A powerful tool for analyzing nested designs in a variety of fields, multilevel/hierarchical modeling allows researchers to account for data collected at multiple levels. Multilevel Modeling Using R provides you with a helpful guide to conducting multilevel data modeling using the R software environment. After reviewing standard linear models, the authors present the basics of multilevel models and explain how to fit these models using R. They then show how to employ multilevel modeling with longitudinal data and demonstrate the valuable graphical options in R. The book also describes models for categorical dependent variables in both single level and multilevel data. The book concludes with Bayesian fitting of multilevel models. For those new to R, the appendix provides an introduction to this system that covers basic R knowledge necessary to run the models in the book.

Features
- Shows how to properly model data structures to avoid incorrect parameter and standard error estimates
- Explains how multilevel models provide insights into your data that otherwise might not be detected
- Illustrates helpful graphical options in R appropriate for multilevel data
- Presents models for categorical dependent variables in single level and multilevel contexts
- Discusses multilevel modeling within the Bayesian framework
- Offers an introduction to R in the appendix for R novices
- Uses various R packages to conduct the analyses and interpret the results, with the code available online

Through the R code and detailed explanations provided, this book gives you the tools to launch your own investigations in multilevel modeling and gain insight into your research.
Multilevel Modeling Using R
Statistics in the Social and Behavioral Sciences Series

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Aims and scope

Large and complex datasets are becoming prevalent in the social and behavioral sciences and statistical methods are crucial for the analysis and interpretation of such data. This series aims to capture new developments in statistical methodology with particular relevance to applications in the social and behavioral sciences. It seeks to promote appropriate use of statistical, econometric and psychometric methods in these applied sciences by publishing a broad range of reference works, textbooks and handbooks.

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Multilevel Modeling Using R

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Preface

The goal of this book is to provide you, the reader, with a comprehensive resource for the conduct of multilevel modeling using the R software package. Multilevel modeling, sometimes referred to as hierarchical modeling, is a powerful tool that allows a researcher to account for data collected at multiple levels. For example, an educational researcher may gather test scores and measures of socioeconomic status (SES) for students who attend a number of different schools. The students would be considered level-1 sampling units, and the schools would be referred to as level-2 units.

Ignoring the structure inherent in this type of data collection can, as we discuss in Chapter 2, lead to incorrect parameter and standard error estimates. In addition to modeling the data structure correctly, we will see in the following chapters that the use of multilevel models can also provide insights into the nature of relationships in our data that might otherwise not be detected.

After reviewing standard linear models in Chapter 1, we will turn our attention to the basics of multilevel models in Chapter 2, before learning how to fit these models using the R software package in Chapters 3 and 4. Chapter 5 focuses on the use of multilevel modeling in the case of longitudinal data, and Chapter 6 demonstrates the very useful graphical options available in R, particularly those most appropriate for multilevel data. Chapters 7 and 8 describe models for categorical dependent variables, first for single-level data, and then in the multilevel context. Finally, we conclude in Chapter 9 with Bayesian fitting of multilevel models.

We hope that you find this book to be helpful as you work with multilevel data. Our goal is to provide you with a guidebook that will serve as the launching point for your own investigations in multilevel modeling. The R code and discussion of its interpretation contained in this text should provide you with the tools necessary to gain insights into your own research, in whatever field it may be. We appreciate your taking the time to read our work and hope that you find it as enjoyable and informative to read as it was for us to write.
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Statistical models provide powerful tools to researchers in a wide array of disciplines. Such models allow for the examination of relationships among multiple variables, which in turn can lead to a better understanding of the world. For example, sociologists use linear regression to gain insights into how factors such as ethnicity, gender, and level of education are related to an individual’s income. Biologists can use the same type of model to understand the interplay between sunlight, rainfall, industrial runoff, and biodiversity in a rain forest. And using linear regression, educational researchers can develop powerful tools for understanding the role that different instructional strategies have on student achievement. In addition to providing a path by which various phenomena can be better understood, statistical models can also be used as predictive tools. For example, econometricians might develop models to predict labor market participation given a set of economic inputs. Higher education administrators may use similar types of models to predict grade point averages for prospective incoming freshmen to identify those who might need academic assistance during their first year of college.

As can be seen from these few examples, statistical modeling is very important across a wide range of fields, providing researchers with tools for both explanation and prediction. Certainly, the most popular of such models over the last 100 years of statistical practice has been the general linear model (GLM). The GLM links a dependent or outcome variable to one or more independent variables and can take the form of such popular tools as analysis of variance (ANOVA) and regression.

Based on GLM’s popularity and utility and its ability to serve as the foundation for many other models including the multilevel types featured in this book, we will start with a brief review of the linear model, focusing on regression. This review starts with a short technical discussion of linear regression models, followed by a description of how they can be estimated using the R language and environment (R Core Team, 2013).

The technical aspects of this discussion are intentionally not highly detailed as we focus on the model from a conceptual perspective. However, sufficient detail is presented so that a reader having only limited familiarity with the linear regression model will be provided with a basis for moving forward to multilevel models so that specific features of these more complex models that are shared with linear models can be explicated.
Readers familiar with linear regression and using R to conduct such analyses may elect to skip this chapter with no loss of understanding of future chapters.

1.1 Simple Linear Regression

As noted above, the GLM framework serves as the basis for the multilevel models that we describe in subsequent chapters. Thus, in order to provide a foundation for the rest of the book, we will focus in this chapter on the linear regression model, although its form and function can easily be translated to ANOVA as well. The simple linear regression model in population form is

\[ y_i = \beta_0 + \beta_1 x_i + \epsilon_i \]  

(1.1)

where \( y_i \) is the dependent variable for individual \( i \) in the data set and \( x_i \) is the independent variable for subject \( i \) \((i = 1, \ldots, N)\). The terms \( \beta_0 \) and \( \beta_1 \), are the intercept and slope of the model, respectively. In a graphical sense, the intercept is the point at which the line in Equation (1.1) crosses the \( y \) axis at \( x = 0 \). It is also the mean, specifically the conditional mean, of \( y \) for individuals with values of 0 on \( x \). This latter definition will be most useful in actual practice. The slope \( \beta_1 \) expresses the relationship between \( y \) and \( x \). Positive slope values indicate that larger values of \( x \) are associated with correspondingly larger values of \( y \), while negative slopes mean that larger \( x \) values are associated with smaller \( y \) values. Holding everything else constant, larger values of \( \beta_1 \) (positive or negative) indicate a stronger linear relationship between \( y \) and \( x \). Finally, \( \epsilon_i \) represents the random error inherent in any statistical model, including regression. It expresses the fact that for any individual, \( i \), the model will not generally provide a perfect predicted value of \( y_i \), denoted \( \hat{y}_i \), and obtained by applying the regression model as

\[ \hat{y}_i = \beta_0 + \beta_1 x_i \]  

(1.2)

Conceptually, this random error is representative of all factors that may influence the dependent variable other than \( x \).

1.1.1 Estimating Regression Models with Ordinary Least Squares

In virtually all real-world contexts, the population is unavailable to the researcher. Therefore, \( \beta_0 \) and \( \beta_1 \) must be estimated using sample data taken from the population. The statistical literature describes several methods for obtaining estimated values of the regression model parameters \((b_0 \text{ and } b_1, \text{ respectively})\) given a set of \( x \) and \( y \). By far, the most popular and widely used
of these methods is ordinary least squares (OLS). The vast majority of other approaches are useful in special cases involving small samples or data that fail to conform to the distributional assumptions undergirding OLS.

The goal of OLS is to minimize the sum of the squared differences between the observed values of $y$ and the model predicted values of $\hat{y}$ across the sample. This difference, known as the residual, is written as

$$e_i = y_i - \hat{y}_i$$

(1.3)

Therefore, the method of OLS seeks to minimize

$$\sum_{i=1}^{n} e_i^2 = \sum_{i=1}^{n} (y_i - \hat{y}_i)^2$$

(1.4)

The actual mechanism for finding the linear equation that minimizes the sum of squared residuals involves the partial derivatives of the sum of squared function with respect to the model coefficients $\beta_0$ and $\beta_1$. We will leave these mathematical details to excellent references such as Fox (2008). Note that in the context of simple linear regression, the OLS criteria reduce to the following equations that can be used to obtain $b_0$ and $b_1$ as

$$b_1 = r \left( \frac{s_y}{s_x} \right)$$

(1.5)

and

$$b_0 = \bar{y} - b_1 \bar{x}$$

(1.6)

where, $r$ is the Pearson product moment correlation coefficient between $x$ and $y$, $s_y$ is the sample standard deviation of $y$, $s_x$ is the sample standard deviation of $x$, $\bar{y}$ is the sample mean of $y$, and $\bar{x}$ is the sample mean of $x$.

### 1.2 Distributional Assumptions Underlying Regression

The linear regression model rests upon several assumptions about the distribution of the residuals in the broader population. Although a researcher typically is never able to collect data from an entire population, it is possible to assess empirically whether the assumptions are likely to hold true based on sample data.

The first assumption that must hold true for linear models to function optimally is that the relationship between $y_i$ and $x_i$ is linear. If the relationship
is not linear, then clearly an equation for a line will not provide adequate fit and the model is thus misspecified. A second assumption is that the variance in the residuals is constant regardless of the value of $x_i$. This assumption is typically referred to as homoscedasticity and is a generalization of the homogeneity of error variance assumption in ANOVA. Homoscedasticity implies that the variance of $y_i$ is constant across values of $x_i$. The distribution of the dependent variables around the regression line is literally the distribution of the residuals, thus making clear the connection of homoscedasticity of errors with the distribution of $y_i$ around the regression line. The third assumption is that the residuals are normally distributed in a population. Fourth is the assumption that the independent variable $x$ is measured without error and that it is unrelated to the model error term $\epsilon$. It should be noted that the assumption of $x$ measured without error is not as strenuous as one might first assume. In fact, for most real-world problems, the model will work well even when the independent variable is not error free (Fox, 2008). Fifth and finally, the residuals for any two individuals in a population are assumed to be independent of one another. This independence assumption implies that the unmeasured factors influencing $y$ are not related from one individual to another and addressed directly with the use of multilevel models, as we will see in Chapter 2.

In many research situations, individuals are sampled in clusters, such that we cannot assume that individuals from the same cluster will have uncorrelated residuals. For example, if samples are obtained from multiple neighborhoods, individuals within the same neighborhoods may tend to be more like one another than they are like individuals from other neighborhoods. A prototypical example of this is children in schools. Due to a variety of factors, children attending the same school often have more in common with one another than they do with children from other schools. These common factors may include neighborhood socioeconomic status, school administration policies, and school learning environment, to name just a few.

Ignoring this clustering or not even realizing it is a problem can be detrimental to the results of statistical modeling. We explore this issue in great detail later in the book, but for now we simply want to mention that a failure to satisfy the assumption of independent errors is (1) a major problem and (2) often a problem that may be overcome with appropriate models, such as multilevel models that explicitly consider the nesting of data.

### 1.3 Coefficient of Determination

When a linear regression model has been estimated, researchers generally want to measure the relative magnitude of the relationships of the variables. One useful tool for ascertaining the strength of the relationship between
\( x \) and \( y \) is the coefficient of determination, which is the squared multiple correlation coefficient denoted \( R^2 \) in Equation (1.7). \( R^2 \) reflects the proportion of variation in the dependent variable that is explained by the independent variable. Mathematically, \( R^2 \) is calculated as

\[
R^2 = \frac{SS_R}{SS_T} = \frac{\sum_{i=1}^{n} (\hat{y}_i - \bar{y})^2}{\sum_{i=1}^{n} (y_i - \bar{y})^2} = 1 - \frac{\sum_{i=1}^{n} (y_i - \hat{y})^2}{\sum_{i=1}^{n} (y_i - \bar{y})^2} = 1 - \frac{SS_E}{SS_T} \tag{1.7}
\]

The terms in Equation (1.7) are as defined previously. The value of this statistic always lies between 0 and 1, with larger numbers indicating a stronger linear relationship between \( x \) and \( y \), implying that the independent variable accounts for more variance in the dependent. \( R^2 \) is a very commonly used measure of the overall fit of a regression model. Along with the parameter inference discussed below, it serves as the primary mechanism by which the relationship between the two variables is quantified.

### 1.4 Inference for Regression Parameters

A second method for understanding the nature of the relationship between \( x \) and \( y \) involves making inferences about the relationship in the population given the sample regression equation. Because \( b_0 \) and \( b_1 \) are sample estimates of the population parameters \( \beta_0 \) and \( \beta_1 \), respectively, they are subject to sampling error as is any sample estimate. This means that although the estimates are unbiased if the aforementioned assumptions hold, they are not precisely equal to the population parameter values. Furthermore, were we to draw multiple samples from the population and estimate the intercept and slope for each, the values of \( b_0 \) and \( b_1 \) would differ across samples even though they would estimate the same population parameter values for \( \beta_0 \) and \( \beta_1 \). The magnitude of this variation in parameter estimates across samples can be estimated from our single sample using a statistic known as the standard error.

The standard error of the slope, denoted as \( \sigma_{b_1} \) in a population, can be thought of as the standard deviation of slope values obtained from all possible samples of size \( n \) taken from the population. Similarly, the standard error of the intercept \( \sigma_{b_0} \) is the standard deviation of the intercept values obtained from all such samples. Clearly, it is not possible to obtain census data from a population in an applied research context. Therefore, we must estimate the standard errors of both the slope (\( s_{b_1} \)) and intercept (\( s_{b_0} \) using
data from a single sample, much as we did with $b_0$ and $b_1$. To obtain $s_{b1}$, we must first calculate the variance of the residuals,

$$S_e^2 = \frac{\sum_{i=1}^{n} e_i^2}{n - p - 1}$$

(1.8)

where $e_i$ is the residual value for individual $i$, $N$ is the sample size, and $p$ is the number of independent variables (one in the case of simple regression). Then

$$S_{b1} = \frac{1}{\sqrt{1 - R^2}} \left[ \frac{S_e}{\sum_{i=1}^{n} (x_i - \bar{x})^2} \right]$$

(1.9)

The standard error of the intercept is calculated as

$$S_{b0} = S_{b1} \sqrt{\frac{\sum_{i=1}^{n} x_i^2}{n}}$$

(1.10)

Because the sample intercept and slope are only estimates of the population parameters, researchers often are interested in testing hypotheses to infer whether the data represent a departure from what would be expected in what is commonly referred to as the null case (the null value holding true in the population can be rejected). Usually (but not always), the inference of interest concerns testing that the population parameter is 0. In particular, a non-0 slope in a population means that $x$ is linearly related to $y$. Therefore, researchers typically are interested in using the sample to make inference about whether the population slope is 0 or not. Inference can also be made regarding the intercept, and again the typical focus is on whether the value is 0 in the population.

Inference about regression parameters can be made using confidence intervals and hypothesis tests. Much as with the confidence interval of the mean, the confidence interval of the regression coefficient yields a range of values within which we have some level of confidence (e.g., 95%) that the population parameter value resides. If our particular interest is in whether $x$ is linearly related to $y$, then we would simply determine whether 0 is in the interval for $\beta_1$. If so, then we could not conclude that the population value differs from 0.
The absence of a statistically significant result (i.e., an interval not containing 0) does not imply that the null hypothesis is true. Rather it means that the sample data contains insufficient evidence to reject the null. Similarly, we can construct a confidence interval for the intercept, and if 0 is within the interval, we would conclude that the value of $y$ for an individual with $x = 0$ could plausibly be but is not necessarily 0. The confidence intervals for the slope and intercept take the following forms:

$$b_1 \pm t_{cv} s_{b_1} \quad (1.11)$$

and

$$b_0 \pm t_{cv} s_{b_0} \quad (1.12)$$

Here the parameter estimates and their standard errors are as described previously, while $t_{cv}$ is the critical value of the $t$ distribution for $1 - \alpha/2$ (e.g., the 0.975 quantile if $\alpha = 0.05$) with $n - p - 1$ degrees of freedom. The value of $\alpha$ is equal to 1 minus the desired level of confidence. Thus, for a 95% confidence interval (0.95 level of confidence), $\alpha$ would be 0.05.

In addition to confidence intervals, inference about the regression parameters can also be made using hypothesis tests. In general, the forms of this test for the slope and intercept, respectively, are

$$t_{b_1} = \frac{b_1 - \beta_1}{s_{b_1}} \quad (1.13)$$

$$t_{b_0} = \frac{b_0 - \beta_0}{s_{b_0}} \quad (1.14)$$

The terms $\beta_1$ and $\beta_0$ are the parameter values under the null hypothesis. Again, most often the null hypothesis posits that there is no linear relationship between $x$ and $y$ ($\beta_1 = 0$) and that the value of $y = 0$ when $x = 0$ ($\beta_0 = 0$). For simple regression, each of these tests is conducted with $n - 2$ degrees of freedom.

### 1.5 Multiple Regression

The linear regression model can be extended very easily to accommodate multiple independent variables at once. In the case of two regressors, the model takes the form

$$y_i = \beta_0 + \beta_1 x_{1i} + \beta_2 x_{2i} + \epsilon_i \quad (1.15)$$
In many ways, this model is interpreted like the one for simple linear regression. The only major difference between simple and multiple regression interpretation is that each coefficient is interpreted in turn holding constant the value of the other regression coefficient. In particular, the parameters are estimated by \( b_0, b_1, \) and \( b_2 \), and inferences about these parameters are made in the same fashion for both confidence intervals and hypothesis tests.

The assumptions underlying this model are also the same as those described for the simple regression model. Despite these similarities, three additional topics regarding multiple regression need to be considered here. These are inference for the set of model slopes as a whole, an adjusted measure of the coefficient of determination, and collinearity among the independent variables. Because these issues will be important in the context of multilevel modeling as well, we will address them in detail.

With respect to model inference, for simple linear regression, the most important parameter is generally the slope, so that inference for it will be of primary concern. When a model has multiple \( x \) variables, the researcher may want to know whether the independent variables taken as a whole are related to \( y \). Therefore, some overall test of model significance is desirable. The null hypothesis for this test is that all of the slopes are equal to 0 in the population; i.e., none of the regressors is linearly related to the dependent variable. The test statistic for this hypothesis is calculated as

\[
F = \frac{SS_R / p}{SS_E / (n - p - 1)} = \left( \frac{n - p - 1}{p} \right) \left( \frac{R^2}{1 - R^2} \right)
\]  

(1.16)

Here, terms are as defined in Equation (1.7). This test statistic is distributed as an \( F \) with \( p \) and \( n - p - 1 \) degrees of freedom. A statistically significant result would indicate that one or more of the regression coefficients are not equal to 0 in the population. Typically, the researcher would then refer to the tests of individual regression parameters described above in order to identify which parameters were not equal to 0.

A second issue to be considered by researchers in the context of multiple regression is the notion of adjusted \( R^2 \). Stated simply, the inclusion of additional independent variables in the regression model will always yield higher values of \( R^2 \), even when these variables are not statistically significantly related to the dependent variable. In other words, there is a capitalization on chance that occurs in the calculation of \( R^2 \).

As a consequence, models including many regressors with negligible relationships with \( y \) may produce an \( R^2 \) that would suggest the model explains a great deal of variance in \( y \). An option for measuring the variance explained in the dependent variable that accounts for this additional model complexity would be helpful to a researcher seeking to understand the true nature of the relationship between the set of independent
variables and the dependent. Such a measure exists in the form of the adjusted $R^2$ value, which is commonly calculated as

$$R^2_A = 1 - \left(1 - R^2\right)\left(\frac{n-1}{n-p-1}\right)$$

(1.17)

$R^2_A$ only increases with the addition of an $x$ if that $x$ explains more variance than would be expected by chance. $R^2_A$ will always be less than or equal to the standard $R^2$. It is generally recommended to use this statistic in practice when models containing many independent variables are used.

A final important issue specific to multiple regression is collinearity, which occurs when one independent variable is a linear combination of one or more of the other independent variables. In such a case, regression coefficients and their corresponding standard errors can be quite unstable, resulting in poor inference. It is possible to investigate the presence of collinearity using a statistic known as the variance inflation factor (VIF). To calculate the VIF for $x_j$, we would first regress all the other independent variables onto $x_j$ and obtain an $R^2_{xi}$ value. We then calculate

$$VIF = \frac{1}{1 - R^2_x}$$

(1.18)

The VIF will become large when $R^2_{xi}$ is near 1, indicating that $x_j$ has very little unique variation when the other independent variables in the model are considered. That is, if the other $p - 1$ regressors can explain a high proportion of $x_j$, then $x_j$ does not add much to the model above and beyond the other $p - 1$ regression. Collinearity in turn leads to high sampling variation in $b_j$, resulting in large standard errors and unstable parameter estimates. Conventional rules of thumb have been proposed for determining when an independent variable is highly collinear with the set of other $p - 1$ regressors. Thus, the researcher may consider collinearity a problem if VIF > 5 or 10 (Fox, 2008). The typical response to collinearity is to remove the offending variable(s) or use an alternative approach to conducting the regression analysis such as ridge regression or regression following a principal components analysis.

1.6 Example of Simple Manual Linear Regression

To demonstrate the principles of linear regression discussed above, let us consider a simple scenario in which a researcher collected data on college grade point averages (GPAs) and test anxiety using a standard measure by
which higher scores indicate greater anxiety when taking a test. The sample consisted of 440 college students who were measured on both variables. The researcher is interested in the extent to which test anxiety is related to college GPA, so that GPA is the dependent variable and anxiety is the independent variable. The descriptive statistics for each variable and the correlations between them appear in Table 1.1.

We can use this information to obtain estimates for both the slope and intercept of the regression model using Equations (1.4) and (1.5). First, the slope is calculated as

\[ b_1 = -0.30 \left( \frac{0.51}{10.83} \right) = -0.014 \]

indicating that individuals with higher test anxiety scores will generally have lower GPAs. Next, we can use this value and information in the table to calculate the intercept estimate:

\[ b_0 = 3.12 - (-0.014) (35.14) = 3.63 \]

The resulting estimated regression equation is then

\[ \hat{GPA} = 3.63 - 0.014 \text{(anxiety)} \]

Thus, this model would predict that for a one-point increase in the anxiety assessment score, the GPA would decrease by \(-0.014\) points.

To better understand the strength of the relationship between test anxiety and GPA, we will want to calculate the coefficient of determination. To do this, we need both the \(SS_R\) and \(SS_T\), which take the values 10.65 and 115.36, yielding

\[ R^2 = \frac{10.65}{115.36} = 0.09 \]

This result suggests that approximately 9% of the variation in GPA is explained by variation in test anxiety scores. Using this \(R^2\) value and Equation (1.14),

<table>
<thead>
<tr>
<th>Variable</th>
<th>Mean</th>
<th>Standard Deviation</th>
<th>Correlation</th>
</tr>
</thead>
<tbody>
<tr>
<td>GPA</td>
<td>3.12</td>
<td>0.51</td>
<td>-0.30</td>
</tr>
<tr>
<td>Anxiety</td>
<td>35.14</td>
<td>10.83</td>
<td></td>
</tr>
</tbody>
</table>
we can calculate the $F$ statistic t-test for whether any of the model slopes (in this case only one) are different from 0 in the population:

$$F = \left( \frac{440 - 1 - 1}{1} \right) \left( \frac{0.09}{1 - 0.09} \right) = \frac{438(0.10)}{43.8} = 43.8$$

This test has $p$ and $n - p - 1$ degrees of freedom, or 1 and 438 in this situation. The $p$ value of this test is less than 0.001, leading us to conclude that the slope in the population is indeed significantly different from 0 because the $p$ value is less than the Type I error rate specified. Thus, test anxiety is linearly related to GPA. The same inference could be conducted using the t-test for the slope. First we must calculate the standard error of the slope estimate:

$$S_{b_1} = \frac{1}{\sqrt{1 - R^2}} \left( \frac{S_E}{\sum (x_i - \bar{x})^2} \right)$$

For these data,

$$S_E = \sqrt{\frac{104.71}{440 - 1 - 1}} = \sqrt{0.24} = 0.49$$

In turn, the sum of squared deviations for $x$ (anxiety) was 53743.64, and we previously calculated $R^2 = 0.09$. Thus, the standard error for the slope is

$$S_{b_1} = \frac{1}{\sqrt{1 - 0.09}} \left( \frac{0.49}{\sqrt{53743.64}} \right) = 1.05(0.002) = 0.002$$

The test statistic for the null hypothesis that $\beta_1 = 0$ is calculated as

$$t = \frac{b_1 - 0}{s_{b_1}} = \frac{-0.014}{0.002} = -7.00$$

with $n - p - 1$ or 438 degrees of freedom. The $p$ value for this test statistic value is less than 0.001 and thus we can probabilistically infer that the value of the slope in the population is not zero, with the best sample point estimate being –0.014.

Finally, we can also draw inference about $\beta_1$ through a 95% confidence interval, as shown in Equation (1.9). For this calculation, we must determine the value of the $t$ distribution with 438 degrees of freedom that correspond to the $1 - 0.05/2$ or 0.975 point in the distribution. We can do so by using a $t$ table in the back of a textbook or with standard computer software.
such as SPSS. In either case, the critical value for this example is 1.97. The confidence interval can then be calculated as

\[-0.014 - 1.97 (0.002), -0.014 + 1.97 (0.002)\]
\[(-0.014 - 0.004, -0.014 + 0.004)\]
\[(-0.018, -0.010)\]

The fact that 0 is not in the 95% confidence interval simply supports the conclusion we reached using the \(p\) value as described above. Also, given this interval, we can infer that the actual population slope value lies between \(-0.018\) and \(-0.010\). Thus, anxiety could plausibly have an effect as small as \(-0.010\) or as large as \(-0.018\).

### 1.7 Regression in R

In R, the function call for fitting linear regression is `lm`, which is part of the `stats` library that is loaded by default each time R is started. The basic form for a linear regression model using `lm` is:

```r
lm(formula, data)
```

where `formula` defines the linear regression form and `data` indicates the data set used in the analysis, examples of which appear below. Returning to the previous example, predicting GPA from measures of physical (BStotal) and cognitive academic anxiety (CTA.tot), the model is defined in R as

```r
Model1.1 <- lm(GPA ~ CTA.tot + BStotal, Cassidy)
```

This line of R code is referred to as a function call and defines the regression equation. The dependent variable `GPA` is followed by the independent variables `CTA.tot` and `BStotal`, separated by `~`. The data set `Cassidy` is also given here, after the regression equation has been defined. Finally, the output from this analysis is stored in the object `Model1.1`. To view this output, we can type the name of this object in R, and hit return to obtain the following:

```r
Call:
  lm(formula = GPA ~ CTA.tot + BStotal, data = Cassidy)

Coefficients:
(Intercept)     CTA.tot     BStotal
   3.61892   -0.02007    0.01347
```

The output obtained from the basic function call will return only values for the intercept and slope coefficients, lacking information regarding
model fit (e.g., $R^2$) and significance of model parameters. Further information on our model can be obtained by requesting a summary of the model.

```
summary(Model1.1)
```

Using this call, R will produce the following:

```
Call:
  lm(formula = GPA ~ CTA.tot + BStotal, data = Cassidy)

Residuals:
   Min     1Q   Median     3Q    Max
-2.99239 -0.29138  0.01516  0.36849  0.93941

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  3.618924   0.079305  45.633  < 2e-16 ***
CTA.tot     -0.020068   0.003065  -6.547  1.69e-10 ***
BStotal      0.013469   0.005077   2.653   0.00828 **

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.4852 on 426 degrees of freedom
(57 observations deleted due to missingness)
Multiple R-squared:  0.1066,   Adjusted R-squared:  0.1024
F-statistic: 25.43 on 2 and 426 DF,  p-value: 3.706e-11
```

From the model summary we can obtain information on model fit (overall $F$ test for significance, $R^2$, and standard error of the estimate), parameter significance tests, and a summary of residual statistics. As the $F$ test for the overall model is somewhat abbreviated in this output, we can request the entire ANOVA result, including sums of squares and mean squares by using the `anova(Model1.1)` function call.

```
Analysis of Variance Table

Response: GPA
            Df Sum Sq  Mean Sq    F value Pr(> F)
CTA.tot     1  10.316  10.3159  43.8125 1.089e-10 ***
BStotal     1   1.657   1.6570  7.0376   0.00828 **
Residuals  426 100.304   0.2355
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Often in a regression model, we are interested in additional information that the model produces such as predicted values and residuals. Using the R call `attributes()`, we can obtain a list of the additional information available for the `lm` function.
This is a list of attributes or information that may be pulled from the fitted regression model. To obtain this information, we can call for the particular attribute. For example, if we want to obtain the predicted GPA for each individual in the sample, we would simply type the following followed by the enter key:

```
Model1.1$fitted.values
```

Thus for example, the predicted GPA for subject 1 based on the prediction equation would be 2.96. By the same token, we can obtain the regression residuals with the following command:

```
Model1.1$residuals
```

From this output, we can see that the predicted GPA for subject 1 based on the prediction equation would be 2.96. By the same token, we can obtain the regression residuals with the following command:
of the interacting variables, so that the moderation model using \texttt{lm()} is defined as:

\begin{verbatim}
Model1.2 <- lm(GPA ~ CTA.tot + BStotal + CTA.tot*BStotal, Cassidy)
\end{verbatim}

\texttt{Model1.2}

\texttt{Call: lm(formula = GPA ~ CTA.tot + BStotal + CTA.tot * BStotal, data = Cassidy)}

\texttt{Residuals:}

\begin{verbatim}
Min 1Q Median 3Q Max
-2.98711 -0.29737 0.01801 0.36340 0.95016
\end{verbatim}

\texttt{Coefficients:}

\begin{verbatim}
Estimate Std. Error t value Pr(>|t|)
(Intercept) 3.8977792 0.2307491 16.892 < 2e-16 ***
CTA.tot -0.0267935 0.0060581 -4.423 1.24e-05 ***
BStotal -0.0057595 0.0157812 -0.365 0.715
CTA.tot:BStotal 0.0004328 0.0003364 1.287 0.199
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
\end{verbatim}

\texttt{Residual standard error: 0.4849 on 425 degrees of freedom}

\texttt{(57 observations deleted due to missingness)}

\texttt{Multiple R-squared: 0.1101, Adjusted R-squared: 0.1038}

\texttt{F-statistic: 17.53 on 3 and 425 DF, p-value: 9.558e-11}

Here the slope for the interaction is denoted \texttt{CTA.tot:BStotal}, takes the value 0.0004, and is nonsignificant (t = 1.287, p = 0.199), indicating that the level of physical anxiety symptoms (\texttt{BStotal}) does not change or moderate the relationship between cognitive test anxiety (\texttt{CTA.tot}) and GPA.

\subsection*{1.7.2 Categorical Independent Variables}

The \texttt{lm} function is also easily capable of incorporating categorical variables into regression. Let us consider an analysis for predicting GPA from cognitive test anxiety (\texttt{CTA.tot}) and the categorical variable gender. To incorporate gender into the model, it must be dummy coded such that one category (e.g., male) takes the value of 1 and the other category (e.g., female) takes the value of 0. In this example, we named the variable \texttt{Male}, where 1 = male and 0 = not male (female). Defining a model using a dummy variable with the \texttt{lm} function then becomes no different from using continuous predictor variables.
Model1.3 <- lm(GPA~CTA.tot + Male, Acad)
summary(Model1.3)

Call:
lm(formula = GPA ~ CTA.tot + Male, data = Acad)

Residuals:
   Min     1Q  Median     3Q    Max  
-3.01149 -0.29005  0.03038  0.35374  0.96294

Coefficients:  Estimate Std. Error t value Pr(>|t|)
(Intercept)   3.740318   0.080940  46.211  < 2e-16 ***
CTA.tot       -0.015184   0.002117  -7.173  3.16e-12 ***
Male           -0.222594   0.047152  -4.721  3.17e-06 ***
---
Signif. codes:  0 '***'  0.001 '**'  0.01 '*'  0.05 '.'  0.1 ' '  1

Residual standard error: 0.4775 on 437 degrees of freedom
(46 observations deleted due to missingness)
Multiple R-squared: 0.1364, Adjusted R-squared: 0.1324
F-statistic: 34.51 on 2 and 437 DF, p-value: 1.215e-14

In this example, the slope for the dummy variable Male is negative and significant ($\beta = -0.223, p < 0.001$), indicating that males have significantly lower mean GPAs than females.

Depending on the format in which the data are stored, the lm function is capable of dummy coding categorical variables. If a variable has been designated as categorical (as often happens if you read data in from an SPSS file in which the variable is designated as such) and is used in the lm function, it will automatically dummy code the variable in your results. For example, if instead of using the Male variable as described above, we used Gender as a categorical variable coded as female and male, we would obtain the following results from the model specification and summary commands.

Model1.4 <- lm(GPA~CTA.tot + Gender, Acad)
summary(Model1.4)

Call:
lm(formula = GPA ~ CTA.tot + Gender, data = Acad)

Residuals:
   Min     1Q  Median     3Q    Max  
-3.01149 -0.29005  0.03038  0.35374  0.96294

Coefficients:  Estimate Std. Error t value Pr(>|t|)
(Intercept)   3.740318   0.080940  46.211  < 2e-16 ***
CTA.tot       -0.015184   0.002117  -7.173  3.16e-12 ***
Gender[T.male] -0.222594   0.047152  -4.721  3.17e-06 ***
---
A comparison of results between models Model1.3 and Model1.4 reveals identical coefficient estimates, $p$ values, and model fit statistics. The only difference between the two sets of results is that for Model1.4 R reported the slope as $\text{Gender}[\text{t.male}]$, indicating that the variable was dummy coded automatically so that male is 1 and not male is 0.

In the same manner, categorical variables consisting of more than two categories can also be incorporated easily into a regression model, either through direct use of the categorical variable or dummy coding prior to analysis. In the following example, the variable Ethnicity includes three possible groups (African American, Caucasian, and Other). By including this variable in the model call, we are implicitly requesting that R automatically dummy code it for us.

```r
GPAmodel1.5 <- lm(GPA~CTA.tot + Ethnicity, Acad)
summary(GPAmodel1.5)
```

Call:
`lm(formula = GPA ~ CTA.tot + Ethnicity, data = Acad)`

Residuals:

<table>
<thead>
<tr>
<th></th>
<th>Min</th>
<th>1Q</th>
<th>Median</th>
<th>3Q</th>
<th>Max</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>-2.95019</td>
<td>-0.30021</td>
<td>0.01845</td>
<td>0.37825</td>
<td>1.00682</td>
</tr>
</tbody>
</table>

Coefficients:

|                         | Estimate | Std. Error | t value | Pr(>|t|) |
|-------------------------|----------|------------|---------|---------|
| (Intercept)              | 3.670308 | 0.079101   | 46.400  | < 2e-16 *** |
| CTA.tot                 | -0.015002 | 0.002147 | -6.989  | 1.04e-11 *** |
| Ethnicity[T.African American] | -0.482377 | 0.131589 | -3.666  | 0.000277 *** |
| Ethnicity[T.Other]      | -0.151748 | 0.136150 | -1.115  | 0.265652 |

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.4821 on 436 degrees of freedom
(46 observations deleted due to missingness)
Multiple R-squared: 0.1215, Adjusted R-squared: 0.1155
F-statistic: 20.11 on 3 and 436 DF, p-value: 3.182e-12

Since we have slopes for African American and Other, we know that Caucasian serves as the reference category, which is coded as 0. Results indicate
a significant positive slope for African American (β = −0.482, p < 0.001), and a nonsignificant slope for Other (β = 0.152, p > 0.05), indicating that African Americans have significantly lower GPAs than Caucasians but the GPA result for the Other ethnicity category was not significantly different from those for Caucasians.

Finally, let us consider some issues associated with allowing R to dummy code categorical variables automatically. First, R will always automatically dummy code the first category listed as the reference category. If a more theoretically suitable dummy coding scheme is desired, it will be necessary to order the categories so that the desired reference category is first or simply recode dummy variables manually.

Also, it is important to remember that automatic dummy coding occurs only when a variable is labeled in a system as categorical. This will occur automatically if the categories are coded as letters. However, if a categorical variable is coded 1, 2 or 1, 2, 3 but not specifically designated as categorical, the system will view it as continuous and treat it as such. To ensure that a variable is treated as categorical when that is what we desire, we simply use the `as.factor` command. For the `Male` variable in which males are coded as 1 and females as 0, we would type

```
Male<-as.factor(Male)
```

We would then be able to assume the `Male` variable is categorical. In addition, if the dummy variable has only two levels, as is the case with `Male`, then it need not be converted to a categorical factor because the results from the regression analysis will be identical either way.

### 1.7.3 Checking Regression Assumptions with R

When checking assumptions for linear regression models, it is often desirable to create a plot of the residuals. Diagnostic residual plots can be easily obtained by using the `residualPlots` function from the `car` R package that we would need to install in our R workspace as explained in the appendix at the end of this book that introduces working with R. Let us again return to `Model1.1` predicting GPA from cognitive test anxiety and physical anxiety symptoms. After the regression model is created (`Model1.1`), we can easily obtain diagnostic residual scatterplots using the following command:

```
Library(car)
residualPlots(Model1.1)
```

This command will produce scatterplots of the Pearson residuals against each predictor variable as well as against the fitted values. In addition,
the \texttt{residualPlots} command will provide lack-of-fit tests in which a t-test for the predictor squared is computed and a fit line added to the plot to help check for nonlinear patterns in the data. A Tukey’s test for non-additivity is also computed for the plot of residuals against the fitted values to acquire further information about the adequacy of model fit along with a lack-of-fit test for each predictor. Tukey’s statistic is obtained by adding the squares of the fitted values to the original regression model. It tests the null hypothesis that the model is additive and that no interactions exist among the independent variables (Tukey, 1949). A nonsignificant result, such as that found for this example, indicates that no interaction is required in the model.

The other tests included here are for the squared term of each independent variable. For example, given that the Test stat results for CTA.tot and BSTotal are not significant, we can conclude that neither of these variables has a quadratic relationship with GPA. See Figure 1.1.

\begin{verbatim}
residualPlots(Model1.1)
\end{verbatim}

\begin{verbatim}
| Test | stat  | Pr(>|t|) |
|------|-------|----------|
| CTA.tot | 0.607 | 0.544    |
| BSTotal  | 0.762 | 0.447    |
| Tukey test | 0.301 | 0.764    |
\end{verbatim}

The \texttt{residualPlots} command provides plots with the residuals on the y axes of the graphs, the values of each independent variable, respectively, on the x axes for the first two graphs, and the fitted values on x for the last graph. In addition, curves were fit linking the x and y axes for each graph.

The researcher would examine these graphs to assess two assumptions about the data. First, the assumption of homogeneity of variance can be checked through an examination of the residual by fitted plot. If the assumption holds, this plot should display a formless cloud of data points with no discernible shapes that are equally spaced across all values of x. In addition, the linearity of the relationships between each independent variable and the dependent variable is assessed by an examination of the plots involving them. For example, it is appropriate to assume linearity for BSTotal if the residual plots show no discernible pattern. This may be further explained by an examination of the fitted line. If this line is essentially flat, as is the case here, we can conclude that any relationship between BSTotal and GPA is only linear.

In addition to linearity and homogeneity of variance, it is also important to determine whether the residuals follow a normal distribution as assumed in regression analysis. To check the normality of residual assumptions, QQ plots (quantile–quantile plots) are typically used.
The `qqPlot` function from the `car` package may be used to easily create QQ plots of run regression models. Interpretation of the QQ plot is quite simple. Essentially, the graph displays the data as it actually is on the $x$ axis and as it would be if normally distributed on the $y$ axis. The individual data points are represented in R by black circles. The solid line represents the data conforming perfectly to the normal distribution. Therefore, the closer the observed data (circles) are to the solid line, the more closely the data conforms to the normal distribution. In addition, R provides a 95% confidence interval for the line, so that when the data points fall within it they are deemed to conform to the normal distribution. In this example, the data appear to follow the normal distribution fairly closely.

```r
qqPlot(Model1.1)
```
Summary

Chapter 1 introduced readers to the basics of linear modeling using R. This treatment was purposely limited, as a number of good texts cover linear modeling and it is not the main focus of this book. However, many of the core concepts presented here for the GLM apply to multilevel modeling as well, and thus are of key importance as we move into more complex analyses. In addition, much of the syntactical framework presented here will reappear in subsequent chapters. In particular, readers should leave this chapter comfortable with interpretation of coefficients in linear models and the concept of variance in outcome variables. We would encourage you to return to this chapter frequently as needed to reinforce these basic concepts. In addition, we would recommend that you also refer to the appendix dealing with the basics of using R when questions about data management and installation of specific R libraries arise. In Chapter 2, we will turn our attention to the conceptual underpinnings of multilevel modeling before delving into estimation in Chapters 3 and 4.
2

Introduction to Multilevel Data Structure

2.1 Nested Data and Cluster Sampling Designs

In Chapter 1, we considered the standard linear model that underlies such common statistical methods as regression and analysis of variance (ANOVA; the general linear model). As noted, this model rests on several primary assumptions about the nature of the data in a population. Of particular importance in the context of multilevel modeling is the assumption of independently distributed error terms for the individual observations within a sample. This assumption essentially means that there are no relationships among individuals in the sample for the dependent variable once the independent variables in the analysis are accounted for. In the example described in Chapter 1, this assumption was indeed met, as the individuals in the sample were selected randomly from the general population. Therefore, nothing linked their dependent variable values other than the independent variables included in the linear model. However, in many cases the method used for selecting the sample does create correlated responses among individuals. For example, a researcher interested in the impact of a new teaching method on student achievement may randomly select schools for placement in treatment or control groups. If school A is placed into the treatment condition, all students within the school will also be in the treatment condition. This is a cluster randomized design in that the clusters (and not the individuals) are assigned to a specific group. Furthermore, it would be reasonable to assume that the school itself, above and beyond the treatment condition, would have an impact on the performances of the students. This impact would manifest as correlations in achievement test scores among individuals attending the school. Thus, if we were to use a simple one-way ANOVA to compare the achievement test means for the treatment and control groups with such cluster sampled data, we would likely violate the assumption of independent errors because a factor beyond treatment condition (in this case the school) would exert an additional impact on the outcome variable.

We typically refer to the data structure described above as nested, meaning that individual data points at one level (e.g., student) appear in only one level
of a higher level variable such as school. Thus, students are nested within school. Such designs can be contrasted with crossed data structures whereby individuals at the first level appear in multiple levels of the second variable. In our example, students may be crossed with after-school activities if they are allowed to participate in more than one. For example, a student might be on the basketball team and a member of the band.

The focus of this book is almost exclusively on nested designs that give rise to multilevel data. Another example of a nested design is a survey of job satisfaction levels of employees from multiple departments within a large business organization. In this case, each employee works within only a single division in the company, making possible a nested design. It seems reasonable to assume that employees working in the same division will have correlated responses on the satisfaction survey, because much of their views of their jobs will be based exclusively upon experiences within their divisions. For a third such example, consider the situation in which clients of several psychotherapists working in a clinic are asked to rate the quality of each therapy session. In this instance, three levels of data exist: (1) time in the form of an individual session, (2) client, and (3) therapist. Thus, session is nested in client, which in turn is nested in therapist. This data structure would be expected to lead to correlated scores on a therapy rating instrument.

### 2.2 Intraclass Correlation

In cases where individuals are clustered or nested within a higher level unit (e.g., classroom, school, school district), it is possible to estimate the correlation among individuals’ scores within the cluster or nested structure using the intraclass correlation (ICC, denoted $\rho_i$ in the population). The $\rho_i$ is a measure of the proportion of variation in the outcome variable that occurs between groups versus the total variation present. It ranges from 0 (no variance among clusters to 1 (variance among clusters but no within-cluster variance). $\rho_i$ can also be conceptualized as the correlation for the dependent measure for two individuals randomly selected from the same cluster. It can be expressed as

$$\rho_i = \frac{\tau^2}{\tau^2 + \sigma^2}$$

(2.1)

where $\tau^2$ denotes population variance between clusters and $\sigma^2$ indicates population variance within clusters. Higher values of $\rho_i$ indicate that a greater share of the total variation in the outcome measure is associated with cluster membership; i.e., a relatively strong relationship among the
scores for two individuals from the same cluster. Another way to frame this issue is that individuals within the same cluster (e.g., school) are more alike on the measured variable than they are like individuals in other clusters.

It is possible to estimate $\tau^2$ and $\sigma^2$ using sample data, and thus it is also possible to estimate $\rho$. Those familiar with ANOVA will recognize these estimates as related (though not identical) to the sum of squared terms. The sample estimate for variation within clusters is simply

$$\hat{\sigma}^2 = \frac{\sum_{j=1}^{C} (n_j - 1) S_j^2}{N - C} \quad (2.2)$$

where $S_j^2$ is the variance within cluster

$$S_j^2 = \sum_{i=1}^{n_j} (y_{ij} - \bar{y}_j)^2$$

$n_j$ is the sample size of cluster $j$, $N$ is the total sample size, and $C$ is the total number of clusters. In other words, $\sigma^2$ is simply the weighted average of within-cluster variances.

Estimation of $\tau^2$ involves a few more steps, but is not much more complex than what we have seen for $\sigma^2$. To obtain the sample estimate for variation between clusters $\hat{\tau}^2$, we must first calculate the weighted between-cluster variance:

$$\hat{S}_B^2 = \frac{\sum_{j=1}^{C} n_j (\bar{y}_j - \bar{y})^2}{\hat{n}(C - 1)} \quad (2.3)$$

where $\bar{y}_j$ is the mean on response variables for cluster $j$ and $\bar{y}$ is the overall mean on the response variable.

$$\hat{n} = \frac{1}{C - 1} \left[ N - \frac{\sum_{j=1}^{C} n_j^2}{N} \right]$$

We cannot use as $S_B^2$ a direct estimate of $\tau^2$ because it is impacted by the random variation among subjects within the same clusters. Therefore, in
order to remove this random fluctuation we will estimate the population between-cluster variance as

$$\hat{\tau}^2 = S_B^2 - \frac{\hat{\sigma}^2}{n}$$  \hspace{1cm} (2.4)$$

Using these variance estimates, we can in turn calculate the sample estimate of \( \rho_I \):

$$\hat{\rho}_I = \frac{\hat{\tau}^2}{\hat{\tau}^2 + \hat{\sigma}^2}$$  \hspace{1cm} (2.5)$$

Note that Equation (2.5) assumes that the clusters are of equal size. Clearly, that will not always be the case, in which case this equation will not hold. However, the purpose for its inclusion here is to demonstrate the principle underlying the estimation of \( \rho_I \), which holds even as the equation changes.

To illustrate estimation of \( \rho_I \), let us consider the following data set. Achievement test data were collected from 10,903 third grade students nested within 160 schools. School enrollment sizes ranged from 11 to 143, with a mean size of 68.14. In this case, we will focus on the reading achievement test scores and use data from only five of the schools to make manual calculations easy to follow. First we will estimate \( \hat{\sigma}^2 \). To do so, we must estimate the variance in scores within each school. These values appear in Table 2.1. Using these variances and sample sizes, we can calculate \( \hat{\sigma}^2 \) as

$$\hat{\sigma}^2 = \frac{\sum_j (n_j - 1)S_j^2}{N - C}$$

$$= \frac{(58 - 1)5.3 + (29 - 1)1.5 + (64 - 1)2.9 + (39 - 1)6.1 + (88 - 1)3.4}{278 - 5}$$

$$= \frac{302.1 + 42 + 182.7 + 231.8 + 295.8}{273} = \frac{1054.4}{273} = 3.9$$

<p>| School Size, Mean, and Variance of Reading Achievement Test |
|---------------|----------------|----------------|</p>
<table>
<thead>
<tr>
<th>School</th>
<th>N</th>
<th>Mean</th>
<th>Variance</th>
</tr>
</thead>
<tbody>
<tr>
<td>767</td>
<td>58</td>
<td>3.952</td>
<td>5.298</td>
</tr>
<tr>
<td>785</td>
<td>29</td>
<td>3.331</td>
<td>1.524</td>
</tr>
<tr>
<td>789</td>
<td>64</td>
<td>4.363</td>
<td>2.957</td>
</tr>
<tr>
<td>815</td>
<td>39</td>
<td>4.500</td>
<td>6.088</td>
</tr>
<tr>
<td>981</td>
<td>88</td>
<td>4.236</td>
<td>3.362</td>
</tr>
<tr>
<td>Total</td>
<td>278</td>
<td>4.149</td>
<td>3.916</td>
</tr>
</tbody>
</table>
Introduction to Multilevel Data Structure

The school means that are required for calculating $S^2_eta$, appear in Table 2.1 as well. First we must calculate $\tilde{n}$:

\[
\tilde{n} = \frac{1}{C - 1} \left( \frac{C}{N} \sum_{j=1}^{C} n_j^2 - 1 \right) = \frac{1}{5 - 1} \left( 278 - \frac{58^2 + 29^2 + 64^2 + 39^2 + 88^2}{278} \right)
\]

\[
= \frac{1}{4} (278 - 63.2) = 53.7
\]

Using this value, we can then calculate $S^2_eta$ for the five schools in our small sample using Equation (2.3):

\[
\frac{58(3.952 - 4.149)^2 + 29(3.331 - 4.149)^2 + 64(4.363 - 4.149)^2}{53.7(5 - 1)} + \frac{39(4.500 - 4.149)^2 + 88(4.236 - 4.149)^2}{53.7(5 - 1)}
\]

\[
= \frac{2.251 + 19.405 + 2.931 + 4.805 + 0.666}{214.8} = \frac{30.057}{214.800} = 0.140
\]

We can now estimate the population between-cluster variance $\tau^2$ using Equation (2.4):

\[
0.140 - \frac{3.9}{53.7} = 0.140 - 0.073 = 0.067
\]

We have now calculated all the parts needed to estimate $\rho_I$ for the population,

\[
\hat{\rho}_I = \frac{0.067}{0.067 + 3.9} = 0.017
\]

This result indicates very little correlation of test scores within the schools. We can also interpret this value as the proportion of variation in the test scores accounted for by the schools. Since $\hat{\rho}_I$ is a sample estimate, we know that it is subject to sampling variation, which can be estimated with a standard error as in Equation (2.6):

\[
s_{\rho_I} = \left(1 - \rho_I\right)\left(1 + (n-1)\rho_I\right)\frac{2}{n(n-1)(N-1)}
\]
The terms in Equation (2.6) are as defined previously, and the assumption is that all clusters are of equal size. As noted earlier, this latter condition is not a requirement, however, and an alternative formulation exists for cases in which it does not hold. However, Equation (2.6) provides sufficient insight for our purposes into the estimation of the standard error of the ICC.

The ICC is an important tool in multilevel modeling, in large part because it indicates the degree to which a multilevel data structure may impact the outcome variable of interest. Larger ICC values are indicative of a greater impact of clustering. Thus, as the ICC increases in value, we must be more cognizant of employing multilevel modeling strategies in data analysis. In the next section, we will discuss the problems associated with ignoring this multilevel structure, before we turn our attention to methods for dealing with it directly.

2.3 Pitfalls of Ignoring Multilevel Data Structure

When researchers apply standard statistical methods to multilevel data such as the regression model described in Chapter 1, the assumption of independent errors is violated. For example, if we have achievement test scores from a sample of students who attend several different schools, it would be reasonable to believe that those attending the same school will have scores that are more highly correlated with one another than they are with scores from students at other schools. This within-school correlation would be due, for example, to a community, a common set of teachers, a common teaching curriculum, a single set of administrative policies, and other factors. The within-school correlation will in turn result in an inappropriate estimate of the of the standard errors for the model parameters, which will lead to errors of statistical inference, such as p-values smaller than they should be and the resulting rejection of null effects above the stated Type I error rate for the parameters.

Recalling our discussion in Chapter 1, the test statistic for the null hypothesis of no relationship between the independent and dependent variable is simply the regression coefficient divided by the standard error. An underestimation of the standard error will cause an overestimation of the test statistic, and thus the statistical significance for the parameter in cases where it should not be, that is, Type I errors at a higher rate than specified. Indeed, the underestimation of the standard error will occur unless $\tau^2$ is equal to 0.

In addition to the underestimation of the standard error, another problem with ignoring the multilevel structure of data is that we may miss important relationships involving each level in the data. Recall our example of two levels of sampling: students (level 1) are nested in schools (level 2). Specifically, by not including information about the school, for example,
we may well miss important variables at the school level that may help explain performance at student level. Therefore, beyond the known problem with misestimating standard errors, we also develop an incorrect model for understanding the outcome variable of interest. In the context of multilevel linear models (MLMs), inclusion of variables at each level is relatively simple, as are interactions among variables at different levels. This greater model complexity in turn may lead to greater understanding of the phenomenon under study.

2.4 Multilevel Linear Models

In the following section we will review some of the core ideas that underlie MLMs. Our goal is to familiarize readers with terms that will repeat throughout the book and explain them in a relatively nontechnical fashion. We will first focus on the difference between random and fixed effects, after which we will discuss the basics of parameter estimation, focusing on the two most commonly used methods, maximum likelihood and restricted maximum likelihood, and conclude with a review of assumptions underlying MLMs, and overview of how they are most frequently used, with examples. In this section, we will also address the issue of centering, and explain why it is an important concept in MLM. After reading the rest of this chapter, the reader will have sufficient technical background on MLMs to begin using the R software package for fitting MLMs of various types.

2.4.1 Random Intercept

As we transition from the one-level regression framework of Chapter 1 to the MLM context, let us first revisit the basic simple linear regression model of Equation (1.1)

\[ y = \beta_0 + \beta_1 x + \varepsilon \]

Here, the dependent variable \( y \) is expressed as a function of an independent variable \( x \), multiplied by a slope coefficient \( \beta_1 \), an intercept \( \beta_0 \), and random variation from subject to subject \( \varepsilon \). We defined the intercept as the conditional mean of \( y \) when the value of \( x \) is 0.

In the context of a single-level regression model such as this, one intercept is common to all individuals in the population of interest. However, when individuals are clustered together in some fashion (e.g., students in classrooms and schools, organizational units within a company), there will potentially be a separate intercept for each cluster, that is, different means may exist for the dependent variable for \( x = 0 \) across the different clusters.
We say potentially here because the single intercept model of Equation (1.1) will suffice if there is no cluster effect. In practice, assessing the existence of different means across clusters is an empirical question described below. It should also be noted that in this discussion we consider only the case where the intercept is cluster specific. It is also possible for $\beta_1$ to vary by group or even other coefficients from more complicated models.

Allowing for group-specific intercepts and slopes leads to the following notation commonly used for the level 1 (micro) model in multilevel modeling

$$y_{ij} = \beta_{0j} + \beta_1 x + \epsilon_{ij}$$

(2.7)

where the $ij$ subscript refers to the $i$th individual in the $j$th cluster. We will begin our discussion of MLM notation and structure with the most basic multilevel model: predicting the outcome from only an intercept that we will allow to vary randomly for each group.

$$y_{ij} = \beta_{0j} + \epsilon_{ij}$$

(2.8)

Allowing the intercept to differ across clusters, as in Equation (2.8), leads to the random intercept that we express as

$$\beta_{0j} = \gamma_{00} + U_{0j}$$

(2.9)

In this framework, $\gamma_{00}$ represents an average or general intercept value that holds across clusters, whereas $U_{0j}$ is a group-specific effect on the intercept. We can think of $\gamma_{00}$ as a fixed effect because it remains constant across all clusters, and $U_{0j}$ is a random effect because it varies from cluster to cluster. Therefore, for a MLM we are interested not only in some general mean value for $y$ when $x$ is 0 for all individuals in the population ($\gamma_{00}$), but also the deviation between the overall mean and the cluster-specific effects for the intercept ($U_{0j}$).

If we go on to assume that the clusters constitute a random sample from the population of all such clusters, we can treat $U_{0j}$ as a kind of residual effect on $y_{ij}$, very similar to how we think of $\epsilon$. In that case, $U_{0j}$ is assumed to be drawn randomly from a population with a mean of 0 (recall that $U_{0j}$ is a deviation from the fixed effect) and a variance $\tau^2$. Furthermore, we assume that $\tau^2$ and $\sigma^2$, the variance of $\epsilon$, are uncorrelated. We have already discussed $\tau^2$ and its role in calculating $\hat{\rho}_1$. In addition, $\tau^2$ can also be viewed as the impact of the cluster on the dependent variable, and therefore testing it for statistical significance is equivalent to testing the null hypothesis that cluster (e.g., school) has no impact on the dependent variable. If we substitute the two components of the random intercept into the regression model, we get

$$y = \gamma_{00} + U_{0j} + \beta_1 x + \epsilon$$

(2.10)
Equation (2.10) is termed the full or composite model in which the multiple levels are combined into a unified equation. Often in MLM, we begin our analysis of a data set with this simple random intercept model known as the null model that takes the form

\[ y_{ij} = \gamma_{00} + U_{0j} + \epsilon_{ij} \]  

(2.11)

While the null model does not provide information about the impacts of specific independent variables on the dependent, it does yield important information regarding how variation in \( y \) is partitioned between variance among the individual \( \sigma^2 \) values and variance among the clusters \( \tau^2 \). The total variance of \( y \) is simply the sum of \( \sigma^2 \) and \( \tau^2 \). In addition, as we have already seen, these values can be used to estimate \( \rho_i \). The null model, as will be seen in later sections, is also used as a baseline for model building and comparison.

### 2.4.2 Random Slopes

It is a simple matter to expand the random intercept model in Equation (2.9) to accommodate one or more independent predictor variables. As an example, if we add a single predictor \( (x_{ij}) \) at the individual level (Level 1) to the model, we obtain

\[ y_{ij} = \gamma_{00} + \gamma_{10}x_{ij} + U_{0j} + \epsilon_{ij} \]  

(2.12)

This model can also be expressed in two separate levels:

**Level 1:**

\[ y_{ij} = \beta_{0j} + \beta_{1j}x_{ij} + \epsilon_{ij} \]  

(2.13)

**Level 2:**

\[ \beta_{0j} = \gamma_{00} + U_{0j} \]  

(2.14)

\[ \beta_{1j} = \gamma_{10} \]  

(2.15)

The model now includes the predictor and the slope relating it to the dependent variable \( \gamma_{10} \), which we acknowledge as being at Level 1 by the subscript 10. We interpret \( \gamma_{10} \) in the same way as \( \beta_1 \) in the linear regression model, i.e., as a measure of the impact on \( y \) of a one-unit change in \( x \). In addition, we can estimate \( \rho_i \) exactly as earlier although now it reflects the correlation between individuals from the same cluster after controlling for the independent variable, \( x \). In this model, both \( \gamma_{10} \) and \( \gamma_{00} \) are fixed effects, while \( \sigma^2 \) and \( \tau^2 \) remain random.

One implication of the model in Equation (2.12) is that the dependent variable is impacted by variations among individuals (\( \sigma^2 \)), variations among clusters (\( \tau^2 \)), an overall mean common to all clusters (\( \gamma_{00} \)), and the impact of the independent variable as measured by \( \gamma_{10} \), which is also common to all clusters.
In practice, however, there is no reason that the impact of \( x \) on \( y \) must be common for all clusters. In other words, it is entirely possible that rather than having a single \( \gamma_{10} \) common to all clusters, there is actually a unique effect for the cluster of \( \gamma_{10} + U_{1j} \), where \( \gamma_{10} \) is the average relationship of \( x \) with \( y \) across clusters, and \( U_{1j} \) is the cluster-specific variation of the relationship between the two variables. This cluster-specific effect is assumed to have a mean of 0 and vary randomly around \( \gamma_{10} \). The random slopes model is

\[
y_{ij} = \gamma_{00} + \gamma_{10}x_{ij} + U_{0j} + U_{1j}x_{ij} + \epsilon_{ij}
\]  

(2.16)

Written in this way, we have separated the model into its fixed (\( \gamma_{00} + \gamma_{10}x_{ij} \)) and random (\( U_{0j} + U_{1j}x_{ij} + \epsilon_{ij} \)) components. The Equation (2.16) model simply indicates an interaction between cluster and \( x \), such that the relationship of \( x \) and \( y \) is not constant across clusters.

Heretofore we discussed only one source of between-group variation, expressed as \( \tau^2 \), that serves as the variation among clusters in the intercept. However, Equation (2.16) adds a second such source of between-group variance in the form of \( U_{1j} \), which indicates cluster variation on the slope relating the independent and dependent variables. To differentiate these two sources of between-group variance, we now denote the variance of \( U_{0j} \) as \( \tau^2_0 \) and the variance of \( U_{1j} \) as \( \tau^2_1 \). Furthermore, within clusters we expect \( U_{1j} \) and \( U_{0j} \) to have a covariance of \( \tau_{01} \). However, across different clusters, these terms should be independent of one another, and in all cases it is assumed that \( \epsilon \) remains independent of all other model terms. In practice, if we find that \( \tau^2_1 \) is not 0, we must be careful in describing the relationship between the independent and dependent variables, as it is not the same for all clusters.

We will revisit this idea in subsequent chapters. For the moment, however, it is most important to recognize that variation in the dependent variable \( y \) can be explained by several sources, some fixed and others random. In practice, we will most likely be interested in estimating all of these sources of variability in a single model.

As a means for further understanding the MLM, let us consider a simple example using the five schools described above. In this context, we are interested in treating a reading achievement test score as the dependent variable and a vocabulary achievement test score as the independent variable. Remember that students are nested within schools so that a simple regression analysis is not appropriate. To understand the issue being estimated in the context of MLM, we can obtain separate intercept and slope estimates for each school as shown in Table 2.2.

Since the schools are of the same sample size, the estimate of \( \gamma_{00} \), the average intercept value is 2.359, and the estimate of the average slope value \( \gamma_{10} \) is 0.375. Notice that for both parameters, the school values deviate from these means. For example, the intercept for school 1 is 1.230. The –1.129 difference between this value and 2.359 is \( U_{0j} \) for that school. Similarly, the
difference between the average slope value of 0.375 and the slope for school 1, 0.552 is 0.177, which is $U_{ij}$ for the school. Table 2.2 includes $U_{0j}$ and $U_{1j}$ values for each school. The differences in slopes also provide information about the relationship between vocabulary and reading test scores. This relationship was positive for all schools, meaning that students who scored higher on vocabulary also scored higher on reading. However, the strength of this relationship was weaker for school 2 than for school 1, as an example.

Based on the values in Table 2.2, it is also possible to estimate the variances associated with $U_{1j}$ and $U_{0j}$, $\tau_1^2$ and $\tau_0^2$, respectively. Again, because the schools in this example had the same numbers of students, the calculation of these variances is a straightforward matter, using

$$\frac{\sum (U_{1j} - \bar{U}_1)^2}{J - 1}$$

for the slopes and an analogous equation for the intercept random variance. We obtain $\tau_0^2 = 0.439$ and $\tau_1^2 = 0.016$. In other words, much more of the variance in the dependent variable is accounted for by variation in the intercepts at school level than is accounted for by variation in the slopes. Another way to think of this result is that the schools exhibited greater differences among one another in the mean level of achievement as compared to differences in the impacts of $x$ on $y$.

The practice of obtaining these variance estimates using the R environment for statistical computing and graphics and interpreting their meaning are subjects for upcoming chapters. Before discussing the practical “nuts and bolts” of conducting this analysis, we first examine the basics for estimating parameters in the MLM framework using maximum likelihood and restricted maximum likelihood algorithms. While similar in spirit to the simple calculations demonstrated above, they are different in practice and will yield somewhat different results from those obtained using least squares as above. First, one more issue warrants our attention as we consider the use of MLM, namely variable centering.

**TABLE 2.2**

<table>
<thead>
<tr>
<th>School</th>
<th>Intercept $U_{0j}$</th>
<th>Slope $U_{1j}$</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1.230</td>
<td>-1.129</td>
</tr>
<tr>
<td>2</td>
<td>2.673</td>
<td>0.314</td>
</tr>
<tr>
<td>3</td>
<td>2.707</td>
<td>0.348</td>
</tr>
<tr>
<td>4</td>
<td>2.867</td>
<td>0.508</td>
</tr>
<tr>
<td>5</td>
<td>2.319</td>
<td>-0.040</td>
</tr>
<tr>
<td>Overall</td>
<td>2.359</td>
<td>0.375</td>
</tr>
</tbody>
</table>
2.4.3 Centering

Centering is simply the practice of subtracting the mean of a variable from each individual value. This implies the mean for the sample of the centered variables is 0 and also that each individual’s (centered) score represents a deviation from the mean rather than representing the meaning of its raw value. In the context of regression, centering is commonly used, for example, to reduce collinearity caused by including an interaction term in a regression model. If the raw scores of the independent variables are used to calculate the interaction and both the main effects and interaction terms are included in the subsequent analysis, it is very likely that collinearity will cause problems in the standard errors of the model parameters. Centering is a way to help avoid such problems (Iversen, 1991).

Such issues are also important to consider in MLM, in which interactions are frequently employed. In addition, centering is also a useful tool for avoiding collinearity caused by highly correlated random intercepts and slopes in MLMs (Wooldridge, 2004). Finally, centering provides a potential advantage in terms of interpretation of results. Remember from our discussion in Chapter 1 that the intercept is the value of the dependent variable when the independent variable is set to 0. In many applications (e.g., a measure of vocabulary), the independent variable cannot reasonably be 0. This essentially renders the intercept as a necessary value for fitting the regression line but not one that has a readily interpretable value. However, when \( x \) has been centered, the intercept takes on the value of the dependent variable when the independent is at its mean. This is a much more useful interpretation for researchers in many situations, and yet another reason why centering is an important aspect of modeling, particularly in the multilevel context.

Probably the most common approach to centering is to calculate the difference between each individual’s score and the overall, or grand mean across the entire sample. This grand mean centering is certainly the most commonly used method in practice (Bickel, 2007). It is not, however, the only manner of centering data. An alternative approach known as group mean centering involves calculating the difference between each individual score and the mean of the cluster to which it belongs. In our school example, grand mean centering would involve calculating the difference between each score and the overall mean across schools, while group mean centering would lead the researcher to calculate the difference between each score and the mean for the school.

While the literature indicates some disagreement regarding which approach may be best for reducing the harmful effects of collinearity (Bryk & Raudenbush, 2002; Snijders & Bosker, 1999), researchers demonstrated that either technique will work well in most cases (Kreft, de Leeuw, & Aiken, 1995). Therefore, the choice of which approach to use must be made on substantive grounds regarding the nature of the relationship between \( x \) and \( y \). By using grand mean centering, we implicitly compare individuals to one another (in the form of the overall mean) across an entire sample.
On the other hand, group mean centering places each individual in relative position on $x$ within his or her cluster. In our school example, using the group mean centered values of vocabulary in the analysis would mean that we are investigating the relationship between a student’s relative vocabulary score in his or her school and his or her reading score. In contrast, the use of grand mean centering would examine the relationship between a student’s relative standing in the sample as a whole on vocabulary and the reading score. This latter interpretation would be equivalent conceptually (but not mathematically) to using the raw score, while the group mean centering would not.

Throughout the rest of this book, we will use grand mean centering by default based on recommendations by Hox (2002), among others. At times, however, we will also demonstrate the use of group mean centering to illustrate how it provides different results and for applications in which interpretation of the impact of an individual’s relative standing in his or her cluster may be more useful than the individual’s relative standing in the sample as a whole.

### 2.5 Basics of Parameter Estimation with MLMs

Heretofore, our discussions of estimation of model parameters have been in the context of least squares—a technique that provides underpinnings of ordinary least squares (OLS) and related linear models. However, as we move from these fairly simple applications to more complex models, OLS is not typically the optimal approach for parameter estimation. Instead, we will rely on maximum likelihood estimation (MLE) and restricted maximum likelihood (REML). In the following sections, we review these approaches to estimation from a conceptual view, focusing generally on how they work, what they assume about the data, and how they differ from one another. For the technical details we refer interested readers to Bryk and Raudenbush (2002) and de Leeuw and Meijer (2008), both of which are excellent resources for those desiring more in-depth coverage of these methods. Our purpose here is to provide readers with a conceptual understanding that will aid their application of MLM techniques in practice.

#### 2.5.1 Maximum Likelihood Estimation

MLE has as its primary goal the estimation of population model parameters that maximize the likelihood of obtaining the sample that we in fact obtained. In other words, the estimated parameter values should maximize the likelihood of our particular sample. From a practical perspective, identifying such sample values takes place by a comparison of the observed data with data predicted by the model associated with the parameter values. The closer the observed and predicted values are to one another, the greater the likelihood
that the observed data arose from a population with parameters close to those used to generate the predicted values. In practice, MLE is an iterative methodology in which the algorithm searches for parameter values that will maximize the likelihood of the observed data (i.e., produce predicted values that are as close as possible to observed values). MLE may be computationally intensive, particularly for complex models and large samples.

2.5.2 Restricted Maximum Likelihood Estimation

A variant of MLE known as restricted maximum likelihood estimation (REML) has proven more accurate than MLE for estimating variance parameters (Kreft & De Leeuw, 1998). In particular, the two methods differ with respect to calculating degrees of freedom in estimating variances. As a simple example, a sample variance is calculated typically by dividing the sum of squared differences between individual values and the mean by the number of observations minus 1 to yield an unbiased estimate. This is a REML estimate of variance.

In contrast, the MLE variance is calculated by dividing the sum of squared differences by the total sample size, leading to a smaller variance estimate than REML and, in fact, one biased in finite samples. In the context of multilevel modeling, REML accounts for the number of parameters being estimated in a model when determining the appropriate degrees of freedom for the estimation of the random components such as the parameter variances described above. In contrast, MLE does not account for these, leading to an underestimate of the variances that does not occur with REML. For this reason, REML is generally the preferred method for estimating multilevel models, although for testing variance parameters (or any random effect), it is necessary to use MLE (Snijders & Bosker, 1999). We should note that as the number of Level 2 clusters increases, the difference in value for MLE and REML estimates becomes very small (Snijders & Bosker, 1999).

2.6 Assumptions Underlying MLMs

As with any statistical model, the appropriate use of MLMs requires that several assumptions about the data hold true. If these assumptions are not met, the model parameter estimates may not be trustworthy, as would be the case with standard linear regression reviewed in Chapter 1. Indeed, while the assumptions for MLM differ somewhat from those for single-level models, the assumptions underlying MLM are akin to those for the simpler models. This section introduces these assumptions and their implications for researchers using MLMs. In subsequent chapters, we describe methods for checking the validity of these assumptions for given sets of data.
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First, we assume that the Level 2 residuals are independent between clusters. In other words, the assumption is that the random intercept and slope(s) at Level 2 are independent of one another across clusters. Second, the Level 2 intercepts and coefficients are assumed to be independent of the Level 1 residuals, i.e., errors for the cluster-level estimates are unrelated to errors at the individual level. Third, the Level 1 residuals are normally distributed and have constant variances. This assumption is very similar to the one we make about residuals in the standard linear regression model. Fourth, the Level 2 intercept and slope(s) have a multivariate normal distribution with a constant covariance matrix. Each of these assumptions can be directly assessed for a sample, as we shall see in forthcoming chapters. Indeed, the methods for checking the MLM assumptions are similar to those for checking the regression model that we used in Chapter 1.

2.7 Overview of Two-Level MLMs

We have described the specific terms of MLM, including the Level 1 and Level 2 random effects and residuals. We will close this chapter about MLMs by considering examples of two- and three-level MLMs and the use of MLMs with longitudinal data. This discussion should prepare the reader for subsequent chapters covering applications of R to the estimations of specific MLMs.

First, we consider the two-level MLM, parts of which we described earlier in this chapter. In Equation (2.16), we considered the random slopes model

\[ y_{ij} = \gamma_{00} + \gamma_{10}x_{ij} + U_{0j} + U_{1j}x_{ij} + \epsilon_{ij} \]

in which the dependent variable \( y_{ij} \) (reading achievement) was a function of an independent variable \( x_{ij} \) (vocabulary test score) and also random error at both the student and school levels. We can extend this model a bit further by including multiple independent variables at both Level 1 (student) and Level 2 (school). Thus, for example, in addition to ascertaining the relationship between an individual’s vocabulary and reading scores, we can also determine the degree to which the average vocabulary score at the school as a whole is related to an individual’s reading score. This model essentially has two parts: (1) one explaining the relationship between the individual level vocabulary (\( x_{ij} \)) and reading and (2) one explaining the coefficients at Level 1 as a function of the Level 2 predictor or average vocabulary score (\( z_{j} \)). The two parts of this model are expressed as

Level 1: \[ y_{ij} = \beta_{0j} + \beta_{1j}x_{ij} + \epsilon_{ij} \] (2.18)

Level 2: \[ \beta_{0j} = \gamma_{00} + \gamma_{01}z_{j} + U_{0j} \] (2.19)
The additional piece of Equation (2.19) is $\gamma_{h1} = \gamma_{h1} z_j$, which represents the slope for ($\gamma_{h1}$), and value of the average vocabulary score for the school ($z_j$). In other words, the mean school performance is related directly to the coefficient linking the individual vocabulary score to the individual reading score. For our specific example, we can combine Equations (2.18) and (2.19) to yield a single equation for the two-level MLM.

$$y_{ij} = \gamma_{00} + \gamma_{10} x_{ij} + \gamma_{01} z_j + \gamma_{1001} x_{ij} z_j + U_{0j} + U_{1j} x_{ij} + \epsilon_{ij}$$ (2.20)

Each of these model terms has been defined previously in this chapter: $\gamma_{00}$ is the intercept or grand mean for the model, $\gamma_{10}$ is the fixed effect of variable $x$ (vocabulary) on the outcome, $U_{0j}$ represents the random variation for the intercept across groups, and $U_{1j}$ represents the random variation for the slope across groups.

The additional pieces of Equation (2.13) are $\gamma_{01}$ and $\gamma_{11}$. The $\gamma_{01}$ represents the fixed effect of Level 2 variable $z$ (average vocabulary) on the outcome and $\gamma_{11}$ represents the slope for and value of the average vocabulary score for the school. The new term in Equation (2.20) is the cross-level interaction $\gamma_{1001} x_{ij} z_j$. As the name implies, the cross-level interaction is simply an interaction of Level 1 and Level 2 predictors. In this context, it represents the interaction between an individual’s vocabulary score and the mean vocabulary score for his or her school. The coefficient for this interaction term, $\gamma_{1001}$, assesses the extent to which the relationship between a student’s vocabulary score is moderated by the mean for the school attended. A large significant value for this coefficient would indicate that the relationship between an individual’s vocabulary test score and overall reading achievement is dependent on the level of vocabulary achievement at his or her school.

### 2.8 Overview of Three-Level MLMs

It is entirely possible to utilize three or more levels of data structures with MLMs. We should note, however, that four-level and larger models are rare in practice. For our reading achievement data in which the second level was school, a possible third level might be the district in which the school is located. In that case, we would have multiple equations to consider when expressing the relationship between vocabulary and reading achievement scores, starting at the individual level:

$$y_{ijk} = \beta_{0jk} + \beta_{1jk} x_{ijk} + \epsilon_{ijk}$$ (2.21)

The subscript $k$ represents the Level 3 cluster to which the individual belongs.
Before formulating the rest of the model, we must evaluate whether the slopes and intercepts are random at both Levels 2 and 3 or only at Level 1, for example. This decision should always be based on the theory surrounding the research questions, what is expected in the population, and what is revealed in the empirical data. We will proceed with the remainder of this discussion under the assumption that the Level 1 intercepts and slopes are random for both Levels 2 and 3 in order to provide a complete description of the most complex model possible when three levels of data structure are present. When the Level 1 coefficients are not random at both levels, the terms in the following models for which this randomness is not present would simply be removed. We will address this issue more specifically in Chapter 4 when we discuss the fitting of three-level models using R. The Level 2 and Level 3 contributions to the MLM described in Equation (2.13) appear below.

**Level 2:**

\[
\beta_{0jk} = \gamma_{00k} + U_{0jk} \\
\beta_{1jk} = \gamma_{10k} + U_{1jk}
\]

**Level 3:**

\[
\gamma_{00k} = \delta_{000} + V_{00k} \\
\gamma_{10k} = \delta_{100} + V_{10k}
\]

(2.22)

We can then use simple substitution to obtain the expression for the Level 1 intercept and slope in terms of both Level 2 and Level 3 parameters.

\[
\beta_{0jk} = \delta_{000} + V_{00k} + U_{0jk} \\
\beta_{1jk} = \delta_{100} + V_{10k} + U_{1jk}
\]

(2.23)

In turn, these terms may be substituted into Equation (2.15) to provide the full three-level MLM.

\[
y_{ijk} = \delta_{000} + V_{00k} + U_{0jk} + (\delta_{100} + V_{10k} + U_{1jk})x_{ijk} + e_{ijk}
\]

(2.24)

There is an implicit assumption in this expression of Equation (2.24) that there are no cross-level interactions, although they certainly may be modeled across all three levels or for any pair of levels. Equation (2.24) expresses individuals’ scores on the reading achievement test as a function of random and fixed components from the school they attend, the district in which the school is located, and their own vocabulary test scores and random variations associated only with them. Although not included in Equation (2.24), it is also possible to include variables at both Levels 2 and 3, similar to what we described for the two-level model structure.
2.9 Overview of Longitudinal Designs and Their Relationship to MLMs

Finally, we will briefly explain how longitudinal designs can be expressed as MLMs. Longitudinal research designs simply involve the collection of data from the same individuals at multiple points in time. For example, we may have reading achievement scores for students tested in the fall and spring of the school year. With such a design, we would be able to investigate aspects of growth scores and changes in achievements over time. Such models can be placed in the context of an MLM where the student represents the Level 2 (cluster) variable, and the individual test administration is at Level 1. We would then simply apply the two-level model described above, including student-level variables that are appropriate for explaining reading achievement. Similarly, if students are nested within schools, we would have a three-level model, with school serving as the third level. We could apply Equation (2.24) again with whichever student- or school-level variables were pertinent to the research question.

One unique aspect of fitting longitudinal data into the MLM context is that the error terms can potentially take specific forms that are not common in other applications of multilevel analysis. These error terms reflect the way in which measurements made over time relate to one another and are typically more complex than the basic error structure described thus far. In Chapter 5, we will consider examples of fitting such longitudinal models with R and focus our attention on these error structures—when each is appropriate and how they are interpreted. In addition, such MLMs need not take linear forms. They may be adapted to fit quadratic, cubic, or other nonlinear trends over time. These issues will be discussed further in Chapter 5.

Summary

The goal of this chapter was to introduce the basic theoretical underpinnings of multilevel modeling, but not to provide an exhaustive technical discussion of these issues. A number of useful resources can provide comprehensive details and are listed in the references at the end of the book. However, the information in this chapter should be adequate as we move forward with multilevel modeling using R software. We recommend that you make liberal use of the information provided here while reading subsequent chapters. This should provide you with a complete understanding of the output generated by R that we will be examining. In particular, when interpreting output from R, it may be helpful for you to return to this chapter to review precisely what each model parameter means.
In the next two chapters, we will take the theoretical information from this chapter and apply it to real data sets using two different R libraries, \texttt{n1me} and \texttt{lme4}, both of which were developed for conducting multilevel analyses with continuous outcome variables. In Chapter 5, we will examine how these ideas can be applied to longitudinal data. Chapters 7 and 8 will discuss multilevel modeling for categorical dependent variables. In Chapter 9, we will diverge from the likelihood-based approaches described here and explain multilevel modeling within the Bayesian framework, focusing on applications and learning when this method may be appropriate and when it may not.
3

Fitting Two-Level Models in R

In the previous chapter, the multilevel modeling approach to analysis of nested data was introduced along with relevant notations and definitions of random intercepts and coefficients. We will devote this chapter to the introduction of the R packages for fitting multilevel models. In Chapter 1, we provided an overview of the `lm()` function for linear regression models. As will become apparent, the estimation of multilevel models in R is very similar to estimating single-level linear models. After providing a brief discussion of the two primary R packages for fitting multilevel models for continuous data, we will devote the remainder of the chapter to extended examples applying the principles introduced in Chapter 2 using R.

3.1 Packages and Functions for Multilevel Modeling in R

Currently, the two main R libraries for devising multilevel models are `nlme` and `lme4`, both of which can be used for fitting basic and advanced multilevel models. The `lme4` package is slightly newer and provides a more concise syntax and more flexibility. Using the `nlme` package, the function call for continuous outcome multilevel models that are linear in their parameters is `lme()`, whereas the function call in `lme4` is `lmer()`.

In the following sections of this chapter, we will demonstrate and provide examples of using these two packages to run basic multilevel models in R. Following is the basic syntax for these two functions. Details regarding their use and various options will be provided in the examples.

\[
\text{lme(fixed, data, random, correlation, weights, subset, method,}
\text{ na.action, control, contrasts = NULL, keep.data = TRUE)}
\]

\[
\text{lmer(formula, data, family = NULL, REML = TRUE,}
\text{ control = list(), start = NULL, verbose = FALSE,}
\text{ doFit = TRUE, subset, weights, na.action, offset,}
\text{ contrasts = NULL, model = TRUE, x = TRUE, ...)}
\]

For simple linear multilevel models, the only necessary R subcommands for the functions are the formula (consisting of fixed and random effects)
and data. The remaining subcommands can be used to customize models and to provide additional output. This chapter focuses first on defining simple multilevel models and then demonstrates options for model customization and assumption checking.

3.2 The \texttt{nlme} Package

3.2.1 Simple (Intercept Only) Multilevel Models Using \texttt{nlme}

To demonstrate the use of R for fitting multilevel models, we return to the example introduced in Chapter 2. Specifically, a researcher wants to determine the extent to which vocabulary scores can be used to predict general reading achievement. Since students were nested within schools, standard linear regression models are not appropriate. In this case, school is a random effect and vocabulary scores are fixed. The first model that we will fit is the null model that has no independent variable. This model is useful for obtaining estimates of the residual and intercept variance when only the clustering by school is considered, as in Equation (2.11). The \texttt{lme} syntax necessary for estimating the null model appears below.

\begin{verbatim}
Model3.0 <- lme(fixed = geread~1, random = ~1|school, data = Achieve)
\end{verbatim}

We can obtain output from this model by typing \texttt{summary(Model3.0)}.

\begin{verbatim}
Linear mixed-effects model fit by REML
Data: Achieve
AIC BIC logLik
46274.31 46296.03 -23134.15
Random effects:
Formula: ~1 | school
 (Intercept) Residual
StdDev: 0.6257119 2.24611
Fixed effects: geread ~ 1
 Value Std.Error DF t-value p-value
 (Intercept) 4.306753 0.05497501 10160 78.3402 0

Standardized Within-Group Residuals:
Min Q1 Med Q3 Max
-2.3229469 -0.6377948 -0.2137753 0.2849664 3.8811630

Number of Observations: 10320
Number of Groups: 160
\end{verbatim}
Although this is a null model in which there is no independent variable, it provides some useful information that will help us understand the structure of the data. In particular, the AIC and BIC values that are of primary interest in this case will be useful in comparing this model with others that include one or more independent variables, as we will see below. In addition, the null model also provides estimates of the variance among the individuals $\sigma^2$ and among the clusters $\tau^2$. In turn, these values can be used to estimate $\rho_I$ (ICC), as in Equation (2.5). Here, the value would be

$$\hat{\rho}_I = \frac{0.6257119}{0.6257119 + 2.24611} = 0.2178797$$

We interpret this value to mean that the correlation of reading test scores among students within the same schools is 0.22 if we round our result.

To fit the model with vocabulary as the independent variable using `lme`, we submit the following syntax in R.

```r
Model3.1 <- lme(fixed = geread~gevocab, random = ~1|school, 
                 data = Achieve)
```

In the first part of the function call, we define the formula for the model fixed effects, very similar to model definition of linear regression using `lm()`. The statement `fixed = geread~gevocab` essentially says that the reading score is predicted with the vocabulary score fixed effect. The `random` part of the function call defines the random effects and the nesting structure. If only a random intercept is desired, the syntax for the intercept is `1`. In this example, `random = ~1|school` indicates that only a random intercepts model will be used and that the random intercept varies within school. This corresponds to the data structure of students nested within schools. Fitting this model, which is saved in the output object `Model3.1`, we obtain the following output by inputting the name of the output object.

```
Model3.1
Linear mixed-effects model fit by REML
  Data: Achieve
  Log-restricted-likelihood: -21568.6
  Fixed: geread ~ gevocab
         (Intercept)   gevocab
         2.0233559 0.5128977

Random effects:
  Formula: ~1 | school
         (Intercept)  Residual
         StdDev: 0.3158785 1.940740

Number of Observations: 10320
Number of Groups: 160
```
Output from the `lme()` function provides parameter estimates for the fixed effects and standard deviations for the random effects along with a summary of the number of Level 1 and Level 2 units in the sample. As with the output from the `lm()` function, however, the output from the `lme()` function provides limited information. If we desire more detailed information about the model, including significance tests for parameter estimates and model fit statistics, we can request a model summary. The `summary()` command will provide the following:

```
summary(Model3.1)
Linear mixed-effects model fit by REML
  Data: Achieve
        AIC       BIC      logLik
   43145.2  43174.17   -21568.6
Random effects:
  Formula: ~1 | school
             (Intercept) Residual
        StdDev: 0.3158785 1.940740
Fixed effects: geread ~ gevocab
  Value Std.Error DF  t-value p-value
(Intercept) 2.0233559  0.04930868  10159  41.03447   0
gevocab     0.5128977  0.00837268  10159  61.25850   0
Correlation:
             (Intr)
gevocab -0.758
Standardized Within-Group Residuals:
        Min         Q1        Med         Q3         Max
-3.0822506 -0.5734728 -0.2103488  0.3206692  4.4334337
Number of Observations: 10320
Number of Groups: 160
```

From this summary we obtain AIC, BIC, and log likelihood information that can be used for model comparisons in addition to parameter significance tests. We can also obtain a correlation between the fixed effect slope and the fixed effect intercept as well as a brief summary of the model residuals including the minimum, maximum, and first, second (median, denoted Med), and third quartiles.

The correlation of the fixed effects represents the estimated correlation if we had repeated samples of the two fixed effects (i.e., the intercept and slope for `gevocab`). Often this correlation is not particularly interesting. From this output, we can see that `gevocab` is a significant predictor of `geread` ($t = 61.258$, $p < 0.05$), and that as vocabulary score increases by 1 point, reading ability increases by 0.513 points. We can compare the fit
for this model with that of the null model by referring to the AIC and BIC statistics. Recall that smaller values reflect better model fit. For Model 3.1, the AIC and BIC are 43145.2 and 43174.17, respectively. For Model 3.0, the AIC and BIC were 46274.31 and 46296.03. Because the values for both statistics are smaller for Model 3.1, we would conclude that it provides a better fit to the data. Substantively, this means that we should include the predictor variable \texttt{geread}, which the results of the hypothesis test also supported.

In addition to the fixed effects in Model 3.1, we can also ascertain how much variation in \texttt{geread} is present across schools. Specifically, the output shows that after accounting for the impact of \texttt{gevocab}, the estimate of variation in intercepts across schools is 0.3158785, while the within-school variation is estimated as 1.940740. We can tie these numbers directly back to our discussion in Chapter 2 where $\tau_0^2 = 0.3158785$ and $\sigma^2 = 1.940740$. In addition, the overall fixed intercept denoted as $\gamma_{00}$ in Chapter 2 is 2.0233559, which is the mean of \texttt{geread} when the \texttt{gevocab} score is 0.

Finally, it is possible to estimate the proportion of variance in the outcome variable accounted for at each level of the model. In Chapter 1, we saw that with single-level OLS regression models, the proportion of response variable variance accounted for by the model is expressed as $R^2$. In the context of multilevel modeling, $R^2$ values can be estimated for each level of the model (Snijders & Bosker, 1999). For Level 1, we can calculate

$$R_{11}^2 = 1 - \frac{\sigma_{M1}^2 + \tau_{M1}^2}{\sigma_{M1}^2 + \tau_{M1}^2}$$

$$= 1 - \frac{1.940740 + 0.3158785}{2.24611 + 0.6257119}$$

$$= 1 - \frac{2.2566185}{2.8718219} = 1 - 0.7857794 = 0.2142206$$

This result tells us that Level 1 of Model 3.1 explains approximately 21% of the variance in the reading score above and beyond that accounted for in the null model. We can also calculate a Level 2 $R^2$ value:

$$R_{12}^2 = 1 - \frac{\sigma_{M1}^2 / B + \tau_{M1}^2}{\sigma_{M0}^2 / B + \tau_{M0}^2}$$

where $B$ is the average size of the Level 2 units (schools in this case). $R$ provides the number of individuals in the sample (10320) and the number of schools (160) so that we can calculate $B$ as 10320/160 = 64.5. We can now estimate
The model in the previous example was quite simple and incorporated only a single Level 1 predictor. In many applications, researchers utilize predictor variables at both Level 1 (student) and Level 2 (school). Incorporation of predictors at higher levels of analysis is straightforward in R and is handled in exactly the same manner as incorporation of Level 1 predictors. For example, let us assume that in addition to a student’s vocabulary test performance, a researcher also wants to determine whether school enrollment size (senroll) also produces a statistically significant impact on overall reading score. In that instance, adding the school enrollment Level 2 predictor would result in the following R syntax:

```r
Model3.2 <- lme(fixed = geread~gevocab + senroll, random = ~1|school, data = Achieve)
summary(Model3.2)
```

**Linear mixed-effects model fit by REML**

**Data:** Achieve

<table>
<thead>
<tr>
<th>AIC</th>
<th>BIC</th>
<th>logLik</th>
</tr>
</thead>
<tbody>
<tr>
<td>43162.1</td>
<td>43198.3</td>
<td>-21576.05</td>
</tr>
</tbody>
</table>

**Random effects:**

Formula: ~1 | school

(Intercept) Residual

*StdDev:* 0.3167654 1.940760

**Fixed effects: geread ~ gevocab + senroll**

<table>
<thead>
<tr>
<th>Value</th>
<th>Std.Error</th>
<th>DF</th>
<th>t-value</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>2.0748819</td>
<td>0.11400758</td>
<td>10159</td>
<td>18.19951</td>
</tr>
<tr>
<td>gevocab</td>
<td>0.5128708</td>
<td>0.00837340</td>
<td>10159</td>
<td>61.25000</td>
</tr>
<tr>
<td>senroll</td>
<td>-0.0001026</td>
<td>0.00020511</td>
<td>158</td>
<td>-0.50012</td>
</tr>
</tbody>
</table>

**Correlation:**

**(Intr) gevocab**

gevocab     -0.327

senroll     -0.901 -0.002
Standardized Within-Group Residuals:

<table>
<thead>
<tr>
<th></th>
<th>Min</th>
<th>Q1</th>
<th>Med</th>
<th>Q3</th>
<th>Max</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>-3.0834462</td>
<td>-0.5728938</td>
<td>-0.2103480</td>
<td>0.3212091</td>
<td>4.4335881</td>
</tr>
</tbody>
</table>

Number of Observations: 10320
Number of Groups: 160

Note that in this specific function call, senroll, is included only in the fixed part of the model and not in the random part. This variable thus has only a fixed (average) effect and is the same across all schools. We will see shortly how to incorporate a random coefficient in this model.

From these results we can see that enrollment did not have a statistically significant relationship with reading achievement. In addition, notice some minor changes in the estimates of the other model parameters and a fairly large change in the correlation between the fixed effect of gevocab slope and the fixed effect of the intercept. The slope for senroll and intercept were strongly negatively correlated and the slopes of the fixed effects exhibited virtually no correlation. As noted earlier, these correlations are typically not very helpful for explaining the dependent variable and are rarely discussed in any detail in reports of analysis results. The $R^2$ values for Levels 1 and 2 appear below.

\[ R_1^2 = 1 - \frac{\sigma^2_{M1} + \tau^2_{M1}}{\sigma^2_{M0} + \tau^2_{M0}} \]
\[ = 1 - \frac{1.940760 + 0.3167654}{2.24611 + 0.6257119} \]
\[ = 1 - \frac{2.2575254}{2.8718219} = 1 - 0.7860952 = 0.2139048 \]

\[ R_2^2 = 1 - \frac{\sigma^2_{M1}/B + \tau^2_{M1}}{\sigma^2_{M0}/B + \tau^2_{M0}} \]
\[ = 1 - \frac{1.940760/64.5 + 0.3167654}{2.24611/64.5 + 0.6257119} \]
\[ = 1 - \frac{0.34685}{0.66053} = 1 - 0.52378 = 0.474884 \]

3.2.2 Random Coefficient Models Using nlme

In Chapter 2, we described the random coefficients model in which the impact of the independent variable on the dependent is allowed to vary across the Level 2 effects. In the context of the current research problem, this would mean that we allow the impact of gevocab on geread to vary from one school to another. Incorporating such random coefficient effects
into a multilevel model using \texttt{lme} occurs in the \texttt{random} part of the model syntax. When defining random effects, as mentioned above, 1 stands for the intercept, so that if all we desire is a random intercepts model as in the previous example, the syntax \texttt{-1|school} is sufficient. If, however, we want to allow a Level 1 slope to vary randomly, we will change this part of the syntax (recall that \texttt{gevocab} is already included in the fixed part of the model).

Let us return to the Model 3.1 scenario, but this time allow both the slope and intercept for \texttt{gevocab} to vary randomly from one school to another. The syntax for this model would now become

\begin{verbatim}
Model3.3 <- lme(fixed = geread~gevocab, random = ~gevocab|school, data = Achieve)
\end{verbatim}

This model differs from Model 3.1 only in that the 1 in the random line is replaced by the variable name whose effect we want to be random. Notice that we no longer explicitly state a random intercept in the specification. After a random slope is defined, the random intercept becomes implicit so we no longer need to specify it (i.e., it is included by default). If we do not want the random intercept while modeling the random coefficient, we would include a \texttt{-1} immediately prior to \texttt{gevocab}. The random slope and intercept syntax will generate the following model summary:

\begin{verbatim}
summary(Model3.3)
\end{verbatim}

Linear mixed-effects model fit by REML
Data: Achieve

AIC   BIC   logLik
43004.85 43048.3 -21496.43

Random effects:
Formula: ~gevocab | school
Structure: General positive-definite, Log-Cholesky parametrization
StdDev Corr
(Intercept) 0.5316640 (Intr)
gevocab 0.1389372 -0.858
Residual  1.9146629

Fixed effects: geread ~ gevocab

\begin{verbatim}
Value  Std.Error  DF  t-value  p-value
(Intercept) 2.0057073 0.06108846 10159 32.83283 0
gevocab 0.5203554 0.01441502 10159 36.09815 0
\end{verbatim}

Correlation:

\begin{verbatim}
(Intr)
gevocab -0.866
\end{verbatim}

Standardized Within-Group Residuals:

\begin{verbatim}
 Min Q1  Med Q3  Max
-3.7101835 -0.5674382 -0.2074307 0.3176354 4.6774104
\end{verbatim}
An examination of the results shows that `gevocab` is statistically significantly related to `geread` across schools. The estimated coefficient 0.5203554 corresponds to $\gamma_0$ from Chapter 2, and is interpreted as the average impact of the predictor on the outcome across schools. In addition, the value 0.1389372 represents the estimate of $\tau^2_1$ from Chapter 2, and reflects the variation in coefficients across schools. A relatively larger value of this estimate indicates that the coefficient varies from one school to another; i.e., the relationship of the independent and dependent variables differs across schools. As before, we also have the estimates of $\tau^2_0$ (0.5316640) and $\sigma^2$ (1.9146629). Taken together these results show that the largest source of random variation in `geread` is variation among students within schools, with lesser variation from differences in the conditional mean (intercept) and coefficient for `gevocab` across schools.

A model with two random slopes can be defined in much the same way as defining a single slope. As an example, suppose a researcher is interested in determining whether the age of a student also impacts reading performance, and wants to allow this effect to vary from one school to another. Such incorporation of two random slopes can be modeled as:

```r
Model3.4 <- lme(fixed = geread~gevocab + age,
    random = ~gevocab + age|school, data = Achieve)
```

```
summary(Model3.4)
```

```
Linear mixed-effects model fit by REML
  Data: Achieve
    AIC  BIC logLik
   43015.77 43088.18 -21497.88
Random effects:  
Formula: ~gevocab + age | school
        Structure: General positive-definite, Log-Cholesky parametrization
            StdDev       Corr
(Intercept) 0.492561805 (Intr) gevocb
gevocab     0.137974552 -0.073
age         0.006388612 -0.649 -0.601
Residual    1.914030323

Fixed effects: geread ~gevocab + age
                Value  Std.Error  DF t-value  p-value
(Intercept) 2.9614102 0.4151894 10158  7.13267 0.00000
gevocab     0.5191491 0.0143562 10158 36.16205 0.00000
age        -0.0088390 0.0038396 10158 -2.30208 0.02137

Correlation:
    (Intr) gevocb
gevocab -0.095
age    -0.989 -0.032
```
Here we see that age is significantly related to \( \text{geread} \) \((p = 0.0214)\), with a negative coefficient indicating that older students had lower scores. In addition, the random variance of coefficients for this variable across schools \((0.006388612)\) is much smaller than that of \( \text{gevocab} \) \((0.137974552)\), leading us to conclude that the relationship of vocabulary on reading varies more across schools than does the impact of age.

### 3.2.3 Interactions and Cross-Level Interactions Using `nlme`

Interactions among the predictor variables, particularly cross-level interactions, can be very important in the application of multilevel models. Cross-level interactions occur when the impact of a Level 1 variable on an outcome (e.g., vocabulary score) differs based on the value of the Level 2 predictor (e.g., school enrollment). Interactions, whether within the same level or across levels, are simply the products of two predictors. Thus, incorporation of interactions and cross-level interactions in multilevel modeling is accomplished in much the same manner as we saw for the `lm()` function in Chapter 1. Following are examples for fitting an interaction model for two Level 1 variables (Model 3.5) and a cross-level interaction involving Level 1 and Level 2 variables (Model 3.6).

```r
Model3.5 <- lme(fixed = geread~gevocab + age + gevocab*age,
                random = ~1|school, data = Achieve)
Model3.6 <- lme(fixed = geread~gevocab + senroll +
                gevocab*senroll, random = ~1|school, data = Achieve)
```

Model 3.5 defines a multilevel model in which two Level 1 (student level) predictors interact with each other. Model 3.5 defines a multilevel model with a cross-level interaction in which a Level 1 (student level) and Level 2 (school level) predictor interact. Note that no difference exists in the treatment of variables at different levels when computing interactions.

```r
summary(Model3.5)
```

```
Linear mixed-effects model fit by REML
Data: Achieve
   AIC     BIC   logLik
43155.49 43198.94 -21571.75
```
Random effects:
    Formula: ~1 | school
      (Intercept) Residual
    StdDev:  0.3142524 1.939708

Fixed effects: geread ~ gevocab + age + gevocab * age
                      Value  Std.Error DF  t-value p-value
    (Intercept)   5.187208 0.8667857 10157 5.984418 0.0000
       gevocab  -0.028078 0.1881452 10157 -0.149233 0.8814
         age    -0.029368 0.0080348 10157 -3.655077 0.0003
      gevocab:age  0.005027 0.0017496 10157  2.873204 0.0041

Correlation:

    (Intr)  gevocab    age
gevocab    -0.879
     age    -0.998  0.879
gevocab:age  0.877 -0.999  0.879

Standardized Within-Group Residuals:

                      Min      Q1     Med      Q3      Max
    Standardized Residuals: -3.0635106 -0.5706179 -0.2108349  0.3190991  4.4467448

Number of Observations: 10320
Number of Groups: 160

We can see from the output of Model 3.5 that both age ($t = -3.65, p < 0.01$) and the interaction (gevocab:age) between age and vocabulary ($t = 2.87, p < 0.01$) are significant predictors of reading. Focusing on the interaction, the sign on the coefficient is positive. This indicates an enhancing effect: as age increases, the relationship of reading and vocabulary becomes stronger.

summary(Model3.6)
Linear mixed-effects model fit by REML
  Data: Achieve
  AIC  BIC  logLik
43175.57 43219.02 -21581.79

Random effects:
    Formula: ~1 | school
      (Intercept) Residual
    StdDev:  0.316492 1.940268

Fixed effects: geread ~ gevocab + senroll + gevocab * senroll
                      Value  Std.Error DF  t-value p-value
    (Intercept)  1.7477004 0.17274011 10158 10.117513 0.0000
       gevocab  0.5851202 0.02986497 10158 19.592189 0.0000
        senroll  0.0005121 0.00031863  158  1.607242 0.1100
    gevocab:senroll -0.0001356 0.00005379 10158 -2.519975 0.0118
Correlation:

<table>
<thead>
<tr>
<th></th>
<th>(Intr)</th>
<th>gevocab</th>
<th>senroll</th>
</tr>
</thead>
<tbody>
<tr>
<td>gevocab</td>
<td>-0.782</td>
<td></td>
<td></td>
</tr>
<tr>
<td>senroll</td>
<td>0.958</td>
<td>0.735</td>
<td></td>
</tr>
<tr>
<td>gevocab:senroll</td>
<td>0.752</td>
<td>-0.960</td>
<td>-0.766</td>
</tr>
</tbody>
</table>

Standardized Within-Group Residuals:

<table>
<thead>
<tr>
<th></th>
<th>Min</th>
<th>Q1</th>
<th>Med</th>
<th>Q3</th>
<th>Max</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>-3.1228018</td>
<td>-0.5697103</td>
<td>-0.2090374</td>
<td>0.3187827</td>
<td>4.4358936</td>
</tr>
</tbody>
</table>

Number of Observations: 10320
Number of Groups: 160

The output from Model 3.6 has a similar interpretation. When school enrollment is used instead of age as a predictor, the main effect of vocabulary ($t = 19.59, p < 0.001$) and the interaction between vocabulary and school enrollment ($t = -2.51, p < 0.05$) are significant predictors of reading achievement. Focusing on the interaction, since the sign on the coefficient is negative we would conclude that there is a buffering or inhibitory effect. In other words, as school size increases, the relationship between vocabulary and reading achievement becomes weaker.

### 3.2.4 Centering Predictors

Based on discussions in Chapter 2, it may be advantageous to center predictors, especially when interactions are incorporated. Centering predictors can provide slightly easier interpretation of interaction terms and also help alleviate multicollinearity arising from inclusion of both main effects and interactions in the same model. Recall that centering of a variable entails the subtraction of a mean value from each score in the variable. Centering of predictors can be accomplished through R by the creation of new variables. For example, returning to Model 3.5, grand mean centered `gevocab` and `age` variables can be created with the following syntax:

```r
Cgevocab <- Achieve$gevocab - mean(Achieve$gevocab)
Cage <- Achieve$age - mean(Achieve$age)
```

After mean centered versions of the predictors are created, they can be incorporated into the model in the same manner used earlier.

```r
Model3.5.C <- lme(fixed = geread~Cgevocab + Cage + Cgevocab*Cage,
                  random = ~1|school, data = Achieve)
```

```
summary(Model3.5.C)
Linear mixed-effects model fit by REML
Data: Achieve
AIC     BIC   logLik
43155.49 43198.94 -21571.75
```
Random effects:
Formula: ~ 1 | school
   (Intercept) Residual
StdDev: 0.3142524 1.939708

Fixed effects: geread ~ Cgevocab + Cage + Cgevocab * Cage

<table>
<thead>
<tr>
<th>Value</th>
<th>Std.Error</th>
<th>DF</th>
<th>t-value</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>4.332326</td>
<td>0.03206185</td>
<td>10157</td>
<td>135.12403</td>
</tr>
<tr>
<td>Cgevocab</td>
<td>0.512480</td>
<td>0.00837950</td>
<td>10157</td>
<td>61.15878</td>
</tr>
<tr>
<td>Cage</td>
<td>-0.006777</td>
<td>0.00391727</td>
<td>10157</td>
<td>-1.72999</td>
</tr>
<tr>
<td>Cgevocab:Cage</td>
<td>0.005027</td>
<td>0.00174965</td>
<td>10157</td>
<td>2.87320</td>
</tr>
</tbody>
</table>

Correlation:

<table>
<thead>
<tr>
<th></th>
<th>(Intr)</th>
<th>Cgevcb</th>
<th>Cage</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cgevocab</td>
<td>0.008</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Cage</td>
<td>0.007</td>
<td>0.053</td>
<td></td>
</tr>
<tr>
<td>Cgevocab:Cage</td>
<td>0.043</td>
<td>0.021</td>
<td>0.205</td>
</tr>
</tbody>
</table>

Standardized Within-Group Residuals:

<table>
<thead>
<tr>
<th>Min</th>
<th>Q1</th>
<th>Med</th>
<th>Q3</th>
<th>Max</th>
</tr>
</thead>
<tbody>
<tr>
<td>-3.0635106</td>
<td>-0.5706179</td>
<td>-0.2108349</td>
<td>0.3190991</td>
<td>4.4467448</td>
</tr>
</tbody>
</table>

Number of Observations: 10320
Number of Groups: 160

First, notice the identical model fit (compare AIC, BIC, and log likelihood) of the centered and uncentered models. This is a good way to ensure that centering worked. Looking now to the fixed effects of the model, we see some changes in their interpretation. These differences are likely due to multicollinearity issues in the original uncentered model. The interaction is still significant (t = 2.87, p < 0.05) but we now see a significant effect of vocabulary (t = 61.15, p < 0.01). Age is no longer a significant predictor (t = -1.73 p > 0.05). Focusing on the interaction, recall that when predictors are centered, an interaction can be interpreted as the effect of one variable while holding the second variable constant. Since the sign on the interaction is positive, vocabulary has a positive impact on reading ability if we hold age constant.

---

### 3.3 The lme4 Package

#### 3.3.1 Random Intercept Models Using lme4

The previous discussion focused on using the lme function from the nlme library to fit multilevel models in R. As noted previously in this chapter, a second function for fitting such models, called lme4, is available in the lmer library. We will see that in some ways the syntax and output from these two functions are virtually identical. However, they exhibit some fundamental
differences that we must consider as we apply them. We will focus on some of these differences and their implications for practice. In particular, the \texttt{lme4} package offers a slightly more streamlined syntax for fitting multilevel models. It also provides a more flexible framework for definition of complex models. In \texttt{lme4}, we would fit Model 3.1 using the following syntax:

\begin{verbatim}
Model3.7 <- lmer(geread~gevocab +(1|school), data = Achieve)
\end{verbatim}

The model is defined in much the same way as we defined the \texttt{lme} function, where the outcome variable is the sum or linear combination of all of the random and fixed effects. The only difference in treatment of fixed and random effects is that the random effects require information on the nesting structure (students within schools in this case) for the parameter within which they vary. The primary difference in model syntax between \texttt{lme} and \texttt{lmer} is that the random effect is denoted by its appearance within parentheses rather than through explicit assignment using the \texttt{random} statement. This syntax will yield the following output:

\begin{verbatim}
Model3.7
Linear mixed model fit by REML
Formula: geread ~ gevocab + (1 | school)
   Data: Achieve
  AIC BIC logLik deviance REMLdev
43145 43174 -21569 43124 43137
Random effects:
 Groups     Name         Variance  Std.Dev.
school   (Intercept) 0.0997790  0.31588
Residual              3.766470  1.94074
Number of obs: 10320, groups: school, 160
Fixed effects:
            Estimate Std. Error   t value
(Intercept)  2.023343  0.049305   41.04
gevocab      0.512901  0.008373   61.26
Correlation of Fixed Effects:
            (Intr)
gevocab -0.758
\end{verbatim}

From this output we can see one obvious benefit of the \texttt{lme4} package is that all important information is presented without requiring the use of a \texttt{summary} statement. The function call alone is enough to provide model fit statistics, parameter estimates, parameter significance tests, parameter estimate correlations, residuals, and sample summaries. We can also see that the \texttt{lme4} package includes deviance and \texttt{REML} estimated deviance values in the model fit statistics in addition to the AIC, BIC, and log likelihood reported in the \texttt{nlme} package. What the \texttt{lme4} package does not include are \textit{p} values for model coefficients.
In comparing the outputs of \texttt{lme} and \texttt{lmer}, we notice that while both \textit{t} values and accompanying \textit{p} values are reported in the \texttt{nlme} package, only the \textit{t} values for fixed effects are reported in \texttt{lme4}. The reason for this discrepancy in the reported results, and specifically for the lack of \textit{p} values is somewhat complex and is not within the scope of this book. However, we should note that the standard approach for finding \textit{p} values based on using the reference \textit{t} distribution, which would seem to be the intuitively correct step, does in fact not yield correct values in many cases. Therefore, some alternative approach for obtaining them is necessary.

Douglas Bates, the developer of \texttt{lme4}, recommends the use of Markov chain Monte Carlo (MCMC) methods to obtain \textit{p} values for mixed model effects. We review MCMC in greater detail in Chapter 9 so that readers may gain an understanding of how this method works. We can say at this point that the computer-intensive MCMC approach relies on generating a posterior distribution for each model parameter, then using the distributions to obtain \textit{p} values and confidence intervals for each parameter estimate. To obtain MCMC \textit{p} values and confidence intervals for \texttt{lme} objects, we must install the \texttt{coda} and \texttt{languageR} packages and then use the following command sequence to obtain the desired statistics for Model 3.7.

\begin{verbatim}
library(coda)
library(languageR)
Model3.7.pvals<-pvals.fnc(Model3.7, nsim = 10000, withMCMC = TRUE)
\end{verbatim}

These commands first load the two libraries we need. We then create an object that contains the \textit{p} values and confidence intervals for the various terms in Model 3.7 in the object \texttt{Model3.7.pvals}. The actual function that we use is \texttt{pvals.fnc}, which is part of the \texttt{languageR} library. In turn, this function calls the \texttt{mcmcsamp} function from the \texttt{coda} library. Three elements are included in this function call, including the name of the \texttt{lmer} object that contains the model fit results (\texttt{Model3.7}), the number of simulated data sets we want to sample by using MCMC (\texttt{nsim}), and whether we want results of each of these 10000 MCMC draws to be saved (\texttt{withMCMC = TRUE}). Setting this last condition to \texttt{TRUE} is not necessary, as we are interested only in summary statistics. We can obtain the relevant information for the fixed and random portions of the model by typing the following commands.

\begin{verbatim}
Model3.7.pvals$fixed
\end{verbatim}

\begin{verbatim}
  Estimate MCMCmean HPD95lower HPD95upper  pMCMC  Pr(>|t|)
(Intercept)  2.0233  2.0218   1.9243    2.1180   0.0001    0
gevocab  0.5129  0.5134   0.4966    0.5300   0.0001    0
\end{verbatim}
From these results, we can determine that the vocabulary score was statistically significantly related to the reading score, and that the random effects school and Residual, were both different from 0 as well, since neither of their confidence intervals included 0.

Returning to model definition using `lmer()`, multiple predictors at any level and interactions between predictors at any level are again entered in the model in the same manner as using the `lm()` or `lme()` functions. The following is the syntax for fitting Model 3.8 using `lmer`.

```
Model3.8 <- lmer(geread ~ gevocab + senroll + (1|school), data = Achieve)
```

Fixed effects:

```
  Estimate Std. Error t value
(Intercept)  2.0748764  0.1139915  18.20
gevocab      0.5128742  0.0083733  61.25
senroll     -0.0001026  0.0002051  -0.50
```

Correlation of Fixed Effects:

```
  (Intr) gevocab
gevocab  -0.327
senroll -0.901 -0.002
```

```
Model3.8.pvals$fixed
```

| Estimate | MCMCmean | HPD95lower | HPD95upper | pMCMC | Pr(>|t|) |
|----------|----------|------------|------------|-------|----------|
| (Intercept) | 2.0749 | 2.0752 | 1.8493 | 2.2950 | 0.0001 | 0.0000 |
| gevocab   | 0.5129 | 0.5133 | 0.4970 | 0.5295 | 0.0001 | 0.0000 |
| senroll   | -0.0001 | -0.0001 | -0.0005 | 0.0003 | 0.5960 | 0.6169 |
Model3.8.pvals$random

<table>
<thead>
<tr>
<th>Groups</th>
<th>Name</th>
<th>Std.Dev.</th>
<th>MCMCmedian</th>
<th>MCMCmean</th>
<th>HPD95lower</th>
<th>HPD95upper</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 school</td>
<td>(Intercept)</td>
<td>0.3168</td>
<td>0.3076</td>
<td>0.3085</td>
<td>0.2501</td>
<td>0.3633</td>
</tr>
<tr>
<td>2 Residual</td>
<td></td>
<td>1.9408</td>
<td>1.9415</td>
<td>1.9415</td>
<td>1.9140</td>
<td>1.9673</td>
</tr>
</tbody>
</table>

### 3.3.2 Random Coefficient Models Using lme4

The definition of random effects for slopes in lme4 is very similar to that in nlme. The only real difference is that again, as in the random intercepts model, the random effects are defined in parentheses as a linear combination of effects. Returning to Model 3.3, we may express the same multilevel model using lmer as:

Model3.9 <- lmer(geread ~ gevocab + (gevocab | school), data = Achieve)

Linear mixed model fit by REML
Formula: geread ~ gevocab + (gevocab | school)
Data: Achieve
AIC  BIC logLik deviance REMLdev
43005 43048 -21496 42981 42993

Random effects:
<table>
<thead>
<tr>
<th>Groups</th>
<th>Name</th>
<th>Variance</th>
<th>Std.Dev.</th>
<th>Corr</th>
</tr>
</thead>
<tbody>
<tr>
<td>school</td>
<td>(Intercept)</td>
<td>0.282692</td>
<td>0.53169</td>
<td>-0.859</td>
</tr>
<tr>
<td></td>
<td>gevocab</td>
<td>0.019305</td>
<td>0.13894</td>
<td>-0.859</td>
</tr>
<tr>
<td>Residual</td>
<td></td>
<td>3.665937</td>
<td>1.91466</td>
<td></td>
</tr>
</tbody>
</table>

Number of obs: 10320, groups: school, 160

Fixed effects:
<table>
<thead>
<tr>
<th>Estimate</th>
<th>Std. Error</th>
<th>t value</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>2.00570</td>
<td>0.06109</td>
</tr>
<tr>
<td>gevocab</td>
<td>0.52036</td>
<td>0.01442</td>
</tr>
</tbody>
</table>

Correlation of Fixed Effects:

(Intr)
gevocab  -0.867

We must note here that the MCMC approach for obtaining hypothesis test results for models estimated using lmer is not currently available for random coefficient models.

Although, for the most part, the syntax of lme4 is fairly similar to that of lme for relatively simple models, incorporating multiple random slopes into multilevel models using lme4 is somewhat different. The random effects discussed for the nlme package assume correlated or nested levels. Random effects in lme4 may be either correlated or uncorrelated. In this respect, lme4 provides greater modeling flexibility. This difference in model specification
is communicated through a different model syntax. As an example, refer to Models 3.10 and 3.11, each of which has the same fixed and random effects. However, the random slopes in Model 3.10 are treated as correlated with one another; in Model 3.11, they are specified as uncorrelated. This lack of correlation in Model 3.11 is expressed by having separate random effect terms (gevocab|school) and (age|school). In contrast, Model 3.10 includes both random effects in a single term (gevocab + age|school).

Model 3.10

```
Model3.10 <- lmer(geread~gevocab + age+(gevocab + age|school), Achieve)
```

Model 3.11

```
Model3.11 <- lmer(geread~gevocab + age+ (gevocab|school) + age|school), Achieve)
```

```
Model3.10
Linear mixed model fit by REML
Formula: geread ~ gevocab + age + (gevocab + age | school)
Data: Achieve

AIC BIC logLik deviance REMLdev
43015 43088 -21498 42974 42995

Random effects:
Groups Name Variance Std.Dev. Corr
school (Intercept) 1.8361e-02 0.135503
gevocab 1.9026e-02 0.137936 0.465
age 2.4641e-05 0.004964 -0.197 -0.960
Residual 3.6641e+00 1.914182

Number of obs: 10320, groups: school, 160

Fixed effects:
Estimate Std. Error t value
(Intercept) 2.965272 0.413052 7.18
gevocab 0.519278 0.014351 36.18
age -0.008881 0.003822 -2.32

Correlation of Fixed Effects:
(Intr) gevocb
gevocab -0.081
age -0.989 -0.047

Model 3.11

```
```
Linear mixed model fit by REML
Formula: geread ~ gevocab + age + (gevocab | school) + (age | school)
Data: Achieve

AIC BIC logLik deviance REMLdev
43017 43089 -21498 42975 42997

Random effects:
Groups Name Variance Std.Dev. Corr
school (Intercept) 2.1436e-01 0.46299441
gevocab 1.9194e-02 0.13854364 -0.976

Model3.11 <- lmer(geread~gevocab + age+ (gevocab|school) + age|school), Achieve)
Fitting Two-Level Models in R

<table>
<thead>
<tr>
<th></th>
<th>Estimate</th>
<th>Std. Error</th>
<th>t value</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>2.973619</td>
<td>0.414551</td>
<td>7.17</td>
</tr>
<tr>
<td>gevocab</td>
<td>0.519191</td>
<td>0.014397</td>
<td>36.06</td>
</tr>
<tr>
<td>age</td>
<td>-0.008956</td>
<td>0.003798</td>
<td>-2.36</td>
</tr>
</tbody>
</table>

Correlation of Fixed Effects:

<table>
<thead>
<tr>
<th></th>
<th>gevocab</th>
<th>age</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intr)</td>
<td>-0.159</td>
<td>-0.989</td>
</tr>
<tr>
<td>gevocab</td>
<td></td>
<td>0.033</td>
</tr>
<tr>
<td>age</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Notice the difference in how random effects are expressed in \texttt{lmer} between Models 3.10 and 3.11. Output in Model 3.10 provides identical estimates to those of the \texttt{nlme} Model 3.4. With random effects, R reports estimates for the variability of the random intercept, variability for each random slope, and the correlations between the random intercept and random slopes. Output in Model 3.11, however, reports two different sets of uncorrelated random effects.

The first set reports variability for the random intercept and variability for the random slope for vocabulary and correlation between the random intercept and random slope for vocabulary. The second set of random effects reports variability of a second random intercept, variability in the random slope for age, and the correlation between the random intercept and the random slope for age. The random slope for vocabulary and the random slope for age are not allowed to correlate. Finally, we can obtain \( p \) values and confidence intervals for each model term using the \texttt{pvals.fnc} function based on the MCMC approach reviewed earlier in this chapter.

3.4 Additional Options

R provides several additional options for applying multilevel models through both the \texttt{nlme} and \texttt{lme4} packages.

3.4.1 Parameter Estimation Method

Both \texttt{nlme} and \texttt{lme4} by default use restricted maximum likelihood (REML) estimation. However, each package also allows use of maximum likelihood (ML) estimation instead. Model 3.12 demonstrates syntax for fitting a multilevel model using ML in the \texttt{nlme} package. To change the estimation
method in nlme, the call is method = "ML". Model 3.13 depicts fitting of the same multilevel model using the lme4 package. The call to designate the use of the ML to be used is REML = FALSE.

Model3.12 <- lme(fixed = geread~gevocab, random = ~1|school,  
    data = Achieve, method = "ML")

Model3.13 <- lmer(geread~gevocab + (1|school), data = Achieve,  
    REML = FALSE)

### 3.4.2 Estimation Controls

Sometimes a correctly specified model will not reach a solution (converge) in the default settings for model convergence. This problem often can be fixed by changing the default estimation controls using the control option. Convergence issues can be fixed frequently by changing the model iteration limit (maxIter) or by changing the model optimizer (opt). To specify which controls will be changed, R must be given a list of controls and their new values. For example, control = list(maxIter = 100, opt = "optim") will change the maximum number of iterations to 100 and the optimizer to optim. These control options are placed in the R code in the same manner as choice of estimation method (separated from the rest of the syntax by a comma). They are the same for both the nlme and lme4 packages. See Models 3.14 and 3.15 below. A comprehensive list of estimation controls can be found on the R help ?lme and ?lme4 pages.

Model3.14 <- lme(fixed = geread~gevocab, random = ~1|school,  
    data = Achieve, method = "ML", control =  
    list(maxIter = 100, opt = "optim"))

Model3.15 <- lmer(geread~gevocab + (1|school), data = Achieve,  
    REML = FALSE, control = list(maxIter = 100,  
    opt = "optim"))

### 3.4.3 Chi Square Test for Comparing Model Fit

We previously explained how the fits of various models can be compared using the AIC and BIC information indices. However, these statistics are descriptive in nature so that no hypotheses about relative model fit can be tested formally. Thus, if the AIC for one model is 1000.5 and 999 for another models, we cannot know whether the apparently small difference in fit within the sample is truly representative of a difference in fit in the general population. Therefore, when we work with nested models and one model is a more constrained (i.e., simpler) version of another, we may wish to test whether overall fit of the two models differs. Such hypothesis testing is possible using the chi-square difference test based on the deviance statistic. When the fits of nested models are compared, the difference in chi-square
values for each model deviance can be used to compare model fit. After each of the models in question has been fit, the difference in chi-square values can be obtained using the \texttt{anova()} function call.

For models run using the \texttt{nlme} package, the \texttt{anova()} command will provide accurate comparisons only if maximum likelihood estimation is used. For models run using \texttt{lme4}, the \texttt{anova()} command will work for both maximum likelihood and restricted maximum likelihood. When maximum likelihood is used, both fixed and random effects are compared simultaneously. When restricted maximum likelihood is used, only random effects are compared. The following is an example of comparing fit with the chi-square difference statistic for Models 3.1 and 3.2 that were discussed in detail above.

\begin{verbatim}
Model3.1 <- lme(fixed = geread~gevocab, random = ~1|school, 
data = Achieve, method = "ML")
Model3.2 <- lme(fixed = geread~gevocab + senroll, random = 
~1|school, data = Achieve, method = "ML")
anova(Model3.1, Model3.2)
\end{verbatim}

\begin{verbatim}
Model3.1 1 4 43132.43 43161.40 -21562.22
Model3.2 2 5 43134.18 43170.39 -21562.09 1 vs 2 0.2550617
\end{verbatim}

3.4.4 Confidence Intervals for Parameter Estimates

Readers who are familiar with multilevel modeling may have noticed that neither \texttt{nlme} nor \texttt{lme4} output provides statistical significance tests for the variance of random effects. As outlined in Chapter 2, statistical significance of random effects provides very useful information about the variability of the clusters under study. Using the example from this chapter, the significance of the random intercept indicates variations in reading ability among schools in the sample; i.e., different schools exhibit significantly different mean reading scores. Similarly, a significant random slope for vocabulary would indicate significant variation in the impact of vocabulary on reading ability across the schools. This is often very useful information by providing insights into the factors that contribute to score differences. However, the current packages do not provide an option for testing the significance of random effects.

It is still possible, however, to obtain information about significance of random effects by creating confidence intervals. With the \texttt{nlme} package, the function call \texttt{intervals()} can be used to generate 95% confidence intervals for the fixed effects and the variances of the random effects. The confidence intervals obtained for the variances of the random effects can
be used to determine the significance of the random effects. For example, returning to Model 3.3 covered earlier in this chapter, we determined that vocabulary was a significant predictor of reading ability. However, we could not determine from the output of Model 3.3 whether the variability in the random intercept or random slope was significantly different from 0. If not different, the result would indicate that the mean reading achievement and/or the relationship of vocabulary score to reading achievement did not differ across schools. To determine the significance of the random effects we can use the `intervals()` function call.

```
intervals(Model3.3)
```

Approximate 95% confidence intervals

**Fixed effects:**

<table>
<thead>
<tr>
<th>Effect</th>
<th>lower est. upper</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>1.8859621 2.0057064 2.1254506</td>
</tr>
<tr>
<td>gevocab</td>
<td>0.4920982 0.5203554 0.5486126</td>
</tr>
</tbody>
</table>

**Random Effects:**

**Level: school**

<table>
<thead>
<tr>
<th>Effect</th>
<th>lower est. upper</th>
</tr>
</thead>
<tbody>
<tr>
<td>sd((Intercept))</td>
<td>0.4250700 0.5316531 0.6649611</td>
</tr>
<tr>
<td>sd(gevocab)</td>
<td>0.1153701 0.1389443 0.1673356</td>
</tr>
<tr>
<td>cor((Intercept),gevocab)</td>
<td>-0.9178709 -0.8585096 -0.7615768</td>
</tr>
</tbody>
</table>

**Within-group standard error:**

<table>
<thead>
<tr>
<th>lower est. upper</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.888327 1.914663 1.941365</td>
</tr>
</tbody>
</table>

For the intercept, the 95% confidence interval lies between 0.425 and 0.665. Thus, we are 95% confident that the actual variance component for the intercept was between these two values. Likewise, the 95% confidence interval for the random slope variance was between 0.115 and 0.167. From these values, we can see that 0 did not lie in the interval for either random effect, intercept, or slope. Thus, we can conclude that both the random intercept and random slope were significantly different from 0.

---

**Summary**

This chapter put to work the concepts learned in Chapter 2 to work using R. We learned the basics of fitting two-level models when a dependent variable is continuous using the `lme` and `lmer` packages. Within this multilevel
framework, we learned how to fit the null, random intercept, and random slopes models. We also covered independent variables at both levels of data and learned how to compare the fits of models with one another. This last point will prove particularly useful as we engage in the process of selecting the most parsimonious (simplest) model that also explains the dependent variable adequately. Of greatest import in this chapter, however, is the ability to fit multilevel models using both \texttt{lme} and \texttt{lme4} in R and correctly interpreting the resultant output. If you have mastered those skills, you are ready to move to Chapter 4, where we extend the model to include a third level in the hierarchy. As we will see, the actual fitting of three-level models is very similar to fitting two-level models studied in the chapter.
Chapters 2 and 3 introduced the multilevel modeling framework and demonstrated the use of the \texttt{nlme} and \texttt{lme4} R packages in fitting two-level models. In Chapter 4, we will expand upon this basic two-level framework by fitting models with additional levels of data structure. As described in Chapter 2, it is conceivable for a Level 1 unit such as student to be nested in higher level units such as classroom. Thus, in keeping with our examples, we may assume that at least a portion of a student’s performance on a reading test is due to the classroom in which he or she learns. Each classroom may have a unique learning context that may contribute to student performance, for example, the quality of the teacher, the presence of disruptive students, and time of day when students are in the class, among others. Furthermore, as we saw in the earlier chapters, the impacts of fixed effects on a dependent variable can vary among Level 2 units, resulting in a random slope model.

We will see that it is possible to estimate models with three or more levels of a nested structure using R and learn that the R commands for defining and fitting these models are very similar to those used in the two-level case. Within the \texttt{nlme} and \texttt{lme4} packages, the same function calls that we used for two-level models can be used to define models with three or more levels:

\begin{verbatim}
  lme(fixed, data, random, correlation, weights, subset, method, 
      na.action, control, contrasts = NULL, keep.data = TRUE)
\end{verbatim}

\begin{verbatim}
  lmer(formula, data, family = NULL, REML = TRUE, 
       control = list(), start = NULL, verbose = FALSE, 
       doFit = TRUE, subset, weights, na.action, offset, 
       contrasts = NULL, model = TRUE, x = TRUE,...)
\end{verbatim}

In this chapter, we will continue working with the data described in Chapter 3. The examples in that chapter included two levels of data structures (students within schools and associated predictors of reading achievement at each level). We will now add a third level of structure, the classroom, which is nested within schools. In this context, \textit{nested} simply means that students within a classroom all attend the same school. Thus, students are nested within classrooms that in turn are nested within schools.
4.1 The \texttt{nlme} Package

4.1.1 Simple Three-Level Models

The R syntax for defining and fitting models incorporating more than two levels of data structures is very similar to that for two-level models that we have already seen. We begin by defining a null model for prediction of student reading achievement in which regressors may include student-level characteristics, classroom-level characteristics, and school-level characteristics. The syntax to fit a three-level null model appears below with the results stored in the object \texttt{Model4.1}.

\begin{verbatim}
Model4.1 <- lme(fixed = geread~1, random = ~1|school/class, 
data = Achieve)
\end{verbatim}

We can see that the syntax for fitting a random intercepts model with three levels is very similar to that for the same model with two levels. To define a model with more than two levels, we must include the variables denoting the higher levels of the nesting structures: \texttt{school} (school-level influence) and \texttt{class} (classroom-level influence) and designate the nesting structure of the levels (students within classrooms within schools). The nested structure in \texttt{lme} is defined as \texttt{A/B} where \texttt{A} is the higher level data unit (e.g., school) and \texttt{B} is the lower unit (e.g., classroom). To view the resulting output, we use the \texttt{summary} command on the fitted model object, as done in previous chapters.

\begin{verbatim}
summary(Model4.1)
\end{verbatim}

\textbf{Linear mixed-effects model fit by REML}
\begin{verbatim}
Data: Achieve
  AIC   BIC  logLik
46154 46182.97 -23073
\end{verbatim}

\textbf{Random effects:}
\begin{verbatim}
Formula: ~1 | school
  (Intercept)  StdDev: 0.558397

Formula: ~1 | class %in% school
  (Intercept) Residual
  StdDev: 0.5221697 2.201589
\end{verbatim}

\textbf{Fixed effects:}
\begin{verbatim}
geread ~ 1

Value  Std.Error  DF  t-value  p-value
(Intercept) 4.308059 0.05499197 9752 78.33979 0
\end{verbatim}

\textbf{Standardized Within-Group Residuals:}
\begin{verbatim}
    Min      Q1    Med      Q3      Max
-2.305201 -0.6289598 -0.2093700 0.3049100 3.8673251
\end{verbatim}
Number of Observations: 10320
Number of Groups:

\[
\text{school class } \%in\% \text{ school}
\]
\[
160 \quad 568
\]

As this is a random intercept-only model, there is not much interpretation required beyond model fit (AIC, BIC, and log likelihood). However, some pieces of information should be noted. For example, we see two different sets of random effects: (1) random effects for \( -1|\text{school} \) to model the intercept to vary across schools and (2) random effects for \( -1|\text{class } \%in\% \text{ school} \) to model the intercept to vary across classrooms within schools. Remember from our discussion in Chapter 2 that we can also interpret these random intercepts as means of the dependent variable (reading) varying across levels of the random effects (classrooms and schools). We should also note that at the end of the output, R summarizes the sample size for each of the higher level units. This is a good place to check to ensure that a model is defined properly and that appropriate data are used. For example, multiple classrooms exist within each school, so it makes sense to have a smaller number of schools (\( \text{school} = 160 \)) and a larger number of classrooms (\( \text{class } \%in\% \text{ school} = 568 \)).

Finally, we can use the `intervals` function component of the `nlme` library to obtain confidence intervals for our random effects.

```r
intervals(Model4.1)
```

**Approximate 95% confidence intervals**

**Fixed effects:**

<table>
<thead>
<tr>
<th></th>
<th>lower</th>
<th>est.</th>
<th>upper</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>4.200265</td>
<td>4.30806</td>
<td>4.415855</td>
</tr>
</tbody>
</table>

attr(, "label")

[1] "Fixed effects:"]

**Random Effects:**

**Level: school**

<table>
<thead>
<tr>
<th></th>
<th>lower</th>
<th>est.</th>
<th>upper</th>
</tr>
</thead>
<tbody>
<tr>
<td>sd((Intercept))</td>
<td>0.4702517</td>
<td>0.5583923</td>
<td>0.6630533</td>
</tr>
</tbody>
</table>

**Level: class**

<table>
<thead>
<tr>
<th></th>
<th>lower</th>
<th>est.</th>
<th>upper</th>
</tr>
</thead>
<tbody>
<tr>
<td>sd((Intercept))</td>
<td>0.4545912</td>
<td>0.5221676</td>
<td>0.5997895</td>
</tr>
</tbody>
</table>

**Within-group standard error:**

<table>
<thead>
<tr>
<th></th>
<th>lower</th>
<th>est.</th>
<th>upper</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>2.170908</td>
<td>2.201589</td>
<td>2.232704</td>
</tr>
</tbody>
</table>

Based on these intervals, we can infer, for example, that the school a student attends has an impact on his or her reading score because the 95% confidence interval for the standard deviation does not include 0. We would reach
a similar inference for a classroom nested within a school, because again, the
95% confidence interval does not include 0.

Since we now know how to define a higher level data structure, we can add
predictors to the fixed portion of a multilevel model with three or more levels
in exactly the same manner as for a two-level model. For example, we may wish
to extend the intercept-only model described above to include several inde-
pendent variables such as a student’s vocabulary test score (gevocab), the size
of the reading classroom (clenroll), and the size of the school (cenroll). In
lme, the R command for fitting this model and viewing the resultant output is

Model4.2 <- lme(fixed = geread~gevocab+clenroll+cenroll,
     random = ~1|school/class, data = Achieve)

summary(Model4.2)

Linear mixed-effects model fit by REML
Data: Achieve
   AIC      BIC   logLik
43144.87 43195.56  -21565.43

Random effects:
   Formula: ~1 | school
         (Intercept)
StdDev: 0.2766194

   Formula: ~1 | class %in% school
         (Intercept) Residual
StdDev: 0.3007871 1.922991

Fixed effects: geread ~ gevocab + clenroll + cenroll
                     Value     Std.Error    DF     t-value     p-value
(Intercept)          1.6751266  0.20809604 9751    8.04978  0.0000000
gevocab              0.5075566  0.00842654 9751   60.23313  0.0000000
clenroll             0.0189860  0.00955860  407    1.98628  0.0477175
cenroll              -0.0000037  0.00000364 158   -1.02193  0.3084245

Correlation:
                (Intr) gevocb clenroll
gevocab -0.124
clenroll -0.961 -0.062
cenroll -0.134  0.025 -0.007

Standardized Within-Group Residuals:
          Min          Q1         Med          Q3         Max
-3.2211629 -0.5672782 -0.2079045  0.3183508  4.4736276

Number of Observations: 10320
Number of Groups:
  school class %in% school
     160           568
When interpreting the output, we first want to ascertain whether including the predictor variables generates a better fitting model. As we saw in Chapter 3, we can compare models by examining the AIC and BIC values for each variable (lower values indicate better fit). For the original null model, these values were 46154 and 46182.97, respectively, which are both larger than the AIC and BIC for Model 4.2. Therefore, we would conclude that this latter model including a single predictor variable at each level provides better fit to the data, and thus is preferable to the null model with no predictors.

We can see from the output for Model 4.2 that a student’s vocabulary score ($t = 60.23, p < 0.001$), and classroom size ($t = 1.99, p < 0.05$) are statistically significantly positive predictors of student reading achievement score, but the size of the school ($t = -1.02, p = 0.308$) does not significantly predict reading achievement.

As a side note, the significant positive relationship between classroom size and reading achievement may seem a bit confusing, suggesting that students in larger classrooms achieved higher reading achievement test scores. However, in this case larger classrooms very frequently included multiple teacher’s aides, so that the actual adult-to-student ratio may have been lower than results for classrooms with fewer students. In addition, estimates for the random intercepts of classroom nested in school and school decreased in value from those of the null model, suggesting that when we account for the three fixed effects, some of the mean differences between schools and between classrooms are accounted for. Using the intervals command, we can obtain confidence intervals for both the fixed and random effects in the model as shown below.

Approximate 95% confidence intervals

<table>
<thead>
<tr>
<th>Fixed effects:</th>
<th>lower</th>
<th>est.</th>
<th>upper</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>1.267215e+00</td>
<td>1.675127e+00</td>
<td>2.083038e+00</td>
</tr>
<tr>
<td>gevocab</td>
<td>4.910389e-01</td>
<td>5.075566e-01</td>
<td>5.240744e-01</td>
</tr>
<tr>
<td>clanroll</td>
<td>1.956547e-04</td>
<td>1.898604e-02</td>
<td>3.777642e-02</td>
</tr>
<tr>
<td>cenroll</td>
<td>-1.091387e-05</td>
<td>-3.721429e-06</td>
<td>3.471016e-06</td>
</tr>
</tbody>
</table>

attr(,”label”)
[1] ”Fixed effects:"

<table>
<thead>
<tr>
<th>Random Effects: Level: school</th>
<th>lower</th>
<th>est.</th>
<th>upper</th>
</tr>
</thead>
<tbody>
<tr>
<td>sd((Intercept))</td>
<td>0.2173971</td>
<td>0.2766194</td>
<td>0.3519749</td>
</tr>
<tr>
<td>Level: class</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>sd((Intercept))</td>
<td>0.2409209</td>
<td>0.3007871</td>
<td>0.3755294</td>
</tr>
</tbody>
</table>

Within-group standard error:

<table>
<thead>
<tr>
<th>lower</th>
<th>est.</th>
<th>upper</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.896210</td>
<td>1.922991</td>
<td>1.950151</td>
</tr>
</tbody>
</table>
In terms of the fixed effects, the 95% confidence intervals demonstrate that vocabulary score and class size are statistically significant predictors of reading scores, but school size is not. In addition, we see that although the variation in random intercepts for schools and classrooms nested in schools declined with the inclusion of the fixed effects, we still conclude that the random intercept terms are different from 0 in the population, indicating that mean reading scores differ across schools and across classrooms nested within schools.

The \( R^2 \) value for Model 4.2 can be calculated as

\[
R^2_1 = 1 - \frac{\sigma^2_{M1} + \tau^2_{M1}}{\sigma^2_{M0} + \tau^2_{M0}}
\]

\[
= 1 - \frac{1.922991 + 0.3007871}{2.201589 + 0.5221697}
\]

\[
= 1 - \frac{2.2237781}{2.7237587} = 1 - 0.81643726 = 0.1835628
\]

From this value, we see that inclusion of the classroom and school enrollment variables along with student vocabulary scores results in a model that explains approximately 18% of the variance in the reading score above and beyond the null model.

Using \texttt{lme}, it is very easy to include both single-level and cross-level interactions of a model if the higher level structure is understood. For example, we may have a hypothesis stating that the impact of vocabulary score on reading achievement varies based on the size of the school that a student attends. To test this hypothesis, we must include the interaction between vocabulary score and size of the school, as in Model 4.3 below.

\[
\text{Model4.3} \leftarrow \text{lme} (\text{fixed} = \text{geread} \sim \text{gevocab} + \text{clenroll} + \text{cenroll} + \text{gevocab} \times \text{cenroll}, \text{random} = \sim 1 | \text{school/class}, \text{data} = \text{Achieve})
\]

\[
\text{summary(model4.3)}
\]

Linear mixed-effects model fit by REML
Data: Achieve

AIC  BIC  logLik
43167.75 43225.69  -21575.88

Random effects:
Formula: ~1 | school
  (Intercept)
StdDev: 0.274096

Formula: ~1 | class %in% school
  (Intercept) Residual
StdDev: 0.2975919  1.923059
Fixed effects: gread ~ gevocab + clenroll + cenroll + gevocab * cenroll

<table>
<thead>
<tr>
<th></th>
<th>Value</th>
<th>Std.Error</th>
<th>DF</th>
<th>t-value</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>1.7515</td>
<td>0.2099</td>
<td>9750</td>
<td>8.3409</td>
<td>0.0000</td>
</tr>
<tr>
<td>gevocab</td>
<td>0.4899</td>
<td>0.0117</td>
<td>9750</td>
<td>41.9401</td>
<td>0.0000</td>
</tr>
<tr>
<td>clenroll</td>
<td>0.0188</td>
<td>0.0095</td>
<td>407</td>
<td>1.9766</td>
<td>0.0488</td>
</tr>
<tr>
<td>cenroll</td>
<td>-0.0000132</td>
<td>0.00000563</td>
<td>158</td>
<td>-2.3372</td>
<td>0.0207</td>
</tr>
<tr>
<td>gevocab:cenroll</td>
<td>0.0000023</td>
<td>0.00000107</td>
<td>9750</td>
<td>2.1896</td>
<td>0.0286</td>
</tr>
</tbody>
</table>

Correlation:

<table>
<thead>
<tr>
<th></th>
<th>(Intr)</th>
<th>gevocb</th>
<th>clnrll</th>
<th>cenrl1</th>
</tr>
</thead>
<tbody>
<tr>
<td>gevocb</td>
<td>-0.203</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>clenroll</td>
<td>-0.949</td>
<td>-0.041</td>
<td></td>
<td></td>
</tr>
<tr>
<td>cenroll</td>
<td>-0.212</td>
<td>0.542</td>
<td>0.000</td>
<td></td>
</tr>
<tr>
<td>gevocab:cenroll</td>
<td>0.166</td>
<td>-0.693</td>
<td>-0.007</td>
<td>-0.766</td>
</tr>
</tbody>
</table>

Standardized Within-Group Residuals:

<table>
<thead>
<tr>
<th></th>
<th>Min</th>
<th>Q1</th>
<th>Med</th>
<th>Q3</th>
<th>Max</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>-3.1901</td>
<td>-0.5682</td>
<td>-0.2060</td>
<td>0.3183</td>
<td>4.4723</td>
</tr>
</tbody>
</table>

Number of Observations: 10320
Number of Groups: 160 568

In this example we can see that other than including a higher level nesting structure in the random effects line, defining a cross-level interaction in a model with more than two levels is no different from the approach for two-level models covered in Chapter 3. The first result we seek is whether or not the model including the interaction provides better fit to the data than Model 4.2 with no interaction. Again, we will make this decision based on the AIC and BIC values.

Because these information indices are larger for Model 4.3, we conclude that including the interaction of vocabulary score and school size does not yield a better fitting model. In terms of hypothesis testing results, student vocabulary ($t = 41.94, p < 0.001$) and classroom size ($t = 1.98, p < 0.05$) remain statistically significant positive predictors of reading ability. In addition, both the cross-level interaction between vocabulary and school size ($t = 2.19, p < .005$) and impact of school size alone ($t = -2.34, p < 0.05$) are also statistically significant predictors of reading score. The statistically significant interaction term indicates that the impact of student vocabulary score on reading achievement is dependent to some degree on the size of the school. Thus the main effects for school and vocabulary cannot be interpreted in isolation and must be considered in light of one another. The interested reader is referred to Aiken and West (1991) for more detail about interpreting interactions in regression. We should note that although this interaction is statistically significant, its inclusion does not yield an overall better fitting model. Thus, a researcher must decide...
whether the primary goal of this analysis is to develop an optimally fitting model or explore relationships in the data. Model 4.2 is a better choice for developing an optimally fitting model. However, if the goal is to ascertain factors related to reading achievement in a broader population, Model 4.3 would be preferable because the cross-level interaction was found to be statistically significant.

Finally, the $R^2$ for Model 4.3 appears below:

$$R^2_1 = 1 - \frac{\sigma^2_{M1} + \tau^2_{M1}}{\sigma^2_{M0} + \tau^2_{M0}}$$

$$= 1 - \frac{1.923059 + 0.2975919}{2.201589 + 0.5221697}$$

$$= 1 - \frac{2.2206509}{2.2237587} = 1 - 0.81528914 = 0.18471086$$

By including the interaction of classroom and school size, we finish with a model that explains approximately 18.5% of variance in the outcome. This value is extremely similar to the portion of variance explained by the model without the interaction, further suggesting that its inclusion contributes little to the analysis of reading test scores.

### 4.1.2 Simple Models with More Than Three Levels

To this point in this chapter, we discussed the use of R for fitting multilevel models with three levels of data structures. In some cases, however, we may wish to fit multilevel models of more than three levels. The `lme` function in R can be used to fit such higher level models in much the same way explained above. As a simple example of such higher order models, we will again fit a null model predicting reading achievement, this time incorporating four levels of data: students nested within classrooms nested within schools nested within school corporations (or districts). As with the previous examples, the part of the code reflecting the multilevel data structure appears in the `random =` line. To represent the three higher levels of influence, this line will be `random = ~1|corp/school/class` in Model 4.4. In addition to fitting the model and obtaining a summary of results, we will also request 95% confidence intervals for the model parameters.

```r
Model4.4 <- lme(fixed = geread~1, random = ~1|corp/school/class, data = Achieve)
summary(Model4.4)
intervals(Model4.4)
```
To ensure that the data set is read by R as we think it should be, we can first examine the last line of the output where we find a summary of the sample sizes for the various data levels. There were 10320 students nested within 568 classrooms (class %in% school %in% corp) nested within 160 schools (school %in% corp) nested within 59 school corporations; this matches what we know about the data. Therefore, we can proceed with interpretation of the results. Because we are working with a null model with no fixed predictors, our primary focus is on the intercept estimates for the random effects and their associated confidence intervals. We can see from the results below that each level of the data yielded intercepts that were significantly different from 0 (given that 0 does not appear in any of the confidence intervals), indicating that mean reading achievement scores differed among the classrooms, the schools, and the school corporations.

Linear mixed-effects model fit by REML
Data: Achieve

AIC   BIC   logLik
46113.22 46149.43 -23051.61

Random effects:
Formula: ~1 | corp
(Intercept)
StdDev: 0.4210368

Formula: ~1 | school %in% corp
(Intercept)
StdDev: 0.2957739

Formula: ~1 | class %in% school %in% corp
(Intercept) Residual
StdDev: 0.5247664 2.201589

Fixed effects: geread ~ 1

Value   Std.Error   DF   t-value   p-value
(Intercept)  4.325832  0.0719804 9752 60.09736   0

Standardized Within-Group Residuals:

Min   Q1  Med   Q3  Max
-2.2995182 -0.6304798 -0.2130699 0.3028559 3.9448301

Number of Observations: 10320
Number of Groups:
corp  school %in% corp  class %in% school %in% corp
59     160               568

Approximate 95% confidence intervals

Fixed effects:

lower   est.   upper
(Intercept)  4.184738  4.32583  4.466923
Random Coefficient Models with Three or More Levels

Chapter 2 discussed the random coefficients multilevel model in which the impact of one or more fixed effects is allowed to vary across the levels of a random effect. Thus, for example, we could assess whether the relationship of vocabulary test score on reading achievement differs by school. In Chapter 3 we learned how to fit such random coefficient models using both \texttt{lme} and \texttt{lmer}. Based on the relative similarity in syntax for fitting two- and three-level models, as may be expected the definition of random coefficient models in the three-level context with \texttt{lme} is very much like that for two-level models. As an example, consider a model intended to determine whether mean reading scores differ between males and females while accounting for the relationship between vocabulary and reading. Furthermore, we believe that the relationship of gender to reading may differ across schools and across classrooms, thus leading to a model where the gender coefficient is allowed to vary across both random effects in a three-level model. Below is the \texttt{lme} command sequence for fitting this model.

\begin{verbatim}
Model4.5 <- lme(fixed = geread~gevocab+gender, 
    random = ~gender|school/class, data = Achieve)
\end{verbatim}

This syntax allows the gender coefficient to vary at both the school and classroom levels. The resulting output appears below. The intervals function is not available for use with models in which coefficients are allowed to vary randomly across two levels of the data structure.

\begin{verbatim}
summary(Model4.5)
Linear mixed-effects model fit by REML
  Data: Achieve

attr(,"label")
[1] "Fixed effects:

Random Effects:
Level: corp
    lower  est.  upper
sd((Intercept))  0.321723  0.4209979  0.5509065
Level: school
    lower  est.  upper
sd((Intercept))  0.2003532  0.295833  0.4368144
Level: class
    lower  est.  upper
sd((Intercept))  0.4578135  0.5247746  0.6015295

Within-group standard error:
    lower  est.  upper
2.170912  2.201587  2.232695
\end{verbatim}
Random effects:
Formula: ~gender | school
Structure: General positive-definite, Log-Cholesky parametrization
  StdDev Corr
(Intercept) 0.2447898 (Intr)
gender[T.MALE] 0.1099837 0.435

Formula: ~gender | class %in% school
Structure: General positive-definite, Log-Cholesky parametrization
  StdDev Corr
(Intercept) 0.302866649 (Intr)
gender[T.MALE] 0.001872273 -0.002
Residual 1.922520180

Fixed effects: geread ~ gevocab + gender

<table>
<thead>
<tr>
<th>Value</th>
<th>Std.Error</th>
<th>DF</th>
<th>t-value</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>2.0325683</td>
<td>0.05261305</td>
<td>9750</td>
<td>38.63240</td>
</tr>
<tr>
<td>gevocab</td>
<td>0.5091249</td>
<td>0.00840838</td>
<td>9750</td>
<td>60.54972</td>
</tr>
<tr>
<td>gender[T.MALE]</td>
<td>0.0175476</td>
<td>0.03929220</td>
<td>9750</td>
<td>0.44659</td>
</tr>
</tbody>
</table>

Correlation:
  (Intr) gevocb
  gevocb -0.728
  gender[T.MALE] -0.343

Standardized Within-Group Residuals:

<table>
<thead>
<tr>
<th>Min</th>
<th>Q1</th>
<th>Med</th>
<th>Q3</th>
<th>Max</th>
</tr>
</thead>
<tbody>
<tr>
<td>-3.2117008</td>
<td>-0.5676468</td>
<td>-0.2071997</td>
<td>0.3160768</td>
<td>4.4474378</td>
</tr>
</tbody>
</table>

Number of Observations: 10320
Number of Groups:
  school class %in% school
  160   568

Interpreting these results, we first note no statistically significant relationship between the fixed gender effect and reading achievement. In other words, across classrooms and schools the difference in mean reading achievement for males and females is not shown to be statistically significant in accounting for vocabulary scores. The estimate for the gender random coefficient term at the school level is approximately 0.11, and approximately 0.002 at the classroom nested in school level. Thus, it appears that the relationship of gender reading achievement varies more across schools than it does across classrooms, at least descriptively.

As noted above in Model 4.5, the coefficients for gender were allowed to vary randomly across both classes and schools. However, in some
situations a researcher may be interested in allowing the coefficient for a fixed effect to vary for only one of the random effects, such as classroom, for example. Using the syntax for Model 4.5 we define the random coefficient with ~gender|school/class, thus allowing both the intercept and slope to vary across both classrooms and schools. This model definition is not flexible enough to allow different random effects structures across nested levels of the data, meaning that we must allow the gender coefficient to vary across both school and classroom if we want it to vary at all across the random effects. Perhaps we would like to hypothesize that the relationship of gender and reading varies significantly across classrooms but not across schools. To model this situation, a more flexible syntax is necessary so that different random effects structures can be defined for each level. Such model syntax for lme appears below, followed by the resulting output and confidence intervals.

```r
Model4.6 <- lme(fixed = geread~gevocab+gender, random =
  list(school = ~1, class = ~gender), data = Achieve)

summary(Model4.6)
intervals(Model4.6)
```

**Linear mixed-effects model fit by REML**

Data: Achieve

<table>
<thead>
<tr>
<th>AIC</th>
<th>BIC</th>
<th>logLik</th>
</tr>
</thead>
<tbody>
<tr>
<td>43125.18</td>
<td>43183.11</td>
<td>-21554.59</td>
</tr>
</tbody>
</table>

**Random effects:**

Formula: ~1 | school

(Intercept)

StdDev: 0.2737245

Formula: ~gender | class %in% school

Structure: General positive-definite, Log-Cholesky parametrization

<table>
<thead>
<tr>
<th>StdDev</th>
<th>Corr</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>0.3020930 (Intr)</td>
</tr>
<tr>
<td>gender[T.MALE]</td>
<td>0.1651159 -0.128</td>
</tr>
<tr>
<td>Residual</td>
<td>1.9215119</td>
</tr>
</tbody>
</table>

**Fixed effects:** geread ~ gevocab + gender

<table>
<thead>
<tr>
<th>Value</th>
<th>Std.Error</th>
<th>DF</th>
<th>t-value</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>2.0319411</td>
<td>0.05357037</td>
<td>9750</td>
<td>37.93031</td>
</tr>
<tr>
<td>gevocab</td>
<td>0.5090472</td>
<td>0.00841459</td>
<td>9750</td>
<td>60.49580</td>
</tr>
<tr>
<td>gender[T.MALE]</td>
<td>0.0190565</td>
<td>0.03880625</td>
<td>9750</td>
<td>0.49107</td>
</tr>
</tbody>
</table>

**Correlation:**

<table>
<thead>
<tr>
<th>(Intr)</th>
<th>gevocb</th>
</tr>
</thead>
<tbody>
<tr>
<td>gevocb</td>
<td>-0.716</td>
</tr>
<tr>
<td>gender[T.MALE]</td>
<td>-0.383 0.039</td>
</tr>
</tbody>
</table>
Standardized Within-Group Residuals:

<table>
<thead>
<tr>
<th>Min</th>
<th>Q1</th>
<th>Med</th>
<th>Q3</th>
<th>Max</th>
</tr>
</thead>
<tbody>
<tr>
<td>-3.2117255</td>
<td>-0.5676850</td>
<td>-0.2072087</td>
<td>0.3182784</td>
<td>4.4324383</td>
</tr>
</tbody>
</table>

Number of Observations: 10320
Number of Groups:

<table>
<thead>
<tr>
<th>school class %in% school</th>
</tr>
</thead>
<tbody>
<tr>
<td>160</td>
</tr>
<tr>
<td>568</td>
</tr>
</tbody>
</table>

Approximate 95% confidence intervals

Fixed effects:

<table>
<thead>
<tr>
<th>lower</th>
<th>est.</th>
<th>upper</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.92693202</td>
<td>2.0319411</td>
<td>2.13695011</td>
</tr>
<tr>
<td>0.49255285</td>
<td>0.5090472</td>
<td>0.52554152</td>
</tr>
<tr>
<td>-0.05701179</td>
<td>0.0190565</td>
<td>0.09512479</td>
</tr>
</tbody>
</table>

Random Effects:

<table>
<thead>
<tr>
<th>lower</th>
<th>est.</th>
<th>upper</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.2147064</td>
<td>0.2737245</td>
<td>0.3489655</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>lower</th>
<th>est.</th>
<th>upper</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.23347625</td>
<td>0.3020931</td>
<td>0.3908758</td>
</tr>
<tr>
<td>0.04241262</td>
<td>0.1651160</td>
<td>0.6428111</td>
</tr>
<tr>
<td>-0.52745676</td>
<td>-0.1282554</td>
<td>0.3173376</td>
</tr>
</tbody>
</table>

Within-group standard error:

<table>
<thead>
<tr>
<th>lower</th>
<th>est.</th>
<th>upper</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.894364</td>
<td>1.921512</td>
<td>1.949049</td>
</tr>
</tbody>
</table>

Using this R syntax, we can more flexibly define models with nested terms while allowing for different random effects data structures at each level. It is important when using this syntax to remember that R infers the nesting structure from the order of the random effects on a list. Thus, the first grouping variable on a list should be the higher level unit (schools in this case), and the second grouping variable should be the lower-level unit (classrooms).

The results of the analysis reveal that the random coefficient for gender across classroom nested in schools is approximately 0.02, which is larger than the result when the coefficient was also allowed to vary by school, as in Model 4.5. In addition, the random coefficient term likely differs from 0 in the population since its 95% confidence interval ranges from 0.04 to 0.64 and does not include 0. From these results, we conclude that our hypothesis stated above is supported, namely that the relationship of gender and reading achievement varies across classrooms nested within schools.
4.2 \texttt{lme4} for Three and More Levels

As we will see below, defining and fitting three-level models using \texttt{lme4} is very similar in most ways to doing so with \texttt{lme} and is also closely aligned with fitting two-level models with \texttt{lme4}. In this section, we will demonstrate the syntax and output for \texttt{lme4} using the examples described above with \texttt{nlme}. To fit the null model including only the random intercept, classroom nested in school, and school with reading as the dependent variable, we would use the following syntax. Note that as with \texttt{lme}, we specify the nested data structure by \texttt{school/class}, which is denoted as a random effect by its inclusion in the parentheses.

\begin{verbatim}
Model4.7 <- lmer(geread~1+(1|school/class), data = Achieve)
\end{verbatim}

To examine the resulting output of our analysis, we will use the \texttt{summary} command.

\begin{verbatim}
summary(Model4.7)
\end{verbatim}

With the exception of rounding errors, these results are essentially identical to those obtained using \texttt{lme}. Specifically, the variance associated with class nested in school is 0.273, while that associated with school is 0.312, and residual variance is 4.847. We can also obtain confidence intervals for the random effects in the model using the MCMC approach discussed in Chapter 3.

\begin{verbatim}
Model4.7.pvals<-pvals.fnc(Model4.7, nsim = 10000, withMCMC = TRUE)
Model4.7.pvals$random
\end{verbatim}

Because the confidence intervals for each term exclude 0, we can conclude from these results that each of the terms included in the model was related to
the outcome variable. In other words, differences were noted in reading scores across the classrooms within schools and across the schools themselves.

Now that we see how to fit three-level models using \texttt{lmer}, we can fit a more complex model including the predictor variables of student vocabulary (\texttt{gevocab}), the size of the student’s class (\texttt{clenroll}), and the size of the student’s school (\texttt{cenroll}) as fixed effects. We continue to fit the three-level model with class nested in school as before. The syntax for fitting this model in \texttt{lmer} and obtaining the resultant output is

\begin{verbatim}
Model4.8 <- lmer(geread~gevocab+clenroll+cenroll+(1|school/class), data = Achieve)

summary(Model4.8)
\end{verbatim}

\begin{verbatim}
Linear mixed model fit by REML
Formula: geread ~ gevocab + clenroll + cenroll + (1 | school/class)
Data: Achieve
AIC BIC logLik deviance REMLdev
43145 43196 -21565 43087 43131
Random effects:
Groups Name Variance Std.Dev.
class:school (Intercept) 0.090473 0.30079
school (Intercept) 0.076518 0.27662
Residual 3.697895 1.92299
Number of obs: 10320, groups: class:school, 568; school, 160
Fixed effects:
Estimate Std. Error t value
(Intercept) 1.675e+00 2.081e-01 8.05
gevocab 5.076e-01 8.426e-03 60.23
clenroll 1.898e-02 9.558e-03 1.99
cenroll -3.721e-06 3.641e-06 -1.02

Correlation of Fixed Effects:
(Intr) gevocab clnrll
gevocab -0.124
clenroll -0.961 -0.062
cenroll -0.134 0.025 -0.007
\end{verbatim}

When interpreting these results, we first want to consider whether this more complex model fits the data better than the simpler null model that does not include the three fixed predictors. The AIC and BIC values for Model 4.8 are 43145 and 43196, respectively. They are lower than those for the null model (Model 4.7)—46154 and 46183. As we noted previously, lower values of these information indices indicate better fit, thereby leading us to the conclusion that the model including the fixed effects provides superior fit.

We will now examine the parameter estimates for the three fixed effects. We see that vocabulary and class size are both positively related to reading
scores, so that higher values of each predictor are associated with higher reading scores. In contrast, school size is negatively associated with reading score. As shown previously, \texttt{lmer} does not provide \textit{p} values for the hypothesis tests of model parameter estimates. Therefore, if we want to identify which parameters in a population are likely to be different from 0 (statistically significant), we must use the MCMC approach described in Chapter 3.

```r
Model4.8.pvals<-pvals.fnc(Model4.8, nsim = 10000, withMCMC = TRUE)
Model4.8.pvals$fixed

\begin{verbatim}
Estimate MCMCmean HPD95lower HPD95upper pMCMC Pr(>|t|)
(Intercept) 1.6751 1.6654 1.2420 2.0506 0.0001 0.0000
gevocab 0.5076 0.5087 0.4920 0.5246 0.0001 0.0000
clenroll 0.0190 0.0192 0.0005 0.0372 0.0076 0.0470
cenroll 0.0000 0.0000 0.0000 0.0000 0.2992 0.3068
\end{verbatim}

```r
Model4.8.pvals$random

\begin{verbatim}
Groups Name Std.Dev. MCMCmedian MCMCmean HPD95lower HPD95upper
1 class:school (Intercept) 0.3008 0.2534 0.2519 0.1789 0.3201
2 school (Intercept) 0.2766 0.2792 0.2800 0.2152 0.3416
3 Residual 1.9230 1.9274 1.9275 1.8996 1.9544
\end{verbatim}

Using this method, we see that both vocabulary score and class enrollment have statistically significant relationships with reading score, while school size does not. This result matches our findings using \texttt{lme}. Additionally, the amount of variance in reading scores associated with the random effects, in particular for classroom nested in school and school, declined in value from the null model. This result suggests that some of the variation associated with these random effects in the null model arises from the sizes of classroom and school, respectively. Finally, \texttt{lmer} provides a correlation matrix for the fixed effects. The low values in the result clearly indicate very little relationship among the estimates for the fixed effects.

A researcher may be interested in including an interaction in the model. In particular, he or she may hypothesize that the relationship between vocabulary and reading is in turn impacted by school size. This cross-level interaction is included in Model 4.9 below.

```r
Model4.9 <- lmer( geread~gevocab+clenroll+cenroll+gevocab* cenroll+(1|school/class), data = Achieve)
summary(Model4.9)

Linear mixed model fit by REML
Formula:  geread ~ gevocab + clenroll + cenroll + gevocab * cenroll + (1 | school/class)
Data: Achieve
AIC BIC logLik deviance REMLdev
43168 43226 -21576 43083 43152
Random effects:
Groups Name Variance Std.Dev.
class:school (Intercept) 0.088561 0.29759
school (Intercept) 0.075129 0.27410
Residual 3.698156 1.92306
Number of obs: 10320, groups: class: school, 568; school, 160

\end{verbatim}
Fixed effects:

<table>
<thead>
<tr>
<th>Estimate</th>
<th>Std. Error</th>
<th>t value</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>1.752e+00</td>
<td>2.100e-01</td>
</tr>
<tr>
<td>gevocab</td>
<td>4.900e-01</td>
<td>1.168e-02</td>
</tr>
<tr>
<td>clenroll</td>
<td>1.880e-02</td>
<td>9.511e-03</td>
</tr>
<tr>
<td>cenroll</td>
<td>-1.316e-05</td>
<td>5.628e-06</td>
</tr>
<tr>
<td>gevocab:cenroll</td>
<td>2.340e-06</td>
<td>1.069e-06</td>
</tr>
</tbody>
</table>

Correlation of Fixed Effects:

<table>
<thead>
<tr>
<th>(Intr)</th>
<th>gevocab</th>
<th>clenroll</th>
<th>cenroll</th>
<th>gevocab:cenroll</th>
</tr>
</thead>
<tbody>
<tr>
<td>-0.203</td>
<td></td>
<td>-0.949</td>
<td>-0.212</td>
<td>0.166</td>
</tr>
<tr>
<td>-0.041</td>
<td>0.542</td>
<td></td>
<td></td>
<td>-0.693</td>
</tr>
<tr>
<td>0.000</td>
<td></td>
<td></td>
<td>-0.007</td>
<td>-0.766</td>
</tr>
</tbody>
</table>

In terms of model fit comparison, the AIC and BIC for Model 4.9 are 43168 and 43226. They are larger than those obtained for the model not including the interaction of vocabulary and school size (43145 and 43196). Therefore, we conclude that the model including the interaction does not fit the data as well as the model without it. We would next want to obtain the MCMC hypothesis testing results.

Model4.9.pvals<-pvals.fnc(Model4.9, nsim = 10000, withMCMC = TRUE)

We see that student vocabulary score, classroom size, school size, and the interaction of vocabulary score and school size were all statistically significant. Additionally, we know that both random effects were significantly different from 0 because the confidence intervals for these terms did not include 0. Finally, the parameter estimates for the interaction term were correlated with estimates for both vocabulary and school enrollment. These parameters were not strongly correlated in the model not including the interaction, suggesting that the interaction induced the relationships among the various estimates.

As with `lme`, it is possible to fit models with more than three levels using `lmer`. In the next example, we fit a four-level model in which students are nested in classrooms nested in schools nested in school corporations. Using this model, we can estimate the amount of variance in student reading test scores associated with each level in the nested data structure. The commands
to estimate this model and obtain the output appear below. We see that the four-level nested structure is simply an amplification of the three-level structure in which the higher levels appear first in the list, separated by slashes (/).

```r
Model4.10 <- lmer(geread ~ 1 + (1|corp/school/class), data = Achieve)
summary(Model4.10)
```

Linear mixed model fit by REML
Formula: geread ~ 1 + (1 | corp/school/class)
Data: Achieve
AIC BIC logLik deviance REMLdev
46113 46149 -23052 46100 46103

Random effects:

<table>
<thead>
<tr>
<th>Groups</th>
<th>Name</th>
<th>Variance</th>
<th>Std.Dev.</th>
</tr>
</thead>
<tbody>
<tr>
<td>class:(school:corp)</td>
<td>(Intercept)</td>
<td>0.275399</td>
<td>0.52478</td>
</tr>
<tr>
<td>school:corp</td>
<td>(Intercept)</td>
<td>0.087452</td>
<td>0.29572</td>
</tr>
<tr>
<td>corp</td>
<td>(Intercept)</td>
<td>0.177256</td>
<td>0.42102</td>
</tr>
<tr>
<td>Residual</td>
<td></td>
<td>4.846993</td>
<td>2.20159</td>
</tr>
</tbody>
</table>

Number of obs: 10320, groups: class:(school:corp), 568; school:corp, 160; corp, 59

Fixed effects:

<table>
<thead>
<tr>
<th>Estimate</th>
<th>Std. Error</th>
<th>t value</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>4.32583</td>
<td>0.07196</td>
</tr>
</tbody>
</table>

Based on these results, we conclude that classroom nested within school within corporation accounts for the largest share of score variance, followed by corporation, and finally school nested within corporation. The MCMC hypothesis random effects confidence intervals for this model appear below. The fact that not one includes 0 indicates that at each level of the data, there were between-cluster differences in average reading performance.

```r
Model4.10.pvals<-pvals.fnc(Model4.10, nsim = 10000, withMCMC = TRUE)
Model4.10.pvals$random
```

<table>
<thead>
<tr>
<th>Groups</th>
<th>Name</th>
<th>Std.Dev.</th>
<th>MCMCmedian</th>
<th>MCMCmean</th>
<th>HPD95lower</th>
<th>HPD95upper</th>
</tr>
</thead>
<tbody>
<tr>
<td>class:(school:corp)</td>
<td>(Intercept)</td>
<td>0.5248</td>
<td>0.4606</td>
<td>0.4605</td>
<td>0.3943</td>
<td>0.5281</td>
</tr>
<tr>
<td>school:corp</td>
<td>(Intercept)</td>
<td>0.2957</td>
<td>0.2999</td>
<td>0.2984</td>
<td>0.1895</td>
<td>0.4054</td>
</tr>
<tr>
<td>corp</td>
<td>(Intercept)</td>
<td>0.4210</td>
<td>0.4203</td>
<td>0.4235</td>
<td>0.3147</td>
<td>0.5327</td>
</tr>
<tr>
<td>Residual</td>
<td></td>
<td>2.2016</td>
<td>2.2086</td>
<td>2.2086</td>
<td>2.1791</td>
<td>2.2405</td>
</tr>
</tbody>
</table>

Using `lmer`, it is possible to estimate a random slopes model in which the coefficient linking a fixed effect to the outcome variable is allowed to vary by level of the random effect. In the case of a three-level data structure, we can fit a random slopes model such that the coefficient is allowed to vary for both random effects simultaneously. In the current example, this would mean allowing the coefficient for a fixed effect (e.g., gender) to vary by classroom nested in school and by school. The R command sequence for fitting a model with a random intercept, and a random coefficient for gender, using `lmer` appears below.
Model4.11 <- lmer(geread~gevocab+gender+(gender|school/class), data = Achieve)

summary(Model4.11)

Linear mixed model fit by REML
Formula: geread ~ gevocab + gender + (gender | school/class)
   Data: Achieve

AIC   BIC  logLik deviance REMLdev
43150 43223 -21565 43113 43130

Random effects:
  Groups     Name       Variance  Std.Dev. Corr
  class:school (Intercept)  2.1424e-09 4.6286e-05
   gender[T.MALE]  8.7588e-02 2.9595e-01  0.000
  school        (Intercept)  8.5786e-02 2.9289e-01
   gender[T.MALE]  4.4282e-04 2.1043e-02  1.000
  Residual       3.7289e+00 1.9310e+00

Number of obs: 10320, groups: class:school, 568; school, 160

Fixed effects:
  Estimate Std. Error   t value
(Intercept)   2.017479   0.052578  38.37
gevocab       0.512175   0.008383  61.10
gender[T.MALE] 0.016858   0.040349   0.42

Correlation of Fixed Effects:
   (Intr) gevocab
gevocab   -0.726
gender[T.MALE] -0.353  0.038

These results indicate that the fixed portion of gender is not statistically significantly related to reading score when the vocabulary score is included in the model (t-value = 0.42, which is below the threshold value of 1.96 that we have been using). In terms of random coefficients, we can see that for classrooms nested within schools, the estimate for the random coefficient for gender is approximately 0.088, whereas it is about 0.004 for schools. As we indicated in Chapter 3, the MCMC approach for obtaining hypothesis test results using \texttt{lmer} is not currently available for random coefficient models.

**Summary**

Chapter 4 is very much an extension of Chapter 3, extending the use of R in fitting two-level models to include data structures at three or more levels. In practice, such complex multilevel data are relatively rare. However, as we saw in this chapter, when faced with such data, we can use either \texttt{lme} or \texttt{lmer} to model it appropriately. Indeed, the basic framework that
we employed in the two-level case works equally well for the more complex data featured in this chapter. If you read the first four chapters, you should now feel fairly comfortable analyzing most common multilevel models with continuous outcome variables. We next turn our attention to the application of multilevel models to longitudinal data. Of key importance as we change directions is that the core ideas already learned, including fitting of the null, random intercept, random coefficients models, and inclusion of predictors at different levels of data do not change with longitudinal data. As we will see, application of multilevel models in this context is no different from applications discussed in Chapters 3 and 4. What is different is the way in which we define data levels. Heretofore, Level 1 has generally been associated with individuals. With longitudinal data, however, Level 1 will refer to a single measurement in time and Level 2 will refer to an individual subject. By recasting longitudinal data in this manner, we take advantage of the flexibility and power of multilevel models.
To this point, we have focused on multilevel models in which a single measurement is made on each individual in a sample and the individuals are in turn clustered. However, as explained in Chapter 2, multilevel modeling can utilize varying data structures in a number of contexts. This chapter will focus on using multilevel modeling to analyze longitudinal data generated when a series of measurements are made on each individual in a sample, usually over a set period of time. While longitudinal data can be measured on bases other than temporal (e.g., measurements at multiple locations on a plot of land), we will focus on the most common—time-based—type of longitudinal data. In this chapter, we will first demonstrate the application to the special case of tools we have already discovered and then briefly describe the correlation structures that are unique to longitudinal data. We will conclude the chapter by describing advantages of using multilevel models with longitudinal data.

5.1 Multilevel Longitudinal Framework

As with the two- and three-level multilevel models described in Chapters 3 and 4, longitudinal analysis in a multilevel framework involves regression-like equations at each level of the data. In the case of longitudinal models, the data structure takes the form of repeated measurements (Level 1) nested within the individual (Level 2) and possibly individual nested within a higher level cluster (e.g., school) at Level 3. A simple two-level longitudinal model involving repeated measurements nested within individuals can be expressed as

\begin{align}
\text{Level 1: } Y_{it} &= \pi_{0i} + \pi_{1i}(T_{it}) + \pi_{2i}(X_{it}) + \varepsilon_{it} \\
\pi_{0i} &= \beta_{00} + \beta_{01}(Z_i) + r_{0i} \\
\pi_{1i} &= \beta_{10} + r_{1i} \\
\pi_{2i} &= \beta_{20} + r_{2i}
\end{align}

(5.1)
where $Y_{it}$ is the outcome variable for individual $i$ at time $t$, $\pi_{it}$ are the Level 1 regression coefficients, $\beta_{it}$ are the Level 2 regression coefficients, $\epsilon_{it}$ is the Level 1 error, $r_{it}$ are the Level 2 random effects, $T_{it}$ is a dedicated time predictor variable, $X_{it}$ is a time-varying predictor variable, and $Z_i$ is a time-invariant predictor. Thus as can be seen in Equation (5.1), although new notation is used to define specific longitudinal elements, the basic framework for the multilevel model is essentially the same as that of the two-level model in Chapter 3. The primary difference is that now we have three different types of predictors: a time predictor, time-varying predictors, and time-invariant predictors. Because these predictor types play unique roles in longitudinal modeling, it is worth spending some time defining them.

Of the three types of predictors possible in longitudinal models, a dedicated time variable is the only one required to make a multilevel model longitudinal. This time predictor, which is literally an index of the time point at which a particular measurement was made, can be very flexible with time measured in fixed intervals or in waves. If time is measured in waves, they can vary in length from person to person or may be measured on a continuum. It is important to note that when working with time as a variable, it is often worthwhile to rescale it so that the first measurement occasion is the zero point, thereby giving the intercept the interpretation of baseline or initial status on the dependent variable.

The other two types of predictors—time varying and time invariant—differ in terms of how they are measured. A predictor is time varying when it is measured at multiple points in time, just as is the outcome variable. In the context of education, a time-varying predictor may be the number of hours in the previous 30 days a student has spent studying. This value could be recorded concurrently with the student taking the achievement test serving as the outcome variable. On the other hand, a predictor is time invariant when it is measured at only one point in time and its value does not change across measurement occasions. An example of this type of predictor would be gender. It may be recorded at the baseline measurement occasion and is unlikely to change over the course of the data collection period. To apply multilevel models to longitudinal data problems, time-varying predictors will appear at Level 1 because they are associated with specific measurements, whereas time-invariant predictors will appear at Level 2 or higher because they are associated with an individual (or higher data level) across all measurement conditions.

### 5.2 Person Period Data Structure

The first step in fitting multilevel longitudinal models with R is to ensure the data are in the proper longitudinal structure. Often such data are entered in what is called a person-level data structure. This structure includes one
row for each individual in the data set and one column for each variable or measurement on that individual. In the context of longitudinal data, this means that each measurement in time would have its own separate column. Although person-level data structure works well in many cases, to apply multilevel modeling techniques to longitudinal analyses, the data must be reformatted into what is called a person-period data structure. Rather than assigning one row for each individual, person-period data utilizes one row for each time that each subject is measured, so that data for an individual in the sample will consist of as many rows as measurements made.

We gathered the data to be used in the following examples from the realm of educational testing. Examinees were given language assessments at six equally spaced times. As always, the data must first be read into R. In this case, the data are in the person-level data structure in a file called Lang. This file includes the total language achievement test score measured over six measurement occasions (outcome variable), four language subtest scores (writing process and features, writing applications, grammar, and mechanics), and variables indicating student and school identification.

Restructuring person-level data into person-period format in R can be accomplished by creating a new data frame from the person-level data using the `stack` command. All time-invariant variables must be copied into the new data file, while time-variant variables (e.g., all test scores measured over the six occasions) must be stacked to create person-period format. The following R command will rearrange the data into the necessary format.

```r
LangPP <- data.frame(ID = Lang$ID, school = Lang$school, 
                      Process = Lang$Process, 
                      Application = Lang$Application, Grammar = Lang$Grammar, 
                      Mechanics = Lang$Mechanics, 
                      stack(Lang, select = LangScore1:LangScore6))
```

This code takes all of the time-invariant variables directly from the raw person-level data while also consolidating the repeated measurements into a single variable called `values`. It also creates a variable measuring time called `ind`. At this point we may wish to do some recoding and renaming of variables. Renaming of variables can be accomplished via the `names` function, and recoding can be done via

```r
recode(var, recodes, as.factor.result, as.numeric. 
      result = TRUE, levels)
```

We could rename the `values` variable to `Language`. The `values` variable is the seventh column, so we would use the following R code to rename it:

```r
names(LangPP)[c(7)] <- c("Language")
```

We may also wish to recode the dedicated time variable `ind`. Currently, this variable is not recorded numerically, but takes on the values "LangScore1", "LangScore2", etc.
"LangScore2", "LangScore3", "LangScore4", "LangScore5", "LangScore6". Thus we may wish to recode the values to make a continuous numeric time predictor as follows.

```r
LangPP$Time <- recode(LangPP$ind,
  "Lang Score1" = 0; "LangScore2" = 1; "LangScore3" = 2;
  "LangScore4" = 3; "LangScore5" = 4; "LangScore6" = 5;,
  as.factor.result = FALSE)
```

The option `as.factor.result = FALSE` tells R that the resulting values should be considered continuous. Thus, we have not only recoded the `ind` variable into a continuous time predictor, but also renamed it as `Time`, and rescaled the variable such that the first time point is 0. As we noted earlier, when time is rescaled in this manner, the intercept can be interpreted as the predicted outcome for baseline or time zero.

### 5.3 Fitting Longitudinal Models Using `nlme` and `lme4` Packages

After data have been restructured into person-period format, we can fit longitudinal models in a multilevel framework in exactly the same manner as we saw in Chapters 3 and 4. As noted earlier, the primary difference between the scenario described here and those in previous chapters is that the nesting structure reflects repeated measurements for each individual. For example, using the `Language` data we just restructured in the previous section, we would use the following syntax for a longitudinal random intercepts model predicting `Language` over time using the `nlme` package:

```r
Model_5.1 <- lme(fixed = Language ~ Time, random = ~1 | ID,
  data = LangPP)
Summary(Model_5.1)
Linear mixed-effects model fit by REML
Data: LangPP
   AIC BIC logLik
135173.6 135204.9 -67582.82
Random effects:
Formula: ~1 | ID
   (Intercept) Residual
StdDev:  15.23617  7.526427
Fixed effects: Language ~ Time
                Value Std.Error    DF  t-value  p-value
(Intercept)  197.21573  0.29356329 15189  671.7997     0
Time         3.24619   0.03264194 15189   99.4483     0
```

```r
Model_5.1 <- lme(fixed = Language ~ Time, random = ~1 | ID,
  data = LangPP)
Summary(Model_5.1)
Linear mixed-effects model fit by REML
Data: LangPP
   AIC BIC logLik
135173.6 135204.9 -67582.82
Random effects:
Formula: ~1 | ID
   (Intercept) Residual
StdDev:  15.23617  7.526427
Fixed effects: Language ~ Time
                Value Std.Error    DF  t-value  p-value
(Intercept)  197.21573  0.29356329 15189  671.7997     0
Time         3.24619   0.03264194 15189   99.4483     0
```
Correlation:
(Intr)
Time -0.278

Standardized Within-Group Residuals:

<table>
<thead>
<tr>
<th></th>
<th>Min</th>
<th>Q1</th>
<th>Med</th>
<th>Q3</th>
<th>Max</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>-6.40395610</td>
<td>-0.49863770</td>
<td>0.03877858</td>
<td>0.56691711</td>
<td>4.86362966</td>
</tr>
</tbody>
</table>

Number of Observations: 18228
Number of Groups: 3038

Because we devoted substantial time in Chapters 3 and 4 to interpreting multilevel model output, we will not spend a great deal of time here for that purpose. However, it is important to note that these results indicate a statistically significant positive relationship between time and performance on the language assessment, such that scores increased over time. In *lme4*, this model would be fit as:

```r
Model_5.2 <- lmer(Language~Time +(1|ID), LangPP)
summary(Model_5.2)
```

Fixed effects:

<table>
<thead>
<tr>
<th></th>
<th>Estimate</th>
<th>Std. Error</th>
<th>t value</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>197.21573</td>
<td>0.29355</td>
<td>671.8</td>
</tr>
<tr>
<td>Time</td>
<td>3.24619</td>
<td>0.03264</td>
<td>99.4</td>
</tr>
</tbody>
</table>

Correlation of Fixed Effects:
(Intr)
Time -0.278

Adding predictors to the model is handled the same way as in earlier examples, whether they are time varying or time invariant. For example, in order
to add Grammar, which is time varying, as a predictor of total language scores over time in \texttt{nlme}, we would use the following:

```r
Model_5.3 <- lme(fixed = Language~Time + Grammar,
             random = ~1|ID, data = LangPP)
summary(Model_5.3)
Linear mixed-effects model fit by REML
  Data: LangPP
  AIC      BIC    logLik
130031.1 130070.2 -65010.56

Random effects:
  Formula: ~1 | ID
             (Intercept) Residual
StdDev:     6.01123   7.526131

Fixed effects: Language ~ Time + Grammar
  Value Std.Error DF  t-value p-value
(Intercept) 73.70355   1.0913675 15179 67.53321     0
Time        3.24548   0.0326514 15179 99.39795     0
Grammar     0.63089   0.0055231  3034 114.22629     0

Correlation:
                     (Intr) Time
Time   -0.075       
Grammar -0.991 0.000

Standardized Within-Group Residuals:
  Min       Q1      Med       Q3      Max
-6.62860687 -0.52600469 0.03741845 0.57880493 4.67614317

Number of Observations: 18216
Number of Groups: 3036
```

From these results, we see again that \texttt{Time} is positively related to scores on the language assessment, indicating that they increased over time. In addition, \texttt{Grammar} is also statistically significantly related to language test scores, meaning that measurement occasions revealing higher \texttt{Grammar} scores also demonstrated higher \texttt{Language} scores. Finally, the AIC and BIC values for the model including \texttt{Grammar} that were lower than the values for the model excluding it indicate that the former is a better fit. In \texttt{lme4} we would fit the model as follows:

```r
Model_5.4 <- lmer(Language~Time + Grammar +(1|ID), LangPP)
summary(Model_5.4)
Linear mixed model fit by REML
  Formula: Language ~ Time + Grammar + (1 | ID)
  Data: LangPP
  AIC      BIC    logLik deviance REMLdev
130031   130070  -65011   130005    130021
```

From these results, we see again that \texttt{Time} is positively related to scores on the language assessment, indicating that they increased over time. In addition, \texttt{Grammar} is also statistically significantly related to language test scores, meaning that measurement occasions revealing higher \texttt{Grammar} scores also demonstrated higher \texttt{Language} scores. Finally, the AIC and BIC values for the model including \texttt{Grammar} that were lower than the values for the model excluding it indicate that the former is a better fit. In \texttt{lme4} we would fit the model as follows:
Random effects:

<table>
<thead>
<tr>
<th>Groups</th>
<th>Name</th>
<th>Variance</th>
<th>Std.Dev.</th>
</tr>
</thead>
<tbody>
<tr>
<td>ID</td>
<td>(Intercept)</td>
<td>36.135</td>
<td>6.0112</td>
</tr>
<tr>
<td>Residual</td>
<td></td>
<td>56.643</td>
<td>7.5261</td>
</tr>
</tbody>
</table>

Number of obs: 18216, groups: ID, 3036

Fixed effects:

<table>
<thead>
<tr>
<th>Estimate</th>
<th>Std. Error</th>
<th>t value</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>73.703551</td>
<td>1.091296</td>
</tr>
<tr>
<td>Time</td>
<td>3.245483</td>
<td>0.032651</td>
</tr>
<tr>
<td>Grammar</td>
<td>0.630888</td>
<td>0.005523</td>
</tr>
</tbody>
</table>

Correlation of Fixed Effects:

<table>
<thead>
<tr>
<th>(Intr)</th>
<th>Time</th>
</tr>
</thead>
<tbody>
<tr>
<td>Time</td>
<td>-0.075</td>
</tr>
<tr>
<td>Grammar</td>
<td>-0.991</td>
</tr>
</tbody>
</table>

Model5.4.pvals$fixed

| Estimate | MCMCmean | HPD95lower | HPD95upper | pMCMC | Pr(>|t|) |
|----------|----------|------------|------------|-------|---------|
| (Intercept) | 73.7036 | 73.7010 | 71.9620 | 75.3295 | 0.0001 | 0 |
| Time | 3.2455 | 3.2451 | 3.1764 | 3.3128 | 0.0001 | 0 |
| Grammar | 0.6309 | 0.6309 | 0.6226 | 0.6396 | 0.0001 | 0 |

Model5.4.pvals$random

<table>
<thead>
<tr>
<th>Groups</th>
<th>Name</th>
<th>Std.Dev.</th>
<th>MCMCmedian</th>
<th>MCMCmean</th>
<th>HPD95lower</th>
<th>HPD95upper</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>ID (Intercept)</td>
<td>4.2004</td>
<td>4.2016</td>
<td>4.0739</td>
<td>4.3318</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>Residual</td>
<td>8.0279</td>
<td>8.0280</td>
<td>7.9331</td>
<td>8.1181</td>
<td></td>
</tr>
</tbody>
</table>

To allow the growth rate to vary randomly across individuals using the nlme package, we would use the following R command.

Model_5.5 <- lme(fixed = Language~Time + Grammar, random = ~Time|ID, data = LangPP)

summary(Model_5.5)

Linear mixed-effects model fit by REML

Data: LangPP

AIC  BIC  logLik
128617.1 128671.7 -64301.54

Random effects:

<table>
<thead>
<tr>
<th>Formula: ~Time</th>
<th>ID</th>
</tr>
</thead>
<tbody>
<tr>
<td>Structure: General positive-definite, Log-Cholesky parametrization</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>StdDev</th>
<th>Corr</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>4.645126</td>
</tr>
<tr>
<td>Time</td>
<td>1.792940</td>
</tr>
<tr>
<td>Residual</td>
<td>6.737546</td>
</tr>
</tbody>
</table>

Fixed effects: Language ~ Time + Grammar

<table>
<thead>
<tr>
<th>Value</th>
<th>Std.Error</th>
<th>DF</th>
<th>t-value</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>54.47082</td>
<td>1.0025930</td>
<td>15179</td>
<td>54.32994</td>
</tr>
<tr>
<td>Time</td>
<td>3.24548</td>
<td>0.0437406</td>
<td>15179</td>
<td>74.19834</td>
</tr>
<tr>
<td>Grammar</td>
<td>0.72912</td>
<td>0.0050825</td>
<td>3034</td>
<td>143.45691</td>
</tr>
</tbody>
</table>
Correlation:  
   (Intr)       Time  
Time  -0.047    
Grammar -0.993  0.000

Standardized Within-Group Residuals:  
         Min        Q1       Med       Q3       Max  
-5.316263678 -0.523957279 -0.001213543 0.536332069 5.032113994

Number of Observations: 18216  
Number of Groups: 3036

In this model, the random effect for Time is assessing the extent to which growth over time differs from one person to the next. Results show that the random effect for Time is statistically significant, given that the 95% confidence interval does not include 0. Thus, we can conclude that growth rates in language scores over the 6 time points do differ across individuals in the sample. Using the lme4 package we would fit this model as follows:

```r
Model_5.6 <- lmer(Language~Time + Grammar + (Time|ID), LangPP)  
summary(Model_5.6)
```

```
Linear mixed model fit by REML  
Formula: Language ~ Time + Grammar + (Time | ID)  
Data: LangPP  
AIC  BIC logLik deviance REMLdev 
128617 128672 -64302.13 128587.26 128603.26
```
Random effects:

<table>
<thead>
<tr>
<th>Groups</th>
<th>Name</th>
<th>Variance</th>
<th>Std.Dev.</th>
<th>Corr</th>
</tr>
</thead>
<tbody>
<tr>
<td>ID</td>
<td>(Intercept)</td>
<td>21.5756</td>
<td>4.6450</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Time</td>
<td>3.2145</td>
<td>1.7929</td>
<td>0.026</td>
</tr>
<tr>
<td></td>
<td>Residual</td>
<td>45.3948</td>
<td>6.7376</td>
<td></td>
</tr>
</tbody>
</table>

Number of obs: 18216, groups: ID, 3036

Fixed effects:

<table>
<thead>
<tr>
<th></th>
<th>Estimate</th>
<th>Std. Error</th>
<th>t value</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>54.475254</td>
<td>1.002524</td>
<td>54.34</td>
</tr>
<tr>
<td>Time</td>
<td>3.245483</td>
<td>0.043740</td>
<td>74.20</td>
</tr>
<tr>
<td>Grammar</td>
<td>0.729096</td>
<td>0.005082</td>
<td>143.46</td>
</tr>
</tbody>
</table>

Correlation of Fixed Effects:

<table>
<thead>
<tr>
<th>(Intr)</th>
<th>Time</th>
</tr>
</thead>
<tbody>
<tr>
<td>Time</td>
<td>-0.047</td>
</tr>
<tr>
<td>Grammar</td>
<td>-0.993 0.000</td>
</tr>
</tbody>
</table>

Recall from Chapter 3 that the pvals.fnc function for obtaining $p$ values using MCMC does not accommodate random coefficients models. Thus, we cannot obtain the hypothesis testing results for Model_5.6.

We could add a third level of data structure to this model by including information about schools within which examinees are nested. To fit this model with nlme we use the following code in R:

```r
Model_5.7 <- lme(fixed = Language~Time, random = ~1|school/ID, data = LangPP)
summary(Model_5.7)
```

Linear mixed-effects model fit by REML
Data: LangPP

AIC      BIC      logLik
134650.4 134689.4 -67320.18

Random effects:

Formula: ~1 | school
(Intercept) StdDev: 8.313249

Formula: ~1 | ID %in% school
(Intercept) Residual StdDev: 13.6812 7.526427

Fixed effects: Language ~ Time

<table>
<thead>
<tr>
<th>Value</th>
<th>Std.Error</th>
<th>DF</th>
<th>t-value</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>197.33787</td>
<td>1.4804399</td>
<td>15189</td>
<td>133.29678</td>
</tr>
<tr>
<td>Time</td>
<td>3.24619</td>
<td>0.0326419</td>
<td>15189</td>
<td>99.44833</td>
</tr>
</tbody>
</table>

Correlation:

<table>
<thead>
<tr>
<th>(Intr)</th>
<th>Time</th>
</tr>
</thead>
<tbody>
<tr>
<td>Time</td>
<td>-0.055</td>
</tr>
</tbody>
</table>
Standardized Within-Group Residuals:

<table>
<thead>
<tr>
<th>Min</th>
<th>Q1</th>
<th>Med</th>
<th>Q3</th>
<th>Max</th>
</tr>
</thead>
<tbody>
<tr>
<td>-6.45895840</td>
<td>-0.50257247</td>
<td>0.03995719</td>
<td>0.56581567</td>
<td>4.85800978</td>
</tr>
</tbody>
</table>

Number of Observations: 18228
Number of Groups:

| school ID %in% school | 35 | 3038 |

Given that the AIC for Model 5.7 is lower than that for Model 5.1, where school is not included as a variable, we can conclude that inclusion of the school level of the data leads to better model fit.

### 5.4 Changing Covariance Structures of Longitudinal Models

When fitting any multilevel model, R will assume by default the independence of random effects with each error variance being equal. However, it is possible to override this default setting and change the error structure modeled in the analysis by using the `correlation` setting. Currently, longitudinal error structure modeling is only possible through the `nlme` package; however, it is likely to be included in the `lme4` package in the future. A popular covariance structure for longitudinal models is the autoregressive error. In general, autoregressive error structures model situations in which measurement occasions close in time to one another have a stronger relationship than measurement occasions that are separated further in time. The `nlme` package provides three common options for autoregressive error structures.

- The `corAR1` error structure is a first-order autoregressive error structure for situations when time is measured in fixed intervals.
- The `corCAR1` error structure is a first-order autoregressive error structure for situations when time is measured in varying intervals.
- The `corARMA` error structure is an error structure that incorporates both an autoregressive component, and a moving average process.

For a list of more possible covariance structures available in the `nlme` package, a user can search the R help using `?corClasses` after the package is loaded.

Returning to Model 5.3 for fitting a random intercepts model for language scores over time, if we believe that the relationships among the longitudinal measures follow an autoregressive process we could use the following commands in R:
Model_5.8 <- lme(fixed = Language~Time, random = ~1|ID,
correlation = corAR1(), data = LangPP)
summary(Model_5.8)
Linear mixed-effects model fit by REML
  Data: LangPP
    AIC   BIC  logLik
   134903.1 134942.2  -67446.55

Random effects:
  Formula: ~1 | ID
        (Intercept) Residual
          StdDev: 15.1301 7.827641

Correlation Structure: AR(1)
  Formula: ~1 | ID
  Parameter estimate(s):
     Phi
          0.1882671

Fixed effects: Language ~ Time
              Value       Std.Error   DF   t-value p-value
(Intercept) 196.928304   0.29727663 15189  662.4413    0
Time          3.324460    0.03677754 15189   90.3936    0

Correlation:
 (Intr)
Time   -0.309

Standardized Within-Group Residuals:
       Min     Q1  Med     Q3    Max
-6.0407998 -0.4756562 0.0531373 0.5632284 4.6866528

Number of Observations: 18228
Number of Groups: 3038

intervals(Model_5.8)
Approximate 95% confidence intervals

  Fixed effects:                 lower  est.  upper
(Intercept) 196.345606 196.928304 197.511002
Time         3.252367  3.324455  3.396544

attr(,"label")
[1] "Fixed effects:

  Random Effects:
Level: ID
       lower  est.  upper
sd((Intercept)) 14.73129 15.1301 15.53971
Correlation structure:

<table>
<thead>
<tr>
<th>lower</th>
<th>est.</th>
<th>upper</th>
</tr>
</thead>
<tbody>
<tr>
<td>Phi</td>
<td>0.1646955</td>
<td>0.1882671</td>
</tr>
</tbody>
</table>

**Within-group standard error:**

<table>
<thead>
<tr>
<th>lower</th>
<th>est.</th>
<th>upper</th>
</tr>
</thead>
<tbody>
<tr>
<td>7.719200</td>
<td>7.827641</td>
<td>7.937606</td>
</tr>
</tbody>
</table>

Taken together, these results indicate that the point estimate for the autocorrelation is 0.188, with a 95% confidence interval between 0.165 and 0.212, meaning that this autocorrelation is significantly different from 0. From a practical perspective, this result indicates a positive relationship between adjacent pairs of scores so that a relatively higher score at one point in time is associated with a relatively higher score at the next point in time.

When specifying error structures, the default used by R is a random intercepts model, i.e., `correlation = corAR1`, which will fit the same structure as `correlation = corAR1(form = 0, ~1|ID)`. However, when adding an error structure to a random coefficients model, the random coefficients structure must be specified in the syntax for specifying the correlation, as we demonstrate below.

```r
Model_5.9 <- lme(fixed = Language~Time, random = ~Time|ID, 
                correlation = corAR1(form = ~Time|ID), data = LangPP)
summary(Model_5.9)
```

**Linear mixed-effects model fit by REML**

Data: LangPP

<table>
<thead>
<tr>
<th>AIC</th>
<th>BIC</th>
<th>logLik</th>
</tr>
</thead>
<tbody>
<tr>
<td>133564.2</td>
<td>133618.9</td>
<td>-66775.11</td>
</tr>
</tbody>
</table>

Random effects:

- Formula: ~Time | ID
- Structure: General positive-definite, Log-Cholesky parametrization

<table>
<thead>
<tr>
<th>StdDev</th>
<th>Corr</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>18.411954</td>
</tr>
<tr>
<td>Time</td>
<td>1.877885</td>
</tr>
<tr>
<td>Residual</td>
<td>6.567266</td>
</tr>
</tbody>
</table>

Correlation Structure: AR(1)

- Formula: ~Time | ID
- Parameter estimate(s):
  - Phi
  - 0.0833605

Fixed effects: Language ~ Time

<table>
<thead>
<tr>
<th>Value</th>
<th>Std.Error</th>
<th>DF</th>
<th>t-value</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>197.32970</td>
<td>0.3439190</td>
<td>15189</td>
<td>573.768</td>
</tr>
<tr>
<td>Time</td>
<td>3.21406</td>
<td>0.0436237</td>
<td>15189</td>
<td>73.677</td>
</tr>
</tbody>
</table>
Correlation:
  (Intr)   
Time  -0.677

Standardized Within-Group Residuals:
                      Min       Q1     Med      Q3      Max
-5.79817245  -0.49068157  0.01554914  0.52059078  5.17526798

Number of Observations: 18228
Number of Groups: 3038

intervals(Model_5.9)
Approximate 95% confidence intervals

Fixed effects:
(Intercept) 196.655574 197.329697 198.003819
Time  3.128554  3.214061  3.299569

attr(,"label")
[1] "Fixed effects:

Random Effects:
Level: ID

                     lower    est.    upper
sd((Intercept)) 17.9271342 18.4119537  18.9098846
sd(Time) 1.7969336 1.8778851  1.9624835
cor((Intercept),Time) -0.7529057 -0.7294741 -0.7041955

Correlation structure:
                     lower    est.    upper
Phi -0.1107705 -0.0833605 -0.05582381

attr(,"label")
[1] "Correlation structure:

Within-group standard error:
                     lower    est.    upper
6.474030 6.567266 6.661844

5.5 Benefits of Using Multilevel Modeling for Longitudinal Analysis

Modeling longitudinal data in a multilevel framework presents several advantages over more traditional methods of longitudinal analysis (e.g., ANOVA designs). For example, a multilevel approach allows the simultaneous modeling of both intra-individual change (how an individual
changes over time) and inter-individual change (differences in temporal change across individuals).

A serious problem that afflicts many longitudinal studies is high attrition within a sample. It is frequently difficult for researchers to keep track of members of a sample over time, especially over a lengthy period. Traditional techniques for longitudinal data analysis, such as repeated measures ANOVA, can analyze only complete data cases. Thus, in studies involving a great deal of missing data, a sophisticated missing data replacement method (e.g., multiple imputation) must be used or the researcher must work with a far smaller sample size. In contrast, multilevel modeling can utilize available data from incomplete observations, thereby not reducing sample size as dramatically as other approaches and not requiring complex techniques for handling missing data.

Repeated measures ANOVA is traditionally one of the most common methods for analysis of change. However, when used with longitudinal data, the assumptions upon which repeated measures rests may be too restrictive. In particular, the assumption of sphericity (assuming equal variances of outcome variable differences) may be unreasonable given that variability may change considerably over time. Conversely, analyzing longitudinal data from a multilevel modeling perspective does not require the assumption of sphericity. It also provides flexibility in model definition, thus allowing the inclusion of information about the anticipated effects of time on error variability in the model design.

Finally, multilevel models can easily incorporate predictors from each of the data levels, thereby allowing for more complex data structures. In the context of longitudinal data, it is possible to incorporate measurement occasion (Level 1), individual (Level 2), and cluster (Level 3) characteristics. We saw an example of this type of analysis in Model 5.7. On the other hand, in the context of repeated measures ANOVA or MANOVA, incorporating these various levels of the data would be much more difficult. Thus, the use of multilevel modeling in this context yields the benefits listed above pertaining specifically to longitudinal analysis and brings the added capability of simultaneous analysis of multiple levels of influence.

Summary

In this chapter, we saw that the multilevel modeling tools we studied in Chapters 2 through 4 may be applied in the context of longitudinal data. The key to this analysis is the treatment of each measurement in time as a Level 1 data point and assigning the individuals on whom the measurements are made to Level 2. Once this shift in thinking is made, the methodology remains very similar to the techniques we employed in the standard
multilevel models in Chapters 3 and 4. Perhaps the only major new aspect to this analysis was the inclusion of specific correlation structures at Level 1. These structures represent the ways in which longitudinal measurements may be related to one another over time and are not applicable to other types of clustered data. For example, autoregressive data may occur when a current data point is correlated most strongly with the data point immediately preceding it in time. The correlation is weaker for measurements that are further removed in time. Such a correlation structure does not occur in the multilevel contexts described in Chapters 3 and 4, in which we typically assumed the correlations between individuals within the same cluster were the same. However, in most other respects, we can see that modeling of longitudinal data is very similar to modeling cross-sectional multilevel data. This technique of modeling longitudinal data enables us to incorporate a wide range of data structures including individuals (Level 2) nested within a higher level of data (Level 3).
Graphing data is an important step in the analysis process. Far too often researchers skip the graphing of their data and move directly into analysis without the insights that can come from a careful visual examination of data. It is certainly tempting for researchers to bypass data exploration through graphical analysis and move directly into formal statistical modeling because models generally serve as the tools used to answer research questions. However, if proper attention is not paid to the graphing of data, the formal statistical analyses may be poorly informed regarding the distribution of variables and their relationships with one another. As an example, a model allowing only a linear relationship between a predictor and a criterion variable would be inappropriate if a nonlinear relationship existed between the two variables. Using graphical tools first, it would be possible to see the nonlinearities and appropriately account for them in the model.

Perhaps one of the most eye-opening examples of the dangers in failing to plot data may be found in Anscombe (1973). Anscombe’s classic paper shows the results of four regression models that are essentially equivalent in terms of the means and standard deviations of the predictor and criterion variable, with the same correlation between the regressor and outcome variables in each data set. However, plots of the data reveal drastically different relationships among the variables. Figure 6.1 shows these four data sets and their regression equations and squared multiple correlations. First, note that the regression coefficients are identical across the models, as are the squared multiple correlation coefficients. However, the actual relationships between the independent and dependent variables are drastically different! Clearly, these data do not come from the same generating process. Thus, modeling the four situations in the same fashion would lead to incorrect conclusions about the nature of the relationships in the population. The moral of the story here is clear: plot your data!

The plotting capabilities in R are outstanding. R can produce high-quality graphics with a great deal of flexibility. As a simple example, consider the Anscombe data from Figure 6.1. These data are included with R and may be loaded into a session with the command data(anscombe). The examination of the data by calling upon the data set leads to

<table>
<thead>
<tr>
<th></th>
<th>x1</th>
<th>x2</th>
<th>x3</th>
<th>x4</th>
<th>y1</th>
<th>y2</th>
<th>y3</th>
<th>y4</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>10</td>
<td>10</td>
<td>10</td>
<td>8</td>
<td>8.04</td>
<td>9.14</td>
<td>7.46</td>
<td>6.58</td>
</tr>
<tr>
<td>2</td>
<td>8</td>
<td>8</td>
<td>8</td>
<td>8</td>
<td>6.95</td>
<td>8.14</td>
<td>6.77</td>
<td>5.76</td>
</tr>
<tr>
<td>3</td>
<td>13</td>
<td>13</td>
<td>13</td>
<td>8</td>
<td>7.58</td>
<td>8.74</td>
<td>12.74</td>
<td>7.71</td>
</tr>
</tbody>
</table>
The way to plot the data for the first data set (i.e., \(x_1\) and \(y_1\) above) is

\[
\text{plot(anscombe$y1 ~ anscombe$x1)}
\]

Notice here that \(y_1\) extracts the column labeled \(y_1\) from the data frame as \(x_1\) extracts the variable \(x_1\). The ~ symbol in the function call positions the data to the left as the dependent variable and plots the data on the

ordinate (y axis). The value to the right is treated as an independent variable and plotted on the abscissa (x axis). Alternatively, we can rearrange the terms so that the independent variable comes first, with a comma separating it from the dependent variable:

```r
plot(anscombe$x1, anscombe$y1)
```

Both approaches lead to the same plot.

Several options within the plotting framework can be utilized. The `plot` function has six base parameters, with the option of calling other graphical parameters including, among others, a `par` function. This function has more than 70 graphical parameters that can be used to modify a basic plot. Discussing all of the available plotting parameters is beyond the scope of this chapter. Rather, we will discuss some of the most important parameters to consider when plotting in R.

The parameters `ylim` and `xlim` modify the starting and ending points for the y and x axes, respectively. For example, `ylim = c(2, 12)` will produce a plot with the y axis scaled from 2 to 12. R typically automates this process, but it can be useful for the researcher to tweak this setting, for example, by setting the same axis across multiple plots. The `ylab` and `xlab` parameters are used to create labels for the y and x axes, respectively. For example, `ylab = "Dependent Variable"` will produce a plot with the y axis labeled “Dependent Variable.” The `main` parameter is used for the main title of a plot. Thus, `main = "Plot of Observed Values"` would produce a plot with the title “Plot of Observed Values” above the graph.

A sub-parameter provides a subtitle that appears at the bottom of a plot, centered and below the `xlab` label. For example, `sub = "Data from Study 1"` would produce such a subtitle. In some situations it is useful to include text, equations, or a combination in a plot. Text is easy to include by using the `text` function. For example, `text(2, 5, "Include This Text")` would place “Include This Text” in the plot centered at x = 2 and y = 5.

Equations can also be included in graphs. Doing so requires the use of an expression within the `text` function call. The function `expression` allows the inclusion of an unevaluated expression (i.e., it displays what is written). The particular syntax for a mathematical expression is available by calling `help` for the `plotmath` function (i.e., `?plotmath`). R provides a demonstration of the `plotmath` functionality via `demo(plotmath)`, which shows the various mathematical expressions that may be displayed in a figure. As an example, to add the $R^2$ information to the figure in the top left sub-figure in Figure 6.1, the following command in R was used:

```r
text(5.9, 9.35, expression(italic(R)^2 = .67))
```

The values of 5.9 (on the x axis) and 9.35 (on the y axis) are simply where we thought the text looked best, and can be easily adjusted to suit a user’s preference.
Combining text and mathematical expressions requires using the `paste` function in conjunction with the `expression` function. For example, if we wanted to add “The Value of $R^2 = 0.67$,” we would replace the previous text syntax with

```r
text(5.9, 9.35, expression(paste("The value of \textit{R}$^2$ is .67", sep = "")))
```

Here, `paste` is used to bind together the text contained within the quotes and the mathematical expression. Note that `sep = ""` is used so that there are no spaces added between the parts pasted together. Although we did not include it in our figure, the implied regression line can be easily included in a scatterplot. One way to do this is through the `abline` function, and to include the intercept (denoted `a`) and the slope (denoted `b`). Thus, `abline(a = 3, b = .5)` would add a regression line to the plot that has an intercept at 3 and a slope of 0.5. Alternatively, to automate the operation, using `abline(lm.object)` will extract the intercept and slope and include the regression line in a scatterplot.

Finally, notice in Figure 6.2 that we have broken the $y$ axis to make very clear that the plot does not start at the origin. Whether this is needed may be debatable; note that base R does not include this option, but we prefer to

![Anscombe's Data Set 1](image)

**FIGURE 6.2**
include it in many situations. A broken axis can be identified with the `axis.break` function from the `plotrix` package. The zigzag break is requested via the `style = "zigzag"` option in `axis.break` and the particular axis (1 for $y$ and 2 for $x$). By default, R will set the axis to a point that is generally appropriate. However, when the origin is not shown, there is no break in the axis by default as some have argued is important.

Now, let us combine the various pieces of information that we have discussed to produce Figure 6.2, which was generated with the following syntax.

```r
data(anscombe)

# Fit the regression model.
data.1 <- lm(y1~x1, data = anscombe)

# Scatterplot of the data.
plot(anscombe$y1 ~ anscombe$x1,
     ylab = expression(italic(Y)),
     ylim = c(2, 12),
     xlab = expression(italic(X)),
     main = "Anscombe's Data Set 1")

# Add the fitted regression line.
abline(data.1)

# Add the text and expressions within the figure.
text(5.9, 9.35,
     expression(paste("The value of \( R^2 \) is \( .67 \),
               sep = "")))

text(5.9, 10.15,
     expression(italic(hat(Y)) = 3+italic(X)*.5))

# Break the axis by adding a zigzag.
require(plotrix)
axis.break(axis = 1, style = "zigzag")
axis.break(axis = 2, style = "zigzag")
```

### 6.1 Plots for Linear Models

To further demonstrate graphing in R, let us recall the Cassidy GPA data from Chapter 1, in which GPA was modeled by `CTA.tot` and `BStotal`. We will now discuss some plots that are useful with single-level data and may be extended easily to the multilevel case with some caveats. See Figure 6.3.

First, let us consider the `pairs` function that plots all pairs of variables in a data set. The resulting graph is sometimes called a scatterplot matrix because
it is in fact a matrix of scatterplots. In the context of a multiple regression model, understanding how the variables all relate to one another can provide useful insights as we conduct our analysis. As an example, consider the following call to `pairs`:

```r
pairs(
  cbind(GPA = Cassidy$GPA, CTA_Total = Cassidy$CTA.tot,
        BS_Total = Cassidy$BStotal))
```

Because our data contains \( p \) variables, we will obtain \( p \cdot (p - 1)/2 \) unique scatterplots (three in this case). The plots below the principal diagonal are the same as those above it; the only difference is the reversal of the \( x \) and \( y \) axes. Such a `pairs` plot allows multiple bivariate relationships to be visualized simultaneously. Of course, we can quantify the degree of linear
Graphing Data in Multilevel Contexts

relation with a correlation. Code to do this can be given as follows, using listwise deletion:

\[
\text{cor(\text{na.omit(}\text{cbind(GPA = Cassidy$GPA, CTA\_Total = Cassidy$CTA\_tot, BS\_Total = Cassidy$BStotal}))})
\]

Other options are available for dealing with missing data (see \texttt{?cor}). We used the \texttt{na.omit} function wrapped around the \texttt{cbind} function to obtain a listwise deletion data set in which the following correlation matrix is computed.

\[
\begin{array}{ccc}
\text{GPA} & \text{CTA\_Total} & \text{BS\_Total} \\
1.000 & -0.300 & -0.115 \\
-0.300 & 1.000 & 0.708 \\
-0.115 & 0.708 & 1.000 \\
\end{array}
\]

Of course, when using multiple regression we must make some assumptions about the distribution of the model residuals, as discussed in Chapter 1. In particular, in order for the \( p \) values and confidence intervals to be exact, we must assume that the distribution of residuals is normal. We can obtain the residuals from a model applying the \texttt{resid} function to a fitted \texttt{lm} object (e.g., \texttt{GPAmodel.1 <- lm(GPA \sim CTA\_tot + BStotal, data = Cass}). Then, \texttt{resid(GPAmodel.1)} returns the model’s residuals that may be plotted in a variety of ways. One useful such plot is a histogram with an overlaid normal density curve (Figure 6.4) that can be obtained using the following R command:

\[
\text{hist(\text{resid.1, freq = FALSE, main = "Density of Residuals for Model 1"}, xlab = "Residuals")}
\lines(\text{density(\text{resid.1}))}
\]

This code first requests that a histogram be produced for the residuals. Note that \texttt{freq = FALSE} is used. It instructs R to make the \( y \) axis scaled in terms of probability, not the default (frequency). The solid line represents the density estimate of the residuals, corresponding closely to the bars in the histogram.

Rather than a histogram and overlaid density, a more straightforward way to evaluate the distribution of the errors to the normal distribution is a quantile-quantile (QQ) plot that includes a straight line reflecting the expected distribution of the data if in fact it is normal. In addition, the individual data points are represented in the figure as dots. In a normal data distribution, the dots will fall along or very close to the straight line. The following code produced the QQ plot in Figure 6.5, based on the residuals from the GPA model.

\[
\text{qqnorm(scale(\text{resid.1}), main = "Normal Quantile-Quantile Plot"})
\text{qqline(scale(\text{resid.1}))}
\]
FIGURE 6.4
Histogram with overlaid density curve of residuals from GPA model in Chapter 1.

FIGURE 6.5
Plot comparing observed quantiles of residuals to theoretical quantiles from standard normal distribution. When points fall along the line that has slope 1 and goes through the origin, sample quantiles follow normal distribution.
Notice that above we use the `scale` function that standardizes the residuals to have a mean of zero (already done due to the regression model) and a standard deviation of 1.

We can see in Figure 6.5 that points in the QQ plot diverge from the line for the higher end of the distribution. This is consistent with the histogram in Figure 6.4 that shows a shorter tail on the high end as compared to the low end of the distribution. This plot and the histogram reveal that the model residuals diverge from a perfectly normal distribution. Of course, the degree of non-normality can be quantified (e.g., with skewness and kurtosis measures). However, in this chapter we are most interested in visualizing the data, and especially looking for gross violations of assumptions. We should note here the grey area between satisfaction of an assumption and a gross violation. At this point, we leave the interpretation to the reader and provide information on how such visualizations can be made.

### 6.2 Plotting Nested Data

Earlier, we illustrated some basic plotting capabilities of R for linear models with only single levels. These tools are also potentially useful in multilevel contexts even though they are not specific to that use. Next, we move on to graphical tools more specifically useful with multilevel data.

Multilevel models are often applied to relatively large, indeed sometimes huge, data sets. Such data sets provide a richness that cannot be realized in studies of small samples. However, a complication that often arises from this vastness of multilevel data is the difficulty of creating plots that can summarize large amounts of information and thereby clearly portray the nature of relationships among the variables. For example, the Prime Time school data set contains more than 10,000 third grade students. A single plot of all 10,000 would be overwhelming and fairly uninformative. Including a nesting structure (e.g., school corporation) can lead to many corporation-specific plots because the data contain 60 corporations. Thus the plotting of nested data necessarily carries more nuances (difficulties) than typically appear with single-level data.

Graphing such data and ignoring the nesting structure can lead to aggregation bias and misinterpretation of results. For example, two variables may be negatively related within nested structures (e.g., classrooms) but positively related overall (e.g., when ignoring classrooms). This is sometimes known as Simpson’s paradox. In addition, sometimes a nested structure of data does not change the sign of the relationship between variables, but rather the estimate of the relationship can be strengthened or suppressed by the nested data structure. This result has been called the reversal paradox (Tu, Gunnell, & Gilthorpe, 2008). Thus, when plotting multilevel data,
the nested structure should be explicitly considered. If not, at minimum, a researcher must realize that the relationships in the unstructured data may differ when the nesting structure is considered. Although dealing with the complexities in plotting nested data can be at times vexing, the richness that nested data provide far outweighs any of the complications that may arise from applying the technique.

6.3 Using the lattice Package

The lattice package in R provides several powerful tools for plotting nested data (Sarkar, 2008).

6.3.1 dotplot

One very useful function in this package is dotplot. One way to use this function is to plot a variable of interest on the x axis with a grouping variable (e.g., classrooms) on the y axis. In the Prime Time data, identifiers for each corporation, each school within corporation, and each individual student are included. Classrooms within a school are simply numbered $1 - n_j$, where $n_j$ is the number of classrooms in the school. This type of structure is typical of large multilevel data sets. Suppose we want to see how reading achievement (geread) is distributed within and between classrooms. To begin, we take a single school (767) in a single corporation (940). This is the first school represented in the data set and we are using it solely for illustrative purposes. Within this school are four classrooms. To compare the distributions of geread scores between classrooms within the school, we can use the dotplot function from the lattice package as follows:

```r
dotplot(
  class ~ geread,
  data = Achieve.940.767, jitter.y = TRUE, ylab = "Classroom",
  main = "Dotplot of \'geread\' for Classrooms in School 767, Which is Within Corporation 940")
```

Several programming points should be noted here. First, we created a new data set containing data for just this individual school, using the following code:

```r
Achieve.940.767 <- Achieve[Achieve$corp == 940 & Achieve$school == 767,]
```

This R command literally identifies the rows in which corp is equal to 940 (equality checks require two equal signs) and school is equal to 767.
The class ~ geread component of the code instructs the function to plot geread for each classroom. The jitter.y parameter is used to jitter or slightly shift overlapping data points in the graph. For example, if multiple students in the same classroom have the same scores for geread, using the jitter option will shift those points on the y axis to indicate clearly the multiple values at the same x value. Finally, labels can be specified. Note that the use of `geread` in the main title puts geread in a single quote in the title. Calling the dotplot function using these R commands yields Figure 6.6.

The figure shows the dispersion of geread for the classrooms in school 767. From this plot, we can see that students in each of the four classrooms had generally similar reading achievement scores. However, it is also clear that classrooms 2 and 4 have multiple students with outlying scores that are higher than those of other individuals within the school. We hope we have shown clearly how a researcher may make use of this type of plot when examining the distributions of scores for individuals at a lower level of data (e.g., students) nested within a higher level such as classrooms or schools.

Because the classrooms within a school are arbitrarily numbered, we can alter the order in which they appear in the graph to make a display more meaningful. Note that if the order of the classrooms had not been arbitrary (e.g., honors classes numbered 1 and 2), we would need to be

![Dotplot of ‘geread’ for Classrooms in School 767](image)

**FIGURE 6.6**
The dotplot of classrooms in school 767 (within corporation 940) for geread.
very careful about changing the order. However, in this case, no such concerns are necessary. In particular, the use of the `reorder` function on the left side of the `~` symbol will reorder the classrooms in ascending order of the variable of interest (`geread` in this case) in terms of the mean. Thus, we can modify Figure 6.6 to place the classes in descending order by the mean of `geread`.

```r
dotplot(
  reorder(class, geread) ~ geread,
  data = Achieve.940.767, jitter.y = TRUE, ylab = "Classroom",
  main = "Dotplot of \'geread\' for Classrooms in School 767, Which is Within Corporation 940")
```

From Figure 6.7, it is easier to see the within-class and between-class variability for school 767. Visually, at least, it is clear that classroom 3 is more homogeneous (smaller variance) and lower performing (smaller mean) than classrooms 2 and 4.

Although plots such as those in Figures 6.6 and 6.7 are useful, creating one for each school would yield so much visual information that it would be difficult to draw any meaningful conclusions from the data. Therefore, suppose that we ignored the classrooms and schools and instead focused on the highest level of data, corporation. Using what we already learned, it is possible

![FIGURE 6.7](image)

The dotplot of classrooms in school 767 (within corporation 940) for `geread` with classrooms ordered by means (lowest to highest).
to create dotplots of student achievement for each corporation. To do so, we would use the following code:

```r
dotplot(reorder(corp, geread) ~ geread, data = Achieve,
        jitter.y = TRUE,
        ylab = "Classroom", main = "Dotplot of \'geread\' for All Corporations")
```

The resulting dotplots that appear in Figure 6.8 demonstrate that with so many students within each corporation, the utility of the plot is, at best, very limited, even at this highest level of data structure. This is an example of what we noted earlier about the difficulties in plotting nested data due to (a) the sheer volume of the data and (b) the need to remain sensitive to the nesting structure of the data.

**FIGURE 6.8**
The dotplot of students in corporations ordered by means (lowest to highest).
One method for visualizing such large and complex data would be to focus on a higher level of data aggregation such as classroom rather than individual students. Recall, however, that classrooms are simply numbered from 1 to \( n \) within each school, and are not given identifiers that mark them as unique across the entire data set. Therefore, to focus on achievement at the classroom level, we must first create a unique classroom number. We can use the following R code to create such a unique identifier that augments the Achieve data with a new column of unique classroom identifiers called \texttt{Classroom \_ Unique}.

\begin{verbatim}
Achieve <- cbind(Achieve, Classroom_Unique = 
paste(Achieve$corp, Achieve$school, Achieve$class, sep = ""))
\end{verbatim}

After forming this unique identifier for classrooms, we then aggregate the data within the classrooms to find the mean of the variables within the classrooms. We do this by using the \texttt{aggregate} function:

\begin{verbatim}
Achieve.Class_Aggregated <- aggregate(Achieve, by = 
list(Achieve$Classroom_Unique), FUN = mean)
\end{verbatim}

This code creates a new data set (\texttt{Achieve.Class \_ Aggregated}) that contains the aggregated classroom data. The \texttt{by = list(Achieve$Classroom \_ Unique)} part of the code instructs the function on which variable name (here \texttt{Classroom \_ Unique}) of the aggregation is to be implemented. Now, with a new data set called \texttt{Achieve.Class \_ Aggregated}, we can examine the distribution of the \texttt{geread} means of the individual classrooms. Thus, our data set has functionally been reduced from over 10,000 students to 568 classrooms. We create a dotplot with the following command:

\begin{verbatim}
dotplot(reorder(corp, geread) ~ geread, data = Achieve.Class_ 
Aggregated, 
jitter.y = TRUE, 
ylab = "Corporation", main = "Dotplot of Classroom Mean \'geread\' Within the Corporations")
\end{verbatim}

Of course, we still know the nesting structure of the classrooms within the schools and the schools within the corporations. We are aggregating here for purposes of plotting, but not modeling the data. We want to remind readers of the potential dangers of aggregation bias discussed earlier. With this caveat in mind, consider Figure 6.9, which shows that classrooms within the corporations vary in terms of their mean levels of achievement (i.e., the within-line corporation spread) and between corporations (i.e., changes in the lines) and produce Figure 6.8.

We can also use dotplots to gain insights into reading performance within specific school corporations. Again, this would yield a unique plot such as the one above for each corporation. Such a graph may be useful when interest concerns a specific corporation or for assessing the variability of specific corporations.
We hope to have demonstrated that dotplots may be useful for gaining an understanding of the variabilities that do or do not exist in one or more variables of interest. Of course, looking only at a single variable can be limiting. Another particularly useful function for multilevel data that can be found in the *lattice* package is *xyplot*. This function creates a graph very similar to a scatterplot matrix for a pair of variables, but it accounts for the nesting structure in the data. For example, the following code produces such a plot for *geread* (y axis) by *gevocab* (x axis), accounting for school corporation.

```r
xyplot(geread ~ gevocab | corp, data = Achieve)
```

**FIGURE 6.9**
The dotplot of *geread* for corporations, with the corporation ordered by means (lowest to highest) of aggregated classroom data. The dots represent means of classrooms scores within each corporation.
Notice that the $|$ symbol defines the grouping or nesting structure. The ~ symbol implies that \texttt{geread} is predicted and modeled by \texttt{gevocab}. By default, the specific names of the grouping structure (corporation numbers here) are not plotted on the strip. To produce Figure 6.10, we added the strip argument with the following options to the above code:

\[
\text{strip} = \text{strip.custom}(\text{strip.names} = \text{FALSE}, \\
\text{strip.levels} = \text{c}((\text{FALSE}, \text{TRUE}))
\]

Our use of the optional strip argument adds the corporation number to the graph, and removes the “corp” variable name from each strip above all the bivariate plots, which itself was removed with the \text{strip.names} = \text{FALSE} sub-command.

Of course, any sort of specific conditioning of interest can be applied to a specific graph. For example, we may want to plot the schools in, say, Students in Each Corporation

\begin{figure}
\centering
\includegraphics[width=\textwidth]{figure610.png}
\caption{The \texttt{xyplot} of \texttt{geread} (y axis) as function of \texttt{gevocab} (x axis) by corporation.}
\end{figure}
corporation 940, which can be done by extracting from the Achieve data only corporation 940, as we did with the code below to produce Figure 6.11.

```r
xyplot(geread ~ gevocab | school, data = Achieve[ Achieve$corp
   = 940, ], strip = strip.custom(strip.names = FALSE, strip.
   levels = c(FALSE, TRUE)), main = "Schools in Corporation 940")
```

We have now discussed two functions that can be useful for visualizing grouped or nested data. An additional plotting strategy involves assessment of the residuals from a fitted model. Doing so can help discern violations of assumptions, much as we saw earlier in this chapter when discussing single-level regression models.

Because residuals are assumed to be uncorrelated with any of the grouping structures in the model, they can be plotted using the R functions discussed

**FIGURE 6.11**
The `xyplot` of `geread` (y axis) as function of `gevocab` (x axis) by school within corporation 940.
earlier for single-level data. For example, to create a histogram with a density line plot of the residuals, we first standardize the residuals and use code as we did earlier. Figure 6.12 was produced with the following syntax:

```r
hist(scale(resid(Model3.1)),
    freq = FALSE, ylim = c(0,.7), xlim = c(-4, 5),
    main = "Histogram of Standardized Residuals from Model 3.1",
    xlab = "Standardized Residuals")
lines(density(scale(resid(Model3.1))))
box()
```

The only differences in the way that we plotted residuals with `hist` earlier in the chapter are purely cosmetic in nature. In particular, here we used the `box` function to draw a box around the plot and specified the limits of the y and x axes. Alternatively, a QQ plot can be used to evaluate the assumption of normality, as described earlier in the chapter. Figure 6.13 depicts a QQ plot. The code to generate such a plot is:

```r
qqnorm(scale(resid(model3.1))
qqline(scale(resid(model3.1)))
```

Clearly, the QQ plot and the associated histogram illustrate issues on the high end of the distribution of residuals. One issue is fairly common in educational research: ceiling effects. In particular, an examination of the previous plots we created reveals that a nontrivial number of students achieved
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maximum scores on *gread*. The multilevel model assumes that the distribution of residuals follows a normal distribution. However, when a maximum value is reached, it is necessarily the case that the residuals will not be normally distributed because a fairly large number of individuals have the same residual values.

The plotting capabilities available in R are impressive. Unfortunately, we were only able to highlight a few of the most useful plotting functions in this chapter. For the most part, we can summarize the graphical ability of R and the available packages as “if you can envision it, you can implement it.” Many useful resources are available for graphics in R. An Internet search will reveal many great (and free) online resources.

**Summary**

This chapter focused on graphing multilevel data. Exploration of data using graphs is always recommended for any data analysis problem, and can be particularly useful in the context of multilevel modeling, as we have seen here. We saw how a scatterplot matrix can provide insights into relationships among variables that may not be readily apparent from a simple review of model coefficients. In addition, we learned the power of dotplots to reveal interesting patterns at multiple levels of a data structure. We were able to
visualize mean differences among classrooms in a school and among individuals within a classroom. Finally, graphical tools can also be used to assess the important assumptions underlying linear models in general and multilevel models in particular, including normality and homogeneity of residual variance. In short, analysts should always be mindful of the power of pictures as they seek to understand relationships in their data.
Brief Introduction to Generalized Linear Models

Heretofore, we focused our attention primarily on models for data in which the outcome variables are continuous. Indeed, we have been even more specific and dealt almost exclusively with models resting on the assumption that errors are normally distributed. However, in many applications, the outcome variable of interest is categorical rather than continuous. For example, a researcher may be interested in predicting whether an incoming freshman is likely to graduate from college in 4 years, using high school grade point average and admissions test scores as the independent variables. Here, the outcome is a dichotomous variable: graduation in 4 years (yes or no). Likewise, consider research conducted by a linguist who interviewed terminally ill patients and wants to compare the number of times those patients use the words death and dying during the interviews. The number of times that each word appears, when compared to the many thousands of words contained in the interviews, is likely to be very small, if not zero for some people.

Another way of considering this outcome variable is the frequency of use of certain target words among all the words used by the interview subjects. Again, this rate will likely be very low, so that the model errors are almost assuredly not normally distributed. Yet another example of categorical outcome variables occurs when a researcher is interested in comparing effects of scores by treatment condition on mathematics performance outcomes that are measured on a Likert scale, such as 1, 2, or 3 (higher scores indicate better performance on mathematics tasks). Thus, the multilevel models that we described in Chapters 2 through 5 are not applicable to these research scenarios.

In each of the previous examples, the outcome variable of interest is not measured on a continuous scale, and will almost surely not produce normally distributed model errors. As we have seen, the linear multilevel models discussed previously work under the assumption of normality of errors. For this reason, they are not appropriate for situations in which these or other types of variables that cannot be appropriately analyzed with a linear model are to be used. However, alternative models for such variables are available. Taken together, these alternatives for categorical outcome variables are often referred to as generalized linear models (GLMs). Before we discuss the multilevel versions of these models in Chapter 8, we should first explore some common GLMs and their applications in the single-level context.
We will expand this discussion in Chapter 8 when we cover multilevel variants of these models and fitting them in R.

The following sections of this chapter focus on three broad types of GLMs: (1) those for categorical outcomes (dichotomous, ordinal, and nominal), (2) counts or rates of events that occur very infrequently, and (3) counts or rates of events that occur somewhat more frequently. After basic theoretical presentations of the three types, we will describe how these single-level GLMs can be fit using functions in R.

### 7.1 Logistic Regression Model for Dichotomous Outcome Variable

As an example of a GLM, we begin the discussion with models for dichotomous outcome data. Consider an example involving a sample of 20 men, 10 of whom have been diagnosed with coronary artery disease and 10 who have not. Each of the 20 individuals was asked to walk on a treadmill until he became too fatigued to continue. The outcome variable in this study was the diagnosis and the independent variable was the time walked until fatigue; i.e., the point at which the subject requested to stop. The goal of the study was to find a model predicting coronary artery status as a function of time walked until fatigue. If an accurate predictive equation could be developed, it might be a helpful tool for physicians to use in helping to diagnose heart problems. In the context of Chapter 1, we might consider applying a linear regression model to these data, as we found that approach useful for estimating predictive equations. However, recall that the technique involves a number of assumptions upon which appropriate inference in the context of linear regression depends, including normal distribution of residuals. Because the outcome variable in the current problem is a dichotomy (coronary disease or no disease), the residuals will almost certainly not follow a normal distribution. Therefore, we must identify an alternative approach for dealing with dichotomous outcome data such as these.

Perhaps the most common model for linking a dichotomous outcome variable with one or more independent variables (continuous or categorical) is logistic regression. The logistic regression model takes the form

\[
\ln \left( \frac{p(y = 1)}{1 - p(y = 1)} \right) = \beta_0 + \beta_1 x
\]

(7.1)

Here, \( y \) is the outcome variable of interest taking the values 1 or 0 where 1 is typically the outcome of interest. Note that these dichotomous outcomes could also be assigned other values, although 1 and 0 are probably
the most commonly used in practice. This outcome is linked to an independent variable $x$ by the slope ($\beta_1$) and intercept ($\beta_0$). Indeed, the right side of this equation should look very familiar: it is identical to the standard linear regression model. However, the left side is very different from what we see in linear regression due to the logistic link function, also known as the logit. Within the parentheses lie the odds that the outcome variable will take the value of 1. For our coronary artery example, 1 is the value for having coronary artery disease and 0 is the value for not having it.

To render the relationship between this outcome and the independent variable (time walking on treadmill until fatigue) linear, we must take the natural log of these odds. Thus, the logit link for this problem is the natural log of the odds of an individual having coronary artery disease. Interpretation of the slope and intercept in the logistic regression model is the same as interpretation in the linear regression context. A positive value of $\beta_1$ would indicate that the larger the value of $x$, the greater the log odds of the target outcome occurring. The parameter $\beta_0$ represents the log odds of the target event occurring when the value of $x$ is 0. Logistic regression models can be fit easily in R using the GLM function within the MASS library, which is a standard package included with the basic installation of R. In the next section, we will see how to call this function and interpret the results it generates.

The data were read into a data frame called `coronary`, using the methods outlined in Chapter 2. The logistic regression model can then be fit in R using the following command sequence, where `group` refers to the outcome variable, and `time` is the number of seconds walked on the treadmill.

```r
coronary.logistic<-glm(group~time, family = binomial)
```

Here we have created a model output object titled `coronary.logistic` that contains the parameter estimates and model fit information. The `glm` command indicates that we are using a GLM that we define within the parentheses (not to be confused with a GLM fitted with the `lm()` function in R, as discussed in Chapter 1). As with other R functions demonstrated in this book, the dependent variable appears on the left side of the `~` symbol and the independent variable(s) appear on the right side. Finally, we indicate that this is a dichotomous logistic regression model with the `family = binomial` command.

We can obtain a summary from this analysis using the `summary(coronary.logistic)` command. When interpreting logistic regression results, it is important to know which of two possible outcomes is modeled by the software in the numerator of the logit. In other words, we must know which category was defined as the target by the software so that we can properly interpret the model parameter estimates. By default, the `glm` command will treat the higher value as the target. In this case, 0 = no disease and 1 = disease. Therefore, the numerator of the logit will be 1 or disease. It is possible to change this so that the lower number is the target, and the interested reader can refer to `help(glm)` for
more information in this regard. This is a very important consideration, as the results would be completely misinterpreted if R used a different specification from the one the user thinks was used. The results of the `summary` command appear below.

Call:
glm(formula = group ~ time, family = binomial)

Deviance Residuals:

<table>
<thead>
<tr>
<th>Min</th>
<th>1Q</th>
<th>Median</th>
<th>3Q</th>
<th>Max</th>
</tr>
</thead>
<tbody>
<tr>
<td>-2.1387</td>
<td>-0.3077</td>
<td>0.1043</td>
<td>0.5708</td>
<td>1.5286</td>
</tr>
</tbody>
</table>

Coefficients:

| Estimate | Std. Error | z value | Pr(>|z|) |
|----------|------------|---------|---------|
| (Intercept) | 13.488949 | 5.876693 | 2.295 | 0.0217 * |
| coronary$time | -0.016534 | 0.007358 | -2.247 | 0.0246 * |

---

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 27.726 on 19 degrees of freedom
Residual deviance: 12.966 on 18 degrees of freedom

AIC: 16.966

Number of Fisher Scoring iterations: 6

Our initial interest is determining whether a significant relationship between the independent variable (time) and the dependent (coronary disease status) exists. Thus, we will first look at the `time` row as it contains this information. The `Estimate` column includes the slope and intercept values. The estimate of $\beta_1$ is $-0.016534$, indicating that the more time an individual could walk on the treadmill before becoming fatigued, the lower the log odds that he had coronary artery disease, i.e., the less likely he was to have heart disease. Through the simple transformation of the slope $e^{\beta_1}$, we can obtain the odds of having coronary artery disease as a function of time. For this example, $e^{-0.016534}$ is 0.984, indicating that for every additional second an individual can walk on a treadmill before becoming fatigued, his estimated odds of having coronary artery disease are multiplied by 0.984. Thus, for an additional minute of walking, the odds decrease by $\exp(-0.016534 \cdot 60) = 0.378$.

Adjacent to the `coefficient` column is the standard error that measures the sampling variation in the parameter estimate. The estimate divided by the standard error yields the test statistic that appears in the `z` column. This is the test statistic for the null hypothesis that the coefficient is equal to 0. Next to `z` is the `p` value for the test. Using standard practice, we would conclude that a `p` value less than 0.05 indicates statistical significance. In addition, R provides a simple heuristic for interpreting these results based on the asterisk (*). For this example, the `p` value of 0.0246 for time indicates
a statistically significant relationship between time on the treadmill to fatigue and the odds of an individual having coronary artery disease. The negative sign for the estimate further tells us that more time spent on the treadmill was associated with a lower likelihood of having heart disease.

One common approach to assessing the quality of the model fit to the data is by examining deviance values. For example, residual deviance compares the fit between a model that is fully saturated, (perfectly fits the data) and our proposed model. Residual deviance is measured using the $\chi^2$ statistic that compares the predicted outcome value with the actual value for each individual in a sample. If the predictions are very far from the actual responses, $\chi^2$ will tend to be a large value, indicating that the model is not very accurate. In the case of residual deviance, we know that the saturated model will always provide optimal fit to the data at hand, although in practice it may not be particularly useful for explaining the relationship between $x$ and $y$ in a population because it will have a separate model parameter for every cell in the contingency table relating the two variables and thus may not generalize well.

The proposed model will always be more parsimonious (have fewer parameters) than the saturated model and therefore will be more interpretable and generalizable to other samples from the same population, assuming that it does in fact provide adequate fit to the data. With appropriately sized samples, the residual deviance can be interpreted as a true $\chi^2$ test and the $p$ value can be obtained to determine whether the fit of the proposed model is significantly worse than that of the saturated model. The null hypothesis for this test is that model fit is adequate, i.e., the fit of the proposed model is close to that of the saturated model. With a very small sample such as the 20 treadmill walkers, this approximation to the $\chi^2$ distribution does not hold (Agresti, 2002) and we must therefore be very careful how we interpret the statistic. For pedagogical purposes, let us obtain the $p$ value for $\chi^2$ of 12.966 with 18 degrees of freedom. This value is 0.7936, which is larger than the $\alpha$ cut-off of 0.05, indicating that we cannot reject that the proposed model fits the data as well as the saturated model. Thus, we would then retain the proposed model as sufficient for explaining the relationships of the independent and dependent variables.

The other deviance statistic that R provides for assessing fit is the null deviance. It tests the null hypothesis that the proposed model does not fit the data better than a model in which the average odds of having coronary artery disease is used as the predicted outcome for every time value (i.e., that $x$ is not linear predictive of the probability of having coronary heart disease). A significant result here would suggest that the proposed model is better than no model. Again, however, we must interpret this test with caution when our sample size is very small, as is the case here. For this example, the $p$ value of the null deviance test ($\chi^2 = 27.726$ with 19 degrees of freedom) was 0.0888. As with the residual deviance test, the result is not statistically significant at $\alpha = 0.05$, suggesting that the proposed model does not provide better fit than the null model with no relationships. Of course, due to the small sample size, we must interpret both hypothesis tests with some caution.
Finally, R also provides the AIC value for the model. As we saw in previous chapters, AIC is a useful statistic for comparing the fits of different and not necessarily nested models with smaller values indicating better relative fit. If we wanted to assess whether including additional independent variables or interactions improved model fit, we could compare AIC values among the various models to ascertain which was optimal. The current example has no other independent variables of interest. However, it is possible to obtain the AIC for the intercept-only model using the following command. The purpose would be to determine whether including the time walking on the treadmill actually improved model fit after the penalty for model complexity was applied.

```r
coronary.logistic.null<-glm(group~1, family = binomial)
```

The AIC for this intercept-only model was 29.726, which is larger than the 16.966 for the model including a time factor. Based on AIC, along with the hypothesis test results discussed above, we would therefore conclude that the full model including time provided a better fit to the outcome of coronary artery disease.

---

### 7.2 Logistic Regression Model for Ordinal Outcome Variable

In the prior example, we considered an outcome variable that could take two possible values (0 = no heart disease and 1 = diseased heart). However, in many cases, a categorical outcome variable may have more than two potential outcomes. In this section we demonstrate the case where the dependent variable is ordinal in nature so that the categories can be interpreted as going from less to more, smaller to larger, or vice versa. Later in the chapter we will work with models that allow the categories to be unordered.

As a way to motivate our discussion of ordinal logistic regression models, consider the following example. A dietician developed a behavior management system designed to encourage healthier lifestyles for individuals suffering from obesity. One such healthy behavior is the preparation of food at home using fresh ingredients rather than dining out or eating prepackaged foods.

Study participants consisted of 100 individuals who were under a physician’s care for health issues directly related to obesity. Members of the sample were randomly assigned to (1) a control condition in which they received no special instruction in planning and preparing healthy meals from scratch or (2) a treatment condition in which they received such instructions. The outcome of interest was a rating provided 2 months after the study began in which all subjects indicated the extent to which they prepared their own meals. The response scale ranged from 0 (prepared all my meals from scratch) to 4 (never prepared any of my meals from scratch) so that lower values were indicative of a stronger
Brief Introduction to Generalized Linear Models

One commonly used method for analyzing ordinal data such as these is the cumulative logits model expressed as

$$\text{logit}[P(Y \leq j)]= \ln \left( \frac{P(Y \leq j)}{1 - P(Y \leq j)} \right)$$

This model has $J - 1$ logits where $J$ is the number of categories in the dependent variable and $Y$ is the actual outcome value. Essentially, this model compares the likelihood that the outcome variable will take a value of $j$ or less versus outcomes larger than $j$. The current example involves four separate logits:

$$\ln \left( \frac{p(Y = 0)}{p(Y = 1) + p(Y = 2) + p(Y = 3) + p(Y = 4)} \right) = \beta_{01} + \beta_{1x}$$

$$\ln \left( \frac{p(Y = 0) + p(Y = 1)}{p(Y = 2) + p(Y = 3) + p(Y = 4)} \right) = \beta_{02} + \beta_{1x}$$

$$\ln \left( \frac{p(Y = 0) + p(Y = 1) + p(Y = 2)}{p(Y = 3) + p(Y = 4)} \right) = \beta_{03} + \beta_{1x}$$

$$\ln \left( \frac{p(Y = 0) + p(Y = 1) + p(Y = 2) + p(Y = 3)}{p(Y = 4)} \right) = \beta_{04} + \beta_{1x}$$

The cumulative logits model has a single slope relating the independent variable to the ordinal response, and each logit has a unique intercept. To apply a single slope across all logits, we must make the proportional odds assumption that states that this slope is identical across logits. To fit the cumulative logits model to our data in R, we use the `polr` function, as in this example.

```r
cooking.cum.logit<-polr(cook~treatment, method = c("logistic"))
```

The dependent variable `cook` must be an R factor object. The independent variable may be either a factor or numeric. In this case, `treatment` is coded as 0 (control) or 1 (treatment). To ensure that `cook` is a factor, we use `cook<-as.factor(cook)` prior to fitting the model. Using `summary(cooking.cum.logit)` after fitting the model, we obtain the following output.

```
Call:
polr(formula = cook ~ treatment, method = c("logistic"))
Coefficients:
            Value Std. Error t value
treatment -0.7963096 0.3677003  -2.165649
```
After the function call, we see the results for the independent variable treatment. The coefficient value is –0.796, indicating that a higher value on the treatment variable (i.e., treatment = 1) was associated with a greater likelihood of providing a lower response on the cooking item. Remember that lower responses to the cooking item reflected a greater propensity to eat scratch-made food at home. Thus, in this example those in the treatment conditions had a greater likelihood of eating scratch-made food at home.

Adjacent to the coefficient value is the standard error for the slope, divided into the coefficient to obtain the \( t \) statistic residing in the final column. We note that no \( p \) value is associated with this \( t \) statistic because in the generalized linear model context, this value only follows the \( t \) distribution asymptotically (i.e., for large samples). In other cases, it simply indicates the relative magnitude of the relationship between the treatment and outcome variable. In this context, we may consider a relationship significant if the \( t \) value exceeds 2, which is approximately the \( t \) critical value for a two-tailed hypothesis test with \( \alpha = 0.05 \) and infinite degrees of freedom. Using this criterion, we would conclude that indeed a statistically significant negative relationship exists between treatment condition and self-reported cooking behavior. Furthermore, by exponentiating the slope we can also calculate the relative odds of a higher level response to the cooking item between the two groups.

Much as we did in the dichotomous logistic regression case, we use the equation \( e^{\beta} \) to convert the slope to an odds ratio. In this case, the value is 0.451, indicating that the odds of a treatment group member selecting a higher level response (less cooking behavior) is only 0.451 as large as the odds of the control group. Note that this odds ratio applies to any pair of adjacent categories, such as 0 versus 1, 1 versus 2, 2 versus 3, or 3 versus 4.

R also provides the individual intercepts along with the residual deviance and AIC for the model. The intercepts are, as with dichotomous logistic regression, the log odds of the target response when the independent variable is 0. In this example, a treatment of 0 corresponds to the control group. Thus, the intercept represents the log odds of the target response for the control condition. As we saw above, it is possible to convert this to the odds scale by exponentiating the estimate. The first intercept provides the log odds of a response of 0 versus all other values for the control group, i.e., plans and prepares all his or her meals versus all other options. The intercept for this
logit is \(-2.9259\), which yields an \(e^{-2.9259}\) of 0.054. We can interpret this to mean that the odds of a member of the control group planning and preparing his or her own meals versus a lower value is less are 0.054. In other words, it is highly unlikely a member of the control group will do this.

We can use the deviance along with the appropriate degrees of freedom to obtain a test of the null hypothesis that the model fits the data. The following command line in R will do this:

```r
1-pchisq(deviance(cooking.cum.logit), df.residual(cooking.cum.logit))
[1] 0
```

The \(p\) value is extremely small (rounded to 0), indicating that the model as a whole does not provide very good fit to the data. This could mean that we may need to include more independent variables with a strong relationship to the dependent to obtain a better fit. However, if our primary interest is in determining the presence of treatment differences in cooking behavior, then this overall test of model fit may not be crucial because we are able to answer the question about the relationship of treatment to cooking behavior.

### 7.3 Multinomial Logistic Regression

A third type of categorical outcome variable involves more than two categories that are not ordered. An example can be seen in a survey of likely voters asked to classify themselves as liberal, moderate, or conservative. A political scientist might be interested in predicting an individual’s political view as a function of age. The most common statistical approach for doing so is the generalized logits or multinomial logistic regression model. This approach, which Agresti (2002) called the baseline category logit model, assigns one of the dependent variable categories as a baseline against which all other categories are compared. More formally, the multinomial logistic regression model can be expressed as

\[
\ln \left( \frac{p(Y = i)}{p(Y = j)} \right) = \beta_{il} + \beta_{il}x
\]  

(7.4)

In this model, category \(j\) will always serve as the reference group against which the other categories \(i\) are compared. A different logit will apply to each non-reference category and each logit will have a unique intercept \((\beta_{il})\) and slope \((\beta_{il})\). Thus, unlike the cumulative logits model in which a single slope represented the relationship between the independent variable and the outcome, the multinomial logits model utilizes multiple slopes.
for each independent variable, one for each logit. Therefore, we do not need to make the proportional odds assumption. This makes this model a useful alternative to the cumulative logits model when that assumption is not tenable. The disadvantage of using the multinomial logits model with an ordinal outcome variable is that the ordinal nature of the data is ignored.

Any of the categories can serve as the reference, with the decision based on the research question of most interest (i.e., against the group that would exhibit the most interesting comparisons) or on pragmatic concerns such the largest group in cases where the research question does not serve as the primary deciding factor. Finally, it is possible to compare the results for two non-reference categories using the equation

\[
\ln \left( \frac{p(Y = i)}{p(Y = m)} \right) = \ln \left( \frac{p(Y = i)}{p(Y = j)} \right) - \ln \left( \frac{p(Y = m)}{p(Y = j)} \right)
\]  

(7.5)

For the present example, we will set the conservative group as the reference and fit a model in which age is the independent variable and political viewpoint is the dependent. We will use the `multinom` function within the `nnet` package that must be installed prior to running the analysis. We would then use the `library(nnet)` command to make the functions in this library available.

The data were read into the R data frame `politics` containing the age and viewpoint variables coded as C (conservative), M (moderate), or L (liberal) for each individual in the sample. Age was expressed in years. The R command to fit the multinomial logistic regression model is

```r
politics.multinom <- multinom(viewpoint ~ age, data = politics)
```

producing the following output.

```
# weights: 9 (4 variable)
initial value 1647.918433
final value 1617.105227
converged
```

This message simply indicates the initial and final values of the maximum likelihood fitting function, along with the information that the model converged. To find parameter estimates and standard errors, we use `summary(politics.multinom)`.

```
Call:
multinom(formula = viewpoint ~ age, data = politics)
Coefficients:
   (Intercept)       age
L  0.4399943 -0.016611846
M  0.3295633 -0.004915465
```

```
Based on these results, we see that the slope relating age to the logit comparing self-identification as liberal (L) is –0.0166, indicating that older individuals had lower likelihoods of being liberal versus conservative. To determine whether this relationship is statistically significant, we can calculate a 95% confidence interval using the coefficient and the standard error for this term. This interval is constructed as

\[-0.0166 \pm 2(0.0040)\]

\[-0.0166 \pm 0.008\]

\((-0.0246, -0.0086)\)

Because 0 is not in this interval, it is not a likely value of the coefficient in the population, leading us to conclude that the coefficient is statistically significant. In other words, we can conclude that older individuals in a population are less likely to identify themselves as liberal than as conservative. We can also construct a confidence interval for the coefficient relating age to the logit for moderate to conservative:

\[-0.0049 \pm 2(0.0034)\]

\[-0.0049 \pm 0.0068\]

\((-0.0117, 0.0019)\)

Thus, because 0 lies within this interval, we cannot conclude that a significant relationship exists between age and the logit. In other words, age is not related to the political viewpoint of an individual in a comparison of moderate versus conservative. Finally, we can calculate estimates for comparing L and M by applying Equation (7.5):

\[
\ln \left( \frac{p(Y = L)}{p(Y = M)} \right) = \ln \left( \frac{p(Y = L)}{p(Y = C)} \right) - \ln \left( \frac{p(Y = M)}{p(Y = C)} \right)
\]

\[
= (0.4400 - 0.0166(age)) - (0.3300 - 0.0049(age))
\]

\[
= 0.4400 - 0.3300 - 0.0166(age) + 0.0049(age)
\]

\[
= 0.1100 - 0.0117(age)
\]

Based on these analyses, we would conclude that older individuals are less likely to be liberal than conservative and less likely to be liberal than moderate.
7.4 Models for Count Data

7.4.1 Poisson Regression

To this point, we have focused on outcome variables of a categorical nature, such as whether an individual cooks for himself or herself and the presence or absence of coronary artery disease. Another type of data that does not fit well into the standard models assuming normally distributed errors involves counts or rates of some outcome, particularly of rare events. Such variables often follow the Poisson distribution, a major property of which is that the mean is equal to the variance. It is clear that if an outcome variable is a count, its lower bound must be 0, i.e., we cannot have negative counts. This presents a problem to researchers applying the standard linear regression model, as it may produce predicted values of the outcome that are less than 0 and thus are nonsensical.

To deal with this potential difficulty, the Poisson regression was developed. This approach for handling count data rests on the application of the log to the outcome variable, thereby overcoming the problem of negative predicted counts, since the log of the outcome can take any real number value. Thus, when dealing with Poisson distributions in the form of counts, we will use the log as the link function in fitting the Poisson regression model:

\[ \ln(Y) = \beta_0 + \beta_1 x \]  

(7.6)

In all other respects, the Poisson model is similar to other regression models in that the relationship between the independent and dependent variables is expressed via the slope \( \beta_1 \). Again, the assumption underlying the Poisson model is that the mean is equal to the variance. This assumption is typically expressed by stating that the overdispersion parameter \( \phi = 1 \). The \( \phi \) parameter appears in the Poisson distribution density and thus is a key component in the fitting function used to determine the optimal model parameter estimates in maximum likelihood. A thorough review of this fitting function is beyond the scope of this book. Interested readers are referred to Agresti (2002) for a complete presentation.

Estimating the Poisson regression model in R can be done with the \texttt{glm} function used previously for dichotomous logistic regression. Consider an example in which a demographer is interested in determining whether a relationship exists between the socioeconomic status (\textit{sei}) of a family and the number of children under the age of 6 months (\textit{babies}) living in the home. We first read the data and name it \texttt{ses_babies}. We then attach it using \texttt{attach(ses_babies)}. To view the distribution of the number of babies, we can use the \texttt{hist(babies)} command. Figure 7.1 is the resulting histogram.
Brief Introduction to Generalized Linear Models

We can see that 0 was the most common response of individuals in the sample; the maximum is 3. To fit the model with the `glm` function, we would use the following function call:

```r
babies.poisson <- glm(babies ~ sei, data = ses_babies, family = c("poisson"))
```

In this command sequence, we create an object called `babies.poisson` that includes the output for the Poisson regression model. The function call is identical to that used for most models in R, and we define the distribution of the outcome variable in the `family` statement. Using `summary(babies.poisson)` yields the following output.

Call:
```r
glm(formula = babies ~ sei, family = c("poisson"), data = ses_babies)
```

Deviance Residuals:
```
  Min     1Q Median     3Q    Max
-0.7312 -0.6914 -0.6676 -0.6217  3.1345
```

Coefficients:
```
            Estimate Std. Error z value Pr(>|z|)  
(Intercept) -1.268353   0.132641  -9.562  <2e-16 ***
sei          -0.005086   0.002900  -1.754    0.0794 .
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

FIGURE 7.1
Histogram of distribution of number of children and socioeconomic status.

We can see that 0 was the most common response of individuals in the sample; the maximum is 3. To fit the model with the `glm` function, we would use the following function call:

```r
babies.poisson <- glm(babies ~ sei, data = ses_babies, family = c("poisson"))
```

In this command sequence, we create an object called `babies.poisson` that includes the output for the Poisson regression model. The function call is identical to that used for most models in R, and we define the distribution of the outcome variable in the `family` statement. Using `summary(babies.poisson)` yields the following output.

Call:
```r
glm(formula = babies ~ sei, family = c("poisson"), data = ses_babies)
```

Deviance Residuals:
```
  Min     1Q Median     3Q    Max
-0.7312 -0.6914 -0.6676 -0.6217  3.1345
```

Coefficients:
```
            Estimate Std. Error z value Pr(>|z|)  
(Intercept) -1.268353   0.132641  -9.562  <2e-16 ***
sei          -0.005086   0.002900  -1.754    0.0794 .
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

(Dispersion parameter for poisson family taken to be 1)
These results show that sei did not have a statistically significant relationship to the number of children under 6 months old living in a home ($p = 0.0794$). We can use the following command to obtain the $p$ value for the test of the null hypothesis that the model fits the data.

\[
1 - \text{pchisq}(\text{deviance(babies.poisson)}, \text{df.residual(babies.poisson)})
\]

\[
[1] 0.9999998
\]

The resulting $p$ is clearly not significant at $\alpha = 0.05$, suggesting that the model does appear to fit the data adequately. The AIC of 1803 will be useful as we compare the relative fit of the Poisson regression model with that of other models for count data.

### 7.4.2 Models for Overdispersed Count Data

Recall that a primary assumption underlying the Poisson regression model is that the mean and variance are equal. When this assumption does not hold, such as when the variance is larger than the mean, estimation of model standard errors is compromised so that errors tend to appear smaller than is actually true in the population (Agresti, 2002). For this reason, it is important that researchers dealing with count data investigate whether this key assumption is likely to hold in a population. Perhaps the most direct way to do this is to fit alternative models that relax the $\phi = 1$ restriction we faced in Poisson regression. One approach is to use the quasi-Poisson model that takes the same form as the Poisson regression model, but does not constrain $\phi$ to be 1. This in turn will lead to different standard errors for the parameter estimates even though the coefficient estimate values will not change. The quasi-Poisson model can be fit in R using the `glm` function, with `family` set to

\[
\text{quasipoisson: babies.quasipoisson<-glm(babies~sei, data =}
\]

\[\text{ses_babies, family = c(”quasipoisson”)).}\]

We can obtain the output using the summary function.

Call:

\[
\text{glm(formula = babies ~ sei, family = c(”quasipoisson”),}
\]

\[\text{data = ses_babies)}\]

Deviance Residuals:

\[
\begin{array}{ccccc}
\text{Min} & \text{1Q} & \text{Median} & \text{3Q} & \text{Max} \\
-0.7312 & -0.6914 & -0.6676 & -0.6217 & 3.1345 \\
\end{array}
\]
Coefficients:

|               | Estimate | Std. Error | t value | Pr(>|t|) |
|---------------|----------|------------|---------|----------|
| (Intercept)   | -1.268353| 0.150108   | -8.45   | <2e-16 ***|
| sei           | -0.005086| 0.003282   | -1.55   | 0.121    |

---

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for quasipoisson family taken to be 1.280709)

Null deviance: 1237.8 on 1496 degrees of freedom
Residual deviance: 1234.7 on 1495 degrees of freedom
(3 observations deleted due to missingness)
AIC: NA
Number of Fisher Scoring iterations: 6

As noted above, the coefficients are the same for both quasi-Poisson and Poisson regression models. However, the standard errors in the former are somewhat larger than those in the latter. In addition, the estimate of \( \phi \) is provided for the quasi-Poisson model and is 1.28 in this case. While this is not exactly equal to 1, it is also not markedly larger, suggesting that the data are not terribly overdispersed. We can test for model fit as we did with the Poisson regression using the command

\[
1 - \text{pchisq}(\text{deviance(babies.quasipoisson)}, \text{df.residual(babies.quasipoisson)})
\]

[1] 0.9999998

As with the Poisson, the quasi-Poisson model also fit the data adequately. An alternative to the Poisson when data are overdispersed is a regression model based on the negative binomial distribution. The mean of this distribution is identical to that of the Poisson; the variance is

\[
\text{var}(Y) = \mu + \frac{\mu^2}{\theta}
\]  

(7.7)

From Equation (7.7), it is clear that as \( \theta \) increases in size, the variance approaches the mean and the distribution becomes more like the Poisson. It is possible for a researcher to provide a value for \( \theta \) if the data come from a particular distribution with a known \( \theta \). For example, when \( \theta = 1 \), the data are modeled from the gamma distribution. However, for most applications, the distribution is not known, in which case \( \theta \) will be estimated from the data.

The negative binomial distribution can be fit to the data in R using the \text{glm.nb} function within the MASS library. For the current example, the R commands to fit the negative binomial model and obtain the output are

\[
\text{babies.nb <- glm.nb(babies~sei, data = ses_babies)}
\]

\text{summary(babies.nb)}
Call:
glm.nb(formula = babies ~ sei, data = ses_babies, init.theta = 
   0.6048359440229,
   link = log)
Deviance Residuals:
   Min       1Q   Median       3Q      Max
-0.6670   -0.6352   -0.6158   -0.5778   2.1973

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -1.26087  0.15637   -8.063  7.42e-16 ***
sei          -0.00526  0.00338   -1.554  0.120
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(0.6048) family
taken to be 1)
Null deviance: 854.08 on 1496 degrees of freedom
Residual deviance: 851.72 on 1495 degrees of freedom
(3 observations deleted due to missingness)
AIC: 1755.4
Number of Fisher Scoring iterations: 1

Theta: 0.605
Std. Err.: 0.127

2 x log-likelihood: -1749.395

As we saw with the quasi-Poisson regression, the parameter estimates
for negative binomial regression are identical to those for the Poisson.
This fact simply reflects the common mean that the distributions all share.
However, the standard errors for the estimates differ across the three
models, although those for the negative binomial are very similar to those
from the quasi-Poisson. Indeed, the resulting hypothesis test results pro-
vide the same answers for all three models: no statistically significant
relationship of sei and the number of babies living in a home. In addi-
tion to the parameter estimates and standard errors, we also obtained an
estimate of $\theta$ of 0.605. To determine the optimal model, we can compare
the AIC from the negative binomial (1755.4) to that of the Poisson (1803)
to conclude that the former provides somewhat better fit to the data than
the latter. In short, it appears that the data are somewhat overdispersed
as the model designed to account for this (negative binomial) provides
better fit than the Poisson that assumes no overdispersion. From a more
practical view, the results of both models are very similar. A researcher
using $\alpha = 0.05$ would reach the same conclusion about the lack of relation-
ship between sei and the number of babies in a home regardless of model selected.
Summary

This chapter marks a major change in direction in terms of the type of data upon which we will focus. The first six chapters were concerned with models in which the dependent variable is continuous and generally assumed to be normally distributed. In Chapter 7 we learned about a variety of models designed for categorical dependent variables. In perhaps the simplest case, such variables can be dichotomous so that logistic regression is most appropriate for data analysis. When an outcome variable has more than two ordered categories, logistic regression can be extended easily via the cumulative logits model. For dependent variables with unordered categories, the multinomial logits model is the typical choice and can be employed easily with R. Finally, we examined dependent variables in the form of counts, and we may choose Poisson regression, the quasi-Poisson model, or the negative binomial model, depending upon the frequency of the outcome counted. As with Chapter 1, the goal of Chapter 7 was to introduce the single-level versions of the multilevel models to come. In Chapter 8, we will see that the model types described here can be extended into multilevel contexts using our old friends \texttt{lme} and \texttt{lmer}. 
Multilevel Generalized Linear Models

In the previous chapter, we introduced generalized linear models (GLMs) that are useful when the outcome variable of interest is categorical in nature. We described a number of models in this broad family, including logistic regression for binary, ordinal, and multinomial data distributions along with Poisson regression models for count or frequency data. In the examples given, the data were collected at a single level. However, just as is true for normally distributed outcome variables, it is common for categorical variables to be gathered in a multilevel framework. The focus of this chapter is on models designed specifically for scenarios in which the outcome of interest is either categorical or counted and the data have been collected in a multilevel framework. Chapter organization will mirror that of Chapter 7. We will start with a description of fitting logistic regression for dichotomous data, followed by models for ordinal and nominal dependent variables. The chapter will conclude with models for frequency count data that fit the Poisson distribution and overdispersed counts.

Chapter 7 provided the relevant mathematical underpinnings for these various models in the single-level case. Chapter 2 introduced some of the theory underlying multilevel models. This chapter will focus almost exclusively on the application of the R software package to fit these models and on the interpretation of the resultant output.

8.1 Multilevel Generalized Linear Model for Dichotomous Outcome Variable

To introduce multilevel generalized linear models (MGLMs) for dichotomous outcomes, let us consider the following example. A researcher has collected testing data indicating whether 9,316 students passed a state mathematics assessment, along with several measures of mathematics aptitude that were obtained before administration of the achievement test. She is interested in whether a relationship exists between the score on number sense aptitude and the likelihood that a student will achieve a passing score on the mathematics achievement test, for which all examinees are categorized as either passing (1) or failing (0). Because the outcome variable is dichotomous, we could use the binary logistic regression method introduced in Chapter 7.
However, students in this sample are clustered by school, as was the case with the data examined in Chapters 3 and 4. Therefore, we will need to account appropriately for this multilevel data structure in our regression analysis.

### 8.1.1 Random Intercept Logistic Regression

As with the standard linear model, R provides two approaches for modeling the data. Within the nlme package, the glmmPQL function can be used for any distributional family available to the glm function used extensively in Chapter 7. This function fits models using penalized quasi-likelihood estimation (Wolfinger & O’Connell, 1993). The technical details of this approach are beyond the scope of this book, and the interested reader is encouraged to investigate the Wolfinger & O’Connell article or works by Breslow and Clayton (1993) and Schall (1991).

The R command for fitting the model and obtaining the summary statistics appear below, following the call to the nlme library and the attachment of the file containing the data. In this initial analysis, we have a fixed effect for the intercept and the slope of the independent variable numsense, but we allow only a random intercept, thereby assuming that the relationship between the number sense score and the likelihood of achieving a passing score on the state math assessment (score2) is fixed across schools, i.e., the relationship of numsense with score2 does not vary from one school to another. As with lme featured in Chapters 3 and 4, the school clustering variable appears in the random sub-command to the left of the vertical line symbol (|). The additional sub-command in glmmPQL identifies the distributional family to which the outcome variable conforms, in this case the binomial. The results are saved to an output object called model8.1, to which we apply the summary command.

```r
library(nlme)
attach(mathfinal)
summary(model8.1<-glmmPQL(score2~numsense,random = ~1|school,
   family = binomial))

Linear mixed-effects model fit by maximum likelihood
  Data: NULL
  AIC BIC logLik
  NA NA NA

Random effects:
  Formula: ~1 | school
     (Intercept) Residual
  StdDev: 0.5363285 0.9676416

Variance function:
  Structure: fixed weights
  Formula: ~invwt
```
Fixed effects: score2 ~ numsense

<table>
<thead>
<tr>
<th></th>
<th>Value</th>
<th>Std.Error</th>
<th>DF</th>
<th>t-value</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>-11.615882</td>
<td>0.29477583</td>
<td>9275</td>
<td>39.40582</td>
<td>0</td>
</tr>
<tr>
<td>numsense</td>
<td>0.058951</td>
<td>0.00139054</td>
<td>9275</td>
<td>42.39450</td>
<td>0</td>
</tr>
</tbody>
</table>

Correlation:

<table>
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<th></th>
<th>(Intr)</th>
<th>numsense</th>
</tr>
</thead>
<tbody>
<tr>
<td>Intr</td>
<td>-0.953</td>
<td></td>
</tr>
</tbody>
</table>

Standardized Within-Group Residuals:

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<tr>
<th></th>
<th>Min</th>
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<th>Med</th>
<th>Q3</th>
<th>Max</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
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<td>-0.7323770</td>
<td>0.2969180</td>
<td>0.6668765</td>
<td>3.5297471</td>
</tr>
</tbody>
</table>

Number of Observations: 9316
Number of Groups: 40

The output that we obtain from this analysis is very similar in format to the output from the lme function. We first examine the variability in intercepts from school to school. This variation is presented as the standard deviation of the variance of the $U_{ij}$ terms from Chapter 2:

$$\sqrt{\tau^2}$$

which is 0.5363285 for this example. The modal value of the intercept across schools is -11.615882. In addition, the variation of individuals within schools (i.e., $\sigma_{error}$) is found to be 0.9676416, indicating variability in the likelihood of passing the exam among students from the same school. This result is not at all surprising, as we would expect such within-school differences in math proficiency.

Most analyses in education involve within-school or within-classroom differences. Here, we are dealing with a pass-or-fail situation. One example of an exception to within-school (or -classroom) variation involves schools working with unique populations of very high- or very low-performing students. For example, consider a school for gifted students in a large school district. It is conceivable that all of the students in the school may pass the examination.

With regard to the slope of the numsense fixed effect, we see that higher scores are associated with a greater likelihood of passing the state math assessment, with the slope being 0.058951 ($p < 0.05$). (Remember that R models the larger value of the outcome in the numerator of the logit, and in this case passing was coded as 1 and failing as 0). The standard error, test statistic, and $p$ value appear in the next three columns. The results are statistically significant ($p < 0.001$), leading to the conclusion that overall number sense scores are positively related to the likelihood of a student achieving a passing score on the assessment. Finally, we see that the correlation between the slope and intercept is strongly negative. Because we are estimating the relationship between two fixed effects, we are not particularly interested in the negative correlation. Information about the residuals appears at the very end of the output.
8.1.2 Random Coefficient Logistic Regression

As with the linear multilevel models, it is also possible to allow for random slopes with multilevel GLMs. The command structure with glmmPQL is very similar to that used with lme, with the inclusion of the numsense independent variable in the random sub-command. In all other respects, the call for model8.2 is very similar to that for model8.1.

```
summary(model8.2<-glmmPQL(score2~numsense,random = ~numsense|school,family = binomial))
```

```
Linear mixed-effects model fit by maximum likelihood
  Data: NULL
    AIC   BIC   logLik
    NA    NA     NA
Random effects:
  Formula: ~numsense | school
  Structure: General positive-definite, Log-Cholesky parametrization
       StdDev       Corr
(Intercept) 4.69544832 (Intr)
  numsense  0.02044981  -0.996
  Residual   0.95847083
Variance function:
  Structure: fixed weights
  Formula: ~invwt
Fixed effects: score2 ~ numsense

Value Std.Error   DF  t-value p-value
(Intercept) -12.774739 0.8197837 9275  -15.58306 0
  numsense    0.064274 0.0036458 9275   17.62953 0
Correlation:
    (Intr)
  numsense  -0.995
Standardized Within-Group Residuals:

    Min      Q1  Med      Q3     Max
-4.992101  -0.7233311 0.2958780 0.6629003 3.8902562

Number of Observations: 9316
Number of Groups: 40
```

We will focus on aspects of the output for the random coefficients model that differ from the output of the random intercepts. In particular, note that we have an estimate of

\[ \sqrt{\tau_1} \]

(the square root of the variance of the \( U_{ij} \) estimates for specific schools). This value, 0.02044981, is relatively small when compared to the variation of intercepts across schools and of individuals within schools. This means that
the relationship of number sense with the likelihood of receiving a passing score on the math achievement test is relatively similar across the schools. The modal slope across schools is 0.064274, again indicating that individuals with higher number sense scores also have higher likelihoods of passing the math assessment. Finally, it is important to note that the correlation between the random components of the slope and intercept—the standardized version of $\tau_{01}$—is very strongly negative.

8.2 Inclusion of Additional Level 1 and Level 2 Effects to MLRM

The researcher in our example is also interested in learning whether a statistically significant relationship exists between gender (female, where 1 = female and 0 = male) and the likelihood of passing the state math assessment and also the relationship of passing and number sense score. To fit the additional Level 1 variable to the random coefficients model, we would use the following command to obtain the subsequent output. This fits a model in which the impact of both the number sense score and gender are allowed to vary across schools.

```r
summary(model8.3<-glmmPQL(score2~numsense+female,random =~numsense+female|school,family = binomial))
```

Linear mixed-effects model fit by maximum likelihood

Data: NULL

AIC BIC logLik
NA NA NA

Random effects:
Formula: ~numsense + female | school
Structure: General positive-definite, Log-Cholesky parametrization

<table>
<thead>
<tr>
<th></th>
<th>StdDev</th>
<th>Corr</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>4.59384937</td>
<td>(Intr)</td>
</tr>
<tr>
<td>numsense</td>
<td>0.02022579</td>
<td>-0.996</td>
</tr>
<tr>
<td>female</td>
<td>0.10974567</td>
<td>0.907</td>
</tr>
<tr>
<td>Residual</td>
<td>0.95801716</td>
<td></td>
</tr>
</tbody>
</table>

Variance function:
Formula: ~invwt

Fixed effects: score2 ~ numsense + female

<table>
<thead>
<tr>
<th></th>
<th>Value</th>
<th>Std.Error</th>
<th>DF</th>
<th>t-value</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>-12.780219</td>
<td>0.8049464</td>
<td>9269</td>
<td>-15.877105</td>
<td>0.0000</td>
</tr>
<tr>
<td>numsense</td>
<td>0.064255</td>
<td>0.0036121</td>
<td>9269</td>
<td>17.788662</td>
<td>0.0000</td>
</tr>
<tr>
<td>female</td>
<td>0.022526</td>
<td>0.0510759</td>
<td>9269</td>
<td>0.441034</td>
<td>0.6592</td>
</tr>
</tbody>
</table>
Correlation:

    (Intr)  numsns
numsense  -0.995
female    0.256  -0.268

Standardized Within-Group Residuals:

                  Min         Q1       Med         Q3        Max
-4.6422483 -0.7244252  0.2977429  0.6653104  4.1120032

Number of Observations: 9316
Number of Groups: 40

These results indicate that being female is not significantly related to likelihood of passing the math achievement test; i.e., no gender differences are seen in the likelihood of passing. There are, however, some differences across schools in the relationship of gender and the likelihood of passing, as evidenced by the variation in the random component of slopes (0.10974567) that exceeds the variation for number sense. The average slope for gender across schools is 0.022526. This result means that the relationship of gender to the likelihood of passing the state math test varies across schools.

We can also include Level 2 independent variables such as the proportion of students receiving free lunch at each school (L_Free). In Model 8.4, we fit a random intercepts model including the Level 2 independent variable L_Free. The random coefficients terms have been removed from this example for the sake of simplicity.

```
summary(model8.4<-glmmPQL(score2~numsense+female+L_Free,random = ~1|school,family = binomial))
```

```
Linear mixed-effects model fit by maximum likelihood
Data: NULL
AIC  BIC  logLik
   NA   NA     NA
Random effects:
  Formula: ~1 | school
           (Intercept) Residual
StdDev:   0.531646 0.9635161

Variance function:
  Structure: fixed weights
  Formula: ~invwt
Fixed effects: score2 ~ numsense + female + L_Free

Value  Std.Error  DF  t-value  p-value
(Intercept) -12.045842  0.4033676  7030 -29.86318 0.0000
numsense     0.063396  0.0016529  7030  38.35493 0.0000
female      -0.025955  0.0556447  7030  -0.46644 0.6409
L_Free       -0.008517  0.0035816   32  -2.37800 0.0235
```
A statistically significant negative relationship exists between the proportion of students in the school receiving free lunches and the likelihood that a student will pass the mathematics assessment based on a coefficient value of −0.008517 and a \( p \) value of 0.0235. In addition, the coefficient for free lunch is unrelated to that of number sense or gender, but is negatively associated with the intercept. Results for the other predictor variables are largely the same as in the prior analyses.

### 8.3 Fitting Multilevel Dichotomous Logistic Regression Using \texttt{lme4}

The previous examples in this chapter were based on the \texttt{nlme} library in R. However, as noted previously in this chapter and earlier in this book, researchers can use functions from the alternative \texttt{lme4} library to conduct essentially the same analyses demonstrated above. The specific function for fitting GLMs with \texttt{lme4} is \texttt{glmer}. From a mathematical perspective, the algorithms used to obtain parameter estimates in \texttt{nlme} and \texttt{lme4} differ in some fundamental ways. While \texttt{glmmPQL} is based on the penalized quasi-likelihood method, \texttt{glmer} relies on an adaptive Gauss–Hermite likelihood approximation (Liu & Pierce, 1994) to fit the model to the data. As with the partial quasi-likelihood, we will not devote time to the technical specifications of this method for fitting the model to the data. However, interested readers are referred to the Liu & Pierce work for a description of this method.

As an introduction to \texttt{glmer}, we will fit the simple random intercept model with number sense as the independent variable. The R command and resultant output appear below.

```r
summary(model8.5<-glmer(score2~numsense+(1|school),family = binomial, nAGQ = 25))
```

Generalized linear mixed model fit by the Laplace approximation
Formula: score2 ~ numsense + (1 | school)
The function call is similar to that for glmmPQL. The only difference is the manner in which the random effect is specified. In addition, the parameter estimates and standard errors for the fixed effects, the correlation between the fixed effects parameters, and the estimate of intercept variation across schools are also very similar to those for Model 8.1. The results from glmer include values for the AIC and BIC. As noted in previous chapters, they can be used to compare the relative fits of various models in an attempt to pick the optimal one. These values were not available with glmmPQL.

The fit of two nested models created by glmer can be compared with one another in the form of a likelihood ratio test with the anova function. The null hypothesis of this test is that the fit of two nested models is equivalent, so that a statistically significant result (i.e., $p \leq 0.05$) would indicate that the models provide different fits to the data, with the more complicated (fuller) model typically providing an improvement in fit beyond what would be expected with the additional parameters added. The anova function is not available for comparing model fits using glmmPQL.

Just as we fit the random intercept model, it is also possible to fit the random coefficients model using glmer, as below.

```r
summary(model8.6<-glmer(score2~numsense+(numsense|school),
 family = binomial))
```

```
Generalized linear mixed model fit by the Laplace approximation
Formula: score2 ~ numsense + (numsense | school)
  AIC BIC logLik deviance
9769 9804 -4879 9759
Random effects:
  Groups Name Variance Std.Dev. Corr
  school (Intercept)  2.1701e+01  4.658438
  numsense  4.1048e-04  0.020260 -0.996
Number of obs: 9316, groups: school, 40
```
Fixed effects:

| Estimate | Std. Error | z value | Pr(>|z|) |
|----------|------------|---------|----------|
| (Intercept) -12.901317 | 0.819828 | -15.74 | <2e-16 *** |
| numsense 0.064902 | 0.003648 | 17.79 | <2e-16 *** |

---

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:

(Intr) numsense -0.995

These results are very closely aligned to those from glmmPQL. We have already discussed the results in some detail and will not do so again here. However, the inclusion of AIC and BIC in GLMER output allows a direct comparison of model fit, thus aiding in the selection of an optimal model for the data. As a brief reminder, AIC and BIC are both measures of unexplained variations in the data with a penalty for model complexity. Therefore, models with lower values provide relatively better fit. Comparison of AIC or BIC with Models 8.5 and 8.6 reveals that BIC provides better fit to the data. We do need to remember that AIC and BIC are not significance tests, but rather are measures of relative model fit. In contrast to the relative fit indices, we can compare the fit of the two models using the anova command:

```
anova(model8.5, model8.6)
```

Data:
Models:

```
model8.5: score2 ~ numsense + (1 | school)
model8.6: score2 ~ numsense + (numsense | school)
```

<table>
<thead>
<tr>
<th>Df</th>
<th>AIC</th>
<th>BIC</th>
<th>logLik</th>
<th>Chisq</th>
<th>Chi Df</th>
<th>Pr(&gt;Chisq)</th>
</tr>
</thead>
<tbody>
<tr>
<td>model8.5 3</td>
<td>10018.9</td>
<td>10040.4</td>
<td>-5006.5</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>model8.6 5</td>
<td>9768.7</td>
<td>9804.4</td>
<td>-4879.4</td>
<td>254.22</td>
<td>2</td>
<td>&lt; 2.2e-16 ***</td>
</tr>
</tbody>
</table>

---

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

These results indicate a statistically significant difference in the relative fits of the two models. Furthermore, the AIC and BIC are both lower for Model 8.6, suggesting that it provides better fit to the data than Model 8.5. Thus, we can conclude that the coefficients for numsense are significantly different across schools. Thus allowing them to vary among the schools leads to a more optimal model than forcing them to be the same. It should be noted that this comparison of model fit carried out by the anova command relies on a two-degrees-of-freedom test in which a significant difference in fit may be due to the fixed effects, the random effects, or both. Another way to interpret this result is that there appear to be school differences in the relationship of number sense and the likelihood of students passing the mathematics achievement test.

The inclusion of additional independent variables at both Level 1 (student) and Level 2 (school) follows the previous model syntax structure. In the
following example commands, we include both gender and the proportion of students at the school receiving free lunches, corresponding to Model 8.4 above.

```r
summary(model8.7<-glmer(score2~numsense+female+L_Free+(1|school),family = binomial))
```

Generalized linear mixed model fit by the Laplace approximation

Formula: score2 ~ numsense + female + L_Free + (1 | school)

<table>
<thead>
<tr>
<th>AIC</th>
<th>BIC</th>
<th>logLik</th>
<th>deviance</th>
</tr>
</thead>
<tbody>
<tr>
<td>7300</td>
<td>7334</td>
<td>-3645</td>
<td>7290</td>
</tr>
</tbody>
</table>

Random effects:

<table>
<thead>
<tr>
<th>Groups</th>
<th>Name</th>
<th>Variance</th>
<th>Std.Dev.</th>
</tr>
</thead>
<tbody>
<tr>
<td>school</td>
<td>(Intercept)</td>
<td>0.28302</td>
<td>0.53199</td>
</tr>
</tbody>
</table>

Number of obs: 7066, groups: school, 34

Fixed effects:

| Estimate | Std. Error | z value | Pr(>|z|) |
|----------|------------|---------|----------|
| (Intercept) | -12.084999 | 0.415491 | -29.08   | <2e-16 *** |
| numsense  | 0.063637   | 0.001718 | 37.04    | <2e-16 *** |
| female    | -0.026007  | 0.057780 | -0.45    | 0.6526    |
| L_Free    | -0.008655  | 0.003604 | -2.40    | 0.0163 *  |

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:

<table>
<thead>
<tr>
<th>(Intr)</th>
<th>numsns</th>
<th>female</th>
</tr>
</thead>
<tbody>
<tr>
<td>numsense</td>
<td>-0.847</td>
<td></td>
</tr>
<tr>
<td>female</td>
<td>-0.070</td>
<td>0.000</td>
</tr>
<tr>
<td>L_Free</td>
<td>-0.492</td>
<td>0.023</td>
</tr>
</tbody>
</table>

anova(model8.6, model8.7)

<table>
<thead>
<tr>
<th>Df</th>
<th>AIC</th>
<th>BIC</th>
<th>logLik</th>
<th>Chisq</th>
<th>Chi Df</th>
<th>Pr(&gt;Chisq)</th>
</tr>
</thead>
<tbody>
<tr>
<td>model8.2b</td>
<td>5</td>
<td>9768.7</td>
<td>9804.4</td>
<td>-4879.4</td>
<td></td>
<td></td>
</tr>
<tr>
<td>model8.4b</td>
<td>5</td>
<td>7299.9</td>
<td>7334.2</td>
<td>-3644.9</td>
<td>2468.9</td>
<td>&lt; 2.2e-16 ***</td>
</tr>
</tbody>
</table>

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Again, the parameter estimates and standard errors for the model terms are very similar for Models 8.4 and 8.7. The inclusion of the relative fit indices in the latter model, however, is very helpful because it allows us to make judgments regarding which model may be optimal for better understanding the population. Both of the relative fit indices are markedly smaller for Model 8.7, as compared to Models 8.5 and 8.6. The likelihood ratio test was significant, indicating that the fits of the two models differed. Thus, we
can conclude that inclusion of gender and/or proportion of students in the schools having free and reduced lunches produced a better model fit than models that excluded them.

### 8.4 MGLM for Ordinal Outcome Variable

As was the case for non-multilevel data, the cumulative logits link function can be used with ordinal data in the context of multilevel logistic regression. Indeed, the link will be the familiar cumulative logit described in Chapter 7. Furthermore, the multilevel aspects of the model including random intercept and coefficient take the same form described above. To provide context, we again consider the math achievement results for students. In this case, the outcome variable takes one of three possible values for each member of the sample: 1 = failure, 2 = pass, and 3 = pass with distinction. The question of most interest to the researcher is whether a computation aptitude score is a good predictor of status on the math achievement test.

#### 8.4.1 Random Intercept Logistic Regression

To fit a multilevel cumulative logits model using R, we install the ordinal package that allows fitting a variety of mixed effects models for categorical outcomes. Within this package, the clmm function is used to fit the multilevel cumulative logits model. Model parameter estimation is achieved using maximum likelihood based on the Newton-Raphson method. After we install this package, we will use the library(ordinal) statement to load it. The R commands to fit the model, obtain the results, and display the results appear below.

```r
summary(model8.8<-clmm(score~computation+(1|school)))

Cumulative Link Mixed Model fitted with the Laplace approximation

formula: score ~ computation + (1 | school)

link threshold nobs logLik AIC niter max.grad cond.H
logit flexible 9316 -7175.07 14358.13 18(786) 1.33e-05 6.9e+05

Random effects:
Var Std.Dev
school 0.3664 0.6053
Number of groups: school 40
```
Coefficients:

|                | Estimate | Std. Error | z value | Pr(>|z|) |
|----------------|----------|------------|---------|----------|
| computation    | 0.049748 | 0.001161   | 42.86   | <2e-16 *** |

---

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Threshold coefficients:

<table>
<thead>
<tr>
<th></th>
<th>Estimate</th>
<th>Std. Error</th>
<th>z value</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>2</td>
<td>9.5741</td>
<td>0.2519</td>
</tr>
<tr>
<td>2</td>
<td>3</td>
<td>12.9107</td>
<td>0.2713</td>
</tr>
</tbody>
</table>

One initial point to note is that the syntax for `clmm` is very similar in form to that for `lmer`. As with most R model syntax, the `score` outcome variable is separated from the `computation` fixed effect by the ~ symbol. The `school` random effect is included in parentheses along with 1, to denote that we are fitting a random intercepts model. It is important to state at this point that no current R package is available to fit a random coefficients model for the cumulative logits model.

An examination of the results presented above reveals that the variance and standard deviation of intercepts across schools are 0.3664 and 0.6053, respectively. Because the variation is not near 0, we conclude that differences in intercepts are present from one school to the next. In addition, we see a significant positive relationship between performance on the computation aptitude sub-test and performance on the math achievement test. This indicates that students who have higher computational skills also are more likely to attain higher ordinal scores on the achievement test (e.g., pass versus fail or pass with distinction versus pass). We also obtain estimates of the model intercepts (termed thresholds by `clmm`). As shown in the single-level cumulative logits model, the intercept represents the log odds of the likelihood of one response versus the other (e.g., 1 versus 2) when the value of the predictor variable is 0. A computation score of 0 would indicate that the student did not answer any of the items on the test correctly. Applying this fact to the first intercept presented above and the exponentiation of the intercept demonstrated in the previous chapter, we can conclude that the odds of a person with a computation score of 1 passing the math achievement exam are $e^{9.5741} = 14,387.28$ to 1 or very high! Finally, we also have available the AIC value (14,358.13) that we can use to compare the relative fit of this to other models.

As an example of fitting models with both Level 1 and Level 2 variables, we include the proportion of students receiving free lunches in the schools (`L_Free`) as an independent variable along with the computation score.

```R
summary(model8.9<-clmm(score~computation+L_Free+(1|school)))
```

Cumulative Link Mixed Model fitted with the Laplace approximation
Multilevel Generalized Linear Models

formula: score ~ computation + L_Free + (1 | school)

link threshold nobs logLik AIC niter max.grad cond.H
logit flexible 7069 -5442.57 10895.14 27(1312) 1.66e-03 1.4e+06

Random effects:
  Var Std.Dev
school 0.2919 0.5402
Number of groups: school 34

Coefficients:
  Estimate Std. Error z value  Pr(>|z|)
computation 0.053010 0.001359 39.018 < 2e-16 ***
L_Free -0.011735 0.003523 -3.331 0.000865 ***
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Threshold coefficients:
  Estimate Std. Error z value
1|2 9.6061 0.3475 27.64
2|3 12.9214 0.3662 35.29

Because we already discussed the results of the previous model in some detail, we will not reiterate the basic ideas again. However, it is important to note aspects that are different here. Specifically, the variability in the intercepts declined somewhat with the inclusion of the school-level variable L_Free. We also found a significant negative relationship between the proportion of students receiving free lunches at school and the likelihood that such individuals would attain higher achievement test scores. Finally, a comparison of the AIC values for the computation-only model (14,358.13) and the computation-and-free-lunch model (10,895.14) shows that the latter provides a somewhat better fit to the data than the former based on its smaller AIC value. In other words, we are better off including both free lunch and computation score when modeling the three-level achievement outcome variable. As was the case with glmmPQL, a likelihood ratio test via the anova command is not available for models fit with clmm.

As of the writing of this book, lme4 does not provide for fitting multilevel ordinal logistic regression models. Therefore, the clmm function in the ordinal package represents perhaps the most straightforward mechanism for fitting such models, albeit with its own limitations. As can be seen above, the basic fitting of these models is not complex and indeed the syntax is similar to that of lme4. In addition, the ordinal package allows for the fitting of ordered outcome variables in the non-multilevel context (see the clm function), and for multinomial outcome variables (see the clmm2 function discussed below). The ordinal package represents another method available for fitting such models in a unified framework.
8.5 MGLM for Count Data

In the previous chapter, we examined statistical models designed for use with outcome variables that represented the frequency of occurrence of some event. Typically these events were relatively rare, such as the addition of babies to a family. Perhaps the most common distribution associated with such counts is the Poisson in which the mean and variance are equal. However, as we saw in Chapter 7, this equality of the two moments does not always hold in all empirical contexts and the result is what is commonly called overdispersed data. In such cases, the Poisson regression model relating one or more independent variables to a count dependent variable is not appropriate, and we must make use of either the quasi-Poisson or negative binomial distribution, each of which is able to model the inequality of the mean and variance appropriately. Extending any of these models to the multilevel context is fairly straightforward, both conceptually and using R with the appropriate packages.

In the following sections, we will demonstrate analysis of multilevel count data outcomes in the context of Poisson regression, quasi-Poisson regression, and negative binomial regression in R. The example involves the number of cardiac warning incidents (e.g., chest pain, shortness of breath, dizzy spell) for 1000 patients associated with 110 cardiac rehabilitation facilities in a large state over a six-month period. Patients who recently suffered heart attacks and were entering rehabilitation agreed to be randomly assigned to a new exercise treatment program or to the standard treatment protocol. Of particular interest to the researcher leading this study is the relationship between treatment condition and the number of cardiac warning incidents. The new approach to rehabilitation is expected to result in fewer such incidents as compared to the traditional method. In addition, the researcher also collected data on patient sex and the number of hours that each rehabilitation facility is open during the week. This latter variable is of interest as it reflects the overall availability of the rehabilitation programs. The new method of conducting cardiac rehabilitation is coded in the data as 1 and the standard approach is coded 0. Males are also coded 1 and females are assigned 0 values.

8.5.1 Random Intercept Poisson Regression

The R commands and resultant output for fitting the Poisson regression model to the data appear below using the glmmPQL function in the nlme library used earlier to fit the dichotomous logistic regression models. This function will accommodate the same link functions available for the glm function, including the quasi-Poisson, as we will see shortly.

```r
summary(model8.10<-glmmPQL(heart~trt+sex,random =~1|rehab,family = poisson))
```

Linear mixed-effects model fit by maximum likelihood
Data: NULL

AIC  BIC  logLik
NA   NA   NA

Random effects:
Formula: ~1  |  rehab
   (Intercept)  Residual
StdDev:  0.6620581  4.010266

Variance function:
Structure: fixed weights
Formula: ~invwt

Fixed effects:  heart ~ trt + sex

<table>
<thead>
<tr>
<th></th>
<th>Value</th>
<th>Std.Error</th>
<th>DF</th>
<th>t-value</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>1.2306419</td>
<td>0.09601707</td>
<td>888</td>
<td>12.816908</td>
<td>0.0000</td>
</tr>
<tr>
<td>trt</td>
<td>-0.2163649</td>
<td>0.06482216</td>
<td>888</td>
<td>-3.337823</td>
<td>0.0009</td>
</tr>
<tr>
<td>sex</td>
<td>0.1354837</td>
<td>0.06305874</td>
<td>888</td>
<td>2.148531</td>
<td>0.0319</td>
</tr>
</tbody>
</table>

Correlation:
(Intr)  trt
trt   -0.152
sex   -0.099  0.045

Standardized Within-Group Residuals:

<table>
<thead>
<tr>
<th></th>
<th>Min</th>
<th>Q1</th>
<th>Med</th>
<th>Q3</th>
<th>Max</th>
</tr>
</thead>
<tbody>
<tr>
<td>Min</td>
<td>-1.48542222</td>
<td>-0.46850088</td>
<td>-0.36061041</td>
<td>0.09957005</td>
<td>12.49933170</td>
</tr>
</tbody>
</table>

Number of Observations: 1000
Number of Groups: 110

In terms of the function call, the syntax for Model 8.10 is virtually identical to that used for the dichotomous logistic regression model. The dependent and independent variables are linked by the usual R technique: `heart ~ trt + sex`. The outcome variable is `heart` to reflect the frequency of the warning signs for heart problems described above. The independent variables are treatment (`trt`) and `sex` while the specific rehabilitation facility data appears in the `rehab` variable. In this model, we are fitting a random intercept only, with no random slope and no rehabilitation center–level variables.

The results of the analysis indicate variation among the intercepts from rehabilitation facility to rehabilitation facility. However, the variation of individuals within the centers is much greater. We can use these values to estimate $\hat{\rho}$, the intra-class correlation coefficient, as $0.6620581/[0.6620581 + 4.010266] = 0.142$. As a reminder, the intercept reflects the mean frequency of events when (in this case) both independent variables are 0 (i.e., females in the control condition).

The average intercept across the 110 rehabilitation centers is 1.2306419, and the nonzero standard deviation for the random slope component of the model suggests that the intercept differs among centers. Stated another way,
we can conclude that the mean number of cardiac warning signs varies across rehabilitation centers, and that the average female in the control condition will have approximately 1.2 such incidents over the course of 6 months. In addition, these results reveal a negative relationship between heart and trt, and a significant positive relationship between heart and sex. Remember that the new treatment is coded as 1 and the control as 0, so that a negative relationship indicates fewer warning signs over 6 months for those in the treatment than those in the control group. Also, males were coded 1 and females 0, so that the positive slope for sex means that males experience more warning signs on average than females.

8.5.2 Random Coefficient Poisson Regression

If we believe that the treatment will exert different impacts on the number of warning signs occurring among the rehabilitation centers, we would want to fit the random coefficient model. This can be done for Poisson regression just as it was syntactically for dichotomous logistic regression, as demonstrated in Model 8.11.

```r
summary(model8.11<-glmmPQL(heart~trt+sex,random =~trt|rehab,family = poisson))
```

```
Linear mixed-effects model fit by maximum likelihood
Data: NULL
AIC BIC logLik
NA NA NA
Random effects:
Formula: ~trt | rehab
Structure: General positive-definite, Log-Cholesky parametrization

StdDev Corr
(Intercept) 0.7152662 (Intr)
trt 0.3016152 0.082
Residual 3.4957831

Variance function:
Structure: fixed weights
Formula: ~invwt

Fixed effects: heart ~ trt + sex

<table>
<thead>
<tr>
<th>Value</th>
<th>Std.Error</th>
<th>DF</th>
<th>t-value</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>1.1961344</td>
<td>0.09459146</td>
<td>888</td>
<td>12.645268</td>
</tr>
<tr>
<td>trt</td>
<td>-0.2288498</td>
<td>0.06877871</td>
<td>888</td>
<td>-3.327335</td>
</tr>
<tr>
<td>sex</td>
<td>0.1444697</td>
<td>0.05523175</td>
<td>888</td>
<td>2.615699</td>
</tr>
</tbody>
</table>

Correlation:

| (Intr) trt
| trt -0.046
| sex -0.093 0.038
```
The syntax for the inclusion of random slopes in the model is identical to that used with logistic regression and thus will not be discussed further here. The random effect for slopes across rehabilitation centers was estimated as approximately 0.302, indicating some differential center impact on the number of cardiac warning signs. However, it is also important to note that the standard deviation for the slopes is less than half as large as the standard deviation for the intercepts, so that this impact on treatment effectiveness is not very large relative to the impact of centers on the number of warning signs in general and is much smaller than differences in the number of warning signs among individuals within the same center. The correlation of the random slope and intercept model components is also very small (0.082). The average slope for treatment across centers remained statistically significantly negative, indicating that those in the treatment condition had fewer warning signs than those in the control group.

8.5.3 Inclusion of Additional Level 2 Effects in Multilevel Poisson Regression Model

Along with testing for treatment and gender differences in the rate of heart warning signs, the researcher conducting this study also wanted to know whether the number of hours per week the rehabilitation centers were open (hours) was related to the outcome variable. To address this question, we will fit a model with both Level 1 (trt and sex) and Level 2 (hours) effects.

summary(model8.12<-glmmPQL(heart~trt+sex+hours,random =~1|rehab,family = poisson))

Linear mixed-effects model fit by maximum likelihood
Data: NULL
AIC BIC logLik
NA NA NA

Random effects:
Formula: ~1 | rehab
(Intercept) Residual
StdDev: 0.618279 3.992570

Variance function:
Structure: fixed weights
Formula: ~invwt
Fixed effects: heart ~ trt + sex + hours
<table>
<thead>
<tr>
<th>Value</th>
<th>Std.Error</th>
<th>DF</th>
<th>t-value</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>1.181874</td>
<td>0.096655</td>
<td>888</td>
<td>12.227757</td>
</tr>
<tr>
<td>trt</td>
<td>-0.2179164</td>
<td>0.06461013</td>
<td>888</td>
<td>-3.372791</td>
</tr>
<tr>
<td>sex</td>
<td>0.1333911</td>
<td>0.06268513</td>
<td>888</td>
<td>2.127954</td>
</tr>
<tr>
<td>hours</td>
<td>-0.2770362</td>
<td>0.09902124</td>
<td>108</td>
<td>-2.797745</td>
</tr>
</tbody>
</table>

Correlation:

<table>
<thead>
<tr>
<th></th>
<th>(Intr)</th>
<th>trt</th>
<th>sex</th>
</tr>
</thead>
<tbody>
<tr>
<td>trt</td>
<td>0.149</td>
<td></td>
<td></td>
</tr>
<tr>
<td>sex</td>
<td>-0.092</td>
<td>-0.044</td>
<td></td>
</tr>
<tr>
<td>hours</td>
<td>0.267</td>
<td>-0.002</td>
<td>-0.018</td>
</tr>
</tbody>
</table>

Standardized Within-Group Residuals:

<table>
<thead>
<tr>
<th>Min</th>
<th>Q1</th>
<th>Med</th>
<th>Q3</th>
<th>Max</th>
</tr>
</thead>
<tbody>
<tr>
<td>-1.4839923</td>
<td>-0.4713802</td>
<td>-0.3546390</td>
<td>0.1157674</td>
<td>12.3346822</td>
</tr>
</tbody>
</table>

Number of Observations: 1000
Number of Groups: 110

These results show that the more hours a center is open, the fewer warning signs patients who attend will experience over a six-month period. In other respects, the parameter estimates for Model 8.12 do not differ substantially from those of the earlier models, generally revealing similar relationships among the independent and dependent variables.

Recall that the signal quality of the Poisson distribution is the equality of the mean and variance. In some instances, however, the variance of a variable may be larger than the mean, leading to the problem of overdispersion described in Chapter 7. In the previous chapter we described alternative statistical models for such situations, including one based on the quasi-Poisson distribution that took the same form as the Poisson, except that it relaxed the requirement of equal mean and variance. It is possible to fit the quasi-Poisson distribution in the multilevel modeling context as well. For \texttt{glmmPQL}, we would use the following syntax for the random intercept model (corresponding to Model 8.10).

\begin{verbatim}
summary(model8.13<-glmmPQL(heart~trt+sex,random = ~1|rehab,family = quasipoisson))
\end{verbatim}

Linear mixed-effects model fit by maximum likelihood

\begin{verbatim}
Data: NULL
AIC  BIC  logLik
NA   NA   NA
\end{verbatim}

Random effects:
Formula: ~1 | rehab
          (Intercept) Residual
StdDev: 0.6620581 4.010266
Variance function:
  Structure: fixed weights
  Formula: ~invwt
Fixed effects: heart ~ trt + sex

<table>
<thead>
<tr>
<th>Value</th>
<th>Std.Error</th>
<th>DF</th>
<th>t-value</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>1.2306419</td>
<td>0.09601707</td>
<td>888</td>
<td>12.816908</td>
</tr>
<tr>
<td>trt</td>
<td>-0.2163649</td>
<td>0.06482216</td>
<td>888</td>
<td>-3.337823</td>
</tr>
<tr>
<td>sex</td>
<td>0.1354837</td>
<td>0.06305874</td>
<td>888</td>
<td>2.148531</td>
</tr>
</tbody>
</table>

Correlation:
  (Intr) trt
  trt -0.152
  sex -0.099 0.045

Standardized Within-Group Residuals:

<table>
<thead>
<tr>
<th>Min</th>
<th>Q1</th>
<th>Med</th>
<th>Q3</th>
<th>Max</th>
</tr>
</thead>
<tbody>
<tr>
<td>-1.48542222</td>
<td>-0.46850088</td>
<td>-0.36061041</td>
<td>0.09957005</td>
<td>12.49933170</td>
</tr>
</tbody>
</table>

Number of Observations: 1000
Number of Groups: 110

The results of the quasi-Poisson regression are essentially identical to those in Model 8.10 using Poisson regression. Thus, it would appear that there is not an overdispersion problem with the data. Indeed, when we conduct the same analysis using lme4 (Model 8.14 below), we will see that the measures of relative fit indicate that the two models fit the data nearly identically. In this instance, we can rely on the Poisson regression results with some confidence.

As we learned in the previous chapter, the negative binomial distribution presents another alternative for use when the outcome variable is overdispersed. Unlike quasi-Poisson regression, in which the distribution is essentially Poisson with a relaxation of the requirement that $\phi = 1$, the negative binomial distribution takes an alternate form from the Poisson, with a difference in the variance parameter (see Chapter 7 for a discussion of this difference). To fit the negative binomial model, we must install and use the gamlss.mx library. The actual function for fitting the model is gamlssNP, as demonstrated below.

```r
summary(model8.14<-gamlssNP(heart~trt+sex, random = 1|rehab,
family = NBI, data = heartdata, mixture = "gq"))
```

******************************************************************************
Family: "NBI Mixture with NO"

Call: gamlssNP(formula = heart ~ trt + sex, random = 1 |
rehab, family = NBI, data = heartdata, mixture = "gq")

Fitting method: RS()
Multilevel Modeling Using R

---

**Mu link function: log**

**Mu Coefficients:**

|                | Estimate | Std. Error | t value | Pr(>|t|)   |
|----------------|----------|------------|---------|------------|
| (Intercept)    | 1.3277   | 0.07823    | 16.970  | 1.994e-62  |
| trt            | -0.3661  | 0.07860    | -4.658  | 3.302e-06  |
| sex            | 0.2856   | 0.07556    | 3.780   | 1.594e-04  |
| z              | 0.1758   | 0.07822    | 2.247   | 2.470e-02  |

---

**Sigma link function: log**

**Sigma Coefficients:**

|                | Estimate | Std. Error | t value | Pr(>|t|)   |
|----------------|----------|------------|---------|------------|
| (Intercept)    | 1.761    | 0.05754    | 30.6    | 5.57e-185  |

---

No. of observations in the fit: 4000

Degrees of Freedom for the fit: 5
Residual Deg. of Freedom: 995

Global Deviance: 3933.643
AIC: 3943.643
SBC: 3968.181

The function call includes the standard model set-up in R for the fixed effects (trt and sex), with the random effect (intercept within school in this example) denoted separately with the random command. The actual structure of the random intercept effect is the same as what we have seen with both glmmPQL and glmer, however. The mixture = "gq" sub-command requests the use of Gaussian quadrature estimation of the model parameters. Essentially this means that the error terms are assumed to be normally distributed and quadrature (a type of simulation-based parameter estimation) is used, as opposed to maximum likelihood that may be mathematically intractable for more complex models.

Because the format of the output from gamlssNP is very different from those of the other functions we used earlier, the format is worth examining in detail. After the function call, we see the table of parameter estimates, standard errors, test statistics, and p values. These results are similar to those described above, indicating the significant relationships between the frequency of cardiac warning signs and both treatment and sex. The variance associated with the random effect is the exponentiated intercept estimate in the Sigma Coefficients table: \( e^{1.761} = 5.818 \). We also are provided the deviance, AIC, and BIC (denoted SBC in the output for Schwartz’s Bayesian criterion).

While it would be interesting to do so, it is currently not possible to fit a random coefficient model for the negative binomial distribution using R.
Multilevel Generalized Linear Models

However, we can include Level 2 independent variables such as number of hours the centers are open in the model and compare the relative fit using the relative fit indices, as in Model 8.15.

```
summary(model8.15<-gamlssNP(heart~trt+sex+hours, random = 1|rehab, family = NBI, data = heartdata, mixture = "gq"))
```

************************************************************
Family: "NBI Mixture with NO"

Call: gamlssNP(formula = heart ~ trt + sex + hours, random = 1 | rehab,
family = NBI, data = heartdata, mixture = "gq")
Fitting method: RS()

- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Mu link function: log
Mu Coefficients:

| Estimate | Std. Error | t value | Pr(>|t|) |
|----------|------------|---------|----------|
| (Intercept) 1.26783 | 0.07898 | 16.0531 | 3.019e-56 |
| trt -0.32611 | 0.07819 | -4.1705 | 3.103e-05 |
| sex 0.25693 | 0.07518 | 3.4175 | 6.384e-04 |
| hours -0.28945 | 0.08155 | -3.5492 | 3.908e-04 |
| z 0.01376 | 0.07780 | 0.1768 | 8.597e-01 |

- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Sigma link function: log
Sigma Coefficients:

| Estimate | Std. Error | t value | Pr(>|t|) |
|----------|------------|---------|----------|
| (Intercept) 1.75 | 0.05878 | 29.77 | 4.468e-176 |

- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
No. of observations in the fit: 4000
Degrees of Freedom for the fit: 6
Residual Deg. of Freedom: 994
at cycle: 1

Global Deviance: 3923.1
AIC: 3935.1
SBC: 3964.546
************************************************************

As shown earlier, the number of hours that the centers are open is significantly negatively related to the number of warning signs over the six-month period of the study. In addition, both AIC and BIC are lower in Model 8.15 than in Model 8.14, yielding evidence that Model 8.15 provides a better fit to the data. Again, we can obtain the variance of the random intercepts through $e^{1.761} = 5.754$. 
8.6 Fitting Multilevel Poisson Regression Using \texttt{lme4}

The \texttt{glmer} function that we used to fit the dichotomous logistic regression model earlier in this chapter can also be used with Poisson regression with a very similar syntax. As can be seen in the commands below, the only difference in fitting the random intercept model for the different distributions is in the specification of the appropriate distributional family (Poisson in this case).

```r
summary(model8.16<-glmer(heart~trt+sex+(1|rehab),family = poisson))
```

**Generalized linear mixed model fit by the Laplace approximation**

**Formula:** heart ~ trt + sex + (1 | rehab)

<table>
<thead>
<tr>
<th>AIC</th>
<th>BIC</th>
<th>logLik</th>
<th>deviance</th>
</tr>
</thead>
<tbody>
<tr>
<td>10116</td>
<td>10136</td>
<td>-5054</td>
<td>10108</td>
</tr>
</tbody>
</table>

**Random effects:**

- Groups: Name Variance Std.Dev.
  - (Intercept) 1.2397 1.1134

- Number of obs: 1000, groups: rehab, 110

**Fixed effects:**

- Estimate Std. Error z value Pr(>|z|)
  - (Intercept) 0.80826 0.10993 7.352 1.95e-13 ***
  - trt -0.20814 0.01676 -12.415 < 2e-16 ***
  - sex 0.13735 0.01635 8.400 < 2e-16 ***

---

**Signif. codes:** 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

**Correlation of Fixed Effects:**

- (Intr) trt
  - trt -0.031
  - sex -0.022 0.058

Based on the similarity in results to those presented for the model fit using \texttt{glmmPQL}, we will not review these in detail here. However, it is important to note that, as stated previously, an advantage to using \texttt{glmer} is that it provides AIC and BIC values that allow for comparison of model fit. Thus, when we alter the model, we may have a better sense of how this action alters its statistical qualities. For example, fitting the random coefficients model with \texttt{glmer} yields the following including the relative fit statistics (AIC and BIC).

```r
summary(model8.17<-glmer(heart~trt+sex+(trt|rehab),family = poisson))
```

**Generalized linear mixed model fit by the Laplace approximation**

**Formula:** heart ~ trt + sex + (trt | rehab)
As noted previously, the variation among the coefficients for treatment across centers was greater than 0, suggesting that the individual centers impacted the effectiveness of the treatment although this impact was smaller than those of the centers on the number of warning signs in general, as measured by the intercept variance and standard deviation. The output from \texttt{glmer} also indicates that the relative fit of Model 8.17 is better than that of Model 8.16 because the AIC and BIC values of the former are smaller than those of the latter. In addition, because they are nested, we can use the \texttt{anova} function to compare the relative fit of the two models from \texttt{glmer} using the likelihood ratio test.

\begin{verbatim}
anova(model8.16, model8.17)
Data:
Models:
 model8.16: heart ~ trt + sex + (1 | rehab)
 model8.17: heart ~ trt + sex + (trt | rehab)

 Df AIC BIC logLik Chisq Chi Df Pr(>Chisq)
model8.16  4 10116.1 10135.7 -5054.0
model8.17  6  9329.7  9359.1 -4658.8  790.4  2 < 2.2e-16 ***

---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
\end{verbatim}

The statistically significant difference in model fit ($p < 0.001$) and the smaller AIC and BIC values in Model 8.17 provide further statistical evidence that the relationship of treatment to the number of cardiac symptoms differs across rehabilitation centers.

The \texttt{glmer} function can also be used to include variables at Level 2 such as the number of hours that a center is open and the Level 1 variables...
including `trt` and `sex`. The syntax is essentially identical to that for the comparable dichotomous logistic regression model with the exception of the definition of the distributional family.

```
summary(model8.18 <- glmer(heart ~ trt + sex + hours + (1 | rehab), family = poisson))
```

Generalized linear mixed model fit by the Laplace approximation
Formula: heart ~ trt + sex + hours + (1 | rehab)
           AIC      BIC   logLik deviance
    10113    10138  -5052.1    10103.3
Random effects:
     Groups   Name        Variance Std.Dev.
        rehab (Intercept) 1.16880   1.0811
Number of obs: 1000, groups: rehab, 110

Fixed effects:
     Estimate Std. Error   z value  Pr(>|z|)
  (Intercept)   0.78262   0.10779    7.260  3.86e-13 ***
trt           -0.20831   0.01677  -12.424 < 2e-16 ***
  sex           0.13734   0.01635    8.400  < 2e-16 ***
hours          -0.25054   0.11245   -2.228  0.0259 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
     (Intr)  trt  sex
trt  -0.033
sex  -0.023  0.058
hours -0.127 0.004 0.000

Because the AIC value for Model 8.18 is slightly lower than that of Model 8.16 and the BIC is slightly higher, we may conclude that the two models provide approximately comparable fit to the data. However, based on the relative fit indices, neither fits the data as well as Model 8.17. Below are the results for the likelihood ratio tests comparing these models. Taken together, these results reinforce our conclusions based on AIC and BIC, that Model 8.17 provides the best fit. Model 8.18 has a slightly lower log-likelihood value than Model 8.16, indicating that Model 8.18 provides slightly better fit than the latter.

```
anova(model8.16, model8.18)
```

Data:
Models:
model8.16: heart ~ trt + sex + (1 | rehab)
model8.18: heart ~ trt + sex + hours + (1 | rehab)
           Df  AIC      BIC   logLik deviance
    model8.16  4 10116.1  10135.7  -5054.0    10108.0
    model8.18  5 10113.3  10137.8  -5051.6    10103.3
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
anova(model8.17, model8.18)

Data:

Models:

model8.17: heart ~ trt + sex + hours + (1 | rehab)
model8.18: heart ~ trt + sex + (trt | rehab)

\[
\begin{array}{cccccc}
\text{DF} & \text{AIC} & \text{BIC} & \text{logLik} & \text{Chisq} & \text{Chi Df Pr(>Chisq)} \\
\hline
\text{model8.17} & 5 & 10113.3 & 10137.8 & -5051.6 & \\
\text{model8.18} & 6 & 9329.7 & 9359.1 & -4658.8 & 785.59 1 < 2.2e-16 *** \\
\end{array}
\]

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

It is also possible to fit the quasi-Poisson model using \texttt{glmer}. In fact, we recommend that researchers working with count data fit models for overdispersed data and compare the AIC and BIC values with those of the Poisson regression model to determine whether the assumption of equal mean and variance should be relaxed. The syntax and output for the quasi-Poisson model with \texttt{glmer} appear below.

\texttt{summary(model8.19<-glmer(heart~trt+sex+(1|rehab),family = quasipoisson))}

Generalized linear mixed model fit by the Laplace approximation
Formula: heart ~ trt + sex + (1 | rehab)

\[
\begin{array}{cccc}
\text{AIC} & \text{BIC} & \text{logLik} & \text{deviance} \\
10118 & 10143 & -5054 & 10108 \\
\end{array}
\]

Random effects:

<table>
<thead>
<tr>
<th>Groups</th>
<th>Name</th>
<th>Variance</th>
<th>Std.Dev.</th>
</tr>
</thead>
<tbody>
<tr>
<td>rehab</td>
<td>(Intercept)</td>
<td>23.142</td>
<td>4.8107</td>
</tr>
<tr>
<td>Residual</td>
<td></td>
<td>18.667</td>
<td>4.3205</td>
</tr>
</tbody>
</table>

Number of obs: 1000, groups: rehab, 110

Fixed effects:

\[
\begin{array}{cccc}
\text{Estimate} & \text{Std. Error} & \text{t value} \\
(Intercept) & 0.80826 & 0.47497 & 1.702 \\
trt & -0.20814 & 0.07243 & -2.874 \\
sex & 0.13735 & 0.07065 & 1.944 \\
\end{array}
\]

Correlation of Fixed Effects:

\[
\begin{array}{cc}
(\text{Intr}) & \text{trt} \\
trt & -0.031 \\
sex & 0.022 0.058 \\
\end{array}
\]

We will first compare the relative fit statistics for Model 8.19 (AIC = 10,118; BIC = 10,143) with those of Model 8.16, the standard Poisson regression approach, (AIC = 10,116; BIC = 10,136) to determine whether we should allow for overdispersion in the data. Because the indices for the Poisson model are slightly lower than those of the quasi-Poisson indicating that the former provides better fit than the latter, it appears that overdispersion is not a problem in this case. However, had the reverse been true, we would have wanted to rely on the results of the quasi-Poisson fit instead. It is not possible to
conduct a likelihood ratio test here because the two models are not nested in one another; i.e. one is not a simpler version of the other. Rather, they differ based on the algorithm used to obtain parameter estimates. Finally, although we will not do so here, it is possible to fit any of the models fit with Poisson regression using the quasi-Poisson distribution, simply by denoting this in the `family` statement as part of the function call.

**Summary**

In this chapter, we learned that the generalized linear models featured in Chapter 7 that accommodate categorical dependent variables can be extended easily to multilevel contexts. Indeed, the basic concepts relating to sources of variation and various types of models covered in Chapter 2 can be extended easily for categorical outcomes. In addition, R provides for easy fitting of such models through the `lme` and `lmer` families of functions. In many ways, this chapter represents a review of material that by now should be familiar even if applied in a new scenario. Perhaps the most important point to take away from this chapter is the notion that modeling multilevel data in the context of generalized linear models is not radically different from the normally distributed continuous dependent variable case. The same types of interpretations can be made and the same types of data structures can be accommodated.
Bayesian statistical modeling represents a fundamental shift from the frequentist methods of model parameter estimation that we used earlier. This paradigm shift is evident in part through the methodology used to obtain the estimates: Markov chain Monte Carlo (MCMC) most commonly for the Bayesian approach, and maximum likelihood (ML) and restricted maximum likelihood (REML) in the frequentist case. In addition, Bayesian estimation involves the use of prior distributional information that is not present in frequentist-based approaches. Perhaps even more than the obvious methodological differences, however, the Bayesian analytic framework involves a very different view from that traditionally espoused in the likelihood-based literature as to the nature of population parameters. In particular, frequentist-based methods estimate the population parameter using a single value obtained using sample data only.

In contrast, in the Bayesian paradigm, the population parameter is estimated as a distribution of values rather than a single number. Furthermore, this estimation is carried out using both sample data and prior distribution information provided by the researcher. Bayesian methods combine this prior information covering the nature of the parameter distribution with information taken from the sample data to estimate a posterior distribution. In practice, when a single value estimate of a model such as a regression coefficient linking dependent and independent variables is desired, the mean, median, or mode of the posterior distribution is calculated. In addition, standard deviations and density intervals for model parameters can also be estimated from this posterior distribution as well.

A key component of conducting Bayesian analysis is the specification of a prior distribution for each model parameter. These prior values may be either one of two types. Informative priors are typically drawn from prior research and their means and variances will be fairly specific. For example, a researcher may find a number of studies in which a vocabulary test score was used to predict reading achievement. Perhaps across these studies the regression coefficient is consistently around 0.5. The researcher may then set the prior for this coefficient as the normal distribution with a mean of 0.5 and a variance of 0.1. In doing so, he or she indicates up front that the coefficient linking these two variables in the study is likely to be near these values. Of course, such may not be the case. Because the data are used also to obtain the posterior distribution, the prior plays only a partial role in its
determination. In contrast to informative priors, noninformative (or diffuse) priors are not based on prior research. Rather, they are selected deliberately so as to constrain the posterior distribution for the parameter as little as possible, in light of the fact that little or no useful information is available for setting the prior distribution. As an example, if the literature contains insufficient evidence for a researcher to know what the distribution of the regression coefficient is likely to be, he or she may set the prior as a normal with a mean of 0 and a large variance of, perhaps, 1000 or even more. By using such a large variance for the prior distribution, the researcher acknowledges the lack of credible information regarding what the posterior distribution might be, thereby leaving the posterior distribution largely unaffected by the prior and relying primarily on the observed data to obtain the parameter estimate.

A reader may rightly question why or when Bayesian multilevel modeling may be particularly useful or even preferable to frequentist methods. One primary advantage of Bayesian methods in some situations including multilevel modeling is that unlike ML and REML, it does not rely on any distributional assumptions about the data. Thus, the determination of Bayesian credibility intervals (corresponding to confidence intervals) can be made without worry even if the data come from a skewed distribution. In contrast, ML or REML confidence intervals may not be accurate if foundational distributional assumptions are not met. In addition, the Bayesian approach can be very useful when the model to be estimated is very complex and frequentist-based approaches such as ML and REML cannot converge. A related advantage is that the Bayesian approach may be better able to provide accurate model parameter estimates in small sample cases. And, of course, the Bayesian approach to parameter estimation can be used in cases where ML and REML also work well. As we will see below, the different methods generally yield similar results in such situations.

9.1 MCMC Estimation

The scope of this book does not encompass the technical aspects of MCMC estimation, which is most commonly used to obtain Bayesian estimates. The interested reader is encouraged to consult any of several good works on the topic. In particular, Lynch (2010) provides a very thorough introduction to Bayesian methods for social scientists including a discussion of the MCMC algorithm. Kruschke (2011) provides a thorough general description of applied Bayesian analysis.

It should be noted here that while MCMC is the most frequently used approach for parameter estimation in the Bayesian context, it is not itself inherently Bayesian. Rather, it is simply an algorithmic approach to sampling from complex sampling distributions such as a posterior distribution.
seen in complicated models such as those in multilevel contexts. Although we will not describe the MCMC process in much detail here, it is necessary to discuss conceptually how it works so that readers will be more comfortable with the derivations of parameter estimates and also we must be able to diagnose whether the method worked appropriately so that we can have confidence in the final parameter estimates.

MCMC is an iterative process in which the prior distribution is combined with information from an actual sample to estimate the posterior distributions for each of the model parameters (e.g., regression coefficients, random effect variances). From this posterior distribution, parameter values are simulated a large number of times to obtain an estimated posterior distribution. After each such sample is drawn, the posterior is updated. This iterative sampling and updating process is repeated many times (e.g., 10,000 or more) until the researcher sees evidence of convergence of the posterior distribution, i.e., a value from one sampling draw is very similar to the previous sample draw. The Markov chain part of MCMC reflects the process of sampling a current value from the posterior distribution, given the previous sampled value. The Monte Carlo segment reflects the random simulation of these values from the posterior distribution. After the chain of values converges, we are left with an estimate of the posterior distribution of the parameter of interest (e.g., regression coefficient). At this point, a single model parameter estimate can be obtained by calculating the mean, median, or mode from the posterior distribution.

When using MCMC, the researcher must be aware of some technical aspects of the estimation that must be assessed to ensure that the analysis has worked properly. The collection of 10,000 (or more) individual parameter estimates form a lengthy time series that must be examined to ensure that two facts are true. First, the parameter estimates must converge, and second the autocorrelation between different iterations in the process should be low. Parameter convergence can be assessed via a trace plot, which is simply a graph of the parameter estimates in order from the first iteration to the last. The autocorrelation of estimates is calculated for a variety of iterations, and the researcher will look for the distance between estimates at which the autocorrelation becomes quite low.

When a researcher determines at what point the autocorrelation between estimates is sufficiently low, the estimates are thinned to remove those that may be more highly autocorrelated with one another than desirable. For example, if the autocorrelation is low when the estimates are 10 iterations apart, the time series of 10,000 sample points would be thinned to include only every tenth observation to create the posterior distribution of the parameter. The mean, median, and mode of this distribution would then be calculated using only the thinned values to yield the single parameter estimate value reported by R. A final issue is what is known as the burn-in period. Regarding distributional convergence, the researcher will not want to include any values in the posterior distribution for iterations prior
to the point at which the time series converged. Thus, iterations prior to convergence are referred to as having occurred during the burn-in and are not used to calculate posterior means, medians, and modes. Each of these MCMC conditions (number of iterations, thinning rate, and burn-in period) can be set by the user in R or default values can be used. The remainder of this chapter will provide detailed examples of the diagnosis of MCMC results along with the setting of MCMC parameters and prior distributions.

9.2 MCMCglmm for Normally Distributed Response Variable

We will begin our discussion of fitting a random intercept model with the Prime Time data we used in numerous examples in previous chapters. In particular, we will fit a model in which reading achievement score is the dependent variable and vocabulary score is the independent variable. Students are nested within schools, which we will treat as a random effect. Bayesian multilevel modeling can be done in R using the MCMCglmm library. As noted earlier in this chapter, a key component of Bayesian modeling is the use of prior distribution information in the estimation of the posterior distribution of the model parameters. MCMCglmm uses a default set of priors for each model parameter. We will rely on this default set for the first example analysis.

The default priors for the model coefficients and intercepts are noninformative; they are taken from the standard normal distribution with a mean of 0 and a variance of 1e+10 or 10 billion. This very large variance for the prior reflects our relative lack of confidence that the mean of the coefficient distributions is in fact 0. The prior distribution for the school random effect is known in MCMCglmm parlance as the G structure and is expressed using two separate terms: (1) $V$ reflecting the variation in the outcome variable (reading score) across schools, and (2) $\nu$ reflecting the degree of belief in the parameter. The default prior distribution for $V$ is the inverse Wishart distribution, with $V = 1$ and $\nu = 0$. This low value for nu reflects the lack of information provided by the prior distribution. There is also a prior distribution for the residual term $R$, with the defaults precisely the same as those for $G$.

To fit the random intercept model with a single predictor under the Bayesian framework with default priors, we will use the following commands in R:

```r
library(MCMCglmm)
prime_time.nomiss<-na.omit(prime_time)
attach(prime_time.nomiss)
model9.1<-MCMCglmm(geread~gevocab, random = ~school, data = prime_time.nomiss)
plot(model9.1)
summary(model9.1)
```
The function call for `MCMCglmm` is fairly similar to what we have seen in previous chapters. One important point to note is that `MCMCglmm` does not accommodate missing data. Therefore, before conducting an analysis, we must expunge all the observations with missing data. We created a data set with no missing observations using the command `prime_time.nomiss<-na.omit(prime_time)` that created a new data frame called `prime_time.nomiss` containing no missing data. We then attached this data frame and fit the multilevel model, indicating the random effect with the `random=~` statement. We subsequently requested a summary of the results and a plot of the relevant graphs that will be used to determine whether the Bayesian model converged properly. It is important to note that by default, `MCMCglmm` uses 13,000 iterations of the MCMC algorithm, with a burn-in of 3,000 and thinning of 10. As we will see below, we can easily adjust these settings to best suit our specific analysis problem.

When interpreting the results of the Bayesian analysis, we first want to know whether we can be confident in the quality of the parameter estimates for both the fixed and random effects. The plots relevant to this diagnosis appear in Figures 9.1 and 9.2. For each model parameter, we have the trace plot on the left, showing the entire set of estimates as a time series across the 13,000 iterations. On the right, we have a histogram of the distribution of parameter estimates.

Our purpose for examining these plots is to ascertain to what extent the estimates converged on a single value. As an example, the first pair of graphs reflects the parameter estimates for the intercept. For the trace, convergence
is indicated when the time series plot hovers around a single value on the $y$ axis and does not meander up and down. In this case, it is clear that the trace plot for the intercept shows convergence. This conclusion is reinforced by the histogram for the estimate, which is clearly centered over a single mean value and shows no bimodal tendencies. We see similar results for the coefficient of vocabulary, the random effect of school, and the residual. Since the parameter estimates appear to have successfully converged, we can have confidence in the actual estimated values that we will examine shortly.

Before we look at the parameter estimates, we want to assess the autocorrelation of the estimates in the time series for each parameter. Our purpose is to ensure that the rate of thinning (taking every tenth observation generated by the MCMC algorithm) that we used is sufficient to ensure that any autocorrelation in the estimates is eliminated. To obtain autocorrelations for the random effects, we use the `autocorr(model9.1$VCV)` command and obtain the following results.

```
, school

<table>
<thead>
<tr>
<th></th>
<th>school</th>
<th>units</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lag 0</td>
<td>1.000000000</td>
<td>-0.05486644</td>
</tr>
<tr>
<td>Lag 10</td>
<td>-0.03926722</td>
<td>-0.03504799</td>
</tr>
<tr>
<td>Lag 50</td>
<td>-0.01636431</td>
<td>-0.04016879</td>
</tr>
<tr>
<td>Lag 100</td>
<td>-0.03545104</td>
<td>0.01987726</td>
</tr>
<tr>
<td>Lag 500</td>
<td>0.04274662</td>
<td>-0.05083669</td>
</tr>
</tbody>
</table>
```
In the first section of this table, we see results for the school random effect. This output includes correlations involving the school variance component estimates. Under the school column are the actual autocorrelations for the school random effect estimate. Under the units column are the cross correlations between estimates for the school random effect and the residual random effect at different lags. Thus, for example, the correlation between the estimates for school and the residual with no lag is –0.0549. The correlation between the school estimate 10 lags prior to the current residual estimate is –0.035. To ascertain whether the rate of thinning is sufficient, the more important numbers are in the school column, where we see the correlation between a given school effect estimate and the school effect 10, 50, 100, and 500 estimates earlier.

The autocorrelation at a lag value of 10, –0.0393, is sufficiently small for us to have confidence in our thinning the results at 10. We would reach a similar conclusion for the autocorrelation of the residual (units). The 10 appears to be a reasonable thinning value for it as well. We can obtain the autocorrelations of the fixed effects using the autocorr(model9.1$Sol) command. It is clear that there is essentially no autocorrelation as far out as a lag of 10, indicating that the default thinning value of 10 is sufficient for both the intercept and the vocabulary test scores.

```
Lag 0  -0.0548664421  1.000000000
Lag 10 -0.0280445140 -0.006663408
Lag 50  -0.0098424151  0.017031804
Lag 100  0.0002654196  0.010154987
Lag 500 -0.0022835508  0.046769152
```

Having established that the parameter estimates converged properly and that our rate of thinning in the sampling of MCMC-derived values is
sufficient to eliminate any autocorrelation in the estimates, we are now ready to examine the specific parameter estimates for our model. The output for this analysis appears below.

**Iterations = 3001:12991**
**Thinning interval = 10**
**Sample size = 1000**

**DIC: 43074.14**

**G-structure: ~school**

<table>
<thead>
<tr>
<th></th>
<th>post.mean</th>
<th>l-95% CI</th>
<th>u-95% CI</th>
<th>eff.samp</th>
</tr>
</thead>
<tbody>
<tr>
<td>school</td>
<td>0.09962</td>
<td>0.06991</td>
<td>0.1419</td>
<td>1000</td>
</tr>
</tbody>
</table>

**R-structure: ~units**

<table>
<thead>
<tr>
<th></th>
<th>post.mean</th>
<th>l-95% CI</th>
<th>u-95% CI</th>
<th>eff.samp</th>
</tr>
</thead>
<tbody>
<tr>
<td>units</td>
<td>3.767</td>
<td>3.668</td>
<td>3.876</td>
<td>1000</td>
</tr>
</tbody>
</table>

**Location effects: geread ~ gevocab**

<table>
<thead>
<tr>
<th></th>
<th>post.mean</th>
<th>l-95% CI</th>
<th>u-95% CI</th>
<th>eff.samp</th>
<th>pMCMC</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>2.0220</td>
<td>1.9323</td>
<td>2.1232</td>
<td>1000</td>
<td>&lt;0.001  ***</td>
</tr>
<tr>
<td>gevocab</td>
<td>0.5131</td>
<td>0.4975</td>
<td>0.5299</td>
<td>1000</td>
<td>&lt;0.001  ***</td>
</tr>
</tbody>
</table>

---

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

We are first given information about the number of iterations, the thinning interval, and the final number of MCMC values sampled (Sample size) and used to estimate the model parameters. Next, we have the model fit index (DIC) that may be used for comparing various models and selecting the one that provides optimal fit. The DIC is interpreted in much the same fashion as the AIC and BIC discussed in earlier chapters, and for which smaller values indicate better model fit. We are then provided with the posterior mean of the distribution for each of the random effects, school and residual that MCMCglmm calls units. The mean variance estimate for the school random effect is 0.09962, with a 95% credibility interval of 0.06991 to 0.1419. Remember that we interpret credibility intervals in Bayesian modeling in much the same way that we interpret confidence intervals in frequentist modeling.

The results indicate that reading achievement scores differ across schools because 0 is not in the interval. Similarly, the residual variance also differs from 0. With regard to the fixed effect of vocabulary score that had a mean posterior value of 0.5131, we also conclude that the results are statistically significant because 0 is not in its 95% credibility interval. We also have a $p$ value for this effect and the intercept, both of which
are significant with values less than 0.05. The positive value of the posterior mean indicates that students with higher vocabulary scores also had higher reading scores.

To demonstrate how we can change the number of iterations, the burn-in period, and the rate of thinning in R, we will re-estimate Model 9.1 with 100,000 iterations, a burn-in of 10,000, and a thinning rate of 50. This will yield 1,800 samples for the purposes of estimating the posterior distribution for each model parameter. The R commands for fitting this model, followed by the relevant output, appear below.

```r
model9.1b<-MCMCglmm(geread~gevocab, random = ~school,
                      data = prime_time.nomiss, nitt = 100000, thin = 50, burnin = 10000)
plot(model9.1b)
summary(model9.1b)
```

As with the initial model, all parameter estimates appear to have successfully converged. (See Figures 9.3 and 9.4.) The results in terms of the posterior means are also very similar to those obtained using the default values for the number of iterations, the burn-in period, and the thinning rate. This result is not surprising, given that the diagnostic information for our initial model

![Trace of Intercept](image1)

![Density of Intercept](image2)

![Trace of gevocab](image3)

![Density of gevocab](image4)

**FIGURE 9.3**

Results after changing iterations, burn-in, and thinning rate: intercept (top) and vocabulary (bottom).
was all very positive. Nonetheless, it was useful for us to see how the default values can be changed if required.

\begin{verbatim}
Iterations = 10001:99951
Thinning interval = 50
Sample size = 1800

DIC: 43074.19

G-structure: ~school

\begin{verbatim}
post.mean  l-95% CI  u-95% CI  eff.samp
school 0.1013 0.06601 0.1366 1800
\end{verbatim}

R-structure: ~units

\begin{verbatim}
post.mean  l-95% CI  u-95% CI  eff.samp
units 3.766 3.664 3.873 1800
\end{verbatim}

Location effects: geread ~ gevocab

\begin{verbatim}
post.mean  l-95% CI  u-95% CI  eff.samp  pMCMC
(Intercept) 2.0240 1.9304 2.1177 1800 <6e-04 ***
gevocab 0.5128 0.4966 0.5287 1846 <6e-04 ***
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
\end{verbatim}
\end{verbatim}

FIGURE 9.4
Results after changing iterations, burn-in, and thinning rate: school (top) and residual (bottom).
9.3 Including Level 2 Predictors with MCMCglmm

In addition to understanding the extent to which reading achievement relates to vocabulary test score (Chapter 3), we were also interested in the relationship of school (senroll), a Level 2 variable, and reading achievement. Including a Level 2 variable in the analysis with MCMCglmm is just as simple as doing so using lme or lme4.

```r
model9.2 <- MCMCglmm(geread ~ gevocab + senroll, random = ~school, data = prime_time.nomiss)
plot(model9.2)
```

An examination of the trace plots and histograms (Figure 9.5) shows that we achieved convergence for all parameter estimates. The autocorrelations appear below the graphs, and reveal that the default thinning rate of 10 may not be sufficient to remove autocorrelation from the estimates for the intercept and school enrollment. Thus, we refit the model with 40,000 iterations, a burn-in of 3,000, and a thinning rate of 100. We selected a 100 thinning rate because for each model term, the autocorrelation at a lag of 100 displayed in the results was sufficiently small.

![Trace plots and histograms](image)

**FIGURE 9.5**
MCMCglmm analysis with Level 2 predictors: intercept (top), vocabulary (middle), and enrollment (bottom).
autocorr(model9.2$VCV)

<table>
<thead>
<tr>
<th>Lag</th>
<th>school</th>
<th>units</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>1.0000000000</td>
<td>-0.05429139</td>
</tr>
<tr>
<td>10</td>
<td>-0.002457293</td>
<td>-0.07661475</td>
</tr>
<tr>
<td>50</td>
<td>-0.020781555</td>
<td>-0.01761532</td>
</tr>
<tr>
<td>100</td>
<td>-0.027670953</td>
<td>0.01655270</td>
</tr>
<tr>
<td>500</td>
<td>0.035838857</td>
<td>-0.03714127</td>
</tr>
</tbody>
</table>

autocorr(model9.2$Sol)

<table>
<thead>
<tr>
<th>(Intercept)</th>
<th>gevocab</th>
<th>senroll</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>1.0000000000</td>
<td>-0.3316674622</td>
</tr>
<tr>
<td>10</td>
<td>0.0801986410</td>
<td>-0.0668713485</td>
</tr>
<tr>
<td>50</td>
<td>0.0581330411</td>
<td>-0.0348434078</td>
</tr>
<tr>
<td>100</td>
<td>0.0004512485</td>
<td>0.0001044589</td>
</tr>
<tr>
<td>500</td>
<td>0.0354993059</td>
<td>-0.0317823452</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>(Intercept)</th>
<th>gevocab</th>
<th>senroll</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>-0.3316674622</td>
<td>1.0000000000</td>
</tr>
<tr>
<td>10</td>
<td>-0.014132944</td>
<td>0.0001538528</td>
</tr>
<tr>
<td>50</td>
<td>-0.001177506</td>
<td>-0.0095964368</td>
</tr>
<tr>
<td>100</td>
<td>-0.010782011</td>
<td>0.0143615330</td>
</tr>
<tr>
<td>500</td>
<td>-0.010100604</td>
<td>0.0464368692</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>(Intercept)</th>
<th>gevocab</th>
<th>senroll</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>-0.8855514315</td>
<td>-0.04335329</td>
</tr>
<tr>
<td>10</td>
<td>-0.0792592927</td>
<td>0.074155593</td>
</tr>
<tr>
<td>50</td>
<td>-0.0542189405</td>
<td>0.04008488</td>
</tr>
<tr>
<td>100</td>
<td>0.0006296875</td>
<td>-0.01189656</td>
</tr>
<tr>
<td>500</td>
<td>-0.0405712255</td>
<td>0.02456735</td>
</tr>
</tbody>
</table>

The summary results for the model with 40,000 iterations and a thinning rate of 100 appear in Figure 9.6. It should be noted that the trace plots and histograms of parameter estimates for Model 9.3 indicate that convergence
Bayesian Multilevel Modeling

had been attained. From these results we can see that overall fit based on the DIC is virtually identical to that of the model not including `senroll`. In addition, the posterior mean estimate and associated 95% credible interval for this parameter show that `senroll` was not statistically significantly related to reading achievement, i.e., 0 is in the interval. These results allow us to conclude that school size does not contribute significantly to the variation in reading achievement scores nor to the overall fit of the model.

\[
\text{summary(model9.3)}
\]
\[
\begin{array}{cccc}
\text{Iterations} & 3001:39901 \\
\text{Thinning interval} & 100 \\
\text{Sample size} & 1700 \\
\text{DIC:} & 43074.86 \\
\end{array}
\]

G-structure: ~school

\[
\begin{array}{cccc}
\text{post.mean} & 1-95\% \ CI & u-95\% \ CI & \text{eff.samp} \\
school & 0.1027 & 0.06611 & 0.1471 & 170 \\
\end{array}
\]

R-structure: ~units

\[
\begin{array}{cccc}
\text{post.mean} & 1-95\% \ CI & u-95\% \ CI & \text{eff.samp} \\
units & 3.768 & 3.661 & 3.865 & 222.7 \\
\end{array}
\]

Location effects: geread ~ gevocab + senroll

FIGURE 9.6
MCMCglmm analysis with Level 2 predictors after changing iterations and thinning rate: school (top) and residual (bottom).
As a final separate example in this section, we will fit a random coefficient model in which we allow the relationship of vocabulary score and reading achievement to vary across schools. The syntax for fitting this model with MCMCglmm appears below.

```
model9.4<-MCMCglmm(geread~gevocab, random = ~school+gevocab, 
                     data = prime_time.nomiss)
plot(model9.4)
summary(model9.4)
autocorr(model9.4$VCV)
```

---

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Lag 50  -0.01334607  0.03583885
Lag 100  0.02850369 -0.01102134
Lag 500  0.03392102 -0.04280691

,, gevocab

(Intercept)  gevocab
Lag 0  -0.863750126  1.0000000000
Lag 10  0.008428317  0.0008246964
Lag 50  0.007928161 -0.0470879801
Lag 100 -0.029552813  0.0237866610
Lag 500 -0.029554289  0.0425010354

The trace plots, histograms, and autocorrelations indicate that the parameter estimation converged properly and that the thinning rate appears satisfactory for removing autocorrelation from the estimate values. The model results appear in Figures 9.7 and 9.8. First, we should note that the DIC for this random coefficients model is smaller than that of the random intercepts-only models above. In addition, the estimate of the random coefficient for vocabulary is 0.2092, with a 95% credible interval of 0.135 to 0.3025. Because this interval does not include 0, we can conclude that the random coefficient is indeed different from 0 in the population, and that the relationship between reading achievement and vocabulary test score varies from one school to another.

FIGURE 9.7
Results of fitting a random coefficient model with MCMCg1mm: intercept (top) and vocabulary (bottom).
FIGURE 9.8
Results of fitting a random coefficient model with \texttt{MCMCglmm}: school (top), vocabulary (middle), and residual (bottom).

Iterations = 3001:12991
Thinning interval = 10
Sample size = 1000

DIC: 42663.14

G-structure: \textasciitilde school

\begin{verbatim}
post.mean  l-95% CI  u-95% CI  eff.samp
school     0.08921  0.0608   0.1256   1000
\end{verbatim}

\textasciitilde gevocab

\begin{verbatim}
post.mean  l-95% CI  u-95% CI  eff.samp
gevocab    0.2092   0.135    0.3025   1000
\end{verbatim}

R-structure: \textasciitilde units

\begin{verbatim}
post.mean  l-95% CI  u-95% CI  eff.samp
units     3.601    3.508    3.7     1000
\end{verbatim}
9.4 User-Defined Priors

Finally, we need to consider a situation in which we want to provide our own prior distribution information rather than rely on the MCMCglmm defaults. To do so, we will make use of the prior command. In this example, we examine the case in which a researcher has informative priors for one of the model parameters. Let us assume that a number of studies in the literature report a small but consistent positive relationship between reading achievement and a measure of working memory. To incorporate this informative prior into a model relating these two variables while also including vocabulary score, and accommodating the random coefficient for this variable, we must first define our prior as below.

The first step is creating the covariance matrix (var) containing the prior of the fixed effects in the model (intercept and memory). In this case, we set the prior variances of the intercept and the coefficient for memory to 1 and 0.1, respectively. We select a fairly small variance for the working memory coefficient because we have much prior evidence regarding the anticipated magnitude of this relationship.

```
var<-matrix(c(1,0,0,0.1), nrow = 2, ncol = 2)
prior.model9.5<-list(B = list(mu = c(0,.15), V = var))
model9.5<-MCMCglmm(geread~npamem, random = ~school, data = prime_time.nomiss, prior = prior.model9.5)
plot(model9.5)
autocorr(model9.5$VCV)
autocorr(model9.5$Sol)
summary(model9.5)
```

The model appears to have converged well, and the autocorrelations suggest that the rate of thinning was appropriate.

```
autocorr(model9.5$VCV)
, , school

          school units
Lag 0 1.0000000000 -0.03320619
Lag 10 -0.007158198 -0.01203254
Lag 50 -0.023838303 -0.03207328
Lag 100 -0.027444606 -0.04150614
Lag 500 0.022895951 0.03123365
```
The summary of the model fit results appear below. Of particular interest is the coefficient for the fixed effect working memory (npamem). The posterior mean is 0.01266, with a credible interval ranging from 0.01221 to 0.01447, indicating that the relationship between working memory and reading achievement is statistically significant. It is important to note, however, that the estimate of this relationship for the current sample is well below that reported in prior research incorporated into the prior distribution. In this case, because the sample is so large, the effect of the prior on the posterior distribution is very small. The impact of the prior would be much greater were we working with a smaller sample.
Bayesian Multilevel Modeling

Location effects: geread ~ npamem

<table>
<thead>
<tr>
<th></th>
<th>post.mean</th>
<th>1-95% CI</th>
<th>u-95% CI</th>
<th>eff.samp</th>
<th>pMCMC</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>3.57999</td>
<td>3.44666</td>
<td>3.71338</td>
<td>1000</td>
<td>&lt;0.001 ***</td>
</tr>
<tr>
<td>npamem</td>
<td>0.01266</td>
<td>0.01121</td>
<td>0.01447</td>
<td>1000</td>
<td>&lt;0.001 ***</td>
</tr>
</tbody>
</table>

---

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

As a point of comparison, we also fit the model using the default priors in MCMCglmm to see what impact the informative priors had on the posterior distribution. We will focus only on the coefficients for this demonstration because they serve as the focus of the informative priors. For the default priors we obtained the following results.

<table>
<thead>
<tr>
<th></th>
<th>post.mean</th>
<th>1-95% CI</th>
<th>u-95% CI</th>
<th>eff.samp</th>
<th>pMCMC</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>3.61713</td>
<td>3.47109</td>
<td>3.75194</td>
<td>1000</td>
<td>&lt;0.001 ***</td>
</tr>
<tr>
<td>npamem</td>
<td>0.01237</td>
<td>0.01080</td>
<td>0.01417</td>
<td>1000</td>
<td>&lt;0.001 ***</td>
</tr>
</tbody>
</table>

---

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Virtually no difference in results is apparent between the user-supplied informative (Figure 9.9) and the default noninformative priors (Figure 9.10). This demonstrates that the selection of priors will exert little bearing on the final results of an analysis when sample sizes are large.

FIGURE 9.9
Results of applying user’s informative priors as model parameters: intercept (top) and memory (bottom).
9.5 MCMCglmm for Dichotomous Dependent Variable

The MCMCglmm library can also be used to fit multilevel models in which the outcome variable is dichotomous in nature. In most respects, the use of the functions from this library will be very similar to what we saw earlier with a continuous outcome. Therefore, we will focus on aspects of model fitting that differ from what we have seen to this point. Our first example involves fitting a model for a dichotomous dependent variable using Bayesian multilevel logistic regression. Specifically, the model of interest involves predicting whether students receive passing scores on a state math assessment (score2) as a function of their number sense (numsense) scores on a formative math assessment. The following is the R code for fitting this model and requesting the plots and output.

```r
model9.6<-MCMCglmm(score2~numsense, random = ~school, family = "ordinal", data = mathfinal,)
plot(model9.6)
autocorr(model9.6$VCV)
autocorr(model9.6$Sol)
summary(model9.6)
```

The default prior parameters are used and the family is defined as ordinal. In other respects, the function call is identical to those for the continuous
outcome variables on which we focused earlier in this chapter. The output from R appears below. From the trace plots and histograms in Figures 9.11 and 9.12, we can see that convergence was achieved for each of the model parameters, and the autocorrelations show that our rate of thinning is sufficient.

<table>
<thead>
<tr>
<th></th>
<th>school</th>
<th>units</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>1.000000000</td>
<td>0.24070410</td>
</tr>
<tr>
<td>10</td>
<td>0.016565749</td>
<td>0.02285168</td>
</tr>
<tr>
<td>50</td>
<td>0.012622856</td>
<td>0.02073446</td>
</tr>
<tr>
<td>100</td>
<td>0.007855806</td>
<td>0.02231629</td>
</tr>
<tr>
<td>500</td>
<td>0.007233911</td>
<td>0.01822021</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th></th>
<th>school</th>
<th>units</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>0.24070410</td>
<td>1.00000000</td>
</tr>
<tr>
<td>10</td>
<td>0.02374442</td>
<td>0.00979023</td>
</tr>
<tr>
<td>50</td>
<td>0.02015865</td>
<td>0.00917857</td>
</tr>
<tr>
<td>100</td>
<td>0.01965188</td>
<td>0.00849276</td>
</tr>
<tr>
<td>500</td>
<td>0.01361470</td>
<td>0.00459030</td>
</tr>
</tbody>
</table>

FIGURE 9.11
Results of fitting model to dichotomous dependent variable: intercept (top) and assessment score (bottom).
In terms of model parameter estimation results, the number sense score was found to be statistically significantly related to whether a student received a passing score on the state mathematics assessment. The posterior mean for the coefficient is 0.04544, indicating that the higher an individual’s number sense score, the greater the likelihood that he or she will pass the state assessment.

\[
\begin{align*}
\text{(Intercept)} & & \text{numsense} \\
\text{Lag 0} & & 1.0000000 & & -0.09818969 \\
\text{Lag 10} & & 0.00862290 & & -0.00878574 \\
\text{Lag 50} & & 0.00688767 & & -0.00707115 \\
\text{Lag 100} & & 0.00580816 & & -0.00603118 \\
\text{Lag 500} & & 0.00300539 & & -0.00314349 \\
\end{align*}
\]

\[
\begin{align*}
\text{numsense} & & \text{(Intercept)} \\
\text{Lag 0} & & -0.09818969 & & 1.0000000 \\
\text{Lag 10} & & -0.00878574 & & 0.00894084 \\
\text{Lag 50} & & -0.00707115 & & 0.00723130 \\
\text{Lag 100} & & -0.00603118 & & 0.00618679 \\
\text{Lag 500} & & -0.00314349 & & 0.00328528 \\
\end{align*}
\]

FIGURE 9.12
Results of fitting model to dichotomous dependent variable: school (top) and residual (bottom).

\[
\begin{align*}
\text{Iterations} = 3001:12991 \\
\text{Thinning interval} = 10 \\
\text{Sample size} = 1000
\end{align*}
\]
Bayesian Multilevel Modeling

DIC: 6929.18

G-structure: ~school

<table>
<thead>
<tr>
<th>post.mean</th>
<th>l-95% CI</th>
<th>u-95% CI</th>
<th>eff.samp</th>
</tr>
</thead>
<tbody>
<tr>
<td>school</td>
<td>0.2169</td>
<td>0.1116</td>
<td>0.3589</td>
</tr>
</tbody>
</table>

R-structure: ~units

<table>
<thead>
<tr>
<th>post.mean</th>
<th>l-95% CI</th>
<th>u-95% CI</th>
<th>eff.samp</th>
</tr>
</thead>
<tbody>
<tr>
<td>units</td>
<td>0.4525</td>
<td>0.1025</td>
<td>0.9084</td>
</tr>
</tbody>
</table>

Location effects: score2 ~ goal1ritscoref10

<table>
<thead>
<tr>
<th>post.mean</th>
<th>l-95% CI</th>
<th>u-95% CI</th>
<th>eff.samp</th>
<th>pMCMC</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>-8.95448</td>
<td>-10.42943</td>
<td>-7.64817</td>
<td>1000</td>
</tr>
<tr>
<td>numsense</td>
<td>0.04544</td>
<td>0.03905</td>
<td>0.05309</td>
<td>1000</td>
</tr>
</tbody>
</table>

*** Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

The exact same command sequence that was used here would also be used to fit a model for an ordinal variable with more than two categories.

---

9.6 MCMCglmm for Count Dependent Variable

Clearly, by using the MCMCglmm R function it is possible to fit the same types of multilevel models in the Bayesian context that we were able to fit using REML with lme and lmer, including count data. As we saw in Chapters 7 and 8, Poisson regression is typically used with such data. To demonstrate the modeling of a count outcome in the Bayesian context, we will revisit the example that was our focus at the end of Chapter 8. Recall that the dependent variable was the number of cardiac warning incidents such as chest pain, shortness of breath, and dizzy spells that occurred over a six-month period for each of 1000 patients treated in 110 cardiac rehabilitation facilities. Study participants were randomly assigned to a new exercise treatment program or to the standard treatment.

At the end of the study, the researchers were interested in comparing the frequency of cardiac warning signs between the two treatments, while controlling for the sexes of the patients. Since the frequency of cardiac warning signs was very small across the six-month period, Poisson regression was deemed to be the optimal analysis for determining whether the new treatment resulted in better outcomes than the old. To fit such a model using MCMCglmm, we use the following commands.
attach(heartdata)
model9.7<-MCMCglmm(heart~trt+sex, random = ~rehab, family = "poisson", data = heartdata)
plot(model9.7)
autocorr(model9.7$VCV)
autocorr(model9.7$Sol)
summary(model9.7)

The key subcommand here is `family = "poisson"`, which indicates that Poisson regression is to be used. In all other respects, the syntax is identical to that used for the continuous and dichotomous variable models. Figures 9.13 and 9.14 show the trace plots and histograms for assessing model convergence.

, , rehab

<table>
<thead>
<tr>
<th></th>
<th>rehab</th>
<th>units</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lag 0</td>
<td>1.000000000</td>
<td>-0.0117468496</td>
</tr>
<tr>
<td>Lag 10</td>
<td>0.004869176</td>
<td>-0.0067184848</td>
</tr>
</tbody>
</table>

FIGURE 9.13
MCMCglmm for a count dependent variable: intercept (top), treatment program (middle), and sex (bottom).
Bayesian Multilevel Modeling

Lag 50  0.000957586 0.0009480950
Lag 100  0.009502289 0.0004500062
Lag 500 -0.009067234 0.0028298115

Lag 0 -0.00117468 1.00000000000
Lag 10 -0.00076201 0.00425938977
Lag 50  0.00013997 0.00065406398
Lag 100  0.00035229 0.00079448090
Lag 500  0.00024450 0.00011262469

:, (Intercept)

Lag 0  1.00000000000  0.0002158950  0.00171708145
Lag 10  0.00268697330  0.0003701961  0.00100571606
Lag 50  0.00013997  0.0001337596  0.00030117833
Lag 100  0.00035229  0.00079448090  0.00033360474
Lag 500  0.00024450  0.00011262469  0.00003672349

FIGURE 9.14
MCMCg1mm for a count dependent variable: rehabilitation facility (top) and residual (bottom).

Lag 50  0.000957586 0.0009480950
Lag 100  0.009502289 0.0004500062
Lag 500 -0.009067234 0.0028298115

Lag 0 -0.00117468 1.00000000000
Lag 10 -0.00076201 0.00425938977
Lag 50  0.00013997 0.00065406398
Lag 100  0.00035229 0.00079448090
Lag 500  0.00024450 0.00011262469

,,,, units

rehab units
Lag 0 -0.00117468 1.00000000000
Lag 10 -0.00076201 0.00425938977
Lag 50  0.00013997 0.00065406398
Lag 100  0.00035229 0.00079448090
Lag 500  0.00024450 0.00011262469

,,,, (Intercept)

(Intercept) trt sex
Lag 0  1.00000000000  0.0002158950  0.00171708145
Lag 10  0.00268697330  0.0003701961  0.00100571606
Lag 50  0.00013997  0.0001337596  0.00030117833
Lag 100  0.00035229  0.00079448090  0.00033360474
Lag 500  0.00024450  0.00011262469  0.00003672349
An examination of the trace plots and histograms shows that the parameter estimation converged appropriately. In addition, the autocorrelations are sufficiently small for all parameters so that we can have confidence in our rate of thinning. Therefore, we can move to discussion of the model parameter estimates that appear below.

\[
\begin{array}{cccc}
\text{Iterations} & = & 3001:12991 \\
\text{Thinning interval} & = & 10 \\
\text{Sample size} & = & 1000 \\
\text{DIC} & = & 2735.293
\end{array}
\]

**G-structure: ~rehab**

<table>
<thead>
<tr>
<th></th>
<th>post.mean</th>
<th>l-95% CI</th>
<th>u-95% CI</th>
<th>eff.samp</th>
</tr>
</thead>
<tbody>
<tr>
<td>rehab</td>
<td>0.5414</td>
<td>0.1022</td>
<td>1.009</td>
<td>1000</td>
</tr>
</tbody>
</table>

**R-structure: ~units**

<table>
<thead>
<tr>
<th></th>
<th>post.mean</th>
<th>l-95% CI</th>
<th>u-95% CI</th>
<th>eff.samp</th>
</tr>
</thead>
<tbody>
<tr>
<td>units</td>
<td>6.102</td>
<td>5.074</td>
<td>7.324</td>
<td>1000</td>
</tr>
</tbody>
</table>

**Location effects: heart ~ trt + sex**

<table>
<thead>
<tr>
<th></th>
<th>post.mean</th>
<th>l-95% CI</th>
<th>u-95% CI</th>
<th>eff.samp</th>
<th>pMCMC</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>-0.96877</td>
<td>-1.23267</td>
<td>-0.68596</td>
<td>1000</td>
<td>&lt;0.001  ***</td>
</tr>
<tr>
<td>trt</td>
<td>-0.21909</td>
<td>-0.40769</td>
<td>-0.01448</td>
<td>1000</td>
<td>0.03    *</td>
</tr>
<tr>
<td>sex</td>
<td>-0.35585</td>
<td>-0.57662</td>
<td>-0.16348</td>
<td>1000</td>
<td>&lt;0.001  ***</td>
</tr>
</tbody>
</table>

---

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
In terms of the primary research question, the results indicate that the frequency of cardiac risk signs was lower among those in the treatment condition than those in the control group when accounting for participants' sexes. In addition, we found a statistically significant difference in the rate of risk symptoms between males and females. With respect to the random effects, the variance in the outcome variable due to rehabilitation facility and the residual were both significantly different from 0. The posterior mean effect of the rehabilitation facility was 0.5414, with a 95% credibility interval of 0.1022 to 1.009. This result indicates that symptom frequency differed among the facilities.

We may also be interested in examining a somewhat more complex explanation of the impact of treatment on the frequency of cardiac symptoms. For instance, previous research indicates that the number of hours the facilities are open may impact the frequency of cardiac symptoms by providing more or fewer opportunities for patients to use their services. In turn, if more participation in rehabilitation activities is associated with the frequency of cardiac risk symptoms, we may expect the hours of operation to impact symptoms. In addition, it is believed that the impacts of treatment on outcomes may vary among rehabilitation centers, leading to a random coefficients model. The R commands to fit the random coefficients (for treatment) model with a Level 2 covariate (hours of operation) appear below followed by the resulting output shown in Figure 9.15. As we have seen in previous examples in this chapter, to specify a random coefficients model, we include the variables of interest (rehab and hours) in the random statement.

\[
\text{model9.8<-MCMCglmm(heart~trt+sex+hours, random = ~rehab+trt, family = "poisson", data = heartdata)}
\]  
\text{plot(model9.8)}
\text{autocorr(model9.8$VCV)}
\text{autocorr(model9.8$Sol)}
\text{summary(model9.8)}

<table>
<thead>
<tr>
<th></th>
<th>rehab</th>
<th>trt</th>
<th>units</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lag 0</td>
<td>1.00000000</td>
<td>-0.266851868</td>
<td>-0.16465715</td>
</tr>
<tr>
<td>Lag 10</td>
<td>0.00378468</td>
<td>-0.021179331</td>
<td>-0.01630321</td>
</tr>
<tr>
<td>Lag 50</td>
<td>0.00190117</td>
<td>-0.018558364</td>
<td>-0.01613084</td>
</tr>
<tr>
<td>Lag 100</td>
<td>0.00215891</td>
<td>-0.015675323</td>
<td>-0.0200173</td>
</tr>
<tr>
<td>Lag 500</td>
<td>0.00134143</td>
<td>-0.004070154</td>
<td>-0.02503848</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th></th>
<th>rehab</th>
<th>trt</th>
<th>units</th>
</tr>
</thead>
<tbody>
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<td>Lag 0</td>
<td>-0.2668519</td>
<td>1.000000000</td>
<td>-0.11400674</td>
</tr>
<tr>
<td>Lag 10</td>
<td>-0.02075032</td>
<td>0.00740803</td>
<td>-0.01180379</td>
</tr>
<tr>
<td>Lag 50</td>
<td>-0.02016743</td>
<td>0.00702657</td>
<td>-0.01022964</td>
</tr>
<tr>
<td>Lag 100</td>
<td>-0.02234751</td>
<td>0.00681188</td>
<td>-0.00740961</td>
</tr>
<tr>
<td>Lag 500</td>
<td>-0.02362045</td>
<td>0.00552936</td>
<td>0.00579908</td>
</tr>
</tbody>
</table>
FIGURE 9.15
Results of fitting random coefficients with Level 2 covariate: intercept (top row), treatment program (second row), sex (third row), and hours open (bottom row).

<table>
<thead>
<tr>
<th></th>
<th>rehab</th>
<th>trt</th>
<th>units</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lag 0</td>
<td>-0.16465715</td>
<td>-0.11400674</td>
<td>1.00000000</td>
</tr>
<tr>
<td>Lag 10</td>
<td>-0.01475261</td>
<td>-0.01183465</td>
<td>0.00967745</td>
</tr>
<tr>
<td>Lag 50</td>
<td>-0.01055799</td>
<td>-0.01229537</td>
<td>0.00862259</td>
</tr>
<tr>
<td>Lag 100</td>
<td>-0.01106924</td>
<td>0.00967745</td>
<td>0.00749455</td>
</tr>
<tr>
<td>Lag 500</td>
<td>-0.00619535</td>
<td>-0.00694997</td>
<td>0.00282392</td>
</tr>
</tbody>
</table>

,, (Intercept)

<table>
<thead>
<tr>
<th></th>
<th>(Intercept)</th>
<th>trt</th>
<th>sex</th>
<th>hours</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lag 0</td>
<td>1.00000000</td>
<td>0.10756409</td>
<td>0.1718756</td>
<td>-0.06742879</td>
</tr>
<tr>
<td>Lag 10</td>
<td>0.00337255</td>
<td>0.01174973</td>
<td>0.0181841</td>
<td>0.01915046</td>
</tr>
<tr>
<td>Lag 50</td>
<td>0.00369810</td>
<td>0.00898286</td>
<td>0.0211193</td>
<td>0.03380228</td>
</tr>
<tr>
<td>Lag 100</td>
<td>0.00373422</td>
<td>0.01070748</td>
<td>0.0187302</td>
<td>0.01015611</td>
</tr>
<tr>
<td>Lag 500</td>
<td>0.00290292</td>
<td>0.00500545</td>
<td>0.0202833</td>
<td>0.04459613</td>
</tr>
</tbody>
</table>
Bayesian Multilevel Modeling

```
,, trt
   (Intercept)    trt      sex    hours
Lag 0  0.10756409  1.00000000  0.1465124  0.09764357
Lag 10 0.01056947  0.00361113  0.0136449  0.01181678
Lag 50 0.00760802  0.00350369  0.0153875  0.00992076
Lag 100 0.00924803  0.00346671  0.0141195  0.00557474
Lag 500 0.00528078  0.00177952  0.0038593  0.00150113

,, sex
   (Intercept)    trt      sex    hours
Lag 0  0.1718756  0.14651224  1.00000000  0.15838758
Lag 10 0.0191615  0.01300171  0.00316606  0.01377718
Lag 50 0.0208031  0.01265926  0.00248169  0.00786715
Lag 100 0.0189574  0.00596110  0.00287549  0.01078291
Lag 500 0.0115626  0.00662074  0.00111150  0.00931525

,, hours
   (Intercept)    trt      sex    hours
Lag 0  -0.06742879  0.09764357  0.15838758  1.00000000
Lag 10 0.00447807  0.00877490  0.01110063  0.01592455
Lag 50 0.00662157  0.01028671  0.00917307  0.01552734
Lag 100 0.00511239  0.00835433  0.00759920  0.00231364
Lag 500 0.00526215  0.01093175  0.00397990  0.00702958
```

The trace plots and histograms reveal that estimation converged for all the parameters estimated in the analysis and the autocorrelations of estimates are small. Thus, we can move on to interpretation of the parameter estimates.

The results of the model fitting revealed several interesting patterns. First, the random coefficient term for treatment was statistically significant, given that the credible interval ranged between 5.421 and 7.607 and did not include 0. Thus, we can conclude that the impact of treatment on the number of cardiac symptoms differed among rehabilitation centers. In addition, the variance in the outcome due to rehabilitation center was also different from 0 based on the confidence interval for rehabilitation of 0.1953 to 1.06. Finally, treatment and sex were negatively statistically significantly related to the number of cardiac symptoms, as they were for Model 9.7 and the centers’ hours of operation were not related to the frequency of cardiac symptoms.

Iterations = 3001:12991
Thinning interval = 10
Sample size = 1000
DIC: 2677.828

G-structure: ~rehab

<table>
<thead>
<tr>
<th></th>
<th>post.mean</th>
<th>l-95% CI</th>
<th>u-95% CI</th>
<th>eff.samp</th>
</tr>
</thead>
<tbody>
<tr>
<td>rehab</td>
<td>0.6261</td>
<td>0.1953</td>
<td>1.06</td>
<td>47.07</td>
</tr>
</tbody>
</table>
Summary

The material presented in this chapter represents a marked departure from that presented in the first eight chapters. In particular, methods presented in the earlier chapters were built upon a foundation of maximum likelihood estimation. Bayesian modeling, which is the focus of this chapter, leaves likelihood-based analyses behind and instead relies on MCMC to derive posterior distributions for model parameters. More fundamentally, however, Bayesian statistics is radically different from likelihood-based frequentist statistics in the ways in which population parameters are estimated. In frequentist methods, they take single values. Bayesian statistics estimates population parameters as distributions so that the sample-based estimate of a parameter is the posterior distribution obtained using MCMC and not a single value calculated from the sample.

Beyond the more theoretical differences among the methods described in this chapter and those presented earlier, are very real differences in application. Analysts using Bayesian statistics work with what is, in many respects, a more flexible modeling paradigm that does not rest on the standard assumptions that must be met for the successful use of maximum likelihood such as normality. At the same time, this greater flexibility comes at the cost of greater complexity in estimating the model. From a practical viewpoint, consider how much more is involved when conducting the analyses featured in this chapter as compared to those described in Chapter 3. In addition, interpretation of Bayesian modeling results requires more from an analyst...
in the form of ensuring model convergence, deciding on the lengths of the chains and degree of thinning required, and determining the summary statistic of the posterior to be used to provide a single parameter estimate. Last and certainly not least, the analyst must consider what the prior distributions of the model parameters should be, knowing that particularly for small samples, the choice will have a direct bearing on the final parameter estimates obtained.

In spite of the many complexities presented by Bayesian modeling, it is also true that such models offer the careful and informed researcher a very flexible and powerful set of tools. In particular, as noted at the beginning of this chapter, Bayesian analysis including multilevel models provides greater flexibility in model form, requires no distributional assumptions, and may be particularly useful for smaller samples. Therefore, we can recommend this approach without reservation even though an interested researcher will need to invest greater time and energy into deciding on priors, determining if and when a model converges, and selecting the most appropriate summary statistic of the posterior distribution. Those willing to invest the time and energy will have the potential to generate very useful and flexible models that may work in situations where standard likelihood-based approaches do not.
Appendix: Introduction to R

R is an open source and freely available computer program that offers a general system—or environment—for statistical computation and graphics for Macintosh, Windows, and Unix/Linux. R uses an interpretative programming language: a program interprets and executes code directly without having to compile the code (as necessary in statistical programs such as SAS, SPSS syntax, and Mplus, and languages like BASIC, C, C++, and Fortran).

The code that R interprets is typically written in the R language, but users can also make use of some basic languages. Typical R users, unlike developers, will interact directly with the R language only by way of R functions. Other than basic mathematical operations, functions are the components by which a user instructs R what data to use and what to do to it. Although R is based on code and requires learning the R language, even those not familiar with computer programming can easily learn how to use the language for many statistical techniques.

The basic way to interact with R is on an R session console, where commands are entered at a prompt (>). For example, consider Figure A.1, where a basic mathematical operation is entered at the prompt. Simply hitting return/enter will submit (i.e., run) the code and the result of the equation will be printed to the screen.

Although it is simple to type an expression at the command prompt, often it is useful to write the code in an editor and run. This is the case for several reasons, for example, allowing easy editing of code, having a record of exactly what was submitted to R, and the speed of performing multiple commands or computations. One way of doing this is to use the basic R script editor. The editor can be opened from the File menu by selecting New Document in Macintosh and Windows machines. R code can then be typed (or pasted from another document) into the script window. The written code can be submitted to R and run by selecting it (either in pieces or all at once, then going to the Edit menu and choosing Execute.

The R environment is extremely flexible and contains a very wide range of statistical options due to its library and package-based structure. R consists of a main base package that contains many basic R mathematical, statistical, and graphical functions and a variety of additional libraries that may be loaded at any time to add additional functionality to the program. However, the base R package represents only a small percentage of its capabilities.

To expand upon and add capabilities to the base R package, a wide variety of additional packages may be downloaded free and installed to add new libraries of functions to the program. For example, this book is concerned with multilevel modeling. The base R package does not include a function allowing for multilevel modeling. In order to run multilevel models in R,
the packages \texttt{nlme} or \texttt{lme4} can be downloaded and installed, thus giving R a new set of options related to multilevel modeling.

Libraries that already exist within the base R package can be called upon at any time with the command \texttt{library()}. For example, the command \texttt{library(foreign)} would install the foreign library necessary for reading SPSS data sets into R. For libraries that do not already exist within the R base package, downloading and installation of R packages is quite easy. On a Macintosh computer, this can be accomplished using the Packages & Data menu (and choosing the Package Installer). (See Figure A.2.) For the PC, access the Packages menu option, followed by Install Packages.

You will be asked to select a computer (referred to as a mirror site) from which to download the packages that you select. Any site selection should be fine. You will then be presented with a lengthy list of all available libraries in R. After you select the one you need, the process of installation begins. Most of it is handled automatically by R. New packages can be downloaded and installed simply by choosing a package or packages from the list and clicking Install Selected. If a package has previously been downloaded, a Package Manager allows you to easily re-install previously downloaded packages.

\section*{A.1 Basic Functions in R}

\subsection*{A.1.1 Running Statistical Analyses in R}

As an example of running basic statistical analyses in R, let's consider the t-test (denoted as \texttt{t.test} in R). The following is an example of running a basic t-test of two independent samples using R. We first define the two
objects as Group1 and Group2 and use them in the \texttt{t.test()} function. To learn about any function in R, typing the \texttt{?name} where \texttt{name} denotes the function (e.g., \texttt{t.test}) will show a help file for the function specified. Also, help files can be found for terms placed inside the \texttt{help.search(" ")} function. Finally, we can also type \texttt{help(name)} to obtain help with specific functions. Again, \texttt{name} would be the name of the function. To access help with \texttt{t.test}, we would type \texttt{help(t.test)}.

First, notice that \texttt{<-} is the assignment operator by which data on the left-hand side is assigned to the value or object on the right. The \texttt{c} in front of a left parenthesis means that the values to follow, separated by commas, are to be \emph{concatenated}, which in the R language means to form the values (which may be text if in quotes) into a vector. In this example, we are creating data for two groups where scores for the first group are 5, 2, 3, 5, 7, and 7. We will then compare the mean of this group with that of the second, using the t-test.
In order to input the data for the two groups, and then run the t-test in R using the default options, the analysis commands can be written as seen below, after which appears the resulting output.

```r
> Group1 <- c(5, 2, 3, 5, 7, 7)
> Group2 <- c(4, 4, 2, 7, 6, 4)
> t.test(Group1, Group2)

Welch Two Sample t-test

data: Group1 and Group2
t = 0.3029, df = 9.789, p-value = 0.7683
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -2.125925  2.792592
sample estimates:
mean of x  mean of y
 4.833333  4.500000
```

We could also specify options within the `t.test` function, such as imposing the assumption of homogeneity of variance and a 99% confidence interval:

```r
> t.test(Group1, Group2, var.equal = TRUE, conf.level = .99)

Two Sample t-test

data: Group1 and Group2
t = 0.3029, df = 10, p-value = 0.7682
alternative hypothesis: true difference in means is not equal to 0
99 percent confidence interval:
 -3.154467  3.821134
sample estimates:
mean of x  mean of y
 4.833333  4.500000
```

### A.1.2 Reading Data into R

We have shown the t-test as an exemplar to give new R users a tiny bit of code that is easy to run for a commonly performed analysis. In this example, data was input directly into R by creating two vectors and running the t-test on those vectors. In many situations, however, the researcher may want to
read in and analyze an external data file from a source such as SPSS, Excel, or a text file.

The most basic R code for reading in external data files is through use of the `read.table` command that allows data in ASCII (text) format to be read into and analyzed by R. If a data file has variable names in the first row, the `header = T` statement should be used for R to recognize the top row of values as variable names. Consider an example in which we have data in the file `data.txt`, with variable names in the first row. In the following command, we read this file in from the appropriate directory into an R data file that we call `DataName`.

```R
DataName <- read.table('/Users/mycomputer/data.txt', header = T)
```

If you would rather find the file through the familiar point-and-click method used in Windows and Mac systems, the use of `file.choose` can help. Running `file.choose` will open a directory search window and allow you to browse and click on the file you want to read into R. Here is an alternative approach for reading the `data.txt` file. We will find it using our operating system's point-and-click functionality.

```R
DataName <- read.table(file.choose(), header = T)
```

R has other specialized commands that are tailored to read in specific file types. Certain of these options, for example, `read.csv` and `read.delim` are available directly from the R base package. Other options for statistics package inputs such as `read.spss` for SPSS files or `read.dta` for STATA files are available in the `foreign` library.

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**A.2 Missing Data**

When reading data into R, it is important to acknowledge that many data sets will be missing data. Missing data is often problematic for statistical analysis and may become an issue for various R functions. Although there are many interesting and sophisticated ways of dealing with missing data, we wanted to call attention to a very simple missing data function in R called `na.omit` that may be used to remove all missing cases from a data set.

The default code for missing data in R is `NA`. Thus, the `na.omit` function will remove all cases with the `NA` code in a data set. It is important to note, however, that only missing data coded `NA` will be removed. Other codes for missing data occurring in a data set will have to be dealt with in a different manner.
A.3 Types of Data

Data in R may take a number of different forms that may be used only for certain functions. Thought of another way, some functions require data to be of a specific type. The two most common types encountered in statistical analyses are numeric and factor data.

As implied by the name, numeric data take the form of numbers that can be added, multiplied, and so on. Factors are variables that R views as including distinct categories. For example, if a data set contains a variable for gender, which is coded as 1 (male) or 2 (female), R will automatically see this as numeric. However, if we want to conduct an analysis in which gender should be treated as a grouping variable, we may need to convert it to a factor. This can be done very easily using the `as.factor` function. For gender, we would simply create a new variable called `gender.factor` using the following command:

```r
gender.factor<-as.factor(gender)
```

We would then use the `gender.factor` variable in all cases where we want to treat gender as a factor variable. One final important point to note is that not every function requires a grouping variable to explicitly act as a factor. Therefore, it is important to read the help manual to determine whether a particular function requires a factor.

A.4 Additional R Environment Options

The R console and use of R scripts provide a framework appropriate for a wide variety of data analysis situations. However, a more sophisticated experience beyond the basic options in R can be obtained through an integrated development environment (IDE) such as RStudio (http://www.rstudio.com/). RStudio, like R, is an open source and freely available program for Macintosh, Windows, and Linux. Figure A.3 shows a session of RStudio and its four windows. A syntax window is shown at top left. The R console appears at bottom left. The top right (blank in the figure) would list objects in the workspace (or history of submitted commands), and a help tab appears at bottom right along with tabs for files and folders in a selected directory, plots, and packages (for installing or loading packages).

Another option, appropriate for more casual statistical users, is the R Commander GUI (Figure A.4). This option adds a more user-friendly interface to the R console by allowing a menu-driven point-and-click accessibility for many basic statistical functions. This interface is considerably more
FIGURE A.3
Screen capture of RStudio windows.

FIGURE A.4
Screen capture of RCommander GUI.
limited in functionality than the full R environment as only a handful of options are programmed into the point-and-click interface. It does, however, still allow the writing of syntax and incorporation of new functionalities via the use of installed packages. The RCommander GUI can be downloaded and installed as a package from the R Package Installer.

This appendix is meant to provide the basic R knowledge necessary to run the models described in this book. More detailed information on the use of R can be found in *The R Book* by Michael J. Crawley and in *Discovering Statistics Using R* by Field, Miles, and Field.
References

A powerful tool for analyzing nested designs in a variety of fields, multilevel/hierarchical modeling allows researchers to account for data collected at multiple levels. Multilevel Modeling Using R provides you with a helpful guide to conducting multilevel data modeling using the R software environment.

After reviewing standard linear models, the authors present the basics of multilevel models and explain how to fit these models using R. They then show how to employ multilevel modeling with longitudinal data and demonstrate the valuable graphical options in R. The book also describes models for categorical dependent variables in both single level and multilevel data. The book concludes with Bayesian fitting of multilevel models. For those new to R, the appendix provides an introduction to this system that covers basic R knowledge necessary to run the models in the book.

Features
- Shows how to properly model data structures to avoid incorrect parameter and standard error estimates
- Explains how multilevel models provide insights into your data that otherwise might not be detected
- Illustrates helpful graphical options in R appropriate for multilevel data
- Presents models for categorical dependent variables in single level and multilevel contexts
- Discusses multilevel modeling within the Bayesian framework
- Offers an introduction to R in the appendix for R novices
- Uses various R packages to conduct the analyses and interpret the results, with the code available online

Through the R code and detailed explanations provided, this book gives you the tools to launch your own investigations in multilevel modeling and gain insight into your research.