of cumulative density function and survival function, we see that the numerator and denominator become

   $$\Pr(t \le T < t + \Delta) \;=\; F(t + \Delta) - F(t)$$

   and

   $$\Pr(T \ge t) \;=\; S(t)$$

   Then from (15.2),

   $$\begin{aligned} h(t) &= \lim_{\Delta \to 0} \left\{ \frac{\Pr(t \le T < t + \Delta | T \ge t)}{\Delta} \right\} \\ &= \lim_{\Delta \to 0} \left[\frac{\{F(t + \Delta) - F(t)\}/S(t)}{\Delta} \right] \\ &= \lim_{\Delta \to 0} \left\{ \frac{F(t + \Delta) - F(t)}{\Delta} \right\} \frac{1}{S(t)} \end{aligned}$$

   Because the density function is the derivative of the cumulative density function,

   $$f(t) \;=\; \frac{\partial F(t)}{\partial t} \equiv \lim_{\Delta \to 0} \left\{ \frac{F(t + \Delta) - F(t)}{\Delta} \right\}$$

   it follows that

   $$h(t) \;=\; \frac{f(t)}{S(t)}$$

2. Demonstrating that $S(t) = \exp\{-H(t)\}$:

   By the chain rule, we obtain

   $$\frac{\partial \ln\{S(t)\}}{\partial t} \;=\; \frac{1}{S(t)} \frac{\partial S(t)}{\partial t} = \frac{1}{S(t)} \frac{\partial [1 - F(t)]}{\partial t} = -\frac{f(t)}{S(t)} \;=\; -h(t)$$

   Integrating both sides, we get

   $$\ln\{S(t)\} \;=\; \int_0^t -h(u)\, \mathrm{d}u \;=\; -H(t)$$

   and exponentiating both sides, it follows that

   $$S(t) \;=\; \exp\{-H(t)\}$$

Display 15.1: Demonstration of two central relations in survival analysis: $h(t) = f(t)/S(t)$ and $S(t) = \exp\{-H(t)\}$

Returning to the divorce data, we start by listing the variables `id`, `dur`, and `divorce` for the first four couples:

```
. list id dur divorce in 1/4, clean noobs
    id        dur   divorce
     9     10.546         0
    11     34.943         0
    13   2.870226         1
    15   18.18403         1
```

We see that the marriage of couple 13 lasted 2.87 years before it ended in divorce (`divorce` takes the value 1), whereas the marriage of couple 9 was still intact after 10.55 years when the couple was censored (`divorce` takes the value 0).

To allow us to use Stata's survival time commands (which have the prefix `st` for "survival time"), we now declare or *set* the data to be survival data by using the `stset` command:

```
. stset dur, failure(divorce) id(id)
                id:  id
     failure event:  divorce != 0 & divorce < .
obs. time interval:  (dur[_n-1], dur]
 exit on or before:  failure
------------------------------------------------------------------------------
     3371  total obs.
        0  exclusions
------------------------------------------------------------------------------
     3371  obs. remaining, representing
     3371  subjects
     1032  failures in single failure-per-subject data
 62098.25  total analysis time at risk, at risk from t =         0
                             earliest observed entry t =         0
                                  last observed exit t =    73.068
```

The first argument, `dur`, declares that this variable contains the time from wedding to divorce or censoring. The Stata documentation calls time scales that are 0 at the time a unit becomes at risk of the event, here the time of the wedding, *analysis time*. If we had used the calendar time at the divorce, we would have to specify the wedding date in the `origin()` option. The observation period is assumed to start when `dur` is zero. If there had been delayed entry, we would need to use the `enter()` option to specify the time observation began on the `dur` time scale. For example, if the survey questions had been about the marriage couples were in at the first panel wave, the `enter()` option would specify a variable containing the number of years couples were already married at the time of the first panel wave.

The option `failure(divorce)` designates `divorce` as the indicator for divorce (and not censoring), and the option `id(id)` designates `id` as the couple identifier. In the output, `failure event: divorce != 0 & divorce < .` means that the event is assumed to occur when the variable `divorce` does not take the value 0 (hence taking the value 1 for divorce) and is not missing. We see that there are 3,371 couples in the dataset and that the marriages of 1,032 of these couples ended in divorce (rather aptly

called "failures" in the output). The total time at risk for the couples is 62,098.25 years, and the longest duration (to divorce or censoring) observed is 73.068 years.

We can estimate the survival function $S(t)$ for the divorce data by using the *Kaplan–Meier estimator* or *product limit estimator* described in display 15.2.

Order the n survival times (all times that end in the event or failure instead of censoring) such that $t_{(1)} \leq t_{(2)} \cdots \leq t_{(n)}$ where $t_{(k)}$ is the kth largest unique survival time. This defines $n-1$ intervals $(t_{(2)} - t_{(1)}), \ldots, (t_{(n)} - t_{(n-1)})$.

The Kaplan–Meier estimator $\widehat{S}(t)$ of the survival function $S(t)$ is defined as

$$\widehat{S}(t) = \prod_{k|t_{(k)} \leq t} \left(1 - \frac{d_k}{r_k}\right)$$

where the product is over all intervals k that end before time t. Here r_k is the number of subjects at risk just before $t_{(k)}$, and d_k is the number who experience the event at time $t_{(k)}$. The ratio d_k/r_k can therefore be interpreted as the estimated probability of experiencing the event at the end of the kth interval, given that the subject is still at risk.

For example, the survival function at the second event time $t_{(2)}$ is equal to the estimated probability of not experiencing the event at time $t_{(1)}$ times the estimated probability of experiencing the event at time $t_{(2)}$, given that the subject is still at risk at $t_{(2)}$.

The form of the Kaplan–Meier estimator is the same as for the life-table estimator for the discrete-time survival function in equation (14.1). The difference is that the intervals are now defined by splitting the analysis time at each of the unique event or failure times in the data.

Display 15.2: Kaplan–Meier estimator of survival function

It is convenient to use the `sts graph` command to produce a plot of the Kaplan–Meier estimates $\widehat{S}(t)$ of the survival function, called a *Kaplan–Meier plot*:

```
. sts graph
        failure _d:  divorce
  analysis time _t:  dur
                id:  id
```

The resulting graph is shown in figure 15.1, where we see that about 10% of the marriages break up within the first 5 years (survival function is at about 0.9), 20% of the marriages break up within the first 10 years, and 35% of the marriages break up within the first 20 years. It appears that about 55% of the marriages are never dissolved in these data.

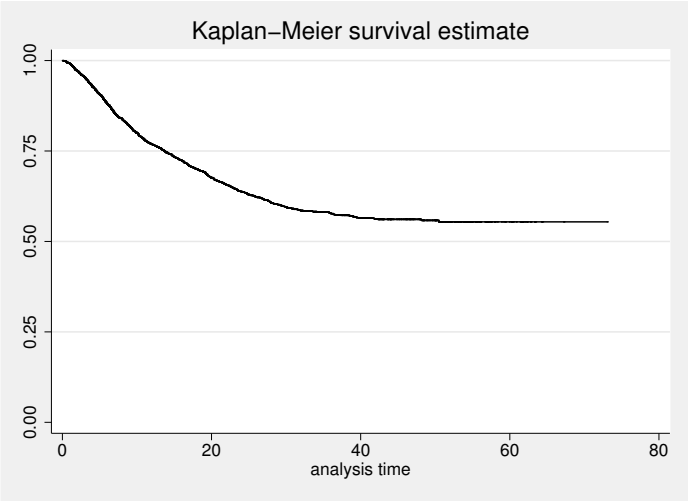


Figure 15.1: Kaplan–Meier survival plot of $\widehat{S}(t)$ for divorce data

We can produce a graph of the estimated hazard function $\widehat{h}(t)$ (using kernel smoothing) by including the `hazard` option in the `sts graph` command:

```
. sts graph, hazard
        failure _d:  divorce
  analysis time _t:  dur
                id:  id
```

The resulting graph is shown in figure 15.2.

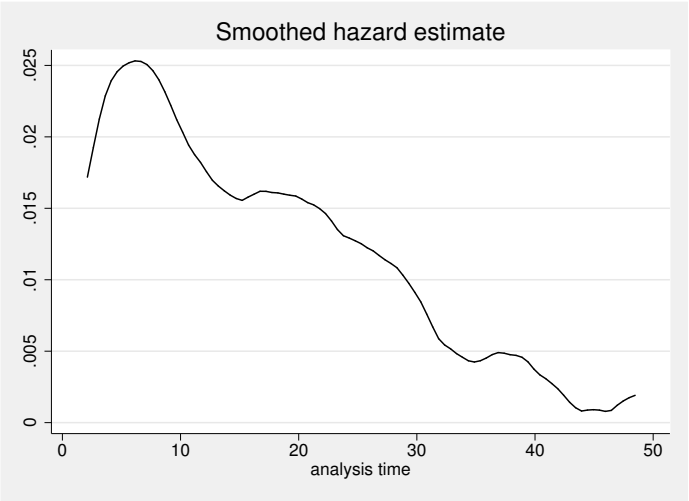


Figure 15.2: Smoothed hazard estimate $\widehat{h}(t)$ for divorce data

The hazard is quite high at the beginning and increases until it reaches a peak at about 7 years of marriage. It is tempting to see this as evidence for the "seven-year itch", famous from a 1955 movie with that title featuring Marilyn Monroe, because the hazard of a given marriage failing apparently increases until 7 years, after which the hazard decreases. However, this hazard function represents the *marginal* or *population-averaged* hazard and does not necessarily reflect the couple-specific hazard for any couple. Later in the chapter (sections 15.9 and 15.10), we discuss models for subject-specific hazards.

15.4 Proportional hazards models

In proportional hazards (PH) models with one covariate x_i, the hazard given the covariate $h(t|x_i)$ is specified as

$$h(t|x_i) \;=\; h_0(t)\exp(\beta x_i) \tag{15.4}$$

where $h_0(t)$ is the *baseline hazard*, the hazard when $x_i = 0$.

The *hazard ratio* or *incidence-rate ratio* associated with a unit increase in x_i, from a value a to $a+1$, becomes

$$\frac{h(t|x_i = a+1)}{h(t|x_i = a)} \;=\; \frac{h_0(t)\exp\{\beta(a+1)\}}{h_0(t)\exp\{\beta(a)\}} = \exp(\beta)$$

Because the hazard ratio is constant over time, the hazard functions of different individuals are proportional, and that is the reason why the model is called a proportional hazards model.

Taking the logarithm on both sides of (15.4), the PH model can alternatively be written as a log-linear model for the hazard

$$\ln\{h(t|x_i)\} \;=\; \ln\{h_0(t)\} + \beta x_i$$

The survival function for the PH model is

$$S(t|x_i) \;\equiv\; \Pr(T_i > t|x_i) \;=\; S_0(t)^{\exp(\beta x_i)}$$

Display 15.3 derives this relationship, but you can skip this if you like.

We start by restating the relation between the survival function $S(t)$ and the cumulative hazards function $H(t)$ given in (15.3)

$$S(t) \;=\; \exp\{-H(t)\} \;=\; \exp\{-\int_0^t h(u)\,\mathrm{d}u\}$$

Substituting the proportional hazards model (15.4) for the hazard $h(u)$, we get

$$\begin{aligned} S(t) &= \exp\{-\int_0^t h_0(u)\exp(\beta x_i)\,\mathrm{d}u\} \\ &= \exp[\{-\int_0^t h_0(u)\,\mathrm{d}u\}\exp(\beta x_i)] \\ &= \exp\{-\int_0^t h_0(u)\,\mathrm{d}u\}^{\exp(\beta x_i)} \end{aligned}$$

Using the definition of the cumulative hazards function and the relation between the survival and cumulative hazards function in (15.3), which also apply to baseline hazards, it follows that

$$\begin{aligned} S(t) &= \exp\{-H_0(t)\}^{\exp(\beta x_i)} \\ &= S_0(t)^{\exp(\beta x_i)} \end{aligned}$$

Display 15.3: Demonstration of $S(t|x_i) = S_0(t)^{\exp(\beta x_i)}$ for proportional hazards model

The simplest and most restrictive assumption for the baseline hazard $h_0(t)$ is that it is constant, $h_0(t) = \lambda$. The corresponding distribution for the survival time is the exponential distribution with mean $1/\lambda$. For example, if the hazard rate is two per day, the average time to the event is half a day. Because the hazard rate λ must be nonnegative, it is convenient to write it as $\lambda = \exp(\alpha_0)$ where there is no constraint on α_0. Note that we use α's instead of β's to refer to coefficients that determine the baseline hazard function $h_0(t)$.

Table 15.1 shows the form of the baseline hazard for the exponential model as well as two more general proportional-hazards models: the Weibull and Gompertz models.

Table 15.1: Parametric proportional hazards models: Name of density $f(t)$, form of baseline hazard function $h_0(t)$, and parameters

$f(t)$	$h_0(t)$	Parameters
Exponential	$\exp(\alpha_0)$	α_0
Weibull	$pt^{p-1}\exp(\alpha_0)$	α_0, p "shape"
Gompertz	$\exp(\gamma t)\exp(\alpha_0)$	α_0, γ "shape"

It is clear that the exponential model is a special case of the Weibull model with $p = 1$ and a special case of the Gompertz model with $\gamma = 0$. The exponential model has a constant baseline hazard, and the Weibull and Gompertz models have monotonic baseline hazards. The hazard of the Weibull model increases with time if $p > 1$ and decreases if $p < 1$, and the hazard of the Gompertz model increases with time if $\gamma > 0$ and decreases if $\gamma < 0$. None of the models therefore appear to be suitable for the divorce data because the smoothed hazard function in figure 15.2 has a peak.

One way to make the parametric proportional hazards models more flexible is to divide the time scale into intervals, each of which has different parameters for the baseline hazard. The most common approach is to construct a piecewise constant baseline hazard $h_0(t)$ by assuming an exponential distribution with different values of α_s for different time intervals. Such a piecewise exponential model is discussed in the next section.

15.4.1 Piecewise exponential model

When using a piecewise exponential model, we have to decide for which intervals or "pieces" we are going to assume that the hazard is constant. Somewhat informed by the shape of the estimated hazard function in figure 15.2, we will use the six intervals (0,1], (1,5], (5,9], (9,15], (15,25], and (25,). Here "(" means that the left-hand-side number is not included in the interval, whereas "[" means that it is included and similarly for the right-hand-side number ")" and "]". So the interval (0,1] does not include 0 (it does however include numbers slightly larger than 0) but does include 1.

We first use the `stptime` (for "person-time") command to estimate the hazard for each of the chosen intervals:

```
. stptime, at(0,1,5,9,15,25)
        failure _d:  divorce
  analysis time _t:  dur
                id:  id
```

Cohort	person-time	failures	rate	[95% Conf.	Interval]
(0 - 1]	3337.4472	30	.00898891	.0062849	.0128562
(1 - 5]	12023.083	270	.0224568	.0199318	.0253017
(5 - 9]	9816.07	251	.02557031	.0225948	.0289377
(9 - 15]	11438	210	.01835985	.0160373	.0210188
(15 - 25]	12509.839	193	.01542786	.0133978	.0177655
> 25	12973.809	78	.00601211	.0048156	.007506
total	62098.248	1032	.01661883	.0156352	.0176643

The total number of couples at risk at year 0 was 3,371 (the number of couples in the dataset). However, we see from the column called `person-time` that the first-year interval (0,1] contains only 3,337.45 person-years. The difference is due to couples being removed from the risk set because their marriages lasted less than a year or due to censoring within the first year of marriage.

For each time interval, the number of divorces during the time interval is given under `failures`, and the estimated hazard is given under `rate`. For instance, the hazard of divorce in the interval (5,9] is estimated as the number of divorces divided by the number of person-years within the interval, 0.02557031 = 251/9816.07. We see that the estimated hazards of divorce follow the same general pattern as seen in the plot of the estimated hazard function in figure 15.2, peaking in the interval (5,9]. The last two columns contain the lower and upper limits for the estimated 95% confidence intervals for the hazards. If we had instead used the `ltable` command (with the `hazard` and `noadjust` options) discussed for discrete-time survival in chapter 14, we would have obtained estimates of the hazards that do not take into account that the risk set is gradually depleted within each interval.

To fit a piecewise exponential survival model, we use the `stsplit` command to expand the data according to the chosen intervals, producing one row of data or one record for each interval a couple is at risk for divorce. Thereafter, we sort and list the data for the first four couples as before.

```
. stsplit interval, at(1,5,9,15,25)
(10754 observations (episodes) created)
. sort id _t
. list id interval _t0 _t _d if id<34, sepby(id) noobs
```

id	interval	_t0	_t	_d
9	0	0	1	0
9	1	1	5	0
9	5	5	9	0
9	9	9	10.546	0
11	0	0	1	0
11	1	1	5	0
11	5	5	9	0
11	9	9	15	0
11	15	15	25	0
11	25	25	34.943001	0
13	0	0	1	0
13	1	1	2.8702259	1
15	0	0	1	0
15	1	1	5	0
15	5	5	9	0
15	9	9	15	0
15	15	15	18.184032	1
33	0	0	1	0
33	1	1	1.418	0

We see that for each couple, there is one record for each interval they are at risk for divorce. For instance, couple 9 has four records because censoring occurred in the fourth interval, whereas couple 15 has five records because a divorce occurred in the

fifth interval. Each record in the expanded dataset hence represents a part of the history for a couple, called an *episode* in Stata.

The `stsplit` command has split each couple's history into episodes and created variables `_t_0` and `_t` for the start and end times of the episodes. All episodes except the final episode for a couple end at one of the predetermined cutpoints (1, 5, 9, 15, 25), and the couple can be viewed as censored at these times (because nothing happened at these times—we just split up the couple's history there). The variable `_d` takes the value 0 for censoring and 1 for divorce. The variable `interval` keeps track of the intervals and takes the value of the lower bound of each interval (here it is equal to `_t0` because there is no delayed entry). The data expansion is the same as for discrete-time survival discussed in section 14.2.2 (where the intervals here correspond to the discrete times there) except that we keep track of the exact timing of divorces and censoring within each interval in the variable `_t`. Stata interprets the expanded data in exactly the same way as it interpreted the original data. All `st` commands will produce the same output before and after the data expansion.

To understand the expanded data better, we produce a summary table. For each interval, there should be as many records as there were couples at risk of divorce (that is, not yet divorced) at the start of the interval. The sum of the time segments `_t`−`_t0` across all couples represented in a given interval should equal the person-years of observation for that interval, and `_d` should take the value 1 for each couple that got divorced during the interval. We can use the `table` command to tabulate these quantities:

```
. generate pers_yr = _t-_t0
. table interval, contents(freq sum pers_yr sum _d)
```

interval	Freq.	sum(pers_yr)	sum(_d)
0	3,371	3337.447	30
1	3,283	12023.08	270
5	2,728	9816.07	251
9	2,205	11438	210
15	1,627	12509.84	193
25	911	12973.81	78

As expected, the last two columns agree with the first two columns produced by the `stptime` command on page 807; namely, `sum(pers_yr)` corresponds to `person_time` and `sum(_d)` corresponds to `failures`.

The reason for expanding the data was to allow us to include dummy variables for the time bands or intervals in a piecewise exponential survival model. Letting the index $s = 1, \ldots, 6$ denote the intervals in the expanded data, we specify the following model:

$$\ln\{h(t|\mathbf{d}_{si})\} \;=\; \alpha_1 d_{1si} + \alpha_2 d_{2si} + \cdots + \alpha_6 d_{6si} \tag{15.5}$$

where $\mathbf{d}_{si} = (d_{1si}, \ldots, d_{6si})'$ are dummy variables for intervals 1 to 6, the intervals starting at 0, 1, 5, 9, 15, and 25, with corresponding coefficients α_1 to α_6.

Using `ibn.interval` to include dummy variables for all the intervals and the option `noconstant` to suppress the intercept, the `streg` command with the option `distribution(exponential)` fits the piecewise exponential model:

```
. streg ibn.interval, distribution(exponential) noconstant
        failure _d:  divorce
  analysis time _t:  dur
                id:  id

Exponential regression -- log relative-hazard form

No. of subjects =         3371                     Number of obs   =     14125
No. of failures =         1032
Time at risk    =  62098.24824
                                                   Wald chi2(6)    =  16685.34
Log likelihood  =    -3077.405                     Prob > chi2     =    0.0000

------------------------------------------------------------------------------
          _t | Haz. Ratio   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
    interval |
           0 |   .0089889   .0016411   -25.81   0.000     .0062849    .0128562
           1 |   .0224568   .0013667   -62.38   0.000     .0199318    .0253017
           5 |   .0255703    .001614   -58.09   0.000     .0225948    .0289377
           9 |   .0183599    .001267   -57.93   0.000     .0160373    .0210188
          15 |   .0154279   .0011105   -57.95   0.000     .0133978    .0177655
          25 |   .0060121   .0006807   -45.17   0.000     .0048156     .007506
------------------------------------------------------------------------------
note: no constant term was estimated in the main equation
```

We see that the estimated hazards and their confidence intervals are identical to those previously produced by the `stptime` command on page 807 (the label `Haz. Ratio` is misleading here because the exponentiated coefficients are hazards due to omission of an intercept).

The benefit of using `streg` is that it makes it straightforward to include covariates in the analysis. Here we include the covariates `heblack` (x_{2i}), `mixrace` (x_{3i}), `hedropout` (x_{4i}), `hecollege` (x_{5i}), `heolder` (x_{6i}), and `sheolder` (x_{7i}), and let the corresponding coefficients be denoted β_2 to β_7. The piecewise exponential model becomes

$$\ln\{h(t|\mathbf{d}_{si},\mathbf{x}_i)\} = \underbrace{\alpha_1 d_{1si}+\alpha_2 d_{2si}+\cdots+\alpha_6 d_{6si}}_{\ln\{h_0(t)\}}+\beta_2 x_{2i}+\cdots+\beta_7 x_{7i} \tag{15.6}$$

where the *baseline hazard* $h_0(t) \equiv \exp(\alpha_1 d_{1si}+\alpha_2 d_{2si}+\cdots+\alpha_6 d_{6si})$ is the hazard when the covariates take the value zero ($\mathbf{x}_i = \mathbf{0}$).

Fitting the model using `streg` with the `distribution(exponential)` option, we obtain

```
. streg ibn.interval heblack mixrace hedropout hecollege heolder sheolder,
> distribution(exponential) noconstant
        failure _d:  divorce
  analysis time _t:  dur
                id:  id
Exponential regression -- log relative-hazard form
No. of subjects =         3371                     Number of obs   =     14125
No. of failures =         1032
Time at risk    =  62098.24824
                                                   Wald chi2(12)   =  16560.43
Log likelihood  =   -3056.2251                     Prob > chi2     =    0.0000
```

_t	Haz. Ratio	Std. Err.	z	P>|z|	[95% Conf.	Interval]
interval						
0	.0093972	.0017478	-25.09	0.000	.0065264	.0135306
1	.0235649	.0016577	-53.28	0.000	.0205299	.0270485
5	.027068	.0019591	-49.87	0.000	.0234881	.0311935
9	.0196236	.0015249	-50.59	0.000	.0168513	.0228519
15	.0168828	.0013671	-50.40	0.000	.0144051	.0197867
25	.0068689	.0008251	-41.46	0.000	.0054279	.0086923
heblack	1.19882	.0956472	2.27	0.023	1.025277	1.401737
mixrace	1.274274	.1015894	3.04	0.002	1.089939	1.489785
hedropout	.7388078	.0504425	-4.43	0.000	.6462718	.8445934
hecollege	.760166	.0801867	-2.60	0.009	.6181854	.9347557
heolder	.7578042	.1640962	-1.28	0.200	.4957199	1.158451
sheolder	1.633342	.4265919	1.88	0.060	.9789543	2.725158

```
note: no constant term was estimated in the main equation
```

The estimated hazard ratios for the six covariates with associated 95% confidence intervals are also reported under "Piecewise exponential" in table 15.2.

Table 15.2: Estimated hazard ratios (HR) for proportional hazards (PH) models and time ratio (TR) for accelerated failure-time (AFT) model with associated 95% confidence intervals

	PH						AFT	
	Piecewise exponential		Cox		Poisson cubic spline		Log normal	
	HR	(95% CI)	HR	(95% CI)	HR	(95% CI)	TR	(95% CI)
`heblack`	1.20	(1.03, 1.40)	1.19	(1.02, 1.39)	1.19	(1.02, 1.39)	0.87	(0.72, 1.05)
`mixrace`	1.27	(1.09, 1.49)	1.27	(1.08, 1.48)	1.27	(1.08, 1.48)	0.73	(0.60, 0.89)
`hedropout`	0.74	(0.65, 0.84)	0.75	(0.65, 0.85)	0.75	(0.65, 0.85)	1.39	(1.18, 1.63)
`hecollege`	0.76	(0.62, 0.93)	0.76	(0.62, 0.93)	0.76	(0.62, 0.93)	1.41	(1.10, 1.79)
`heolder`	0.76	(0.50, 1.16)	0.77	(0.50, 1.18)	0.77	(0.50, 1.18)	1.14	(0.73, 1.79)
`sheolder`	1.63	(0.98, 2.73)	1.64	(0.98, 2.74)	1.64	(0.98, 2.73)	0.53	(0.28, 0.98)
Log likelihood	−3,056.23		−7,821.91†		−9,442.73		−3,077.61	

†Partial log likelihood

Controlling for the other covariates, the estimated hazard ratios suggest that the hazard of marriage dissolution is about 20% [$= 100\%(1.19882 - 1)$] higher for black husbands than for white husbands and 27% [$= 100\%(1.274274 - 1)$] higher for mixed couples than for nonmixed couples. The model implies that couples where the husband is black and the wife is white have a 53% [$= 100\%(1.19882 \times 1.274274 - 1)$] higher hazard than white couples (see table 15.3 for hazard ratios comparing each type of couple with white couples).

		mixrace	
		0	1
heblack	0	both white 1	he white & she black 1.27
	1	both black 1.20	he black & she white $1.20 \times 1.27 = 1.53$

Table 15.3: Estimated hazards ratios for combinations of the spouses' race (both spouses white as reference category and adjusted for other covariates)

For a husband having less than 12 years of education, the hazard of marriage dissolution is about 26% lower [$-26\% = 100\%(0.7388078 - 1)$] than for the reference category (12 to 16 years of education), and the hazard is 24% lower [$-24\% = 100\%(0.760166 - 1)$] for husband having more than 16 years of education compared with the reference, controlling for the other covariates. Still controlling for the other covariates, the hazard is estimated as 24% *lower* [$-24\% = 100\%(0.7578042 - 1)$] if the husband is more than 10 years older than the wife than if he is not (not significant at the 5% level), whereas the hazard is 63% [$= 100\%(1.633342 - 1)$] *higher* if the wife is more than 10 years older than the husband than if she is not (not significant at the 5% level).

We now plot the estimated piecewise constant baseline hazard function, which was omitted from the model. The postestimation command `stcurve` cannot be used to accomplish this because Stata interprets the baseline hazard to be just the exponential of the intercept $\exp(\widehat{\alpha}_1)$. Therefore we calculate the estimated baseline hazard ourselves from the estimated coefficients:

```
. generate h0 = exp(_b[0.interval]*(interval==0) + _b[1.interval]*(interval==1)
> + _b[5.interval]*(interval==5) + _b[9.interval]*(interval==9)
> + _b[15.interval]*(interval==15) + _b[25.interval]*(interval==25))
```

(An alternative method for making predictions with a subset of coefficients that requires less typing uses the `matrix score` command as described on page 821.) We can then produce a graph using the `twoway` command:

```
. twoway line h0 _t, connect(J) sort xtitle(Time since wedding in years)
> ytitle(Baseline hazard)
```

Here the `connect(J)` option (synonymous with the `connect(stairstep)` option) connects the estimated hazards using a step function, because the hazard at the previous time point persists until the next time point. The resulting graph is shown in figure 15.3.

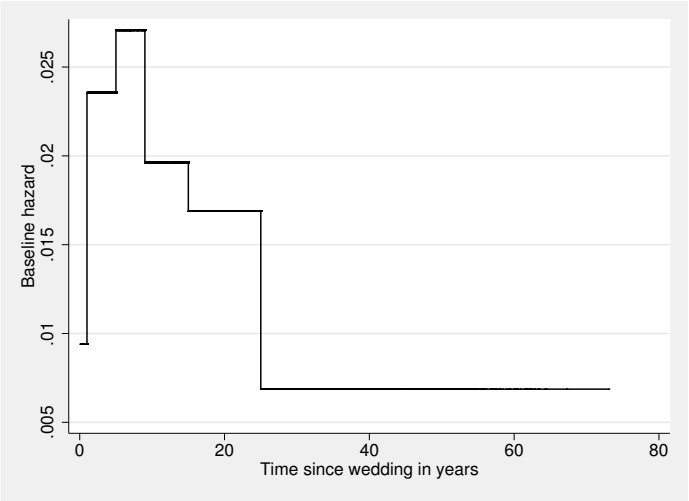


Figure 15.3: Piecewise constant baseline hazard curve

Because the baseline hazard represents the hazard when $\mathbf{x}_i = \mathbf{0}$, it is the hazard for a couple where the husband is white and has between 12 and 16 years of education, the spouses have the same race (that is, the wife is also white), and the age difference is less than 10 years. The estimated baseline hazard from the piecewise exponential model has a similar shape to the smoothed curve in figure 15.2 but that figure showed the marginal hazard, not conditioning on covariate values.

The piecewise exponential model can alternatively be fit using a Poisson regression model (see chapter 13) with the logarithm of the time at risk or exposure (the length of the interval) as an offset (a covariate without a coefficient). The model is

$$\ln(\mu_{si}) \;=\; \ln(t_{si}) + \alpha_1 + \alpha_2 d_{2si} + \cdots + \alpha_6 d_{6si} + \beta_2 x_{2i} + \cdots + \beta_7 x_{7i}$$

where μ_{si} is the mean parameter of the Poisson distribution and t_{si} is the time at risk in interval s for couple i. It may appear strange to use a model for counts (0,1,...) in this context because the event can only happen once in each episode. However, we could count the number of events that occur for each combination of interval and covariate values, and Poisson regression on such aggregated data would yield the same results as shown in section 13.3. Using Poisson regression in this way to estimate a piecewise exponential survival model is useful when random effects are introduced in the survival model (because `streg` can fit random-intercept models only, whereas `xtmepoisson` and `gllamm` can fit models with random coefficients).

We first construct the offset containing the log time at risk,

```
. generate lexposure = ln(_t - _t0)
```

and fit the Poisson regression model with the `offset()` option to include the offset and the `irr` option to express parameter estimates for the covariates as incidence-rate ratios:

```
. poisson _d ibn.interval heblack mixrace hedropout hecollege heolder sheolder,
> offset(lexposure) noconstant irr
Poisson regression                              Number of obs   =      14125
                                                Wald chi2(12)   =   16560.43
Log likelihood = -4541.2426                     Prob > chi2     =     0.0000
```

_d	IRR	Std. Err.	z	P>|z|	[95% Conf.	Interval]
interval						
0	.0093972	.0017478	-25.09	0.000	.0065264	.0135306
1	.0235649	.0016577	-53.28	0.000	.0205299	.0270485
5	.027068	.0019591	-49.87	0.000	.0234881	.0311935
9	.0196236	.0015249	-50.59	0.000	.0168513	.0228519
15	.0168828	.0013671	-50.40	0.000	.0144051	.0197867
25	.0068689	.0008251	-41.46	0.000	.0054279	.0086923
heblack	1.19882	.0956472	2.27	0.023	1.025277	1.401737
mixrace	1.274274	.1015894	3.04	0.002	1.089939	1.489785
hedropout	.7388078	.0504425	-4.43	0.000	.6462718	.8445934
hecollege	.760166	.0801867	-2.60	0.009	.6181854	.9347557
heolder	.7578042	.1640962	-1.28	0.200	.4957199	1.158451
sheolder	1.633342	.4265919	1.88	0.060	.9789543	2.725158
lexposure	1	(offset)				

As you can see, the parameter estimates and the estimated standard errors are identical to those produced by the `streg` command above.

Before discussing Cox regression in the next section, we return to the original non-expanded data format by using the `stjoin` command, after first removing the variables `interval`, `lexposure`, and `h0` that vary within couples between the episodes:

```
. drop interval pers_yr lexposure h0
. stjoin
(option censored(0) assumed)
(10754 obs. eliminated)
```

15.4.2 Cox regression model

A disadvantage of parametric proportional hazards models, such as the exponential, Weibull, or Gompertz models, is that a parametric form must be assumed for the baseline hazard $h_0(t)$.

We showed in the previous section that the parametric form can, at least partly, be relaxed by using a piecewise parametric model with different values of the parameters in

each interval. The narrower the intervals, the more flexible the model becomes, and the less we are smoothing the data. Taking this idea to the extreme, we can let the intervals be so small that each interval contains only one event. This can be accomplished by defining intervals to start just after each failure that occurs in the data and end just after the next failure (see also display 15.2 on the Kaplan–Meier estimator). Such intervals capturing a single event are sometimes referred to as *clicks*.

Specifying a piecewise exponential model such as (15.6) with a dummy variable for each click s corresponds to the Cox regression model,

$$\ln\{h(t|\mathbf{x}_i)\} \;=\; \ln\{h_0(t)\} + \beta_2 x_{2i} + \cdots + \beta_7 x_{7i}$$

which can equivalently be expressed as

$$h(t|\mathbf{x}_i) \;=\; h_0(t)\exp(\beta_2 x_{2i} + \cdots + \beta_7 x_{7i})$$

The model is sometimes described as *semiparametric* because no parametric shape is assumed for the baseline hazard $h_0(t)$, whereas the covariate effects are parametric.

We first demonstrate the `stcox` command, which fits the model without any need to expand the data. We then show how to expand the data and fit the same model using Poisson regression. This is useful for fitting random-effects models that are not accommodated by the `stcox` command (see section 15.9). The appropriate `stcox` command is

```
. stcox heblack mixrace hedropout hecollege heolder sheolder
         failure _d:  divorce
   analysis time _t:  dur
                 id:  id
Cox regression -- no ties
No. of subjects =         3371                     Number of obs   =      3371
No. of failures =         1032
Time at risk    =  62098.24824
                                                   LR chi2(6)      =     40.46
Log likelihood  =   -7821.9073                     Prob > chi2     =    0.0000
```

_t	Haz. Ratio	Std. Err.	z	P>|z|	[95% Conf.	Interval]
heblack	1.192658	.095109	2.21	0.027	1.020085	1.394426
mixrace	1.266902	.1009307	2.97	0.003	1.083752	1.481003
hedropout	.7458869	.0509019	-4.30	0.000	.6525054	.8526325
hecollege	.7594514	.080115	-2.61	0.009	.6175985	.9338858
heolder	.769728	.166686	-1.21	0.227	.5035098	1.176702
sheolder	1.640293	.4284575	1.89	0.058	.9830622	2.73692

The estimated hazard ratios were also reported under "Cox" in table 15.2 on page 812. We see that the estimates are nearly identical to those for the piecewise exponential model.

The log likelihood in the output is actually a *partial log likelihood* (see display 15.4) where the coefficients of the dummy variables for the clicks are viewed as nuisance

parameters and have been eliminated. The output also mentions that there are no ties because ties pose a challenge in Cox regression and can be handled in different ways as briefly described in display 15.4.

Partial likelihood

The partial likelihood that is maximized with respect to $\boldsymbol{\beta}$ is given by

$$\prod_f \frac{\exp(\mathbf{x}_f'\boldsymbol{\beta})}{\sum_{i\in R(f)}\exp(\mathbf{x}_i'\boldsymbol{\beta})}$$

where the product is over all failures f, and the summation in the denominator is over all subjects who are still at risk at the time of failure, the members of the risk set $R(f)$.

The term in the product represents the conditional probability that the event happens to a subject with covariates $\mathbf{x}_f$ given that it has happened to one of the subjects still at risk [a member of the risk set $R(f)$]. The partial likelihood is equivalent to the conditional likelihood for conditional logistic regression for discrete choice (see display 12.2), with risk sets corresponding to alternative sets and failures corresponding to the chosen alternatives.

The partial likelihood can also be viewed as a profile likelihood (that is, the likelihood in which the baseline hazard parameters have been replaced by functions of $\boldsymbol{\beta}$ that maximize the likelihood for fixed $\boldsymbol{\beta}$).

The partial likelihood estimator does not depend on the exact timing of the events but only on their ranking or chronological order (because time does not appear in the partial likelihood).

Ties

When several subjects experience the event at exactly the same time, we have ties.

By default, `stcox` uses *Breslow's method* for ties, where the risk sets $R(f)$ above contain all subjects who failed at or after the failure time of the subject contributing to the numerator. For a group of subjects with tied survival times, the contributions to the partial likelihood therefore all have the same denominator.

Because risk sets usually decrease by one after each failure, *Efron's method* downweights contributions to the risk set from the subjects with tied failure times in successive risk sets. Efron's method is requested by using the `efron` option of `stcox`.

In the *exact method*, the contribution to the partial likelihood from a group of tied survival times is the sum, over all possible orderings (or permutations) of the tied survival times, of the contributions to the partial likelihood corresponding to these orderings. The exact method is obtained by using the `exactp` option of `stcox` (the `exactm` option is an approximation to the truly exact method).

Display 15.4: Partial likelihood and ties in Cox regression

We can plot a kernel smoothed version of estimated hazard functions from Cox regression for different covariate values using the `stcurve` command with the `hazard` option. For instance, to plot separate curves for `sheolder` equal to 0 and 1, and with the other covariates evaluated at their mean, we use

```
. stcurve, hazard xtitle(Time since wedding in years) at1(sheolder=0)
> at2(sheolder=1)
```

The resulting graph is shown in figure 15.4.

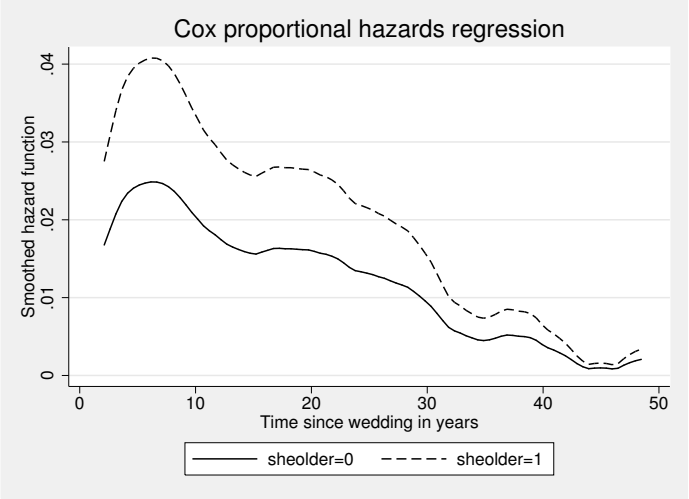


Figure 15.4: Kernel smoothed hazard curves from Cox regression

The model-implied curves are proportional, the curve for `sheolder`=1 being a constant multiple of the curve for `sheolder`=0.

We also want to save the kernel-smoothed estimated baseline hazard for later use, which requires that we explicitly set all covariates to 0 in the `at()` option and that we save the predictions in a file by using the `outfile()` option (predictions cannot be saved in the data because the values for `_t` required to make a nice graph are not necessarily the same as the values of `_t` in the data),

```
. stcurve, hazard xtitle(Time since wedding in years)
> at(heblack=0 mixrace=0 hedropout=0 hecollege=0 heolder=0 sheolder=0)
> outfile(temp, replace)
```

(graph not shown).

15.4.3 Poisson regression with smooth baseline hazard

Now we demonstrate how the Cox regression model can be fit using Poisson regression by expanding the data with the `stsplit` command. This data expansion will allow us to model the baseline hazard using a smooth function such as a spline or polynomial.

Each divorce that occurred corresponds to an interval or click. For each click, the new dataset will contain a row of data (or episode) for the index couple that got divorced and all the couples that stayed married until the next click. This collection of records is called the *risk set* because it is the set of couples who were at risk of divorce at the time the index couple got divorced. We saw from the `stset` output that the dataset contains 1,032 divorces, so the expanded data will be huge. In the `stsplit` command, we specify that the limits between the intervals are the divorce times, called `failures`, and that the risk sets should have the identifier `click` (the command will take some time to run and, in Stata 11 or earlier, may require increasing the memory by using `set memory`):

```
. stsplit, at(failures) riskset(click)
(1032 failure times)
(2243134 observations (episodes) created)
```

We see that there are 1,032 unique times of divorce and that 2,243,134 new rows of data have been created!

We now list the data for the first four and last four clicks for the first couple in the dataset (`id`=9):

```
. list id click _t0 _t _d _st if id==9 & (click<5 | click>624), separator(4)
> noobs
```

id	click	_t0	_t	_d	_st
9	1	0	.10110053	0	1
9	2	.10110053	.11268183	0	1
9	3	.11268183	.13671894	0	1
9	4	.13671894	.35028338	0	1
9	625	10.41302	10.443006	0	1
9	626	10.443006	10.458218	0	1
9	627	10.458218	10.500483	0	1
9	.	10.500483	10.546	0	1

The last completed episode for the couple was click 627 with censoring occurring at time 10.546 during click 628. (This last contribution does not contribute to Cox regression.)

At this point, we could attempt to use maximum likelihood to fit a Poisson model with a dummy variable for each of the 1,032 risk sets. However, this is computationally very demanding, so we use an equivalent but less taxing approach based on maximizing the conditional likelihood, where the coefficients for the dummy variables are treated as nuisance parameters (see section 13.11.1).

As before, we first construct the offset, the logarithm of the time at risk for each risk set:

```
. generate lexposure = ln(_t - _t0)
```

We then fit a Poisson regression model by conditional maximum likelihood, using the `xtpoisson` command with the `fe` (for "fixed effects") option. We first `xtset` the data, declaring `click` as the grouping variable:

```
. quietly xtset click
```

In the `xtpoisson` command, we also specify `offset(lexposure)` to define the offset, and `irr` to display incidence-rate ratios:

```
. xtpoisson _d heblack mixrace hedropout hecollege heolder sheolder,
> fe offset(lexposure) irr
Conditional fixed-effects Poisson regression    Number of obs      =   2244166
Group variable: click                           Number of groups   =      1032
                                                Obs per group: min =       139
                                                               avg =    2174.6
                                                               max =      3370
                                                Wald chi2(6)       =     41.40
Log likelihood  = -7821.9073                    Prob > chi2        =    0.0000
------------------------------------------------------------------------------
          _d |        IRR   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
     heblack |   1.192658    .095109     2.21   0.027     1.020085    1.394426
     mixrace |   1.266902   .1009307     2.97   0.003     1.083752    1.481003
   hedropout |   .7458869   .0509019    -4.30   0.000     .6525054    .8526325
   hecollege |   .7594514    .080115    -2.61   0.009     .6175985    .9338858
     heolder |   .7697281   .1666861    -1.21   0.227     .5035099    1.176702
    sheolder |   1.640318   .4284608     1.89   0.058     .9830807    2.736951
   lexposure |          1  (offset)
------------------------------------------------------------------------------
```

The estimates are identical to those produced by `stcox`. The offset is not needed here because it is constant within each risk set and drops out of the conditional likelihood. Identical estimates could also be obtained by using the following conditional logistic regression (see display 12.2):

```
clogit d heblack mixrace hedropout hecollege heolder sheolder, group(click)
```

As an alternative to this semiparametric approach, we can instead impose a smooth function on the baseline hazard, using, for instance, a polynomial or some kind of spline function. Here we adopt the latter strategy and use a cubic spline (see section 7.3.2 on linear splines). The necessary basis functions can be constructed using the `mkspline` command,

```
. mkspline sp = _t, cubic knots(1,5,7,9,12,15,20,25)
```

where the knots we have chosen for the spline are given in the `knots()` option. We then fit an ordinary Poisson model, including the offset (which is now needed), by maximum likelihood using the `poisson` command:

```
. poisson _d sp* heblack mixrace hedropout hecollege heolder sheolder,
> offset(lexposure) irr
Poisson regression                              Number of obs   =    2246505
                                                LR chi2(13)     =     279.14
                                                Prob > chi2     =     0.0000
Log likelihood = -9442.7291                     Pseudo R2       =     0.0146
```

_d	IRR	Std. Err.	z	P>|z|	[95% Conf.	Interval]
sp1	1.304973	.0751225	4.62	0.000	1.165738	1.460838
sp2	.044862	.0506301	-2.75	0.006	.0049117	.4097547
sp3	391459.9	3116978	1.62	0.106	.0653191	2.35e+12
sp4	1.88e-08	2.96e-07	-1.13	0.259	7.24e-22	486979.6
sp5	587734.7	8223518	0.95	0.342	7.23e-07	4.78e+17
sp6	.000776	.0064476	-0.86	0.389	6.57e-11	9160.43
sp7	2.955591	12.49459	0.26	0.798	.0007451	11723.31
heblack	1.192452	.0950753	2.21	0.027	1.019938	1.394145
mixrace	1.265812	.1008347	2.96	0.003	1.082836	1.479709
hedropout	.7464898	.0509393	-4.28	0.000	.6530391	.8533135
hecollege	.7587815	.0800423	-2.62	0.009	.6170569	.9330571
heolder	.7700903	.1667609	-1.21	0.228	.5037515	1.177245
sheolder	1.637608	.4277325	1.89	0.059	.9814807	2.732362
_cons	.0110737	.0016838	-29.62	0.000	.0082198	.0149184
lexposure	1	(offset)				

The estimated incidence-rate ratios or hazard ratios were also reported under "Poisson cubic spline" in table 15.2 on page 812. The estimates are almost identical to those reported for Cox regression, giving us some confidence that we are not over-smoothing the baseline hazard.

We now produce a graph of the baseline hazard, based on the cubic spline estimated above. The estimated baseline hazard could be calculated using the same kind of `generate` commands used on page 813, but here we demonstrate an approach that requires less typing, especially if the baseline hazard depends on many coefficients. First, we place the coefficients for the baseline hazard in a matrix, `coeff`,

```
. matrix a=e(b)
. matrix coeff = a[1,1..7],a[1,14..14]
```

where element 14 is the intercept. We then use the `matrix score` command to calculate the predicted log-baseline hazards, $\widehat{\alpha}_0 + \widehat{\alpha}_1$`sp1` $+ \cdots$,

```
. matrix score lhazard = coeff
```

and exponentiating this, we obtain the baseline hazard,

```
. generate h0=exp(lhazard)
```

Before plotting this baseline hazard, we append the data in `temp.dta` for the baseline hazard from Cox regression,

```
. append using temp
```

and plot both baseline hazards together using

```
. twoway (line h0 _t if divorce<., sort)  (line haz1 _t , sort),
> xtitle(Time since wedding in years)
> ytitle(Baseline hazard) legend(order(1 "Cubic spline" 2 "Cox"))
```

In the `line` subcommand used to plot the cubic spline version of the baseline hazard `h0`, we specified `if divorce<.` to plot the predictions only for the original 3,371 observations, which is much faster than plotting predictions for over 2 million expanded observations but produces an identical graph because the unique values of `_t` are just repeated in the expanded data. The resulting graph is presented in figure 15.5.

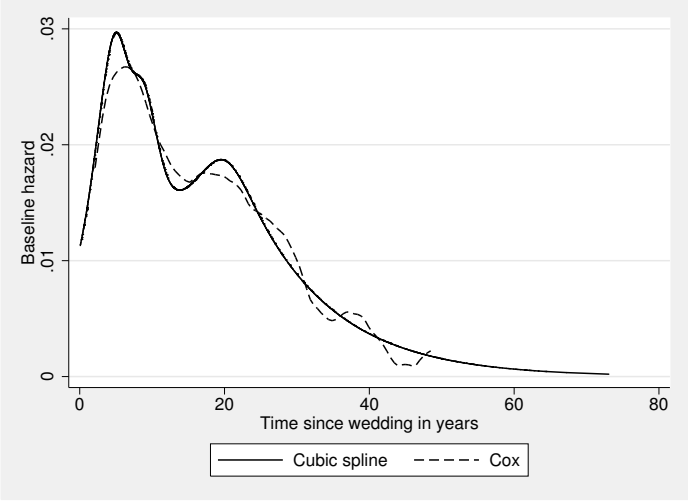


Figure 15.5: Estimated baseline hazard curve from piecewise exponential model with cubic spline and Cox model

We see that the cubic spline appears to be an appropriately smoothed version of the nonparametric baseline hazard from Cox regression (it is not too smooth and not too rough).

Before we proceed to a discussion of accelerated failure-time models, we restore the data to their unexpanded form. We first delete the observations from `temp.dta` and variables that vary within couples between the episodes created by `stsplit`,

```
. drop if _st >= .
(93 observations deleted)
. drop sp* h0 haz1 lexposure lhazard click
```

and then use `stjoin`,

```
. stjoin
(option censored(0) assumed)
(2243134 obs. eliminated)
```

Multilevel versions of proportional hazard models are discussed in section 15.9.

15.5 Accelerated failure-time models

Many parametric survival models can be written as log-linear models for the survival time T_i,

$$\ln(T_i) \;=\; \alpha_0 + \beta_2 x_i + \epsilon_i \tag{15.7}$$

or equivalently as multiplicative models of the form

$$T_i \;=\; \exp(\beta_2 x_i)\underbrace{\exp(\alpha_0 + \epsilon_i)}_{\tau_i} \tag{15.8}$$

The parametric distribution assumed for $\tau_i \equiv \exp(\alpha_0 + \epsilon_i)$ provides the name for the model. For example, in the log-normal survival model, τ_i is log normal (the log of τ_i has a normal distribution). The log-normal model is particularly interesting because if τ_i is log normal, then ϵ_i is normal, giving a standard linear regression model with a normally distributed residual for the log survival time in (15.7).

The parametric models for τ_i available in Stata are the following:

- *Log normal*, so ϵ_i is normal with variance σ^2
- *Log logistic*, so ϵ_i is logistic with variance $\gamma^2\pi^2/3$ (the standard logistic distribution used in chapters 10 and 11 on dichotomous and ordinal responses is obtained when $\gamma = 1$)
- *Exponential*, so ϵ_i is standard extreme value type I or Gumbel distributed (this distribution was used in chapter 12 on nominal responses)
- *Weibull*, so ϵ_i is extreme value type I distributed with scale parameter p
- *Generalized gamma* with parameters α_0, κ, and σ (there is no simple distribution for ϵ_i in this case)

The exponential and Weibull models have both proportional hazards (PH) and accelerated failure time (AFT) parameterizations. The `time` option can be used in the `streg` command to switch from the default PH to the AFT parameterization for these models.

For model selection, it is useful that the Weibull, exponential, and log-normal models are all nested in the generalized gamma model. For other models, the Akaike information criterion (AIC) or the Bayesian information criterion (BIC) can be used for model selection (see section 6.5).

For log-normal and log-logistic models, the distribution of ϵ_i is symmetric around 0 so that the median log-survival time is simply $\alpha_0 + \beta_2 x_i$, and the median survival time is therefore $\exp(\alpha_0 + \beta_2 x_i)$. (For monotonic functions, such as the exponential, the quantile of the function of a random variable is the function of the quantile of the random variable). For the other distributions, the median of ϵ_i, denoted Median(ϵ_i), is not zero, but we can write the median survival time as

$$\text{Median}(T_i|x_i) \;=\; \exp(\beta_2 x_i)\text{Median}(\tau_i)$$

and similarly for any other quantiles or percentiles. The expected survival time is also multiplicative in the covariate:

$$E(T_i|x_i) \;=\; \exp(\beta_2 x_i)E(\tau_i)$$

When x_i changes from a to $a+1$, the ratio of the median survival times and the ratio of the expected survival times both are

$$\frac{\exp\{\beta_2(a+1)\}}{\exp\{\beta_2(a)\}} \;=\; \exp(\beta_2)$$

Therefore, $\exp(\beta_2)$ is called the *time ratio* (TR) of x_i.

The models are called accelerated failure time (AFT) models because the survival function can be written as

$$S(t|x_i) \;=\; S_0\{t\exp(-\beta_2 x_i)\} \tag{15.9}$$

where $S_0(t)$ is the survival function when $x_i = 0$. For example, consider survival after onset of a terminal illness. If $\beta_2 = 0.69$ and some individual has $x_i = 1$ so that $\exp(-\beta_2 x_i) = 1/2$, then that individual reaches the same point in the survival curve, or the same probability of survival, in half the time as an individual with $x_i = 0$. The disease processes affecting survival are in that sense *accelerated*. When plotted against time, the survival curves for both individuals look the same, but the tick-mark on the time axis that represents 1 year since onset for the individual with $x_i = 1$ represents 2 years for the individual with $x_i = 0$.

To derive (15.9) from the AFT model, we first substitute for T_i from model (15.8) in the survival function and obtain

$$S(t|x_i) \;=\; \Pr(T_i > t|x_i) \;=\; \Pr\{\exp(\beta_2 x_i)\tau_i > t|x_i\} \;=\; \Pr\{\tau_i > t\exp(-\beta_2 x_i)|x_i\}$$

For the special case of $x_i = 0$, we then get

$$S_0(t) \equiv S(t|x_i = 0) \;=\; \Pr(T_i > t|x_i = 0) \;=\; \Pr(\tau_i > t)$$

because $\exp(-\beta_2 \times 0) = \exp(0) = 1$. Comparing the two expressions, we see that (15.9) follows.

15.5.1 Log-normal model

The log-normal survival model can be written as

$$\ln(T_i) \;=\; \alpha_0 + \beta_2 x_i + \epsilon_i, \quad \epsilon_i \sim N(0, \sigma^2) \tag{15.10}$$

where we assume that $E(\epsilon_i|x_i) = 0$. It follows that the mean survival time becomes

$$E(T_i|x_i) \;=\; \exp(\alpha_0 + \beta_2 x_i)\exp(\sigma^2/2)$$

We can fit the model using `streg` with the `distribution(lognormal)` option and the `time` option for the AFT parameterization:

```
. streg heblack mixrace hedropout hecollege heolder sheolder,
> distribution(lognormal) time
        failure _d:  divorce
  analysis time _t:  dur
                id:  id
Lognormal regression -- accelerated failure-time form
No. of subjects =         3371                     Number of obs   =      3371
No. of failures =         1032
Time at risk    =  62098.24824
                                                   LR chi2(6)      =     36.35
Log likelihood  =   -3077.6061                     Prob > chi2     =    0.0000
```

_t	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
heblack	-.137753	.0968523	-1.42	0.155	-.3275801	.0520742
mixrace	-.314885	.0988419	-3.19	0.001	-.5086115	-.1211584
hedropout	.3289508	.0818263	4.02	0.000	.1685742	.4893274
hecollege	.3404015	.123536	2.76	0.006	.0982754	.5825275
heolder	.1330227	.2304122	0.58	0.564	-.318577	.5846224
sheolder	-.6399424	.3181989	-2.01	0.044	-1.263601	-.016284
_cons	3.798159	.066096	57.46	0.000	3.668613	3.927705
/ln_sig	.5481884	.0241329	22.72	0.000	.5008887	.5954881
sigma	1.730116	.0417528			1.650187	1.813916

The exponentiated estimated coefficients or time ratios represents multiplicative factors for the time to reach a given survival probability. For instance, if the wife is more than 10 years older than the husband, the couple reaches a given survival probability in just over half the time [$0.53 = \exp(-0.6399424)$] as couples with an age difference of less than 10 years. The mean or median survival time is correspondingly halved. Estimated coefficients greater than zero have time ratios greater than one corresponding to slower progression of the process. For example, if the husband completed fewer than 12 years of schooling, the process takes 39% longer [$1.39 = \exp(0.3289508)$] to reach a given point, and the median or mean survival time is 39% longer.

The `tr` option can be used to display time ratios (TRs), which correspond to the exponentiated regression coefficients for the log-linear model. We can accomplish this by replaying the previous command with the `tr` option:

```
. streg, tr
Lognormal regression -- accelerated failure-time form
No. of subjects =         3371                     Number of obs   =      3371
No. of failures =         1032
Time at risk    =  62098.24824
                                                   LR chi2(6)      =     36.35
Log likelihood  =   -3077.6061                     Prob > chi2     =    0.0000
```

_t	Tm. Ratio	Std. Err.	z	P>|z|	[95% Conf.	Interval]
heblack	.8713139	.0843888	-1.42	0.155	.7206656	1.053454
mixrace	.7298728	.072142	-3.19	0.001	.6013299	.8858936
hedropout	1.389509	.1136984	4.02	0.000	1.183616	1.631219
hecollege	1.405512	.1736313	2.76	0.006	1.103267	1.790558
heolder	1.142276	.2631943	0.58	0.564	.7271831	1.794313
sheolder	.5273228	.1677935	-2.01	0.044	.2826345	.9838479
_cons	44.61896	2.949137	57.46	0.000	39.1975	50.79027
/ln_sig	.5481884	.0241329	22.72	0.000	.5008887	.5954881
sigma	1.730116	.0417528			1.650187	1.813916

The estimated time ratios are given under `Tm. Ratio` in the output and were also reported together with estimates from other models in table 15.2 (under "log normal").

We can look at the model-implied hazard functions for `sheolder` equal to 0 and 1 when all other covariates are evaluated at their mean by using the postestimation command `stcurve` for `streg` with the `hazard` option,

```
. stcurve, hazard xtitle(Time since wedding in years) at1(sheolder=0)
> at2(sheolder=1)
```

which produces the curves presented in figure 15.6.

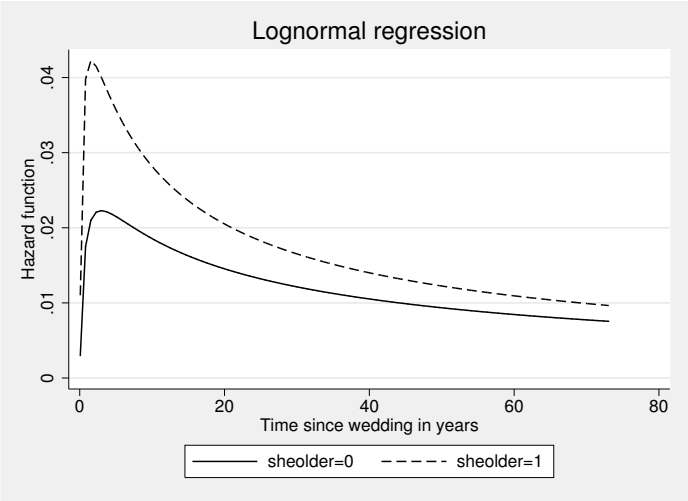


Figure 15.6: Hazards for log-normal survival model according to value taken by `sheolder`

The hazard curves in figure 15.6 have a similar shape as those based on Cox regression in figure 15.4, but they are much more smooth, as would be expected.

Model (15.10) is just a linear regression model for log survival times. If there were no censoring, we could simply log transform the survival times and fit a standard linear regression model by ordinary least squares (OLS) using the `regress` command. However, censoring is ubiquitous in survival data and also occurs frequently in the divorce data. For right-censored observations, all we know is that the survival time exceeds the censoring time. For such observations, the contribution to the likelihood is an integral from the censoring time to infinity. Such *censored regression models* are typically referred to as *tobit models* in economics (after the prominent economist James Tobin).

Stata's `tobit` command cannot handle censoring limits that are different across subjects, and we therefore use the `intreg` command instead (for "interval-censored regression"). The `intreg` command is very flexible, handling limits differing between couples and allowing for left-censoring, right-censoring, and interval-censoring. The command requires that two response variables be specified, representing the lower and upper limits of interval-censored data, respectively. If the lower limit is missing, we have left-censoring, and if the upper limit is missing, we have right-censoring, which is the only censoring we are concerned with in the divorce data.

Because we require a *log*-linear model for survival, we must log transform the durations,

```
. generate ldur = ln(dur)
```

before proceeding.

We now consider a log-normal survival model with *right-censoring*. In this case, the lower limit equals `ldur` and the upper limit should also be `ldur` unless right-censoring occurred, in which case it should be missing:

```
. generate ldur2 = ldur if divorce==1
(2339 missing values generated)
```

The model is fit using the `intreg` command:

```
. intreg ldur ldur2 heblack mixrace hedropout hecollege heolder sheolder
Interval regression                             Number of obs   =       3371
                                                LR chi2(6)      =      36.35
Log likelihood = -3077.6061                     Prob > chi2     =     0.0000
------------------------------------------------------------------------------
             |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
    heblack  |   -.137753   .0968523    -1.42   0.155    -.3275801    .0520742
    mixrace  |   -.314885   .0988419    -3.19   0.001    -.5086115   -.1211584
  hedropout  |   .3289508   .0818263     4.02   0.000     .1685742    .4893274
  hecollege  |   .3404015    .123536     2.76   0.006     .0982754    .5825276
    heolder  |   .1330227   .2304122     0.58   0.564     -.318577    .5846224
    sheolder |  -.6399424   .3181989    -2.01   0.044    -1.263601    -.016284
       _cons |   3.798159    .066096    57.46   0.000     3.668613    3.927705
-------------+----------------------------------------------------------------
    /lnsigma |   .5481884   .0241329    22.72   0.000     .5008887    .5954881
-------------+----------------------------------------------------------------
       sigma |   1.730116   .0417528                      1.650187    1.813916
------------------------------------------------------------------------------

  Observation summary:         0  left-censored observations
                            1032     uncensored observations
                            2339 right-censored observations
                               0       interval observations
```

The estimates, p-values, and confidence intervals reported in the output are identical to those produced by the `streg` command.

We mentioned in section 15.2 that the time from wedding to divorce could not be determined exactly and that the variables `lower` and `upper` represented lower and upper bounds for the durations. We could use `intreg` to take this interval-censoring into account; see exercise 15.2.

Multilevel versions of accelerated failure-time models are discussed in section 15.10.

15.6 Time-varying covariates

We now want to include the number of children of each couple as a covariate. This covariate is time varying because it increases by one at every birth of a new child. Information about time-varying covariates can be stored in the data by splitting the survival time into episodes, from time 0 to the first birth, from the first to second birth, and so on, and finally until divorce or censoring.

We read in the dataset `divorce2.dta`, which is in this format,

```
. use http://www.stata-press.com/data/mlmus3/divorce2, clear
```

and list data for the first five couples:

```
. list id dur numkids divorce if id<34, sepby(id) noobs
```

id	dur	numkids	divorce
9	3.734	0	0
9	10.546	1	0
11	.767	0	0
11	32.512	1	0
11	34.943	2	0
13	2.585	0	0
13	2.870226	1	1
15	18.18403	0	1
33	1.418	0	0

The time-varying covariate, number of children, is called `numkids` in the dataset. We see that couple 9 had zero children during the first episode, from time 0 to 3.73 years when they had a child, then no more children before censoring occurred at 10.55 years. Couple 11 had two children by the time they were censored at 34.94 years, whereas couple 13 got divorced shortly after having a child. Couples 15 and 33 had no children by the time they got divorced and censored, respectively. Note the `divorce` takes the value 0 for each episode that does not end in divorce.

We define the survival time, failure indicator, and subject identifier by using the `stset` command with the `failure()` and `id()` options:

```
. stset dur, failure(divorce) id(id)
                id:  id
     failure event:  divorce != 0 & divorce < .
obs. time interval:  (dur[_n-1], dur]
 exit on or before:  failure
------------------------------------------------------------------------------
     8728  total obs.
        0  exclusions
------------------------------------------------------------------------------
     8728  obs. remaining, representing
     3371  subjects
     1032  failures in single failure-per-subject data
 62098.25  total analysis time at risk, at risk from t =         0
                             earliest observed entry t =         0
                                  last observed exit t =    73.068
```

This command created new variables `_t0` and `_t` for the start and end times of each episode, as can be seen by listing the data:

```
. sort id dur
. list id _t0 _t numkids divorce if id<34, sepby(id) noobs
```

id	_t0	_t	numkids	divorce
9	0	3.734	0	0
9	3.734	10.546	1	0
11	0	.76700002	0	0
11	.76700002	32.512001	1	0
11	32.512001	34.943001	2	0
13	0	2.585	0	0
13	2.585	2.8702259	1	1
15	0	18.184032	0	1
33	0	1.418	0	0

Before we can fit the models described in the previous sections but now with `numkids` as an additional time-varying covariate, we must create several dummy variables as before:

```
. generate mixrace = (heblack & !sheblack) | (sheblack & !heblack)
. generate hedropout = hiseduc<12
. generate hecollege = hiseduc>=16 if hiseduc<.
. generate heolder = agediff > 10 if agediff<.
. generate sheolder = agediff< -10
```

We can use the `stcox` or `streg` commands, but not the `intreg` command, to fit all the models considered so far with the additional time-varying covariate `numkids`. For example, the log-normal accelerated failure-time model is fit like this:

```
. streg heblack mixrace hedropout hecollege heolder sheolder numkids,
> distribution(lognormal) time tr
        failure _d:  divorce
  analysis time _t:  dur
                id:  id
Lognormal regression -- accelerated failure-time form
No. of subjects =         3371                     Number of obs   =      8728
No. of failures =         1032
Time at risk    =  62098.24824
                                                   LR chi2(7)      =     73.70
Log likelihood  =   -3058.9311                     Prob > chi2     =    0.0000
```

_t	Tm. Ratio	Std. Err.	z	P>|z|	[95% Conf.	Interval]
heblack	.92643	.0817663	-0.87	0.387	.7792663	1.101385
mixrace	.6900399	.061664	-4.15	0.000	.579173	.8221292
hedropout	1.350578	.0999625	4.06	0.000	1.168203	1.561425
hecollege	1.383798	.1545178	2.91	0.004	1.111798	1.722343
heolder	1.162471	.2440743	0.72	0.473	.7703046	1.754292
sheolder	.5572091	.1611488	-2.02	0.043	.3161147	.9821814
numkids	1.178646	.0287783	6.73	0.000	1.12357	1.236422
_cons	34.19375	2.400638	50.31	0.000	29.79795	39.23801
/ln_sig	.4662275	.0259057	18.00	0.000	.4154533	.5170017
sigma	1.59397	.0412928			1.515057	1.676992

Here the `tr` option was used to obtain time ratios. According to the fitted model, each extra child increases the mean and median survival time by 18%, controlling for the other covariates. However, the probability of having a child could be partly determined by the hazard of divorce. It is dangerous to interpret the effect as causal because the number of children is likely to be an endogenous covariate or "internal" covariate, as discussed by Lillard (1993).

Time-varying covariates can also be used to assess and relax proportionality assumptions in survival models. The models discussed so far assume that the covariates have multiplicative effects on the survival time (AFT models) or the hazards (PH models), and that these effects are constant over time. To relax these proportionality assumptions, we can introduce interactions between covariates and functions of analysis time.

For Cox regression, `stcox` provides two convenient options called `tvc()` and `texp()` for relaxing the proportional hazards assumption. The covariates for which the assumption is relaxed are specified in `tvc(`*varlist*`)`. If `texp()` is not specified, interactions with untransformed analysis time are included for all of these covariates. Alternatively, to include interactions between these covariates and a function of analysis time, the function is specified in `texp()`, for instance, `texp(log(_t))` represents the log of analysis time. For categorical explanatory variables, proportionality can also be relaxed by specifying category-specific (for example, group-specific) baseline hazards by using the `strata()` option in `stcox`; see section 15.8.1 for an example.

For other survival models, proportionality can be relaxed by splitting the observation period into episodes, as shown for the piecewise exponential model, and forming interactions between interval dummies and covariates (see exercise 15.6).

15.7 Does nitrate reduce the risk of angina pectoris?

Angina pectoris is severe chest pain due to insufficient blood and hence oxygen supply to the heart muscle. Severe angina attacks, sudden onset of angina at rest, and angina lasting more than 15 minutes are symptoms that may herald myocardial infarction or heart attack. In more than half of patients with angina, the severity of symptoms seriously limits their everyday activities, often leading to premature retirement. According to a meta-analysis reported by Hemingway et al. (2008), the prevalence of angina varied between about 6% and 9% for people aged 45 and above depending on the gender and age. The mean of the study-specific prevalences (weighted by population size) was 6.7% for women and 5.7% for men.

We will analyze a subset of the data published in Danahy et al. (1976) and previously analyzed by Pickles and Crouchley (1994, 1995) and Skrondal and Rabe-Hesketh (2004). Subjects with coronary heart disease participated in a randomized crossover trial comparing isosorbide dinitrate (ISDN) with placebo. The subjects were asked to exercise on exercise bikes until the onset of angina pectoris or, if angina did not occur, to exhaustion. The exercise time and outcome (angina or exhaustion) were recorded.

Each subject repeated the exercise test four times under each of two regimes: a placebo regime and a treatment regime (ISDN). For both regimes, the first exercise test of the day was a control test where the subjects were given neither placebo nor drug. Before the second test, which took place 1 hour after the initial test, the subjects were administered either ISDN or placebo orally. For each regime, the exercise test was repeated 1, 3, and 5 hours after drug or placebo administration. A crossover design was used where the regimes were implemented on 2 successive days and the order of the regimes was randomized. Unfortunately, we do not know the order for individual subjects because this was not reported in the original paper.

Each subject j therefore has repeated survival times to angina or exhaustion for eight exercise test occasions i in two regimes. Data on the timing of several events per subject are often called multivariate or multilevel survival data. The event could be of different types (for example, onset of different diseases) or of the same kind (as here). In the latter case, the data are typically called recurrent-event data (see section 15.12 for further discussion). The multiple events are not absorbing; otherwise, we would have competing risks.

Because the subjects started each of the four exercise tests at rest, so that a similar process leading to angina or exhaustion can be assumed to begin at the start of each test, we define the origin of analysis time to be at the beginning of each test. Such a time scale, that resets to 0 when subjects start being at risk for the next event, is called *gap time*.

The dataset `angina8.dta` contains the following variables for 42 subjects:

- `subject`: identification number for subject (j)
- `regime`: treatment regime (1: ISDN; 0: placebo)
- `occ`: exercise test number within each of the treatment regimes (i, $i = 1, 2, 3, 4$)
- `second`: time from start of exercise to angina or censoring in seconds
- `uncen`: dummy variable for type of event observed (1: angina; 0: censored)

We first read in the data and list the 16 observations for the first two subjects in the dataset:

```
. use http://www.stata-press.com/data/mlmus3/angina8, clear
. list subj regime occ second uncen in 1/16, sepby(subj) noobs
```

subj	regime	occ	second	uncen
1	0	1	150	1
1	0	2	172	1
1	0	3	118	1
1	0	4	143	1
1	1	1	136	1
1	1	2	445	0
1	1	3	393	0
1	1	4	226	1
2	0	1	205	1
2	0	2	287	1
2	0	3	211	1
2	0	4	207	1
2	1	1	250	1
2	1	2	306	1
2	1	3	206	1
2	1	4	224	1

The data are already in long form with eight records per subject representing the times to angina or exhaustion.

We now construct dummy variables x_{2i}, x_{3i}, and x_{4i}, called `occ2`, `occ3`, and `occ4` in the dataset, for the second, third, and fourth exercise test occasion within each regime

```
. tabulate occ, generate(occ)
```

occ	Freq.	Percent	Cum.
1	42	25.00	25.00
2	42	25.00	50.00
3	42	25.00	75.00
4	42	25.00	100.00
Total	168	100.00	

and construct a treatment dummy x_{5ij}, called `treat`, that is equal to 1 after administration of the drug and equal to 0 otherwise:

```
. generate treat = regime==1 & occ>1
```

For the `id()` option of the `stset` command, we need an identifier for each survival time (or set of episodes constituting a survival time), not for each subject. We therefore construct an observation index, `id`, that labels all combinations of subjects and exercise test occasions,

```
. generate id=_n
```

The data now look like this:

```
. list id subj regime occ2 occ3 occ4 treat second uncen in 1/16, sepby(subj)
> noobs
```

id	subj	regime	occ2	occ3	occ4	treat	second	uncen
1	1	0	0	0	0	0	150	1
2	1	0	1	0	0	0	172	1
3	1	0	0	1	0	0	118	1
4	1	0	0	0	1	0	143	1
5	1	1	0	0	0	0	136	1
6	1	1	1	0	0	1	445	0
7	1	1	0	1	0	1	393	0
8	1	1	0	0	1	1	226	1
9	2	0	0	0	0	0	205	1
10	2	0	1	0	0	0	287	1
11	2	0	0	1	0	0	211	1
12	2	0	0	0	1	0	207	1
13	2	1	0	0	0	0	250	1
14	2	1	1	0	0	1	306	1
15	2	1	0	1	0	1	206	1
16	2	1	0	0	1	1	224	1

We are now ready to `stset` the dataset to define it as survival data:

```
. stset second, failure(uncen) id(id)
                id:  id
     failure event:  uncen != 0 & uncen < .
obs. time interval:  (second[_n-1], second]
 exit on or before:  failure
------------------------------------------------------------------------------
      168  total obs.
        0  exclusions
------------------------------------------------------------------------------
      168  obs. remaining, representing
      168  subjects
      155  failures in single failure-per-subject data
    47267  total analysis time at risk, at risk from t =         0
                             earliest observed entry t =         0
                                  last observed exit t =       743
```

15.8 Marginal modeling

The basic idea of marginal or population-averaged modeling is to estimate the parameters as if the data were single level or nonclustered and take clustering into account when estimating standard errors.

15.8.1 Cox regression

We start by considering the following Cox regression model with a nonparametric baseline hazard function $h_0(t)$; occasion-specific dummy variables x_{2i}, x_{3i}, and x_{4i}; and treatment dummy x_{5ij}:

$$\ln\{h(t|\mathbf{x}_{ij})\} = \ln\{h_0(t)\} + \beta_2 x_{2i} + \beta_3 x_{3i} + \beta_4 x_{4i} + \beta_5 x_{5ij} \tag{15.11}$$

The dummy variables for exercise test occasions are included to allow the hazard to change throughout the day as the drug concentration in the blood, the time of day, state of rest/tiredness, etc., change. The hazards for different test occasions are, however, assumed to be proportional (because the log-hazards are parallel). The hazards implied by the Cox model with occasion-specific dummy variables are shown under "Occ.spec. dummies" in table 15.4. In the literature on recurrent-event data, assuming a common form of the baseline hazard with different intercepts for different events is sometimes referred to as a semicommon baseline hazard.

The baseline hazard $h_0(t)$ is the hazard at the first or control exercise test occasion, where neither placebo nor ISDN is administered in either the placebo or the treatment regimes. At subsequent occasions, $i = 2, 3, 4$, the hazard for the treatment regime is $\exp(\beta_5)$ times the hazard for the placebo regime. It follows that $\exp(\beta_5)$ can be interpreted as a *hazard ratio*, comparing the hazards for subjects who are given the treatment with subjects who are given the placebo at each test occasion.

Table 15.4: Hazards implied by Cox models. "Occ.spec. dummies" refers to model (15.11) with occasion-specific dummy variables, and "Occ.spec. baselines" refers to model (15.12) with occasion-specific baseline hazards.

		Hazards	
Regime	Test occasion	Occ.spec. dummies	Occ.spec. baselines
Placebo	1 (control)	$h_0(t)$	$h_{01}(t)$
Placebo	2	$\{h_0(t)\exp(\beta_2)\}$	$h_{02}(t)$
Placebo	3	$\{h_0(t)\exp(\beta_3)\}$	$h_{03}(t)$
Placebo	4	$\{h_0(t)\exp(\beta_4)\}$	$h_{04}(t)$
Treatment	1 (control)	$h_0(t)$	$h_{01}(t)$
Treatment	2	$\{h_0(t)\exp(\beta_2)\}\exp(\beta_5)$	$h_{02}(t)\exp(\beta_5)$
Treatment	3	$\{h_0(t)\exp(\beta_3)\}\exp(\beta_5)$	$h_{03}(t)\exp(\beta_5)$
Treatment	4	$\{h_0(t)\exp(\beta_4)\}\exp(\beta_5)$	$h_{04}(t)\exp(\beta_5)$

We fit the Cox regression model with occasion-specific dummy variables by using `stcox` with the `vce(cluster subj)` option to obtain robust standard errors for clustered data:

```
. stcox occ2 occ3 occ4 treat, vce(cluster subj)
        failure _d:  uncen
  analysis time _t:  second
                id:  id
Cox regression -- Breslow method for ties
No. of subjects      =          168                 Number of obs   =       168
No. of failures      =          155
Time at risk         =        47267
                                                    Wald chi2(4)    =     31.21
Log pseudolikelihood =   -648.95214                 Prob > chi2     =    0.0000
                                  (Std. Err. adjusted for 21 clusters in subj)
------------------------------------------------------------------------------
             |               Robust
          _t | Haz. Ratio   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
        occ2 |   .7283773   .0957445    -2.41   0.016     .5629461    .9424233
        occ3 |   .9171277   .0861531    -0.92   0.357     .7629036    1.102529
        occ4 |   1.228249   .1236968     2.04   0.041     1.008236    1.496273
       treat |   .4031625    .079238    -4.62   0.000     .2742736     .59262
------------------------------------------------------------------------------
```

The estimates suggest that treatment with ISDN reduces the hazard of angina by 60% [$-60\% = 100\%(0.4031625 - 1)$]. This estimate is also given under "Marginal" in table 15.5 on page 844. We also see that the hazard of angina within a given regime decreases by 27% [$-27\% = 100\%(0.7283773 - 1)$] from occasion 1 to 2, does not change significantly at the 5% level from occasion 1 to 3, and increases by 23% [$= 100\%(1.228249 - 1)$] from occasion 1 to 4.

To visualize the treatment effect, we plot smoothed estimated hazard curves at test occasion 2 (after placebo or ISDN has been administered) for the treatment and placebo groups,

```
. stcurve, hazard at1(occ2=1 occ3=0 occ4=0 treat=1)
> at1(occ2=1 occ3=0 occ4=0 treat=0) legend(order(1 "Treatment" 2 "Placebo"))
> xtitle(Time in seconds) ytitle(Hazard function)
```

producing the graph shown in figure 15.7.

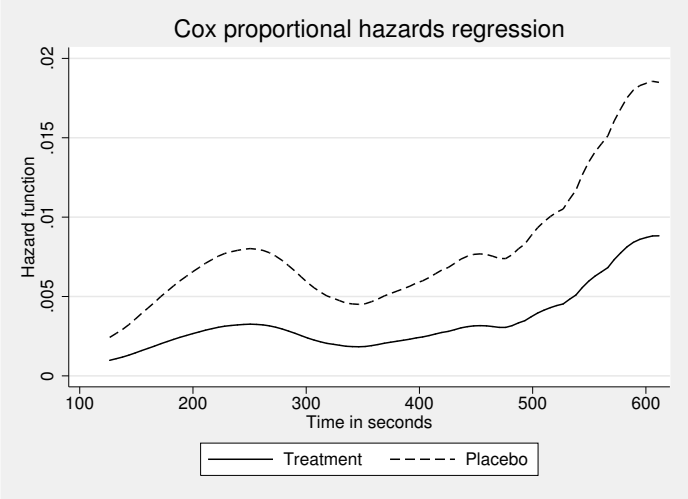


Figure 15.7: Smoothed estimated hazard functions at second exercise test occasion for treatment and placebo groups

Before proceeding, we store the smoothed estimated baseline hazard function (the hazard for the control test occasions) in `temp.dta` for later use,

```
. stcurve, hazard name(cox, replace) at(occ2=0 occ3=0 occ4=0 treat=0)
> outfile(temp, replace)
```

(graph not shown).

Instead of assuming that the log-baseline hazard functions at different exercise test occasions are parallel, we can let the baseline hazards in the Cox regression model be completely different at each occasion i (but identical across regimes for a given test occasion),

$$\ln\{h(t|\mathbf{x}_{ij})\} \;=\; \ln\{h_{0i}(t)\} + \beta_5 x_{5ij} \tag{15.12}$$

where $h_{0i}(t)$ is the occasion-specific baseline hazard for test occasion i. The hazards implied by this model are shown under "Occ.spec. baselines" in table 15.4.

The Cox model with occasion-specific baseline hazards can be fit using `stcox` with the `strata()` option:

```
. stcox treat, strata(occ) vce(cluster subj)
        failure _d:  uncen
  analysis time _t:  second
                id:  id
Stratified Cox regr. -- Breslow method for ties
No. of subjects      =          168                 Number of obs   =       168
No. of failures      =          155
Time at risk         =        47267
                                                    Wald chi2(1)    =     23.38
Log pseudolikelihood =   -441.86794                 Prob > chi2     =    0.0000
                                  (Std. Err. adjusted for 21 clusters in subj)
------------------------------------------------------------------------------
             |               Robust
          _t | Haz. Ratio   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       treat |   .4185219   .0753937    -4.84   0.000     .2940225    .5957389
------------------------------------------------------------------------------
                                                          Stratified by occ
```

The `strata()` option causes the risk set for an event occurring at a particular exercise test occasion to be restricted to episodes for the same occasion. We see that the estimated treatment effect is close to that from model (15.11) with a nonparametric baseline hazard for the control condition and occasion-specific dummy variables. We will therefore use the latter and simpler specification of the fixed part of the model henceforth.

15.8.2 Poisson regression with smooth baseline hazard

Instead of a fully nonparametric specification of the baseline hazard function $h_0(t)$, we will now model the log-baseline hazard as a smooth function of time by using orthogonal polynomial terms (where the pth order term is a linear combination of t, t^2, ..., t^p such that the different order terms are mutually uncorrelated). An alternative would be to use a piecewise exponential model. That model is less smooth, but it also does not require the data to be expanded to episodes defined by clicks, only to episodes defined by the intervals within which the hazards are assumed to be constant. Yet another alternative would be to use splines as we did for the divorce data in section 15.4.2 or fractional polynomials.

Stata's `stsplit` command can be used to expand the data to episodes defined by clicks:

```
. stsplit, at(failures) riskset(click)
(118 failure times)
(10013 observations (episodes) created)
```

As explained in section 15.4.1, this command produces variables `_t0`, `_t`, and `_d` representing the start time, end time, and failure indicator for each episode. We then compute the lengths of the intervals between unique failure times so that we can use the log interval lengths as an offset in the Poisson regression.

```
. generate lny = ln(_t - _t0)
```

We could check whether the data expansion and the construction of the binary response variable and the offset is correct by fitting a Poisson regression model that corresponds to Cox regression by typing

```
xtset click
xtpoisson _d occ2 occ3 occ4 treat, fe offset(lny) irr
```

Both models give identical parameter estimates, confirming that our data have been set up correctly (at the time of writing this book, `xtpoisson` cannot be combined with `vce(cluster subj)` to obtain standard errors taking clustering into account).

Orthogonal polynomials of the desired degree, say, degree 4, can be created by using `orthpoly`:

```
. orthpoly _t, gen(t1-t4) degree(4)
```

Denoting the linear, quadratic, cubic, and quartic terms of the polynomial as p_{1sij} to p_{4sij} and the corresponding coefficients as δ_1 to δ_4, we specify a Poisson regression model with smooth baseline hazard as

$$\ln(\mu_{sij}) \;=\; \ln(t_{sij}) + \delta_0 + \delta_1 p_{1sij} + \cdots + \delta_4 p_{4sij} + \beta_2 x_{2i} + \beta_3 x_{3i} + \beta_4 x_{4i} + \beta_5 x_{5ij}$$

This model can be fit using `poisson`, and we obtain cluster-robust standard errors with the `vce(cluster subj)` option:

```
. poisson _d t1-t4 occ2 occ3 occ4 treat, offset(lny) irr vce(cluster subj)
Poisson regression                                Number of obs   =      10181
                                                  Wald chi2(8)    =      48.21
                                                  Prob > chi2     =     0.0000
Log pseudolikelihood = -811.77386                 Pseudo R2       =     0.0839
                                  (Std. Err. adjusted for 21 clusters in subj)
------------------------------------------------------------------------------
             |               Robust
          _d |        IRR   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
          t1 |   1.759941    .334701     2.97   0.003     1.212324    2.554921
          t2 |   .6195466    .101207    -2.93   0.003     .4498054    .8533423
          t3 |   1.415135   .1151696     4.27   0.000     1.206489    1.659862
          t4 |   .8220619     .03362    -4.79   0.000     .7587397    .8906688
        occ2 |   .7357576   .0895868    -2.52   0.012     .5795506    .9340673
        occ3 |   .9158704   .0907676    -0.89   0.375     .7541806    1.112225
        occ4 |   1.213588   .1214511     1.93   0.053     .9974391    1.476577
       treat |   .4103732   .0797539    -4.58   0.000     .2803834    .6006281
       _cons |   .0054372   .0010889   -26.04   0.000      .003672    .0080508
         lny |          1  (offset)
------------------------------------------------------------------------------
```

The estimated coefficients are quite close to those of the Cox model, and using higher-order polynomials does not improve the approximation appreciably.

We can also compare the orthogonal polynomial baseline hazard function with the nonparametric baseline hazard from Cox regression. We first predict the baseline hazard

function for the model just fit. The estimated coefficients for the baseline hazard are placed in a matrix, `coeff`,

```
. matrix a=e(b)
. matrix coeff=a[1,1..4], a[1,9..9]
```

where element 9 is the intercept $\widehat{\delta}_0$. We then use the `matrix score` command to calculate the predicted log-baseline hazards, $\widehat{\delta}_0 + \widehat{\delta}_1 p_{1sij} + \widehat{\delta}_2 p_{2sij} + \widehat{\delta}_3 p_{3sij} + \widehat{\delta}_4 p_{4sij}$,

```
. matrix score lhazard = coeff
```

and after exponentiating, we get the baseline hazard

```
. generate haz0 = exp(lhazard)
```

Appending the data in `temp.dta` for the smoothed predicted baseline hazard from Cox regression,

```
. append using temp
```

we are now ready to plot both curves together in the same graph:

```
. twoway (line haz0 _t, sort) (line haz1 _t, sort),
> xtitle(Time in seconds) ytitle(Baseline hazard function)
> legend(order(1 "Polynomial" 2 "Cox"))
```

The resulting graph is shown in figure 15.8:

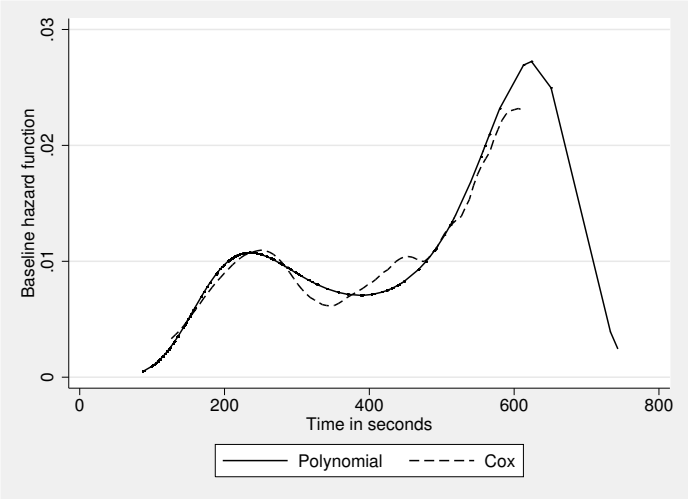


Figure 15.8: Estimated baseline hazard functions from Poisson regression with orthogonal polynomials and Cox regression

The dotted curve represents the baseline hazard from Cox regression, and the solid curve represents the baseline hazard from Poisson regression with orthogonal polynomials. We see that the baseline hazards are very similar. The nonparametric curve from Cox regression ends at about 600 seconds because only a few events happen later, whereas the curve based on the polynomials is parametric and ends at 743 seconds when the last event happened.

15.9 Multilevel proportional hazards models

We now discuss multilevel survival models where the dependence among multiple survival times is explicitly modeled using random effects.

15.9.1 Cox regression with gamma shared frailty

Consider a Cox regression model with a random intercept ζ_j for subject j:

$$\begin{aligned}\ln\{h(t|\mathbf{x}_{ij})\} &= \ln\{h_0(t)\} + \beta_2 x_{2i} + \beta_3 x_{3i} + \beta_4 x_{4i} + \beta_5 x_{5ij} + \zeta_j \\ &= [\ln\{h_0(t)\} + \zeta_j] + \beta_2 x_{2i} + \beta_3 x_{3i} + \beta_4 x_{4i} + \beta_5 x_{5ij}\end{aligned}$$

The random intercept ζ_j induces dependence among the hazards at different exercise test occasions for each subject. The exponential of the random intercept, $\exp(\zeta_j)$, is called a *shared frailty*, because it represents the unobserved frailty or proneness for angina shared across test occasions for a subject. It is assumed that the random intercept and frailty are independent of the covariates. We see that the subject-specific baseline hazard becomes $h_0(t)\exp(\zeta_j)$ in the model, so $h_0(t)$ is multiplied by the subject-specific frailty.

We now consider a Cox regression model with a frailty $\exp(\zeta_j)$ that is assumed to have a gamma distribution with expectation 1 and variance θ (scale=θ, shape=$1/\theta$). To fit the Cox model with a gamma frailty using `stcox`, we return to the unexpanded data by using the `stjoin` command (after deleting `click` and other variables we created after `stsplit`):

```
. drop click lny lhazard haz0 haz1 t1-t4
. stjoin
```

We can then fit the model by using the `stcox` command with the `shared()` option:

```
. stcox occ2 occ3 occ4 treat, shared(subj)
        failure _d:  uncen
  analysis time _t:  second
                id:  id
Cox regression --
        Breslow method for ties                 Number of obs      =       168
        Gamma shared frailty                    Number of groups   =        21
Group variable: subj
No. of subjects =          168                  Obs per group: min =         8
No. of failures =          155                                 avg =         8
Time at risk    =        47267                                 max =         8
                                                Wald chi2(4)       =     68.45
Log likelihood  =   -580.70822                  Prob > chi2        =    0.0000
------------------------------------------------------------------------------
          _t | Haz. Ratio   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
        occ2 |   .5001758   .1354445    -2.56   0.011     .2941864     .850399
        occ3 |   .9019859   .2320675    -0.40   0.688     .5447513    1.493486
        occ4 |   1.697274   .4156496     2.16   0.031     1.050266    2.742867
       treat |   .2210261   .0514855    -6.48   0.000     .1400123    .3489162
-------------+----------------------------------------------------------------
       theta |   2.695165   .7875161
------------------------------------------------------------------------------
Likelihood-ratio test of theta=0: chibar2(01) =   136.49 Prob>=chibar2 = 0.000
Note: standard errors of hazard ratios are conditional on theta.
```

The estimated hazard ratios (HRs) for the treatment along with corresponding standard errors and the estimate of the variance θ of the gamma distribution (not to be confused with our use of θ as the level-1 residual variance in linear multilevel models) are reported under "Gamma frailty" in table 15.5. We note that the estimated subject-specific or conditional hazard ratio is more different from 1 than the marginal or population-averaged counterpart. This is in accordance with the results in Gail et al. (1984), which can be used to contrast conditional and marginal effects in many survival models.

We can plot conditional or subject-specific hazard functions when the frailty is 1 (the mean) for the placebo and treatment groups at the second test occasion by using

```
. stcurve, at1(occ2=1 occ3=0 occ4=0 treat=1) at2(occ2=1 occ3=0 occ4=0 treat=0)
> hazard xtitle(Time in seconds) ytitle(Hazard function)
> legend(order(1 "Treatment" 2 "Placebo")) range(87 430)
```

giving the graph in figure 15.9. (We plotted the curves only up to 430 seconds because, for subjects with frailty equal to 1, survival goes to zero above 430 seconds, making the hazard irrelevant in that range.)

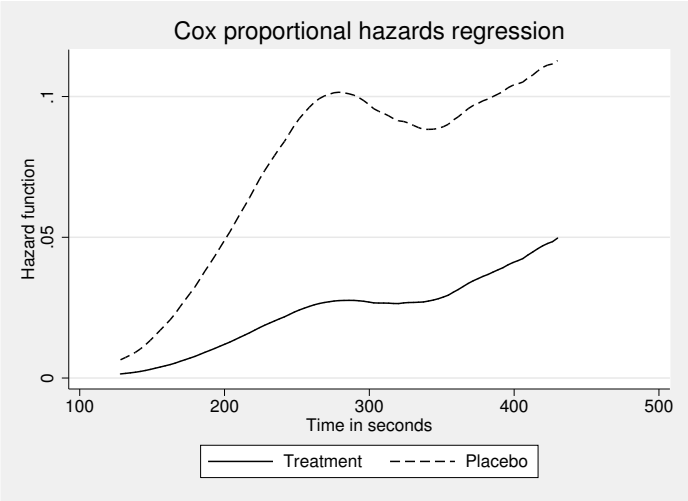


Figure 15.9: Smoothed estimated conditional hazard functions for the second exercise test occasion from Cox regression with gamma frailty evaluated at mean

We see that for subjects with mean frailty, the smoothed conditional or subject-specific hazard function increases almost linearly up to about 280 seconds, and because of the proportionality, the gap between treatment and placebo subjects increases markedly in that range. The shape of the subject-specific hazards from the shared frailty model are markedly different from the marginal hazards shown in figure 15.7. This illustrates the dangers of interpreting marginal hazards curves (and hence survival curves) as if they were subject specific.

Identical estimates to those produced by Cox regression with a gamma frailty can alternatively be obtained by expanding the data to clicks, as we did in the previous section, and fitting a Poisson regression model with a subject-specific random intercept ζ_j:

$$\ln(\mu_{sij}) \;=\; \ln(t_{sij}) + \alpha_s + \beta_2 x_{2i} + \beta_3 x_{3i} + \beta_4 x_{4i} + \beta_5 x_{5ij} + \zeta_j \tag{15.13}$$

Here, μ_{sij} is the mean parameter of the Poisson distribution, t_{sij} is the time at risk in interval s for experiment i of subject j, α_s is a interval-specific parameter, and $\exp(\zeta_j)$ has a gamma distribution with expectation 1 and variance θ. The model can be fit by using the `xtpoisson` command,

```
xtset subj
xtpoisson _d i.click occ2 occ3 occ4 treat, re offset(lny) irr
```

which by default fits a model with a gamma-distributed frailty.

Table 15.5: Proportional hazards models for angina data. Estimated hazards ratios (HRs) for treatment ISDN versus placebo with corresponding 95% confidence intervals reported under "Fixed part" (other estimated regression coefficients not shown). Estimated variance parameters reported under "Random part".

	Marginal		Random effects						Fixed effects	
	Cox regression		Gamma frailty		Log-normal frailty		Normal RI & RC		Subject-spec. baseline hazard	
	Est	(95% CI)[†]	Est	(95% CI)	Est	(95% CI)	Est	(95% CI)	Est	(95% CI)
Fixed part										
$\exp(\beta_5)$ [`treat`]	0.40	(0.27, 0.59)	0.22	(0.14, 0.35)	0.23	(0.14, 0.36)	0.14	(0.05, 0.37)	0.26	(0.16, 0.42)
Random part										
$\theta^{\ddagger}$			2.70							
ψ_{11}					4.32		6.19			
ψ_{22}							3.54			
ρ_{21}							0.26			
Log likelihood	$-648.95^{\bullet}$		-580.71		-735.81		-717.56		$-189.32^{\bullet}$	

[†] Robust standard errors taking clustering into account
[‡] Variance of gamma distribution with expectation 1 for frailty
[•] Partial log likelihood

15.9.2 Poisson regression with normal random intercepts

We could assume that the frailty $\exp(\zeta_j)$ in (15.13) is distributed as log normal (and hence that the random intercept ζ_j is normal) instead of gamma. However, in contrast to the model based on a gamma frailty, this model is considerably more complicated to fit because the marginal likelihood cannot be expressed in closed form and the frailty must be integrated out using numerical integration or Monte Carlo integration. The reason for nevertheless considering models with normal random intercepts is that they are straightforward to extend to situations with *several* random effects. To reduce the computational burden, in particular for larger datasets than that considered here, we will smooth the baseline hazards. If appropriately implemented, this approach will considerably reduce the number of parameters to be estimated and yet produce estimates that are very similar to those produced without smoothing.

Because we have previously shown that a Poisson regression including a fourth-degree orthogonal polynomial for the risk sets produced parameter estimates that closely approximated those from Cox regression for the angina data, we now consider such a model with a normally distributed random intercept ζ_j or log-normal frailty $\exp(\zeta_j)$:

$$\ln(\mu_{sij}) \;=\; \ln(t_{sij}) + \delta_0 + \delta_1 p_{1sij} + \cdots + \delta_4 p_{4sij} + \beta_2 x_{2i} + \beta_3 x_{3i} + \beta_4 x_{4i} + \beta_5 x_{5ij} + \zeta_j$$

The random intercept is assumed to have zero mean, variance ψ, and to be independent of the covariates.

We first expand the data to clicks and re-create the orthogonal polynomial terms:

```
. stsplit, at(failures) riskset(click)
(118 failure times)
(10013 observations (episodes) created)
. generate lny = ln(_t - _t0)
(87 missing values generated)
. orthpoly _t, gen(t1-t4) degree(4)
```

We can then fit the model using `xtpoisson` with the `re` and `normal` options:

```
. quietly xtset subj
. xtpoisson _d t1-t4 occ2 occ3 occ4 treat, re normal offset(lny) irr
Random-effects Poisson regression               Number of obs      =     10181
Group variable: subj                            Number of groups   =        21
Random effects u_i ~ Gaussian                   Obs per group: min =        86
                                                               avg =     484.8
                                                               max =       873
                                                Wald chi2(8)       =    150.09
Log likelihood  = -735.80547                    Prob > chi2        =    0.0000
```

_d	IRR	Std. Err.	z	P>|z|	[95% Conf.	Interval]
t1	6.016739	.9847173	10.96	0.000	4.365671	8.29223
t2	.3748918	.0415088	-8.86	0.000	.3017582	.46575
t3	1.620945	.1169195	6.70	0.000	1.407248	1.867092
t4	.8047381	.0411539	-4.25	0.000	.7279884	.8895792
occ2	.5387437	.1450992	-2.30	0.022	.3177818	.913346
occ3	.9221486	.2367601	-0.32	0.752	.5575148	1.525266
occ4	1.731507	.4247124	2.24	0.025	1.070625	2.800342
treat	.2271963	.0525722	-6.40	0.000	.1443568	.3575735
_cons	.006078	.0029611	-10.47	0.000	.0023393	.0157924
lny	1	(offset)				
/lnsig2u	1.462888	.3473601	4.21	0.000	.7820747	2.143701
sigma_u	2.078079	.3609208			1.478514	2.92078

```
Likelihood-ratio test of sigma_u=0: chibar2(01) =   151.94 Pr>=chibar2 = 0.000
```

The estimated regression coefficients have been exponentiated in the output to give incidence rate-ratios (IRR) because we used the `irr` option. These IRRs can be interpreted as conditional hazard ratios (conditional on the random intercepts or frailties). The estimate for `treat`, also reported under "Log-normal frailty" in table 15.5, is close to the corresponding estimate for the model with a gamma frailty. Note that the random-intercept variance $\psi \equiv \mathrm{Var}(\zeta_j)$ cannot be compared directly with the frailty variance $\theta \equiv \mathrm{Var}\{\exp(\zeta_j)\}$.

There is a large random-intercept standard deviation. Comparing the log likelihood with that of the ordinary Poisson model suggests that the intercept varies significantly between subjects. We can interpret the heterogeneity by estimating the median incidence-rate ratio as discussed in section 13.7.2,

$$\mathrm{IRR}_{\mathrm{median}} \;=\; \exp\left\{\sqrt{2\psi}\,\Phi^{-1}(3/4)\right\}$$

Plugging in $\widehat{\psi}$, we obtain

```
. display exp(sqrt(2*2.078079^2)*invnormal(3/4))
7.258858
```

For two randomly sampled subjects with the same covariate values, the incidence-rate ratio (or hazard ratio) comparing the subject who has the larger random intercept with the other subject is as large or larger than 7.3 half the time.

15.9.3 Poisson regression with normal random intercept and random coefficient

In addition to including a random intercept ζ_{1j}, we now also allow the treatment effect to vary randomly between subjects by introducing a random coefficient ζ_{2j} for the dummy variable `treat`:

$$\begin{aligned}\ln(\mu_{sij}) &= \ln(t_{sij}) + \delta_0 + \delta_1 p_{1sij} + \cdots + \delta_4 p_{4sij} \\ &\quad + \beta_2 x_{2i} + \beta_3 x_{3i} + \beta_4 x_{4i} + \beta_5 x_{5ij} + \zeta_{1j} + \zeta_{2j} x_{5ij} \\ &= \ln(t_{sij}) + \delta_1 p_{1sij} + \cdots + \delta_4 p_{4sij} \\ &\quad + \beta_2 x_{2i} + \beta_3 x_{3i} + \beta_4 x_{4i} + (\delta_0 + \zeta_{1j}) + (\beta_5 + \zeta_{2j}) x_{5ij}\end{aligned}$$

Here ζ_{1j} and ζ_{2j} have a bivariate normal distribution with zero means, variances ψ_{11} and ψ_{22}, respectively, and covariance ψ_{21}. The random effects are assumed to be independent of the covariates.

Because the covariate x_{5ij} that has a random coefficient is binary in this model, the random intercept ζ_{1j} represents the (residual) between-subject variability in the log hazard when ISDN is *not* administered, whereas $\zeta_{1j} + \zeta_{2j}$ represents the between-subject variability when ISDN is administered. The conditional or subject-specific hazards implied by the model with a random intercept and a random treatment effect are shown in table 15.6.

Table 15.6: Conditional or subject-specific hazards implied by Cox model with random intercept and random treatment effect

Regime	Test occasion	Hazard
Placebo	1 (control)	$h_0(t)\exp(\zeta_{1j})$
Placebo	2	$\{h_0(t)\exp(\zeta_{1j})\}\exp(\beta_2)$
Placebo	3	$\{h_0(t)\exp(\zeta_{1j})\}\exp(\beta_3)$
Placebo	4	$\{h_0(t)\exp(\zeta_{1j})\}\exp(\beta_4)$
Treatment	1 (control)	$h_0(t)\exp(\zeta_{1j})$
Treatment	2	$\{h_0(t)\exp(\zeta_{1j})\}\exp(\beta_2)\{\exp(\beta_5)\exp(\zeta_{2j})\}$
Treatment	3	$\{h_0(t)\exp(\zeta_{1j})\}\exp(\beta_3)\{\exp(\beta_5)\exp(\zeta_{2j})\}$
Treatment	4	$\{h_0(t)\exp(\zeta_{1j})\}\exp(\beta_4)\{\exp(\beta_5)\exp(\zeta_{2j})\}$

We can use `xtmepoisson` to fit a Poisson regression model with both a random intercept and a random coefficient for treatment (models with random coefficients cannot be fit in `xtpoisson`):

```
. xtmepoisson _d t1-t4 occ2 occ3 occ4 treat || subj: treat,
> covariance(unstructured) offset(lny) irr
Mixed-effects Poisson regression                Number of obs      =     10181
Group variable: subj                            Number of groups   =        21
                                                Obs per group: min =        86
                                                               avg =     484.8
                                                               max =       873
Integration points =   7                        Wald chi2(8)       =    138.45
Log likelihood =   -717.556                     Prob > chi2        =    0.0000
```

_d	IRR	Std. Err.	z	P>|z|	[95% Conf.	Interval]
t1	10.31293	2.157379	11.15	0.000	6.844124	15.53983
t2	.3308228	.044848	-8.16	0.000	.2536311	.4315077
t3	1.688182	.1440924	6.14	0.000	1.428125	1.995595
t4	.7879996	.0466569	-4.02	0.000	.7016604	.8849627
occ2	.4359863	.1274784	-2.84	0.005	.2458042	.7733147
occ3	.8654263	.2323399	-0.54	0.590	.5113393	1.464708
occ4	1.780738	.4521346	2.27	0.023	1.082624	2.929022
treat	.1423461	.0695404	-3.99	0.000	.0546396	.3708372
_cons	.0061234	.0035093	-8.89	0.000	.0019914	.0188286
lny	1	(offset)				

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
subj: Unstructured				
sd(treat)	1.880437	.4138663	1.221567	2.894677
sd(_cons)	2.488696	.4428286	1.755951	3.527209
corr(treat,_cons)	.2635586	.2416877	-.2346751	.652126

```
LR test vs. Poisson regression:      chi2(3) =   188.44   Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference.
```

Using a likelihood-ratio test, there is significant variability in the treatment effect (twice the difference in log likelihoods is 36.50, which corresponds to a tiny p-value also when taking into account that the null is on the boundary of the parameter space). The estimated hazard-ratio for `treat`, also reported under "Normal RI & RC" in table 15.5, is smaller than the corresponding estimate for the model with just a normally distributed random intercept.

Before proceeding to multilevel accelerated failure-time models, we return to the nonexpanded form of the data:

```
. drop lny click t1-t4
. stjoin
(option censored(0) assumed)
(10013 obs. eliminated)
```

15.10 Multilevel accelerated failure-time models

15.10.1 Log-normal model with gamma shared frailty

Stata's `streg` command allows gamma and inverse normal frailties but not a log-normal frailty. Here we illustrate a log-normal survival model with a shared frailty $\exp(\zeta_j)$ having a gamma distribution:

$$\ln(T_{ij}) \;=\; \beta_1 + \beta_2 x_{2i} + \beta_3 x_{3i} + \beta_4 x_{4i} + \beta_5 x_{5ij} + \zeta_j + \epsilon_{ij}, \qquad \epsilon_{ij} \sim N(0, \sigma^2)$$

This model may be fit using `streg` with the `distribution(lognormal)`, `shared()`, and `frailty(gamma)` options:

```
. streg occ2 occ3 occ4 treat, distribution(lognormal) shared(subj) frailty(gamma)
        failure _d:  uncen
  analysis time _t:  second
                id:  id

Lognormal regression --
        accelerated failure-time form          Number of obs      =       168
        Gamma shared frailty                   Number of groups   =        21
Group variable: subj

No. of subjects =          168                 Obs per group: min =         8
No. of failures =          155                                avg =         8
Time at risk    =        47267                                max =         8

                                               LR chi2(4)         =     24.73
Log likelihood  =   -73.791288                 Prob > chi2        =    0.0001

------------------------------------------------------------------------------
          _t |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
        occ2 |   .1145159   .0698114     1.64   0.101    -.0223118    .2513437
        occ3 |   .0216564   .0697459     0.31   0.756    -.1150431    .1583559
        occ4 |  -.0927119   .0689199    -1.35   0.179    -.2277925    .0423687
       treat |   .1992808   .0575947     3.46   0.001     .0863973    .3121643
       _cons |    5.18272   .0782714    66.21   0.000     5.029311    5.336129
-------------+----------------------------------------------------------------
     /ln_sig |  -1.331404   .1065086   -12.50   0.000    -1.540157   -1.122651
     /ln_the |   .6189547   .3417248     1.81   0.070    -.0508136    1.288723
-------------+----------------------------------------------------------------
       sigma |   .2641063   .0281296                      .2143475    .3254161
       theta |   1.856986    .634578                      .9504559     3.62815
------------------------------------------------------------------------------
Likelihood-ratio test of theta=0: chibar2(01) =    99.88 Prob>=chibar2 = 0.000
```

Exponentiating the estimated treatment coefficient, we get 1.22 [= exp(0.1992808)]. This means that the subject-specific effect of taking the treatment is to prolong the time it takes to reach a given survival probability by about 22%.

Because we used a parametric (log-normal) baseline hazard, `stcurve` can produce graphs for conditional hazards, given that the frailty takes the mean value of 1, or unconditional or marginal hazards, integrating out the frailty. The conditional hazards at the second exercise test occasion are obtained using

```
. stcurve, at1(occ2=1 occ3=0 occ4=0 treat=1)
> at2(occ2=1 occ3=0 occ4=0 treat=0) hazard
> xtitle(Time in seconds) ytitle(Hazard function)
> legend(order(1 "Treatment" 2 "Placebo"))
(option alpha1 assumed)
```

and the marginal hazards are obtained using the above command with the option `unconditional`. The graphs are shown in figure 15.10.

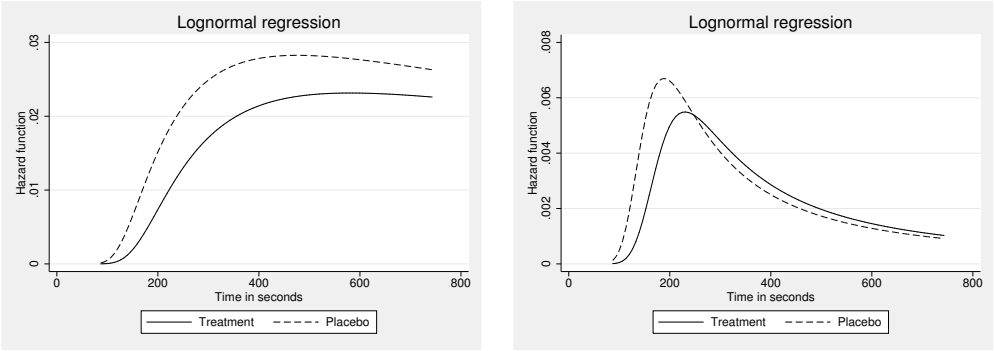


Figure 15.10: Subject-specific or conditional hazard functions (left) and population-averaged or marginal hazard functions (right) at second exercise test for treatment and placebo groups

These graphs nicely illustrate the *frailty* phenomenon. According to the fitted frailty model, the subject-specific or conditional hazard functions shown in the left panel increase until they become practically constant. In contrast, the population-averaged or marginal hazard functions in the right panel have pronounced peaks. This shape of the marginal hazard function can be explained by the fact that frail subjects tend to experience angina early and leave behind more resilient subjects.

15.10.2 Log-normal model with log-normal shared frailty

We now consider the log-normal survival model (15.10.1) with normally distributed subject-specific intercepts $\zeta_j \sim N(0, \psi)$, or in other words, log-normal frailties instead of gamma frailties. This model can be fit using `xtintreg`, the random-intercept version of the `intreg` command used earlier to fit the log-normal survival model.

Two variables are required when using `xtintreg`: the lower limit of the time to event or censoring (which we will call `dep_lo`) and the higher limit (called `dep_hi`). Because there is no left-censoring here, `dep_lo` contains the logarithm of the time to angina or censoring in seconds, whereas `dep_hi` contains the log time to angina if uncensored and Stata's missing indicator, ".", if right-censored.

```
. generate lnsecond = ln(second)
. generate dep_lo = lnsecond
. generate dep_hi = lnsecond if uncen==1
(100 missing values generated)
. replace dep_hi = . if uncen==0
(0 real changes made)
```

We can now fit the model using `xtintreg`:

```
. quietly xtset subj
. xtintreg dep_hi dep_lo occ2 occ3 occ4 treat
Random-effects interval regression              Number of obs      =       168
Group variable: subj                            Number of groups   =        21
Random effects u_i ~ Gaussian                   Obs per group: min =         8
                                                               avg =       8.0
                                                               max =         8
                                                Wald chi2(4)       =     50.31
Log likelihood  =  7.7822407                    Prob > chi2        =    0.0000
------------------------------------------------------------------------------
             |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
        occ2 |   .0844567   .0426664     1.98   0.048     .0008321    .1680813
        occ3 |   .0343252   .0423786     0.81   0.418    -.0487353    .1173858
        occ4 |  -.0450026   .0422627    -1.06   0.287    -.1278359    .0378307
       treat |   .1889437   .0337492     5.60   0.000     .1227965     .255091
       _cons |   5.391495   .0918128    58.72   0.000     5.211546    5.571445
-------------+----------------------------------------------------------------
     /sigma_u |   .4016115   .0635735     6.32   0.000     .2770098    .5262132
     /sigma_e |   .1773681   .0108113    16.41   0.000     .1561783    .1985579
-------------+----------------------------------------------------------------
          rho |   .8367873   .0465668                      .729419    .9117519
------------------------------------------------------------------------------
  Observation summary:        13  left-censored observations
                             155     uncensored observations
                               0 right-censored observations
                               0       interval observations
```

The estimated treatment effect is close to the corresponding estimate for the model with a gamma shared frailty.

Important limitations of the `xtintreg` command are that random slopes are not allowed and that time-varying covariates cannot be handled. However, `gllamm` can be used to fit models with random coefficients for interval-censored data (see `gllamm` companion).

15.11 A fixed-effects approach

15.11.1 Cox regression with subject-specific baseline hazards

Instead of modeling unobserved heterogeneity via subject-specific random effects, we can use a fixed-effects approach. Cox regression models include a baseline hazard func-

tion, making them more complex than standard regression models that include only an intercept when the covariates are all zero. Whereas a subject-specific intercept is often sufficient for representing heterogeneity in standard regression models, Cox regression may require subject-specific baseline hazards. Furthermore, estimation of Cox regression models with fixed cluster-specific intercepts is problematic when censoring occurs at different times for units nested in a given cluster (Holt and Prentice 1974).

We now consider a Cox regression model with subject-specific baseline hazards $h_{0j}(t)$,

$$\ln\{h(t|\mathbf{x}_{ij})\} = \ln\{h_{0j}(t)\} + \beta_2 x_{2i} + \beta_3 x_{3i} + \beta_4 x_{4i} + \beta_5 x_{5ij} \tag{15.14}$$

The shape of the log baseline hazards are not restricted in any way within or across subjects here, in contrast to section 15.9.1 where a common baseline hazard was multiplied by a subject-specific frailty.

The conditional or subject-specific hazards implied by the Cox model with subject-specific baseline hazards are shown in table 15.7.

Table 15.7: Conditional or subject-specific hazards implied by Cox model with subject-specific baseline hazards

Regime	Test occasion	Hazard
Placebo	1 (control)	$h_{0j}(t)$
Placebo	2	$\{h_{0j}(t)\}\exp(\beta_2)$
Placebo	3	$\{h_{0j}(t)\}\exp(\beta_3)$
Placebo	4	$\{h_{0j}(t)\}\exp(\beta_4)$
Treatment	1 (control)	$h_{0j}(t)$
Treatment	2	$\{h_{0j}(t)\}\exp(\beta_2)\exp(\beta_5)$
Treatment	3	$\{h_{0j}(t)\}\exp(\beta_3)\exp(\beta_5)$
Treatment	4	$\{h_{0j}(t)\}\exp(\beta_4)\exp(\beta_5)$

Such a model can be specified by considering each subject as a *stratum* with a separate baseline hazard function $h_{0j}(t)$ and fit using `stcox` with the `strata()` option.

```
. stcox occ2 occ3 occ4 treat, strata(subj)
        failure _d:  uncen
  analysis time _t:  second
                id:  id
Stratified Cox regr. -- Breslow method for ties
No. of subjects =          168                     Number of obs   =       168
No. of failures =          155
Time at risk    =        47267
                                                   LR chi2(4)      =     58.85
Log likelihood  =   -189.31811                     Prob > chi2     =    0.0000
```

_t	Haz. Ratio	Std. Err.	z	P>|z|	[95% Conf.	Interval]
occ2	.5633327	.1643431	-1.97	0.049	.31801	.9979048
occ3	.7497439	.215071	-1.00	0.315	.4273049	1.315491
occ4	1.593586	.4344607	1.71	0.087	.9339245	2.719188
treat	.2594194	.0640238	-5.47	0.000	.1599296	.4208004

Stratified by subj

The estimated hazard ratio of 0.26 for the treatment represents the within-subject ratio of the hazards when treated versus not treated at a given exercise test occasion. In this sense, each subject serves as his or her own control in this analysis.

We see that estimated treatment effect is very similar to that from the model with a random intercept. This suggests that there is no endogeneity problem for the treatment variable, which is indeed true by design in this case because of randomization. This need not be the case in observational studies where different estimates would suggest endogeneity as discussed in section 3.7.4.

The approach with subject-specific baseline hazards is unproblematic when the number of occasions is determined by the design of the study as in the angina experiment. However, observational studies typically have a fixed observation period and a varying number of events observed per subject. In this case, Chamberlain (1985) pointed out that the approach is problematic because the censoring time for the last spell depends on the lengths of the preceding spells. This problem can be avoided by considering only the first $n^* > 1$ spells if all persons have experienced at least n^* spells, at the cost of a potentially large loss in efficiency. Interestingly, Allison (1996) conducted a simulation study from which he concluded that the approach based on subject-specific baseline hazards works satisfactorily for fixed observation periods and varying number of spells as long as the proportion of spells that are censored is not extreme and the number of previous events is not included as a covariate.

15.12 Different approaches to recurrent-event data

Recurrent event or multi-episode data are a special case of multivariate or multilevel survival data and can be modeled as described in the previous sections by including shared frailties in the model. There are, however, several important decisions that must be made for recurrent-event data that need not concern us in other kinds of multilevel survival data. In this section, we closely follow the review by Kelly and Lim (2000).

We will consider the following artificial dataset for three subjects A, B, and C:

```
. use http://www.stata-press.com/data/mlmus3/recurrent, clear
. list, sepby(id) noobs
```

id	number	stop	event
A	1	2	1
A	2	5	1
A	3	14	0
B	1	7	1
B	2	11	1
B	3	17	1
C	1	14	0

Subject A experienced the first event (`number`=1) at time 2 (`stop`=2, `event`=1), the second event (`number`=2) at time 5 (`stop`=5, `event`=1), and the third event (`number`=3) is censored at time 14 (`stop`=14, `event`=0). Subject B experiences three events at times 7, 11, and 17, and subject C experiences no event and is censored at time 14. It is important to remember to define an identifier variable that uniquely labels each "level-1" unit, here each combination of `id` and event `number`. This identifier will be used for the `id()` option of the `stset` command.

```
. egen idnum = group(id number)
```

Using `id(id)` instead of `id(idnum)` would make Stata interpret multiple rows of data per person as episodes for one duration.

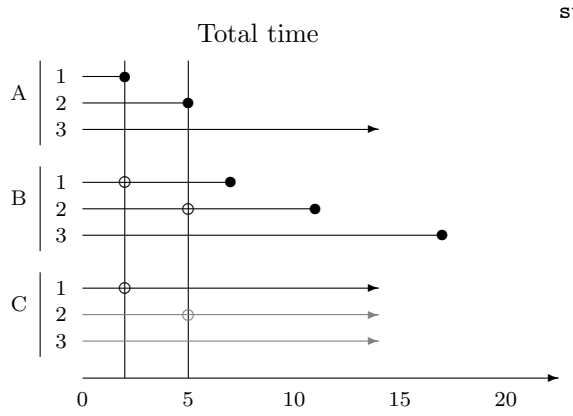
Kelly and Lim (2000) describe three model components that need to be determined for recurrent-event data (besides methods for handling within-subject dependence): 1) definition of risk intervals, 2) definition of risk sets, and 3) common versus event-specific baseline hazards.

The following three subsections consider three definitions of risk intervals: total time, counting process, and gap time. For each type of risk interval, risk set definitions are discussed together with the choice between common and event-specific baseline hazard. These definitions will be discussed in the context of Cox regression, but they are equally relevant when other types of analyses are used, including discrete-time survival.

15.12.1 Total time

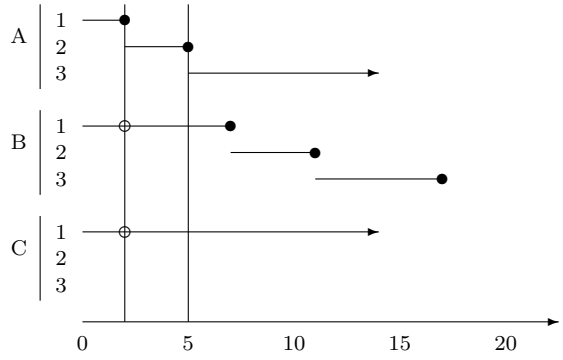
In this case, the *clock continues to run from the start of observation (time zero), undisturbed by event occurrences, and subjects are at risk for all events from time zero.* An example might be the risk of different kinds of infection following surgery.

In the top panel of figure 15.11, the risk intervals for events 1, 2, and 3 in the artificial dataset are shown as lines that start from zero and end when the event occurs (filled circle) or when censoring occurs (arrowhead). (The gray dummy risk intervals for subject C's second and third events will be explained below.)



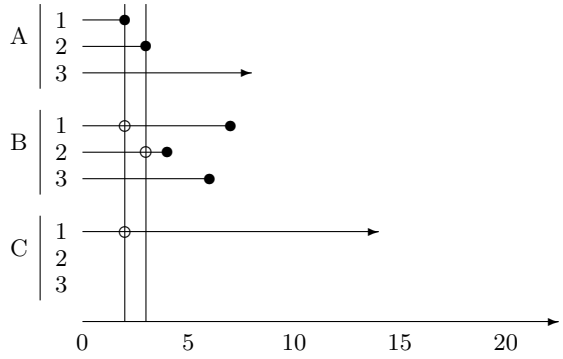

```
stset stop, failure(event)
   id(idnum)
```

		_t0	_t	_d
A	1	0	2	1
	2	0	5	1
	3	0	14	0
B	1	0	7	1
	2	0	11	1
	3	0	17	1
C	1	0	14	0
	2	0	14	0
	3	0	14	0




```
stset stop, failure(event)
   enter(start) id(idnum)
```

		_t0	_t	_d
A	1	0	2	1
	2	2	5	1
	3	5	14	0
B	1	0	7	1
	2	7	11	1
	3	11	17	1
C	1	0	14	0




```
stset stop, failure(event)
   origin(start) id(idnum)
```

		_t0	_t	_d
A	1	0	2	1
	2	0	3	1
	3	0	9	0
B	1	0	7	1
	2	0	4	1
	3	0	6	1
C	1	0	14	0

Figure 15.11: Illustration of risk intervals for total time, counting process, and gap time. Unrestricted risk sets shown as intersections between vertical and horizontal lines and restricted risk sets shown as circles (adapted from Kelly and Lim [2000]).

Total time risk intervals can be defined using the following `stset` command:

```
. stset stop, failure(event) id(idnum)
                id:  idnum
     failure event:  event != 0 & event < .
obs. time interval:  (stop[_n-1], stop]
 exit on or before:  failure
------------------------------------------------------------------------------
         7  total obs.
         0  exclusions
------------------------------------------------------------------------------
         7  obs. remaining, representing
         7  subjects
         5  failures in single failure-per-subject data
        70  total analysis time at risk, at risk from t =         0
                          earliest observed entry t =         0
                               last observed exit t =        17
```

They can be inspected using the `list` command:

```
. list id number stop event _t0 _t _d if _st==1, sepby(id) noobs
```

id	number	stop	event	_t0	_t	_d
A	1	2	1	0	2	1
A	2	5	1	0	5	1
A	3	14	0	0	14	0
B	1	7	1	0	7	1
B	2	11	1	0	11	1
B	3	17	1	0	17	1
C	1	14	0	0	14	0

The `stset` command produces the variables `_t0`, the start times of the risk intervals; `_t`, the end times; and `_d`, the corresponding failure indicator. We only listed data that contribute information for survival analysis (for which `_st` takes the value 1).

Total time can be combined with *unrestricted risk sets*, meaning that all subjects' risk intervals contribute to the risk set for a given event, regardless of the number of events experienced by the subjects. This can be implemented by specifying a *common baseline hazard* across events. Lee, Wei, and Amato (2010) specified such a model for time to blindness in each eye due to diabetes. In the top panel of figure 15.11, unrestricted risk sets for the first two events of subject A are shown as all the intervals that intersect with the vertical lines at the corresponding event times (regardless of whether there are hollow circles). Kelly and Lim (2000) point out that this specification does not make sense because it allows subjects to make several contributions to a given risk set.

Another possibility is to use *semirestricted risk sets*, where subjects must have experienced fewer than k events to contribute to the risk set for a kth event (Wei, Lin, and Weissfeld 1989). In this case, the baseline hazard is specified as event specific by using the `strata(number)` option in the `stcox` command. Stratifying by event number

means that only risk intervals for the same event number contribute to a given risk set. The risk intervals contributing to the risk sets for the first and second events of subject A are shown as hollow circles in the figure.

We see that it is now necessary to define *dummy risk intervals* for subject C (shown in gray) to make this subject contribute to the risk sets of events 2 and 3. We can create these dummy risk intervals by using the `fillin` command:

```
. fillin id number
```

This command fills in any missing combinations of the values of `id` and `number` and creates the dummy variable `_fillin` for newly created observations. We set the `stop` time for these observations equal to the previous stop time and set the failure indicator, `event`, to zero:

```
. by id (number), sort: replace stop = stop[_n-1] if _fillin==1
(2 real changes made)
. replace event = 0 if _fillin==1
(2 real changes made)
```

We also need to replace the missing values of `idnum` with unique values (because the variable appears in the `stset` command), and the easiest way to accomplish this is to drop `idnum` and define it from scratch:

```
. drop idnum
. egen idnum = group(id number)
```

The complete set of risk intervals, including the two shown in gray in figure 15.11, are then defined using

```
. stset stop, failure(event) id(idnum)
                id:  idnum
     failure event:  event != 0 & event < .
obs. time interval:  (stop[_n-1], stop]
 exit on or before:  failure
------------------------------------------------------------------------------
        9  total obs.
        0  exclusions
------------------------------------------------------------------------------
        9  obs. remaining, representing
        9  subjects
        5  failures in single failure-per-subject data
       98  total analysis time at risk, at risk from t =         0
                         earliest observed entry t =         0
                              last observed exit t =        17
```

and listed using

```
. list id number stop event _t0 _t _d if _st==1, sepby(id) noobs
```

id	number	stop	event	_t0	_t	_d
A	1	2	1	0	2	1
A	2	5	1	0	5	1
A	3	14	0	0	14	0
B	1	7	1	0	7	1
B	2	11	1	0	11	1
B	3	17	1	0	17	1
C	1	14	0	0	14	0
C	2	14	0	0	14	0
C	3	14	0	0	14	0

15.12.2 Counting process

Here the *clock continues to run from time zero, but subjects are not at risk of the kth event until they have experienced the $k-1$th event.* An example would be HIV infection (event 1) and AIDS (event 2), or onset of cancer (event 1) and recurrence of cancer after treatment (event 2). Counting process risk intervals are shown in the middle panel of figure 15.11.

Counting process risk sets are defined by specifying the `enter()` option in `stset` to define the start times of the risk intervals as being equal to the end times of the previous intervals. We first generate a variable, `start`, equal to 0 before the first event and equal to the previous value of `stop` for subsequent events:

```
. by id (number), sort: generate start = stop[_n-1] if _n>1
(3 missing values generated)
. replace start = 0 if start == .
(3 real changes made)
```

We can now specify `start` in the `enter()` option of the `stset` command,

```
. stset stop, failure(event) enter(start) id(idnum)
                id:  idnum
     failure event:  event != 0 & event < .
obs. time interval:  (stop[_n-1], stop]
 enter on or after:  time start
 exit on or before:  failure
------------------------------------------------------------------------------
        9  total obs.
        2  ignored because idnum missing
------------------------------------------------------------------------------
        7  obs. remaining, representing
        7  subjects
        5  failures in single failure-per-subject data
       45  total analysis time at risk, at risk from t =         0
                         earliest observed entry t =         0
                              last observed exit t =        17
```

and list the risk intervals,

```
. list id number stop event _t0 _t _d if _st==1, sepby(id) noobs
```

id	number	stop	event	_t0	_t	_d
A	1	2	1	0	2	1
A	2	5	1	2	5	1
A	3	14	0	5	14	0
B	1	7	1	0	7	1
B	2	11	1	7	11	1
B	3	17	1	11	17	1
C	1	14	0	0	14	0

(Note that the dummy risk intervals now do not contribute to the survival analysis because `start` equals `stop` for these intervals.) By looking at the intersections of the vertical lines for the first and second events of subject A, we can see that it is no longer problematic to specify *unrestricted risk sets* and a *common baseline hazard*. This approach was proposed by Andersen and Gill (1982).

Alternatively, we can use the `strata(number)` option to specify *restricted risk sets*, shown as hollow circles, as was done by Prentice, Williams, and Peterson (1981) in their model (2).

15.12.3 Gap time

In this case, the *clock is reset to zero for a subject every time an event occurs*. This type of risk interval makes sense if the subject is restored to a similar state after each event. The angina dataset analyzed earlier in this chapter was an example where this was deemed to be appropriate. Another example might be multiple tumor recurrences, each happening after removing the previous tumor. Gap time risk intervals are shown in the bottom panel of figure 15.11.

Gap times can be defined by specifying `start` in the `origin()` option,

```
. stset stop, failure(event) origin(start) id(idnum)
                id:  idnum
     failure event:  event != 0 & event < .
obs. time interval:  (stop[_n-1], stop]
 exit on or before:  failure
    t for analysis:  (time-origin)
            origin:  time start
--------------------------------------------------------------------------------
        9  total obs.
        2  ignored because idnum missing
--------------------------------------------------------------------------------
        7  obs. remaining, representing
        7  subjects
        5  failures in single failure-per-subject data
       45  total analysis time at risk, at risk from t =         0
                            earliest observed entry t =         0
                                 last observed exit t =        14
```

which produces the following risk intervals:

```
. list id number stop event _t0 _t _d if _st==1, sepby(id) noobs
```

id	number	stop	event	_t0	_t	_d
A	1	2	1	0	2	1
A	2	5	1	0	3	1
A	3	14	0	0	9	0
B	1	7	1	0	7	1
B	2	11	1	0	4	1
B	3	17	1	0	6	1
C	1	14	0	0	14	0

In the angina data, the time variable `second` was already a gap time, corresponding with `stop-start`, so it was not necessary to use the `origin()` option.

In section 15.8.1, we initially used *unrestricted risk sets* but allowed the hazard function for different events (or exercise test occasions `occ`) to differ by a multiplicative constant by including dummy variables for test occasion in the model for the log hazard [see model (15.11)].

Later in the same section, we used *restricted risk sets* with *event-specific baseline hazards* by specifying the `strata(occ)` option in the `stcox` command [see model (15.14)]. In their model (3), Prentice, Williams, and Peterson (1981) also used gap times with restricted risk sets and event-specific baseline hazards, which would here be implemented by using the `strata(number)` option. The risk intervals contributing to the restricted risk sets for the first and second events of subject A are shown as hollow circles in the bottom panel of figure 15.11. See exercises 15.4 (with solutions provided) and 15.8 for analyses of real data using the different approaches to recurrent-event data discussed here.

15.13 Summary and further reading

In this chapter, we have introduced the basic notions of survival analysis and discussed various models for single-level survival modeling, such as proportional hazards models (including piecewise exponential models and Cox regression) and accelerated failure-time models (including the log-normal survival model). To accommodate clustered or multilevel survival data, we have extended proportional hazards models and accelerated failure-time models to include frailties and other subject-specific effects. We have also given an overview of important issues in survival modeling of recurrent events.

We have discussed *shared frailty models* for multivariate or multilevel survival data but have not considered *"unshared" frailty models* for single-level data where the frailty takes on a unique value for each observation. The latter models are identified only if, conditional on the frailties, a proportional hazards model is assumed, or if the hazard function is assumed to have a specific parametric form. The marginal hazard function (integrating out the frailty) then departs from the structure assumed for the conditional hazard function and thus provides information on the frailty variance. Unshared frailty models only make sense if we have a strong reason to assume proportional hazards or a parametric hazard function conditionally on the frailties.

Continuous-time survival models for competing risks have not been discussed in this chapter. In this case, there are multiple types of absorbing events, a classical example being different causes of death in mortality studies. Fortunately, it is straightforward to handle competing risks in continuous-time survival analysis if the times to the different events are conditionally independent given the covariates: simply analyze one event at a time as if it were the only event and treat the other events as censoring together with the truly censored observations.

Good introductory books on continuous-time survival analysis include Collett (2003b), Klein and Moeschberger (2003), and Hosmer, Lemeshow, and May (2008) for medicine and Allison (1984, 1995) and Box-Steffensmeier and Jones (2004) for social science. We also recommend Blossfeld, Golsch, and Rohwer (2007) and Cleves et al. (2010) for Stata-specific treatments.

Continuous-time survival modeling of clustered data is discussed in the paper by Pickles and Crouchley (1995) and the book by Skrondal and Rabe-Hesketh (2004, chap. 12). Advanced treatments of multivariate survival analysis include Duchateau and Janssen (2008) and Hougaard (2000). Models with discrete random effects, and many other issues in survival analysis, are discussed in Vermunt (1997).

The first two exercises of this chapter do not involve any clustering. The first is on reimprisonment following prison release (exercise 15.1) and the second revisits the divorce data discussed in this chapter (exercise 15.2). Exercises on recurrent events include multiple divorces (exercise 15.3), blindness in two eyes of patients suffering from diabetic retinopathy (exercise 15.6), recurrence of bladder cancer (exercise 15.4), and multiple infections (exercises 15.7 and 15.8). Exercise 15.5 is on single events for units nested in clusters, specifically, child mortality among children nested in mothers.

Exercises 15.4 and 15.8 illustrate the different approaches for modeling recurrent survival data discussed in section 15.12.

15.14 Exercises

15.1 Reimprisonment data

In this exercise, we consider reimprisonment of former prisoners after release, often called recidivism, in the state of North Carolina in the U.S.A. The main research question is whether participation in the North Carolina prisoner work release program reduces the risk of recidivism after controlling for the nature and severity of the original crime and other covariates.

Here we consider data on 1,445 prisoners provided by Wooldridge (2010). The data are part of a dataset collected by Chung, Schmidt, and Witte (1991) that includes information on prisoners released from the North Carolina prison system between July 1, 1977, and June 30, 1978. Follow-up information on these prisoners was collected through a search of North Carolina Department of Correction records in April 1984. Because of the 1-year window for selection of releases, the follow-up period ranged from 70 to 81 months. The variables were all recorded either at the beginning of the original sentence or at the time of release from prison, and no information is available on changes in the variables after release.

We will use the following variables from the dataset `recid.dta`:

- `durat`: minimum time in months from release until either return to prison or censoring due to end of follow-up period
- `ldurat`: ln(`durat`)
- `cens`: dummy variable for censoring (1: right censoring; 0: event)
- `workprg`: dummy variable for participation in North Carolina prisoner work release program during sentence (1: participation; 0: no participation)
- `priors`: number of previous incarcerations (not including the current incarceration)
- `tserved`: time served in prison (rounded to months)
- `felon`: dummy variable for conviction for felony (1: conviction for felony; 0: conviction for misdemeanor); felony means that the prison sentence is for more than 1 year, whereas misdemeanor means that the sentence is for 1 year or less
- `alcohol`: dummy variable for record indicating serious problem with alcohol (1: alcohol problem; 0: otherwise)
- `drugs`: dummy variable for record indicating use of hard drugs (1: hard drugs; 0: otherwise)
- `black`: dummy variable for being black (1: black; 0: otherwise)
- `married`: dummy variable for being married at time of release (1: married; 0: otherwise)

- `educ`: number of years of schooling completed
- `age`: age in months at time of release

1. Following Wooldridge, fit a Weibull model to the data with `workprg`, `priors`, `tserved`, `felon`, `alcohol`, `drugs`, `nonwhite`, `married`, `educ`, and `age` as covariates. Use the proportional hazards parameterization.
2. Interpret the estimated exponentiated coefficients of `workprg` and `drugs`.
3. Now fit the same model using the accelerated failure-time parameterization.
4. Interpret the estimated exponentiated coefficients of `workprg` and `drugs`.
5. Fit a log-normal accelerated failure-time model, and compare the estimated coefficients of `workprg` and `drugs` with the estimate from step 4.
6. Fit a piecewise exponential model assuming constant hazards in year 1, year 2, year 3, and the remaining time after year 3.
7. Compare the estimated exponentiated coefficients of `workprg` and `drugs` with those from step 1.

15.2 Divorce data

We mentioned in section 15.2 that the time from wedding to divorce could not be determined exactly and that the variables `lower` and `upper` represented lower- and upper-bounds for the durations. To take this *interval-censoring* into account, fit an interval-censored log-normal survival model using `intreg`.

1. Generate the lower and upper bound variables, keeping in mind that we want to fit a model to the log durations.
2. Fit the model with `heblack`, `mixrace`, `hedropout`, `hecollege`, `heolder`, and `sheolder` as covariates. (See section 15.2 on how to create these variables.)
3. Compare the estimates with those based on assuming that the divorce time is known in section 15.5.1.

15.3 Multiple divorce data

Up to now we have restricted our analysis of the divorce data provided by Lillard and Panis (2003) to the first marriage. Here we consider a larger dataset also made available by Lillard and Panis (2003) (and converted to Stata by Germán Rodríguez) that contains times from wedding to divorce for multiple marriages per respondent.

The data `divorce3.dta` contains a row of data for each marriage and most of the variables are as described in section 15.2. Additional variables we will use here are

- `id`: identifier for respondent
- `marnum`: marriage number (1, 2, etc.)
- `censor`: dummy variable for censoring due to loss to follow-up or death of spouse or respondent

1. Generate dummy variables, `second` and `thirdplus`, for the second marriage and for the third and subsequent marriages, respectively. Also create the explanatory variables `mixrace`, `hedropout`, `hecollege`, `heolder`, and `sheolder` as in section 15.2.
2. Create a variable, `dur`, by drawing a random number from the uniform distribution on the interval from `lower` to `upper`. (This can be done by drawing a number from a uniform on the interval from 0 to 1 and applying a linear transformation so that 0 becomes `lower` and 1 becomes `upper`.) Also create an appropriate identifier for the marriages (see section 15.12). Now define the data as survival data by using `stset`.
3. Fit a piecewise exponential model, cutting time at 1, 5, 9, 15, and 25 years, with the variables created in step 1 and `heblack` as covariates. Use robust standard errors for marriages clustered in respondents.
4. Now fit the same model but include a shared gamma frailty instead of using robust standard errors.
5. Compare the estimates of the marginal model in step 3 and the frailty model in step 4. In particular, comment on the change in the estimates of the coefficients of `second` and `thirdplus`.
6. What kind of risk interval did you use in the above analyses? Were the risk sets restricted or unrestricted? (See section 15.12.)

15.4 Bladder cancer data Solutions

Here we consider data from a bladder cancer study conducted by the Veterans Administration Cooperative Urological Research Group (Byar 1980). The data were previously analyzed by Wei, Lin, and Weissfeld (1989) and have been made available by Therneau and Grambsch (2000). Patients who had just had a superficial bladder tumor removed were randomly assigned to one of three treatments to prevent tumor recurrence: placebo, thiotepa, and pyridoxine. Here we consider only the placebo and thiotepa groups. The patients were followed up and information about recurrent tumors was collected, including the recurrence times from the beginning of initial treatment. Only the first four recurrence times will be analyzed here.

The data in `bladder.dta` contain the following variables:

- `id`: patient identifier
- `enum`: recurrence number
- `treat`: dummy variable for receiving thiotepa (1: thiotepa; 0: placebo)
- `number`: number of initial tumors (except 8 denotes 8 or more)
- `size`: size of largest initial tumor in centimeters
- `start`: timing of previous event in months
- `stop`: timing of event in months
- `event`: failure indicator (1: tumor recurrence; 0: censoring)

Each patient has data for each recurrence although censoring for a given recurrence implies censoring for all subsequent recurrences.

```
. list id treat number size enum start stop event if id>6&id<10, sepby(id)
> noobs
```

id	treat	number	size	enum	start	stop	event
7	0	1	1	1	0	18	0
7	0	1	1	2	18	18	0
7	0	1	1	3	18	18	0
7	0	1	1	4	18	18	0
8	0	1	3	1	0	5	1
8	0	1	3	2	5	18	0
8	0	1	3	3	18	18	0
8	0	1	3	4	18	18	0
9	0	1	1	1	0	12	1
9	0	1	1	2	12	16	1
9	0	1	1	3	16	18	0
9	0	1	1	4	18	18	0

For subject 7, the risk intervals for the second to fourth recurrences are therefore dummy risk intervals as shown in the top panel of figure 15.11. Refer to section 15.12 for this exercise. Use the `efron` option for handling ties in all Cox regression analyses below.

1. Wei, Lin, and Weissfeld (1989) specify a marginal Cox regression model based on total time and semirestricted risk sets, where the risk set for a kth event includes risk intervals for all previous events ($< k$). They specify event-specific baseline hazards and allow the effects of `treat`, `number`, and `size` to differ between events. Fit this model.
2. Use `testparm` to test whether the coefficients of `treat` differ significantly between events (at the 5% level) and similarly for `number` and `size`.
3. Fit the model by Wei, Lin, and Weissfeld (1989) but constraining all coefficients to be the same across events.

4. In their model (2), Prentice, Williams, and Peterson (1981) use counting process risk intervals with restricted risk sets and event-specific baseline hazards. Fit this model, assuming that `treat`, `number`, and `size` have the same coefficients across events.
5. Andersen and Gill (1982) also use counting process risk intervals, but they use unrestricted risk sets and assume that all events have a common baseline hazard function. Fit this model, again assuming that `treat`, `number`, and `size` have the same coefficients across events.
6. In their model (3), Prentice, Williams, and Peterson (1981) use gap time with restricted risk sets and event-specific baseline hazards. Fit this model, assuming that `treat`, `number`, and `size` have the same coefficients across events.
7. Compare and interpret the treatment effect estimates from steps 3 to 6.

15.5 Child mortality data

Here we analyze the Guatemalan child mortality data from Pebley and Stupp (1987) and Guo and Rodríguez (1992), which were described in detail in section 14.3.

The data `mortality.dta` contain the survival times in months (variable `time`) of several children per mother (variable `momid`) together with a dummy variable, `death`, indicating whether the survival time ended in death or censoring. For instance, for mother 26, these variables are

```
. list kidid time death if momid==26, noobs
```

kidid	time	death
2601	60	0
2602	.25	1
2603	48	1
2604	.25	1
2605	60	0

We see that children 2601 and 2605 (children 1 and 5 of mother 26) were censored at 60 months, whereas children 2602 and 2604 died at 0.25 months and child 2603 died at 48 months.

1. Fit a piecewise exponential model assuming that the incidence rate is constant for the age bands 1–5 months, 6–11 months, 12–23 months, and 24 or more months. Use `stset` and `stsplit` to prepare the data for this analysis. Define dummy variables for the age bands, called `ageband1`, `ageband2`, etc.
2. Create the covariates used in section 14.6:

```
. generate mage2 = mage^2
. generate comp12 = f0011*(ageband4==1)
. generate comp24e = f0011*(ageband5==1)
. generate comp24l = f1223*(ageband5==1)
```

3. Use `streg` to fit a marginal piecewise exponential model with covariates `mage`, `mage2`, `border`, `p0014`, `p1523`, `p2435`, `p36up`, `pdead`, `comp12`, `comp24e`, and `comp24l`.
4. Fit the same piecewise exponential model as in step 3 but with a gamma frailty that is shared by children having the same mother.
5. Use `xtpoisson` to fit the same model as in step 4.
6. Compare the estimates with those in table 14.3 for the random-intercept complementary log-log model that treats the data as interval-censored.

15.6 Blindness data

Here will use the piecewise exponential survival model to analyze the data from exercise 14.6. The study was a randomized trial of a treatment to delay the onset of blindness in patients suffering from diabetic retinopathy. One eye of each patient was randomly selected for treatment, and patients were assessed at 4-month intervals. The endpoint used to assess the treatment effect was the occurrence of visual acuity less than 5/200 at two consecutive assessments.

The variables in the dataset `blindness.dta` are described in exercise 14.6.

1. Expand the data for analysis using the piecewise exponential model with time intervals (6,10], (10,14], ..., (50,54], (54,58], (58,66], (66,83].
2. Use Poisson regression to fit a piecewise exponential model with dummy variables for the intervals, `treat`, `late`, and the `treat` by `late` interaction as covariates.
3. Fit the same model as in step 2 but with a normally distributed random intercept.
   a. Is there evidence for residual within-subject dependence?
   b. Interpret the estimated incidence-rate ratios for `treat`, `late`, and their interaction.
4. For the model in step 3, test the proportional hazards assumption for `treat` by including an interaction between `treat` and a variable containing the start times of the intervals. (Hint: You can use `_t0` or the variable created using the `stsplit` command in step 1.)

15.7 Randomized trial of infection prevention I

Chronic gramulomatous disease (CGD), also known as Bridges-Good syndrome or Quie syndrome, is a diverse group of immunodeficiencies. The disease usually begins in early childhood and is characterized by recurrent bouts of infection (such as pneumonia, skin abscesses, or suppurative arthritis). In the United States, about 20 new cases are diagnosed each year. In 1986, Genentech, Inc., conducted a randomized, double-blind, placebo-controlled trial with 128 CGD patients. Sixty-three patients received Genentech's humanized interferon gamma (rIFN-g) three times daily for a year, and 65 patients received placebo three times daily for a year. The primary endpoint was the time to the first serious infection, but here we

analyze the times to up to seven serious infections that occurred during the study. The data were provided by Therneau and Grambsch (2000) and have previously been discussed by Fleming and Harrington (1991) among others.

The variables in `infections.dta` we will use here are

- `id`: patient identifier
- `number`: infection number
- `stop`: time of infection in days since randomization
- `start`: time of previous infection
- `infection`: indicator for infection (1: infection; 0: censoring)
- `treat`: dummy for interferon gamma versus placebo (1: rIFN-g; 0: placebo)

1. Fit a marginal Cox regression using counting process risk intervals and unrestricted risk sets with a common baseline hazard (see section 15.12). Use `treat` as the only covariate with a common coefficient across events.
2. Expand the data to clicks by using `stsplit` and fit an equivalent model using Poisson regression.
3. Fit a Poisson model with a smooth baseline hazard function, using a fifth-degree orthogonal polynomial. Is the estimate of the hazard ratio for `treat` similar to that from Cox regression?
4. Create a variable in the data representing the predicted baseline hazard function for the model from step 3. Run Cox regression again (on the expanded data) and use `stcurve` to plot the baseline hazard function. Overlay the predicted baseline hazard function for the model from step 3 by using the `addplot()` option (see section 4.8.5 for an example of using `addplot()` in the `serrbar` command).
5. Now include a frailty for subjects in the model from step 3 and fit the model first assuming a gamma frailty distribution and then a log-normal frailty distribution. Does the distributional assumption affect the estimate of the treatment effect?

See also exercise 16.9, where a three-level model is fit to these data.

15.8 Randomized trial of infection prevention II

Here we continue using the dataset `infections.dta` that was used in exercise 15.7, now focusing on different approaches to recurrent events. We will use the following additional variables:

- `age`: age of patient in years at the time of randomization
- `inherit`: pattern of inheritance (1: X-linked; 2: autosomal recessive)
- `steroids`: use of corticosteroids (1: used corticosteroids; 2: did not use corticosteroids)

Use Efron's method for handling ties throughout this exercise.

1. Wei, Lin, and Weissfeld (1989) specify a marginal Cox regression model based on total time and semirestricted risk sets, where the risk set for a kth event includes risk intervals for all previous events ($< k$). Fit such a model with `treat`, `age`, and dummy variables for X-linked inheritance and for using corticosteroids as covariates, with common regression coefficients across events.
2. In their model (2), Prentice, Williams, and Peterson (1981) use counting process risk intervals with restricted risk sets and event-specific baseline hazards. Fit this model, assuming that the covariates have the same coefficients across events.
3. Andersen and Gill (1982) also use counting process risk intervals, but they use unrestricted risk sets and assume that all events have a common baseline hazard function. Fit this model, again assuming that the covariates have the same coefficients across events.
4. In their model (3), Prentice, Williams, and Peterson (1981) use gap time with restricted risk sets and event-specific baseline hazards. Fit this model, assuming that the covariates have the same coefficients across events.
5. Compare and interpret the treatment effect estimates from steps 1 to 4.

Part VIII

Models with nested and crossed random effects

16 Models with nested and crossed random effects

16.1 Introduction

We have until now in this volume considered two-level data where units are nested in groups or clusters.

In this chapter, we first discuss higher-level multilevel or hierarchical models where units are classified by some factor (for instance, community) into top-level clusters. The units in each top-level cluster are then (sub)classified by a further factor (for instance, mother) into clusters at a lower level and so on (for instance, children nested in mothers). The factors defining the classifications are nested if a lower-level cluster can only belong to one higher-level cluster (for instance, a mother and her children can only belong to one community).

We also discuss nonhierarchical models where units are cross-classified by two or more factors. In this case, each unit can potentially belong to any combination of values of the different factors, for instance, children may be cross-classified by the elementary school and high school they attended. If the main effects of a such a cross-classification are represented by random effects, the models have crossed random effects.

For *continuous* responses, we previously discussed higher-level models with nested random effects in chapter 8 and models with crossed random effects in chapter 9. Before reading this chapter on *noncontinuous* responses, we strongly recommend that you read chapters 8 and 9.

16.2 Did the Guatemalan immunization campaign work?

Pebley, Goldman, and Rodríguez (1996) and Rodríguez and Goldman (2001) analyzed data on Guatemalan families' decisions about whether to immunize their children. Data are available from the National Survey of Maternal and Child Health (ENSMI) conducted in Guatemala in 1987. A nationally representative sample of 5,160 women aged between 15 and 44 was interviewed. The questionnaire included questions regarding factors that could affect the immunization status of children who were born in the previous 5 years and alive at the time of the interview.

Beginning in 1986, the Guatemalan government undertook a series of campaigns to immunize the population against major childhood diseases. The immunization campaign visited most of the country and often located children in their own households. The full set of recommended immunizations included three doses of DPT vaccine (against diphtheria, whooping cough, and tetanus), three doses of polio vaccine, one dose of BCG (antituberculosis), and one dose of measles vaccine.

The data considered here comprise 2,159 children aged 1–4 years for whom we have community data on health services and who received at least one immunization. The response variable of interest is whether the children received the full set of immunizations. An important explanatory variable is whether the child was at least 2 years old at the time of the interview, in which case the child was eligible to receive all immunizations during the campaign. If this variable is associated with immunization status, there is some indication that the campaign worked.

The dataset `guatemala.dta` comprises children i nested in mothers j nested in communities k. The multilevel structure of the data is displayed in figure 16.1.

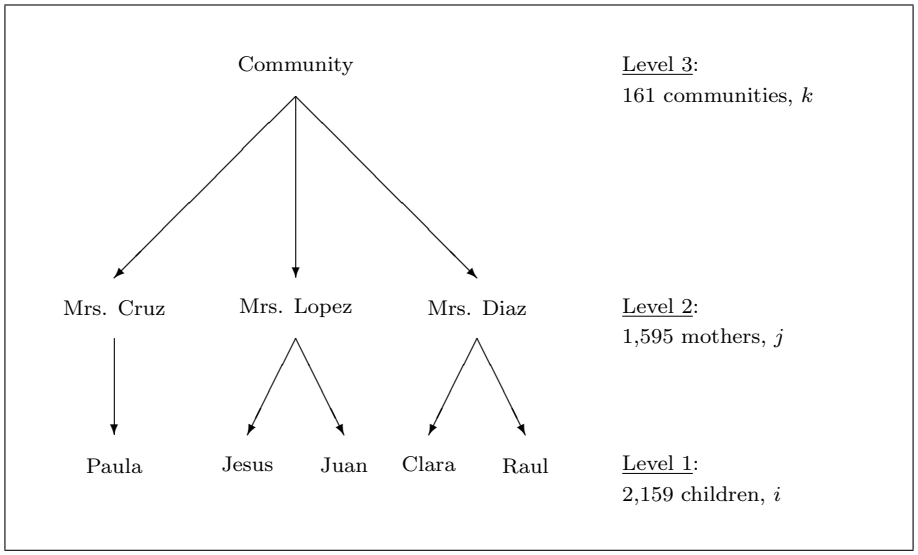


Figure 16.1: Three-level structure of Guatemalan immunization data

The dataset contains the following subset of variables from Pebley, Goldman, and Rodríguez (1996):

- Level 1 (child):
  - `immun`: indicator variable for child receiving full set of immunizations (y_{ijk})
  - `kid2p`: dummy variable for child being at least 2 years old at time of the interview and hence eligible for full set of immunizations (x_{2ijk})
- Level 2 (mother):
  - `mom`: identifier for mothers (j)
  - Ethnicity (dummy variables with Latino as reference category)
    - `indNoSpa`: mother is indigenous, not Spanish speaking (x_{3jk})
    - `indSpa`: mother is indigenous, Spanish speaking (x_{4jk})
  - Mother's education (dummy variables with no education as reference category)
    - `momEdPri`: mother has primary education (x_{5jk})
    - `momEdSec`: mother has secondary education (x_{6jk})
  - Husband's education (dummy variables with no education as reference category)
    - `husEdPri`: husband has primary education (x_{7jk})
    - `husEdSec`: husband has secondary education (x_{8jk})
    - `husEdDK`: husband's education is not known (x_{9jk})
- Level 3 (community):
  - `cluster`: identifier for communities (k)
  - `rural`: dummy variable for community being rural ($x_{10,k}$)
  - `pcInd81`: percentage of population that was indigenous in 1981 ($x_{11,k}$)

We read in the Guatemalan immunization data by typing

```
. use http://www.stata-press.com/data/mlmus3/guatemala
```

16.3 A three-level random-intercept logistic regression model

In section 10.6, we introduced two-level random-intercept logistic regression models where random intercepts varied between clusters. We now extend such models to include random intercepts varying at both the cluster and the supercluster levels.

16.3.1 Model specification

We specify a three-level random-intercept logistic regression model for childhood immunization with children i nested in mothers j who are nested in communities k:

$$\begin{aligned}\text{logit}\{\Pr(y_{ijk}=1|\mathbf{x}_{ijk},\zeta^{(2)}_{jk},\zeta^{(3)}_{k})\} &= \beta_1+\beta_2 x_{2ijk}+\cdots+\beta_{11}x_{11,k}+\zeta^{(2)}_{jk}+\zeta^{(3)}_{k}\\ &= (\beta_1+\zeta^{(2)}_{jk}+\zeta^{(3)}_{k})+\beta_2 x_{2ijk}+\cdots+\beta_{11}x_{11,k} \quad (16.1)\end{aligned}$$

Here $\mathbf{x}_{ijk}=(x_{2ijk},\ldots,x_{11,k})'$ is a vector containing all covariates, $\zeta^{(2)}_{jk}\sim N(0,\psi^{(2)})$ is a random intercept varying over mothers (level 2), and $\zeta^{(3)}_{k}\sim N(0,\psi^{(3)})$ is a random intercept varying over communities (level 3). The random intercepts $\zeta^{(2)}_{jk}$ and $\zeta^{(3)}_{k}$ are assumed to be independent of each other and independent across communities, and $\zeta^{(2)}_{jk}$ is assumed to be independent across mothers as well. Both random intercepts are assumed to be independent of the covariates $\mathbf{x}_{ijk}$. The responses y_{ijk} are independently Bernoulli distributed given the random effects and covariates.

The model can alternatively be written as a latent-response model (see section 10.2.2),

$$y^*_{ijk} = \beta_1+\beta_2 x_{2ijk}+\cdots+\beta_{11}x_{11,k}+\zeta^{(2)}_{jk}+\zeta^{(3)}_{k}+\epsilon_{ijk}$$

where ϵ_{ijk} has a standard logistic distribution with variance $\pi^2/3$. The ϵ_{ijk} are assumed to be mutually independent and to be independent of $\zeta^{(2)}_{jk}$, $\zeta^{(3)}_{k}$, and $\mathbf{x}_{ijk}$. The observed binary responses are then presumed to be generated by the threshold model

$$y_{ijk} = \begin{cases}1 & \text{if } y^*_{ijk}>0\\ 0 & \text{otherwise}\end{cases}$$

16.3.2 Measures of dependence and heterogeneity

Types of residual intraclass correlations of the latent responses

As discussed for two-level models in section 10.9.1, we can consider residual intraclass correlations for the latent responses of two children i and i'. The difference in three-level models is that we can now consider two kinds of residual intraclass correlations (as we saw for linear models in section 8.5).

For the same community k but different mothers j and j', we obtain

$$\rho(\text{comm.})\equiv \text{Cor}(y^*_{ijk},y^*_{i'j'k}\mid \mathbf{x}_{ijk},\mathbf{x}_{i'j'k}) = \frac{\psi^{(3)}}{\psi^{(2)}+\psi^{(3)}+\pi^2/3}$$

whereas for the same mother j (and then obviously the same community k), we get

$$\rho(\text{mother, comm.})\equiv \text{Cor}(y^*_{ijk},y^*_{i'jk}\mid \mathbf{x}_{ijk},\mathbf{x}_{i'jk}) = \frac{\psi^{(2)}+\psi^{(3)}}{\psi^{(2)}+\psi^{(3)}+\pi^2/3}$$

In a three-level model, $\psi^{(2)}>0$ and $\psi^{(3)}>0$, and it follows that $\rho(\text{mother, comm.}) > \rho(\text{comm.})$. This makes sense because responses for children of the same mother are more similar than responses for children from the same community having different mothers.

Types of median odds ratios

As previously discussed for two-level models in section 10.9.2, we can quantify the unobserved heterogeneity by considering the median odds ratio for pairs of randomly sampled units having the same covariate values, where the unit that has the larger random intercept is compared with the unit that has the smaller random intercept. Again, we obtain two versions of the median odds ratio for three-level models.

Comparing children of different mothers in the same community gives the median odds ratio

$$\text{OR(comm.)}_{\text{median}} \;=\; \exp\left\{\sqrt{2\psi^{(2)}}\Phi^{-1}(3/4)\right\}$$

and comparing children of different mothers from different communities gives

$$\text{OR}_{\text{median}} \;=\; \exp\left\{\sqrt{2(\psi^{(2)}+\psi^{(3)})}\Phi^{-1}(3/4)\right\}$$

There is no unexplained heterogeneity between children of the same mother (median OR=1), some unexplained heterogeneity if the mothers are different, and even more heterogeneity if the communities are also different.

16.3.3 Three-stage formulation

Retaining the distributional assumptions for the random intercepts, we can specify the same model as in (16.1) using the three-stage formulation of Raudenbush and Bryk (2002).

Following Raudenbush and Bryk, we use different letters to denote covariates at different levels: a_{ijk} for level 1, X_{jk} for level 2, and W_k for level 3. The only level-1 covariate, `kid2p`, is therefore denoted a_{1ijk}. The child-level (level-1) model can then be written as

$$\text{logit}\{\Pr(y_{ijk}=1|\pi_{0jk},a_{1ijk})\} \;=\; \pi_{0jk}+\pi_1 a_{1ijk}$$

where the intercept π_{0jk} varies between mothers j and communities k. Denoting the seven covariates at the mother level as X_{1jk} to X_{7jk}, the mother-level (level-2) model for the intercept becomes

$$\pi_{0jk} \;=\; \beta_{00k}+\beta_{01}X_{1jk}+\cdots+\beta_{07}X_{7jk}+r_{0jk}$$

Here the only coefficient having a k subscript is the intercept β_{00k}, which therefore requires a community-level (level-3) model,

$$\beta_{00k} \;=\; \gamma_{000}+\gamma_{001}W_{1k}+\gamma_{002}W_{2k}+u_{0k}$$

where W_{1k} is `rural` and W_{2k} is `pcInd81`, the covariates at level 3.

Substituting the model for β_{00k} into the level-2 model and subsequently for π_{0jk} into the level-1 model, we obtain the reduced-form model (16.1)

$$\begin{aligned}\text{logit}\{\Pr(y_{ijk}=1|\mathbf{x}_{ijk},\zeta_{jk}^{(2)},\zeta_k^{(3)})\} &= \underbrace{\gamma_{000}}_{\beta_1}+\underbrace{\pi_1}_{\beta_2}\underbrace{a_{1ijk}}_{x_{2ijk}}+\underbrace{\beta_{01}}_{\beta_3}\underbrace{X_{1jk}}_{x_{3jk}}+\cdots+\underbrace{\beta_{07}}_{\beta_9}\underbrace{X_{7jk}}_{x_{9jk}}\\ &\quad+\underbrace{\gamma_{001}}_{\beta_{10}}\underbrace{W_{1k}}_{x_{10,k}}+\underbrace{\gamma_{002}}_{\beta_{11}}\underbrace{W_{2k}}_{x_{11,k}}+\underbrace{r_{0jk}}_{\zeta_{jk}^{(2)}}+\underbrace{u_{0k}}_{\zeta_k^{(3)}}\end{aligned}$$

16.4 Estimation of three-level random-intercept logistic regression models

Two Stata commands can be used to fit three-level (and higher-level) logistic regression models: `xtmelogit` and `gllamm` (`xtlogit` can only be used for two-level models). For the applications considered here, `gllamm` is faster, so we start with `gllamm`.

16.4.1 Using gllamm

In `gllamm`, the clustering variables for the different levels in the model are given in the `i()` option, starting from level 2 and then going up the levels. This ordering is the reverse of that used in `xtmelogit` (and `xtmixed`).

When all the random effects are random intercepts, as in the present example, `gllamm` does not require the `eqs()` option. The `gllamm` command for the three-level random-intercept logistic regression model (16.1) is therefore simply

```
. gllamm immun kid2p indNoSpa indSpa momEdPri momEdSec husEdPri husEdSec
> husEdDK rural pcInd81, family(binomial) link(logit) i(mom cluster) nip(5)

number of level 1 units = 2159
number of level 2 units = 1595
number of level 3 units = 161

Condition Number = 10.125574

gllamm model

log likelihood = -1328.0727
```

immun	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
kid2p	1.712282	.2139083	8.00	0.000	1.293029	2.131535
indNoSpa	-.2992919	.4837166	-0.62	0.536	-1.247359	.6487753
indSpa	-.2178983	.361165	-0.60	0.546	-.9257688	.4899721
momEdPri	.3789441	.215497	1.76	0.079	-.0434222	.8013104
momEdSec	.3836723	.4605474	0.83	0.405	-.518984	1.286329
husEdPri	.4934885	.2244022	2.20	0.028	.0536683	.9333087
husEdSec	.4466857	.4008267	1.11	0.265	-.3389201	1.232291
husEdDK	-.0079424	.3485074	-0.02	0.982	-.6910043	.6751195
rural	-.8642705	.300585	-2.88	0.004	-1.453406	-.2751347
pcInd81	-1.17417	.4953427	-2.37	0.018	-2.145023	-.2033157
_cons	-1.054729	.4085558	-2.58	0.010	-1.855484	-.2539746

```
Variances and covariances of random effects
------------------------------------------------------------------------------


***level 2 (mom)

    var(1): 5.4272669 (1.3185042)

***level 3 (cluster)

    var(1): 1.1338841 (.37262628)
------------------------------------------------------------------------------
```

Here we have used only five quadrature points (by using the `nip(5)` option) because estimation would otherwise be slow for this sample. With as few as five points, the version of adaptive quadrature implemented in `gllamm` is sometimes unstable, so we have used ordinary quadrature by omitting the `adapt` option.

We now increase the number of quadrature points to the default of eight per dimension and use adaptive quadrature to get more accurate results. We first place the current estimates in the row matrix `a` and then specify the `from(a)` option in `gllamm` to use these estimates as starting values.

```
. matrix a = e(b)
. gllamm immun kid2p indNoSpa indSpa  momEdPri momEdSec husEdPri husEdSec
> husEdDK rural pcInd81, family(binomial) link(logit) i(mom cluster)
> from(a) adapt

number of level 1 units = 2159
number of level 2 units = 1595
number of level 3 units = 161

Condition Number = 9.6723285

gllamm model

log likelihood = -1328.496
```

immun	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
kid2p	1.713088	.2154478	7.95	0.000	1.290818	2.135357
indNoSpa	-.299316	.4778503	-0.63	0.531	-1.235885	.6372535
indSpa	-.1576852	.3568031	-0.44	0.659	-.8570065	.5416361
momEdPri	.3840802	.2170398	1.77	0.077	-.0413101	.8094705
momEdSec	.3616156	.4738778	0.76	0.445	-.5671679	1.290399
husEdPri	.4988694	.2274981	2.19	0.028	.0529813	.9447575
husEdSec	.4377393	.4042692	1.08	0.279	-.3546138	1.230092
husEdDK	-.0091557	.3519029	-0.03	0.979	-.6988728	.6805614
rural	-.8928454	.2990444	-2.99	0.003	-1.478962	-.3067291
pcInd81	-1.154086	.4935178	-2.34	0.019	-2.121363	-.1868085
_cons	-1.027388	.4061945	-2.53	0.011	-1.823514	-.2312612

```
Variances and covariances of random effects
------------------------------------------------------------------------------


***level 2 (mom)

    var(1): 5.1872364 (1.1927247)

***level 3 (cluster)

    var(1): 1.0274006 (.31690328)
------------------------------------------------------------------------------
```

The maximum likelihood estimates have changed somewhat but not drastically. Fitting the model with 12 points per dimension (not shown) gives nearly the same results as for 8 points, indicating that the latter estimates, reported under "Est" in table 16.1, are reliable. We store these estimates for later use under the name `glri8`:

```
. estimates store glri8
```

To obtain estimated odds ratios with 95% confidence intervals, we can simply replay the results with the `eform` option:

```
. gllamm, eform

number of level 1 units = 2159
number of level 2 units = 1595
number of level 3 units = 161

Condition Number = 9.6723285

gllamm model

log likelihood = -1328.496
```

immun	exp(b)	Std. Err.	z	P>|z|	[95% Conf.	Interval]
kid2p	5.546059	1.194886	7.95	0.000	3.635758	8.46007
indNoSpa	.7413251	.3542425	-0.63	0.531	.2905774	1.891279
indSpa	.8541186	.3047522	-0.44	0.659	.4244307	1.718817
momEdPri	1.468263	.3186716	1.77	0.077	.9595316	2.246718
momEdSec	1.435647	.6803213	0.76	0.445	.5671293	3.634237
husEdPri	1.646858	.3746571	2.19	0.028	1.05441	2.57219
husEdSec	1.549201	.6262943	1.08	0.279	.7014443	3.421546
husEdDK	.9908861	.3486957	-0.03	0.979	.4971454	1.974986
rural	.4094889	.1224554	-2.99	0.003	.2278742	.7358499
pcInd81	.3153457	.1556287	-2.34	0.019	.1198682	.8296026
_cons	.3579408	.1453936	-2.53	0.011	.1614573	.7935322

```
Variances and covariances of random effects
------------------------------------------------------------------------------


***level 2 (mom)

    var(1): 5.1872364 (1.1927247)

***level 3 (cluster)

    var(1): 1.0274006 (.31690328)
------------------------------------------------------------------------------
```

The estimated conditional odds ratios with confidence intervals are also reported under "OR" in table 16.1. The explanatory variable of main interest `kid2p` has a large estimated odds ratio of 5.55, adjusted for the other observed covariates and given the random intercepts at the mother and community levels. There is thus some evidence of an effect of the government campaign on child immunization, although it should be emphasized that the study is observational and thus vulnerable to confounding.

Table 16.1: Maximum likelihood estimates for three-level random-intercept logistic model (using eight-point adaptive quadrature in `gllamm`)

	Est	(SE)	OR	(95% CI)
Fixed part				
β_1 [_cons]	−1.03	(0.41)		
β_2 [kid2p]	1.71	(0.22)	5.55	(3.64, 8.46)
β_3 [indNoSpa]	−0.30	(0.48)	0.74	(0.29, 1.89)
β_4 [indSpa]	−0.16	(0.36)	0.85	(0.42, 1.72)
β_5 [momEdPri]	0.38	(0.22)	1.47	(0.96, 2.25)
β_6 [momEdSec]	0.36	(0.47)	1.44	(0.57, 3.63)
β_7 [husEdPri]	0.50	(0.23)	1.65	(1.05, 2.57)
β_8 [husEdSec]	0.44	(0.40)	1.55	(0.70, 3.42)
β_9 [husEdDK]	−0.01	(0.35)	0.99	(0.50, 1.97)
β_{10} [rural]	−0.90	(0.30)	0.41	(0.23, 0.74)
β_{11} [pcInd81]	−1.15	(0.49)	0.32	(0.12, 0.83)
Random part				
$\psi^{(2)}$	5.19			
$\psi^{(3)}$	1.03			
Log likelihood		−1328.50		

To interpret the random part of the model, it is instructive to consider the estimated residual intraclass correlations of the latent responses. For children of the same mother, $\widehat{\rho}(\text{mother}, \text{comm.})$ is obtained as

```
. display (1.0274+5.1872)/(1.0274+5.1872+_pi^2/3)
.65386089
```

and for children of different mothers in the same community, $\widehat{\rho}(\text{comm.})$ is obtained as

```
. display 1.0274/(1.0274+5.1872+_pi^2/3)
.10809653
```

Comparing children of different mothers from different communities, we obtain the estimated median odds ratio

```
. display exp(sqrt(2*(1.0274+5.1872))*invnorm(3/4))
10.782434
```

and comparing children of different mothers from the same community, we obtain

```
. display exp(sqrt(2*(5.1872))*invnorm(3/4))
8.7800782
```

These odds ratios are large compared with the estimated odds ratio for `kid2p`.

16.4.2 Using xtmelogit

In `xtmelogit`, the clustering variables for the different levels in the model are given starting from the top level and then going down the levels, just as in `xtmixed`. In the current three-level application, we first specify random intercepts for communities using `|| cluster:` and then random intercepts for mothers using `|| mom:`.

Because estimation of this model is time consuming, we start by using the computationally efficient Laplace method, which is obtained in `xtmelogit` by specifying the `intpoints(1)` or `laplace` option (even this command will take a long time):

```
. xtmelogit immun kid2p indNoSpa indSpa momEdPri momEdSec husEdPri husEdSec
> husEdDK rural pcInd81 || cluster: || mom:, intpoints(1)
Mixed-effects logistic regression               Number of obs      =      2159
```

Group Variable	No. of Groups	Observations per Group Minimum	Average	Maximum	Integration Points
cluster	161	1	13.4	55	1
mom	1595	1	1.4	3	1

```
                                                Wald chi2(10)      =     93.95
Log likelihood =  -1359.709                     Prob > chi2        =    0.0000
```

immun	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
kid2p	1.28234	.158357	8.10	0.000	.9719658	1.592714
indNoSpa	-.2017537	.3312773	-0.61	0.543	-.8510452	.4475378
indSpa	-.0893714	.2481248	-0.36	0.719	-.5756871	.3969443
momEdPri	.262748	.1495222	1.76	0.079	-.0303101	.5558061
momEdSec	.2554452	.3288252	0.78	0.437	-.3890403	.8999307
husEdPri	.3687133	.1566719	2.35	0.019	.0616421	.6757846
husEdSec	.3216275	.2795014	1.15	0.250	-.2261852	.8694402
husEdDK	.0096085	.2430354	0.04	0.968	-.4667321	.4859491
rural	-.6601202	.2075705	-3.18	0.001	-1.066951	-.2532896
pcInd81	-.8580105	.3431571	-2.50	0.012	-1.530586	-.1854348
_cons	-.7624847	.2861215	-2.66	0.008	-1.323272	-.2016969

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
cluster: Identity				
sd(_cons)	.7207785	.1005431	.5483599	.9474101
mom: Identity				
sd(_cons)	1.111227	.1579589	.841019	1.468248

```
LR test vs. logistic regression:     chi2(2) =    88.72   Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference.
Note: log-likelihood calculations are based on the Laplacian approximation.
```

The estimates from the Laplace method are placed in the row matrix `a` for subsequent use as starting values:

```
. matrix a = e(b)
```

We now perform maximum likelihood estimation using adaptive quadrature with five integration points in `xtmelogit` by specifying the `intpoints(5)` option. We can save time by using the Laplace estimates just placed in the matrix `a` as starting values instead of letting `xtmelogit` compute its own starting values. This is accomplished by using the `from()` option to pass the starting values to `xtmelogit` and the `refineopts(iterate(0))` option to specify 0 iterations for "refining" the starting values:

```
. xtmelogit immun kid2p indNoSpa indSpa momEdPri momEdSec husEdPri husEdSec
> husEdDK rural pcInd81 || cluster: || mom:, intpoints(5) from(a)
> refineopts(iterate(0))
Mixed-effects logistic regression               Number of obs      =      2159
```

Group Variable	No. of Groups	Observations per Group Minimum	Average	Maximum	Integration Points
cluster	161	1	13.4	55	5
mom	1595	1	1.4	3	5

```
                                                Wald chi2(10)      =     91.18
Log likelihood =  -1329.993                     Prob > chi2        =    0.0000
```

immun	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
kid2p	1.640996	.2003109	8.19	0.000	1.248394	2.033598
indNoSpa	-.293059	.4533644	-0.65	0.518	-1.181637	.595519
indSpa	-.1521803	.3383808	-0.45	0.653	-.8153945	.511034
momEdPri	.3615499	.2047625	1.77	0.077	-.0397772	.762877
momEdSec	.3411994	.4484829	0.76	0.447	-.5378109	1.22021
husEdPri	.4748191	.2145763	2.21	0.027	.0542574	.8953809
husEdSec	.4164453	.3824737	1.09	0.276	-.3331894	1.16608
husEdDK	-.0073808	.3328712	-0.02	0.982	-.6597963	.6450347
rural	-.8526129	.2837777	-3.00	0.003	-1.408807	-.2964189
pcInd81	-1.098836	.4679617	-2.35	0.019	-2.016024	-.1816477
_cons	-.9821477	.3854029	-2.55	0.011	-1.737524	-.2267719

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
cluster: Identity				
sd(_cons)	.9768667	.1458175	.7290813	1.308864
mom: Identity				
sd(_cons)	2.093691	.2102444	1.719636	2.54911

```
LR test vs. logistic regression:     chi2(2) =   148.15   Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference.
```

The maximum likelihood estimates based on five-point adaptive quadrature are placed in the row matrix `a` for use as starting values:

```
. matrix a = e(b)
```

The estimated standard deviation $\sqrt{\widehat{\psi}^{(2)}}$ of the mother-level random intercept and the estimated effects of the covariates are substantially larger than the estimates obtained from the Laplace method. It is evident that the rather crude Laplace method should be used with considerable caution.

However, the five-point estimates using `xtmelogit` differ from the eight-point solution using `gllamm`, so it appears that more integration points are required. We therefore use eight-point adaptive quadrature with the five-point estimates in the vector `a` as starting values (this takes some time to run):

```
. xtmelogit immun kid2p indNoSpa indSpa momEdPri momEdSec husEdPri husEdSec
> husEdDK rural pcInd81 || cluster: || mom:, intpoints(8) from(a)
> refineopts(iterate(0))
Mixed-effects logistic regression               Number of obs      =      2159
```

Group Variable	No. of Groups	Observations per Group Minimum	Average	Maximum	Integration Points
cluster	161	1	13.4	55	8
mom	1595	1	1.4	3	8

```
                                                Wald chi2(10)      =     82.76
Log likelihood =  -1328.437                     Prob > chi2        =    0.0000
```

immun	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
kid2p	1.715209	.2156215	7.95	0.000	1.292599	2.137819
indNoSpa	-.300494	.4779275	-0.63	0.530	-1.237215	.6362266
indSpa	-.158379	.3573174	-0.44	0.658	-.8587083	.5419502
momEdPri	.3851237	.2173339	1.77	0.076	-.0408429	.8110903
momEdSec	.3623701	.4742332	0.76	0.445	-.5671098	1.29185
husEdPri	.4999467	.22774	2.20	0.028	.0535845	.9463089
husEdSec	.4393949	.4048559	1.09	0.278	-.354108	1.232898
husEdDK	-.0091831	.3521292	-0.03	0.979	-.6993437	.6809775
rural	-.8959982	.3001188	-2.99	0.003	-1.48422	-.3077761
pcInd81	-1.15788	.494736	-2.34	0.019	-2.127545	-.1882149
_cons	-1.027295	.4065234	-2.53	0.012	-1.824066	-.2305236

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
cluster: Identity				
sd(_cons)	1.015412	.1566953	.7503911	1.374033
mom: Identity				
sd(_cons)	2.281914	.2604568	1.824498	2.854007

```
LR test vs. logistic regression:     chi2(2) =   151.27   Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference.
```

These estimates are close to the estimates from `gllamm`.

The likelihood-ratio test for the null hypothesis that both random intercept variances are zero that is reported at the bottom of the output is conservative, that is, the p-value

is too large. Because the p-value is tiny although it is conservative, we can reject the null hypothesis. As discussed in display 8.1, the asymptotic null distribution is $\frac{1}{4}\chi^2(0) + \frac{1}{2}\chi^2(1) + \frac{1}{4}\chi^2(2)$, so we could also obtain the asymptotic p-value as

```
display chi2tail(1,151.27)/2 + chi2tail(2,151.27)/4
```

Note that $\frac{1}{4}\chi^2(0)$ is a mass at 0 and does not contribute to the tail probability.

16.5 A three-level random-coefficient logistic regression model

We have already seen that the communities vary in their overall levels of immunization, due to both fixed effects and random effects. It would be interesting to investigate whether the effect of the campaign also varies between communities. This can be achieved by including a random coefficient $\zeta_{2k}^{(3)}$ of `kid2p` (x_{2ijk}) at level 3. To keep the model simple, we retain only `kid2p` and the community-level covariates:

$$\begin{aligned}\text{logit}\{\Pr(y_{ijk}=1|\mathbf{x}_{ijk},\zeta_{jk}^{(2)},\zeta_{1k}^{(3)},\zeta_{2k}^{(3)})\} &= \beta_1+\beta_2 x_{2ijk}+\beta_{10}x_{10,ijk}+\beta_{11}x_{11,ijk} \\ &\quad +\zeta_{jk}^{(2)}+\zeta_{1k}^{(3)}+\zeta_{2k}^{(3)}x_{2ijk} \\ &= (\beta_1+\zeta_{jk}^{(2)}+\zeta_{1k}^{(3)})+(\beta_2+\zeta_{2k}^{(3)})x_{2ijk} \\ &\quad +\beta_{10}x_{10,ijk}+\beta_{11}x_{11,ijk} \qquad (16.2)\end{aligned}$$

The random intercept $\zeta_{1k}^{(3)}$ and the random coefficient $\zeta_{2k}^{(3)}$ at the community level have a bivariate normal distribution with zero means and covariance matrix

$$\boldsymbol{\Psi}^{(3)} = \begin{bmatrix}\psi_{11}^{(3)} & \psi_{12}^{(3)} \\ \psi_{21}^{(3)} & \psi_{22}^{(3)}\end{bmatrix}, \qquad \psi_{21}^{(3)}=\psi_{12}^{(3)} \qquad (16.3)$$

The random effects at the community level $\zeta_{1k}^{(3)}$ and $\zeta_{2k}^{(3)}$ are assumed to be independent of the random intercept $\zeta_{jk}^{(2)}$ at the mother level. All random effects are assumed to be independent of the covariates $\mathbf{x}_{ijk}$.

It is unusual to include a random coefficient for a given variable at a higher level and not at the lower level(s). Here we have done so because the "treatment" was applied at the community level, and we believe that its effect will vary more between communities than between mothers within communities. Furthermore, individual mothers do not provide much information on the mother-specific effect of `kid2p` because they do not have many children of each type.

16.6 Estimation of three-level random-coefficient logistic regression models

16.6.1 Using gllamm

We first fit a three-level random-intercept logistic regression model that only includes the treatment variable x_{2ijk} and the community-level variables $x_{10,k}$ and $x_{11,k}$ as covariates,

$$\text{logit}\{\Pr(y_{ijk}=1|\mathbf{x}_{ijk},\zeta_{jk}^{(2)},\zeta_{k}^{(3)})\} = \beta_1+\beta_2 x_{2ijk}+\beta_{10}x_{10,k}+\beta_{11}x_{11,k}+\zeta_{jk}^{(2)}+\zeta_{k}^{(3)}$$

using the previous estimates for the three-level random-intercept model with the full set of covariates as starting values. These estimates are retrieved using

```
. estimates restore glri8
```

We then copy the starting values into the matrix `a`,

```
. matrix a = e(b)
```

and pass that to `gllamm` using the `from()` option. We must also specify the `skip` option, because `a` contains extra parameters (the regression coefficients of the covariates we have dropped):

```
. gllamm immun kid2p rural pcInd81, family(binomial) link(logit)
> i(mom cluster) from(a) skip adapt eform

number of level 1 units = 2159
number of level 2 units = 1595
number of level 3 units = 161

Condition Number = 5.4620661

gllamm model

log likelihood = -1335.0426
```

immun	exp(b)	Std. Err.	z	P>|z|	[95% Conf.	Interval]
kid2p	5.369864	1.151166	7.84	0.000	3.527661	8.174097
rural	.3450857	.0979057	-3.75	0.000	.1978923	.6017623
pcInd81	.1905651	.0678821	-4.65	0.000	.0948053	.3830485
_cons	.8051822	.2467615	-0.71	0.480	.4416002	1.468112

```
Variances and covariances of random effects
------------------------------------------------------------------------------

***level 2 (mom)

    var(1): 5.2136851 (1.2063284)

***level 3 (cluster)

    var(1): 1.0333637 (.31347077)
------------------------------------------------------------------------------
```

We store the estimates for later use under the name `glri0`:

```
. estimates store glri0
```

The maximum likelihood estimates are shown under "Random intercept" in table 16.2. The estimate of the conditional odds ratio for `kid2p` has not changed considerably compared with the estimate for the full model in table 16.1, suggesting that discarding the level-2 covariates does not seriously distort the estimate.

We then turn to estimation of model (16.2), which has a random coefficient $\zeta_{2k}^{(3)}$ for `kid2p` at the community level, as well as random intercepts $\zeta_{jk}^{(2)}$ and $\zeta_{1k}^{(3)}$ at the mother and community levels, respectively. We first specify equations for the intercept(s) and slope:

```
. generate cons = 1
. eq inter: cons
. eq slope: kid2p
```

The new model has two extra parameters: the variance $\psi_{22}^{(3)}$ of the random coefficient and the covariance $\psi_{21}^{(3)}$ between the random intercept and the random coefficient at the community level. We can therefore use the matrix containing the previous estimates as starting values if we add two more values:

```
. matrix a = e(b)
. matrix a = (a,.2,0)
```

As in two-level random-coefficient models, we must use the `nrf()` option to specify the number of random effects. However, in the three-level case, we must specify two numbers of random effects, `nrf(1 2)`, for levels 2 and 3. In the `eqs()` option, we must then specify one equation for level 2 and two equations for level 3. To speed up estimation (although it will still be slow), we reduce the number of quadrature points per dimension for the two random effects at level 3 from the default of eight to four by using the `nip()` option. (More points are often required at the lowest level than at the higher levels.)

```
. gllamm immun kid2p rural pcInd81, family(binomial) link(logit) i(mom cluster)
> nrf(1 2) eqs(inter inter slope) nip(8 4 4) from(a) copy adapt eform

number of level 1 units = 2159
number of level 2 units = 1595
number of level 3 units = 161

Condition Number = 7.1155374

gllamm model

log likelihood = -1330.8285
```

immun	exp(b)	Std. Err.	z	P>|z|	[95% Conf.	Interval]
kid2p	6.729718	1.975344	6.50	0.000	3.785711	11.96317
rural	.3296138	.0989118	-3.70	0.000	.1830516	.5935225
pcInd81	.1769139	.0667759	-4.59	0.000	.0844261	.3707207
_cons	.6861712	.2465649	-1.05	0.295	.3392864	1.387709

```
Variances and covariances of random effects
------------------------------------------------------------------------------

***level 2 (mom)

    var(1): 5.8320415 (1.4186368)

***level 3 (cluster)

    var(1): 2.4200309 (1.0925729)
    cov(2,1): -1.5234084 (.94663254) cor(2,1): -.72984351

    var(2): 1.8003307 (.98477224)
------------------------------------------------------------------------------
```

We store the estimates under the name `glrc`:

```
. estimates store glrc
```

The estimates of the conditional odds ratios and the residual between-mother variance (at level 2) have not changed considerably compared with the three-level random-intercept model. At the community level (level 3), the estimated elements of the covariance matrix of the random intercept and random slope are given under `***level 3 (cluster)`. The random-intercept variance, now interpretable as the residual between-community variance of the latent responses for children who were too young to be immunized at the time of the campaign (`kid2p`=0), has increased considerably to $\widehat{\psi}_{11}^{(3)} = 2.42$. The variance of the slope of `kid2p` can be interpreted as the residual variability in the effectiveness of the campaign across communities and is estimated as $\widehat{\psi}_{22}^{(3)} = 1.80$. The estimated correlation between the random intercepts and slopes is

$$\frac{\widehat{\psi}_{21}^{(3)}}{\sqrt{\widehat{\psi}_{11}^{(3)}\widehat{\psi}_{22}^{(3)}}} = -0.73$$

which suggests that for given covariate values, the immunization campaign was less effective in communities where immunization rates are already high for children who were too young to be immunized during the campaign (`kid2p`=0). The estimates are also shown in table 16.2 under "Random coefficient". Practically the same estimates (not shown) are obtained with eight quadrature points per dimension.

The three-level random-intercept logistic model, which is nested in the random-coefficient logistic regression model, is rejected at the 5% significance level (using a conservative likelihood-ratio test because the null hypothesis is on the border of parameter space).

```
. lrtest glrc glri0
Likelihood-ratio test                                 LR chi2(2)  =      8.43
(Assumption: glri0 nested in glrc)                    Prob > chi2 =    0.0148
```

As a next step, we could include cross-level interactions between `kid2p` and the community-level covariates to try to explain the variability in the effect of `kid2p` between communities, but we will not pursue this here.

Table 16.2: Maximum likelihood estimates from `gllamm` for three-level random-intercept and random-coefficient logistic regression models

	Random intercept		Random coefficient	
	Est	(95% CI)	Est	(95% CI)
Fixed part				
Conditional odds ratios				
$\exp(\beta_2)$ [`kid2p`]	5.37	(3.53, 8.17)	6.73	(3.79, 11.96)
$\exp(\beta_{10})$ [`rural`]	0.35	(0.20, 0.60)	0.33	(0.18, 0.59)
$\exp(\beta_{11})$ [`pcInd81`]	0.19	(0.09, 0.38)	0.18	(0.08, 0.37)
Random part				
$\psi^{(2)}$	5.21		5.83	
$\psi_{11}^{(3)}$	1.03		2.42	
$\psi_{22}^{(3)}$			1.80	
$\psi_{21}^{(3)}$			−1.52	
Log likelihood	−1,335.04		−1,330.83	

16.6.2 Using xtmelogit

We can fit the three-level random-coefficient model (16.2) by using the following `xtmelogit` command (this takes a long time to run):

```
. xtmelogit immun kid2p rural pcInd81 || cluster: kid2p, covariance(unstructured)
> || mom:, intpoints(4 8) or
Mixed-effects logistic regression               Number of obs      =      2159
```

Group Variable	No. of Groups	Observations per Group Minimum	Average	Maximum	Integration Points
cluster	161	1	13.4	55	4
mom	1595	1	1.4	3	8

```
                                                Wald chi2(3)       =     60.78
Log likelihood = -1330.7479                     Prob > chi2        =    0.0000
```

immun	Odds Ratio	Std. Err.	z	P>|z|	[95% Conf.	Interval]
kid2p	6.758302	1.986326	6.50	0.000	3.798934	12.02302
rural	.3276506	.0988741	-3.70	0.000	.1813622	.5919368
pcInd81	.1751774	.0666157	-4.58	0.000	.0831355	.3691216
_cons	.6885445	.2472419	-1.04	0.299	.3406304	1.391812

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
cluster: Unstructured				
sd(kid2p)	1.342271	.3678758	.7844257	2.29683
sd(_cons)	1.555728	.350135	1.00083	2.41828
corr(kid2p,_cons)	-.7284215	.137793	-.9052754	-.3363832
mom: Identity				
sd(_cons)	2.424341	.2929176	1.913147	3.072125

```
LR test vs. logistic regression:     chi2(4) =   163.69   Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference.
```

We store the estimates under the name `xtrc`:

```
. estimates store xtrc
```

In the random part for the community level, specified after the first double pipe, `||`, the syntax `cluster: kid2p` is used to include a random slope for `kid2p`, and a random intercept is included by default. The `covariance(unstructured)` option is used to estimate the covariance matrix in (16.3) without any restrictions. Without this option, the covariance is set to zero, which is rarely recommended in practice (see section 4.4.2). The random part for the mother level is specified after the second double pipe, `||`, where `mom:` means that there should be only a random intercept. We specified the `intpoints(4 8)` option to use four integration points for each random effect at level 3 and eight integration points at level 2.

16.7 Prediction of random effects

16.7.1 Empirical Bayes prediction

At the time of writing this book, `gllapred` (after estimation with `gllamm`) is the only command that can produce empirical Bayes predictions of the random effects for multilevel logistic models (`predict` for `xtmelogit` produces empirical Bayes modal predictions). After retrieving the `gllamm` estimates for the three-level random-coefficient logistic regression model,

```
. estimates restore glrc
```

we use `gllapred` with the `u` option,

```
. gllapred zeta, u
(means and standard deviations will be stored in zetam1 zetas1 zetam2 zetas2
> zetam3 zetas3)
```

and list the predicted random effects for the first nine children in the dataset:

```
. sort cluster mom
. list cluster mom zetam1 zetam2 zetam3 in 1/9, sepby(mom) noobs
```

cluster	mom	zetam1	zetam2	zetam3
1	2	1.0097228	.15487673	.04783502
36	185	-2.0246433	-.42102637	-.01032988
36	186	-2.0246433	-.42102637	-.01032988
36	187	-2.0246433	-.42102637	-.01032988
36	188	-.69007018	-.42102637	-.01032988
36	188	-.69007018	-.42102637	-.01032988
36	189	1.1806865	-.42102637	-.01032988
36	190	2.2574648	-.42102637	-.01032988
36	190	2.2574648	-.42102637	-.01032988

Here `zetam1` is the predicted random intercept $\widetilde{\zeta}_{jk}^{(2)}$ for mothers, `zetam2` is the predicted random intercept $\widetilde{\zeta}_{1k}^{(3)}$ for communities, and `zetam3` is the predicted random slope $\widetilde{\zeta}_{2k}^{(3)}$ for communities. The order of these random effects is the same as in the `eqs()` option and always from the lowest to the highest level.

The random intercept for mothers can vary between mothers but is constant across multiple children of the same mother (mothers 188 and 190). Mothers 185, 186, and 187 all have the same predictions because they have the same covariate values and responses. The predicted random intercepts and slopes at the community level are constant across children and mothers from the same community (clusters 1 and 36). We can plot the predicted random intercepts $\widetilde{\zeta}_{1k}^{(3)}$ and slopes $\widetilde{\zeta}_{2k}^{(3)}$ for the communities by using

```
. egen pick_com = tag(cluster)
. twoway scatter zetam3 zetam2 if pick_com==1, xtitle(Intercept) ytitle(Slope)
```

The resulting graph is shown in figure 16.2.

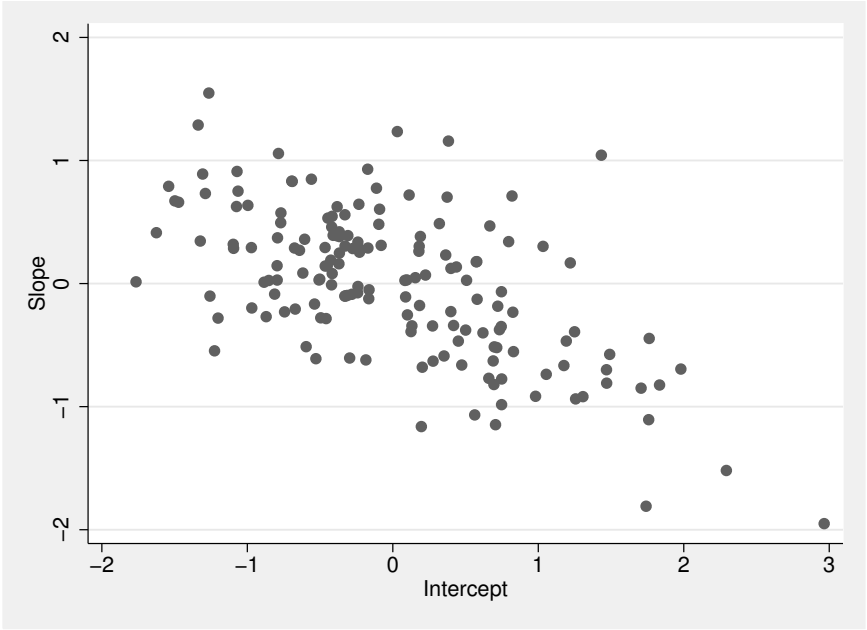


Figure 16.2: Empirical Bayes predictions of community-level random slopes versus community-level random intercepts; based on three-level random-coefficient logistic regression model

Approximate comparative standard errors for the predicted random effects are in the variables `zetas1`, `zetas2`, and `zetas3`.

16.7.2 Empirical Bayes modal prediction

The `predict` command for `xtmelogit` provides the *modes* of the posterior distributions instead of the means. We first restore the estimates for the three-level random-coefficient regression model from `xtmelogit`,

```
. estimates restore xtrc
```

and then use the `predict` command with the `reffects` option:

```
. predict comms commi mother, reffects
```

Here we have chosen variable names `comms` and `commi` for the slopes and intercepts at the community level, respectively, and `mother` for the mother-level random intercepts, to remind us which random effects have been stored in which variable (the `predict` command also produces informative variable labels). `xtmelogit` starts from the highest level, and the random intercept always comes last, exactly as in the output.

We list the empirical Bayes modal predictions by using

```
. sort cluster mom
. list cluster mom mother commi comms in 1/9, sepby(mom) noobs
```

cluster	mom	mother	commi	comms
1	2	.6343669	.0970523	.0302855
36	185	-1.786311	-.4229505	-.0808258
36	186	-1.786311	-.4229505	-.0808258
36	187	-1.786311	-.4229505	-.0808258
36	188	-.7136105	-.4229505	-.0808258
36	188	-.7136105	-.4229505	-.0808258
36	189	.8373247	-.4229505	-.0808258
36	190	1.886907	-.4229505	-.0808258
36	190	1.886907	-.4229505	-.0808258

These predictions are similar but not identical to the empirical Bayes counterparts listed (in the same order) earlier. Approximate comparative standard errors can be obtained using the `reses` option.

16.8 Different kinds of predicted probabilities

16.8.1 Predicted population-averaged or marginal probabilities: New clusters

At the time of writing this book, marginal or population-averaged probabilities can be predicted for multilevel logistic regression models only by using `gllapred` after estimation using `gllamm`. Here we have to integrate out all three random effects (the random intercept at level 2 and the random intercept and random coefficient at level 3).

The command for obtaining predicted marginal probabilities of immunization is the same as for two-level models discussed in section 10.13.1:

```
. estimates restore glrc
(results glrc are active now)
. gllapred margp, mu marginal
(mu will be stored in margp)
```

These probabilities can be interpreted as the probabilities of immunization for randomly chosen children of randomly chosen mothers from randomly chosen communities, with given covariate values.

16.8.2 Predicted median or conditional probabilities

Median probabilities are just conditional probabilities given that the random effects are zero. We can obtain median probabilities of immunization by setting the random effects equal to their median values of zero,

```
. generate z1 = 0
. generate z2 = 0
. generate z3 = 0
```

and then using `gllapred` with the `us()` option to base the predictions on these particular values for the random effects:

```
. gllapred condp, mu us(z)
(mu will be stored in condp)
```

Plotting both these conditional probabilities and the marginal probabilities from the previous section by using

```
. label define r 0 "Urban" 1 "Rural"
. label values rural r
. twoway (line condp pcInd81 if kid2p==0, lpatt(solid) sort)
> (line condp pcInd81 if kid2p==1, lpatt(solid) sort)
> (line margp pcInd81 if kid2p==0, lpatt(dash) sort)
> (line margp pcInd81 if kid2p==1, lpatt(dash) sort),
> by(rural) legend(order(1 "Conditional" 3 "Marginal"))
> xtitle(Percentage Indigenous) ytitle(Probability)
```

we obtain the graph in figure 16.3. It is clear that the marginal effects of both percentage indigenous (slopes of dashed curves) and the child being eligible for vaccination during the campaign (vertical distances between dashed curves) are attenuated compared with the conditional effects (solid curves) as usual.

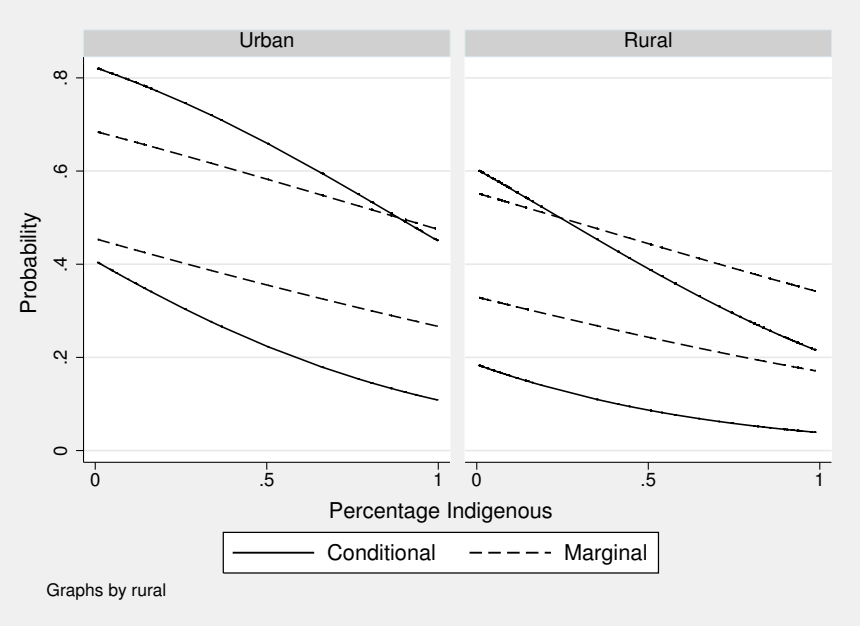


Figure 16.3: Predicted median or conditional probabilities of immunization with random effects set to zero (solid curves) and marginal probabilities of immunization (dashed curves). Curves higher up in each graph correspond to `kid2p` = 1 and curves lower down to `kid2p` = 0. Based on three-level random-coefficient logistic regression model.

16.8.3 Predicted posterior mean probabilities: Existing clusters

We now consider predicting the probability of immunization for a child of a particular mother in a particular community. This prediction will benefit from the data we already have for the mother's other children and for the other children in the community. The information these data provide about the community and mother-level random effects is expressed by the posterior distribution of the random effects, given the immunization status and covariates of all children in the community. We therefore integrate the conditional probability of immunization for the child over the posterior distribution of the random effects, as shown for two-level models in (13.11).

The `gllapred` command is also the same as for two-level models:

```
. gllapred postp, mu
(mu will be stored in postp)
```

We now list the predicted posterior mean probabilities together with the empirical Bayes predictions of the random effects:

```
. sort cluster mom
. list cluster mom kid2p zetam1 zetam2 zetam3 postp in 1/9, sepby(mom) noobs
```

cluster	mom	kid2p	zetam1	zetam2	zetam3	postp
1	2	1	1.0097228	.15487673	.04783502	.82746602
36	185	1	-2.0246433	-.42102637	-.01032988	.34772187
36	186	1	-2.0246433	-.42102637	-.01032988	.34772187
36	187	1	-2.0246433	-.42102637	-.01032988	.34772187
36	188	1	-.69007018	-.42102637	-.01032988	.55892132
36	188	1	-.69007018	-.42102637	-.01032988	.55892132
36	189	1	1.1806865	-.42102637	-.01032988	.79839256
36	190	0	2.2574648	-.42102637	-.01032988	.70573537
36	190	1	2.2574648	-.42102637	-.01032988	.90750043

For community 36, all covariates are constant except that `kid2p` changes from 0 to 1 for mother 190 (the other covariates are community specific). Mothers 185, 186, and 187 have a low predicted random intercept of -2.02 and correspondingly a low predicted posterior mean probability of immunization of 0.35, whereas mother 190 has a large predicted random intercept of 2.26 and a correspondingly large predicted probability of 0.91 for the child with `kid2p` $= 1$. For the other child with `kid2p` $= 0$, the predicted probability of 0.71 is lower as expected.

16.9 Do salamanders from different populations mate successfully?

We now consider the famous salamander mating data from three experiments conducted by S. J. Arnold and P. A. Verrell; see Verrell and Arnold (1989) for the background of the experiments. The data were first introduced into the statistical literature by McCullagh and Nelder (1989) and then analyzed by Karim and Zeger (1992), Breslow and Clayton (1993), and many others. The purpose of the experiments considered here was to investigate the extent to which mountain dusky salamanders from two geographically isolated populations in North Carolina, U.S.A., would cross-breed. The two populations were named after the location where the salamanders were collected, the Rough Butt Bald in the Great Balsam Mountains ("roughbutt") and the Whiteside Mountain in the Highlands Plateau ("whiteside").

The first experiment in the summer of 1986 used two groups of 20 salamanders. Each group comprised five roughbutt males (RBM), five whiteside males (WSM), five roughbutt females (RBF), and five whiteside females (WSF). Within each group, 60 male–female pairs were formed so that each salamander had three potential partners from the same population and three partners from the other population. This design is shown under

"Experiment 1" in table 16.3, where the pairs are indicated by a 1 (successful mating) or 0 (unsuccessful mating). Two further similar experiments were conducted in the fall of 1987 as shown under "Experiment 2" and "Experiment 3" in table 16.3. Experiment 2 actually used the same salamanders as experiment 1, with salamander 21 corresponding to salamander 1, salamander 31 to salamander 11, etc. Experiment 3 used a new set of salamanders.

Table 16.3: Salamander mating data (layout adapted from Vaida and Meng [2005])

Experiment 1

Group 1

		RBM					WSM				
		01	02	03	04	05	06	07	08	09	10
RBF	01	1			1	1	0			1	1
	02	1		1		1		1	1		1
	03	1	1	1			0		1	1	
	04		1		1	1		1		1	0
	05		1	1	1		1	1	1		
WSF	06	0	0		0			0	1		0
	07	1	0			1	1			1	1
	08			0	0	0	1	1			1
	09	1		1	0		1		1	1	
	10		0	1		0		1	1	0	

Group 2

		RBM					WSM				
		11	12	13	14	15	16	17	18	19	20
RBF	11		0	1	1		1			1	1
	12	0		0	1			0	0	0	
	13	1			1	0	0	0			1
	14	1	0			1			1	1	0
	15		0	0		0	1	0	1		
WSF	16		1		0	0			1	1	1
	17	0	0		0		0	1			0
	18	0	0	0			1	0		0	
	19			1	0	0			1	1	1
	20	0		0		0	0	0	1		

Experiment 2

Group 3

		RBM					WSM				
		21	22	23	24	25	26	27	28	29	30
RBF	21	1			1	1	0			0	0
	22	0		1		1		1	0		1
	23	1	0	1			1		1	1	
	24		0		1	0		0		0	0
	25		0	1	1		0	0	0		
WSF	26	1	0		1			1	1		1
	27	0	0			0	0			1	1
	28			0	0	0	0	0			0
	29	1		1	1		1		1	1	
	30		0	1		0		1	1	1	

Group 4

		RBM					WSM				
		31	32	33	34	35	36	37	38	39	40
RBF	31		0	0	1		0			1	1
	32	1		1	1			0	1	0	
	33	0			0	0	1	0			1
	34	1	1			1			1	0	1
	35		0	1		0	1	0	1		
WSF	36		0		0	0			1	1	0
	37	0	0		0		1	0			1
	38	0	0	0			1	1		1	
	39			1	0	0			1	1	0
	40	0		0		0	0	0	0		

Experiment 3

Group 5

		RBM					WSM				
		41	42	43	44	45	46	47	48	49	50
RBF	41	1			1	1	0			1	1
	42	0		0		0		0	1		0
	43	1	1	1			1		1	0	
	44		1		1	0		0		0	1
	45		1	0	1		0	0	1		
WSF	46	0	0		0			0	1		0
	47	0	0			0	0			1	1
	48			0	0	0	0	1			1
	49	0		0	0		0		1	1	
	50		0	0		0		0	1	1	

Group 6

		RBM					WSM				
		51	52	53	54	55	56	57	58	59	60
RBF	51		1	1	1		1			0	1
	52	0		1	0			0	0	0	
	53	1			0	1	1	1			1
	54	0	0			1			1	1	0
	55		1	1		1	1	0	1		
WSF	56		0		0	0			1	0	1
	57	0	0		0		1	1			1
	58	1	0	1			1	0		0	
	59			1	0	1			0	0	1
	60	0		0		1	1	1	1		

The dataset `salamander.dta` has the following variables:

- `y`: indicator for successful mating (1: successful; 0: unsuccessful)
- `male`: male identifier as in table 16.3 (1–60)
- `female`: female identifier as in table 16.3 (1–60)
- `experiment`: experiment number (1–3)
- `group`: identifiers of six groups of 20 salamanders as in table 16.3 with groups {1,2}, {3,4}, and {5,6} used in experiments 1, 2, and 3, respectively
- `rbm`, `wsm`, `rbf`, `wsf`: dummy variables for salamander being of the given type: roughbutt males, whiteside males, roughbutt females, and whiteside females, respectively

We read in the salamander data by typing

```
. use http://www.stata-press.com/data/mlmus3/salamander, clear
```

Because the design is complicated, we should first make sure that we understand the data correctly by, for instance, producing the cross-tabulation for the first groups for experiment 1.

```
. table female male if group==1, contents(mean y)
```

	male									
female	1	2	3	4	5	6	7	8	9	10
1	1			1	1	0			1	1
2	1		1		1		1	1		1
3	1	1	1			0		1	1	
4		1		1	1		1		1	0
5		1	1	1		1	1	1		
6	0	0		0			0	1		0
7	1	0			1	1			1	1
8			0	0	0	1	1			1
9	1		1	0		1		1	1	
10		0	1		0		1	1	0	

16.10 Crossed random-effects logistic regression

We now consider Model A from Karim and Zeger (1992) that treated the salamanders from experiments 1 and 2 as independent. A logistic regression model with crossed random effects was specified for successful mating. The model included the covariates `wsm` (x_{2i}), `wsf` (x_{3j}), and their interaction, as well as random intercepts ζ_{1i} for males i ($i = 1, \ldots, I$) and ζ_{2j} for females j ($j = 1, \ldots, J$)

$$\text{logit}\{\Pr(y_{ij} = 1 | x_{2i}, x_{3j}, \zeta_{1i}, \zeta_{2j})\} = \beta_1 + \beta_2 x_{2i} + \beta_3 x_{3j} + \beta_4 x_{2i} x_{3j} + \zeta_{1i} + \zeta_{2j}$$

The random intercepts are assumed to be distributed as $\zeta_{1i} \sim N(0, \psi_1)$ and $\zeta_{2j} \sim N(0, \psi_2)$, to be independent of each other, and to be independent of the covariates x_{2i}

and x_{3j}. The random intercepts are crossed because each male i has the same value of his random intercept ζ_{1i} across all females and each female j has the same value of her random intercept ζ_{2j} across all males.

In section 9.3.3, we described in detail how to fit models with crossed random effects by defining the entire dataset to be a cluster at level 3, specifying level-3 random coefficients of dummy variables for the levels of one of the factors, say, males, and defining females to be clusters at level 2 with level-2 random intercepts. The random part of the model is expressed as

$$\zeta_{1i} + \zeta_{2j} \equiv \sum_{r=1}^{I} \zeta_{ra}^{(3)} d_{ri} + \zeta_j^{(2)}$$

where a denotes the entire dataset ("all") and $\zeta_{ra}^{(3)}$ is the random coefficient of the dummy variable d_{ri} for male i (equal to 1 if $r = i$ and 0 otherwise) so that

$$\sum_{r=1}^{I} \zeta_{ra}^{(3)} d_{ri} = \zeta_{ia}^{(3)} \equiv \zeta_{1i}$$

The syntax `_all: R.male` makes it easy to specify random coefficients for male dummy variables varying at level 3 (the entire dataset). The complete syntax for the random part of the model is `|| _all: R.male || female:`.

Unfortunately, this model has 60 random coefficients and 1 random intercept, and computation time for generalized linear mixed models increases exponentially with the number of random effects. We will therefore exploit the fact that salamanders are nested within six groups with no matings occurring across groups. This allows us to use the trick described in section 9.8 with `group` as the highest level in the model instead of `_all`. We then only need 10 random coefficients for males (10 males per group); the first random coefficient multiplies a dummy variable for the salamander being the first male in each group (male salamanders 1, 11, 21, 31, 41, and 51); the second is for the second male in each group (male salamanders 2, 12, 22, 32, 42, and 52); and so forth. These sets of six salamanders do not share the same value of the random coefficient because they are in different groups and the random coefficient is nested in groups.

A model with 10 random coefficients and 1 random intercept is still computationally demanding to fit. We will therefore initially use one integration point, which corresponds to the Laplace approximation. We generally do not recommend relying on this approach alone without conducting some simulations to make sure that the estimates are reasonable.

We first relabel the males so that the sets of six salamanders (for example, the set of first salamanders in the six groups) described above have the same label (we do the same for females although this is not necessary):

```
. generate m = male - (group-1)*10
. generate f = female - (group-1)*10
```

To list the new labels, we use the `egen` function `tag()` to define a dummy variable, `pickmale`, for picking out one observation per male:

```
. egen pickmale = tag(male)
```

We can then sort and display the data for the first two sets of six males:

```
. sort m group
. list group male m if pickmale==1&m<3, sepby(m) noobs
```

group	male	m
1	1	1
2	11	1
3	21	1
4	31	1
5	41	1
6	51	1
1	2	2
2	12	2
3	22	2
4	32	2
5	42	2
6	52	2

Consider the data for the first set of six males with `m` equal to 1. A dummy variable for this set of six males will multiply the random coefficient $\zeta_{1k}^{(3)}$, where k denotes `group` (and replaces the subscript a we used previously before implementing the trick). Importantly, the random coefficient $\zeta_{1k}^{(3)}$ takes on a different value for each male in the set, depending on the group it belongs to (namely, $\zeta_{11}^{(3)}$, $\zeta_{12}^{(3)}$, $\zeta_{13}^{(3)}$, $\zeta_{14}^{(3)}$, $\zeta_{15}^{(3)}$, or $\zeta_{16}^{(3)}$).

We start by generating the interaction term,

```
. generate ww = wsf*wsm
```

and fit the model using `xtmelogit` with the `laplace` option:

```
. xtmelogit y wsm wsf ww || group: R.m || f:, laplace
Mixed-effects logistic regression               Number of obs      =       360
```

Group Variable	No. of Groups	Observations per Group Minimum	Average	Maximum	Integration Points
group	6	60	60.0	60	1
f	60	6	6.0	6	1

```
                                                Wald chi2(3)       =     37.57
Log likelihood = -209.27659                     Prob > chi2        =    0.0000
```

y	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
wsm	-.7020417	.4614756	-1.52	0.128	-1.606517	.2024339
wsf	-2.90421	.5608211	-5.18	0.000	-4.003399	-1.805021
ww	3.588444	.6390801	5.62	0.000	2.33587	4.841018
_cons	1.008221	.3937705	2.56	0.010	.2364454	1.779997

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
group: Identity				
sd(R.m)	1.020296	.2483604	.6331794	1.64409
f: Identity				
sd(_cons)	1.083683	.2530921	.6856555	1.712769

```
LR test vs. logistic regression:     chi2(2) =    27.02   Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference.
Note: log-likelihood calculations are based on the Laplacian approximation.
```

Having reduced the dimensionality of integration to 10 at level 3 and 1 at level 2 (compared with 60 at level 3 and 1 at level 2 without the trick), it becomes feasible to use adaptive quadrature in `xtmelogit` with two integration points. To speed things up, we use the estimates from the Laplace approximation as starting values. The `refineopts(iterate(0))` option is used to prevent `xtmelogit` from computing its own starting values:

```
. matrix a = e(b)
. xtmelogit y wsm wsf ww || group: R.m || f:, intpoints(2) from(a)
> refineopts(iterate(0))
Mixed-effects logistic regression               Number of obs      =       360
```

Group Variable	No. of Groups	Observations per Group Minimum	Average	Maximum	Integration Points
group	6	60	60.0	60	2
f	60	6	6.0	6	2

```
                                                Wald chi2(3)       =     37.40
Log likelihood = -208.39862                     Prob > chi2        =    0.0000
```

y	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
wsm	-.6946282	.4668329	-1.49	0.137	-1.609604	.2203474
wsf	-2.910889	.5661132	-5.14	0.000	-4.020451	-1.801328
ww	3.587045	.6378697	5.62	0.000	2.336843	4.837246
_cons	1.003062	.3996581	2.51	0.012	.2197465	1.786377

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
group: Identity				
sd(R.m)	1.058889	.2481503	.6689157	1.676213
f: Identity				
sd(_cons)	1.114577	.2522591	.7152533	1.736841

```
LR test vs. logistic regression:     chi2(2) =    28.78   Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference.
```

This did not take long, so we increase the number of integration points to three (this command took a very long time to run!):

```
. matrix a=e(b)
. xtmelogit y wsm wsf ww || group: R.m || f:, intpoints(3) from(a)
> refineopts(iterate(0))
Mixed-effects logistic regression               Number of obs      =       360
```

Group Variable	No. of Groups	Observations per Group Minimum	Average	Maximum	Integration Points
group	6	60	60.0	60	3
f	60	6	6.0	6	3

```
                                                Wald chi2(3)       =     37.07
Log likelihood = -207.71151                     Prob > chi2        =    0.0000
```

y	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
wsm	-.6962912	.4750503	-1.47	0.143	-1.627373	.2347903
wsf	-2.946427	.5785634	-5.09	0.000	-4.080391	-1.812464
ww	3.621843	.6442771	5.62	0.000	2.359083	4.884603
_cons	1.013944	.4097109	2.47	0.013	.2109251	1.816962

Random-effects Parameters	Estimate	Std. Err.	[95% Conf.	Interval]
group: Identity				
sd(R.m)	1.100838	.2558109	.6981081	1.735898
f: Identity				
sd(_cons)	1.161527	.2610426	.7477042	1.804385

```
LR test vs. logistic regression:     chi2(2) =    30.15   Prob > chi2 = 0.0000
Note: LR test is conservative and provided only for reference.
```

The null hypothesis that the male and female random-effects variances are both zero is rejected even using the conservative test. As discussed in display 8.1, the asymptotic null distribution is $\frac{1}{4}\,\chi^2(0) + \frac{1}{2}\,\chi^2(1) + \frac{1}{4}\,\chi^2(2)$, so we could also obtain the p-value as

```
. display chi2tail(1,30.15)/2 + chi2tail(2,30.15)/4
9.094e-08
```

The estimates using the Laplace approximation and adaptive quadrature with three integration points (AQ-3pt) are given in table 16.4 together with estimates using Monte Carlo EM (MCEM) from Vaida and Meng (2005), Markov chain Monte Carlo (MCMC) with noninformative priors from Karim and Zeger (1992), and penalized quasilikelihood (PQL) from Breslow and Clayton (1993). Treating the estimates from MCEM as the gold standard (because they are maximum likelihood estimates employing Monte Carlo integration), the Laplace estimates are considerably better than the PQL estimates, and the adaptive quadrature estimates with just three quadrature points are nearly identical to the MCEM estimates.

Table 16.4: Different estimates for the salamander mating data

	Laplace		AQ-3pt		MCEM	MCMC		PQL	
	Est	(SE)	Est	(SE)	Est	Est	(SE)*	Est	(SE)
Fixed part									
β_1 [_cons]	1.00	(0.39)	1.01	(0.41)	1.02	1.03	(0.43)	0.79	(0.32)
β_2 [wsm]	−0.70	(0.46)	−0.70	(0.48)	−0.70	−0.69	(0.50)	−0.54	(0.39)
β_3 [wsf]	−2.90	(0.56)	−2.95	(0.58)	−2.96	−3.01	(0.60)	−2.29	(0.43)
β_4 [wsm×wsf]	3.59	(0.64)	3.62	(0.64)	3.63	3.74	(0.68)	2.82	(0.50)
Random part									
$\sqrt{\psi_1}$ [Males]	1.02		1.10		1.11	1.16		0.79	
$\sqrt{\psi_2}$ [Females]	1.08		1.16		1.18	1.22		0.84	

*Range of 90% CI divided by 3.3

When the random intercepts are zero, $\zeta_{1i}=\zeta_{2j}=0$, the odds of successful mating for salamander pairs where both male and female are roughbutts (RBM–RBF) are estimated as

```
. lincom _cons, or
 ( 1)  [eq1]_cons = 0
```

y	Odds Ratio	Std. Err.	z	P>|z|	[95% Conf.	Interval]
(1)	2.75645	1.129348	2.47	0.013	1.23482	6.153139

For RBM–WSF, we get

```
. lincom _cons + wsf, or
 ( 1)  [eq1]wsf + [eq1]_cons = 0
```

y	Odds Ratio	Std. Err.	z	P>|z|	[95% Conf.	Interval]
(1)	.1447882	.0675077	-4.14	0.000	.0580576	.3610831

For WSM–RBF, we get

```
. lincom _cons + wsm, or
 ( 1)  [eq1]wsm + [eq1]_cons = 0
```

y	Odds Ratio	Std. Err.	z	P>|z|	[95% Conf.	Interval]
(1)	1.373899	.5370912	0.81	0.416	.6385558	2.956042

And for WSM–WSF, we get

```
. lincom _cons + wsm + wsf + ww, or
 ( 1)  [eq1]wsm + [eq1]wsf + [eq1]ww + [eq1]_cons = 0
```

y	Odds Ratio	Std. Err.	z	P>|z|	[95% Conf.	Interval]
(1)	2.699504	1.099259	2.44	0.015	1.215256	5.996529

Within the same population, the odds of successful mating are high for both whitesides and roughbutts. Across populations, the odds are considerably lower, particularly if the male is a roughbutt and the female a whiteside. However, for a given type of pairing, the estimated median odds ratio comparing the more fertile of two randomly chosen pairs with the less fertile pair is large,

```
. display exp(sqrt(2*(1.10^2+1.16^2))*invnormal(3/4))
4.5946103
```

indicating that there is considerable unexplained heterogeneity.

16.11 Summary and further reading

We have applied models with nested random effects to a three-level dataset on immunization of children in Guatemala where children are nested in mothers who are nested in communities. Different kinds of median odds ratios and residual intraclass correlations between latent responses were described for dichotomous responses. Intraclass correlations between latent responses can also be used in cumulative logit and probit models for ordinal responses and the idea of median odds ratios, median incidence-rate ratios, etc., is applicable for all response types.

We also considered a model with crossed random effects for male and female salamanders, where each male salamander mated with six female salamanders and each female salamander mated with six male salamanders. Although many fundamental issues regarding nested and crossed random effects remain the same as in the continuous case, we have emphasized some of the special challenges in modeling noncontinuous responses.

Raudenbush and Bryk (2002) and Goldstein (2011) discuss generalized linear mixed models with nested and crossed random effects. Guo and Zhao (2000) is a review paper on two- and three-level models for binary responses. We also recommend an excellent encyclopedia entry by Rasbash (2005) on crossed random-effects models and multiple-membership models.

The exercises cover all the response types discussed in this volume. Exercises 16.1, 16.2, 16.3, 16.10, and 16.11 are on binary responses; exercise 16.4 is on an ordinal response; exercise 16.8 is on a nominal response; exercises 16.6 and 16.7 are on counts; exercise 16.5 is on discrete-time survival; and exercise 16.9 is on continuous-time survival. Exercise 16.10 is about multilevel and random-item item-response models and

involves crossed and nested random effects. In exercise 16.11, a biometrical genetic model is fit to binary twin data.

16.12 Exercises

16.1 Dairy-cow data

Consider again the data on dairy cows from Dohoo et al. (2001) and Dohoo, Martin, and Stryhn (2010) that was used in exercise 8.8 (see also exercise 10.5).

1. Fit a two-level random-intercept logistic regression model for the response variable `fscr`, an indicator for conception at the first insemination attempt (first service). Include a random intercept for cow and the covariates `lncfs`, `ai`, and `heifer`.
2. Now extend the model by including a random intercept for herds as well. Use `xtmelogit` or `gllamm` with five integration points to speed up estimation. Is there any evidence for unobserved heterogeneity in fertility between herds?

16.2 Tower-of-London data Solutions

Rabe-Hesketh, Toulopoulou, and Murray (2001a) analyzed data on patients with schizophrenia, their relatives, and controls. Cognitive performance was assessed by the Tower of London (a computerized task), which was repeated at three levels of difficulty, starting with the easiest and ending with the hardest. The data have a three-level structure with measurements at occasion i for person j in family k. We will consider the dichotomous response y_{ijk}, equal to 1 if the tower was completed in the minimum number of moves and 0 otherwise.

The dataset `towerl.dta` contains the following variables:

- `famnum`: family identifier
- `id`: person identifier
- `dtlm`: indicator for completing the task in the minimum number of moves
- `level`: level of difficulty of the Tower of London (x_{ijk})
- `group`: group (1: controls; 2: relatives; 3: schizophrenics)

1. Fit the two-level random-intercept model (random intercept for persons):

$$\text{logit}\{\Pr(y_{ijk}=1 \mid \mathbf{x}_{ijk}, \zeta_{jk}^{(2)})\} \;=\; \beta_0 + \beta_1 x_{ijk} + \beta_2 g_{2ijk} + \beta_3 g_{3ijk} + \zeta_{jk}^{(2)}$$

   where g_{2ijk} and g_{3ijk} are dummy variables for groups 2 and 3, respectively, and $\zeta_{jk}^{(2)} \sim N(0, \psi^{(2)})$ is independent of the covariates $\mathbf{x}_{ijk}$. Here and throughout the exercise, `level` is treated as continuous.
2. Fit the three-level random-intercept model (random intercepts for persons and families):

$$\text{logit}\{\Pr(y_{ijk}=1 \mid \mathbf{x}_{ijk}, \zeta_{jk}^{(2)}, \zeta_{k}^{(3)})\} \;=\; \beta_0+\beta_1 x_{ijk}+\beta_2 g_{2ijk}+\beta_3 g_{3ijk}+\zeta_{jk}^{(2)}+\zeta_{k}^{(3)}$$

where $\zeta_{jk}^{(2)} \sim N(0, \psi^{(2)})$ is independent of $\zeta_k^{(3)} \sim N(0, \psi^{(3)})$ and both random effects are assumed independent of $\mathbf{x}_{ijk}$.

3. Compare the models in steps 1 and 2 using a likelihood-ratio test, but retain the three-level model even if the null hypothesis is not rejected at the 5% level.
4. Include a group (controls, relatives, schizophrenics) by level of difficulty interaction in the three-level model. Test the interaction using both a Wald test and a likelihood-ratio test.
5. For the model in step 4, obtain predicted marginal or population-averaged probabilities using `gllapred`. (This requires fitting the model in `gllamm`.) Plot the probabilities against the levels of difficulty with different curves for the three groups.

16.3 Antibiotics data

Acute respiratory tract infection (ARI) is a common disease among children, pneumonia being a leading cause of death in young children in developing countries. In China, the standard medication for ARI is antibiotics, which has led to concerns about antibiotics misuse and resultant drug resistance. As a response, the World Health Organization (WHO) introduced a program of case management for ARI in children under 5 years old in China in the 1990s.

Here we consider data on physicians' prescribing behavior of antibiotics in two Chinese counties, only one of which was in the WHO program. These data have previously been analyzed by Yang (2001); see also Skrondal and Rabe-Hesketh (2003b) and Skrondal and Rabe-Hesketh (forthcoming).

Medical records were examined for medicine prescribed and a correct diagnosis determined from symptoms and clinical signs. The antibiotic prescription was defined as abuse if there were no clinical indications.

The dataset `antibiotics.dta` has the following variables:

- Level 1 (child):
  - `abuse`: classification of prescription (1: correct use; 2: abuse of one antibiotic; 3: abuse of several antibiotics)
  - `age`: age in years (0–4)
  - `temp`: body temperature in Centigrade, centered at 36 degrees
  - `Paymed`: dummy variable for patient paying for his or her own medication
  - `Selfmed`: dummy variable for self-medication before seeing doctor
  - `Wrdiag`: dummy variable for diagnosis classified as wrong
- Level 2 (doctor):
  - `doc`: doctor identifier
  - `DRed`: doctor's education (ordinal with six categories from self-taught to medical school)

- Level 3 (hospital):
  - `hosp`: hospital identifier
  - `WHO`: dummy variable for hospital being in the WHO program

1. Recode `abuse` into a dichotomous variable equal to 1 if there was abuse of one or more antibiotics and 0 otherwise.
2. Fit a three-level logistic regression model for the dichotomized variable `abuse` with random intercepts for doctors and hospitals and no covariates. Use adaptive quadrature with five quadrature points.
3. Add the dummy variable for hospital being in the WHO program to the model. Obtain and interpret the estimated odds ratio for the WHO program, as well as its 95% confidence interval. Does this analysis suggest that the program has been effective?
4. Include all the other covariates in the model and reassess the apparent effect of the WHO program. Comment on the change in the estimated random-intercept variances between the model without covariates (step 2) and the model with all the covariates (step 4).

16.4 Smoking-intervention data

In this exercise, we use the dataset `tvsfpors.dta` from Flay et al. (1988) that was described in exercise 11.3.

1. Investigate how tobacco and health knowledge is influenced by the interventions by fitting a three-level proportional odds model with students nested in classes nested in schools. Include `cc`, `tv`, their interaction, and `prethk` as covariates. Use five-point adaptive quadrature.
2. Does this model fit better than the two-level models with a random intercept either at the class level or at the school level?

16.5 Cigarette data

Use the dataset `cigarette.dta` from Flay et al. (1988) that was described in exercise 14.7.

1. Expand the data to person–period data.
2. Fit the discrete-time survival model that assumes the continuous-time hazards to be proportional. Use dummy variables for periods; include `cc`, `tv`, their interaction, and `male` as explanatory variables; and specify random intercepts for classes and schools. (Five quadrature points at each level should suffice.)
3. Interpret the exponentials of the estimated regression coefficients.
4. Perform likelihood-ratio tests of the null hypotheses that each of the variance components is zero using a 5% level of significance.
5. ❖ Perform a likelihood-ratio test of the joint null hypothesis that both variance components are zero using a 5% level of significance (see display 8.1).

16.6 Health-care reform data

This exercise is based on the health-care reform dataset `drvisits.dta` from Winkelmann (2004) that was discussed in section 13.4.

1. Fit the random-intercept Poisson model specified on page 696.
2. Write down and fit the three-level model that also includes an occasion and person-specific random intercept in addition to a person-specific random intercept. Use five-point adaptive quadrature.
3. Does the three-level model appear to fit better than the two-level model?
4. ❖ Consider the total random part in the three-level model, and compare the variances for 1996 and 1998 and the covariance with the corresponding estimates for the random-coefficient model fit in section 13.8 (see also section 13.8.3). Comment on the difference between the random-coefficient and three-level models. Is one more general than the other?

16.7 Skin-cancer data

Here we consider the dataset `skincancer.dta` from Langford, Bentham, and McDonald (1998) that was described in exercise 13.7.

1. Use `gllamm` to fit a Poisson model for the number of male deaths using the log expected number of male deaths as an offset (see page 724) and `uv` and squared `uv` as covariates. Include random intercepts for county, region, and nation. This is a four-level model requiring the option `i(county region nation)`. To speed up estimation in `gllamm`, use eight quadrature points at level 2 and five points at levels 3 and 4 (the `nip(8 5 5)` option).
2. Write down the model, and interpret the estimates.
3. Obtain empirical Bayes predictions for the nations.
4. Instead of using a random intercept for nation, include dummy variables for all the nations and exclude the constant (use `xtmelogit`). How do the estimated regression coefficients of the nation dummy variables compare with the empirical Bayes predictions from step 3? How do the estimated standard errors for these regression coefficients compare with the standard errors for the empirical Bayes predictions?

16.8 British election data

In exercise 12.4, several models are fit to British national election data from 1987 and 1992. In addition to the variables described in exercise 12.4, the dataset `elections.dta` contains the variable `constit`, an identifier for the constituency (the district for which a member of parliament is elected) where the respondent lives.

1. Create a variable `chosen` equal to 1 for the party voted for (`rank` equal to 1) and zero for the other parties, and standardize `lrdist` and `inflation` to have mean 0 and variance 1.

2. Consider a discrete-choice model for party voted for with `yr87` and `yr92` as the only covariates with party-specific coefficients. Use Conservatives as base outcome and fit the model using `clogit` and `gllamm`.
3. Extend the model to include a random slope for `lrdist` at the voter and constituency levels and fit the extended model in `gllamm`. Use five quadrature points to speed up estimation.
4. Test whether the constituency-level random slope is needed.

16.9 Randomized trial of infection prevention

1. Solve exercise 15.7.
2. Extend the model with a lognormal frailty at the subject level (fit in step 5 of exercise 15.7) by adding another lognormal frailty at the center level (variable `center`). Fit the model using `xtmepoisson`.
3. Is there evidence for between-center variability in the baseline hazards?

16.10 Item-response data

Here we consider a dataset collected by Doolaard (1999) and previously analyzed by Fox and Glas (2001) and Vermunt (2008).

The data are from an 18-item math test taken by 2,156 students belonging to 97 schools in the Netherlands. We will fit a standard one-parameter logistic item response (IRT) model, also known as a *Rasch model* (see also exercises 10.4 and 11.2) as well as more advanced IRT models.

The variables in the dataset `cito.dta` that we will use here are

- `y1`, `y2`, ... , `y18`: binary item responses for items 1 through 18 (1: correct; 0: incorrect)
- `school`: school identifier

1. Create a person identifier and reshape the data to long form.
2. Fit a Rasch model, that is, a logistic regression model with a random intercept for person, fixed coefficients for dummy variables for the 18 items, and no fixed intercept (this is fastest using `xtlogit`). The coefficients of the item dummies are minus the item difficulties, and the random intercept is the person ability.
3. Use the `predict` command with the `xb` option to store estimates of minus the difficulties in the data.
4. Now consider a model with random effects of items and persons. The random-item model for the log odds that person j responds correctly to item i can be written as

$$\text{logit}\{\Pr(y_{ij}=1|\zeta_{1i},\zeta_{2j})\} \;=\; \beta+\zeta_{1i}+\zeta_{2j}$$

where ζ_{1i} and ζ_{2j} are uncorrelated normally distributed random item effects and random person effects, respectively, both with zero mean and with variances ψ_1 and ψ_2. The random item effects and random person effects are

assumed to be independent of each other. Fit the model using `xtmelogit` with the `laplace` option.

5. Predict the random effects and add the estimated fixed intercept to the predicted item effects.
6. Produce a scatterplot to compare the estimated fixed item effects from step 2 with the predicted random item effects from step 5. Include a $y = x$ line in the graph.
7. Now add a random intercept for school and fit the model using `xtmelogit` with the `laplace` option.
8. For a given item, what is the estimated median odds ratio comparing randomly chosen students from different schools?

16.11 ❖ Twin hayfever data

In this exercise, we consider a biometrical genetic model for twin data on hayfever. Twin models for binary responses are typically probit models and the model for the latent response, referred to as "liability" in this context, is analogous to the model for twin data with observed continuous responses (see exercises 2.3 and 8.10). The latent response y^*_{ij} underlying hayfever status for twin i in twin-pair j is modeled as

$$y^*_{ij} \;=\; \mu + A_{ij} + D_{ij} + C_{ij} + \epsilon_{ij}$$

where A_{ij} are additive genetic effects, D_{ij} are dominance genetic effects, C_{ij} is a common environment effect, and ϵ_{ij} is a unique environment effect. The terms are independent of each other and have variances σ^2_A, σ^2_D, σ^2_C, and 1, respectively. The genetic effects A_{ij} and D_{ij} are each perfectly correlated between members of the same twin pair for MZ (monozygotic or identical) twins and have correlations 1/2 and 1/4, respectively, for DZ (dizygotic or fraternal) twins. The shared environment effect C_{ij} is perfectly correlated for both types of twins, whereas ϵ_{ij} is uncorrelated for both types of twins. The mean and variance of y^*_{ij} is constant. Because the full model is not identifiable using twin data, the ACE or ADE models are usually estimated (omitting either D_{ij} or C_{ij} from the model).

Rabe-Hesketh, Skrondal, and Gjessing (2008) show that the covariance structure implied by the biometrical model can be induced using the following three-level model:

$$y^*_{ikj} \;=\; \beta_1 + \zeta^{(2)}_{kj} + \zeta^{(3)}_{j} + \epsilon_{ikj} \tag{16.4}$$

where k is an artificially created identifier that equals the twin pair identifier j for MZ twins and the person identifier i for DZ twins. The variance ψ_3 of $\zeta^{(3)}_j$ is shared by both members of the twin pair for both MZ and DZ twins. In contrast, the variance ψ_2 of $\zeta^{(2)}_{kj}$ is shared by members of the twin pair only for MZ twins, producing the additional covariance for MZ twins while keeping the total variance constant across twin types. The covariances are therefore

$$\text{Cov}(y_{ij}, y_{i'j}) = \begin{cases} \psi_2 + \psi_3 = \sigma_A^2 + \sigma_D^2 + \sigma_C^2 & \text{for MZ twins} \\ \psi_3 = \sigma_A^2/2 + \sigma_D^2/4 + \sigma_C^2 & \text{for DZ twins} \end{cases}$$

For the ACE model ($\sigma_D^2 = 0$), we have

$$\sigma_A^2 = 2\psi_2 \qquad \sigma_C^2 = \psi_3 - \psi_2 \qquad \sigma_e^2 = 1$$

and for the ADE model ($\sigma_C^2 = 0$), we have

$$\sigma_A^2 = 3\psi_3 - \psi_2 \qquad \sigma_D^2 = 2(\psi_2 - \psi_3) \qquad \sigma_e^2 = 1$$

The data in `twin_hay` are from Hopper et al. (1990) and contain the following variables:

- `pair`: twin-pair identifier (j)
- `member`: twin identifier (1,2 for each twin-pair) (i)
- `M`: dummy variable for monozygotic (identical) twin pair (1: monozygotic; 2: dizygotic)
- `h`: hayfever status (1: present; 0: absent)
- `male`: dummy variable for being male
- `freq`: number of twin-pairs having the same pattern of values in `M`, `h`, and `male`

The data are in collapsed or aggregated form with `freq` representing the number of twin-pairs having a given set of values of `M`, `h`, and `male`. For MZ twins, there are six patterns of `h` and `male` (`h` equal to 00, 11, 01 for `male` equal to 00 and 11) and for DZ twins there are the same six patterns for same-sex twins, plus four patterns for mixed-sex twins (with {`h`, `male`} equal to {00,01}, {11,01}, {01,01}, {10,01}), giving 6+6+4=16 patterns and 32 rows of data (representing 7,614 individuals). Fitting the model with the data in such a collapsed form is extremely efficient.

1. Create the artificial identifier k described above and rename `freq` to `num3` so that this variable can be specified as level-3 (twin-pair level) frequency weights in `gllamm`. (`gllamm` requires that frequency weight variables end in a number that denotes the level that the weights pertain to.)
2. Fit the `probit` model in (16.4) using `gllamm`. Use the option `weight(num)` to specify that the level-3 weights are in `num3`. Note that the last character of the variable name is omitted in the `weight()` option, and that `gllamm` looks for `num1`, `num2`, and `num3`, assuming that the weights at a given level are 1 if the corresponding variable is not found.
3. Calculate the estimated variance components for the liability according to the ADE model.
4. Calculate the estimated heritability according to the ADE model, where the heritability h^2 is defined as

$$h^2 = \frac{\sigma_A^2 + \sigma_D^2}{\sigma_A^2 + \sigma_D^2 + 1}$$

A Syntax for gllamm, eq, and gllapred: The bare essentials

Here we describe the features of `gllamm` and `gllapred` that are most important for multilevel and longitudinal modeling. We also describe the `eq` command that is required for fitting random-coefficient models in `gllamm`. The full set of options for `gllamm`, `gllapred`, and `gllasim` is given in appendices B, C, and D, respectively. See Stata's *Longitudinal-Data/Panel-Data Reference Manual* for [XT] **xtmixed**.

Title

gllamm — Generalized linear latent and mixed models

Syntax

`gllamm` *depvar* [*indepvars*] [*if*] [*in*], `i(`*varlist*`)` [*options*]

options	Description
Model	
`i(``varlist`*`)`	cluster identifiers from level 2 and up
`nrf(`#`,...,`#`)`	number of random effects at each level
`eqs(`*eqnames*`)`	equation for each random effect
`family(`*familyname*`)`	distribution of *depvar*, given the random effects; default is `family(gaussian)`
`link(`*linkname*`)`	link function; default is canonical link for `family()` specified
Model 2	
`noconstant`	suppress constant or intercept
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1
Integration method	
`adapt`	use adaptive quadrature; default is ordinary quadrature
`nip(`#`)`	number of integration points
Reporting	
`eform`	report exponentiated coefficients

`i(``varlist`*`)` is required.

familyname	Description
gaussian	Gaussian (normal)
poisson	Poisson
binomial	Bernoulli

linkname	Description
identity	identity
log	log
logit	logit
probit	probit
ologit	ordinal logit, proportional odds
oprobit	ordinal probit

Description

`gllamm` fits a wide range of models. Here we consider multilevel generalized linear models.

In the two-level case, units i (for example, students) are nested in clusters j (for example, schools). In this case, the `i()` option specifies a single variable, the identifier for the clusters. The conditional expectation or mean μ_{ij} of the response y_{ij} (*depvar*) given the covariates and random effects is linked to the linear predictor ν_{ij} via a *link function* $g(\cdot)$, specified using the `link()` option,

$$g(E[y_{ij}|\nu_{ij}]) \equiv g(\mu_{ij}) \;=\; \nu_{ij}$$

The distribution of y_{ij} given its mean is a member of the *exponential family*, specified using the `family()` option. In a simple random-coefficient model, the *linear predictor* has the form

$$\nu_{ij} \;=\; \beta_1 + \beta_2 x_{ij} + \zeta_{1j}^{(2)} + \zeta_{2j}^{(2)} x_{ij}$$

where x_{ij} is a covariate, β_1 is a *constant* or intercept, and β_2 is the slope or regression coefficient of x_{ij}. This *fixed part* of the model is specified using *indepvars* (the constant is not explicitly specified but included by default). $\zeta_{1j}^{(2)}$ is a *random intercept*, whereas $\zeta_{2j}^{(2)}$ is a *random slope* or *random coefficient*. These two *random effects* at level 2 represent deviations for cluster j from the mean intercept β_1 and slope β_2, respectively. The fact that there are two random effects is declared using the `nrf()` option. The `eqs()` option is used to specify two corresponding equations previously defined using the `eq` command. Each equation consists of a single variable, containing the values multiplying the random effect, 1 and x_{ij}, respectively.

In a three-level model for units i nested in clusters j nested in superclusters k (for example, students in classes in schools), an example of a linear predictor would be

$$\nu_{ijk} = \beta_1 + \beta_2 x_{ijk} + \zeta_{1jk}^{(2)} + \zeta_{2jk}^{(2)} x_{ijk} + \zeta_k^{(3)}$$

where $\zeta_k^{(3)}$ is the deviation for supercluster k from the mean intercept. The three-level structure can be communicated to `gllamm` by specifying the identifiers for levels 2 and 3 in the `i()` option. The `nrf()` option now requires two numbers of random effects, one for level 2 and one for level 3, here `nrf(2 1)`. The `eqs()` option expects three equation names, first two equations for level 2 and then another equation for level 3. Here the first and last equation names could be the same.

Options

Model

`i(`*varlist*`)` gives the variables that define the hierarchical, nested clusters from the lowest level (finest clusters) to the highest level, for example, `i(student class school)`.

`nrf(#,...,#)` specifies the number of random effects at each level, that is, for each variable in `i(`*varlist*`)`. The default is `nrf(1,...,1)`.

`eqs(`*eqnames*`)` specifies the equation names (defined before running `gllamm` using `eq`; see page 918). In multilevel models, these equations simply define the variables multiplying the random effects. The number of equations per level is specified in the `nrf()` option.

`family(`*family*`)` specifies the family to be used for the distribution of the response given the mean. The default is `family(gaussian)`.

`link(`*link*`)` specifies the link function to be used, linking the conditional expectation of the response to the linear predictor.

Model 2

`noconstant`, `offset(`*varname*`)`; see [R] **estimation options**.

Integration method

`adapt` specifies adaptive quadrature. The default is ordinary quadrature.

`nip(#)` specifies the number of integration points.

Reporting

`eform` displays the exponentiated coefficients and corresponding standard errors and confidence intervals. For `family(binomial) link(logit)` (that is, logistic regression), exponentiated coefficients are odds ratios; for `family(poisson) link(log)` (that is, Poisson regression), exponentiated coefficients are rate ratios.

Title

eq — Equations

Syntax

`eq` [`define`] *eqname*`:` *varlist*

Description

`eq` [`define`] can be used to define an equation having the name *eqname* for use with estimation commands such as `gllamm`. The equation is just a linear combination of the variables in *varlist*. For instance,

```
eq slope: x
```

implies the equation λx, whereas

```
eq longer: x1 x2 x3 x4
```

implies the equation $\lambda_1 x_1 + \lambda_2 x_2 + \lambda_3 x_3 + \lambda_4 x_4$. If used to specify a component of a model in an estimation command, the λ parameters will typically be estimated. In `gllamm`, the `eqs()` option sets the coefficient of the first variable to 1. The `thresh()` and `peqs()` options add an intercept or constant to the linear combination, giving $\lambda_0 + \lambda_1 x_1 + \lambda_2 x_2 + \lambda_3 x_3 + \lambda_4 x_4$ in the previous example.

Title

gllapred — predict command for gllamm

Syntax

`gllapred` *varname* [*if*] [*in*] [`,` *statistic option*]

statistic	Description
`u`	empirical Bayes predictions of random effects
`ustd`	standardized empirical Bayes predictions
`xb`	fixed part of linear predictor
`linpred`	linear predictor with empirical Bayes predictions of random effects plugged in
`mu`	mean of response; by default, posterior mean
`pearson`	Pearson residual; by default, posterior mean

option	Description
`marginal`	combined with `mu`, gives marginal or population-averaged mean

Description

`gllapred` is the prediction command for `gllamm`.

For numerical integration, `gllapred` uses the same number of integration points as the preceding `gllamm` command and the same method (adaptive or nonadaptive quadrature).

For predictions of quantities that are linear in the random effects (`u`, `ustd`, and `linpred`), posterior means or empirical Bayes predictions are substituted for the random effects. These are means of the posterior distributions of the random effects given the observed responses, with parameter estimates plugged in. With the `u` option, standard deviations of the posterior distributions are also returned. The `ustd` option returns the empirical Bayes predictions divided by their approximate sampling standard deviations. The sampling standard deviation is approximated by the square root of the difference between the estimated prior variance $\hat{\psi}$ and the posterior variance. For linear models, this approximation is exact (except that the parameter estimates are plugged in).

For predictions of quantities that are nonlinear functions of the random effects, the expectation of the nonlinear function is returned, by default, with respect to the posterior distribution of the random effects. The `marginal` option specifies that the expectation should be taken with respect to the prior distribution of the random effects (not conditioning on the observed responses).

Only one of the statistics may be requested at a time. With the `u` and `ustd` options, *varname* is the prefix used for the variables that will contain the predictions.

Options

`u` returns posterior means (empirical Bayes predictions) and posterior standard deviations of the random effects in *varname*`m1`, *varname*`m2`, etc., and *varname*`s1`, *varname*`s2`, etc., respectively, where the order of the random effects is the same as in the call to `gllamm`.

`ustd` returns standardized empirical Bayes predictions of the random effects in *varname*`m1`, *varname*`m2`, etc. Each empirical Bayes prediction is divided by the square root of the difference between the estimated prior and posterior variances, which equals the sampling standard deviation in linear models but only approximates it in other models.

`xb` returns the fixed-effects part of the linear predictor in *varname*.

`linpred` returns the linear predictor, including the fixed- and random-effects part, where empirical Bayes predictions are substituted for the random effects.

`mu` returns the expectation of the response, for example, the predicted probability in the case of dichotomous responses. By default, the expectation is with respect to the posterior distribution of the random effects; also see the `marginal` option.

`pearson` returns Pearson residuals. By default, the posterior expectation with respect to the random effects is returned.

`marginal` together with the `mu` option gives the expectation of the response with respect to the prior distribution of the random effects. This is useful for looking at the marginal or population-averaged effects of covariates.

B Syntax for gllamm

Here we give the full syntax for `gllamm` with all available options.

Title

gllamm — Generalized linear latent and mixed models

Syntax

`gllamm` *depvar* [*indepvars*] [*if*] [*in*], `i(`*varlist*`)` [*options*]

options	Description
Linear predictor	
*`i(`*_varlist_`)`	cluster identifiers from level 2 and up
`nrf(`#`,...,`#`)`	number of random effects at each level
`eqs(`*eqnames*`)`	equation for each random effect
†`frload(`#`,...,`#`)`	free first factor loading
Linear predictor 2	
`noconstant`	suppress constant or intercept
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1
Response model	
`family(`*familynames*`)`	distributions of *depvar*, given the random effects; default is `family(gaussian)`
†`fv(`*varname*`)`	variable assigning distributions to units or observations
`link(`*linknames*`)`	link functions; default is canonical link for `family()` specified (if only one *familyname* is given)
†`lv(`*varname*`)`	variable assigning links to units or observations
†`denom(`*varname*`)`	variable containing binomial denominator if `link(binomial)` is used; default denominator is `1`
`s(`*eqname*`)`	equation for log of residual standard deviation
`thresh(`*eqnames*`)`	equations for threshold models
†`ethresh(`*eqnames*`)`	equations for alternative threshold models
†`expanded(`*varname*`...)`	combined with `link(mlogit)` specifies that data are in expanded form
†`basecategory(`#`)`	reference category for multinomial logit models
†`composite(`*varname*`...)`	composite link

*`i(`*varlist*`)` is required.

options (cont'd)	Description
Random-effects distribution	
† `nocorrel`	uncorrelated random effects
`ip(`*string*`)`	continuous or discrete random effects
Structural model	
`geqs(`*eqnames*`)`	equations for regressions of random effects on covariates
† `bmatrix(`*matrix*`)`	matrix for regressions among random effects
† `peqs(`*eqname*`)`	equation for multinomial logit model for probabilities of discrete distribution
Weights	
`weight(`*varname*`)`	frequency weights at different levels
`pweight(`*varname*`)`	inverse probability sampling weights at different levels
Constraints	
† `constraints(`*clist*`)`	linear parameter constraints
Integration method	
`adapt`	use adaptive quadrature; default is ordinary quadrature
`ip(m)`	use spherical integration rules; default is cartesian product
`nip(#)`	number of integration points
SE/Robust	
`robust`	standard errors based on sandwich estimator
`cluster(`*varname*`)`	adjust standard errors for intragroup correlation
Reporting	
`eform`	report exponentiated coefficients
† `level(#)`	confidence level for confidence intervals; default is 95%
† `trace`	report model details and more detailed iteration log
† `nolog`	suppress iteration log
† `nodisplay`	do not display estimates
† `allc`	display all parameters as they are estimated (sometimes transformation of parameters usually reported)
`lf0(# #)`	specify number of parameters and log likelihood of nested model for likelihood-ratio test
† `eval`	evaluate log likelihood for parameters given in `from(`*matrix*`)`
† `init`	fit the model where random part is set to 0
† `noest`	do not fit the model
† `dots`	display dots each time the log likelihood is evaluated

options (cont'd)	Description
Starting values	
`from(`*matrix*`)`	row matrix of starting values
`copy`	ignore equation and column names of matrix specified in `from(`*matrix*`)`, relying on values being in correct order
`skip`	matrix of starting values has extra parameters
† `long`	matrix of starting values is for model without constraints (with `constraints()` option)
† `search(#)`	number of values to try in search for starting values for random part of model
Max options	
† `iterate(#)`	maximum number of Newton–Raphson iterations
† `adoonly`	use ado-version of `gllamm`
Gâteaux derivative	
`gateaux(# # #)`	range and number of steps for Gâteaux derivative search

† Options not used elsewhere in this book.

familyname	Description
`gaussian`	Gaussian (normal)
`poisson`	Poisson
`binomial`	Bernoulli or binomial (with `denom(`*varname*`)`)
† `gamma`	gamma

† Options not used elsewhere in this book.

linkname	Description
`identity`	identity
`log`	log
† `reciprocal`	reciprocal (power −1)
`logit`	logit
`probit`	probit
† `sprobit`	scaled probit
`cll`	complementary log-log
`ologit`	ordinal logit, proportional odds
`oprobit`	ordinal probit
`soprobit`	scaled ordinal probit
† `ocll`	ordinal complementary log-log
† `mlogit`	multinomial logit

† Options not used elsewhere in this book.

Description

`gllamm` fits generalized linear latent and mixed models (GLLAMMs). The models include random effects or latent variables varying at different levels. Here we use *random effect* instead of *latent variable* because we regard the terms more or less as synonyms and because this book is essentially about random-effects models. GLLAMMs consist of a linear predictor, response model, random-effects distribution, and structural model.

Linear predictor

For an L-level model, the most general form of the linear predictor is

$$\begin{aligned}\nu \;=\;& \beta_1 x_1 + \cdots + \beta_p x_p \\ &+ \eta_1^{(2)}(\lambda_{11}^{(2)} z_{11}^{(2)} + \cdots + \lambda_{1q_{12}}^{(2)} z_{1q_{12}}^{(2)}) + \cdots \\ &+ \eta_{M_2}^{(2)}(\lambda_{M_2,1}^{(2)} z_{M_2,1}^{(2)} + \cdots + \lambda_{M_2,1}^{(2)} z_{M_2,q_{M_2,2}}^{(2)}) + \cdots \\ &+ \eta_1^{(L)}(\lambda_{11}^{(L)} z_{11}^{(L)} + \cdots + \lambda_{1q_{1L}}^{(L)} z_{1q_{1L}}^{(L)}) + \cdots \\ &+ \eta_{M_L}^{(L)}(\lambda_{M_L,1}^{(L)} z_{M_L,1}^{(L)} + \cdots + \lambda_{M_L,1}^{(L)} z_{M_L,q_{M_L,L}}^{(L)}), \\ &\text{where } \lambda_{m1}^{(l)} = 1, \text{ for } l = 2,\ldots,L,\ m = 1,\ldots,M_l\end{aligned}$$

where we have omitted subscripts for the units at the different levels ($ijk\ldots$) to simplify notation. Here the fixed part in the first line has the usual form. In the random part, $\eta_m^{(l)}$ is a random effect at level l, where l goes from 2 to L and, at each level, m goes from 1 to M_l. Each random effect is multiplied by a linear combination of covariates $z_{mk}^{(l)}$ with coefficients $\lambda_{mk}^{(l)}$, $k = 1,\ldots,q_{ml}$. These coefficients sometimes function as factor loadings in measurement models. In ordinary random-coefficient models, each term in parentheses collapses to a single variable $z_m^{(l)}$.

Using vector notation and summation signs, we can write the linear predictor more compactly as

$$\nu \;=\; \mathbf{x}'\boldsymbol{\beta} + \sum_{l=2}^{L}\sum_{m=1}^{M_l} \eta_m^{(l)} \mathbf{z}_m^{(l)\prime} \boldsymbol{\lambda}_m^{(l)}, \quad \lambda_{m1}^{(l)} = 1$$

In `gllamm`, the `i()` option is used to define the levels 2 to L of the model, and the `nrf()` option is used to specify the numbers of random effects M_l at each level. The `eqs()` option is used to specify equations defining the linear combinations $\mathbf{z}_m^{(l)\prime}\boldsymbol{\lambda}_m^{(l)}$ multiplying the random effects.

Response model

The response model is a generalized linear model with unit-specific link function and distribution from the exponential family, specified using the `link()`, `lv()`, `family()`, and `fv()` options. In addition, the variance of the response, given the linear predictor,

can depend on covariates as can the thresholds in ordinal response models (via the `s()` and `thresh()` options, respectively).

Random-effects distribution

The random effects can be either continuous or discrete. In the continuous case, the following applies to the disturbances if there is a structural model (see below). The random effects are multivariate normal with zero means. Random effects at the same level may be correlated, but there are no correlations across levels.

In the discrete case, the M_l random effects at level l take on discrete values that can be thought of as locations in M_l dimensions. The locations together with the associated probabilities are parameters of the model. Random effects at different levels are again assumed to be mutually independent. Discrete random effects can be used for latent-class or finite-mixture models or for *nonparametric maximum likelihood* estimation. The `ip()` option is used to specify whether the random effects are continuous or discrete.

Structural model

Continuous case

In the structural model, each random effect can be regressed on covariates w,

$$\eta_m^{(l)} \;=\; \gamma_{m1}^{(l)} w_{m1}^{(l)} + \cdots + \gamma_{m,r_{ml}}^{(l)} w_{m,r_{ml}}^{(l)} + \zeta_m^{(l)}$$

where $\zeta_m^{(l)}$ is a disturbance or residual. These linear combinations of covariates are defined as equations and passed to `gllamm` using the `geqs()` option.

The structural model also allows random effects to be regressed on other random effects. These relations, together with the regressions on observed covariates given above, are easiest to express using a column vector $\boldsymbol{\eta}$ for all random effects from levels 2 to L and $\boldsymbol{\zeta}$ for the corresponding disturbances

$$\boldsymbol{\eta} \;=\; \mathbf{B}\boldsymbol{\eta} + \boldsymbol{\Gamma}\mathbf{w} + \boldsymbol{\zeta}$$

where $\mathbf{B}$ (specified using the `bmatrix()` option) is an upper triangular matrix of regression coefficients allowing random effects to be regressed on other random effects. The term $\boldsymbol{\Gamma}\mathbf{w}$ represents the regressions of random effects on covariates written more explicitly above.

Discrete case

In the discrete case, the `peqs()` option can be used to specify multinomial logit models for the probabilities of the different locations for the random effects.

Options

Linear predictor

`i(`*varlist*`)` gives the variables that define the hierarchical, nested clusters from the lowest level (finest clusters) to the highest level, for example, `i(student class school)`.

`nrf(#,...,#)` specifies the number of random effects M_l at each level l, that is, for each variable in `i(`*varlist*`)`. The default is `nrf(1,...,1)`.

`eqs(`*eqnames*`)` specifies the equation names (defined before running `gllamm`) for the linear combinations $\mathbf{z}_m^{(l)\prime}\boldsymbol{\lambda}_m^{(l)}$ multiplying the random effects. The equations for the level-2 random effects are listed first, followed by those for the level-3 random effects, etc., the number of equations per level being specified in the `nrf()` option. If required, constants should be explicitly included in the equation definitions using variables equal to 1. If the option is not used, the random effects are assumed to be random intercepts, and only one random effect is allowed per level. The first coefficient $\lambda_{m1}^{(l)}$ is set to one, unless the `frload()` option is specified. The other coefficients are estimated together with the (co)variances of the random effects.

`frload(#,...,#)` lists the random effects for which the first coefficient $\lambda_{m1}^{(l)}$ should be freely estimated instead of set to 1. It is up to the user to define appropriate constraints to identify the model. Here the random effects are referred to as 1, 2, 3, etc., in the order in which they are defined by the `eqs()` option.

Linear predictor 2

`noconstant`, `offset(`*varname*`)`; see [R] **estimation options**.

Response model

`family(`*familynames*`)` specifies the family (or families) to be used for the response probabilities (or densities) given the random effects. The default is `family(gaussian)`. Several families may be given, in which case, the variable allocating families to units or observations must be given using `fv(`*varname*`)`.

`fv(`*varname*`)` is required if several families are specified in the `family()` option. The variable indicates which family applies to which unit or observation. A value of one refers to the first family specified in `family()`, etc.

`denom(`*varname*`)` gives the variable containing the binomial denominator for the responses whose family was specified as `binomial`. The default denominator is 1.

`s(`*eqname*`)` specifies that the log of the standard deviation (or of the coefficient of variation) at level 1 for normally (or gamma) distributed responses (or the scale for the `sprobit` or `soprobit` links) is given by the linear combination of covariates defined by `eqname`. This allows for heteroskedasticity at level 1. For example, if dummy variables for groups are used in the definition of *eqname*, different residual variances are estimated for different groups.

`link(`*linknames*`)` specifies the link functions linking the conditional means to the linear predictors. If a single family is specified, the default link is the canonical link. Several links may be given, in which case, the variable assigning links to units or observations must be given using `lv(`*varname*`)`.

`lv(`*varname*`)` is the variable whose values indicate which link applies to which unit or observation. See `fv(`*varname*`)` for details.

`thresh(`*eqnames*`)` specifies equations for the thresholds for ordinal responses. One equation is specified for each ordinal response, and constants are automatically added. This option allows the effects of some covariates to differ between the categories of the ordinal outcome rather than assuming a constant effect—the parallel-regression assumption, or with the `ologit` link, the proportional odds assumption. Variables used in the model for the thresholds generally should not appear in the fixed part of the linear predictor.

`ethresh(`*eqnames*`)` is the same as `thresh(`*eqnames*`)`, except that a different parameterization is used for the threshold model. To ensure that $\kappa_{s-1} \leq \kappa_s$, the model is $\kappa_s = \kappa_{s-1} + \exp(\mathbf{x}'\boldsymbol{\alpha})$, for $s = 2, \ldots, S-1$, where S is the number of response categories.

`expanded(`*varname varname string*`)` is used with the `mlogit` link and specifies that the data have been expanded as illustrated below:

```
A                          B
choice                     response altern selected
   1                           1       1       1
   2                           1       2       0
                               1       3       0
                               2       1       0
                               2       2       1
                               2       3       0
```

The variable `choice` is the multinomial response (possible values 1, 2, 3), `response` labels the original lines of data, `altern` gives the possible responses or alternatives, and `selected` indicates the response that was given. The syntax would be `expanded(response selected m)`, and `altern` would be used as the dependent variable. This expanded form allows the user to have alternative-specific covariates, apply different random effects to different alternatives, and have different alternative sets for different individuals. The third argument is `o` if one set of coefficients should be estimated for the explanatory variables and `m` if one set of coefficients is to be estimated for each category of the response except the reference category.

`basecategory(#)` specifies the value of the response to be used as the reference category when the `mlogit` link is used. This option is ignored if the `expanded()` option is used with the third argument equal to `m`.

`composite(`*varname varname* `...)` specifies that a composite link be used. The first variable is a cluster identifier (`cluster` below) so that linear predictors within the cluster can be combined into a single composite link. The second variable (`ind` below) indicates to which response the composite links defined by the subsequent weight variables belong. Observations with `ind`=0 have a missing link. The remaining variables (`c1` and `c2` below) specify weights for the composite links. The composite link based on the first weight variable will go to where `ind`=1, etc.

```
Example:

Data setup with form of inverse link       Interpretation of
h_i determined by link() and lv():         composite(cluster ind c1 c2)

cluster ind  c1  c2  inverse link           cluster  composite link
  1      1    1  0    h_1                      1       h_1 - h_2
  1      2   -1  1    h_2                      1       h_2 + h_3
  1      0    0  1    h_3           ==>        1       missing
  2      1    1  0    h_4                      2       h_4 + h_5
  2      2    1  1    h_5                      2       h_5 + 2*h_6
  2      0    0  2    h_6                      2       missing
```

Random-effects distribution

`nocorrel` may be used to constrain all correlations to zero if there are several random effects at any of the levels and if these are modeled as multivariate normal.

`ip(`*string*`)` requests that the random effects be multivariate normal (Gaussian) if *string* is `g` and be discrete with freely estimated mass points if *string* is `f`. The default is Gaussian quadrature. With the `ip(f)` option, only `nip-1` mass-point locations are estimated, the last being determined by setting the mean of the mass-point distribution to 0. The `ip(fn)` option can be specified to estimate all `nip` masses freely—the user must then make sure that the mean is not modeled in the linear predictor, for example, by specifying the `noconstant` option. See integration method for a description of `ip(m)`.

Structural model

`geqs(`*eqnames*`)` specifies equations for regressions of random effects on explanatory variables. The second character of the equation name indicates which random effect is regressed on the variables used in the equation definition; for example, `f1:a b` means that the first random effect is regressed on `a` and `b` (without a constant).

`bmatrix(`*matrix*`)` specifies a square matrix $\mathbf{B}$ of regression coefficients for the dependence of the random effects on other random effects. The matrix must be upper diagonal and have number of rows and columns equal to the total number of random effects. Elements of *matrix* are 1 where coefficients in $\mathbf{B}$ should be estimated and 0 where they should be set to 0.

`peqs(`*eqname*`)` can be used with the `ip(f)` or `ip(fn)` option to allow the (prior) probabilities of the discrete distribution to depend on covariates via a multinomial logit model. A constant is automatically included in addition to the covariates specified in the `eq` command.

Weights

`weight(`*wt*`)` specifies that variables *wt*`1`, *wt*`2`, etc., contain frequency weights. The suffixes (1,2,...) in the variable names should not be included in the `weight()` option. They determine at what level each weight applies. If only some of the weight variables exist, for example, only level-2 weights, the other weights are assumed to be equal to 1. For example, if the level-1 units are occasions (or panel waves) in longitudinal data and the level-2 units are individuals, and the only variable used in the analysis is a binary variable, `result`, then we can collapse dataset A into dataset B by defining level-1 weights as follows:

A

ind	occ	result
1	1	0
1	2	0
2	3	0
2	4	1
3	5	0
3	6	1

B

ind	occpat	result	wt1
1	1	0	2
2	2	0	1
2	3	1	1
3	4	0	1
3	5	1	1

The two occasions for individual 1 in dataset A have the same result. The first row in B therefore represents two occasions (occasions 1 and 2), as indicated by `wt1`. The variable `occpat` labels the unique patterns of responses at level 1.

The two individuals 2 and 3 in dataset B have the same pattern of results over the measurement occasions (both have two occasions with values 0 and 1). We can therefore collapse the data into dataset C by using level-2 weights:

B

ind	occpat	result	wt1
1	1	0	2
2	2	0	1
2	3	1	1
3	4	0	1
3	5	1	1

C

indpat	occpat	result	wt1	wt2
1	1	0	2	1
2	2	0	1	2
2	3	1	1	2

The variable `indpat` labels the unique patterns of responses at level 2, and `wt2` indicates that `indpat` 1 in dataset C represents one individual and `indpat` 2 represents two individuals; that is, all the data for individual 2 are replicated once. Collapsing the data in this way can make `gllamm` run faster.

`pweight(`*varname*`)` specifies that variables *varname*`1`, *varname*`2`, etc., contain inverse probability sampling weights for levels 1, 2, etc. As far as the estimates and log likelihood are concerned, the effect of specifying these weights is the same as for frequency weights, but the standard errors will be different. Robust standard errors will automatically be provided. This pseudolikelihood approach should be used with

caution if the sampling weights apply to units at a lower level than the highest level in the multilevel model. The weights are not rescaled; scaling is the responsibility of the user.

Constraints

`constraint(`*clist*`)` specifies the constraint numbers of the linear constraints to be applied. Constraints are defined using the `constraint()` command; see [R] **constraint**. To find out the equation names needed to specify the constraints, run `gllamm` with the `noest` and `trace` options.

Integration method

`adapt` specifies adaptive quadrature; the default is ordinary quadrature.

`ip(m)` specifies spherical quadrature that can be more efficient than the default cartesian product quadrature when there are several random effects.

`nip(#,...,#)` specifies the number of integration points or masses to be used for each integral or summation. When quadrature is used, a value may be given for each random effect. When freely estimated masses are used, a value may be given for each level of the model. If only one argument is given, the same number of integration points will be used for each summation. The default value is 8. When used with `ip(m)`, `nip()` specifies the degree d of the approximation (corresponds in accuracy approximately to $(d+1)/2$ points per dimension for cartesian product quadrature). Only certain values are available for spherical quadrature: for two random effects, 5, 7, 9, 11, and 15; for more than two random effects, 5 and 7.

SE/Robust

`robust` specifies that the Huber/White/sandwich estimator of the covariance matrix of the parameter estimates is to be used. If a model has been fit without the `robust` option, the robust standard errors can be obtained by simply typing `gllamm, robust`.

`cluster(`*varname*`)` specifies that the highest-level units of the GLLAMM model are nested in even higher-level clusters, where *varname* contains the cluster identifier. Robust standard errors will be provided that take this clustering into account. If a model has been fit without this option, the robust standard errors for clustered data can be obtained using the command `gllamm, cluster(`*varname*`)`.

Reporting

`eform` displays the exponentiated coefficients and corresponding standard errors and confidence intervals. For `family(binomial) link(logit)` (that is, logistic regression), exponentiated coefficients are odds ratios; for `family(poisson) link(log)` (that is, Poisson regression), exponentiated coefficients are rate ratios.

`level(#)` specifies the confidence level as a percentage for confidence intervals of the fixed coefficients. The default is 95.

`trace` displays details of the model being fit, as well as details of the maximum likelihood iterations.

`nolog` suppresses output for maximum likelihood iterations.

`nodisplay` suppresses output of the estimates but still shows the iteration log, unless `nolog` is used.

`allc` causes all estimated parameters to be displayed in a regression table, which may be transformations of the parameters usually reported, in addition to the usual output.

`lf0(##)` gives the number of parameters and the log likelihood for a likelihood-ratio test to compare the model to be fit with a simpler model. A likelihood-ratio chi-squared test is only performed if the `lf0()` option is used.

`eval` causes the program to evaluate the log likelihood for values passed to `gllamm` using the `from(matrix)` option.

`init` sets random part of model to zero so that only the fixed part is fit. This is also how initial values or starting values for the fixed part are computed in `gllamm`.

`noest` is used to prevent the program from carrying out the estimation. This may be used with the `trace` option to check that the model is correct and get the information needed to set up a matrix of initial values. Global macros are available that are normally deleted. Particularly useful may be `M_initf` and `M_initr`, matrices for the parameters (fixed part and random part, respectively).

`dots` causes a dot to be printed (if used together with `trace`) each time the likelihood-evaluation program is called by `ml`. This helps the user to assess how long `gllamm` is likely to take to run and reassures the user that it is making some progress when it is very slow.

Starting values

`from(`*matrix*`)` specifies the matrix (one row) to be used as starting values. The column names and equation names must be correct (see `help matrix`), unless the `copy` option is used. The parameter values given may be previous estimates, obtained using `e(b)`. This is useful if new covariates are added or if the number of integration points (or locations in a discrete distribution) is increased. The `skip` option must be used if the model to be fit contains fewer parameters than are included in *matrix*, for instance, if covariates are dropped.

`copy`; see `from(`*matrix*`)`.

`skip`; see `from(`*matrix*`)`.

`long` can be used with the `from(`*matrix*`)` option when parameter constraints are used to indicate that the matrix of initial values corresponds to the unconstrained model; that is, it has more elements than will be fit.

`search(#)` causes the program to search for initial values for the random-effects variances at level 2 (in range 0 to 3). The argument specifies the number of random searches. This option may only be used with `ip(g)` and when `from(`*matrix*`)` is not used.

Max options

`iterate(#)` specifies the maximum number of iterations. With the `adapt` option, using the `iterate(#)` option will cause `gllamm` to skip the Newton–Raphson iterations usually performed at the end without updating the quadrature locations. `iterate(0)` is like `eval`, except that standard errors are computed.

`adoonly` causes `gllamm` to use only ado-code instead of internalized code. `gllamm` will be faster if it uses internalized versions of some of the functions available from Stata 7 (if updated on or after 26 October 2001).

gateaux derivative

`gateaux(###)` can be used with the `ip(f)` or `ip(fn)` options to increase the number of mass points by one from a previous solution with parameter estimates specified using `from(`*matrix*`)`. The number of parameters and log likelihood of the previous solution must be specified using the `lf0(##)` option. The program searches for the location of the new mass point by placing a small mass at the location given by the first argument and moving it to the second argument in the number of steps specified by the third argument. (If there are several random effects, this search is done in each dimension, resulting in a regular grid of search points.) If the maximum increase in likelihood is greater than 0, the location corresponding to this maximum is used as the initial value of the new location; otherwise, the program stops. If the program stops, this suggests that the nonparametric maximum likelihood estimator has been obtained.

C Syntax for gllapred

After you fit a model using `gllamm`, you can use `gllapred` to obtain predictions of various quantities.

Title

gllapred — predict command for gllamm

Syntax

`gllapred` *varname* [*if*] [*in*] [`,` *statistic options*]

statistic	Description
`u`	empirical Bayes predictions of random effects; disturbances if there is a structural model
`corr`	posterior correlations between random effects or disturbances
`fac`	empirical Bayes predictions of random effects
`ustd`	standardized empirical Bayes predictions
`xb`	fixed part of linear predictor
`linpred`	linear predictor with empirical Bayes predictions of random effects plugged in
`mu`	mean of response; by default, posterior mean
`pearson`	Pearson residual; by default, posterior mean
`deviance`	deviance residual; by default, posterior mean
`anscombe`	Anscombe residual; by default, posterior mean
`cooksd`	Cook's distance for top-level clusters
`p`	posterior probabilities if random effects are discrete
`s`	standard deviations if `s()` option was used
`ll`	log-likelihood contributions from top-level clusters

options	Description
marginal	combined with mu, gives marginal or population-averaged mean
us(*varname*)	substitute specific values for random effects in *varname*1, etc.
above(#,...,#)	for ordinal responses with mu option, return probability that y exceeds # (several values if more than one ordinal link)
outcome(#)	for mlogit link with mu option, probability that y=#
nooffset	suppress offset
fsample	predict for full sample, not just estimation sample
from(*matrix*)	use parameters in *matrix* instead of estimated parameters
adapt	use adaptive quadrature even if gllamm did not
adoonly	use ado-version of gllapred

Description

See description for gllapred on page 919.

Options

u returns posterior means (empirical Bayes predictions) and posterior standard deviations of the random effects in *varname*m1, *varname*m2, etc., and *varname*s1, *varname*s2, etc., respectively, where the order of the random effects is the same as in the call to gllamm. In the case of continuous random effects, the integration method (ordinary versus adaptive quadrature) and the number of quadrature points used is the same as in the previous call to gllamm. If the gllamm model includes equations for the random effects (geqs or bmatrix), the posterior means and standard deviations of the disturbances ζ are returned.

corr returns posterior correlations of the random effects in *varname*c21, etc. This option only works together with the u option. If there is a structural model, posterior correlations of the disturbances are returned.

fac returns posterior means (empirical Bayes predictions) and posterior standard deviations of the random effects in *varname*m1, *varname*m2, etc., and *varname*s1, *varname*s2, etc. If there is a structural model, predictions of the random effects on the left-hand side of the structural equations are returned.

xb returns the fixed-effects part of the linear predictor in *varname* including the offset (if there is one), unless the nooffset option is used.

ustd returns standardized posterior means (empirical Bayes predictions) of the disturbances in *varname*m1, *varname*m2, etc. Each posterior mean is divided by the square root of the difference between the prior and posterior variances, which approximates the sampling standard deviation.

cooksd returns Cook's distances for the top-level units in *varname*.

linpred returns the linear predictor including the fixed- and random-effects part where posterior means (empirical Bayes predictions) are substituted for the random effects.

`mu` returns the expectation of the response, for example, the predicted probability in the case of dichotomous responses. By default, the expectation is with respect to the posterior distribution of the random effects; also see the `marginal` and `us()` options. The offset is included (if there is one in the `gllamm` model), unless the `nooffset` option is specified.

`pearson` returns Pearson residuals. By default, the posterior expectation with respect to the random effects is returned. The `us()` option can be used to obtain the conditional residual when specific values are substituted for the random effects.

`deviance` returns deviance residuals. By default, the posterior expectation with respect to the random effects is returned. The `us()` option can be used to obtain the conditional residual when specific values are substituted for the random effects.

`anscombe` returns Anscombe residuals. By default, the posterior expectation with respect to the random effects is returned. The `us()` option can be used to obtain the conditional residual when specific values are substituted for the random effects.

`p` can only be used for two-level models fit using the `ip(f)` or `ip(fn)` option. `gllapred` returns the posterior probabilities in *varname*1, *varname*2, etc., giving the probabilities of classes 1, 2, etc. `gllapred` also displays the (prior) probability and location matrices to help interpret the posterior probabilities.

`s` returns the scale. This is useful if the `s()` option was used in `gllamm` to specify level-1 heteroskedasticity.

`ll` returns the log-likelihood contributions of the highest-level (level-L) units.

`marginal` together with the `mu` option gives the expectation of the response with respect to the prior distribution of the random effects. This is useful for looking at the marginal or population-averaged effects of covariates.

`us(`*varname*`)` specifies values for the random effects to calculate conditional quantities, such as the conditional mean of the responses (`mu` option), given the values of the random effects. Here *varname* specifies the prefix for the variables, and `gllapred` will look for *varname*`1`, *varname*2, etc.

`above(#,...,#)` returns probabilities that *depvar* exceeds # (ordinal responses). If there are several ordinal responses, a different value can be specified for each ordinal response or a single value given for all ordinal responses.

`outcome(#)` specifies the outcome for which the predicted probability should be returned (`mu` option) if there is a nominal response. This option is not necessary if the `expanded()` option was used in `gllamm` because in this case predicted probabilities are returned for all outcomes.

`nooffset` excludes the offset from the predictions (with the `xb`, `linpred`, or `mu` options). It will only make a difference if the `offset()` option was used in `gllamm`.

`fsample` causes `gllapred` to return predictions for the full sample (except units or observations excluded in the `if` and `in` qualifiers), not just the estimation sample. The returned log likelihood may be missing because `gllapred` will not exclude observations with missing values on any of the variables used in the likelihood calculation. It is up to the user to exclude these observations using `if` or `in`.

`from(`*matrix*`)` specifies a row matrix of parameter values for which the predictions should be made. The column and equation names will be ignored. Without this option, the parameter estimates from the last `gllamm` model will be used.

`adapt` specifies that numerical integration should be performed using adaptive quadrature instead of ordinary quadrature. This option is not necessary if estimation in `gllamm` used adaptive quadrature.

`adoonly` causes `gllamm` to use only ado-code. This option is not necessary if `gllamm` was run with the `adoonly` option.

D Syntax for gllasim

After you fit a model using `gllamm`, you can use `gllasim` to simulate responses from the model.

Title

gllasim — simulate command for gllamm

Syntax

`gllasim` *varname* [*if*] [*in*] [`,` *statistic options*]

statistic	Description
`y`	response
`u`	random effects (or disturbances if there is a structural model)
`fac`	random effects
`linpred`	linear predictor
`mu`	mean of response (substituting simulated values for random effects)

options	Description
`us(`*varname*`)`	substitute specific values for random effects in *varname*`1`, etc.
`above(#,...,#)`	for ordinal responses with `mu` option, return probability that y exceeds # (several values if more than one ordinal link)
`outcome(#)`	for `mlogit` link with `mu` option, probability that y=#
`nooffset`	suppress offset
`fsample`	simulate for full sample, not just estimation sample
`from(`*matrix*`)`	use parameters in *matrix* instead of estimated parameters
`adoonly`	use ado-version of `gllasim`

Description

`gllasim` is the simulation command for `gllamm`. The command is somewhat similar to `gllapred`, except that random effects are simulated from the prior random-effects distribution instead of predicted as the posterior means.

By default, the response is simulated. If other statistics are requested, the response can be simulated as well if the `y` option is used. With the `u`, `fac`, `linpred`, and `mu` options, *varname* is just the prefix of the variable names in which results are stored.

Options

`y` returns simulated responses in *varname*. This option is only necessary if `u`, `fac`, `linpred`, or `mu` is also specified.

`u` returns simulated random effects in *varname*`p1`, *varname*`p2`, etc., where the order of the random effects is the same as in the call to `gllamm` (in the order of the equations in the `eqs()` option). If the `gllamm` model includes equations for the random effects (`geqs` or `bmatrix`), the simulated disturbances are returned.

`fac` returns the simulated random effects in *varname*`p1`, *varname*`p2`, etc., instead of the disturbances if the `gllamm` model includes equations for the random effects (`geqs()` or `bmatrix()` options in `gllamm`), that is, the random effects on the left-hand side of the structural model.

`linpred` returns the linear predictor, including the fixed and simulated random parts in *varname*`p`. The offset is included (if there is one in the `gllamm` model), unless the `nooffset` option is specified.

`mu` returns the expected value of the response conditional on the simulated values for the random effects, for example, a probability if the responses are dichotomous.

`us(`*varname*`)` specifies that, instead of simulating the random effects, `gllasim` should use the variables in *varname*`1`, *varname*`2`, etc.

`above(#,...,#)` returns probabilities that *depvar* exceeds # (with the `mu` option) if there are ordinal responses. A single number can be given for all ordinal responses.

`outcome(#)` specifies the outcome for which the predicted probability should be returned (`mu` option) if there is a nominal response and the `expanded()` option has not been used in `gllamm` (with the `expanded()` option, predicted probabilities are returned for all outcomes).

`nooffset` can be used with the `linpred` and `mu` options to exclude the offset from the simulated value. This will only make a difference if the `offset()` option was used in `gllamm`.

`fsample` causes `gllasim` to simulate values for the full sample (except observations excluded in the `if` and `in` qualifiers), not just the estimation sample.

`from(`*matrix*`)` specifies a matrix of parameters for which the simulations should be made. The column and equation names will be ignored. Without this option, the parameter estimates from the last `gllamm` model will be used.

`adoonly` causes `gllasim` to use only ado-code. This option is not necessary if `gllamm` was run with the `adoonly` option.

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