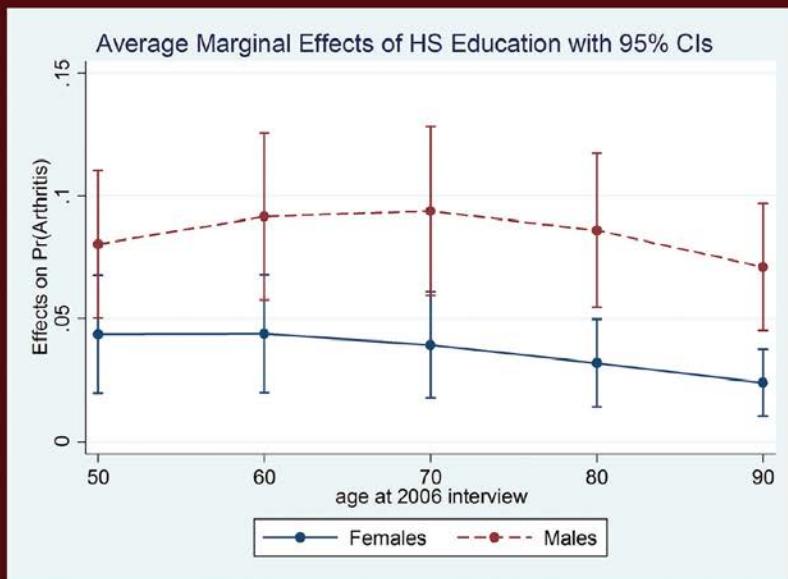


Applied Survey Data Analysis

Second Edition



Steven G. Heeringa
Brady T. West
Patricia A. Berglund



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Second Edition



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Preface

Applied Survey Data Analysis, Second Edition, is written as a current guide to the applied statistical analysis and interpretation of survey data. When the editors initially raised the question of a second edition, the first questions that came to our mind were, “Is there sufficient new material?” and “Have there been important advances in theory, methods, and software to justify an update to our 2010 first edition of *Applied Survey Data Analysis*?” After a short period of deliberation, the consensus among our author group was a definite “yes.”

Writing a second edition provided us with an opportunity to update the previous material and communicate new advances in applied methods and software, and also opened the door to adding important new content areas. New to this second edition is coverage of: bootstrap methods of variance estimation ([Chapter 3](#)); estimation and inference for specialized functions such as the Gini coefficient ([Chapter 5](#)) and log-linear models ([Chapter 6](#)); updated approaches to examining model diagnostics, testing goodness of fit, and estimation and display of marginal effects in linear and generalized linear models ([Chapters 7 through 9](#)); state-of-the-art methods for analysis of longitudinal survey data ([Chapter 11](#)); fractional imputation methods for item missing data ([Chapter 12](#)); and enhanced treatment of methods and software for fitting multilevel models, structural equation models, and other latent variable models to complex sample survey data ([Chapter 13](#)). Appendix A provides an updated review of software packages and procedures that are currently available for the analysis of complex sample survey data in the major software systems.

In addition to updates of previous content and the addition of new topics in this second edition, the majority of the analysis examples based on the National Health and Nutrition Examination Survey (NHANES) and the Health and Retirement Study (HRS) are now based on more recent public-use versions of these data sets. At the request of instructors and students who have used ASDA for graduate-level courses on survey data analysis, we have added example analyses using the European Social Survey (ESS), which includes measures on a wide range of social, political, economic, cultural, and religion topics. Data analysis exercises for [Chapters 5 through 12](#) have also been revised to incorporate the updated versions of NHANES and HRS data as well as the new ESS public-use file.

The general outline for this second edition continues to be based on the syllabus for a course entitled *Analysis of Complex Sample Survey Data* that we have taught for more than 15 years in the Joint Program in Survey Methodology (JPSM) based at the University of Maryland (College Park), in the University of Michigan’s Program in Survey Methodology (MPSM), and

the Summer Institute in Survey Research Techniques at the University of Michigan Institute for Social Research. We have also presented this material at a number of domestic and international short course programs.

As was the case for the original edition, the motivation for this second edition lies both in years of teaching graduate courses in applied methods for survey data analysis and extensive consultation with social and physical scientists, educators, medical researchers, and public health professionals on best methods for approaching applied survey data analysis problems. Readers may initially find the topical outline and content choices a bit unorthodox, but our instructional and consultation experience has shown it to be effective for teaching this complex subject to students and professionals who have a minimum of a two-semester graduate-level course in applied statistics. The practical, everyday relevance of the chosen topics and the emphasis each receives in this text has also been informed by over 80 years of combined experience in consulting on survey data analysis with research colleagues and students under the auspices of the Survey Methodology Program of the Institute for Social Research (ISR) and the University of Michigan Consulting for Statistics, Computing, and Analytics Research (CSCAR) team. For example, the emphasis placed on topics as varied as weighted estimation of population quantities, sampling error calculation models, coding of indicator variables in regression models, and interpretation of results from generalized linear models derives directly from our long-term observation of how often naïve users make critical mistakes in these areas.

This book, like the many courses that it will serve, is designed to provide an intermediate-level statistical overview of the analysis of complex sample survey data—emphasizing methods and worked examples while reinforcing the principles and theory that underlie those methods. The intended audience includes graduate students, survey practitioners, and research scientists from the wide array of disciplines that use survey data in their work. Students and practitioners in the statistical sciences should also find that this text provides a useful framework for integrating their further, more in-depth studies of the theory and methods for survey data analysis.

Balancing theory and application in any text is no simple matter. The distinguished statistician D.R. Cox begins the outline of his view of applied statistical work by stating: “Any simple recommendation along the lines *in applications one should do so and so* is virtually bound to be wrong in some or, indeed, possibly many contexts. On the other hand, descent into yawning vacuous generalities is all too possible” (Cox, 2007). Since the ingredients of each applied survey data analysis problem vary—the aims, the sampling design, the available survey variables—there is no single set of recipes that each analyst can simply follow without additional thought and evaluation on their part. On the other hand, a book on applied methods should not leave survey analysts alone, fending for themselves, with only abstract theoretical explanations to guide their way through an applied statistical analysis of survey data.

THEORY BOX 0.1 AN EXAMPLE THEORY BOX

Theory boxes are used in this book to develop or explain a fundamental theoretical concept underlying statistical methods. The content of these theory boxes is intended to stand alone, supplementing the interested reader's knowledge, but should not be necessary for understanding the general discussion of applied statistical approaches to the analysis of survey data.

On balance, the discussion in this book will tilt toward proven recipes where theory and practice have demonstrated the value of a specific approach. In cases where theoretical guidance is less clear, we identify the uncertainty but still aim to provide advice and recommendations based on experience and current thinking on best practices.

The chapters of this book are organized to be read in sequence, with each chapter building on material covered in the preceding chapters. Chapter 1 provides important context for the remaining chapters, briefly reviewing historical developments and laying out a step-by-step process for approaching a survey analysis problem. The updated and extended content of Chapters 2 through 4 of this second edition will introduce the reader to the fundamental features of *complex sample designs* and demonstrate how design characteristics such as stratification, cluster sampling, and weighting are easily incorporated into the statistical methods and software for survey estimation and inference.

Treatment of statistical methods for survey data analysis begins in Chapters 5 and 6 with coverage of univariate (i.e., single-variable) descriptive and simple bivariate (i.e., two-variable) analyses of continuous and categorical variables. Chapter 7 presents the linear regression model for continuous dependent variables. Generalized linear regression modeling methods for survey data are treated in Chapters 8 and 9. Chapter 10 pertains to methods for event-history analysis of survey data, including models such as the Cox proportional hazard model and discrete time models. Chapter 11 is completely new to this second edition and covers the latest developments in analysis of longitudinal survey data. Chapter 12 introduces methods for handling missing data problems in survey data sets, expanding on the first edition's coverage of multiple imputation to include new developments in design-based fractional imputation methods. Finally, the coverage of statistical methods for survey data analysis concludes in Chapter 13 with a discussion of new developments in the area of advanced statistical techniques for survey data, including multilevel analysis and structural equation modeling.

To avoid repetition in the coverage of more general topics such as the recommended steps in a regression analysis or testing hypotheses concerning regression parameters, topics will be introduced as they become relevant to

the specific discussion. For example, the iterative series of steps that we recommend analysts follow in regression modeling of survey data is introduced in [Chapter 7](#) (linear regression models for continuous outcomes), but the series applies equally to estimation, evaluation, and inference for generalized linear regression models ([Chapters 8](#) and [9](#)). By the same token, specific details of the appropriate procedures for each step (e.g., regression model diagnostics) are covered in the chapter on a specific technique. Readers who use this book primarily as a reference volume will find cross-references to earlier chapters useful in locating important background for discussion of specific analysis topics.

There are many quality software choices out there for survey data analysts. We have once again selected Stata for most of the book examples, due to its ease of use and flexibility for survey data analysis, but we will also demonstrate the use of available programs and command syntax for SAS, SUDAAN, SPSS, R, and Mplus for specific types of analyses. All example analyses presented in the book chapters have been replicated to the greatest extent possible using the SAS®, SPSS®, SUDAAN®, IVEware®, R, WesVar®, and Mplus® software packages on the book’s web site (<http://www.isr.umich.edu/src/smp/asda/>).

Examples based on the analysis of major survey data sets are routinely used in this book to demonstrate statistical methods and software applications. To ensure diversity in sample design and substantive content, example exercises and illustrations are drawn from four major survey data sets: the 2011–2012 NHANES, the 2006–2012 HRS data, the National Comorbidity Survey Replication (NCS-R), and the ESS 2012 (Round 6) data for the Russian Federation. A description of each of these survey data sets is provided in Section 1.3. Practical exercises based on these data sets are included at the end of each chapter on an analysis topic to provide readers and students with examples enabling practice with using statistical software for applied survey data analysis.

Clear and consistent use of statistical notation is important. [Table 0.1](#) provides a summary of the general notational conventions used in this book. Special notation and symbol representation will be defined as needed for discussion of specific topics.

The materials and examples presented in the chapters of this book (which we refer to in subsequent chapters as ASDA) are supplemented through a companion web site (<http://www.isr.umich.edu/src/smp/asda/>). This web site provides survey analysts and instructors with additional resources in the following areas: links to new publications and an updated bibliography for the survey analysis topics covered in [Chapters 5](#) through [13](#); links to web sites, for example, survey data sets; replication of the command setups and output for the analysis examples in the Stata®, SAS, SUDAAN, IVEWare, R, SPSS, WesVar, and Mplus software systems; answers to frequently asked questions (FAQs); short technical reports related to special topics in applied survey data analysis; and reviews of statistical software system updates and

TABLE 0.1

Notational Conventions for Applied Survey Data Analysis

Notation	Properties	Explanation of Usage
<i>Indices and Limits</i>		
N, n	Standard usage	Population size, sample size
h	Subscript	Stratum index, for example, \bar{y}_h
α	Subscript	Cluster or Primary Stage Unit (PSU) index, for example, \bar{y}_{ha}
i	Subscript	Element (respondent) index, for example, y_{hai}
j, k, l	Subscripts	Used to index vector or matrix elements, for example, β_j
<i>Survey Variables and Variable Values</i>		
y, x	Roman, lower case, italicized, end of alphabet	Survey variables, for example, systolic blood pressure (mmHg), weight (kg)
Y_i, X_i	Roman, upper case, end of alphabet, subscript	True population values of y, x for individual i , with $i = 1, \dots, N$ comprising the population
y_i, x_i	Roman, lower case, end of alphabet, subscript	Sample survey observation for individual i , for example, $y_i = 124.5$ mmHg, $x_i = 80.2$ kg
$\mathbf{y}, \mathbf{x}, \mathbf{Y}, \mathbf{X}$	As above, bold	Vectors (or matrices) of variables or variable values, for example, $\mathbf{y} = \{y_1, y_2, \dots, y_n\}$
<i>Model Parameters and Estimates</i>		
β_j, γ_j	Greek, lower case	Regression model parameters, subscripts
$\hat{\beta}_j, \hat{\gamma}_j$	Greek, lower case, “^” hat	Estimates of regression model parameters
$\boldsymbol{\beta}, \boldsymbol{\gamma}, \hat{\boldsymbol{\beta}}, \hat{\boldsymbol{\gamma}}$	As above, bold	Vectors (or matrices) of parameters or estimates, for example, $\boldsymbol{\beta} = \{\beta_0, \beta_1, \dots, \beta_p\}$
$B, b, \mathbf{B}, \mathbf{b}$	Roman, otherwise as above	As above, but used to distinguish finite population regression coefficients from probability model parameters and estimates
<i>Statistics and Estimates</i>		
$\bar{Y}, P, \sigma_y^2, S_y^2,$ \bar{y}, p, s_y^2	Standard usage	Population mean, proportion, and variance; sample estimates as used in Cochran (1977)
$\Sigma, \hat{\Sigma}$	Standard usage	Variance–covariance matrix; sample estimate of variance–covariance matrix
R^2, r, ψ	Standard usage	Multiple-coefficient of determination (R-squared), Pearson product moment correlation, odds ratio
ρ_y	Greek, lower case	Intraclass correlation for variable y
Z, t, χ^2, F	Standard usage	Probability distributions

any resulting changes to the software commands or output for the analysis examples.

We owe a debt to our many students in the JPSM, MPSM, and Summer Institute programs who over the years have studied with us—we only hope that you learned as much from us as we did from working with you. As lifelong

students ourselves, we owe a debt to our mentors and colleagues who over the years have instilled in us a passion for statistical teaching and consultation: Leslie Kish, Irene Hess, Graham Kalton, Morton Brown, Jim Lepkowski, Julian Faraway, Edward Rothman, Rod Little, and Trivellore Raghunathan. Finally, we wish to thank the staff at Chapman Hall/CRC Press, especially Rob Calver and Rebecca Davies, for their continued guidance.

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1

Applied Survey Data Analysis: An Overview

1.1 Introduction

Our modern society—its governments, businesses, educational institutions, nonprofit organizations, and individuals—continues to apply the *survey method* as a principal tool for looking at itself—“a telescope on society” in the words of House et al. (2004). Scientific surveys designed to measure labor force participation and employment, earnings and expenditures, health and healthcare, commodity stocks and flows, business and agricultural production, environmental conditions, and many other topics are critically important to social scientists, health professionals, policy makers and administrators, and thus to society itself.

Since the first edition of this book was published in 2010, the topics of *big data* and computationally intensive *data analytic methods* have exploded onto the scene in the popular and business media as well as in scientific communications, leaving many of us wondering what the future role will be for statistics in general and survey methodology and survey statistics in particular (Foster et al., 2016). We adopt the viewpoints expressed by our colleagues: “... demand for survey statistics has never been higher” and “Survey research is not dying, it is changing” (Groves, 2011; Couper, 2013). In fact, we can go further and say that since its origins in the early twentieth century, the scientific survey method has undergone continual change: improvements in sampling design and methods, emergence of new modes of data collection, shifts in *essential survey conditions* such as demands on survey respondents and declining response rates, and most importantly for readers of this book, an ongoing evolution of new statistical approaches and refinement of old approaches to the applied analysis of survey data. This second edition builds on the foundational theory and methods of applied survey data analysis and will introduce important new developments and tools that in a changing world promise to update and improve our statistical treatments of survey data.

The focus of this book will be on statistical methods—both old and new—for the analysis of *complex sample survey data* typically seen in large-scale scientific surveys, but the general approach to survey data analysis

and specific statistical methods described here should apply to all forms of survey data. To set the historical context for this work, Section 1.2 briefly reviews the history of developments in theory and methods for applied survey data analysis. Section 1.3 provides some needed background on the data sets that will be used for the analysis examples in [Chapters 2](#) through [13](#). This short overview chapter concludes in Section 1.4 with a general review of the sequence of steps required in any applied analysis of survey data.

1.2 A Brief History of Applied Survey Data Analysis

Today's survey data analysts approach a problem armed with substantial background in the theory of survey statistics, a literature filled with empirical results and high-quality software tools for the task at hand. However, before turning to the best methods currently available for the analysis of survey data, it is useful to look back at how we arrived at where we are today. The brief history described here is certainly a selected interpretation, chosen to emphasize the evolution of probability sampling design and related statistical analysis techniques that are most directly relevant to the material in this book. Readers interested in a comprehensive review of the history and development of survey research in the United States should see Converse (1987). Bulmer (2001) provides a more international perspective on the history of survey research in the social sciences. For the more statistically inclined, Skinner et al. (1989) provide an excellent review of the development of methods for descriptive and analytical treatment of survey data. A comprehensive history of the impacts of sampling theory on survey practice can be found in O'Muircheartaigh and Wong (1981).

1.2.1 Key Theoretical Developments

The science of survey sampling, survey data collection methodology, and the analysis of survey data date back a little more than 100 years. By the end of the nineteenth century, an open and international debate established the *representative sampling method* as a statistically acceptable basis for the collection of observational data on populations (Kaier, 1895). Over the next 30 years, work by Bowley (1906), Fisher (1925), and other statisticians developed the role of randomization in sample selection and large-sample methods for estimation and statistical inference for simple random sample (SRS) designs.

The early work on the representative method and inference for simple random and stratified random samples culminated in a landmark paper by Jerzy Neyman (1934), which outlined a cohesive framework for estimation

and inference based on estimated confidence intervals for population quantities that would be derived from the probability distribution for selected samples over repeated sampling. Following the publication of Neyman's paper, there was a major proliferation of new work on sample designs, estimation of population statistics, and variance estimation techniques required to develop confidence intervals for sample-based inference, or what in more recent times has been labeled *design-based inference* (Yates, 1949; Deming, 1950; Hansen et al., 1953; Sukatme, 1954; Kish, 1965; Cochran, 1977). House et al. (2004) credit J. Steven Stock (U.S. Department of Agriculture) and Lester Frankel (U.S. Bureau of the Census) with the first applications of area probability sampling methods for household survey data collections. Even today, the primary techniques for sample design, population estimation, and inference developed by these pioneers and published during the period 1945–1975 remain the basis for almost all descriptive analysis of survey data.

The developments of the World War II years firmly established the probability sample survey as a tool for describing population characteristics, beliefs, and attitudes. Based on Neyman's theory of inference, survey sampling pioneers in the United States, Britain, India, and elsewhere developed optimal methods for sample design, estimators of survey population characteristics, and confidence intervals for population statistics. As early as the late 1940s, social scientists led by sociologist Paul Lazarsfeld of Columbia University began to move beyond using survey data to simply describe populations to using these data to explore relationships among the measured variables (Kendall and Lazarsfeld, 1950; Klein and Morgan, 1951). Skinner et al. (1989) and others before them labeled these two distinct uses of survey data as "descriptive" and "analytical." Hyman (1955) used the term "explanatory" to describe scientific surveys whose primary purpose was the analytical investigation of relationships among variables.

During the period 1950–1990, analytical treatments of survey data expanded as new developments in statistical theory and methods were introduced, empirically tested, and refined. Important classes of methods that were introduced during this period included log-linear models and related methods for contingency tables, generalized linear models (e.g., logistic regression), survival analysis models, general linear mixed models (e.g., hierarchical linear models), structural equation models, and latent variable models. Many of these new statistical techniques applied the method of maximum likelihood to estimate model parameters and standard errors of the estimates, assuming that the survey observations were *independent* observations from a known probability distribution (e.g., binomial, multinomial, Poisson, product multinomial, normal). As discussed in [Chapter 2](#), data collected under most contemporary survey designs do not conform to the key assumptions of these methods.

As Skinner et al. (1989) point out, survey statisticians were aware that straightforward applications of these new methods to complex sample

survey data could result in underestimates of variances and biased estimates of confidence intervals and test statistics. However, except in limited situations of relatively simple designs, exact determination of the size and nature of the bias (or a potential correction) was difficult to express analytically. Early investigations of such “design effects” were primarily empirical studies, comparing design-adjusted variances for estimates to the variances that would be obtained if the data were truly identically and independently distributed (equivalent to an SRS of equal size). Over time, survey statisticians developed special approaches to estimating these models that enabled the survey analyst to take into account the complex characteristics of the sample design (e.g., Koch and Lemeshow, 1972; Kish and Frankel, 1974; Rao and Scott, 1981; Binder, 1983; Pfeffermann et al., 1998). These approaches (and related developments) are described in [Chapters 5](#) through [13](#) of this book.

1.2.2 Key Software Developments

Development of the underlying statistical theory and empirical testing of new methods was obviously important, but the survey data analyst needed computational tools in order to apply these techniques. We can have nothing but respect for the pioneers who in the 1950s fitted multivariate regression models to survey data using only hand computations (sums, sums of squares, sums of cross products, matrix inversions, etc.) performed on a rotary calculator and possibly a tabulating machine (Klein and Morgan, 1951). The first Hewlett Packard electronic calculator with square root, logarithm, and trigonometric functions was advertised in *Scientific American* in 1971. The origin of statistical software as we know it today dates back to the 1960s, with the advent of the first mainframe computer systems. Software systems such as BMDP and OSIRIS and later SPSS, SAS, GLIM, S, and GAUSS were developed for mainframe users; however, with limited exceptions, these major software packages did not include programs that were adapted to complex sample survey data.

To fill this void during the 1970s and early 1980s, a number of stand-alone programs, often written in the Fortran language and distributed as compiled objects, were developed by survey statisticians (e.g., OSIRIS: PSALMS and REPERR, CLUSTERS, CARP, SUDAAN, and WesVar). By today’s standards, these programs had a steep “learning curve,” limited data management flexibility, and typically supported only descriptive analysis (means, proportions, totals, ratios, and functions of descriptive statistics) and linear regression modeling of multivariate relationships. A review of the social science literature of this period shows that only a minority of researchers actually employed these special software programs when analyzing complex sample survey data, resorting instead to standard analysis programs with their default assumption that the data originated with an SRS of the survey population.

The appearance of microcomputers in the mid-1980s was quickly followed by a transition to personal computer versions of the major statistical software (BMDP, SAS, SPSS) as well as the advent of new statistical analysis software platforms (e.g., SYSTAT, Stata, S-Plus). However, with the exception of specialized software systems (WesVar PC, PC CARP, PC SUDAAN, Micro-OOSIRIS, CLUSTERS for PC, IVEware) that were often designed to read data sets stored in the formats of the larger commercial software packages, the microcomputing revolution still did not put tools for the analysis of complex sample survey data in the hands of most survey data analysts. Nevertheless, throughout the late 1980s and early 1990s, the scientific and commercial pressures to incorporate programs of this type into the major software systems were building. Beginning with Version 6.12, SAS users had access to PROC SURVEYMEANS and PROC SURVEYREG, two new SAS procedures that permitted simple descriptive analysis and linear regression analysis for complex sample survey data. At about the same time, the Stata system for statistical analysis appeared on the scene, providing complex sample survey data analysts with the “svy” versions of the more important analysis programs. SPSS’s entry into the world of complex sample survey data analysis came later with the introduction of the Complex Samples add-on module in Version 13. Software programs for the analysis of complex sample survey data have also appeared in the contributed survey package for the R system (Lumley, 2010) and the MPlus system (Muthén and Muthén, 2015). Appendix A of this book presents updated coverage of the capabilities of all of these different systems in detail.

The survey researcher who sits down today at their personal computing workstation, laptop, or tablet has access to powerful software systems, high-speed processing and high-density data storage capabilities that the analysts in the 1970s, 1980s, and even the 1990s could not have envisioned. All of these recent advances have brought us to a point at which today’s survey analyst can approach both simple and complex problems with the confidence gained through a fundamental understanding of the theory, empirically tested methods for design-based estimation and inference, and software tools that are sophisticated, accurate, and easy to use.

Now that we have had a glimpse at our history, let us begin our study of applied survey data analysis.

1.3 Example Data Sets and Exercises

Examples based on the analysis of major survey data sets are routinely used in this book to demonstrate statistical methods and software applications. To ensure diversity in sample design and substantive content, example exercises

and illustrations in this second edition are drawn from four major U.S. and international survey data sets:

1. *The National Comorbidity Survey Replication (NCS-R)*: The NCS-R was a 2002 study of mental illness in the U.S. household population aged 18 and over, funded by the U.S. National Institutes of Health (NIH). The core content of the NCS-R is based on a lay-administered interview using the World Health Organization (WHO) Composite International Diagnostic Interview (CIDI) diagnostic tool, which is designed to measure primary mental health diagnostic symptoms, symptom severity, and use of mental health services (Kessler et al., 2004). The NCS-R was based on interviews with randomly chosen adults in an equal probability, multistage sample of households selected from the University of Michigan National Sample master frame. The survey response rate was 70.9%. The survey was administered in two parts: a Part I core diagnostic assessment of all respondents ($n = 9,282$), followed by a Part II in-depth interview with 5,692 of the 9,282 Part I respondents, including all Part I respondents who reported a lifetime mental health disorder and a probability subsample of the disorder-free respondents in the Part I screening.

The NCS-R was chosen as an example data set for the following reasons: (1) the scientific content and, in particular, its binary measures of mental health status; (2) the multistage design with primary stage stratification and cluster sampling typical of many large-scale public-use survey data sets; and (3) the two-phase aspect of the data collection.

2. *The Health and Retirement Study (HRS)*—2012: The HRS is a longitudinal study of the American population 50 years of age and older. Beginning in 1992, the HRS has collected data every 2 years on a longitudinal panel of sample respondents born between the years of 1931 and 1941. Originally, the HRS was designed to follow this probability sample of age-eligible individuals and their spouses or partners as they transitioned from active working status to retirement, measuring aging-related changes in labor force participation, financial status, physical and mental health, and retirement planning. The HRS observation units are age-eligible individuals and “financial units,” or couples in which at least one spouse or partner is HRS eligible. Beginning in 1993 and again in 1998, 2004, 2010, and 2016, the original HRS 1931–1941 birth cohort panel sample was augmented with probability samples of U.S. adults and spouses/partners from: (1) pre-1924 (added in 1993); (2) 1924–1930 and 1942–1947 (added in 1998); (3) 1948–1953 (added in 2004); and (4) 1954–1959 (added in 2010). The baseline response

rates for the original 1992 cohort sample exceeded 80%. The corresponding baseline survey response rates for the 1993–2010 new cohort updates ranged from 70% to 80%. In 2012, the HRS interviewed over 20,500 eligible sample adults aged 50+ in the composite panel.

The HRS samples were primarily identified through in-person screening of large, multistage area probability samples of U.S. households. For the pre-1931 birth cohorts, the core area probability sample screening was supplemented through sampling of age-eligible individuals from the U.S. Medicare Enrollment Database. Sample inclusion probabilities for HRS respondents vary slightly across birth cohorts and are approximately two times higher for African-Americans and Hispanics. Data from the 2012 wave of the HRS panel are used for many the examples in this book, and we consider a longitudinal analysis of multiple waves of HRS data in [Chapter 11](#).

3. *The National Health and Nutrition Examination Survey (NHANES)—2011–2012:* Sponsored by the National Center for Health Statistics (NCHS) of the Centers for Disease Control (CDC), the NHANES is a survey of the adult, noninstitutionalized population of the United States. The NHANES is designed to study the prevalence of major disease in the U.S. population and monitor the change in prevalence over time as well as trends in treatment and major disease risk factors including personal behaviors, environmental exposure, diet, and nutrition. The NHANES survey includes both an in-home medical history interview with sample respondents and a detailed medical examination at a local mobile examination center (MEC).

The NHANES surveys were conducted on a periodic basis between 1971 and 1994 (NHANES I, II, III), but beginning in 1999, the study transitioned to a continuous interviewing design. Since 1999, yearly NHANES data collections have been performed in a multistage sample that includes 15 primary stage unit (PSU) locations with new sample PSUs added in each data collection year. Approximately 7,000 probability sample respondents complete the NHANES in-home interview phase each year and roughly 5,000 of these individuals also consent to the detailed MEC examination. To meet specific analysis objectives, the NHANES oversamples low-income persons, adolescents between the ages of 12 and 19, persons aged 60 and older, African-Americans and Hispanics of Mexican ancestry. To ensure adequate precision for sample estimates, NCHS recommends pooling data for 2 or more consecutive years of NHANES data collection. The NHANES example analyses provided in this text are based on the combined data collected in 2011 and 2012. The

unweighted response rate for the interview phase of the 2011–2012 NHANES was approximately 72%.

4. *The European Social Survey (ESS): Russian Federation, Round 6 (2012):* The ESS is a multinational survey conducted in over 30 European nations. ESS is jointly funded by the European Commission (EC), the European Science Foundation as well as collaborating academic institutions in the participating countries. The ESS follows a *repeated cross-sectional survey design* ([Chapter 11](#)), with independent samples of persons from a given country measured in each survey year. Each country's ESS questionnaire includes a common core module of questions focusing on social, political, economic, cultural, and religious topics as well as several special modules of questions that rotate across rounds of ESS data collection. The inclusion of the ESS data set for analysis examples and exercises in this second edition of ASDA reflects not only the importance of this multinational data resource to comparative social science research in Europe but also a deliberate decision to include analysis topics that are not so health research focused, such as those based on the NHANES, HRS, and the NCS-R data sets.

Beginning with Round 1 in 2002, a new round of ESS sampling and interviewing has been conducted every 2 years. The examples in this book are based on data from the Round 6 ESS:Russian Federation (ESS:RF) survey that was conducted in 2012. The sample design for Round 6 of the ESS:RF survey can be described as a stratified, clustered, multistage probability sample of individual respondents aged 15 years and older. The Round 6 ESS:RF response rate was just under 70%. Interviews were completed with $n = 2,484$ sample respondents.

Each record in the ESS:RF Round 6 data file includes a STRATIFY variable containing codes for eight primary stage strata defined geographically by “okrug” administrative units. A total of $a = 151$ PSUs were selected from the eight strata, with multiple PSUs selected per stratum. Codes for these 151 primary stage clusters are contained in the PSU variable. Each data record also contains a sample selection weight DWEIGHT and a post-stratified survey weight (PSPWGHT). Unless otherwise stated, all ESS:RF analysis examples in this book will use the post-stratified weight (PSPWGHT). ESS public-use data files also include a population size weight (PWEIGHT) intended to be used when analysts wish to combine data from multiple ESS country samples in a single analysis on a “proportionate to population size” basis. Since our analysis examples will focus only on the Round 6 ESS:RF data, this “combining” weight will not be used in this book.

Public-use versions of each of these four major survey data sets are available online. The companion web site for this book

provides the most current links to the official public-use data and documentation archives for each of these example survey data sets.

1.4 Steps in Applied Survey Data Analysis

Applied survey data analysis—both in daily practice and here in this book—is a process that requires more of the analyst than simple familiarity and proficiency with statistical software tools. It requires a deeper understanding of the sample design, the survey data, and the interpretation of the results of the statistical methods. Following a more general outline for applied statistical analysis presented by Cox (2007), [Figure 1.1](#) outlines a sequence of six steps that are fundamental to applied survey data analysis, and we describe these steps in more detail below.

Step 1: Definition of the problem and statement of the objectives—The first of the six steps involves a clear specification of the problem to be addressed and formulation of objectives for the analysis exercise. For example, the “problem” may be ambiguity among physicians over whether there should be a lower threshold for prostate biopsy following prostate-specific antigen (PSA) screening in African-American men (Cooney et al., 2001). The corresponding objective would be to estimate the 95th percentile and the 95% confidence bounds for this quantity (± 0.2 ng/mL PSA) in a population of African-American men. The estimated 95% confidence bounds can in turn be used by medical experts to determine if the biopsy

Step	Activity
1	Definition of the problem and statement of the objectives
2	Understanding the sample design
3	Understanding design variables, underlying constructs, and missing data
4	Analyzing the data
5	Interpreting and evaluating the results of the analysis
6	Reporting of estimates and inferences from the survey data

FIGURE 1.1
Steps in applied survey data analysis.

threshold for African-American men should be different than for men of other race and ethnic groups.

As described above, the problems to which survey data analyses may be applied span many disciplines and real-world settings. Likewise, the statistical objectives may vary. Historically, the objectives of most survey data analyses were to describe characteristics of a target population: its average household income, the median blood pressure of men, or the proportion of eligible voters who favor candidate X. However, survey data analyses can also be used for decision-making: For example, should a pharmaceutical company recall its current products from store shelves due to a perceived threat of contamination? In a population case-control study, does the presence of silicone breast implants significantly increase the odds that a woman will contract a connective tissue disease such as scleroderma (Burns et al., 1996)? In recent decades, the objective of many sample survey data analyses has been to explore and extend the understanding of multivariate relationships among variables in the target population. Sometimes multivariate modeling of survey data is seen simply as a descriptive tool, defining the form of a functional relationship as it exists in a finite population. However, it is increasingly common for researchers to use observational data from complex sample surveys to probe causality in the relationships among variables.

Step 2: Understanding the sample design—The survey data analyst must understand the sample design that was used to collect the data that they are about to analyze. Without an understanding of key properties of the sample design, the analysis may be inefficient, biased, or otherwise lead to incorrect inference. An experienced researcher who designs and conducts a randomized block experimental design to test the relative effectiveness of new instructional methods should not proceed to analyze the data as a simple factorial design, ignoring the blocking that was built into her experiment. Likewise, an economics graduate student who elects to work with the longitudinal HRS data should understand that the nationally representative sample of older adults includes stratification, cluster sampling and disproportionate sampling (i.e., compensatory population weighting), and that these design features may require special approaches to population estimation and inference.

At this point, we may have discouraged the reader into thinking that an in-depth knowledge of sample design is required to work with survey data or that they may need to relearn what was learned in general courses on applied statistical methods. This is not the case. [Chapters 2 through 4](#) will introduce the reader to the fundamental features of *complex sample designs* and demonstrate how

design characteristics such as stratification, cluster sampling, and weighting are easily incorporated into the statistical methods and software for survey estimation and inference. [Chapters 5 through 13](#) will then show the reader that relatively simple extensions of their current knowledge of applied statistical analysis methods provide the necessary foundation for efficient and accurate analysis of the data collected in sample surveys.

Step 3: Understanding design variables, underlying constructs, and missing data—The typical scientific survey data set is *multipurpose*, with the final data sets often including hundreds of variables that span many domains of study—income, education, health, family. The sheer volume of available data and the ease by which it can be accessed can cause survey data analysts to become complacent in their attempts to fully understand the properties of the data that are important to their choice of statistical methods and the conclusions that they will ultimately draw from their analysis. Step 2 described the importance of understanding the sample design. In the survey data, the key features of the sample design will be encoded in a series of *design variables*. Before analysis begins, some simple questions need to be put to the candidate data set: What are the empirical distributions of these design variables and do they conform to the design characteristics outlined in the technical reports and online study documentation? Does the original survey question that generated a variable of interest truly capture the underlying construct of interest? Are the response scales and empirical distributions of responses and independent variables suitable for the intended analysis? What is the distribution of missing data across the cases and variables, and is there a potential impact on the analysis and the conclusions that will be drawn? [Chapter 4](#) discusses techniques for answering these and other questions before proceeding to statistical analysis of the survey data.

Step 4: Analyzing the data—Finally, we arrive at the step to which many researchers rush to enter the process. We are all guilty of wanting to jump ahead. Identifying the problem and objectives seems intuitive. We tell ourselves that formalizing that step wastes time. Understanding the design and performing data management and exploratory analysis to better understand the data structure is boring. After all, the statistical analysis step is where we obtain the results that enable us to describe populations (through confidence intervals), to extend our understanding of relationships (through statistical modeling), and possibly even to test scientific hypotheses.

In fact, the statistical analysis step lies at the heart of the process. Analytic techniques must be carefully chosen to conform to the

analysis objectives and the properties of the survey data. Specific methodology and software choices must accommodate the design features that influence estimation and inference. Treatment of statistical methods for survey data analysis begins in [Chapters 5](#) and [6](#) with coverage of univariate (i.e., single-variable) descriptive and simple bivariate (i.e., two-variable) analyses of continuous and categorical variables. [Chapter 7](#) presents the linear regression model for continuous dependent variables, and generalized linear regression modeling methods for survey data are treated in [Chapters 8](#) and [9](#). [Chapter 10](#) pertains to methods for event-history analysis of survey data, including models such as the Cox proportional hazards model and discrete time logistic models. New to this second edition, methods of longitudinal analysis for complex sample survey data are addressed in [Chapter 11](#). [Chapter 12](#) introduces methods for handling missing data problems in survey data sets. Finally, the coverage of statistical methods for survey data analysis concludes in [Chapter 13](#) with a discussion of survey applications of specialized statistical models and techniques.

Step 5: Interpreting and evaluating the results of the analysis—Knowledge of statistical methods and software tools is fundamental to success as an applied survey data analyst. However, setting up the data, running the programs, and printing the results are not sufficient to constitute a thorough treatment of the analysis problem. Likewise, scanning a column of p -values in a table of regression model output does not inform us concerning the form of the “final model” or even the pure effect of a single predictor. As described in Step 3 above, interpretation of the results from an analysis of survey data requires a consideration of the error properties of the data. Variability of sample estimates will be reflected in the *sampling errors* (i.e., confidence intervals, test statistics) estimated in the course of the statistical analysis. *Nonsampling errors*, including potential bias due to survey nonresponse and item missing data, cannot generally be estimated from the survey data (Lessler and Kalsbeek, 1992). However, it may be possible to use ancillary data to explore the potential direction and magnitude of such errors. For example, an analyst working for a survey organization may statistically compare survey respondents with nonrespondents in terms of known correlates of key survey variables that are readily available on the sampling frame, to assess the possibility of nonresponse bias.

As survey data analysts have pushed further into the realm of multivariate modeling of survey data, care is required in interpreting fitted models. Is the model reasonably identified and do the data meet the underlying assumptions of the model estimation technique? Are there alternative models that explain the observed data

equally well? Is there scientific support for the relationship implied in the modeling results? Are interpretations that imply causality in the modeled relationships supported (Rothman, 1988)?

Step 6: Reporting of estimates and inferences from the survey data—The end products of applied survey data analyses are reports, papers, or presentations designed to communicate the findings to fellow scientists, policy analysts, and administrators/decision makers. This book includes discussion of standards and proven methods for effectively presenting the results of applied survey data analyses, including table formatting, statistical contents, and the use of statistical graphics.

With these six steps in mind, we now can now begin our updated walk through the process of planning, formulating, and conducting analysis of survey data.



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2

Getting to Know the Complex Sample Design

2.1 Introduction

The first step in any applied analysis of survey data involves defining the research questions that will be addressed using a given set of survey data. The next step is to study and understand the sampling design that generated the sample of elements (e.g., persons, businesses) from the target population of interest, given that the actual survey data with which the reader will be working were collected from the elements in this sample. This chapter aims to help readers understand the complex sample designs that they are likely to encounter in practice and identify the features of the designs that have important implications for correct analyses of the survey data.

Although a thorough knowledge of sampling theory and methods can benefit the survey data analyst, it is not a requirement. With a basic understanding of complex sample design features, including stratification, cluster sampling and weighting, readers will be able to specify the key design parameters required by today's survey data analysis software systems. Readers who are interested in a more in-depth treatment of sampling theory and methods are encouraged to review work by Hansen et al. (1953), Kish (1965), or Cochran (1977). More recent texts that blend basic theory and applications include Valliant et al. (2013), Levy and Lemeshow (2007), and Lohr (1999). A short monograph by Kalton (1983) provides an excellent summary of survey sample designs.

The sections in this chapter outline the key elements of complex sample designs that analysts need to understand to proceed knowledgeably and confidently to the next step in the analysis process.

2.1.1 Technical Documentation and Supplemental Literature Review

The path to understanding the complex sample design and its importance to the reader's approach to the analysis of the survey data should begin with a review of the technical documentation for the survey and the sample design. A review of the literature, including both supplemental methodological reports and papers that incorporate actual analyses of the survey

data, will be quite beneficial for the reader's understanding of the data to be analyzed.

Technical documentation for the sample design, weighting, and analysis procedures should be part of the "metadata" that are distributed with a survey data set. In the real world of survey data, the quality of this technical documentation can be highly variable; but at a minimum, the reader should expect to find a summary description of the sample, a discussion of weighting and estimation procedures, and, ideally, specific guidance on how to perform analyses of the survey data that correctly account for the complex sample design features. Readers who plan to analyze a public-use survey data set may find that the documentation of the design is lacking or inadequate. In these cases, readers should contact the help desk for the data distribution web site or inquire with the study team directly to obtain or clarify the basic information needed to correctly specify the sample design when analyzing the survey data.

Before diving into the statistical analysis of a survey data set, time is well spent in reviewing supplemental methodological reports or published scientific papers that used the same data. This review can identify important new information or even guide the reader's choice of an analytic approach given the statistical objectives of their research.

2.2 Classification of Sample Designs

As illustrated in [Figure 2.1](#), Hansen et al. (1983) define a sampling design to include two components: the sampling plan and a method for drawing inferences from the data generated under the sampling plan. The vast majority of survey data sets will be based on sample designs that fall in Cell A of [Figure 2.1](#), that is, designs that include a sampling plan based on probability sampling methods and assume that statistical inferences concerning population characteristics and relationships will be derived using the "design-based" theory initially proposed by Neyman (1934). Consequently, in this book, we will focus almost exclusively on sample designs of this type.

Sampling plan	Method of inference	
	Design-based	Model-based
Probability sample	A	B
Model-dependent sample	C	D

FIGURE 2.1

Classification of sample designs for survey data, per Hansen et al. (1983).

2.2.1 Sampling Plans

Probability sampling plans assign each member of the population a known nonzero probability of inclusion in the sample. A probability sampling plan may include features such as stratification and clustering of the population prior to selection—it does not require that the selection probability of one population element be independent of that for another. Likewise, the sample inclusion probabilities for different population elements need not be equal. In a probability sample of students in a coeducational secondary school, it is perfectly appropriate to sample women at a higher rate than men with the requirement that weights will be needed to derive unbiased estimates for the combined population. Randomization of sample choice is always introduced in probability sampling plans.

Model-dependent sampling plans assume that the variables of interest in the research follow a known probability distribution and that the choice of sample elements maximizes the precision of estimation for statistics of interest. For example, a researcher interested in estimating total annual school expenditures for teacher salaries (y) may assume the following relationship of the expenditures to known school enrollments (x): $y_i = \beta x_i + \varepsilon_i$, $\varepsilon_i \sim N(0, \sigma^2 x_i)$, where i indexes a school. Model-dependent sampling plans may employ stratification and clustering but strict adherence to randomized selection is not a requirement. Model-dependent sampling plans have received considerable attention in the literature on sampling theory and methods (Valliant et al., 2000). However, they are not common in survey practice due to a number of factors: the multipurpose nature of most surveys; uncertainty regarding the most appropriate model, where inappropriate models can lead to biased estimates (Hansen et al., 1983); and lack of high-quality ancillary data (e.g., the x variable in the example above).

Though not included in [Figure 2.1](#), *quota sampling*, *convenience sampling*, *snowball sampling*, and *peer nomination* are nonprobability methods for selecting sample members (Kish, 1965). Practitioners who employ these methods base their choices on assumptions concerning the “representativeness” of the selection process and often analyze the survey data using inferential procedures that are appropriate for probability sampling plans. However, these sampling plans do not adhere to the fundamental principles of either probability sampling plans or a rigorous probability model-based approach. Is it impossible to draw correct inferences from nonprobability sample data? No, because by chance an arbitrary sample could produce reasonable results; however, the survey analyst is left with no theoretical basis to measure the variability and bias associated with their inferences. Survey data analysts who plan to work with data collected under nonprobability sampling plans should carefully evaluate and report the potential selection biases and other survey errors that could affect their final results. Since there is presently no true statistical basis of support for the analysis of data collected under these nonprobability designs, they will not be addressed further in this book. For

a summary of recent thinking on approaches to the analysis of survey data collected from nonprobability samples, we refer readers to Baker et al. (2013).

2.2.2 Other Types of Study Designs Involving Probability Sampling

Occasionally, *case-control study designs* will be embedded in complex probability samples, where at the stage of sampling elements for eventual measurement, elements will be stratified based on whether they are “cases” (e.g., patients at a hospital with a particular type of illness or disease) or “controls” (e.g., patients at a hospital without the illness or disease). These studies are designed to enable the researcher to make inferences about differences in outcomes between the cases and controls, and rely on the same principles of random selection as probability sampling. In the case that the sampled cases and controls are still different on available covariates or outcomes despite the randomized selection, various techniques may be employed to ensure balance among the two groups, such as *propensity score matching*. There is a vast literature on the design and analysis of case-control studies, along with propensity score matching and related techniques; see, for example, Schlesselman and Schneiderman (1982), Rosenbaum and Rubin (1983), and Schulz and Grimes (2002). Secondary analysts working with survey data from a complex sample with an embedded case-control design need to carefully consider the ways in which the complex sample design features should be incorporated into their analyses. Recent work by Hahs-Vaughn and Onwuegbuzie (2006) and Landsman and Graubard (2013) provides important practical guidance in this regard.

Many research studies collect repeated measurements from individuals over time, in what are generally known as *prospective study designs*. These study designs often give rise to *longitudinal survey data* or *panel survey data*, where an initial probability sample of individuals or establishments is surveyed at some baseline time point, and then measured repeatedly over time in follow-up waves of the survey. The Health and Retirement Study (HRS), which we analyze in this book, provides a good example of a prospective study design. Secondary analysts of survey data collected as part of a prospective study design need to carefully consider the design features of the initial probability sample, and how these features (including time-varying survey weights for the respondents) should be accounted for in their analysis of the longitudinal data. We dedicate an entire chapter of this second edition to current thinking on how one should perform these types of analyses ([Chapter 11](#)).

In many cases, large probability samples selected from diverse target populations of interest will feature multiple stages of cluster sampling (discussed in more detail later in this chapter). For example, a sampling plan may feature random selection of counties, followed by smaller geographic areas, and finally households within the sampled areas. In most design-based approaches to survey data analysis, the primary sampling

units (PSUs; e.g., counties or groups of counties) are most critical for making robust inferences regarding the target population of interest, and the secondary analyst only needs to identify codes that indicate these PSUs (or use *replicate weights* reflecting the cluster sampling) in the analysis. However, some researchers may be interested in taking more of a *model-based approach* to the analysis, and making inferences regarding the *components of variance* for a particular survey measure of interest across *all stages* of the multistage cluster sample design.

For example, what proportion of the variability in the survey measure of interest arises from counties? And what proportion arises from the smaller areas within counties? And if covariates are available describing features of these sampled “clusters,” do they effectively explain variance at each stage of the sample design? To answer these types of questions, researchers can employ *multilevel models*, and it is important that relevant features of the probability sample design, including selection probabilities for the clusters at each stage of sample selection, be accounted for when estimating the components of variance that define these models. We discuss these types of analytic approaches in more detail in [Chapters 11 and 13](#).

2.2.3 Inference from Survey Data

In the Hansen et al. (1983) framework for sample designs, a sampling plan is paired with an approach for deriving inferences from the data that are collected under the chosen plan. *Statistical inferences* from sample survey data may be “design-based” or “model-based.” The natural design pairings of sampling plans and methods of inference are the diagonal cells (A and D) of [Figure 2.1](#); however, the hybrid approach of combining probability sampling plans with model-based approaches to inference is not uncommon in survey research, as discussed in the section above. Both approaches to statistical inference use probability models to establish the correct forms of confidence intervals (CIs) or hypothesis tests for the intended statistical inference. Under the “design-based” or “randomization-based” approach formalized by Neyman (1934), the inferences are derived based on the distribution of all possible samples that could have been chosen under the specified probability sampling design. This approach is sometimes labeled “nonparametric” or “distribution free” because it relies only on the known probability that a given sample was chosen and not on the specific probability distribution for the underlying variables of interest, for example, $y \sim N(\beta_0 + \beta_1 x, \sigma_{y|x}^2)$ ([Chapter 3](#)).

As the label implies, *model-based inferences* are based on a probability distribution for the random variable of interest—not the distribution of probability for the sample selection. Estimators, standard errors, CIs, and hypothesis tests for the parameters of the distribution (e.g., means, regression coefficients, and variances) are typically derived using the method of maximum likelihood or possibly Bayesian models (Little, 2003).

2.3 Target Populations and Survey Populations

The next step in becoming acquainted with the sample design and its implications for the reader's analysis is to verify the survey designers' intended study population—who, when, and where. Probability sample surveys are designed to describe a *target population*. The target populations for survey designs are *finite populations* that may range from as few as 100 *population elements* for a survey of special groups to millions and even billions for national population surveys. Regardless of the actual population size, each discrete population element ($i = 1, \dots, N$) could, in theory, be counted in a census or sampled for survey observation.

In contrast to the target population, the *survey population* is defined as the population that is truly eligible for sampling under the survey design (Groves et al., 2009). In survey sampling practice, there are geographical, political, social, and temporal factors that restrict our ability to identify and access individual elements in the complete target population and the de facto *coverage* of the survey is limited to the survey population. Examples of geographic restrictions on the survey population could include persons living in remote, sparsely populated areas such as islands, deserts, or wilderness areas. Rebellions, civil strife, and governmental restrictions on travel can limit access to populations living in the affected areas. Homelessness, institutionalization, military service, nomadic occupations, physical and mental conditions, and language barriers are social and personal factors that can affect the coverage of households and individuals in the target population. The timing of the survey can also affect the coverage of the target population. The target population definition for a survey assumes that the data are collected as a "snapshot" in time when in fact the data collection may span several months (or even years).

We now consider an example of this distinction. The target population for the National Comorbidity Survey Replication (NCS-R) is defined to be adults aged 18 and over, living in households in the United States as of July 1, 2002. Here is the exact definition of the survey population for the NCS-R:

The survey population for the NCS-R included all U.S. adults aged 18+ years residing in households located in the coterminous 48 states. Institutionalized persons including individuals in prisons, jails, nursing homes and long term medical or dependent care facilities were excluded from the survey population. Military personnel living in civilian housing were eligible for the study, but due to security restrictions residents of housing located on a military base or military reservation were excluded. Adults who were not able to conduct the NCS-R interview in English were not eligible for the survey (Heeringa et al., 2004).

Note that among the list of exclusions in this definition, the NCS-R survey population excludes residents of Alaska and Hawaii, institutionalized persons, and non-English speakers. Furthermore, the survey observations were

collected over a window of time that spanned several years (February 2001–April 2003). For populations that remain stable and relatively unchanged during the survey period, the time lapse required to collect the data may not lead to bias for target population estimates. However, if the population is mobile or experiences seasonal effects in terms of the survey variables of interest, considerable change can occur during the window of time that the survey population is being observed.

As the survey data analyst, the reader will also be able to restrict their analysis to *subpopulations* of the survey population represented in the survey data set, but their analysis can only use the available data and cannot directly reconstruct coverage of the unrepresented segments of the target population. Therefore, it is important to carefully review the definition of the survey population and assess the implications of any exclusion for the inferences to be drawn from the analysis.

2.4 Simple Random Sampling: A Simple Model for Design-Based Inference

Simple random sampling with replacement (SRSWR) is the most basic of sampling plans, followed closely in theoretical simplicity by simple random sampling without replacement (SRSWOR). Survey data analysts are unlikely to encounter true simple random sampling (SRS) designs in survey practice. Occasionally, SRS may be used to select samples of small localized populations or samples of records from databases or file systems, but this is rare. Even in cases where SRS is practicable (feasible), survey statisticians will aim to introduce simple stratification in order to improve the efficiency of sample estimates (see below). Furthermore, if SRS is employed but weighting is required to compensate for nonresponse or to apply poststratification adjustments (Section 2.7), the survey data now include complex features that cannot be ignored in estimation and inference.

2.4.1 Relevance of SRS to Complex Sample Survey Data Analysis

So why is SRS even relevant for the material in this book? There are several reasons:

1. SRS designs produce samples that most closely approximate the assumptions (*i.i.d.*—observations are *independent* and *identical in distribution*), defining the theoretical basis for the estimation and inference procedures found in standard analysis programs in the major statistical software systems. Survey analysts who use the standard programs in Stata®, SAS®, and SPSS® are essentially defaulting to the assumption

that their survey data were collected under SRS. In general, the SRS assumption results in underestimation of variances of survey estimates of descriptive statistics and model parameters. CIs based on computed variances that assume independence of observations will be biased (generally too narrow) and design-based inferences will be affected accordingly. Likewise, test statistics (t, χ^2, F) computed in complex sample survey data analysis using standard programs will tend to be biased upward and overstate the significance of tests of effects.

2. The theoretical simplicity of the SRS designs provides a basic framework for design-based estimation and inference on which to build a bridge to the more complicated approaches used for complex samples.
3. SRS provides a comparative benchmark that can be used to evaluate the relative efficiency of the more complex designs that are common in survey practice.

Let us examine the second reason listed above more closely, using SRS as a theoretical framework for design-based estimation and inference. In Section 2.5, we will turn to SRS as a benchmark for the efficiency of complex sample designs.

2.4.2 SRS Fundamentals: A Framework for Design-Based Inference

Most students of statistics were introduced to SRS designs through the example of an urn containing a population of blue and red balls. To estimate the proportion of balls in the urn that were blue, the instructor described a sequence of random draws of $i = 1, \dots, n$ balls from the N balls in the urn. If a drawn ball was returned to the urn before the next draw was made, the sampling was “with replacement” (SRSWR). If a selected ball was not returned to the urn until all n random selections were completed, the sampling was “without replacement” (SRSWOR).

In each case, the SRSWR or SRSWOR sampling procedure assigned each population element an equal probability of sample selection, $f = n/N$. Furthermore, the overall probability that a specific ball was selected to be in the sample was independent of the probability of selection for any of the remaining $N - 1$ balls in the urn. In survey practice, random sampling is not typically performed by drawing balls from an urn. Instead, survey sampling uses devices such as tables of random numbers or computerized random number generators to select sample elements from the population.

Let us assume that the objective of a sample design was to estimate the mean of a characteristic, y , in the population:

$$\bar{Y} = \frac{\sum_{i=1}^N Y_i}{N}. \quad (2.1)$$

Under SRS, an unbiased estimate of the population mean is the sample mean:

$$\bar{y} = \frac{\sum_{i=1}^n y_i}{n}. \quad (2.2)$$

The important point to note here is that there is a true population parameter of interest, \bar{Y} , and the estimate of the parameter, \bar{y} , which can be derived from the sample data. The sample estimate \bar{y} is subject to sampling variability, denoted as $\text{var}(\bar{y})$, from one sample to the next. Another measure of the sampling variability in sample estimates is termed the *standard error*, or $SE(\bar{y}) = \sqrt{\text{var}(\bar{y})}$. If one selected all possible samples of size n from the population of size N and computed the estimate of the population mean for each sample, the standard error would describe the standard deviation of the distribution of the sample estimates. For simple random samples of size n selected from populations of size N , the standard error for the estimated population mean is calculated as follows:

$$\begin{aligned} SE(\bar{y}) &= \sqrt{\text{var}(\bar{y})} = \sqrt{(1 - n/N) \cdot \frac{S^2}{n}} \\ &\approx \sqrt{\frac{S^2}{n}} \text{ if } N \text{ is large} \end{aligned} \quad (2.3)$$

where:

$$S^2 = \sum_{i=1}^N (Y_i - \bar{Y})^2 / (N - 1); n = \text{SRS sample size; and } N = \text{the population size.}$$

Note that the calculation of the standard error in Equation 2.3 relies on the knowledge of values of y for all elements in the population. Since we observe only a single sample and not all possible samples of size n from the population of size N , the true (or theoretical) standard error, $SE(\bar{y})$, must be estimated from the data in our chosen sample:

$$\begin{aligned} se(\bar{y}) &= \sqrt{\text{var}(\bar{y})} = \sqrt{(1 - n/N) \cdot \frac{s^2}{n}} \\ &\approx \sqrt{\frac{s^2}{n}} \text{ if } N \text{ is large} \end{aligned} \quad (2.4)$$

where:

$$s^2 = \sum_{i=1}^n (y_i - \bar{y})^2 / (n - 1); n = \text{SRS sample size; and } N = \text{the population size.}$$

The term $(1 - n/N)$ in the expressions for $SE(\bar{y})$ and $se(\bar{y})$ is the *finite population correction (fpc)*. It applies only where selection of population elements is

THEORY BOX 2.1 THE FINITE POPULATION CORRECTION (FPC)

The fpc reflects the expected reduction in the sampling variance of a survey statistic due to sampling WOR. For SRSWOR, the fpc factor arises from the algebraic derivation of the expected sampling variance of a survey statistic over all possible WOR samples of size n that could be selected from the population of N elements (Cochran, 1977).

In most practical survey sampling situations, the population size, N , is very large, and the ratio n/N is so close to zero that the fpc ~ 1.0 . As a result, the fpc can be safely ignored in the estimation of the standard error of the sample estimate. Since complex samples may also employ sampling WOR at one or more stages of selection, in theory, variance estimation for these designs should also include fpes. Where applicable, software systems such as Stata and SUDAAN provide users with the flexibility to input population size information and incorporate the fpc values in variance estimation for complex sample survey data. Again, in most survey designs, the size of the population at each stage of sampling is so large that the fpc factors can be safely ignored.

without replacement (WOR) (Theory Box 2.1), and is generally assumed to be equal to 1 in practice if $f = n/N < 0.05$.

If the sample size, n , is large, then under Neyman's (1934) method of design-based inference, a 95% CI for the true population mean, \bar{Y} , can be constructed as follows:

$$\bar{y} \pm t_{0.975, n-1} \cdot se(\bar{y}). \quad (2.5)$$

2.4.3 Example of Design-Based Inference under SRS

To illustrate the simple steps in design-based inference from SRS, [Table 2.1](#) presents a hypothetical sample data set of $n = 32$ observations from a very large national adult population (because the sampling fraction, n/N , is small, the fpc will be ignored). Each subject was asked to rate his or her view of the strength of the national economy (y) on a 0–100 scale, with 0 representing the weakest possible rating and 100 the strongest possible rating. The sample observations are drawn from a large population with population mean $\bar{Y} = 40$ and population variance $S_y^2 \approx 12.80^2 = 164$. The individual case identifiers for the sample observations are provided in Column (1) of [Table 2.1](#). For the time being, we can ignore the columns labeled Stratum, Cluster, and Case Weight.

If we assume that the sample of size $n = 32$ was selected using SRS, the sample estimate of the mean, the estimated standard error of the sample

TABLE 2.1

Sample Data Set for Sampling Plan Comparisons

Case No. (1)	Stratum (2)	Cluster (3)	Economy Rating Score, y_i (4)	Case Weight, w_i (5)
1	1	1	52.8	1
2	1	1	32.5	2
3	1	1	56.6	2
4	1	1	47.0	1
5	1	2	37.3	1
6	1	2	57.0	1
7	1	2	54.2	2
8	1	2	71.5	2
9	2	3	27.7	1
10	2	3	42.3	2
11	2	3	32.2	2
12	2	3	35.4	1
13	2	4	48.8	1
14	2	4	66.8	1
15	2	4	55.8	2
16	2	4	37.5	2
17	3	5	49.4	2
18	3	5	14.9	1
19	3	5	37.3	1
20	3	5	41.0	2
21	3	6	45.9	2
22	3	6	39.9	2
23	3	6	33.5	1
24	3	6	54.9	1
25	4	7	26.4	2
26	4	7	31.6	2
27	4	7	32.9	1
28	4	7	11.1	1
29	4	8	30.7	2
30	4	8	33.9	1
31	4	8	37.7	1
32	4	8	28.1	2

estimate, and the 95% CI for the population mean would be calculated as follows:

$$\bar{y} = \frac{\sum_{i=1}^n y_i}{n} = \frac{\sum_{i=1}^{32} y_i}{32} = 40.77$$

$$se(\bar{y}) = \sqrt{var(\bar{y})} = \sqrt{\frac{\sum_{i=1}^{32} (y_i - \bar{y})^2}{[n \cdot (n-1)]}} = 2.41$$

$$95\% \text{ CI} = \bar{y} \pm t_{0.975, n-1} \cdot se(\bar{y}) = (35.87, 45.68).$$

The fundamental results that have been illustrated here for SRS are that for a sample of size n , unbiased estimates of the population mean and the standard error of the sample estimate can be computed. For samples of reasonably large size, a CI for the population parameter of interest can be derived. As our discussion transitions to more complex samples and more complex statistics we will build on this basic framework for constructing CIs for population parameters, adapting each step to the features of the sample design and the analysis procedure.

2.5 Complex Sample Design Effects

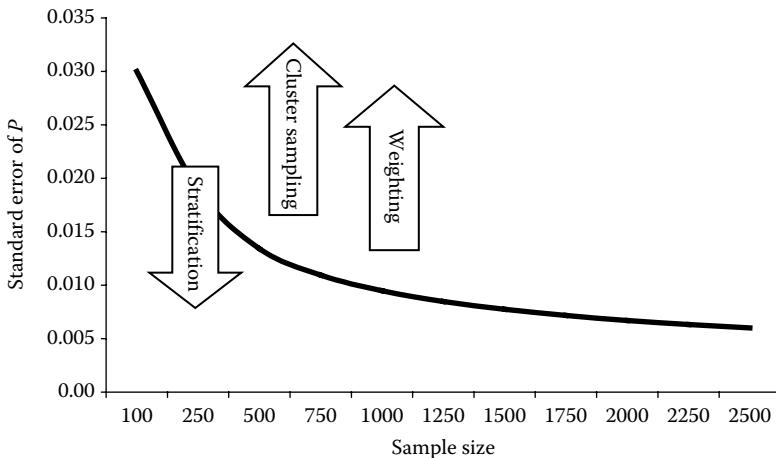
Most practical sampling plans employed in scientific surveys are not SRS designs. Stratification is introduced to increase the statistical and administrative efficiency of the sample. Sample elements are selected from naturally occurring clusters of elements in multistage designs to reduce travel costs and improve interviewing efficiency. Disproportionate sampling of population elements may be used to increase the sample sizes for subpopulations of special interest, resulting in the need to employ weighting in the descriptive estimation of population statistics. All of these features of more commonly used sampling plans will have effects on the accuracy and precision of survey estimators, and we discuss those effects in this section.

2.5.1 Design Effect Ratio

Relative to SRS, the need to apply weights to complex sample survey data changes the approach to estimation of population statistics or model parameters. Also relative to SRS designs, stratification, cluster sampling, and weighting all influence the sizes of standard errors for survey estimates. [Figure 2.2](#) illustrates the general effects of these design features on the standard errors of survey estimates. The curve plotted in this figure represents the SRS standard error of a sample estimate of a proportion P (where the estimate of P is assumed to be 0.5) as a function of the sample size n . At any chosen sample size, the effect of sample stratification is generally a reduction in standard errors relative to SRS. Clustering of sample elements and designs that require weighting for unbiased estimation generally tend to yield estimates with larger standard errors than a simple random sample of equal size.

Relative to a simple random sample of equal size, the complex effects of stratification, cluster sampling, and weighting on the standard errors of estimates are termed the *design effect*, and are measured by the following ratio (Kish, 1965):

$$D^2(\hat{\theta}) = \frac{SE(\hat{\theta})_{\text{complex}}^2}{SE(\hat{\theta})_{\text{srs}}^2} = \frac{\text{var}(\hat{\theta})_{\text{complex}}}{\text{var}(\hat{\theta})_{\text{srs}}}, \quad (2.6)$$

**FIGURE 2.2**

Complex sample design effects on standard errors of prevalence estimates.

where:

$D^2(\hat{\theta})$ = the design effect for the sample estimate, $\hat{\theta}$.

$var(\hat{\theta})_{complex}$ = the complex sample design variance of $\hat{\theta}$.

$var(\hat{\theta})_{SRS}$ = the SRS variance of $\hat{\theta}$.

A somewhat simplistic but practically useful model of design effects that survey statisticians may use to plan a sample survey is:

$$D^2(\hat{\theta}) \approx 1 + f(G_{strat}, L_{cluster}, L_{weighting}),$$

where:

G_{strat} = the relative gain in precision from stratified sampling compared to SRS.

$L_{cluster}$ = the relative loss of precision due to cluster sampling.

$L_{weighting}$ = the relative loss due to unequal weighting for sample elements.

The value of the design effect for a particular sample design will be the net effect of the combined influences of stratification, cluster sampling, and weighting. In Sections 2.5 through 2.7, we will introduce very simple models that describe the nature and rough magnitude of the effects attributable to stratification, cluster sampling and weighting. In reality, the relative increase in variance measured by D^2 will be a complex and most likely nonlinear function of the influences of stratification, cluster sampling and weighting, and their interactions. Over the years, there have been a number of attempts to analytically quantify the anticipated design effect for specific complex samples, estimates, and subpopulations (Skinner et al., 1989; Kish, 1995; Spencer,

2000; Park and Lee, 2004; Gabler et al., 2006; Lohr, 2014; Henry and Valliant, 2015). While these more advanced models are instructive, the sheer diversity in real-world survey designs and analysis objectives generally requires the empirical approach of estimating design effects directly from the available survey data:

$$d^2(\hat{\theta}) = \frac{se(\hat{\theta})_{complex}^2}{se(\hat{\theta})_{srs}^2} = \frac{var(\hat{\theta})_{complex}}{var(\hat{\theta})_{srs}}, \quad (2.7)$$

where:

$d^2(\hat{\theta})$ = the estimated design effect for the sample estimate, $\hat{\theta}$.

$var(\hat{\theta})_{complex}$ = the estimated complex sample design variance of $\hat{\theta}$.

$var(\hat{\theta})_{srs}$ = the estimated SRS variance of $\hat{\theta}$.

As a statistical tool, the concept of the complex sample design effect is more directly useful to the designer of a sample than to the analyst of the survey data. The sample designer can use the concept and its component models to optimize the cost and error properties of specific design alternatives or to adjust SRS sample size computations for the design effect anticipated under a specific sampling plan (Kish et al., 1976). Using the methods and software presented in this book, the survey data analyst will compute CIs and test statistics that incorporate the estimates of standard errors corrected for the complex sample design—generally bypassing the need to estimate the design effect ratio.

Nevertheless, knowledge of estimated design effects and the component factors does permit the analyst to gauge the extent to which the sampling plan for their data has produced efficiency losses relative to an SRS standard and to identify features such as extreme cluster sampling or weighting influences that might affect the stability of the inferences that they will draw from the analysis of the data. In addition, there are several analytical statistics, such as the Rao–Scott modifications of the Pearson χ^2 or Likelihood Ratio χ^2 test statistics (Rao and Scott, 1984; Rao and Thomas, 1988), where estimated design effects are used directly in adapting conventional hypothesis test statistics for the effects of the complex sample design ([Chapter 6](#)).

2.5.2 Generalized Design Effects and Effective Sample Sizes

The design effect statistic permits us to estimate the variance of complex sample estimates relative to the variance for a simple random sample of equal size:

$$\begin{aligned} var(\hat{\theta})_{complex} &= d^2(\hat{\theta}) \cdot var(\hat{\theta})_{srs}; \quad \text{or} \\ se(\hat{\theta})_{complex} &= \sqrt{d^2(\hat{\theta})} \cdot se(\hat{\theta})_{srs}. \end{aligned} \quad (2.8)$$

Under an SRS assumption, the variances of many forms of sample estimates are approximately proportionate to the reciprocal of the sample size, that is, $\text{var}(\hat{\theta}) \propto 1/n$.

For example, if we ignore the fpc, the estimated SRS variances of estimates of a population proportion, mean, or simple linear regression coefficient are:

$$\begin{aligned}\text{var}(\hat{p}) &\approx \frac{\hat{p}(1-\hat{p})}{(n-1)}; \\ \text{var}(\bar{y}) &\approx \frac{s^2}{n}; \\ \text{var}(\hat{\beta}) &\approx \frac{\hat{\sigma}_y^2 \cdot x}{\sum_{i=1}^n (x_i - \bar{x})^2} = \frac{\sum_{i=1}^n (y_i - \hat{y}_i)^2 / (n-2)}{\sum_{i=1}^n (x_i - \bar{x})^2}.\end{aligned}$$

Before today's statistical software was conveniently available to analysts, many public-use survey data sets were released without the detailed stratification and cluster variables that are required for complex sample variance estimation. Instead, the users were provided with tables of generalized design effects for key survey estimates that had been computed and summarized by the data producer. Users were instructed to perform analyses of the survey data using standard SAS, Stata, or SPSS programs under the SRS assumptions, obtain SRS variance estimates, and then apply the design effect factor as shown in Equation 2.8 to approximate the correct complex sample variance estimate and corresponding CI for the parameter of interest. Even today, several major public-use survey data sets, including the National Longitudinal Survey of Youth (NLSY) and the Monitoring the Future (MTF) Survey, require analysts to use this approach.

Survey designers make extensive use of design effects to translate between the simple analytical computations of sampling variance for SRS designs and the approximate variances expected from a complex sample design alternative. In working with clients, samplers may discuss design effect ratios, or they may choose a related measure of design efficiency termed the *effective sample size*:

$$n_{\text{eff}} = \frac{n_{\text{complex}}}{d^2(\hat{\theta})}, \quad (2.9)$$

where:

n_{eff} = the effective sample size, or the size of a simple random sample required to achieve the same precision as the actual complex sample design.

n_{complex} = the actual or "nominal" sample size selected under the complex sample design.

The design effect ratio and effective sample size are, therefore, two means of expressing the precision of a complex sample design relative to a simple random sample of equal size. For a fixed sample size, the statements “the design effect for the proposed complex sample is 1.5” and “the complex sample of size $n = 1000$ has an effective sample size of $n_{\text{eff}} = 667$ ” are equivalent statements of the precision loss expected from the complex sample design.

2.6 Complex Samples: Cluster Sampling and Stratification

We noted above that survey data collections are rarely based on SRS. Instead, sample designs for large survey programs often feature stratification, cluster sampling, and disproportionate sampling. Survey organizations use these “complex” design features to optimize the variance/cost ratio of the final design or meet precision targets for subpopulations of the survey population. The authors’ mentor, Leslie Kish (1965, 1987), was fond of creating classification systems for various aspects of the sample design process. One such system was a taxonomy of complex sample designs. Under the original taxonomy, there were six binary keys to characterize all complex probability samples. Without loss of generality, we will focus on four of the six keys that are most relevant to the survey data analyst and aim to correctly identify the design features that are most important in applications:

- Key 1: Is the sample selected in a single stage or multiple stages?
- Key 2: Is clustering of elements used at one or more sample stages?
- Key 3: Is stratification employed at one or more sample stages?
- Key 4: Are elements selected with equal probabilities?

In the full realm of possible sampling approaches, this implies that there are at least 2^4 or 16 possible permutations of general choices for complex sample designs. In fact, the number of complex sample designs encountered in practice is far fewer, and one complex design—multistage stratified cluster sampling with unequal probabilities of selection for elements—is used in most in-person surveys of household populations. Because they are so important in major programs of household population survey research, we will cover these multistage probability sampling plans in detail in Section 2.8. Before we do that, let us take a more basic look at the common complex sample design features of cluster sampling, stratification, and weighting for unequal selection probabilities and nonresponse.

2.6.1 Cluster Sampling Plans

Cluster sampling of elements is a common feature of most complex sample survey data. In fact, to simplify our classification of sample designs, it is possible to view population elements as “clusters of size 1.” By treating elements as single-unit clusters, the general formulas for estimating statistics and standard errors for cluster samples can be applied to correctly estimate standard errors for simpler stratified element samples ([Chapter 3](#)).

Survey designers employ cluster sampling for several reasons:

- Geographic clustering of elements for household surveys reduces interviewing costs by amortizing travel and related expenditures over a group of observations. By definition, multistage sample designs such as the area probability samples employed in the NCS-R, National Health and Nutrition Examination Survey (NHANES), HRS, and European Social Survey (ESS) incorporate clustering at one or more stages of the sample selection.
- Sample elements may not be individually identified on the available sampling frames, but can be linked to aggregate cluster units (e.g., voters at precinct polling stations, students in colleges and universities). The available sampling frame often identifies only the clusters of elements. Identification of the sample elements requires an initial sampling of clusters and on-site work to select the elements for the survey interview.
- One or more stages of the sample are deliberately clustered to enable the estimation of multilevel models and components of variance in variables of interest (e.g., students in classes, classes within schools). This is not common but does occur in educational research.

Therefore, while cluster sampling can reduce survey costs or simplify the logistics of the actual survey data collection, the survey data analyst must recognize that clustered selection of elements affects their approach to variance estimation and developing inferences from the sample data. In almost all cases, sampling plans that incorporate cluster sampling result in standard errors for survey estimates that are greater than those from a simple random sample of equal size; furthermore, special approaches are required to estimate the correct standard errors. The SRS variance estimation formulae and approaches incorporated in the standard programs of most statistical software packages no longer apply, because they are based on assumptions of independence of the sample observations, and sample observations from within the same cluster generally tend to be correlated (e.g., students within a classroom, or households within a neighborhood).

The appropriate choice of a variance estimator required to correctly reflect the effects of cluster sampling on the standard errors of survey statistics depends on the answers to a number of questions:

1. Are all clusters equal in size?
2. Is the sample stratified?
3. Does the sample include multiple stages of selection?
4. Are units selected with unequal probability?

Fortunately, modern statistical software includes simple conventions that the analyst can use to specify the complex design features. Based on a simple set of user-supplied “design variables,” the software selects the appropriate variance estimation formula and computes correct design-based estimates of standard errors.

The general increase in design effects due to either single-stage or multistage cluster sampling is caused by correlations (non-independence) of observations within sample clusters. Many characteristics measured on sample elements within naturally occurring clusters, such as children in a school classroom or adults living in the same neighborhood, are correlated. Socioeconomic status, access to healthcare, political attitudes, and even environmental factors such as the weather are all examples of characteristics that individuals in sample clusters may share to a greater or lesser degree. When such group similarity is present, the amount of “statistical information” contained in a cluster sample of n persons is less than in an independently selected simple random sample of the same size. Hence, cluster sampling increases the standard errors of estimates relative to a simple random sample of equivalent size. A statistic that is frequently used to quantify the amount of homogeneity that exists within sample clusters is the *intraclass correlation*, ρ (Kish, 1965). See Kish et al. (1976) for an in-depth discussion of intraclass correlations observed in the World Fertility Surveys.

A simple example is useful to explain why intraclass correlation influences the amount of “statistical information” in cluster samples. A researcher has designed a study that will select a sample of students within a school district and collect survey measures from the students. The objective of the survey is to estimate characteristics of the full student body and the instructional environment. A probability sample of $n = 1,000$ is chosen by randomly selecting 40 classrooms of 25 students each. Two questions are asked of the students:

1. What is your mother’s highest level of completed education?

Given the degree of socioeconomic clustering that can exist even among schools within a district, it is reasonable to expect that the intraclass correlation for this response variable is positive, possibly as high as $\rho = 0.2$.

2. What is your teacher's highest level of completed education?

Assuming students in a sampled class have only one teacher, the intraclass correlation for this measure is 1.0! The researcher need not ask the question of all $n = 1,000$ students in the sample. An identical amount of information could be obtained by asking a single truthful student from each sample classroom. The effective sample size for this question would be 40, or the number of sample classrooms.

When the primary objective of a survey is to estimate proportions or means of population characteristics, the following model can be used to approximate the design effect that is attributable to the clustered sample selection (Kish, 1965):

$$D^2(\bar{y}) = 1 + L_{cluster} \approx 1 + \rho \cdot (B - 1). \quad (2.10)$$

where:

ρ = the intraclass correlation for the characteristic of interest.

B = the size of each cluster or primary sampling unit (PSU).

The value of ρ is specific to the population characteristic (e.g., income, low-density cholesterol level, candidate choice) and the size of the clusters (e.g., counties, enumeration areas [EAs], schools, classrooms) over which it is measured. Generally, the value of ρ decreases as the geographical size and scope (i.e., the heterogeneity) of the cluster increases. Typical values of ρ observed for general population characteristics range from 0.00 to 0.20 with most between 0.005 and 0.100 (Kish et al., 1976).

In practice, it is sometimes valuable to estimate the value of ρ for a survey characteristic y . While it is theoretically possible to estimate ρ as a function of the sample data ($y_i, i = 1, \dots, n$) and the sample cluster labels ($\alpha = 1, \dots, a$), in most survey designs such direct estimates tend to be unstable. Kish (1965) suggested a synthetic estimator of ρ which he labeled the *rate of homogeneity* (roh). Using the simple model for the estimated design effect for a sample mean, the expression is rearranged to solve for roh as:

$$roh(y) = \frac{d^2(\bar{y}) - 1}{\bar{b} - 1}, \quad (2.11)$$

where \bar{b} is the average sample size per cluster.

Algebraically, this synthetic estimate of the intraclass correlation is restricted to a range of values from $-1/(\bar{b} - 1)$ to 1.0. Since ρ is almost always positive for most survey variables of interest, this restricted range of the synthetic approximation roh is not a problem in practice. As the analyst (and not the designer) of the sample survey, the calculation of roh is not essential to the reader's work; however, when the reader begins to work with a new

survey data set, it can be valuable to compute the roh approximation for a few key survey variables simply to get a feel for the level of intraclass correlation in the variables of interest.

Let us return to the hypothetical sample data set provided in [Table 2.1](#). Previously, we assumed a simple random sample of size $n = 32$, and estimated the mean, the SRS standard error, and a 95% CI for the mean of the economic conditions index. Now, instead of assuming SRS, let us assume that eight clusters, each of size four elements, were selected with equal probability. The cluster codes for the individual cases are provided in Column (3) of [Table 2.1](#). Without digressing to the specific estimators of the mean and variance for this simple cluster sample (Cochran, 1977), let us look at the correct numerical values for the estimated mean, standard error of the mean, and the 95% CI for \bar{Y} :

$$\bar{y}_{cl} = 40.77, se_{cl}(\bar{y}) = 3.65, \text{CI}(\bar{y}_{cl}) = (32.12, 49.49).$$

Comparing these results with those for the SRS example based on the same data (Section 2.4.3), the first thing we observe is that the estimate of \bar{y} is identical. The change that occurs when clustering is introduced to the example is that the standard error of the mean is increased (due to the presence of the intraclass correlation that was used in developing the clusters for this example). The width of the 95% CI is also increased, due to the increase in standard error and the reduction in the degrees of freedom for the Student t statistic used to develop the CI limits (degrees of freedom determination for complex sample designs will be covered in [Chapter 3](#)). The relative increase in $se(\bar{y})$ for the simple cluster sample compared to the simple random sample of $n = 32$ and the synthetic estimate of the intraclass correlation are computed as follows:

$$d(\bar{y}) = \sqrt{d^2(\bar{y})} = \frac{se_{cl}(\bar{y})}{se_{srs}(\bar{y})} = \frac{3.65}{2.41} = 1.51;$$

$$roh(y) \approx \frac{1.51^2 - 1}{4 - 1} = 0.4267.$$

2.6.2 Stratification

Strata are nonoverlapping, homogeneous groupings of population elements or clusters of elements that are formed by the sample designer prior to the selection of the probability sample. In multistage sample designs (Section 2.8), a different stratification of units can be employed at each separate stage of the sample selection. Stratification can be used to sample elements or clusters of elements. As noted above, if elements are viewed as “clusters of size $B = 1$,” then the general formulas for estimating statistics and standard errors for stratified clustered samples can be applied to correctly compute these statistics for the simpler stratified element samples ([Chapter 3](#)). To take this “unification” one

step further, if the sample design does not incorporate explicit stratification, it may be viewed as sampling from a single stratum (i.e., $H = 1$).

In survey practice, stratified sampling serves several purposes:

- Relative to a simple random sample of equal size, stratified samples that employ *proportional allocation* or *optimal allocation* of the sample size to the individual strata have smaller standard errors for sample estimates (Cochran, 1977).
- Stratification provides the survey statistician with a convenient framework to disproportionately allocate the sample to subpopulations, that is, to oversample specific subpopulations to ensure sufficient sample sizes for analysis.
- Stratification of the probability sample can facilitate the use of different survey methods or procedures in the separate strata ([Chapter 3](#)).

Every stratified sample design involves the following four steps in sample selection and data analysis:

1. Strata ($h = 1, \dots, H$) of N_h clusters/elements are formed.
2. Probability samples of a_h clusters or $a_h = n_h$ elements are independently selected from each stratum.
3. Separate estimates of the statistic of interest are computed for sample cases in each stratum and then weighted and combined to form the total population estimate.
4. Sampling variances of sample estimates are computed separately for each stratum and then weighted and combined to form the estimate of sampling variance for the total population estimate.

Because stratified sampling selects independent samples from each of the $h = 1, \dots, H$ explicit strata of relative size $W_h = N_h/N$, and the same H strata would be used to select every hypothetical sample, any variance attributable to differences among strata is eliminated from the sampling variance of the estimate. Hence, the goal of any stratification designed to increase sample precision is to form strata that are “homogeneous within” and “heterogeneous between”—units assigned to a stratum are like one another and different from those in other strata, in terms of the measurements being collected.

To illustrate how stratification works to reduce sampling variance, let us consider the case of a simple stratified random sample of size $n = \sum_{h=1}^H n_h$, where the stratum sample sizes are proportional to the individual strata: $n_h = n \cdot N_h/N$. This *proportionate allocation* of the sample ensures that each population element has an equal probability of being included in the sample,

denoted by $f_h = n_h/N_h = n/N = f$. Let us compare $\text{var}(\bar{y}_{st,pr})$ for this stratified sample to $\text{var}(\bar{y}_{srs})$, ignoring the fpc:

$$\begin{aligned}
 \Delta &= \text{var}(\bar{y}_{srs}) - \text{var}(\bar{y}_{st,pr}) \\
 &= \frac{S_{\text{total}}^2}{n} - \frac{S_{\text{within}}^2}{n} = \frac{\left[S_{\text{within}}^2 + S_{\text{between}}^2 \right]}{n} - \frac{S_{\text{within}}^2}{n} \\
 &= \frac{S_{\text{between}}^2}{n} \\
 &= \frac{\sum_{h=1}^H W_h (\bar{Y}_h - \bar{Y})^2}{n}.
 \end{aligned} \tag{2.12}$$

A simple random sample of size n includes the variance of y both within the strata, S_{within}^2 , and between the strata, S_{between}^2 , but the stratified sample has eliminated the between-stratum variance component and consequently yields a sampling variance for the mean that is less than or equal to that for a simple random sample of equal size. The expected amount of the reduction in the variance of the mean is a weighted function of the squared differences between the stratum means, \bar{Y}_h , and the overall population mean, \bar{Y} . Hence the importance of forming strata that differ as much as possible in the $h = 1, \dots, H$ values of the \bar{Y}_h .

Let us return to the example data set in [Table 2.1](#) and assume that the $n = 32$ observations were selected from four population strata of equal size, such that $W_h = N_h/N = 0.25$. The stratum identifiers for each sample case are provided in Column (2) of [Table 2.1](#). Under this proportionately allocated, stratified random sample design, we compute the following:

$$\begin{aligned}
 \bar{y}_{st,pr} &= \sum_{h=1}^H W_h \cdot \bar{y}_h \\
 &= 0.25 \times 51.1 + 0.25 \times 43.32 + 0.25 \times 39.60 + 0.25 \times 29.04 \\
 &= 40.77
 \end{aligned}$$

$$\text{se}(\bar{y}_{st,pr}) = \sqrt{\text{var}(\bar{y}_{st,pr})} = \sqrt{\sum_{h=1}^H \frac{W_h^2 s_h^2}{n_h}}$$

$$= 2.04$$

$$d(\bar{y}_{st,pr}) = \frac{\text{se}(\bar{y}_{st,pr})}{\text{se}(\bar{y}_{srs})} = \frac{2.04}{2.41} = 0.85$$

$$d^2(\bar{y}_{st,pr}) = 0.85^2 = 0.72$$

$$n_{\text{eff}} = \frac{n}{d^2(\bar{y}_{st,pr})} = \frac{32}{0.72} = 44.44.$$

Note that the unbiased sample estimate, $\bar{y}_{st,pr} = 40.77$, is identical to that obtained when we assumed that the 32 observations were sampled using SRS, and also identical to that obtained when we assumed that the 32 observations arose from a cluster sample. The estimated standard error, $se(\bar{y}_{st,pr}) = 2.04$, is much smaller, resulting in an estimated design effect ratio of 0.72. For this example, it appears that the stratified sample of size $n = 32$ (8 cases from 4 strata) yields the sample precision of a simple random sample of more than 44 cases.

The simple algebraic illustration and exercise calculation above demonstrate how stratification of the sample can lead to reductions in the variance of sample estimates relative to an SRS. In contrast to this simple example, the precision gains actually achieved by stratification, G_{strat} , in complex samples are difficult to determine analytically. The gains will be a function of the stratum means, the variances of y within individual strata, and whether the sampling within strata includes additional stages, clustering, unequal probabilities of selection, or other complex sample design features.

2.6.3 Joint Effects of Sample Stratification and Cluster Sampling

To see how the two design features of stratification and cluster sampling contribute to the design effect for a complex sample, let us revisit the sample data in [Table 2.1](#), treating it as a stratified sample from $h = 1, \dots, 4$ strata. Within each stratum, a proportionately allocated sample of two clusters ($a_h = 2$) of size 4 is selected with equal probability. This is a very simple example of a stratified “two-per-stratum” or “paired selection” cluster sample design that is very common in survey practice ([Chapter 4](#)). [Table 2.2](#) compares the results for this stratified cluster sample design scenario to those for the simpler SRS, cluster sample, and stratified designs considered earlier.

Note that for the stratified cluster sample design scenario, the estimated design effect falls between the high value for the “cluster sample only” scenario and the low value for the scenario where only stratification effects are considered. As illustrated in [Figure 2.2](#), real survey designs result in a “tug of war” between the variance inflation due to cluster sampling and the variance reduction due to stratification. From [Table 2.2](#), the design effect for

TABLE 2.2

Sample Estimates of the Population Mean and Related Measures of Sampling Variance under Four Alternative Sample Designs

Sample Design Scenario	Estimator	\bar{y}	$se(\bar{y})$	$d(\bar{y})$	$d^2(\bar{y})$	n_{eff}
SRS	\bar{y}_{srs}	40.77	2.41	1.00	1.00	32
Cluster sample	\bar{y}_{cl}	40.77	3.66	1.51	2.31	13.9
Stratified	\bar{y}_{st}	40.77	2.04	0.85	0.72	44.7
Stratified cluster sample	$\bar{y}_{st,cl}$	40.77	2.76	1.15	1.31	24.4

Source: [Table 2.1](#).

the stratified cluster sample is greater than 1, indicating a net loss of precision relative to a simple random sample of size n —cluster sampling “won” the contest. Estimates of design effects greater than 1 are common for most complex sample designs that combine stratification and cluster sample selection. In population surveys, large stratification gains are difficult to achieve unless the survey designer is able to select the sample from a frame that contains rich ancillary data, x , that are highly correlated with the survey variables, y . The survey data analyst needs to be aware of these design effects on the precision of sample estimates. Correctly recognizing the stratum and cluster codes for sample respondents provided by a data producer for use by data analysts is essential for correct and unbiased analyses of the survey data. We discuss the importance of identifying these codes in a survey data set in [Chapter 4](#).

2.7 Weighting in Analysis of Survey Data

2.7.1 Introduction to Weighted Analysis of Survey Data

When probability sampling is used in survey practice, it is common to find that sample inclusion probabilities for individual observations vary. Weighting of the survey data is thus required to “map” the sample back to an unbiased representation of the survey population. A simple but useful device for “visualizing” the role of case-specific weights in survey data analysis is to consider the weight as the number (or share) of the population elements that is represented by the sample observation. Observation i , sampled with probability $f_i = 1/10$, represents 10 individuals in the population (herself and 9 others). Observation j , selected with probability $f_j = 1/20$, represents 20 population elements. In fact, if each sample case is assigned a weight equal to the reciprocal of its probability of selection, $w_i = 1/f_i$, the sum of the sample weights will in expectation equal the population size: $E(\sum_{i=1}^n w_i) = N$. As a survey data analyst, the reader can use this fact during their pre-analysis “checklist” to understand the distribution of the sampling weights that the data producer has provided ([Chapter 4](#)).

Generally, the *final survey weights* in survey data sets (sometimes referred to as *estimation weights*) are the product of the sample selection weight (w_{sel}), a nonresponse adjustment factor (w_{nr}), and the poststratification factor (w_{ps}):

$$w_{final,i} = w_{sel,i} \times w_{nr,i} \times w_{ps,i}. \quad (2.13)$$

The sample selection weight factor (or *base weight*) is simply the reciprocal of the probability that a population element was selected in the sample, $w_{sel,i} = 1/f_i$. Under the theory of design-based inference for probability samples,

weighted estimation using these “inverse probability” weight factors will yield unbiased (or nearly unbiased) estimates of population statistics.

For example:

$$\bar{y}_w = \frac{\sum_{i=1}^n w_{sel,i} \cdot y_i}{\sum_{i=1}^n w_{sel,i}} \text{ is unbiased for } \bar{Y};$$

$$s_w^2 = \frac{\sum_{i=1}^n w_{sel,i} \cdot (y_i - \bar{y}_w)^2}{\sum_{i=1}^n w_{sel,i} - 1} \text{ is an unbiased estimate of } S^2.$$
(2.14)

Note how in each of these estimators, the selection weight “expands” each sample observation’s contribution to reflect its share of the population representation. Throughout this book, weighted estimation of population parameters will follow a similar approach, even for procedures as complex as the pseudo maximum likelihood (PML) estimation of the coefficients in a multiple logistic regression model.

If we were able to always complete an observation on each selected sample case, the development of the survey weights would be very straightforward. The computation of the weight would only require knowledge of the sample selection probability factors (Section 2.7.2). In a carefully designed and well-managed survey, these probability factors are known and carefully recorded for each sample case. The computation of w_{sel} is therefore an accounting function, requiring only multiplication of the probabilities of selection at each stage of sampling and then taking the reciprocal of the product of the probabilities.

As we will see in [Chapter 4](#), *survey data producers* who in most cases have the responsibility for developing the final survey weights have a more difficult task than the simple arithmetic required to compute w_{sel} . First, weighting by w_{sel} will only yield unbiased estimators of population parameters if all n elements in the original sample are observed. Unfortunately, due to *survey nonresponse*, observations are only collected for r cases of the original probability sample of n elements (where $r <= n$). Therefore, survey data producers must develop statistical models of the conditional probability that a sample element will be an observed case. In general terms, the nonresponse adjustment factor, w_{nr} , in the survey weight is the reciprocal of the estimated conditional probability that the sample case responds. The objective in applying nonresponse factors in survey weights is to attenuate bias due to differential nonresponse across sample elements. A price that may be paid for the bias reduction through nonresponse weighting takes the form of increases in standard errors for the weighted estimates. The potential magnitude of the

increases in standard errors is discussed below in the context of weighting for unequal selection probabilities.

Even after computing w_{sel} and adjusting for nonresponse through the factor w_{nr} , most survey data producers also introduce the poststratification factor w_{ps} into the final weight. As its label implies, the poststratification factor is an attempt to apply stratification corrections to the observed sample “post” or after the survey data have been collected. While not as effective as estimation for samples that were stratified at the time that they were selected, the use of poststratification weight factors can lead to reduced standard errors (variance) for sample estimates. Furthermore, poststratification weighting can attenuate any sampling biases that may have entered the original sample selection due to sample frame noncoverage or omissions that occurred in implementing the sample plan. An example of the latter would be systematic underreporting of young males in the creation of household rosters for the selection of the survey respondent.

In the sections that follow, we describe the development of these three important weighting factors in more detail.

2.7.2 Weighting for Probabilities of Selection (w_{sel})

As described above, the selection weight factor, w_{sel} , is introduced in the calculation of the final survey weight to account for the probability that a case was selected for the sample. Common reasons for varying probabilities of case selection in sample surveys include:

1. Disproportionate sampling within strata to achieve an optimally allocated sample for a specific population estimate (Cochran, 1977)
2. Disproportionate sampling within a stratum or group of strata to deliberately increase the sample size and precision of analysis for certain domains of the survey population
3. The use of sample screening across the sample strata and clusters to identify and differentially sample subpopulations, for example, the NHANES oversampling of household members with disabilities
4. Unequal probabilities that arise from subsampling of observational units within sample clusters, for example, the common procedure of selecting a single random respondent from the eligible members of sample households
5. Unequal probabilities that reflect information on final sampling probability that can only be obtained in the process of the survey data collection, for example, in a *random digit dialing* (RDD) telephone sample survey, the number of distinct landline telephone numbers that serve a respondent’s household

Due to the multipurpose nature of modern population surveys (many variables, many statistical aims), the use of disproportionate sampling to optimize

a sample design for purposes of estimating a single population parameter is rare in survey practice. Far more common are designs in which geographic domains or subpopulations of the survey population are oversampled to boost the sample size and precision for stand-alone or comparative analysis. For example, the HRS employs a roughly twofold oversampling of age-eligible African-Americans and Hispanic individuals to improve precision of cross-sectional and longitudinal analyses of these two population subgroups (Heeringa and Connor, 1995). The NCS-R employs a Part 1 screening interview to obtain profiles of respondents' mental health-related symptoms but disproportionately samples persons with positive symptom counts for the more intensive Part 2 questionnaire (Kessler et al., 2004). As these examples illustrate, the selection probability for individual observational units often includes multiple components—for example, a base factor for housing unit (HU) selection, a factor for subsampling targeted groups within the full population, and a probability of selecting a single random respondent within the household. For HRS sample respondents, the selection weight factor, w_{sel} , is computed as the product of the reciprocals of three probabilities: (1) $w_{sel,hh}$, the reciprocal of the multistage probability of selecting the respondent's HU from the area frame (Section 2.8); (2) $w_{sel,sub}$, the reciprocal of the probability of retaining the sample HU under the design objective of a 2:1 oversampling of eligible African-American and Hispanic adults; and (3) $w_{sel,resp}$, the reciprocal of the conditional probability of selecting a single financial unit within the eligible household. This calculation is illustrated below:

$$\begin{aligned} f_{sel} &= f_{sel,hh} \times f_{sel,sub} \times f_{sel,resp} \\ \Rightarrow \\ w_{sel} &= \frac{1}{f_{sel}} = w_{sel,hh} \times w_{sel,sub} \times w_{sel,resp}. \end{aligned}$$

Drawing on the general features of the HRS sample selection, Table 2.3 illustrates the sample selection weight calculations for four hypothetical respondents from different race/ethnicity groups who have different numbers of eligible respondents (Rs) in their sample households.

TABLE 2.3

Illustration of Example w_{sel} Computations

Sample ID	Description of Sample Case					
	Race/Ethnicity of Respondent	Eligible Rs/Household	$w_{sel,hh}$	$w_{sel,sub}$	$w_{sel,resp}$	w_{sel}
A	Black	2	2000	1	2	4000
B	Black	1	2000	1	1	2000
C	White	2	2000	2	2	8000
D	White	1	2000	2	1	4000

2.7.3 Nonresponse Adjustment Weights (w_{nr})

As described above, the most widely accepted approach to compensate for *unit nonresponse* in surveys is for the data producer to develop and apply a nonresponse adjustment factor to the sample selection weight that is used in analysis. Underlying the weighting adjustment for nonresponse is a model of the *response propensity*—conditional on sample selection, the probability that the unit will cooperate with the survey request. In a sense, the concept of response propensity treats response to the survey as another step in the “sample selection process.” However, unlike true sample selection in which the sampling statistician predetermines the sampling probability for each unit, an underlying propensity model—for the most part outside the control of a statistician—determines the probability that a sampled case will be observed. The multiplication of the original sample selection weight for each sample unit by the reciprocal of its modeled response propensity creates a new weight, which, if the model is correct, enables unbiased or nearly unbiased estimation of population statistics from the survey data.

Two related methods for estimating response propensity and computing the nonresponse adjustment are commonly used in survey practice: a simple weighting class adjustment method and a propensity score weighting approach.

2.7.3.1 Weighting Class Approach ($w_{nr,wc}$)

The “weighting class method” (Little and Rubin, 2002) assigns all eligible elements of the original sample—survey respondents and nonrespondents—to classes or cells based on categorical variables (age categories, gender, region, sample stratum, etc.) that are predictive of response rates. Original sample cases that were found to be ineligible for the survey are excluded from the nonresponse adjustment calculation. The weighting class method makes the simple assumption that the response propensities for cases within a given weighting class cell are equal (i.e., nonrespondents are missing at random (MAR), conditional on the categorical variables and interactions implicit in the defined cells). The common response propensity for cases in a cell is estimated by the empirical response rate for the cases assigned to that cell. The weighting class nonresponse adjustment is then computed as the reciprocal of the response rate for the cell $c = 1, \dots, C$ to which the case was assigned:

$$w_{nr,wc,i} = \frac{1}{rrate_c}, \quad (2.15)$$

where $rrate_c$ = the response rate for weighting class $c = 1, \dots, C$.

Little and Vartivarian (2005) showed that reductions in both the bias and variance of an estimate are possible if weighting classes are formed based on

variables related to *both* response propensity and the survey variable of interest. This important result was recently explored in more detail by Kreuter et al. (2010) and Krueger and West (2014), who considered the utility of survey paradata and other auxiliary information in improving nonresponse adjustments.

Aside from identifying effective auxiliary variables for forming weighting classes, another important consideration is the role of the selection weights in forming the nonresponse adjustments. Should the estimate of the response rate within a given nonresponse adjustment cell be weighted by the selection weights? Kott (2012) addressed this question in theoretical detail, concluding that use of the selection weights in these adjustments will improve the mean squared error of the resulting estimates. West (2009) and Flores Cervantes and Brick (2016) provide further empirical support for this idea, finding evidence of substantial benefits of using the selection weights in estimating the response rates in each cell. Flores Cervantes and Brick (2016) show that this is especially true if the implicit model for response propensity is misspecified, and the weighting classes are not “ideal” classes that vary in terms of both response propensity and the survey measures of interest. In short, a failure to use the selection weights in estimation of the response rates in each weighting class has the potential to lead to estimates with substantial bias. We revisit this idea in Theory Box 2.2.

2.7.3.2 Propensity Cell Adjustment Approach ($w_{nr,prop}$)

The propensity cell weighting approach also assigns an adjustment factor to each respondent’s sample selection weight that is equal to the reciprocal of the estimated probability that they participated in the survey. However, in the propensity adjustment method, the assignment of cases to adjustment cells is based on individual response propensity values estimated (via logit transform) from a logistic regression model:

$$\hat{p}_{resp,i} = prob(respondent = yes | X_i) = \left(\frac{e^{X_i \hat{\beta}}}{1 + e^{X_i \hat{\beta}}} \right), \quad (2.16)$$

where:

X_i is a vector of values of response predictors for $i = 1, \dots, n$.

$\hat{\beta}$ is the corresponding vector of estimated logistic regression coefficients.

Grau et al. (2006) and Wun et al. (2007) suggest that the selection weights should once again be used when estimating the coefficients in this response propensity model. Given the estimated coefficients, adjustment cells are then defined based on quantile ranges—often deciles, 0–0.099, 0.10–0.199, and so on—of the distribution of predicted response propensities (Little and Rubin, 2002). The propensity score nonresponse weighting adjustments are then

computed as the reciprocal of the response rate in the quantile range cell $d = 1, \dots, D$ to which the case was assigned:

$$w_{nr,prop,i} = \frac{1}{rrate_d}, \quad (2.17)$$

where $rrate_d$ = the weighted response rate for propensity cell $d = 1, \dots, D$.

The use of individual estimated response propensities for these adjustments (i.e., $\hat{p}_{resp,i}$ as opposed to the response rates, $rrate_d$, within the quantile range cells, as shown in Equation 2.17) is often not recommended, as extremely low estimated response propensities (e.g., $\hat{p}_{resp,i} = 0.001$) could result in more variance in the weights. This increased variance in the weights would decrease the precision of weighted estimates based on the survey data (Section 2.7.5).

THEORY BOX 2.2 ESTIMATING RESPONSE PROPENSITIES IN NONRESPONSE ADJUSTMENTS

In our discussion, both the weighting class and propensity cell adjustments for nonresponse require estimation of response rates within defined cells. Traditionally, many survey statisticians have employed the sample selection weight, w_{sel} , to compute weighted estimates of response rates in these cells:

$$rrate_{weighted,cell} = \frac{\sum_{i \in cell}^{n_{cell}} w_{sel,i} \cdot y_i}{\sum_{i \in cell}^{n_{cell}} w_{sel,i}}, \quad (2.18)$$

where:

$y_i = 1$ if sample person i is a respondent, 0 otherwise.

$w_{sel,i}$ = the sample selection weight for case i .

n_{cell} = the total count of eligible sample cases in cell $c = 1, \dots, C$.

Little and Vartivarian (2003) suggested that the unweighted response rate may be the preferred estimate of the response propensity for the cell, depending on what design variables are used to construct the cells:

$$rrate_{cell} = \sum_{i \in cell}^{n_{cell}} \frac{y_i}{n_{cell}}. \quad (2.19)$$

As mentioned earlier, Kott (2012) presented theoretical rationale arguing for the use of the selection weights in estimating the within-cell response rates more generally (2.18). We advise readers responsible for developing nonresponse adjustments to selection weights to consider both approaches, and examine the sensitivity of a variety of estimates to the approach used (along with any shifts in standard errors due to the different approaches).

Note that under the propensity modeling approach, the computed value of the empirical response rate for cases in a modeled propensity quantile need not always fall within the range of scores for the quantile. For example, the range of propensity scores used to define an adjustment cell might be 0.75–0.79, but the corresponding response rate for cases in the cell could be 0.73. This is a reflection of lack of fit in the propensity model. Standard tests may be used to evaluate the goodness of fit of the logistic regression model of response propensity. We recommend including as many theoretical predictors of responding as possible in the model, and especially predictors that are also correlated with the survey variables of primary interest (Little and Vartivarian, 2005).

To employ either method for nonresponse adjustment, the characteristics used to define the cells or model the response propensities must be known for both respondents and nonrespondents. In cross-sectional sample surveys such as the NCS-R or NHANES, this limits the nonresponse adjustment to characteristics of sample persons or households that are known from the sampling frame or are completely observed in the screening process. In the case of the 1992 HRS baseline sample, a simple weighting class adjustment approach was employed to develop the nonresponse adjustment (Heeringa and Connor, 1995). Region (Northeast, South, Midwest, West), urban/rural status of the PSU, and race of the respondent (Black, Hispanic, White, and Other) were used to define weighting class adjustment cells. See Table 2.4 for an illustration of typical values of w_{ns} for various cells and how the values of this adjustment factor influence the final composite weight.

2.7.4 Poststratification Weight Factors (w_{ps})

The nonresponse adjustment procedures described above have the property that only data available for sampled respondent and nonrespondent cases are used to compute weighting adjustments. Another weighting technique used in practice to improve the quality of sample survey estimates is to incorporate known information for the full survey population—borrowing strength from data sources external to the sample. *Poststratification* is one such method for using population data in survey estimation. *Raking ratio estimation*, *generalized regression (GREG) estimation*, and *calibration* are other

TABLE 2.4Illustration of Example w_{final} Computations Including w_{sel} , w_{nr} , and w_{ps}

Description of Sample Case						
Sample ID	Nonresponse Adjustment Cell	Poststratum	w_{sel} (from Table 2.3)	w_{nr}	w_{ps}	w_{final}
A	Black, Northeast, urban	Age 50–54, male, married	4,000	1.3	1.04	5,408
B	Black, South, rural	Age 55–61, female, single	2,000	1.15	0.96	2,208
C	White, West, urban	Age 50–54, male, married	8,000	1.25	1.06	10,600
D	White, Midwest, rural	Age 55–61, female, single	4,000	1.18	0.97	4,578

forms of postsurvey weight adjustment that may be employed to improve the precision and accuracy of survey estimates. For example, Kott and Liao (2012) present a technique based on calibration weighting that can provide “double protection” against nonresponse bias, which means that as long as the variables used in the calibration procedure define either a well-specified substantive model for a variable of interest or a well-specified response propensity model, weighted estimates based on the technique (implemented in the WTADJUST procedure of the SUDAAN software) will still be unbiased asymptotically. Here, we will focus on poststratification, the most common technique applied in general social and health survey weighting.

Simple poststratification forms $l = 1, \dots, L$ poststrata of respondent cases (just as the sample designer might form $h = 1, \dots, H$ design strata prior to sample selection). The auxiliary variables used to form the L poststrata should satisfy the following three criteria: (1) they should be variables such as age, gender, and region for which accurate population control totals are available from external sources; (2) they should be highly correlated with key survey variables; and (3) they may be predictive of noncoverage in the sampling frame. Cross-classifications of these variables are then used to define the $l = 1, \dots, L$ poststrata. To ensure efficiency in the poststratification, poststrata are generally required to include a minimum of $n_l = 15–25$ observations. If the cross-classification of poststratification variables results in cells with fewer than this minimum number, similar poststrata are collapsed to form a larger grouping.

Poststratification weighting involves adjusting the final weights for respondent sample cases so that weighted sample distributions conform to the known population distributions across the $l = 1, \dots, L$ poststrata. The poststratification factor applied to each respondent weight is computed as follows:

$$w_{ps,l,i} = \frac{N_l}{\sum_{i=1}^{n_l} (w_{sel,i} \times w_{nr,i})} = \frac{N_l}{\hat{N}_l}, \quad (2.20)$$

where:

$w_{ps,l,i}$ = the poststratification weight for cases in poststratum $l = 1, \dots, L$.

N_l = the population count in poststratum l obtained from a recent Census, administrative records, or a large survey with small sampling variance.

In the case of the 1992 HRS baseline sample, post-strata of sample respondents were defined based on age category (50–54, 55–61) for the 1931–1941 birth cohorts, gender, and marital status (married, single). Population control totals, N_l , for each poststratum were obtained as weighted population totals from the March 1992 demographic supplement to the U.S. Current Population Survey (Heeringa and Connor, 1995). See [Table 2.4](#) for an illustration of typical values of w_{ps} for various poststrata and how the values of this adjustment factor influence the final survey weight (w_{final}).

We have covered the basics of weight construction thus far in this chapter, providing enough background to help survey analysts understand what information goes into the final survey weights that are typically provided in public-use survey data sets. For more detailed practical guidance on the construction of weights for complex sample surveys, we refer readers to Valliant et al. (2013).

2.7.5 Design Effects Due to Weighted Analysis

The weights that readers will be using in their survey data analysis are therefore compound products of several adjustments—unequal probabilities of selection, differential patterns of response, and poststratification. Each of these factors can have a different effect on the precision and bias reduction for a design-based population estimate (Valliant, 2004). Along with stratification and cluster sampling, weighted estimation contributes to the final design effect for a survey estimate. In [Figure 2.1](#) shown earlier in this chapter, the large arrow representing the net effect of weighting could be split into three smaller arrows—the small arrows for selection weighting and nonresponse adjustment pointing up to higher variance, and the small poststratification arrow pointing down to lower variance. It is difficult if not impossible in most surveys to analytically partition out the size of the contribution of each factor (stratification, cluster sampling, selection weights, nonresponse adjustment, poststratification weighting) to the variance of sample estimates; see Park and Lee (2004) for discussion of this point. Recently, Henry and Valliant (2015) described how to compute design effects due to calibration weighting.

Changes in standard errors due to weighting are related to the variance of the weight values assigned to the individual cases and the correlations of the weights with the values and standard deviations of the variable(s) of interest (Spencer, 2000). We generally find in survey practice that the net effect of weighted estimation is inflation in the standard errors of estimates. This reflects the empirical fact that through the sequence of steps—selection weighting, nonresponse weighting, and poststratification—case weights can

be quite variable. Furthermore, most survey weights are at best only moderately correlated with the distributional properties of the survey variables.

In recent years, the survey literature has used the term “weighting loss” to describe the inflation in variances of sample estimates that can be attributed to weighting. A simple approximation used by sampling statisticians to anticipate $L_{\text{weighting}}$, the proportional increase in variance of the sample mean due to weighted estimation, is:

$$L_{\text{weighting}}(\bar{y}) \approx cv^2(w) = \frac{s^2(w)}{\bar{w}^2} = \left\{ \frac{\sum_{i=1}^n w_i^2}{\left(\sum_{i=1}^n w_i \right)^2} \cdot n - 1 \right\}, \quad (2.21)$$

where:

$cv^2(w)$ = the relative variance of the sample weights.

$s(w)$ = the standard deviation of the sample weights.

\bar{w} = the mean of the sample weights.

This simple model of weighting loss was introduced by Kish (1965), and despite its widespread use, it was intended more as a design tool than as a strong model of true weighting effects on variances of sample estimates. The Kish model of weighting loss was originally presented in the context of proportionate stratified sampling and represented the proportional increase in the variance of means (and proportions as means of binary variables) due to arbitrary disproportionate sampling of strata. It assumes that proportionate allocation is the optimal stratified design (i.e., variances of y are approximately equal in all strata) and that the weights are uncorrelated with the values of the random variable y . Spencer (2000) would later develop design effects due to weighting that relaxed the latter assumption.

Little and Vartivarian (2005) provide clear examples where this simple Kish model of weighting loss breaks down. As in any model, the quality of the predictions is tied to how closely the data scenario matches the model assumptions. Even within a survey data set, there may be variables for which the weighting actually improves the precision of estimates (due to intended or chance optimality for that variable) and many others for which the variability and randomness of the weights simply produces an increase in the variance of estimates. Mendelson and Huang (2016) recently demonstrated that reductions in sample size can substantially increase weighting loss based on Kish’s simple model when using poststratification or raking to adjust sample selection weights.

To illustrate the application of Kish’s weighting loss model to a sample design problem, consider the following example. A survey is planned for a target population that includes both urban and rural populations of children. Eighty percent of the target population lives in the urban domain and

20% lives in the rural villages. The agency sponsoring the survey is interested in measuring the mean body mass index (BMI) of these children. The agency would like to have roughly equal precision for mean estimates for urban and rural children and decides to allocate the sample equally (50:50) to the two geographic domains (or strata). They recognize that this will require weighting to obtain unbiased estimates for the *combined* area. Urban cases will need to be weighted up by a factor proportional to $0.80/0.50 = 1.6$, and rural cases will need to be down-weighted by a factor proportional to $0.20/0.50 = 0.4$. To estimate $L_{weighting}$, they compute the relative variance of these weights for a sample that is 50% urban and 50% rural. They determine that $L_{weighting} \approx cv^2(w) = 0.36$. Ignoring any cluster sampling that may be included in the sampling plan, this implies that the final sample size for the survey must be $n_{complex} = n_{srs} \times 1.36$, or 36% larger than the SRS sample size required to meet a set precision level for estimating mean BMI for the combined population of urban and rural children.

The reader should note that $L_{weighting}$ is often nontrivial. Survey data sets that include disproportionate sampling of geographic areas or other sub-populations should be carefully evaluated. Despite what may appear to be large nominal sample sizes for the total survey, the effective sample sizes for pooled analysis may be much smaller than the simple case count suggests.

Fortunately, a detailed understanding of each of these contributions to the final design effect for a complex sample survey is more important to the survey designer than it is to the survey analyst. In the role of survey analyst, the reader will often not have access to the detailed information that the survey producer's statisticians used to develop the final weights. As analysts, we must certainly be able to identify the correct weight variable to use in our analysis, be able to perform checks that the designated weight has been correctly carried forward to the data set that we will use for analysis, and be familiar with the syntax required to perform weighted estimation in our chosen statistical analysis software. Subsequent chapters in this book will provide the explanation and examples needed to become proficient in applying weights in survey data analysis.

2.8 Multistage Area Probability Sample Designs

The applied statistical methods covered in Chapters 5 through 13 of this volume are intended to cover a wide range of complex sample designs. However, because the majority of large public-use survey data sets that are routinely used in the social and health sciences are based on multistage area probability sampling of households, it is important to describe this particular probability sampling technique in greater detail. The generic illustration presented here is most applicable to national household sampling in

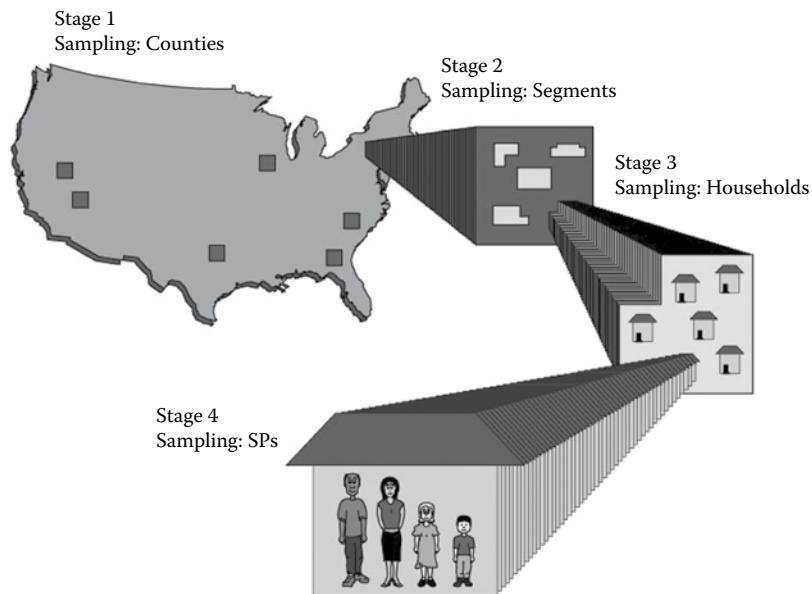


FIGURE 2.3

Schematic illustration of multistage area probability sampling. (Mohajer, L., *The National Assessment of Adult Literacy (NAAL) Sample Design*, Westat, Rockville, MD, 2002. Reprinted with permission.)

the United States and Canada. With minor changes in the number of stages and the choice of sampling units, similar household sample designs are used throughout Central and South America, Africa, Asia, and Europe (Heeringa and O'Muircheartaigh, 2010).

Figure 2.3 illustrates the selection of a multistage, area probability sample of respondents. The design illustrated in this figure conforms closely to the actual procedure used in the selection of the NCS-R, HRS, and NHANES samples of the U.S. household populations. Under the general procedure illustrated by the figure, the selection of each study respondent requires a four-step sampling process: a primary stage sampling of the U.S. counties or groupings of adjacent counties, followed by a second-stage sampling of area segments and a third-stage sampling of HUs within the selected area segments, and concluding with the random selection of eligible respondents from the sampled HUs.

2.8.1 Primary Stage Sampling

The *primary stage units* (PSUs) of the multistage sample are single counties or groupings of geographically contiguous counties. The PSUs are therefore the highest level groupings or “clusters” of sample observations (this will be important to remember when we discuss variance estimation in

[Chapters 3 and 4](#)). All land area in the target population is divided into PSUs (e.g., the land area of the 50 United States is uniquely divided into roughly 3100 county and parish [Louisiana] divisions). For comparison, the land area of Chile is uniquely divided into *comuna* units, Russia into *raions* (regions), and South Africa and many other countries into Census *EAs*. Ideally, the populations within PSUs will be reasonably heterogeneous to minimize intraclass correlations for survey variables (and therefore cluster sample design effects, per [2.10]). At the same time, the geographically defined PSUs must be small enough in size to facilitate cost-efficient travel to second-stage interview locations. Each designated PSU in the population is assigned to one of $h = 1, \dots, H$ sampling strata based on region of the country, urban/rural status, PSU size, geographic location within regions, and population characteristics. Designs with approximately $H = 100$ primary stage strata are common in multistage samples of the U.S. households, but the actual number of strata employed in the primary stage sample can range from less than ten to hundreds depending on available stratification variables and the number of PSUs, a_h , that will be selected from each stratum.

Depending on the study sample design, some of the primary stage strata contain only a single *self-representing (SR)* metropolitan PSU. Each SR PSU is included in the sample with certainty in the primary stage of selection—for these strata, “true sampling” begins at the second stage of selection. The remaining *nonself-representing (NSR)* primary stage strata in each design contain more than one PSU. From each of these NSR strata, one or more PSUs are sampled with *probability proportionate to size (PPS)* as measured in occupied HU counts reported at the most recent Census. The number of PSUs selected from each primary stage stratum is decided by the sample allocation. The University of Michigan Survey Research Center (SRC) National Sample Design (Heeringa and Connor, 1986) allocates one primary stage selection per stratum. More commonly, a minimum of two sample PSUs are selected from each primary stage stratum. A “two-per-stratum” design in which exactly two PSUs ($a_h = 2$) are selected with PPS from each stratum maximizes the number of strata that can be formed for selecting a primary stage sample of $a = \sum_{h=1}^H a_h$ PSUs. The two-per-stratum allocation is also common because a minimum of two PSUs per primary stage stratum is required to estimate sampling variances of estimates from complex samples. One-per-stratum primary stage samples, like that used by the University of Michigan’s SRC for HRS and NCS-R, maximize the stratification potential but require a collapsing of design strata to create pseudo-strata for complex sample variance estimation ([Chapter 4](#)).

2.8.2 Secondary Stage Sampling

The designated second-stage sampling units (SSUs) in multistage samples are commonly termed *area segments*. Area segments are formed by linking

geographically contiguous Census blocks to form units with a minimum number of occupied HUs (typically 50–100 based on the needs of the study). Within sample PSUs, SSUs may be stratified at the county level by geographic location and race/ethnicity composition of residents' households. Within each sample PSU, the actual probability sampling of SSUs is performed with probabilities proportionate to Census counts of the occupied HUs for the Census blocks that comprise the area segment. The number of SSUs that are selected within each sample PSU is determined by survey statisticians to optimize the cost and error properties of the multistage design. The number of SSUs selected in an SR PSU varies in proportion to the total size of the PSU selected with certainty (e.g., HRS and NCS-R use approximately 48 area segments in the New York SR PSU). Depending on the total size of the survey and the cost structure for data collection operations, typically from 6 to 24 SSUs are selected from each NSR PSU.

2.8.3 Third- and Fourth-Stage Sampling of HUs and Eligible Respondents

Prior to the selection of the third-stage sample of households, field staff from the survey organization visit each sample SSU location and conduct an up-to-date enumeration or "listing" of all HUs located within the physical boundaries of the selected area segments. A third-stage sample of HUs is then selected from the enumerative listing according to a predetermined sampling rate. The third-stage sampling rates for selecting households in the multistage area probability samples are computed using the following "selection equation" (Kish, 1965):

$$\begin{aligned} f &= f_1 \times f_2 \times f_3 \\ &= \frac{MOS_{\alpha} \times a_h}{MOS_h} \times \frac{b_{\alpha} \times MOS_{\beta(\alpha)}}{MOS_{\alpha}} \times \frac{C_h}{MOS_{\beta(\alpha)}}. \end{aligned} \quad (2.22)$$

In the final selection equation derived in Equation 2.22, we have the following notation: f = the overall multistage sampling rate for HUs; MOS_{α} = total population measure of size in the selected PSU α ; MOS_h = total population measure of size in the design stratum h ; a_h = number of PSUs to be selected from design stratum h ; b_{α} = number of area segments selected in the PSU α ; $MOS_{\beta(\alpha)}$ = total household measure of size for the SSU $\beta = 1, \dots, b_{\alpha}$; and C_h = a stratum-specific constant $= (f \times MOS_h) / a_h b_{\alpha}$.

For example, the third-stage sampling rate for selecting an equal probability national sample from the listed HUs for the selected PSUs and area segment SSUs is:

$$f_3 = \frac{f}{f_1 \times f_2} = \frac{f \times MOS_h}{a_h \times b_{\alpha} \times MOS_{\beta(\alpha)}}. \quad (2.23)$$

The third-stage sampling rate is computed for each selected SSU in the sample design. This rate is then used to select a random sample of actual HUs from the area segment listing.

Each sample HU is then contacted in person by an interviewer. Within each cooperating sample household, the interviewer conducts a short screening interview with a knowledgeable adult to determine if household members meet the study eligibility criteria. If the informant reports that one or more eligible adults live at the sampled HU address, the interviewer prepares a complete listing of household members and proceeds to randomly select a respondent for the study interview. The random selection of the respondent is often performed using a special adaptation of the objective household roster/selection table method developed by Kish (1949).

Despite the obvious effort and complexity that goes into fielding a multistage area probability sample, relatively simple specifications of primary stage stratum, primary stage cluster (PSU), and final survey weight variables will be required for analysts desiring appropriate analyses of survey data from this common household sampling design. A detailed discussion of a unified approach to variance estimation for multistage samples is given in [Chapter 4](#).

2.9 Special Types of Sampling Plans Encountered in Surveys

As described above, most large-scale social, economic, demographic, and health-related surveys are designed to provide the capability to make descriptive inferences about specific survey populations or to analyze multivariate relationships in a population. Although the techniques for applied survey data analysis presented in the following chapters are generally applicable to all forms of probability sample designs suitable for population estimation and inference, some fields of population survey research (such as surveys of businesses, hospitals, and other nonhousehold units that vary in size and “importance”) have developed special methods that will not be covered in detail in this volume. Researchers who are working with survey data for these populations are encouraged to use the survey literature to determine current best practices for these special population surveys.

Survey research on natural populations in environmental (e.g., forestry or fisheries), geological, and some human and animal epidemiological studies is increasingly turning to *adaptive sample designs* to optimize observation, estimation, and inference. If the reader’s data are of these types, they will need to use special procedures for estimation and inference. An excellent reference on adaptive sample design can be found in Thompson and Seber (1996).

Increasingly, adaptive sampling procedures are being employed in major population surveys. Groves and Heeringa (2006) apply the term *responsive design* to surveys that adapt sampling, survey measurement, and nonresponse follow-ups to empirical information that is gathered in the survey process. One sampling technique that is critical to the responsive design of

surveys is the use of multiphase sampling, in which sample cases may be subsampled for further contact and interview at a time point, t , conditional on the prior disposition (e.g., number of calls, success with contact, resistance to interview) of the case. Presently, the stochastic nature of the sample disposition of each case at time t is ignored and the data are weighted for estimation as though the disposition of cases was a deterministic (fixed) outcome. Current and future research is expected to lead to improved procedures for estimation and inference in multiphase sample designs.

Occasionally, population-based survey methods are employed to perform research that is purely analytical. These include studies that fall in the category of epidemiological case-control designs; randomized population-based experiments including “group randomized trials”; or model-based designs for research on hierarchical or multilevel populations (e.g., research on student, classroom, and school effects). As discussed earlier in this chapter, the analysis of “survey” data from these types of analytical research designs requires special approaches. Chapter 13 will explore approaches to several of the more common analytical designs that use survey-like procedures to collect data; but again, with data of this type, the reader is encouraged to also turn to the statistical literature for an up-to-date and more in-depth description of best practices. See, for example, Burns et al. (1996), Heeringa et al. (2001), and Raudenbush (2000).

3

Foundations and Techniques for Design-Based Estimation and Inference

3.1 Introduction

The fundamental theory and practical procedures for estimation and inference for complex sample survey data have been under development for almost a century. The foundations are present in the work on randomization and the “representative method” (Bowley, 1906; Fisher, 1925) and what is generally agreed to be the breakthrough paper by Neyman (1934) on the theory of design-based inference from probability sample designs. Even today, estimation and inference for survey data remains an evolving field with important new developments in applications of survey data to hierarchical and latent variable modeling (Rabe-Hesketh and Skrondal, 2006), estimation of small area statistics (Rao and Molina, 2015), and Bayesian approaches to model estimation and inference using survey data (Little, 2003). The general concept of design-based inference and its application to survey data analysis was introduced in Section 2.2. The aim of this chapter is to expand the reader’s understanding of the key components of design-based approaches to estimation and inference from survey data: consistent estimation of population statistics; robust, distribution-free methods for estimating the sampling variance of estimates; construction and interpretation of confidence intervals (CIs); and design-adjusted test statistics for hypothesis testing.

The chapter opens in Section 3.2 with a simple introduction to finite populations and a superpopulation model—two theoretical concepts that have only subtle implications for how the survey data are actually analyzed but are important concepts for interpretation and reporting of the survey findings. CIs are a primary tool for presenting survey estimates and the corresponding degree of uncertainty due to population sampling. Section 3.3 introduces the CI as the organizing framework for discussion of the three main components of design-based inference: weighted sample estimates of population statistics (Section 3.4); critical values from the sampling distribution of the estimates (Section 3.5); and robust estimates of the standard error of the sample estimate (Section 3.6). Inference from survey data is not limited

to CI construction and interpretation. Tests of specific hypotheses concerning the true population value of a statistic may also be performed based on survey data. Section 3.7 compares approaches to common hypothesis tests under simple random sampling assumptions to the corresponding test procedures for complex sample survey data. The chapter concludes in Section 3.8 with a discussion of the potential impact of sources of total survey error (TSE) on estimation and inference for survey data.

3.2 Finite Populations and Superpopulation Models

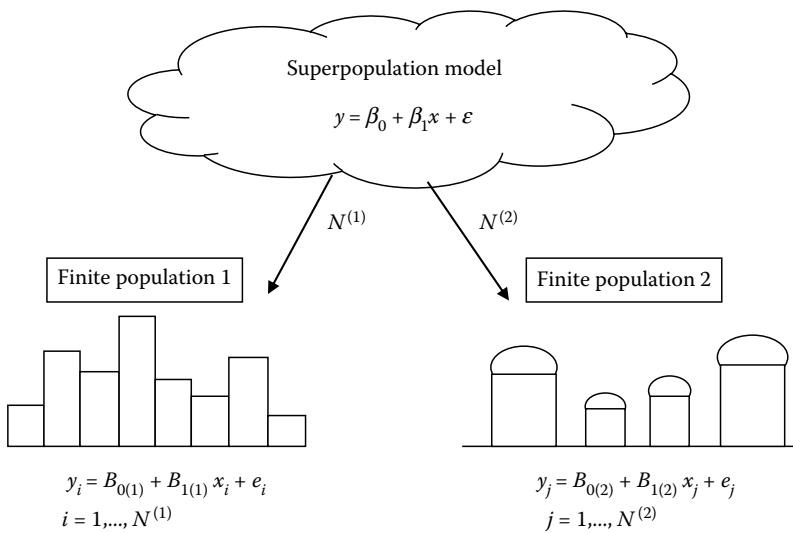
Chapters 1 and 2 have touched on the healthy tension in the historical statistical literature between design-based and model-based approaches to survey inference. There has generally been little debate over the application of design-based inference for *descriptive analysis* of probability samples of survey populations. The objectives of the analysis are clear—to describe with measurable uncertainty due to sampling a population characteristic or process as it exists in a defined *finite population*. More controversy arises when researchers go beyond descriptive analysis to *analytic uses* of survey data sets—uses that estimate models to explore more universal, multivariate relationships or even to possibly attempt to understand causality in relationships among variables. To unify our thinking about finite population statistics versus a more universal model of processes or outcomes, sampling theoreticians have introduced the concept of a *superpopulation model*.

Figure 3.1 illustrates this concept. The figure shows two finite survey populations, each somewhat different, yet each generated by the same overarching superpopulation model. Research teams conducting probability sample surveys in the two respective finite populations would estimate their finite population regression parameter as

$$b_{1(1)} = \hat{B}_{1(1)} = \frac{\sum_{i=1}^{n(1)} w_i \cdot (y_i - \bar{y}_w) \cdot (x_i - \bar{x}_w)}{\sum_{i=1}^{n(1)} w_i \cdot (x_i - \bar{x}_w)^2}; \quad b_{1(2)} = \hat{B}_{1(2)} = \frac{\sum_{j=1}^{n(2)} w_j \cdot (y_j - \bar{y}_w) \cdot (x_j - \bar{x}_w)}{\sum_{j=1}^{n(2)} w_j \cdot (x_j - \bar{x}_w)^2} \quad (3.1)$$

In each case, the design-based estimates, $b_{1(1)}$ or $b_{1(2)}$, would be consistent estimates of the corresponding finite population regression coefficients, $B_{1(1)}$ or $B_{1(2)}$. Note that survey weights (denoted by w_i or w_j) are used to compute the estimates.

What if the statistical objective of each research team was not to simply estimate the best regression model for their survey population but to infer

**FIGURE 3.1**

Superpopulation model and finite populations.

about the universal model that governs the relationship between y and x ? The concept of a superpopulation model provides a bridge to the broader inference by postulating that the two finite populations are simply a size $N_{(1)}$ or $N_{(2)}$ “sample” of pairs of (x,y) observations generated from the superpopulation regression model: $y = \beta_0 + \beta_1 x + \varepsilon$. (See Theory Box 7.1 later in [Chapter 7](#) for more details.)

The theoretical linkage of finite population samples to a superpopulation model is not foremost in the mind of applied survey data analysts as they sit down at their computer to begin their work with a survey data set. It will also have little bearing on how that analyst applies the design-based statistical analysis techniques described in the second half of this book. Many survey researchers can become careless about reporting conclusions from their data analysis, suggesting universality of their findings when in fact the sample data may have been drawn from a small or very unique survey population. It is important for research analysts reporting analysis results to be clear with their audiences concerning the nature of their inferential statements. Are the inferences targeted to the specific survey population, or is the aim to broaden the scope of the inference to imply more generalizable findings that extend beyond the boundaries of the finite population? If it is the latter, one should expect to provide scientific support for the inferential arguments. Is there a replication of one’s findings in surveys of other distinct finite populations? Can one make a convincing theoretical argument for a single universal model for the relationships observed in the finite population?

3.3 CIs for Population Parameters

....The form of this solution consists in determining certain intervals which I propose to call confidence intervals....

Jerzy Neyman, 1934

This quote from Neyman (1934) capped nearly three decades of research and experimentation by leading statisticians of the day (including R.A. Fisher and E.S. Pearson) to establish a theory of estimation for the representative method of sampling (i.e., simple random samples and other probability samples). Since the mid-1930s when the paper was published, Neyman's CIs have played a leading role in population estimation and inference for survey data. A generic form for an approximate $100(1 - \alpha)$ % CI for a population parameter (θ), where α represents a level of significance (e.g., 0.05, corresponding to a 95% CI), is:

$$\hat{\theta} \pm t_{1-\alpha/2, df} \cdot se(\hat{\theta}), \quad (3.2)$$

where:

$\hat{\theta}$ is an unbiased or consistent estimate of the population parameter, θ .

$t_{1-\alpha/2, df}$ is the value of the Student t distribution with df degrees of freedom.

df is the degrees of freedom for variance estimation under the sample design.

$se(\hat{\theta})$ is a robust estimate of the standard error of $\hat{\theta}$.

The CI summarizes our uncertainty in inferring a true population value from a single sample. In simple terms, if the identical sample design was used to repeatedly draw samples from the survey population and the 95% CI was created for each sample, 95 in 100 of all such sample CIs would be expected to contain the true population value. Note that it is the theoretical distribution of sample estimates over repeated sampling from the population that provides "support" for the statement of uncertainty.

Construction of CIs for population parameters therefore requires three components: a consistent estimate, $\hat{\theta}$; the appropriate critical value from $t_{1-\alpha/2, df}$; and the standard error of the estimate, $se(\hat{\theta})$. The following three sections describe the underlying theory and derivation of each component.

3.4 Weighted Estimation of Population Parameters

Survey weights play a key role in consistent, design-based estimation of finite population parameters. *Consistent estimators* may be *unbiased estimators*. They may also be estimators such as the ratio mean for stratified, cluster sample data that have a small bias that decreases as the sample size, n , increases and disappears as the sample size approaches the population size, N . Some examples of consistent, weighted estimators of population statistics include:

$$\bar{y}_w = \frac{\sum_{i=1}^n w_i \cdot y_i}{\sum_{i=1}^n w_i} \text{ to estimate the population mean, } \bar{Y}; \quad (3.3)$$

$$b_{1,w} = \frac{\sum_{i=1}^n w_i \cdot (y_i - \bar{y}_w) \cdot (x_i - \bar{x}_w)}{\sum_{i=1}^n w_i \cdot (x_i - \bar{x}_w)^2} \text{ to estimate the simple linear regression coefficient, } B_1. \quad (3.4)$$

Weighted estimation is also employed in iterative estimation of parameters for a large class of generalized linear models (GLMs). Estimation of GLMs from survey data involves a “weighted” likelihood function, weighted first derivatives (the score or estimating equations), and then application of the *Newton–Raphson algorithm* to find the coefficient estimates that maximize the weighted *pseudo-likelihood*. To illustrate how weights enter GLM estimation, the weighted pseudo-log-likelihood function used in fitting a logistic regression model to survey data takes the following form:

Pseudo ln(Likelihood):

$$\sum_{h=1}^H \sum_{\alpha=1}^{a_h} \sum_{i=1}^{n_\alpha} w_{h\alpha i} y_{h\alpha i} \cdot \ln(\hat{\pi}(x_{h\alpha i})) + \sum_{h=1}^H \sum_{\alpha=1}^{a_h} \sum_{i=1}^{n_\alpha} w_{h\alpha i} (1 - y_{h\alpha i}) \cdot \ln(1 - \hat{\pi}(x_{h\alpha i})), \quad (3.5)$$

where:

$y_{h\alpha i} \in (0, 1)$ is the binary dependent variable in the logistic model.

$w_{h\alpha i}$ is the weight value for case i in cluster α and stratum h .

$x_{h\alpha i}$ is the vector of predictor variables in the logistic regression model.

$\hat{\pi}(x_{h\alpha i}) = e^{x_{h\alpha i} b} / (1 + e^{x_{h\alpha i} b})$ is the predicted probability that $y_{h\alpha i} = 1$.

These and other weighted approaches to estimating population parameters and model coefficients will be introduced as we cover each of the major procedures for survey data analysis.

Since the early 1950s, survey statisticians, economists, and researchers in other disciplines have debated the role that weights should play in model-based inferences from survey data. Lohr (1999, Section 11.3) provides an excellent review of this debate, including a discussion of contributions from Brewer and Mellor (1973), Hansen et al. (1983), and DuMouchel and Duncan (1983). A strong argument that emerges from papers by Pfeffermann and Holmes (1985) and Kott (1991) is that the survey weights protect the analyst against unknowingly misspecifying the model by omitting predictor variables or variable interactions that may be associated with the survey weight value (Section 2.7). Within the past 20 years, leading statisticians who approach survey data from a model-based perspective have endorsed this view that survey weights can serve as a “proxy” for important features of the sample design that have a bearing on the response variable of interest (Little, 1991).

To illustrate this property of weighted estimation, consider the Health and Retirement Study (HRS) sample of Black adults. HRS employs a two-fold oversampling of households in U.S. Census blocks with 10% or greater Black households to increase the size of the Black subpopulation sample in a cost-effective manner. Black adults living in the geographic domain of higher density blocks have twice the selection probability of those who live on a block with fewer than 10% Black households. The HRS weights for Black respondents adjust for the differential selection probabilities. The HRS public-use data set does contain a variable that is coded for the race/ethnicity of the respondent; however, the only source of information about whether the respondent lives in a low- or high-density Black neighborhood is encoded in the relative value of the survey weight. If the survey weights were ignored in a regression analysis, the potentially crucial influence of the disproportionate representation of Black adults from higher density (and often lower income) blocks would be omitted from the model.

Table 3.1 compares two estimated regression models where the dependent variable is the natural log of 2006 household income for HRS Black respondents. Each model includes demographic covariates of interest (age, gender of head of household, education level) as well as predictors that control for geographic region and urbanicity of residence. The first estimated model ignores the weights in the computation of model coefficients and their standard errors. The estimated coefficients in the second model correctly incorporate the HRS weights, and the estimated standard errors for the estimated coefficients correctly incorporate design effects for stratification, cluster sampling, and weighting. Both estimated models point to the importance of education level in determining the income level of HRS Black households; however, the estimated effect of a bachelor’s degree or even some college training (13–15 years) is much larger when the survey

TABLE 3.1

Regression Models of Log-Transformed Household Income for the 2006 HRS Black Subpopulation ($n = 2,465$)

Independent Variable	Regression Parameter Estimate (Standard Error, p -value)	
	Unweighted	Weighted (Design-Based SE)
<i>Age (Continuous)</i>	0.0026 (0.0058, $p = 0.66$)	0.0056 (0.0093, $p = 0.54$)
<i>Gender</i>		
Female	−0.4629 (0.1246, $p < 0.001$)	−0.3034 (0.2199, $p = 0.17$)
Male	Reference category	Reference category
<i>Education</i>		
Grade 0–11	−1.5585 (0.1991, $p < 0.0001$)	−1.9016 (0.2610, $p < 0.0001$)
Grade 12	−1.0304 (0.2011, $p < 0.0001$)	−1.5177 (0.2871, $p < 0.0001$)
Grade 13–15	−0.5145 (0.2152, $p < 0.0001$)	−0.7114 (0.1330, $p < 0.0001$)
Grade 16+	Reference category	Reference category
<i>Region</i>		
Northeast	0.0804 (0.2743, $p = 0.77$)	0.1462 (0.1680, $p = 0.38$)
Midwest	−0.3331 (0.2635, $p = 0.21$)	−0.2423 (0.2614, $p = 0.36$)
South	−0.2525 (0.2476, $p = 0.31$)	−0.3519 (0.2405, $p = 0.15$)
West	Reference category	Reference category
<i>Urbanicity</i>		
Urban	−0.0697 (0.1690, $p = 0.68$)	−0.0553 (0.3751, $p = 0.88$)
Suburban	0.05878 (0.1965, $p = 0.76$)	−0.0262 (0.4764, $p = 0.58$)
Rural	Reference category	Reference category

weights are employed in the estimation. This can be attributed to the fact that a higher proportion of the more highly educated HRS Black respondents will reside in the more integrated neighborhoods of the low density Black domain. Consequently, their contribution to the estimated model will be “up-weighted” when the survey weights are applied. (For a second illustration of how survey weights can influence the estimation of a regression model, see the [Chapter 7](#) example of estimation of a model of diastolic blood pressure based on the National Health and Nutrition Examination Survey [NHANES] data.)

There will be situations where the application of survey weights will have no real impact on a survey analysis and may even result in a loss of statistical precision relative to the unweighted alternative. Chambers and Skinner (2003) use a likelihood framework to demonstrate that the benefit of weighted analysis occurs when the sample and corresponding weights reflect an *informative sample design*. In simple terms, an informative design is one in which the design features—stratification, cluster sampling, disproportionate sampling—are associated with the response variable of interest. Korn and Graubard (1999, Sections 4.3 and 4.4) also provide examples of

situations where the application of survey weights does not have a substantial impact on inferences, and discuss methods for computing the inefficiency in survey estimates that can arise when sampling weights are used unnecessarily.

The general approach that we adopt in this book is to begin with the assumption that the features of the complex sample design and the associated survey weights are in fact related to the response variable of interest. Consequently, the design-based analyses illustrated in [Chapters 5 through 13](#) will employ weighted estimation of population parameters. However, we agree with Lohr (1999) on the value of comparing models estimated both with and without the survey weights. If the estimated model parameters are very different, the analyst should be able to explain the difference based on documented knowledge about how the weights were constructed—for example, oversampling of low-income households, persons with disabilities, older adults, and so on.

3.5 Probability Distributions and Design-Based Inference

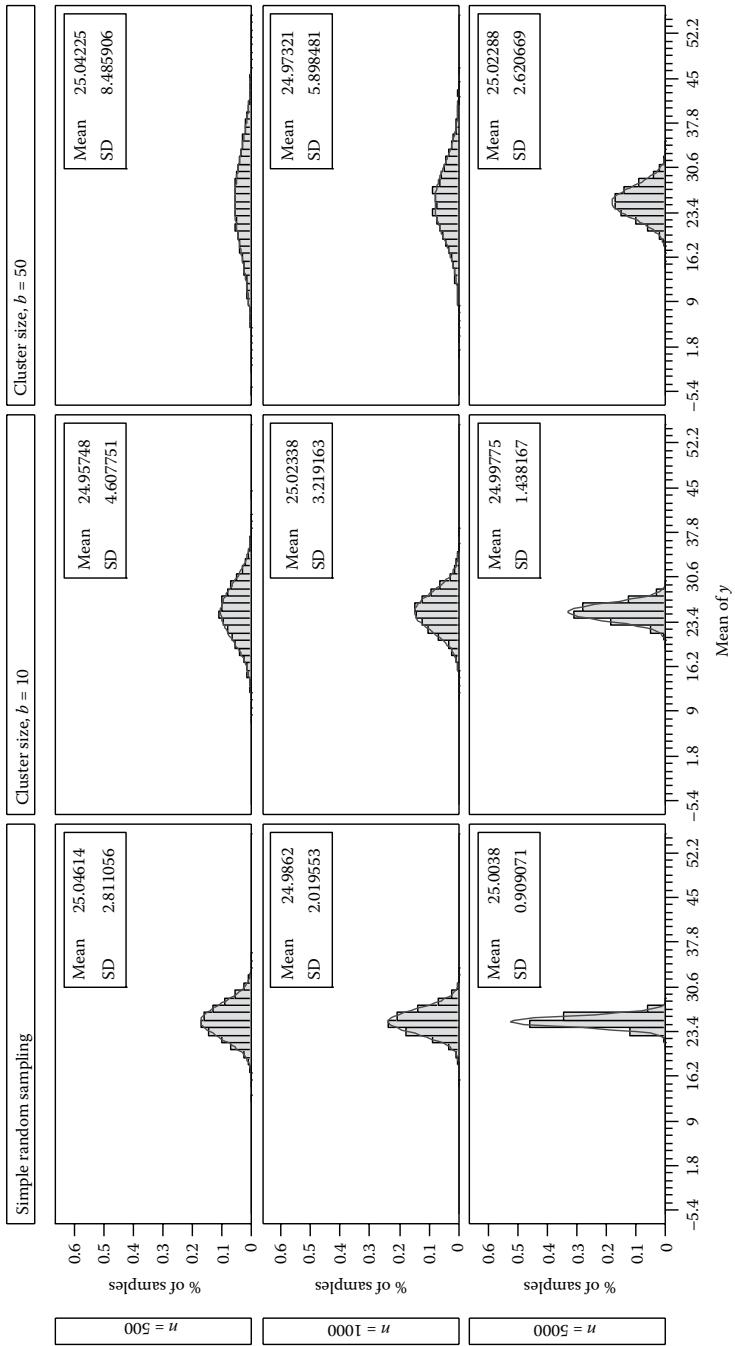
The whole procedure consists really in solving the problems which Professor Bowley termed direct problems: given a hypothetical population, to find the distribution of certain characters in repeated samples. If this problem is solved, then the solution of the other problem, which takes the place of the problem of inverse probability, can be shown to follow.

Jerzy Neyman, 1934

3.5.1 Sampling Distributions of Survey Estimates

Professor Neyman's "distribution of certain characters in repeated samples" is termed the *sampling distribution* of a sample estimate. The theoretical sampling distribution is based on all possible samples of size n that could be selected from a finite population of N elements. Using a single sampling plan, if all possible samples of size n from the N population elements were drawn in sequence, sample estimates were computed for each selected sample, and a histogram of the estimated values was plotted, the shape of the sampling distribution would emerge. Provided that the sample size, n , was sufficiently large, the distribution that would begin to appear as each new sample estimate was added to the histogram would be the familiar bell-shaped curve of a Normal distribution.

[Figure 3.2](#) illustrates a set of nine simulated sampling distributions for sample estimates of the population mean. Each individual graph in this

**FIGURE 3.2**

Simulated sampling distributions for a survey estimate of a mean (5000 simulated samples, $\bar{Y} = 25$).

figure represents the histogram of sample estimates, \bar{y} , computed from 5000 independent samples from a large finite population with known mean $\bar{Y} = 25$. The nine simulated sampling distributions displayed in this figure represent nine different probability sampling plans—three levels of sample size ($n = 500$, $n = 1,000$, $n = 5,000$), and three levels of cluster sampling (no cluster sampling, and clusters of size $b = 10$ and $b = 50$). Since \bar{y} is an unbiased estimator regardless of the sampling plan or the sample size, each sampling distribution is centered at the population mean, $\bar{Y} = 25$. As the sample size decreases or the sizes of the sampled clusters increase, the dispersion of sample estimates about the population mean value increases. The degree of dispersion of the sample estimates about the mean of the sampling distribution is the *sampling variance* associated with the sample design, which can be written as

$$\text{var}(\bar{y}) = \sum_{s=1}^S P(s) \cdot (\bar{y}_s - E(\bar{y}_s))^2, \quad (3.6)$$

where:

$s = 1, \dots, S$ indexes all possible samples of size n under the design.

$P(s)$ = the probability that sample s was chosen from the set of S possibilities.

\bar{y}_s = the estimate for sample s .

The square root of the sampling variance is the *standard error* of a probability sample estimate, denoted by $SE(\bar{y})$. Or equivalently, the standard error of a design-based estimate is simply the *standard deviation* of the sampling distribution.

In real-world survey samples, a single sample is observed. It is never practically feasible to observe the full sampling distribution of an estimate, its mean, its variance, or its distributional shape. So how is it possible to make inferential statements based on a sampling distribution that is never observed? Briefly, statistical theory shows that if the sample size n is sufficiently large (e.g., 100 cases), and $\hat{\theta}$ is an unbiased or otherwise consistent estimator of the population parameter θ , the sampling distribution converges to an approximately Normal distribution: $f(\hat{\theta}) \sim N(\hat{\theta}, \text{var}(\hat{\theta}))$. Consequently, the test statistic $t = (\hat{\theta} - \theta) / se(\hat{\theta})$, where both $\hat{\theta}$ and $se(\hat{\theta})$ are estimated from the survey sample data, follows the Student t probability distribution with df degrees of freedom (to be defined in the next section). This test statistic can be “inverted” to derive the following probability statement: $P_s \{ \hat{\theta} - t_{1-\alpha/2, df} \cdot se(\hat{\theta}) \leq \theta \leq \hat{\theta} + t_{1-\alpha/2, df} \cdot se(\hat{\theta}) \} \equiv 1 - \alpha$. This re-expression of the test statistic as a range of values for θ is the basis for the $100(1 - \alpha)\%$ CI presented in Equation 3.2.

3.5.2 Degrees of Freedom for t under Complex Sample Designs

Probability distributions such as the Student t , χ^2 , and F play a critical role in the construction of CIs for population values or as the reference distributions for formal tests of hypotheses concerning population parameters. Included in the quantities that define the shape of these distributions are *degree(s) of freedom (df)* parameters. The degrees of freedom are indices of how precisely the true variance parameter(s) of the reference distribution have been estimated from the sample design. Sample designs with large numbers of degrees of freedom for variance estimation enable more precise estimation of the true variance parameters of the reference distribution. Conversely, the smaller the degrees of freedom afforded by the sample design, the less precisely these variance parameters are estimated. Consider the $(1 - \alpha/2 = 0.975)$ critical values for the Student t distribution with varying degrees of freedom: $t_{0.975,1} = 12.706$; $t_{0.975,20} = 2.0860$; $t_{0.975,40} = 2.0211$; $t_{0.975,\infty} = Z_{0.975} = 1.9600$. Whenever an analyst (or their computer software) derives a CI or test statistic from sample data, variance parameters that define the appropriate t , χ^2 , or F reference distribution must be estimated from the sample data.

Precise determination of the degrees of freedom for variance estimation available under complex sample designs used in practice is difficult. Currently, computer software programs for the analysis of complex sample survey data employ a *fixed degrees of freedom rule* to determine the degrees of freedom for the reference distribution used to construct a CI (e.g., $t_{1-\alpha/2,df}$) or a p -value for a hypothesis test (e.g., $P(F_{k,d} > F)$):

$$df_{des} = \sum_{h=1}^H (a_h - 1) = \sum_{h=1}^H a_h - H = \# \text{clusters} - \# \text{strata}. \quad (3.7)$$

Interested readers are referred to Theory Box 3.1 for a more in-depth (yet not strictly theoretical) explanation of the basis for this rule.

The fixed rule for determining degrees of freedom for complex sample designs is applied by software procedures designed for the analysis of survey data whenever the full survey sample is being analyzed. However, programs may use different rules for determining degrees of freedom for subpopulation analyses. For subpopulations, improved CI coverage of the true population value is obtained using a “variable” degrees-of-freedom calculation method (Korn and Graubard, 1999):

$$df_{var} = \sum_{h=1}^H I_h \cdot (a_h - 1), \quad (3.8)$$

where:

$I_h = 1$ if stratum h has 1 or more subpopulation cases, 0 otherwise.

a_h = the number of clusters (PSUs) sampled in stratum $h = 1, \dots, H$.

THEORY BOX 3.1 DEGREES OF FREEDOM FOR VARIANCE ESTIMATION

Consider the pivotal t statistic, $t = (\bar{y} - \bar{Y}_0) / se(\bar{y})$. Under simple random sampling (SRS):

$$t_{n-1,SRS} = \frac{(\bar{y} - \bar{Y}_0)}{se(\bar{y})} = \frac{(\bar{y} - \bar{Y}_0)}{\sqrt{s^2/n}} = \frac{(\bar{y} - \bar{Y}_0)}{\sqrt{\sum_{i=1}^n [(y_i - \bar{y})^2 / (n-1)] / n}}.$$

A total of $n - 1$ independent contrasts (squared differences) contribute to the SRS estimate of S^2 (once the mean is known, there are only $n - 1$ unique pieces of information for estimating the variance). Consequently, for an SRS design, the t statistic is referred to a Student t distribution with $n - 1$ degrees of freedom.

Now, consider this same test statistic under a more complex stratified cluster sample design:

$$\begin{aligned} t_{df, complex} &= \frac{(\bar{y}_{st,cl} - \bar{Y}_0)}{\sqrt{var(\bar{y}_{st,cl})_{complex}}} = \frac{(\bar{y}_{st,cl} - \bar{Y}_0)}{se(\bar{y}_{st,cl})_{complex}} \\ var(\bar{y}_{st,cl}) &= \sum_{h=1}^H W_h^2 \frac{1}{a_h} \left[\frac{1}{(a_h - 1)} \cdot \frac{1}{b_h^2} \left\{ \sum_{\alpha=1}^{a_h} y_{h\alpha}^2 - \frac{y_h^2}{a_h} \right\} \right] \\ &= \sum_{h=1}^H \frac{W_h^2}{a_h b_h^2} \left[\frac{1}{(a_h - 1)} \left\{ \sum_{\alpha=1}^{a_h} \left(y_{h\alpha} - \frac{y_h}{a_h} \right)^2 \right\} \right] \end{aligned}$$

Under a design with $h = 1, \dots, H$ strata and $\alpha = 1, \dots, a_h$ equal-sized primary stage units (PSUs) per stratum (i.e., the sample size in each PSU in stratum h is b_h), each stratum contributes $a_h - 1$ independent contrasts to the estimate of the $var(\bar{y}_{st,cl})$. The t statistic for the complex sample design is no longer referred to a Student t distribution with $n - 1$ degrees of freedom. Instead, the correct degrees of freedom for variance estimation under this complex sample design are:

$$design\ df_{fixed} = \sum_{h=1}^H (a_h - 1) = \sum_{h=1}^H a_h - H = \# clusters - \# strata.$$

The variance estimation technique known as Taylor Series Linearization (TSL) in particular (Section 3.6.2) involves approximating

complex nonlinear statistics with simpler linear functions of linear statistics, and then estimating the variances of the linear statistics (enabling the use of known variance estimation formulae for complex designs, as above). This gives rise to the use of the fixed degrees-of-freedom rule when using this variance estimation procedure.

For additional theoretical details on the determination of degrees of freedom in variance estimation under complex sample designs, we refer readers to Valliant and Rust (2010), Korn and Graubard (1999, Section 5.2), and Rust and Rao (1996).

The variable degrees of freedom are determined as the total number of clusters in strata with 1+ subpopulation cases minus the number of strata with at least one subpopulation observation. Rust and Rao (1996) suggest the same rule for calculating degrees of freedom for test statistics when replicated variance estimation methods are used to develop standard errors for subpopulation estimates. (See Section 4.5 for a more in-depth discussion of survey estimation for subpopulations.)

In theory, both the “fixed” and “variable” rules only yield an approximation to the true degrees of freedom for a complex sample design. Valliant and Rust (2010) propose a simple estimator of degrees of freedom that leads to improved CI coverage relative to the simple rule above which is currently used by most software packages. At the time of this writing, the approach suggested by Valliant and Rust (2010) has yet to make its way into major statistical software packages including procedures for the analysis of survey data. Our hope is that there will be more work in this area in the near future, including implementation of improved methods for estimating degrees of freedom based on different types of complex sample designs.

3.6 Variance Estimation

Survey analysis that employs CIs (or hypothesis test statistics and p -values) requires estimation of the sampling variability of the sample estimates. For simple statistics computed from data collected under equal-probability SRS designs or stratified random sample designs, exact expressions for the estimator of the sampling variance may be derived (Cochran, 1977). Survey analysis programs in Stata or SUDAAN and many other software packages allow the user to choose the exact formula for these simple sample designs.

Consider estimating the population mean under a stratified (*st*), random sample (*ran*) design:

$$\bar{y}_{st,ran} = \sum_{h=1}^H W_h \cdot \bar{y}_h = \sum_{h=1}^H \frac{N_h}{N} \cdot \bar{y}_h. \quad (3.9)$$

An unbiased estimate of the sampling variance of the mean estimate is computed using the following analytical formula:

$$var(\bar{y}_{st,ran}) = \sum_{h=1}^H W_h^2 \cdot var(\bar{y}_h) = \sum_{h=1}^H \left(1 - \frac{n_h}{N_h}\right) \cdot W_h^2 \cdot \frac{s_h^2}{n_h}. \quad (3.10)$$

Note that this exact expression includes the finite population correction factor for each stratum ($1 - f_n = 1 - n_h/N_h$). The variance expression for this most basic of stratified sample designs illustrates an important fact. For stratified samples, the sampling variance of an estimator is simply the sum of the variance contributions from each stratum. There is no between-stratum component of variance! This simple rule applies equally to more complex designs which utilize cluster sampling or unequal probability sampling within strata.

When survey data are collected using a complex sample design with unequal size clusters or weights are used in estimation, most statistics of interest will not be simple linear functions of the observed data, as in the case of Equation 3.9, and alternative methods for estimating the variances of the more complex statistics are required. Over the past 50 years, advances in survey sampling theory have guided the development of a number of methods for correctly estimating variances from complex sample survey data sets. The two most common approaches to the estimation of sampling errors for estimates computed from complex sample survey data sets are (1) through the use of a TSL of the estimator (and corresponding approximation to its variance) or (2) through the use of resampling variance estimation procedures such as Balanced Repeated Replication (BRR) or Jackknife Repeated Replication (JRR) (Rust, 1985; Wolter, 2007). BRR, JRR, and the bootstrap technique comprise a second class of non-parametric methods for conducting estimation and inference from complex sample survey data. As suggested by the generic label for this class of methods, BRR, JRR, and the bootstrap utilize replicated subsampling of the sample data to develop sampling variance estimates for linear and nonlinear statistics.

The following sections describe the basic features of the TSL technique and the alternative replication methods for estimating the variance of sample estimates from complex sample survey data.

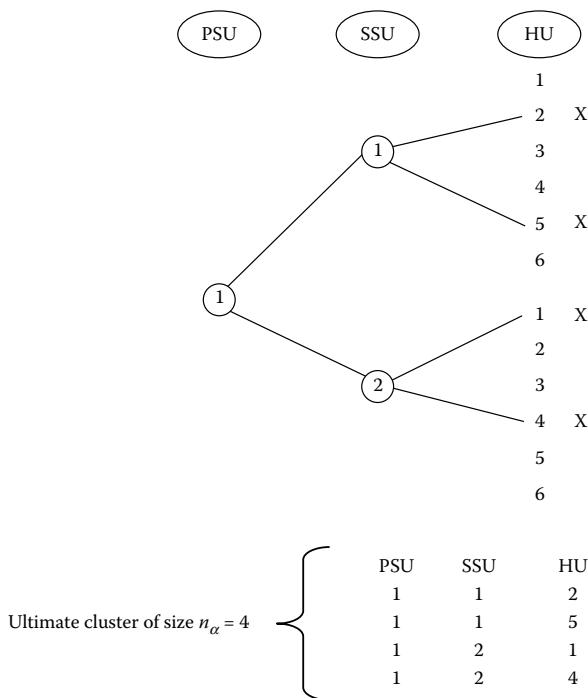
3.6.1 Simplifying Assumptions Employed in Complex Sample Variance Estimation

Before turning to the computational methods, it is important to consider two simplifying assumptions that are routinely used in TSL, JRR, and BRR variance estimation programs available in today's statistical software packages:

1. PSUs in multistage sample designs are considered to be selected *with replacement* from the primary stage strata. Any finite population correction for the primary stage sample is ignored. The resulting estimates of sampling variance will be slight overestimates.
2. Multistage sampling within selected PSUs results in a single *ultimate cluster* of observations for that PSU. Variance estimation methods based on the ultimate clusters "roll up" the components of variance for the multiple stages into a single-stage formula that only requires knowledge of the primary stage stratum and PSU identifiers to perform the final calculations. All sources of variability nested within the PSU are captured in the composite variance estimate.

[Figure 3.3](#) illustrates the concept of an ultimate cluster for a single sample PSU. Within the sample PSU, two additional stages of sampling identify a unique cluster of four elements (units 2 and 5 within sample secondary stage unit [SSU] 1 and units 1 and 4 within sample SSU 2). Under assumption 1, PSUs are initially selected with replacement within first-stage sampling strata. Following this with-replacement selection of PSUs, all possible ultimate clusters that could arise from the multistage sampling procedure could be enumerated (in theory) within each selected PSU. (The multistage selection process emulates this process of enumerating and sampling a single ultimate cluster of elements to represent the PSU, but at substantially reduced cost and effort.) Then, the survey statistician could (in theory) select a without-replacement sample of these ultimate clusters from all of the PSUs. In practice, one ultimate cluster is generally selected within each PSU, as shown in [Figure 3.3](#). The resulting sample can be thought of as a single-stage, with-replacement selection of ultimate clusters, where all elements within each selected ultimate cluster are sampled. This greatly simplifies variance estimation through the use of formulae for stratified, with-replacement sampling of ultimate clusters of observations. Since PSUs are typically sampled *without* replacement from within the primary stage strata in practice, use of the simpler variance estimation formulae results in a slight overestimate of the true variance (Kish, 1965, Section 5.3), which is an acceptably conservative approach for making inferences.

[Figure 3.4](#) provides a simple illustration of a survey data set that is ready for analysis. The data set includes $n = 16$ cases. From each of $h = 1, \dots, 4$ strata, a total of $a_h = 2$ PSUs has been selected *with replacement*. An ultimate cluster of $b = 2$ observations has been selected from each sample PSU. The data set

**FIGURE 3.3**

Schematic illustration of the ultimate cluster concept.

contains a unique stratum code, a PSU (or cluster) code within each stratum, and a case-specific value for the weight variable, w_i . As discussed in more detail in Section 4.3, the stratum, cluster, and weight variables represent the minimum set of *design variables* that are required to perform analyses of sampling variability for complex sample designs. (Note: As an alternative to releasing the detailed stratum and cluster codes, survey data sets may include “replicate weights” for use by software that supports replicated variance estimation—see Section 4.2.1.) This simple example data set will be used in the following sections to illustrate the computational steps in the TSL, JRR, BRR and Bootstrap variance estimation methods.

3.6.2 TSL Method

Taylor series approximations of complex sample variances for weighted sample estimates of finite population means, proportions, and linear regression coefficients have been available since the 1950s (Hansen et al., 1953; Kish and Hess, 1959). Woodruff (1971) summarized the general application of the TSL methods to a broader class of survey statistics. Binder (1983) advanced the application of the TSL method to variance estimation for analysis techniques

Stratum	PSU (cluster)	Case	y_i	w_i
1	1	1	0.58	1
	1	2	0.48	2
1	2	1	0.42	2
	2	2	0.57	2
2	1	1	0.39	1
	1	2	0.46	2
2	2	1	0.50	2
	2	2	0.21	1
3	1	1	0.39	1
	1	2	0.47	2
3	2	1	0.44	1
	2	2	0.43	1
4	1	1	0.64	1
	1	2	0.55	1
4	2	1	0.47	2
	2	2	0.50	2

FIGURE 3.4

Data set for example TSL, JRR, BRR, and Bootstrap sampling variance calculations: four strata, two PSUs per stratum, ultimate clusters of two elements per PSU.

such as logistic regression and other GLMs. In general, the TSL approach to variance estimation involves a noniterative process of five steps.

TSL Step 1: The estimator of interest is written as a function of weighted sample totals. Consider a weighted, combined ratio estimator of the population mean of the variable y (Kish, 1965):

$$\bar{y}_w = \frac{\sum_{h=1}^H \sum_{\alpha=1}^{a_h} \sum_{i=1}^{n_{h\alpha}} w_{h\alpha i} y_{h\alpha i}}{\sum_{h=1}^H \sum_{\alpha=1}^{a_h} \sum_{i=1}^{n_{h\alpha}} w_{h\alpha i}} = \frac{\sum_{h=1}^H \sum_{\alpha=1}^{a_h} \sum_{i=1}^{n_{h\alpha}} u_{h\alpha i}}{\sum_{h=1}^H \sum_{\alpha=1}^{a_h} \sum_{i=1}^{n_{h\alpha}} v_{h\alpha i}} = \frac{u}{v}. \quad (3.11)$$

Notice that the estimator of the ratio mean can be expressed as a ratio of two weighted totals, u and v , which are sums over design strata ($h = 1, \dots, H$), PSUs ($\alpha = 1, \dots, a_h$), and individual ($i = 1, \dots, n_{h\alpha}$) cases of the constructed variables $u_{h\alpha i} = w_{h\alpha i} y_{h\alpha i}$ and $v_{h\alpha i} = w_{h\alpha i}$. The concept of a sample total is not limited to sums of single variables or sums of weighted values. For reasons that will be explained more fully in later sections, the individual case-level variates used to construct the sample totals for complex sample survey data may be more complex functions involving many variates and functional forms. For example, under a stratified, cluster sample design, the following estimated

totals are employed in TSL variance estimation for simple linear and simple logistic regression coefficients:

$$\begin{aligned} u &= \sum_{h=1}^H \sum_{\alpha=1}^{a_h} \sum_{i=1}^{n_\alpha} w_{h\alpha i} \cdot (y_{h\alpha i} - \bar{y}_w)(x_{h\alpha i} - \bar{x}_w); \\ v &= \sum_{h=1}^H \sum_{\alpha=1}^{a_h} \sum_{i=1}^{n_\alpha} w_{h\alpha i} \cdot (x_{h\alpha i} - \bar{x}_w)^2; \text{ or even} \\ sc &= \sum_{h=1}^H \sum_{\alpha=1}^{a_h} \sum_{i=1}^{n_\alpha} \left[w_{h\alpha i} \cdot x_{h\alpha i} \cdot y_{h\alpha i} - w_{h\alpha i} \cdot x_{h\alpha i} \frac{e^{\hat{\beta}_0 + \hat{\beta}_1 \cdot x_{h\alpha i}}}{1 + e^{\hat{\beta}_0 + \hat{\beta}_1 \cdot x_{h\alpha i}}} \right]. \end{aligned}$$

TSL Step 2: Like many other survey estimators for complex sample survey data, the weighted estimator of the population mean is a nonlinear function of the two weighted sample totals. Consequently,

$$var(\bar{y}_w) = var\left(\frac{u}{v}\right) \neq \frac{var(u)}{var(v)}.$$

To solve the problem of the nonlinearity of the sample estimator, a standard mathematical tool, the Taylor Series expansion, is used to derive an approximation to the estimator of interest, rewriting it as a linear combination of weighted sample totals:

$$\begin{aligned} \bar{y}_{w,TSL} &= \frac{u_0}{v_0} + (u - u_0) \left[\frac{\partial \bar{y}_{w,TSL}}{\partial u} \right]_{u=u_0, v=v_0} + (v - v_0) \left[\frac{\partial \bar{y}_{w,TSL}}{\partial v} \right]_{v=v_0, u=u_0} + \text{remainder} \\ \bar{y}_{w,TSL} &\equiv \frac{u_0}{v_0} + (u - u_0) \left[\frac{\partial \bar{y}_{w,TSL}}{\partial u} \right]_{u=u_0, v=v_0} + (v - v_0) \left[\frac{\partial \bar{y}_{w,TSL}}{\partial v} \right]_{v=v_0, u=u_0} \\ \bar{y}_{w,TSL} &\equiv \text{constant} + (u - u_0) \cdot A + (v - v_0) \cdot B, \end{aligned}$$

where A and B symbolically represent the derivatives with respect to u and v , evaluated at the expected values of the sample estimates u_0 and v_0 .

The quadratic, cubic, and higher order terms in the full Taylor series expansion of \bar{y}_w are dropped (i.e., the “remainder” is assumed to be negligible). Further, consistent (and preferably unbiased) sample estimates are generally used in place of the expected values of the sample estimates (Rao and Wu, 1985).

TSL Step 3: A standard statistical result for the variance of a linear combination (sum) is applied to obtain the approximate variance of the “linearized” form of the estimator, $\bar{y}_{w,TSL}$:

$$\begin{aligned}
\text{var}(\bar{y}_{w,TSL}) &\equiv \text{var}[\text{constant} + (u - u_0) \cdot A + (v - v_0) \cdot B] \\
&\equiv 0 + A^2 \text{var}(u - u_0) + B^2 \text{var}(v - v_0) + 2AB \text{cov}(u - u_0, v - v_0) \\
&\equiv A^2 \text{var}(u) + B^2 \text{var}(v) + 2AB \text{cov}(u, v),
\end{aligned}$$

where $A = \frac{\delta \bar{y}_{w,TSL}}{\delta u} \Big|_{u=u_0, v=v_0} = \frac{1}{u_0}$; $B = \frac{\delta \bar{y}_{w,TSL}}{\delta v} \Big|_{u=u_0, v=v_0} = -\frac{u_0}{v_0^2}$; and

u_0, v_0 are the weighted sample totals computed from the survey data.

\Rightarrow

$$\text{var}(\bar{y}_{w,TSL}) \equiv \frac{\text{var}(u) + \bar{y}_{w,TSL}^2 \cdot \text{var}(v) - 2 \cdot \bar{y}_{w,TSL} \cdot \text{cov}(u, v)}{v_0^2}.$$

The sampling variance of the nonlinear estimator, $\bar{y}_{w,TSL}$, is thus approximated by a simple algebraic function of quantities that can be readily computed from the complex sample survey data. The sample estimates of the ratio mean, $\bar{y}_{w,TSL}$, and the sample total of the analysis weights, v_0 , are computed from the survey data. The estimates of $\text{var}(u)$, $\text{var}(v)$, and $\text{cov}(u, v)$ are computed using the relatively simple computational formulae described in Step 4 (below).

TSL Step 4: Under the TSL method, the variance approximation in Step 3 has been derived for most survey estimators of interest, and software systems such as Stata and SUDAAN provide programs that permit TSL variance estimation for virtually all of the analytical methods used by today's survey data analyst. The sampling variances and covariances of individual weighted totals, u or v , are easily estimated using simple formulae (under an assumption of with-replacement sampling of PSUs within strata at the first stage) that require only knowledge of the subtotals for the primary stage strata and clusters.

$$\begin{aligned}
\text{var}(u) &= \sum_{h=1}^H \frac{a_h}{(a_h - 1)} \cdot \left[\sum_{\alpha=1}^{a_h} u_{h\alpha}^2 - \frac{u_h^2}{a_h} \right]; \\
\text{var}(v) &= \sum_{h=1}^H \frac{a_h}{(a_h - 1)} \cdot \left[\sum_{\alpha=1}^{a_h} v_{h\alpha}^2 - \frac{v_h^2}{a_h} \right]; \\
\text{cov}(u, v) &= \sum_{h=1}^H \frac{a_h}{(a_h - 1)} \cdot \left[\sum_{\alpha=1}^{a_h} u_{h\alpha} \cdot v_{h\alpha} - \frac{u_h \cdot v_h}{a_h} \right];
\end{aligned}$$

where $u_{h\alpha}$, u_h , $v_{h\alpha}$, and v_h are defined below.

Provided that the sample stratum codes, cluster codes, and weights are included in the survey data set, the *weighted totals* for strata and clusters are easily calculated. These calculations are illustrated here for u :

$$u_{h\alpha} = \sum_{i=1}^{n_\alpha} u_{h\alpha i}; \quad u_h = \sum_{\alpha=1}^{a_h} \sum_{i=1}^{n_\alpha} u_{h\alpha i}.$$

Returning to the example data set in [Figure 3.4](#):

$$\begin{aligned}\bar{y}_{w,TSL} &= \frac{\sum_h \sum_{\alpha} \sum_i w_{h\alpha i} y_{h\alpha i}}{\sum_h \sum_{\alpha} \sum_i w_{h\alpha i}} = \frac{\sum_h \sum_{\alpha} \sum_i u_{h\alpha i}}{\sum_h \sum_{\alpha} \sum_i v_{h\alpha i}} = \frac{u}{v} = \frac{11.37}{24} = 0.47375 \\ v_0 &= \sum_h \sum_{\alpha} \sum_i w_{h\alpha i} = 24 \\ var(u) &= 0.9777; \quad var(v) = 6.0000; \quad cov(u, v) = 2.4000 \\ var(\bar{y}_{w,TSL}) &\equiv \frac{var(u) + \bar{y}_{w,TSL}^2 \cdot var(v) - 2 \cdot \bar{y}_{w,TSL} \cdot cov(u, v)}{v_0^2} \\ &= \frac{0.9777 + 0.4737^2 \cdot 6.0000 - 2 \cdot 0.4737 \cdot 2.4000}{24^2} \\ &= 0.00008731 \\ se(\bar{y}_{w,TSL}) &= 0.009344.\end{aligned}$$

TSL Step 5: CIs (or hypothesis tests) based on estimated statistics, standard errors, and correct degrees of freedom based on the complex sample design are then constructed and reported as output from the TSL variance estimation program. We show this calculation for a 95% CI for the population mean based on the example data set in [Figure 3.4](#) (note that $df = 8$ clusters – 4 strata = 4):

$$\begin{aligned}CI(\bar{y}_{w,TSL}) &= \bar{y}_{w,TSL} \pm t_{1-\alpha/2, df} \cdot \sqrt{var_{TSL}(\bar{y}_{w,TSL})} \\ \text{e.g., } CI(\bar{y}_{w,TSL}) &= 0.47375 \pm t_{1-\alpha/2, 4} \cdot 0.009344 \\ &= 0.47375 \pm 2.7764 \cdot (0.009344) = (0.44780, 0.49969).\end{aligned}$$

Most contemporary software packages employ the TSL approach as the default method of computing sampling variances for complex sample survey data. TSL approximations to sampling variances have been derived for virtually all of the statistical procedures that have important applications in survey data analysis. The following Stata (Version 14+) syntax illustrates the command sequence and output for an analysis of the prevalence of at least one lifetime episode of major depression in the National Comorbidity Survey Replication (NCS-R) adult survey population.

```

. svyset seclustr [pweight=ncsrwtsh], strata(sestrat)///
vce(linearized) singleunit(missing)
      pweight: ncsrwtsh
      VCE: linearized
Single unit: missing
Strata 1: sestrat
  SU 1: seclustr
  FPC 1: <ZERO>
. svy: mean mde
(running mean on estimation sample)
Survey: Mean estimation
Number of strata =        42          Number of obs      =    9282
Number of PSUs   =         84          Population size  =    9282
                                         Design df       =        42
-----
                                         | Linearized
                                         |     Mean   Std. Err.    [95% Conf. Interval]
----- | -----
mde  |   .1917112   .0048768   .1818694   .201553
----- |

```

Note that Stata explicitly reports the linearized estimate of the standard error (0.0049) of the weighted estimate of the population mean (0.1917). These Stata commands will be explained in more detail in the upcoming chapters.

3.6.3 Replication Methods for Variance Estimation

JRR, BRR, and the bootstrap form a second class of nonparametric methods for computing sampling variances of survey estimates. As suggested by the generic label for this class of methods, JRR, BRR, and the bootstrap use replicated subsampling of the database of sample observations to develop sampling variance estimates for linear and nonlinear statistics (Rust, 1985; Rao et al., 1992; Shao and Tu, 1995; Wolter, 2007).

The precursor to today's JRR, BRR, and bootstrap techniques for replicated variance estimation was a simple yet statistically elegant technique of interpenetrating samples or replicated sampling developed by Mahalanobis (1946) for agricultural surveys in Bengal, India. Mahalanobis' method requires selecting the complete probability sample of size n as a set of $c = 1, \dots, C$ independent sample replicates from a common sampling plan. The replicated estimate of θ and the sampling variance of the simple replicated estimate are:

$$\hat{\theta}_{rep} = \sum_{c=1}^C \hat{\theta}_c / C, \text{ the mean of the replicate sample estimates;} \quad (3.12)$$

$$var(\hat{\theta}_{rep}) = \sum_{c=1}^C (\hat{\theta}_c - \hat{\theta}_{rep})^2 / C \cdot (C - 1).$$

Despite their simplicity, simple replicated sample designs are rarely used in population survey practice. If a large number of replicate samples are used to obtain adequate degrees of freedom for variance estimation, the requirement that each replicate sample be a “miniature” of the full sample design restricts the design efficiency by limiting the numbers of strata that can be employed at each stage of selection. If a highly efficient stratified design is employed, the number of independent replicates and corresponding degrees of freedom for variance estimation may be seriously limited.

Mahalanobis’ pioneering idea that replicated samples could be used to estimate sampling variances was extended to the BRR, JRR, and bootstrap methods. These techniques draw on the principles of the simple replication method but yield a more efficient procedure for creating the replicates and provide greater efficiency for estimating sampling variances by increasing degrees of freedom for comparable sample sizes and survey costs.

Each of these replication-based methods employs a generic sequence of five steps:

1. Sample replicates ($r = 1, \dots, R$) of the full survey sample are defined based on assignment rules tailored to the BRR, JRR, and bootstrap techniques.
2. Full sample survey weights are revised for each replicate to create $r = 1, \dots, R$ replicate weights.
3. Weighted estimates of a population statistic of interest are computed for the full sample and then separately for each replicate (using the replicate weights).
4. A replicated variance estimation formula tailored to the BRR, JRR, or bootstrap method is used to compute standard errors.
5. CIs (or hypothesis tests) based on the estimated statistics, standard errors, and correct degrees of freedom are constructed.

JRR, BRR, and the bootstrap employ different methods to form the replicates (Step 1) which in turn requires minor modifications to Steps 2–4 of the general replicated variance estimation algorithm. The following sections describe each of the basic steps for the most common JRR and BRR methods as well as the resampling bootstrap method of Rao et al. (1992).

3.6.3.1 Jackknife Repeated Replication

The JRR method of replicated variance estimation is applicable to a wide range of complex sample designs. There are several JRR approaches to constructing JRR replicates and estimating the variance of a survey estimate, including the JK1 and JK_n approaches (Wolter, 2007; Valliant et al., 2013). We describe these two approaches for JRR replicate formation and the corresponding variance estimation formulae below.

The *JK1 method* assumes that the sample of $\alpha = 1, \dots, a$ PSUs (or elements) is selected under an unstratified design. Replicates are formed by dropping a single unit from the sample and rescaling the full sample weights for all observations in the undeleted units by a factor of $a/(a - 1)$. The JK1 estimate of variance for a statistic, q , is then computed using the formula:

$$\text{var}_{\text{JRR}, \text{JK1}}(\hat{q}) = \frac{a-1}{a} \sum_{k=1}^a (\hat{q}_k - \hat{q})^2$$

$$df = a - 1.$$

The *JKn method* is the default method in most survey analysis software (e.g., SAS®, Stata, SUDAAN, and R). The *JKn* (or Delete One) method applies to stratified sample designs with two or more PSUs selected per stratum, and is the form of JRR estimation that will be used here for an example. This method employs the following five-step sequence:

JRR Step 1: Each JRR replicate is constructed by “deleting” a single PSU from a single primary stage stratum. Operationally, the statistical software systems that provide JRR capability do not physically remove the cases for the deleted PSUs in creating each replicate sample. Instead, by assigning a zero or missing weight value to each case in the deleted PSU, the “replicate weight” sweeps the deleted cases out of the computation of the replicate estimate. Sample cases in all remaining PSUs (including those in all other strata) constitute the JRR replicate. See [Figure 3.5](#), in which the first PSU in the first stratum is deleted to form a first JRR replicate.

For the *JKn* variance estimator, each stratum will contribute $a(h)$ replicates, where for each replicate one of the clusters in a single stratum is deleted. In our data example, $H = 4$ and $a(h) = 2$ for $h = 1, \dots, 4$, so the total number of required JRR replicates for the *JKn* variance estimation is:

$$R = \sum_{h=1}^4 (a_h) = 8.$$

Each stratum will contribute only $a_h - 1$ unique JRR replicates, yielding a total of $df = \sum_{h=1}^H (a_h - 1) = a - H = \# \text{clusters} - \# \text{strata}$ degrees of freedom for estimating standard errors of sample estimates. In our example, with two PSUs per stratum, once the total for the stratum and one PSU is known, the total for the second PSU is known (meaning that it is not unique information).

JRR Step 2: A new *replicate weight* is computed for each of the JRR replicates. Replicate weight values for cases in the deleted PSU are assigned a value of “0” or “missing.” The replicate weight values for the retained PSU cases

Stratum	PSU (cluster)	Case	y_i	$w_{i,rep}$
1	1	1	0.00	0
	1	2	0.00	0
1	2	1	0.42	2x2
	2	2	0.57	2x2
<hr/>				
2	1	1	0.39	1
	1	2	0.46	2
2	2	1	0.50	2
	2	2	0.21	1
<hr/>				
3	1	1	0.39	1
	1	2	0.47	2
3	2	1	0.44	1
	2	2	0.43	1
<hr/>				
4	1	1	0.64	1
	1	2	0.55	1
4	2	1	0.47	2
	2	2	0.50	2

FIGURE 3.5

Formation of a single JRR replicate for the data example.

in the “deletion stratum” are formed by multiplying the full sample survey weights by a factor of $a_h/(a_h - 1)$. This factor equals 2 in our example. Note that, for all strata except the deletion stratum, the replicate weight value is the unaltered full sample weight.

The second JRR replicate is formed by dropping the second PSU in Stratum 1 and weighting up the first PSU in Stratum 1, with the process continuing until all replicates have been formed.

JRR Step 3: Using the replicate weights developed for each JRR replicate sample, the weighted estimates of the population statistic are computed for each replicate. The statistic of interest in our example is the weighted estimate of the population mean, so each replicate estimate takes the following form:

$$\hat{q}_r = \bar{y}_k = \frac{\sum_{i \in rep}^{n_{rep}} y_i \cdot w_{i,rep}}{\sum_{i \in rep}^{n_{rep}} w_{i,rep}} \text{ for each of } k = 1, \dots, 8 \text{ replicates.}$$

$$\begin{aligned} \hat{q}_{1(\text{del 1_1})} &= 0.47240; & \hat{q}_{3(\text{del 2_1})} &= 0.46958; & \hat{q}_{5(\text{del 3_1})} &= 0.47434; & \hat{q}_{7(\text{del 4_1})} &= 0.46615; \\ \hat{q}_{2(\text{del 1_2})} &= 0.47521; & \hat{q}_{4(\text{del 2_2})} &= 0.47791; & \hat{q}_{6(\text{del 3_2})} &= 0.47320; & \hat{q}_{8(\text{del 4_2})} &= 0.48272. \end{aligned}$$

The full sample estimate of the mean is also computed:

$$\hat{q} = \frac{\sum_{i=1}^n y_i \cdot w_i}{\sum_{i=1}^n w_i} = 0.47375.$$

JRR Step 4: Using the $r = 1, \dots, R$ replicate estimates and the full sample estimate, the sampling variance is estimated using the following simple formula:

$$\begin{aligned} var_{JRR_DelOne}(\hat{q}) &= \sum_{h=1}^H \frac{a_h - 1}{a_h} \sum_{\alpha=1}^{a_h} (\hat{q}_{(h\alpha)} - \hat{q})^2 \\ &= 0.5 \cdot \sum_{k=1}^8 (\hat{q}_k - \hat{q})^2 \\ &= 0.5 \cdot \sum_{k=1}^8 (\bar{y}_k - \bar{y})^2 \\ &= 0.0000801449 \\ se_{JRR}(\bar{y}) &= \sqrt{0.0000801449} = 0.008952. \end{aligned}$$

If only R replicate weights are provided with the data set, the JRR estimate of variance is the slightly simpler expression:

$$\begin{aligned} var_{JRR}(\hat{q}) &= \frac{R-1}{R} \sum_{r=1}^R (\hat{q}_r - \hat{q})^2 \\ df &= R-1. \end{aligned}$$

JRR Step 5: A $100(1-\alpha)\%$ CI for the population parameter is then constructed:

$$\begin{aligned} CI(q) &= \hat{q} \pm t_{1-\alpha/2, df} \sqrt{var_{JRR, JK}}(\hat{q}) \\ \text{e.g., } CI(\bar{y}) &= 0.47375 \pm t_{1-\alpha/2, 4} \cdot 0.008952 \\ &= 0.47375 \pm 2.7764 \cdot (0.008952) = (0.44890, 0.49860). \end{aligned}$$

Note that this variance estimation technique only requires the full sample weight and the R sets of *replicate weights* in order to perform the appropriate

variance estimation. This is what enables survey organizations concerned about protecting respondent confidentiality to produce public-use complex sample survey data sets that do not include stratum or cluster codes (which might be used, in theory, to identify a respondent), and only include the required weight variables for estimation of population parameters and replicated variance estimation. In contrast, stratum and cluster codes would be required to estimate variances using TSL.

3.6.3.2 Balanced Repeated Replication

The BRR method of variance estimation is a “half-sample” method that was developed specifically for estimating sampling variances under two PSU-per-stratum sample designs. The 2011–2012 NHANES, NCS-R, and 2012 HRS data sets used in the example analyses described in this book employ such a sampling error calculation model (Section 4.3), with two PSUs (clusters) per stratum. The evolution of the BRR method began with the concept of forming replicates by choosing one-half of the sample. For a complex sample design with $h = 1, \dots, H$ strata and exactly $a_h = 2$ PSUs per stratum, a *half-sample replicate* could be formed by choosing one of the two PSUs from each stratum (e.g., in [Figure 3.4](#), choose PSU 1 in strata 1, 2, and 3 and PSU 2 in stratum 4). By default, this choice of one PSU per stratum would define a *half-sample complement* (e.g., PSU 2 in strata 1, 2, and 3 and PSU 1 in stratum 4). For H strata and two PSUs per stratum, there are 2^H possible different half samples that could be formed—a total of 16 for the simple sample in [Figure 3.4](#), and 4,398,000,000,000 for the $H = 42$ strata in the NCS-R design. Since a complex sample design with H strata and two PSUs per stratum provides only H degrees of freedom for variance estimation, the formation of $R > H$ half-sample replicates will not yield additional gains in efficiency for a replicated half-sample variance estimate.

BRR variance estimation proceeds using the following five steps:

BRR Step 1: So what is the optimal procedure for selecting which half-sample replicates to employ in the variance estimation? McCarthy (1969) introduced the concept of BRR in which individual replicates are formed according to a pattern of “+” and “–” symbols that are found in the columns of a *Hadamard matrix*. The optimal efficiency of the BRR method for variance estimation based on half samples is due to its “balancing”—that is, complete algebraic cancellation of unwanted between-stratum cross-product terms, for example, $(y_{h1} - y_{h2}) \cdot (y_{g1} - y_{g2})$, that enter the half-sample variance computation formula. Readers interested in a more complete mathematical development of this idea are referred to Wolter (2007).

Fortunately, contemporary software for survey data analysis makes it easy to apply the BRR variance estimation method. Using only sampling error stratum and cluster codes (Section 4.3.1) provided with the survey data set, the software will invoke the correct form of the Hadamard matrix to

BRR rep	Stratum (h)			
	1	2	3	4
1	+	+	+	-
2	+	-	-	-
3	-	-	+	-
4	-	+	-	-

FIGURE 3.6

Example Hadamard matrix used to define BRR replicates for an $H = 4$ stratum design.

construct the sample replicates. [Figure 3.6](#) illustrates the 4×4 Hadamard matrix that can be used to define BRR replicates for the 4-strata sample design in [Figure 3.4](#). Each row of the matrix defines one BRR replicate. For BRR replicate 1, the “+” sign in the columns for Strata 1, 2, and 3 indicates that the first PSU in the stratum is assigned to the replicate. The “–” sign in the Stratum 4 column indicates the second PSU is to be included in replicate 1. Likewise, BRR replicate 2 will include PSU 1 from stratum 1 and PSU 2 from strata 2, 3, and 4.

When a BRR half-sample replicate is created by choosing one PSU from each stratum, a “complementary” half sample is also created from the unchosen paired PSUs in each stratum. There are several BRR variance estimation formulae that utilize both the BRR half samples and their complementary half samples to estimate variance (Rust, 1985). A special case of BRR that utilizes replicate sample estimates from both the original half samples and their complements is Fay’s method (see below). [Figure 3.7](#) illustrates the form of the first BRR replicate for the [Figure 3.4](#) data set.

Hadamard matrices are defined only for dimensions that are multiples of four. Whenever the number of primary strata defined for a complex sample design is a multiple of four, exactly H BRR replicates are defined according to the patterns of “+/-” indicators in the rows and columns of the $H \times H$ Hadamard matrix. The corresponding BRR variance estimates are said to be *fully balanced*. If the number of primary strata in the complex sample design is not a multiple of four, the Hadamard matrix of dimension equal to the next multiple of four greater than H is used, and any additional columns beyond H are dropped. For example, a Hadamard matrix of dimension 44×44 is used to define the 44 half-sample replicates for the NCS-R which has $H = 42$ strata for variance estimation, and the final two columns of this matrix are dropped. In such cases, the corresponding BRR variance estimates are said to be *partially balanced*.

BRR Step 2: A new replicate weight is then created for each of the $h = 1, \dots, H$ BRR half-sample replicates created in Step 1. Replicate weight values for cases in the complement half-sample PSUs are assigned a value of “0” or “missing.” The replicate weight values for the cases in the PSUs retained in the half sample are formed by multiplying the full sample analysis weights by a factor of 2.

Stratum	PSU (cluster)	Case	y_i	$w_{i,rep}$
1	1	1	0.58	1×2
	1	2	0.48	2×2
1	2	1	0.00	0
	2	2	0.00	0
2	1	1	0.39	1×2
	1	2	0.46	2×2
2	2	1	0.00	0
	2	2	0.00	0
3	1	1	0.39	1×2
	1	2	0.47	2×2
3	2	1	0.00	0
	2	2	0.00	0
4	1	1	0.00	0
	1	2	0.00	0
4	2	1	0.47	2×2
	2	2	0.50	2×2

FIGURE 3.7

Illustration of BRR replicate 1 for the example data set.

BRR Step 3: Following the same procedure outlined for JRR and using the replicate weights developed for each BRR replicate sample, the weighted replicate estimates of the population statistic are computed. The full sample estimate of the population statistic is also computed:

$$\hat{q}_r = \bar{y}_r = \frac{\sum_{i \in rep}^{n_{rep}} y_i \cdot w_{i,rep}}{\sum_{i \in rep}^{n_{rep}} w_{i,rep}};$$

$$\hat{q}_1 = 0.4708; \quad \hat{q}_2 = 0.4633; \quad \hat{q}_3 = 0.4614; \quad \hat{q}_4 = 0.4692;$$

$$\bar{y}_w = \hat{q} = \frac{\sum_{i=1}^n y_i \cdot w_i}{\sum_{i=1}^n w_i} = 0.4737.$$

BRR Step 4: The BRR estimate of sampling variance of the sample estimate is estimated using one of several simple formulae. Here, we illustrate the computation using one of the more common half-sample variance estimation formulae:

$$\begin{aligned}
var_{BRR}(\bar{y}_w) &= var_{BRR}(\hat{q}) = \frac{1}{R} \sum_{r=1}^R (\hat{q}_r - \hat{q})^2 \\
&= \frac{1}{4} \sum_{r=1}^4 (\bar{y}_r - \bar{y})^2 \\
&= 0.00007248 \\
se_{BRR}(\bar{y}_w) &= \sqrt{0.0000748} = 0.008515.
\end{aligned}$$

Several software packages such as WesVar® PC permit users to choose alternative half-sample variance estimation formulae including a method proposed by Fay (Judkins, 1990). Interested users are referred to Rust (1985) or Wolter (2007) for more information on alternative half-sample variance estimation formulae.

BRR Step 5: A $100(1 - \alpha)\%$ CI for the population parameter is then constructed (recall that in the case of BRR, $df = H$):

$$\begin{aligned}
CI(q) &= \hat{q} \pm t_{1-\alpha/2, df} \sqrt{var_{BRR}(\hat{q})} \\
\text{e.g., } CI(\bar{y}) &= 0.4737 \pm t_{1-\alpha/2, 4} \cdot 0.008515 \\
&= 0.4737 \pm 2.7764 \cdot (0.008515) = (0.45011, 0.49739).
\end{aligned}$$

3.6.3.3 Fay's BRR Method

As noted above, the literature on BRR variance estimation for complex sample survey data includes a number of alternatives to the estimators presented in Step 4 above. One alternative that deserves mention is Fay's BRR method. Each Fay BRR replicate "blends" PSU contributions from the $a(h) = 2$ PSUs in each stratum using a Fay factor or coefficient (ε) with $0 < \varepsilon < 1$. If element $(r = \text{replicate}, h = \text{stratum})$ of the Hadamard matrix equals "+," then the survey weight for cases in the second PSU is multiplied by the ε factor and the survey weight for the first PSU in stratum h is multiplied by $(2 - \varepsilon)$ to form the replicate weight for replicate $r = 1, \dots, R$. If element (r, h) of the Hadamard matrix equals "-", the scaling is reversed. Weights for cases in the second PSU in stratum h are multiplied by $(2 - \varepsilon)$ and those in the first PSU by ε to form the r -th replicate weight.

The replicated variance estimator for BRR replicates that are formed using the Fay factor in this fashion is:

$$var_{BRR,FAY}(\hat{q}) = \frac{1}{R \cdot (1 - \varepsilon)^2} \sum_{r=1}^R (\hat{q}_r - \hat{q})^2.$$

Note that if the Fay factor, ε , is set to zero, this expression reduces to the standard BRR variance estimator in Step 4 above. In practice, Fay factors in the range of $\varepsilon = (0.3 \text{ to } 0.5)$ have been shown to work well (Judkins, 1990; Valliant et al., 2013).

All of the major software systems for the analysis of complex sample survey data now support BRR estimation of variances, including the optional Fay method.

3.6.3.4 Bootstrap (Rao–Wu Rescaling Bootstrap)

Next, we consider the five steps involved in estimating variance using a popular variation of the bootstrap technique for complex sample survey data known as the Rao–Wu Rescaling Bootstrap.

Bootstrap Step 1: The Rao–Wu Rescaling Bootstrap (Rao et al., 1992) forms $b = 1, \dots, B$ bootstrap replicates by sampling with replacement (SWR) m_h PSUs from each of the $h = 1, \dots, H$ primary stage strata. Rust and Rao (1996) recommend setting $m_h = a_h - 1$ (one less than the number of sample PSUs in stratum h). In the example that we consider here, a total of $B = 100$ bootstrap samples is selected from the data displayed in [Figure 3.4](#).

Bootstrap Step 2: For $m_h = a_h - 1$, the bootstrap weight for the each of the B selected replicates is:

$$w_{h\alpha i}^{(b)} = w_{h\alpha i} \cdot \frac{a_h}{(a_h - 1)} \cdot r_{h\alpha i}^{(b)};$$

where $r_{h\alpha i}^{(b)}$ = the number of times PSU α is selected in replicate b .

Bootstrap Step 3: Using the replicate weights developed for each bootstrap replicate sample, the weighted replicate estimates of the population statistic are computed. The full sample estimate of the population statistic is also estimated:

$$\hat{q}_{(b)} = \bar{y}_r = \frac{\sum_{i \in rep}^{n_{rep}} y_i \cdot w_{i,rep}}{\sum_{i \in rep}^{n_{rep}} w_{i,rep}}; \quad \hat{q}_{(b)} \in (0.4620, \dots, 0.4900)$$

$$\bar{y}_w = \hat{q} = \frac{\sum_{i=1}^n y_i \cdot w_i}{\sum_{i=1}^n w_i} = 0.4737.$$

Bootstrap Step 4: The variance estimate based on the $b = 1, \dots, B$ bootstrap estimates is the Monte Carlo approximation:

$$\begin{aligned} var_{Boot}(\hat{q}) &= \frac{1}{B} \sum_{r=1}^B (\hat{q}_{(b)} - \bar{q})^2 \\ var_{Boot}(\bar{y}_w) &= \frac{1}{100} \sum_{b=1}^{100} (\bar{y}_{(b)} - \bar{y})^2 \\ &= 0.0000844 \\ se_{Boot}(\bar{y}_w) &= \sqrt{0.0000844} = 0.0091865. \end{aligned}$$

Bootstrap Step 5: Symmetric CIs can be constructed based on bootstrap estimates of the standard error:

$$\begin{aligned} CI(q) &= \hat{q} \pm t_{1-\alpha/2, df} \sqrt{var_{Boot}(\hat{q})} \\ \text{e.g., } CI(\bar{y}) &= 0.4737 \pm z_{1-\alpha/2} \cdot 0.0092 \\ &= 0.4737 \pm 1.9600 \cdot (0.0092) = (0.4557, 0.4918). \end{aligned}$$

For large numbers of bootstrap replicates (e.g., $b > 1000$), a histogram of the bootstrap replicates simulates the sampling distribution of the estimator. The bootstrap “simulation” of the sampling distribution may be used to examine the asymptotic normality assumption or used directly to derive asymmetric CIs for population values. See Kolenikov (2010) for additional discussion of these ideas.

Rao (2016) has recently proposed a general framework for hypothesis testing with complex samples that relies on bootstrap replicates to approximate the distribution of a given *test statistic* (e.g., the Rao–Scott chi-square test statistic; [Chapter 6](#)) under a null hypothesis. Given this approximate distribution of the test statistic under a null hypothesis (based on the bootstrap replicates), one would reject the null hypothesis if the weighted test statistic based on the full sample exceeds some critical value based on the approximated distribution.

3.6.3.5 Construction of Replicate Weights for Replicated Variance Estimation

At the foundation of replicate methods of variance estimation for complex samples is the concept that each JRR, BRR, or bootstrap replicate is itself a weighted replication of the full sample design. As a default, most replicated variance estimation software requires the analyst to supply the stratum codes, cluster codes, and full sample weights that are needed to define the sample replicates and compute replicate weights. Under this default, replicate sample adjustments are applied to the full sample weight; postselection

weighting adjustments for nonresponse or poststratification are *not* recomputed based only on the replicate samples. In theory, to capture the true variability introduced by these added weighting steps and minimize bias for estimated variances, these postsurvey weighting adjustment steps should be repeated for each replicate sample (Rust and Rao, 1996). Since replicate reweighting for nonresponse or poststratification requires detailed and possibly confidential data (e.g., detailed characteristics of respondents and nonrespondents) that is not generally available to public data users, the reweighting process must be typically performed by the data producer and the resulting replicate weights must be released with the data set.

But what should an analyst do if the data producer does not supply replicate weights and only the stratum codes, cluster codes, and full sample weights are available? Analytically, it is impossible to accurately determine when replicate reweighting will make a significant difference in reducing the bias in replicated variance estimates. A substantial amount of empirical evaluation based on large household survey data sets has found that replicate reweighting for nonresponse and poststratification produces few significant changes in estimated variances (Saavedra and Harding, 2009; Chowdhury, 2014), and that any bias associated with using only the full sample weight in replicate weighting will not result in serious bias. The absence of major differences in these and other empirical examples should not be taken as evidence that recomputation of weighting adjustments for replicate samples does not improve the accuracy of complex sample variance estimates for survey statistics. In complex sample designs for populations such as school students and businesses where extensive population data can be used effectively to achieve large poststratification gains, reweighted replicate creation on the part of the data producer will ensure that those gains are reflected in the variance estimates.

3.6.4 Example Comparing Results from the TSL, JRR, BRR, and Bootstrap Methods

The previous sections have presented simple illustrations of the TSL, JRR, BRR, and bootstrap variance calculations based on the example data set in [Figure 3.4](#). While these simple example calculations point out that estimated standard errors for the four calculation methods may in fact differ, these differences are magnified by the small sample size of the example data set. In this section, we present a more realistic comparison based on the NCS-R survey data set.

A number of empirical and simulation-based studies have compared the properties of the TSL, JRR, and BRR methods of variance estimation for complex sample designs, including Kish and Frankel (1974), Kovar et al. (1988), Valliant (1990), and Rao and Wu (1985). Across a range of estimators and sample designs, these studies have shown few important differences in the results obtained using these three methods. The methods are unbiased and produce identical results in the special case where the estimator of interest

is a linear statistic such as a weighted sample total. For nonlinear estimators commonly employed in survey analysis (e.g., regression coefficients), the TSL and JRR methods tend to have slightly lower bias (smaller mean square error [MSE]) for the estimates of sampling variance. However, CIs constructed using BRR or bootstrap estimates of standard errors provide better nominal coverage (e.g., 95 in 100 for a 95% CI) of the true population value. For non-smooth functions of the sample data (e.g., sample quantiles), linearization cannot be applied directly (due to the need for smooth, continuous functions to compute derivatives), and the JRR method is known to result in biased estimates of the variance. As a result, BRR is often used in these situations to estimate variances (Chapter 5).

Tables 3.2 and 3.3 present the results of simple analyses of the HRS Wave 1 (1992) data that illustrate the general equivalency of the TSL, JRR, BRR, and bootstrap methods for sampling variance estimation. The methods comparison includes estimates of the statistic/parameter of interest (identical for all methods) and standard errors of estimates computed using seven methods: (1) SRS; (2–3) WesVar (W) BRR and JRR estimates computed using replicate weights that incorporate HRS nonresponse and poststratification adjustments specific to each replicate sample; (4–6) TSL, JRR, and BRR estimates computed in Stata/SAS (S) using only replication based on the full sample weight; and (7) bootstrap estimates from the *survey* package in R that also use only the full sample weight to derive bootstrap weights.

The analysis summarized in Table 3.2 focuses on three descriptive estimates of characteristics of the HRS Wave 1 survey population: (1) mean years of schooling completed; (2) body weight in pounds; and (3) number (out of 10) of words recalled in a test of memory. Table 3.3 presents the estimated coefficients and comparative standard errors for the parameters of a linear regression of the number of words recalled measure on respondent gender, race/ethnicity, and years of schooling.

Since each method employs the same overall weighted estimate, the point estimates of the population statistics (Table 3.2) or regression parameters (Table 3.3) are identical under the TSL, JRR, BRR, and bootstrap methods. We also see clear evidence of design effects, as the TSL, JRR, BRR, and bootstrap variance estimates are each larger than the variance estimates assuming SRS. To two decimal places, estimated standard errors are virtually identical under the TSL, JRR, BRR, and bootstrap methods and any differences in the third decimal place are sufficiently small that they would be negligible in any practical survey analysis setting. Furthermore, comparison of the BRR and JRR estimates with replicate-specific adjustments for nonresponse to those that use only the full sample weight shows few important trends or differences in the two series of standard error estimates. As discussed in Section 3.6.3.5, the absence of major differences in this empirical example should not be taken as evidence that recomputation of weighting adjustments for replicate samples does not improve the accuracy of complex sample variance estimates for survey statistics.

TABLE 3.2
 Comparison of the TSL, JRR, BRR, and Bootstrap Variance Estimation Methods for the Estimation of Descriptive Population Parameters

Statistic	<i>n</i>	Estimated				Standard Error by Method		
		SRS	W-BRR	W-JRR	S-TSL	S-BRR	S-JRR	R-Boot
Years of school	9,759	12.31	0.031	0.078	0.077	0.077	0.077	0.076
Body weight (lbs)	9,759	172.35	0.374	0.447	0.432	0.435	0.434	0.404
Words recalled	9,759	7.57	0.028	0.064	0.064	0.066	0.066	0.067

Source: 1992 HRS.

TABLE 3.3

Comparison of the TSL, JRR, BRR, and Bootstrap Variance Estimation Methods for the Estimation of a Linear Regression Model for Number of Words Recalled

Coefficient	$\hat{\beta}$	Standard Error by Method						
		SRS	W-BRR	W-JRR	S-TSL	S-BRR	S-JRR	R-Boot
Intercept	4.88	0.120	0.170	0.170	0.166	0.170	0.166	0.178
Male	-0.93	0.052	0.063	0.065	0.064	0.064	0.064	0.061
Black	-1.24	0.084	0.089	0.091	0.093	0.094	0.093	0.096
Hispanic	-0.51	0.107	0.140	0.143	0.141	0.141	0.141	0.139
School years	0.27	0.009	0.011	0.012	0.011	0.011	0.011	0.012

Source: 1992 HRS.

3.7 Hypothesis Testing in Survey Data Analysis

Throughout this book, we will emphasize the use of CIs as the basis for making inferences concerning the population value of a descriptive statistic or to display the uncertainty associated with model-based estimates of the relationship of a covariate with a dependent variable. However, inference in the analysis of complex sample survey data is not limited to the construction of CIs for population parameters.

While we advise caution in using p -values to establish a “bright line” demarcation between significant and nonsignificant findings (Nuzzo, 2014), complex sample survey data may also be used to derive familiar test statistics (t , χ^2 , F) for formal hypothesis tests of the form: $H_0: \theta = \theta_0$ versus $H_A: \theta \neq \theta_0$. In fact, as the discussion in Section 3.5.1 pointed out, the Student t -test statistic is the *pivotal statistic* from which the expression for the $100(1 - \alpha)\%$ CI is derived. Table 3.4 compares the test statistics and hypothesis testing approaches for SRS (or independently and identically distributed) data to the modified approaches that have been developed for complex sample survey data.

Simple Student t -tests based on single weighted estimates of means, proportions, regression coefficients, and differences or linear combinations of these statistics incorporate the complex sample design by using correct standard errors in the computation of the test statistic. To test the null hypothesis, the test statistic is referred to a Student t distribution with degrees of freedom adjusted for the complex sample design. Chapter 5 will describe design-adjusted Student t -tests for means, proportions, differences of means and proportions, subpopulation estimates, and general linear combinations of estimates. Design-adjusted t -tests for single parameters in linear regression or GLMs are addressed in Chapters 7 through 9.

For tests of association between two cross-classified categorical variables, the standard Pearson X^2 , Likelihood Ratio G^2 , and Wald X^2 are replaced by design-adjusted forms of these traditional test statistics. Like their SRS

TABLE 3.4

Comparisons of Hypothesis Testing Procedures for Simple Random Sample Data versus Complex Sample Survey Data

Simple Random Sample (iid) Data	Complex Sample Survey Data
Student t -tests of hypotheses ($H_0 \mid H_A$) for means, proportions, single model parameters; for example, $\bar{Y} = \bar{Y}_0; \beta_j = 0$	Design-adjusted Student t -test <ul style="list-style-type: none"> • Correct standard error in denominator • Design-adjusted degrees of freedom
Student t -tests of simple hypotheses concerning differences of linear combinations of means; for example, $(\bar{Y}_1 - \bar{Y}_2) = 0; \sum_j a_j P_j = 0$	Design-adjusted Student t -test <ul style="list-style-type: none"> • Correct standard error in denominator reflecting separate estimates of variance and covariance of component estimates • Design-adjusted degrees of freedom
X^2 test of independence (association) in bivariate and multiway tables: <ul style="list-style-type: none"> • Pearson X^2, Likelihood Ratio G^2 	Design-adjusted X^2 and F -tests <ul style="list-style-type: none"> • Rao–Scott first- and second-order corrections adjust for design effects in $\hat{\Sigma}(p)$ • X^2 transformed to F-test statistic
Full and partial F -tests for hypotheses for linear regression model goodness of fit and full versus reduced model, for example, $H_0: \beta = \{\beta_1, \beta_2, \dots, \beta_p\} = 0$; $H_0: \beta_{(q)} = \{\beta_{p-q}, \dots, \beta_p\} = 0$.	Design-adjusted Wald X^2 or F -test <ul style="list-style-type: none"> • Correct $\hat{\Sigma}(\hat{\beta})$ under complex design • Adjusted degrees of freedom
F -tests based on expected mean squares for ANOVA-type linear models	Linear regression parameterization of the ANOVA model. Design-adjusted Wald X^2 or F -tests as in linear regression above
Likelihood Ratio X^2 tests for maximum likelihood estimates of parameters in generalized linear models, for example, $H_{0,MLE}: \beta = \{\beta_1, \beta_2, \dots, \beta_p\} = 0$; $H_{0,MLE}: \beta_{(q)} = \{\beta_{p-q}, \dots, \beta_p\} = 0$.	Design-adjusted Wald X^2 or F -test <ul style="list-style-type: none"> • Correct $\hat{\Sigma}(\hat{\beta})$ under complex design • Adjusted degrees of freedom
	Design-adjusted likelihood ratio test (Lumley and Scott, 2014)

counterparts, under the null hypothesis, the Rao–Scott “adjusted” X^2 and G^2 statistics and the adjusted Wald X^2 (computed with a design-based variance–covariance matrix) are expected to follow a central chi-square distribution. Software packages offer the user the option of using the standard χ^2 version of each test statistic or a modified version that under H_0 is referred to an F distribution. More details on these design-adjusted tests of association for cross-classified data with accompanying examples are provided in [Chapter 6](#).

F -tests are used in standard normal linear regression to test the overall fit of the model as well as to perform joint tests concerning the significance of subsets of the model parameters: for example, $H_0: \beta = \{\beta_1, \beta_2, \dots, \beta_p\} = \mathbf{0}$; $H_0: \beta_{(q)} = \{\beta_{p-q}, \dots, \beta_p\} = \mathbf{0}$. In the analysis of complex sample survey data, these conventional F -tests are replaced with a Wald X^2 test statistic that is provided both as a chi-square test and as a transformed F -test statistic. [Chapter 7](#) addresses the use of the Wald test statistic for joint hypothesis tests involving multiple parameters in estimated linear regression models.

Standard approaches to analyses involving GLMs (e.g., logistic, probit, and Poisson regression models) typically employ maximum likelihood methods to estimate parameters and standard errors. Tests of hypotheses concerning the significance of a nested subset of the full vector of model parameters, that is, $H_0: \beta_{(q)} = \{\beta_{p-q}, \dots, \beta_p\} = \mathbf{0}$, are therefore performed using the standard *likelihood ratio test (LRT)*. When GLMs are fitted to complex sample survey data, multiparameter tests of this type are generally conducted using a design-adjusted Wald X^2 or F statistic. More recently, Lumley and Scott (2014) have outlined design-adjusted versions of LRTs as well. These design-adjusted tests for GLM analyses are described in more detail in [Chapters 8 and 9](#).

3.8 TSE and Its Impact on Survey Estimation and Inference

Probability sampling provides a theoretical basis for unbiased estimation of population parameters and the associated sampling variance of the sample estimates. However, a successful scientific survey depends not only on control of sampling variances but also on other sources of error. The collection of all sources of error that can influence the precision and accuracy of survey estimates of population parameters is termed *TSE* (Lessler and Kalsbeek, 1992; Groves, 2004). The TSE for a survey estimate is measured as the MSE, $\text{Mean Square Error} = \text{Variance} + \text{Bias}^2$, or the variance of the estimate plus the square of the bias in the sample estimate. [Table 3.5](#) provides a typical taxonomy of survey errors.

3.8.1 Variable Errors

The sources of error that cause sample estimates to disperse randomly about the true and unknown population value of interest across replications of the survey process are termed *variable errors*.

Sampling variances or standard errors that have been described at length in the preceding sections derive from the statistical fact that only a subset of the full target population is observed in any given sample. As sample sizes increase, the sampling variance decreases and disappears entirely if a

TABLE 3.5
A Taxonomy of Survey Errors

Variable Errors	Biases
Sampling variance	Sample selection bias
Interviewer variance	Frame coverage bias
Response (measurement) variance	Measurement bias
Coding variance	Nonresponse bias

complete census of the target population is conducted. Probability sampling theory provides well-defined guidance for estimating sampling variances for survey estimates.

Interviewer variance and *response variance* (Fuller, 1987; Groves, 2004) enter the data during the actual interview, and may be attributed to random inaccuracies in the way that interviewers ask survey questions or record the survey answers (see West and Blom, 2016 for a recent review of the literature explaining interviewer effects), or the way that the respondents report the responses. In scientific surveys, interviewer and response variance is minimized by carefully training interviewers and designing and pretesting questions so that they are clearly worded and have comprehensive, easy-to-interpret response categories. Readers interested in an in-depth treatment of interviewer variance and other measurement errors are referred to Biemer et al. (1991).

Coding variance is primarily a technical source of random error in the data set. Research staff responsible for coding the survey data and transcribing the information to a computer file for analysis may make errors in a random manner. As the technology for computer-assisted interviewing and data collection has advanced, this source of error has been reduced.

Each of these sources of variance—sampling, interviewer, response, and coding—contributes to the combined total variability in observed survey data. Short of conducting elaborate experiments, it will not be possible for the data producer, let alone the survey analyst, to decompose the total variance of a survey estimate into components attributable to each of these sources. Nevertheless, it is important to note that the combined influences of these multiple sources of variability will all be captured in the estimated standard errors that are computed from the survey data.

3.8.2 Biases in Survey Data

The English word *bias* has many meanings, but in a statistical context it refers to the tendency of a statistical estimate to deviate systematically from the true value it is intended to estimate across replications of the survey process. Students of statistics, including survey researchers, have long been taught that “unbiasedness”—the absence of bias—is one of the most desirable properties of a statistical estimator or procedure. In survey practice, bias should certainly be avoided; however, elimination of all sources of bias in survey data is probably neither practical nor even efficient when both the costs and benefits of reducing bias are considered. In fact, survey analysts tend to be less interested in purely unbiased estimators and more interested in estimators that have the property of being a *consistent estimator* of the population parameter of interest. *Consistent estimators* converge to the true population value as the sample size n increases to the population size N . Survey biases listed in the survey error taxonomy given in [Table 3.5](#) may be collapsed into two major types: *sampling bias* and *nonsampling bias* (Kish, 1965).

In probability samples, the greatest potential for *sampling bias* can be attributed to noncoverage of survey population elements. *Sample frame noncoverage* occurs when population elements are systematically excluded from the population registry or the data sources (maps and census counts) used to develop area probability frames and therefore have no probability of being included in the sample. Sample noncoverage bias may also occur in the process of screening selected dwelling units to identify and select eligible survey respondents. Survey producers minimize sampling bias through careful design and attention to detail in the sample selection process, field testing of screening and respondent selection procedures prior to the data collection period, and rigorous training and on-site supervision of the field staff for the actual survey data collection. After the survey is complete, poststratification weighting may be employed to attenuate any remaining sample bias in the survey data.

Survey data are also vulnerable to *nonsampling bias* from two primary sources: *measurement bias*, or systematic bias in the way respondents interpret and respond to questions, and *survey nonresponse*. Measurement bias may be deliberate on the part of the respondent or it may be the unconscious result of poor questionnaire construction or interviewer training. Survey respondents who are asked to report their household income may underreport or fail to mention sources of income such as the sale of a parcel of land. Survey questions that ask about participation in elections, educational activities, or religious observances may be subject to overreporting of participation, a phenomenon termed "social desirability" bias. Poorly worded or "leading" questions or questionnaires that place questions out of context may yield biased measures for the constructs in which the research investigator is truly interested. Across disciplinary areas, survey methodologists work very hard to understand the survey measurement process, and to design questions and questionnaire formats that accurately measure the underlying constructs of interest.

Survey nonresponse is another potential source of bias in sample-based estimates of population characteristics. The failure to obtain any data on a sample household or individual is termed *unit nonresponse*. A missing response to one or more individual variable items in an otherwise complete interview questionnaire is termed *item nonresponse* (Little and Rubin, 2002). Nonresponse to voluntary surveys including those conducted by universities and other scientific research organizations has become a major problem in countries in Western Europe and North America. Nonresponse bias in survey estimates of simple statistics such as population means or proportions is a function of the response rate and the difference in the values of the statistic for responding and nonresponding members of the sample. For estimates of a population proportion, for example, the nonresponse bias can be expressed using the following formula:

$$\text{Bias}_{NR}(p) = (1 - R\text{Rate}) \times (p_R - p_{NR}). \quad (3.13)$$

In Equation 3.13, $RRate$ is the expected value of the population response rate, p_R is the value of the proportion for respondents, and p_{NR} is the value of the proportion for nonrespondents. The absolute value of the expected nonresponse bias increases with the product of nonresponse rate and the difference in p for respondents and nonrespondents. If the response rate is high or proportions for respondents and nonrespondents do not differ, the nonresponse bias will be very small. Unlike sampling variance, which decreases as sample size increases, nonresponse bias is persistent. Its expected value is not a function of sample size but remains unchanged regardless of how large or small the size of the survey sample.

The potential impact of nonresponse bias on the analysis of survey data may be best illustrated through a simple example. Assume a researcher is interested in studying parents' views on the need for increased government spending (hence potential increases in taxes) for elementary science education. Among parents who agree to participate in the survey, the expected proportion that supports increased spending on elementary science education is $p_R = 0.6$, while for noncooperating parents $p_{NR} = 0.4$ —a major difference between respondents and nonrespondents. If only 50% of the original random sample of $n = 1000$ parents agreed to participate, the expected nonresponse bias for the proportion of interest would be:

$$Bias_{NR}(\hat{p}) = (1 - RR) \times (p_R - p_{NR}) = (1 - .5) \times (.6 - .4) = 0.10.$$

Assuming for simplicity that the original sample of parents was selected using SRS, the researcher would develop the following 95% CI for this estimate:

$$\hat{p}_R \pm 1.96 \cdot [\hat{p} \cdot (1 - \hat{p})/(n)]^{1/2} \equiv \hat{p}_R \pm 1.96 \cdot [0.6(1 - 0.6)/(0.5 \cdot 1000)]^{1/2} = \hat{p}_R \pm 0.043.$$

In this case, the size of the expected nonresponse bias is relatively large in comparison to the size of the 95% CI half width—a result of the low response rate and the major difference in expected proportions for respondent and nonrespondent cases.

The purpose of this example is not to magnify the potential seriousness of nonresponse bias in survey estimation—high response rates and/or smaller differences in the expected statistics for respondents and nonrespondents would decrease the size of the expected bias. Some recent research has suggested that we may be overly concerned about the seriousness of nonresponse bias for certain types of survey measures, and especially measures of respondent attitudes and expectations (Curtin et al., 2000; Keeter et al., 2000). However, the example makes the point that we cannot be complacent and ignore the potential for nonresponse bias in the survey estimation process.

As described in Section 2.7, detailed data on respondents and nonrespondents and a model for the nonresponse mechanism are used to develop nonresponse adjustments to the survey analysis weights in actual survey practice. To the extent that the estimated model accurately describes the underlying nonresponse process, these adjustments to the analysis weight serve to attenuate potential nonresponse bias and its impact on estimates and the corresponding inference that the analyst draws from the survey data.



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4

Preparation for Complex Sample Survey Data Analysis

4.1 Introduction

This chapter guides the survey analyst through a sequence of steps that are important to properly prepare for the analysis of a complex sample survey data set. The steps in this chapter should only be considered *after* steps 1 and 2 in [Chapter 1](#) (defining the research problem, stating the research objectives, and understanding the sample design). These steps include reviewing the weights and the sampling error calculation model for the survey data set, examining the amount of missing data for key variables, and preparing for the analysis of sample subclasses. The chapter concludes with a short checklist to remind the reader of these critical preliminary steps.

We remind readers about two important terms. The term *data producer* applies to the statistical agency or the research team that is responsible (with the assistance of survey statisticians) for designing a probability sample from a larger population, collecting the survey data, developing survey weights, and producing information about the complex sample design that can be used by research analysts for statistical analysis of the data. For example, the National Center for Health Statistics (NCHS) along with its contractor, Westat, Inc., was responsible for producing the 2011–2012 National Health and Nutrition Examination Survey (NHANES) data that is analyzed throughout this book. The term *data user* is applied to the survey analyst or researcher who will use the survey data to develop and test scientific hypotheses concerning the survey population.

In most cases, the data producer has access to far more detailed information about the complex sample design and personal information concerning study respondents than the data user. To maintain confidentiality for survey respondents and minimize *disclosure risk*, the data producer is responsible for making optimal use of detailed and often confidential information on the individual sample cases to develop sampling error codes and final survey weights for the survey data set. In addition, the data producer is responsible for providing the data user with a cleaned data set, a codebook for the survey variables and technical documentation describing the sample and survey

procedures. Many survey programs are now providing data users with a guide for statistical analysis of their survey data set. For example, NCHS provides analytic guidelines online* that include detailed instructions for how to correctly analyze the NHANES data sets.

4.2 Final Survey Weights: Review by the Data User

Experience as survey statisticians and consultants has taught us that many survey data analysts struggle with the correct use of final survey weights in survey estimation and inference. For whatever reason, many otherwise sophisticated data users wish to place a “black box” around the process of weight development and the application of weights in their analysis. As described in Section 2.7, the final survey weights provided in survey data sets are generally the product of a sample selection weight (w_{sel}), a nonresponse adjustment factor (w_{nr}), and a poststratification factor (w_{ps}): $w_{final,i} = w_{sel,i} \cdot w_{nr,i} \cdot w_{ps,i}$. For the reasons outlined above, the data producer is responsible for developing individual weights for each sample case and linking the final survey weight variable to each observational unit in the survey data file.

The final survey weight assigned to each survey respondent is a measure of the number of population members represented by that respondent, or alternatively, the relative share of the population that the respondent represents. When weights are applied in the statistical analysis of survey data, weighted calculations simply expand each respondent’s contribution to reflect its representative share of the target population. Because the process of weight development has been discussed extensively in Section 2.7, the aim of this section is to remove any remaining mystique surrounding the weights that are provided with a survey data set.

Although data analysts will not typically be responsible for the actual weight calculations, they should familiarize themselves with the survey weight variable(s) and how weighted analysis may influence estimation and inference from their survey data. Key steps in this process of verification and familiarization include:

- Verifying the variable name for the appropriate weight for the intended analysis
- Checking and reviewing the scaling and general distribution of the weights
- Evaluating the impact of the weights on key survey statistics

The subsequent sections describe these three activities in more detail.

* http://www.cdc.gov/nchs/data/series/sr_02/sr02_161.pdf

4.2.1 Identification of the Correct Weight Variable(s) for the Analysis

The data user will need to refer to the survey documentation (technical report, codebook, analytic guidelines, etc.) to identify the correct variable name for the final survey weight. Unfortunately, there are no standard naming conventions for weight variables, and we recommend great caution in this step as a result. A number of years ago, a student mistakenly chose a variable labeled WEIGHT and produced a wonderful paper based on the NHANES data in which each case was weighted by their body weight in kilograms. The correct survey weight variable in the student's data file was stored under a different, less obvious variable label.

Depending on the variables to be analyzed, there may be more than one weight variable provided with the survey data set. The 2012 Health and Retirement Study (HRS) data set includes one weight variable (NWGTHH) for the analysis of financial unit (single adult or couple) variables, such as home value or total net worth, and a separate weight variable (NWGTR) for individual-level analysis of variables such as health status or earnings from a job. The 2011–2012 NHANES documentation instructs analysts to use the weight variable WTINT2YR for analyses of the medical history interview variables and another weight variable (WTMEC2YR) for analyses of data collected from the medical examination phase of the study. The larger sample of National Comorbidity Survey Replication (NCS-R) Part I mental health screening data ($n = 9,282$) is to be analyzed using one weight variable (NCSRWTSH), while another weight variable (NCSRWTLG) is the correct weight for analyses involving variables measured only for the in-depth Part II subsample ($n = 5,692$). Finally, the European Social Survey (ESS) Round 6 Russian Federation data set includes the “design weight” variable DWEIGHT and the “poststratification” weight variable PSPWGHT. We use the poststratified weight (PSPWGHT) for all analysis examples in this text.

Some public-use data sets may contain a large set of weight variables known as *replicate weights*. For example, the 1999–2000 NHANES public-use data file included the replicate weight variables WTMREP01, WTMREP02,..., WTMREP52. As mentioned in [Chapter 3](#), replicate weights are used in combination with software that employs a replicated method of variance estimation, such Balanced Repeated Replication (BRR), Jackknife Repeated Replication (JRR), or bootstrapping. When a public-use data set includes replicate weights, design variables for variance estimation (stratum and cluster codes) will generally *not* be included (Section 4.3), and the survey analyst needs to use the program syntax to specify the replicated variance estimation approach (BRR, JRR, BRR-Fay, etc.) and identify the sequence of variables that contain the replicate weight values (see Appendix A for more details on these software options).

4.2.2 Determining the Distribution and Scaling of the Weight Variable(s)

In everyday practice, it is always surprising to learn that an analyst who is struggling with the weighted analysis of survey data has never actually looked at the distribution of the weight variable. This is a critical step in preparing for analysis. Assessing a simple univariate distribution of the final survey weight variable provides information on: (1) the scaling of the weights; (2) the variability and skew in the distribution of weights across sample cases; (3) extreme weight values; and (4) (possibly) missing data on the survey weight. Scaling of the weights is important for interpreting estimates of totals and in older versions of software may affect variance estimates. The variance and distribution of the weights may influence the precision loss for sample estimates (Section 2.7). Extreme weights, especially when combined with outlier values for variables of interest, may produce instability in estimates and standard errors for complete sample or subclass estimates. Missing data or zero (0) values on weight variables may indicate an error in building the data set or a special feature of the data set. For example, 2011–2012 NHANES cases that completed the Medical History Interview but did not participate in the mobile examination center (MEC) phase of the study will have a positive, nonzero weight value for WTINT2YR but will have a zero value for WTMEC2YR ([Table 4.1](#)).

[Table 4.1](#) provides simple distributional summaries of the survey weight variables for the NCS-R, 2012 HRS, 2011–2012 NHANES, and ESS Russian Federation (Round 6) data sets. Inspection of these weight distributions quickly identifies that the scale of the weight values is quite different from one study to the next. For example, the sum of the NCS-R Part I weights is 9,282 (equal to the sample size), while the sum of the 2012 HRS individual weights is 90,698,760 (which would seem to approximate the size of the target HRS population).

With the exception of weighted estimates of population totals, weighted estimation of population parameters and standard errors should be invariant to a linear scaling of the weight values, that is, $w_{scale,i} = k \cdot w_{final,i}$, where k is an arbitrary constant. That is, the data producer may choose to multiply or divide the weight values by any constant and with the exception of estimates of population totals, weighted estimates of population parameters and their standard errors should not change.

For many surveys such as the 2011–2012 NHANES and the 2012 HRS, the weights for individual cases will be *population scale weights*, and the expected

value of the sum of the weights will be the population size: $E\left(\sum_{i=1}^n w_i\right) = N$.

For other survey data sets, a *normalized* version of the overall survey weight is provided with the survey data. To “normalize” the final overall survey weights, data producers divide the final population scale weight for each sample respondent by the mean final weight for the entire sample:

TABLE 4.1
Descriptive Statistics for the Survey Weights in the Data Sets Analyzed in This Book

	NCS-R: NCSRWTLG	NCS-R: NCSRWTSH	NHANES: WTMEC2YR ^c	NHANES: WTINT2YR ^c	HRS: NWGTR	HRS: NWGTHH	ESS-Russian Federation: DWEIGHT	ESS-Russian Federation: PSPWGHT
<i>n</i>	5,692	9,282	5,864	5,864	20,554	20,554	2,484	2,484
Sum	5,692	9,282	232,002,539	231,898,519	90,698,760	89,174,512	2,484	2,484
Mean	1.00 ^a	1.00 ^a	39,653.87	39,546.13	4,412.71	4,338.55	1.00 ^a	1.00 ^a
SD	0.96	0.52	40,104.81	38,741.87	3,923.57	3,654.94	0.59	0.59
Min	0.11	0.17	0 ^b	4,300	0 ^b	0 ^b	0.16	0.10
Max	10.10	7.14	220,579.78	220,233.32	19,866	17,875	4.00	4.00
Pctls.								
1%	0.24	0.36	0	6,800.60	0	0	0.22	0.22
5%	0.32	0.49	6,857.04	9,048.96	0	0	0.33	0.31
25%	0.46	0.69	15,096.34	15,497.84	1,738	1,746	0.57	0.57
50%	0.64	0.87	23,508.42	23,599.80	3,479	3,358.50	0.88	0.88
75%	1.08	1.16	43,508.42	42,892.68	5,692	5,536	1.28	1.28
95%	2.95	1.85	133,985.24	130,577.03	12,370	11,819	2.08	2.12
99%	4.71	3.17	169,896.24	167,711.39	19,618	17,855	3.06	3.08

^a Suggests that the survey weights have been normalized to sum to the sample size.

^b Cases with weights of zero will be dropped from analyses and usually correspond to individuals who were not eligible to be in a particular sample.

^c Adults aged 18+.

$w_{norm,i} = w_i / \left(\sum_i w_i / n \right) = w_i / \bar{w}$. Many public-use data sets such as the NCS-R will have *normalized weights* available as the final overall survey weights. The resulting normalized weights will have a mean value of $\bar{w}_{norm} = 1.0$, and the normalized weights for all sample cases should add up to the sample size: $\sum_i w_{norm,i} = n$.

Normalizing survey weight values is a practice that has its roots in the past when computer programs for the analysis of survey data often misinterpreted the “sample size” for weighted estimates of variances and covariances required in computations of standard errors, confidence intervals, or test statistics. As illustrated in Section 3.5.2, the degrees of freedom for variance estimation in analyses of complex sample survey data are determined by the sampling features (stratification, cluster sampling) and not by the nominal sample size. Also, some data analysts feel more comfortable with weighted frequency counts that closely approximate the nominal sample sizes for the survey. However, there is a false security in assuming that a weighted frequency count of $\Sigma w_i = 1000$ corresponds to an effective sample size of $n_{eff} = 1000$. As discussed in Section 2.7, the effective sample size for 1000 nominal cases will be determined in part by the weighting loss, L_w that arises due to variability in the weights and the correlation of the weights with the values of the survey variables of interest. Fortunately, normalizing weights is *not necessary* when analysts use computer software capable of incorporating any available complex design information for a sample into analyses of the survey data. This is especially important when estimation of population totals is a primary analytic objective; the use of normalized weights in these analyses will result in severe under-estimation of population totals; and population scale weights need to be used instead. We will return to this issue in [Chapter 5](#).

4.2.3 Weighting Applications: Sensitivity of Survey Estimates to the Weights

A third step that we recommend survey analysts consider the first time that they work with a new survey data set is to conduct a simple investigation of how the application of the survey weights affects the estimates and standard errors for several key parameters of interest.

To illustrate this step, we consider data from the NCS-R data set, where the documentation indicates that the overall survey weight to be used for the *subsample* of respondents responding to both Part I and Part II of the NCS-R survey ($n = 5,692$) is NCSRWTLG. A univariate analysis of these survey weights in Stata reveals a mean of 1.00, a standard deviation of 0.96, a minimum of 0.11, and a maximum of 10.10 ([Table 4.1](#)). These values indicate that the weights have been normalized and have moderate variance. In addition, we note that some survey weight values are below 0.50. Many standard

statistical software procedures will round noninteger weights and set the weight to 0 if the normalized weight is less than 0.5—excluding such cases from certain analyses. This is an important consideration that underscores the need to use specialized software that incorporates the overall survey weights correctly (and does not round them).

We first consider unweighted estimation of the proportions of NCS-R Part II respondents with lifetime diagnoses of either a major depressive episode (MDE), measured by a binary indicator equal to 1 (yes) or 0 (no), or alcohol dependence (ALD, also a binary indicator), in Stata:

```
mean mde ald if ncsrwtlg !=.
```

Variable	Mean	Standard Error	95% Confidence Interval	
MDE	0.3155	0.0062	0.3035	0.3276
ALD	0.0778	0.0036	0.0709	0.0845

Note that we explicitly limit the unweighted analysis to Part II respondents (who have a nonmissing value on the Part II analysis weight variable NCSRWTLG). The unweighted estimate of the MDE proportion is 0.316, suggesting that almost 32% of the NCS-R population has had a lifetime diagnosis of MDE. The unweighted estimate of the ALD proportion is 0.078, suggesting that almost 8% of the NCS-R population has had a diagnosis of alcohol dependence at some point in their lifetime.

We then request *weighted* estimates of these proportions in Stata, first identifying the final survey weight to Stata with the svyset command, and then requesting weighted estimates by using the svy: mean command:

```
svyset [pweight = ncsrwtlg]
svy: mean mde ald
```

Variable	Mean	Linearized Standard Error	95% Confidence Interval	
MDE	0.1918	0.0054	0.1813	0.2023
ALD	0.0541	0.0031	0.0481	0.0601

The weighted estimates of population prevalence of MDE and ALD are 0.192 and 0.054, respectively. The unweighted estimates for MDE and ALD therefore have a positive bias for the true population proportions (there would be a big difference in reporting a population estimate of 32% for lifetime MDE versus an estimate of 19%).

In this simple example, the weighted estimates differ significantly from the unweighted means of the respondent measures. We would say that the survey weights in this case are *informative* for the two variables of interest

(MDE and ALD). This is not always the case. Depending on the sample design and the nonresponse factors that contributed to the computation of individual weight values, weighted and unweighted estimates may or may not show significant differences. When this simple comparison of weighted and unweighted estimates of key population parameters shows a significant difference, the survey analyst should aim to understand why this difference occurs. Specifically, what are the factors contributing to the case-specific weights that would cause the weighted population estimates to differ from an unweighted analysis of the nominal set of sample observations?

Consider the NCS-R example. We know from the [Chapter 1](#) description that according to the survey protocol, all Part I respondents reporting symptoms of a mental health disorder and a random subsample of symptom-free Part I respondents continued on to complete the Part II in-depth interview. Therefore, the unweighted Part II sample contains an “enriched” sample of persons who qualify for one or more mental health diagnoses. As a consequence, when the corrective population weight is applied to the Part II data, the unbiased weighted estimate of the true population value is substantially lower than the simple unweighted estimate. Likewise, a similar comparison of estimates of the prevalence of physical function limitations using the 2011–2012 NHANES data would yield weighted population estimates that are lower than the simple unweighted prevalence estimates for the observed cases. The explanation for that difference lies in the fact that persons who self-report a disability are oversampled for inclusion in the NHANES, and the application of the weights adjusts for this initial oversampling.

Repeating this exercise for a number of key variables should provide the user with confidence that they understand both how and why the application of the survey weights will influence estimation and inference for the population parameters that they will estimate from the sample survey data. We note that these examples were designed only to illustrate the calculation of weighted sample estimates; standard errors for the weighted estimates were not appropriately estimated to incorporate complex design features of the NCS-R sample. [Chapter 5](#) considers estimation of descriptive statistics and their standard errors in more detail.

4.3 Understanding and Checking the Sampling Error Calculation Model

The next step in preparing to work with a complex sample survey data set is to identify, understand, and verify the *sampling error calculation model* that the data producer has developed and encoded for the survey data set. Information about the sampling error calculation model can often be found

in sections of the technical documentation for survey data sets entitled “sampling error calculations” or “variance estimation” (to name a couple of possibilities). In this section, we discuss the notion of a sampling error calculation model, and how to identify the appropriate variables in a survey data set that represent the model for variance estimation purposes.

A sampling error calculation model is an approximation or “model” for the actual complex sample design that permits practical estimation of sampling variances for survey statistics. Such models are necessary because in many cases, the most practical, cost-efficient sample designs for survey data collection pose analytical problems for complex sample variance estimation. Examples of sample design features that complicate direct analytic approaches to variance estimation include:

- Multistage sampling of survey respondents
- Sampling units without replacement (WOR) at each stage of sample selection
- Sampling of a single PSU from non-self-representing (NSR) primary stage strata
- Small primary stage clusters that are not optimal for subclass analyses or pose an unacceptable disclosure risk

The data producer has the responsibility of creating a sampling error calculation model that retains as much essential information about the original complex design as possible while eliminating the analytical problems that the original design might pose for variance estimation.

4.3.1 Stratum and Cluster Codes in Complex Sample Survey Data Sets

The specification of the sampling error calculation model for a complex sample design entails the creation of a *sampling error stratum* and a *sampling error cluster* variable.

These *sampling error codes* identify the strata and “clusters” to which the survey respondents belong, approximating the original sample design as closely as possible while at the same time conforming to the analytical requirements of several methods for estimating variances from complex sample survey data. Because these codes approximate the stratum and cluster codes that would be assigned to survey respondents based on the original complex sample design, they will not be equal to the original design codes, and the approximate codes are often scrambled (or masked) to prevent the possibility of identifying the original design codes in any way. Sampling error stratum and cluster codes are *essential* for data users who elect to use statistical software programs that employ the Taylor Series Linearization (TSL) method for variance estimation. Software for replicated variance estimation (BRR,

JRR, or bootstrapping) does not require these codes, provided that the data producer has generated replicate weights. If replicate weights are not available, software enabling replicated variance estimation can use the sampling error stratum and cluster codes to create sample replicates and develop the corresponding replicate weights.

In some complex sample survey data sets where confidentiality is of utmost importance, variables containing sampling error stratum and cluster codes may not be provided directly to the research analyst (even if they represent approximations of the original design codes). In their place, the data producer's survey statisticians calculate *replicate weights* which reflect the sampling error calculation model and can be used for repeated replication methods of variance estimation (Chapter 3). We provide examples of analyses using replicate weights on the book web page, and interested readers can refer to Appendix A to see how replicate weights would be identified in various software procedures.

Unfortunately, as is true for final survey weights, data producers have not adopted standard conventions for naming the sampling error stratum and cluster variables in public-use survey data sets. The variable containing the stratum code often has a label that includes some reference to stratification. Two examples from this book include the variable SDMVSTRA from the 2011–2012 NHANES data set, and the variable SESTRAT from the NCS-R data set.

The variable containing the sampling error cluster codes is sometimes referred to as a *sampling error computation unit* (SECU) variable, or it may be generically called the “cluster” code, the primary sampling unit (PSU) code or pseudo primary sampling unit (PPSU) variable. Two examples that will be used throughout the example exercises in this book include the SDMVPSU variable from the 2011–2012 NHANES data set and the SECLUST variable from the NCS-R data set.

As discussed in Section 2.5.2, some large survey data sets are still released without sampling error codes or replicate weight values that are needed for complex sample variance estimation. In such cases, analysts may be able to submit an application to the data producer for restricted access to the sampling error codes, or they may elect to use the generalized design effect that is advocated by these data producers. For a limited number of survey data sets, online, interactive analysis systems such as the Survey Documentation Analysis (SDA) system* provide survey analysts with the capability of performing analysis without gaining direct access to the underlying sampling error codes for the survey data set. Analysts who are working with older public-use data sets may find that

* The SDA system is available at the website of the University of Michigan Inter-University Consortium for Political and Social Research (ICPSR) and is produced by the Computer-Assisted Survey Methods Program at the University of California—Berkeley. Visit www.icpsr.umich.edu for more details.

these data sets were released with the sampling error stratum and cluster codes concatenated into a single code (e.g., 3001 for stratum = 30 and cluster = 01). In these cases, the variable containing the unified code will need to be divided into two variables (stratum and cluster) by the survey data analyst for variance estimation purposes.

4.3.2 Building the NCS-R Sampling Error Calculation Model

We now consider the sample design for the NCS-R as an illustration of the primary concepts and procedures for constructing a sampling error calculation model for a complex sample survey data set. Table 4.2 presents a side-by-side comparison of the features of the original NCS-R complex sample design and the procedures employed to create the corresponding sampling error calculation model. Interested readers can refer to Kessler et al. (2004) for more details on the original sample design for the NCS-R.

Note from Table 4.2 that in the NCS-R sampling error calculation model, the assumption of with-replacement sampling of ultimate clusters described in Chapter 3 is employed to address the analytic complexities associated with the multistage sampling and the without-replacement selection of NCS-R PSUs. The assumption that ultimate clusters are selected with replacement within primary stage strata ignores the finite population correction factor

TABLE 4.2

Original Sample Design and Associated Sampling Error Calculation Model for the NCS-R

Original Sample Design	Sampling Error Calculation Model
The sample is selected in multiple stages.	The concept of <i>ultimate clusters</i> is employed (Chapter 3). Under the assumption that PSUs (ultimate clusters) are sampled with replacement, only PSU-level statistics (totals, means) are needed to compute estimates of sampling variance.
Primary stage units (PSUs), second stage units (SSUs), and third stage units are selected without replacement (WOR).	The ultimate clusters are assumed to be <i>sampled with replacement</i> (SWR) at the primary stage. Finite population corrections are ignored, and simpler SWR variance formulas may be used for variance estimation.
Sixteen of the primary stage strata are self-representing (SR) and contain a single PSU. True sampling begins with the selection of SSUs within the SR PSU.	<i>Random groups</i> are formed for sampling error calculation. Each SR PSU becomes a sampling error stratum. Within the SR stratum, SSUs are randomly assigned to a pair of sampling error clusters.
Forty-six of the primary stage strata are non-self-representing (NSR). A single PSU is selected from each NSR stratum.	<i>Collapsed strata</i> are formed for sampling error calculation. Two similar NSR design strata (e.g., Strata A and B) are collapsed to form one sampling error computation stratum. The Stratum A PSU is the first sampling error cluster in the stratum, and the Stratum B PSU forms the second sampling error cluster.

TABLE 4.3

Illustration of NCS-R Sampling Error Code Assignments

		Original Sample Design						Sampling Error Calculation Model	
		Stratum		PSU ^a				Stratum	Cluster
SR	15			1	2	3	4	5	6
				7	8	9	10	11	12
	16			1	2	3	4	5	6
				7	8	9	10	11	12
								
NSR	17			1701				17	1 = 1701
	18			1801					2 = 1801
	19			1901				18	1 = 1901
	20			2001					2 = 2001

^a Recall from Section 2.8 and Table 4.2 that in self-representing (SR) strata, sampling begins with the selection of the smaller area segment units. Hence, in the NCS-R, the sampled units (coded 1–12) in each SR stratum (serving as its own PSU) are actually secondary sampling units. We include them in the PSU column because this was the first stage of noncertainty sampling in the SR strata. Unlike the SR PSUs, which serve as both strata and PSUs (each SR stratum is a PSU, i.e., they are one in the same), the non-self-representing (NSR) strata can include multiple PSUs. In the NCS-R, one PSU was randomly selected from each NSR stratum (e.g., PSU 1701). NSR strata were then collapsed to form sampling error strata with two PSUs each, for the purpose of facilitating variance estimation.

(Section 2.4.2) and therefore results in a slight overestimation of true sampling variances for survey estimates.

To introduce several other features of the NCS-R sampling error calculation model, Table 4.3 illustrates the assignment of the sampling error stratum and cluster codes for six of the NCS-R sample design strata. In self-representing (SR) design strata 15 and 16, the “area segments” constitute the first actual stage of noncertainty sample selection—hence they are the ultimate cluster units with these two strata. To build the sampling error calculation model within each of these two SR design strata, the *random groups method* is used to assign the area segment units to two sampling error clusters. This is done to simplify the calculations required for variance estimation. As illustrated, NCS-R NSR strata 17–20 contain a single PSU selection. The single PSU selected from each of these NSR strata constitutes an ultimate cluster selection. Because a minimum of two sampling error clusters per stratum is required for variance estimation, pairs of NSR design strata (e.g., 17 and 18, 19, and 20) are collapsed to create single sampling error strata with two SECUs (PSUs) each.

Randomly grouping PSUs to form a sampling error cluster does not bias the estimates of standard errors that will be computed under the sampling error calculation model. However, forming random clusters by combining units does forfeit degrees of freedom, so the “variance of the variance estimate” may increase slightly.

If the collapsed stratum technique is used to develop the sampling error calculation model, slight overestimation of standard errors occurs because the collapsed strata ignore the true differences in the design strata that are collapsed to form the single sampling error calculation stratum. The following section provides interested readers with more detail on the combined strata, random groups, and collapsed strata techniques used in building sampling error calculation models for complex sample survey data.

4.3.3 Combining Strata, Randomly Grouping PSUs, and Collapsing Strata

Combining strata in building the sampling error calculation model involves the combination of PSUs from two or more different strata to form a single stratum with larger pooled sampling error clusters. Consider Figure 4.1. The original complex sample design involved paired selection of two PSUs within each primary stage stratum. For variance estimation, PSUs from the two design strata are combined, with the PSUs being randomly assigned into two larger sampling error clusters.

The technique of combining strata for variance estimation is typically used for one of two reasons: (1) the sample design has large numbers of primary stage strata and small numbers of observations per PSU, which could lead to variance estimation problems (especially when subclasses are being analyzed); or (2) the data producer wishes to group design PSUs to mask individual PSUs as part of a disclosure protection plan. The sampling error calculation model for the NHANES has traditionally employed combined strata to mask the identity of individual PSUs.

The *random groups method* randomly combines multiple clusters from a single design stratum to create two or more clusters for sampling error estimation. This is the technique illustrated for NCS-R SR design strata 15 and 16

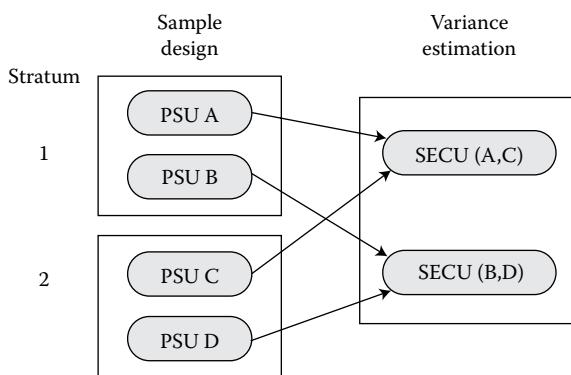


FIGURE 4.1

Illustration of the combined stratum method.

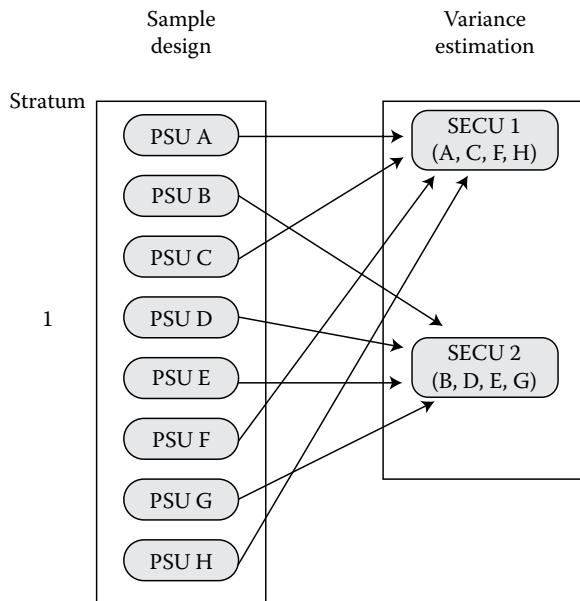


FIGURE 4.2
Illustration of the random groups method.

in Table 4.3. Figure 4.2 presents an illustration of forming random groups of clusters for variance estimation purposes. In this illustration, there are eight area segment selections within an original SR design stratum. (The New York Metropolitan Statistical Area [MSA] is a common example of a geographic area that forms an SR stratum in national area probability samples of the U.S. population.) Figure 4.2 shows how the eight area segment clusters are randomly assigned into two larger sampling error clusters containing four of the original segments each.

The random groups method is typically used when a large number of small design PSUs has been selected within a single stratum and the data producer wishes to simplify the calculation of variance for that stratum or to minimize disclosure risk that could result from releasing the original stratification and cluster coding. This technique is commonly used to create sampling error clusters in SR primary stage strata of multistage sample designs.

Collapsing strata is another technique that data producers may employ in building a sampling error calculation model for a complex sample design. This technique is generally used when a single primary sampling unit is selected from each primary stage design stratum (which precludes direct estimation of sampling variance for the stratum). The technique involves “collapsing” or “erasing” the boundary between adjacent strata, so that similar strata become one larger pseudo- or “collapsed” stratum with multiple

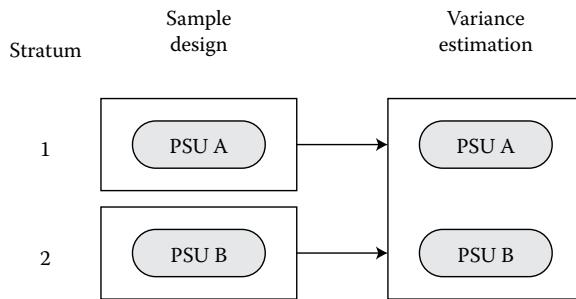
**FIGURE 4.3**

Illustration of the collapsed stratum method.

primary sampling units. In contrast to the combined stratum method, the original design PSUs remain distinct as sampling error clusters in the collapsed sampling error stratum. We illustrate the idea of collapsing strata in Figure 4.3.

4.3.4 Checking the Sampling Error Calculation Model for the Survey Data Set

As discussed previously in this chapter, identification of the variables identifying the sampling error strata and clusters is an essential step in preparing for the analysis of a complex sample survey data set. When these variables have been identified, a useful first step is to cross-tabulate these variables to get a sense of the sample sizes in each stratum and cluster.

The Stata software system provides the `svyset` and `svydes` commands that enable users to define these key sample design variables (including final survey weights) for a data set and then describe the distributions of the cases to sampling error strata and clusters. These commands need to be submitted only once in a given Stata session, unlike other software procedures that require these variables to be identified for each individual analysis (e.g., PROC SURVEYMEANS in SAS, PROC DESCRIPT in SUDAAN); readers can refer to Appendix A for details.

We illustrate the use of the `svyset` and `svydes` commands to show how these key design variables are identified and described in Stata for the NCS-R. First, the correct design variables were determined based on the documentation for the survey data set. Next, the following two Stata commands (`svyset` and `svydes`) were submitted, which produced the output that follows the commands:

```
svyset seclustr [pweight=ncsrwtlg], strata(sestrat) ///
vce(linearized) singleunit(missing)
svydes
```

Stratum	#Units included	#Units omitted	#Obs with complete data		#Obs with missing data	#Obs per included Unit		
	min	mean	max					
1	2	0	44	0	22	22.0	22	
2	2	0	53	0	26	26.5	27	
3	2	0	77	0	31	38.5	46	
4	2	0	87	0	42	43.5	45	
5	2	0	72	0	32	36.0	40	
6	2	0	68	0	31	34.0	37	
7	2	0	127	0	61	63.5	66	
8	2	0	84	0	38	42.0	46	
9	2	0	89	0	44	44.5	45	
10	2	0	78	0	23	39.0	55	
11	2	0	57	0	28	28.5	29	
12	2	0	61	0	24	30.5	37	
13	2	0	63	0	26	31.5	37	
14	2	0	45	0	20	22.5	25	
15	2	0	73	0	36	36.5	37	
16	2	0	66	0	30	33.0	36	
17	2	0	41	0	18	20.5	23	
18	2	0	55	0	26	27.5	29	
19	2	0	62	0	29	31.0	33	
20	2	0	159	0	70	79.5	89	
21	2	0	187	0	75	93.5	112	
22	2	0	178	0	82	89.0	96	
23	2	0	186	0	84	93.0	102	
24	2	0	197	0	94	98.5	103	
25	2	0	264	0	124	132.0	140	
26	2	0	155	0	58	77.5	97	
27	2	0	172	0	79	86.0	93	
28	2	0	117	0	45	58.5	72	
29	2	0	199	0	99	99.5	100	
30	2	0	121	0	57	60.5	64	
31	2	0	267	0	131	133.5	136	
32	2	0	191	0	86	95.5	105	
33	2	0	82	0	37	41.0	45	
34	2	0	236	0	108	118.0	128	
35	2	0	236	0	94	118.0	142	
36	2	0	203	0	100	101.5	103	
37	2	0	218	0	106	109.0	112	
38	2	0	197	0	84	98.5	113	
39	2	0	215	0	76	107.5	139	
40	2	0	164	0	66	82.0	98	
41	2	0	211	0	94	105.5	117	
42	2	0	235	0	116	117.5	119	
42	84	0	5692	0	18	67.8	142	
<hr/>								
5692								
3590 = #Obs with missing values in the								
----- survey characteristics								
9282								

The Stata output above illustrates the frequency distributions of the design variables that are produced by running the `svyset` and `svydes` commands for the NCS-R data set. The sampling error calculation model for the NCS-R sample design recognizes stratification of the population, and the variable containing the stratum codes for sampling error calculations is `SESTRAT`. The sampling

error cluster (SECLUSTR) and final survey weight (NCSRWTLG) variables are also identified, in addition to the method of variance estimation (TSL). We also indicate what Stata should do if strata containing a single sampling error cluster are encountered in an analysis (variance estimates should be set to missing). Additional options for the svyset command are described in Appendix A. We note that if Stata users wish to reset the design variables declared in the svyset command, the svyset, clear command can be submitted.

The output from the svydes command displayed above indicates that the NCS-R sampling error calculation model has been specified as a paired selection design, with two sampling error clusters (# Units included) in each of the 42 sampling error strata (for 84 sampling error clusters total). Sample sizes in the clusters (denoted in the Stata output by "# Obs per included Unit") range from 18 to 142, with an average of 67.8 sample respondents per ultimate cluster. This "two per stratum" sampling error coding is common in many public-use survey data sets and enables survey analysts to employ any of the variance estimation techniques (TSL, BRR, JRR, bootstrapping) discussed in [Chapter 3](#). Stata also reports that 3,590 observations have missing data on at least one key design variable. This does not come as a surprise, because the Part II survey weight variable for NCS-R cases (NCSRWTLG) takes on missing values for cases that were not selected or subsampled for Part II of the NCS-R survey.

These simple initial tabulations help to familiarize data users with the sampling error calculation models that will be used for variance estimation and can be useful for describing complex sample design information and methods of variance estimation in scientific and technical publications. Analysts using other statistical software packages (e.g., SAS, SPSS, and SUDAAN) can easily perform these simple descriptive analyses using standard procedures for cross-tabulation.

4.4 Addressing Item Missing Data in Analysis Variables

Many survey data analysts, initially excited to begin the analysis of a new survey data set, are disappointed to find that many of the key survey variables they hope to analyze suffer from problems of missing data. As they move from simple univariate analysis to multivariate analysis, the missing data problem is compounded due to the deletion from analysis by statistical software of any cases with missing values on one or more variables.

The first fact that all data users should recognize is that no survey data set is immune to some form of missing data problem. Therefore, addressing missing data should be as commonplace an analytic activity as choosing the form of a regression model to apply to a dependent variable of interest. Section 2.7 has already introduced weighting adjustments for unit nonresponse—one major source of missing data in sample surveys.

Here we will focus briefly on the implications of ignoring item missing data in analysis and then describe a convenient method for investigating the rates and patterns of missing data in a chosen set of analysis variables. [Chapter 12](#) will examine methods for statistical imputation of item missing data using today's powerful new software tools.

4.4.1 Potential Bias due to Ignoring Missing Data

Many analysts simply choose to ignore the missing data problem when performing analyses. If the rates of missing data on key analysis variables are very low (say <1%–2% of cases), the penalty for not taking active steps (i.e., weighting or imputation) to address the missing data is probably small. Consider a univariate analysis to estimate the population mean of a variable y . Under a simple deterministic assumption that the population is comprised of “responders” and “nonresponders,” the expected bias in the respondent mean of the variable y is defined as follows:

$$\text{Bias}(\bar{Y}_R) = \bar{Y}_R - \bar{Y} = P_{NR} \times (\bar{Y}_R - \bar{Y}_{NR}). \quad (4.1)$$

In Equation 4.1, \bar{Y} is the true population mean, \bar{Y}_R is the population mean for responders in the population, \bar{Y}_{NR} is the population mean for nonresponders in the population, and P_{NR} is the expected proportion of nonrespondents in a given sample. For the bias to be large, the rate of missing data must be sizeable, and respondents must differ in their characteristics from nonrespondents. In statistical terms, the potential bias due to missing data depends on both the missing data pattern and the missing data mechanism. [Chapter 12](#) will provide a more detailed review of missing data patterns and mechanisms.

4.4.2 Exploring Rates and Patterns of Missing Data Prior to Analysis

Newer versions of Stata (Versions 13+) provide data analysts with the `misstable` patterns and `misstable summarize` commands to display the patterns and rates of missing data across a set of variables that will be included in an analysis. The following example uses these commands to explore the missing data for six 2011–2012 NHANES variables that will be included in the multiple imputation regression example that is presented later in Section 12.6. The variables are diastolic blood pressure (`BPXDI1_1`), marital status (`MARCAT`), gender (`RIAGENDR`), race/ethnicity (`RIDRETH1`), age (`AGEC` and `AGECSQ`), body mass index (`BMXBMI`), and family poverty index (`INDFMPIR`). The command syntax to request the missing data summary for this set of six variables (where `AGECSQ` is simply `AGEC` squared) is:

```
misstable summarize bpmdi1_1 bmxbmi indfmpir marcat ///
riagendr ridreth1 agec agecsq if age18p==1 & ///
wtmec2yr > 0 , all
```

The command syntax to request the missing data patterns for the same six variables is:

```
misstable patterns bpxdil_1 bmxbmi indfmpir ///
marcat riagendr ridreth1 agec agecsq, freq
```

The actual Stata output produced by the `misstable patterns` and `misstable summarize` commands is provided below. In the `summarize` output, the first portion of the output lists the number of observed and missing values for each variable that has at least one missing value and also variables with full data since the `all` option was specified. The missing-value patterns output summarizes the frequencies of various patterns of missing data across the four variables with missing data, using a coding of "1" for observed and "0" for missing. For example, 4,416 observations have no missing data for these four variables, and a total of nine observations have missing data only for the BMXBMI (body mass index) variable.

```
misstable summarize bpxdil_1 bmxbmi indfmpir marcat riagendr ridreth1 agec agecsq, all
```

Variable	Obs=.	Obs>.	Obs<.	Obs<.		
				Unique values	Min	Max
bpxdil_1	503		5,112	49	10	120
bmxbmi	90		5,525	385	13.4	82.1
indfmpir	487		5,128	406	0	5
marcat	300		5,315	3	1	3
riagendr			5,615	2	1	2
ridreth1			5,615	5	1	5
agec			5,615	63	-28.35516	33.64484
agecsq			5,615	63	.1261386	1131.975

Missing-value patterns

(1 means complete)

Frequency	Pattern			
	1	2	3	4
4,416	1	1	1	1
386	1	1	1	0
369	1	1	0	1
230	1	0	1	1
62	1	1	0	0
48	0	1	1	1
31	1	0	0	1
22	1	0	1	0
18	0	1	1	0
12	0	1	0	1
9	1	0	0	0
6	0	0	1	1
4	0	1	0	0
2	0	0	1	0
5,615				

Variables are (1) bmxbmi (2) marcat (3) indfmpir (4) bpxdil_1

With recent advances in the theory of statistical analysis with missing data (Little and Rubin, 2002; Raghunathan, 2016) and today's improved software (e.g., Raghunathan et al., 2001; Berglund and Heeringa, 2014; StataCorp, 2015), data producers or data users often consider different methods for the *imputation* (or prediction) of missing data values. Depending on the patterns of missing data and the underlying process that generated the missingness, statistically sound imputation strategies can produce data sets with complete cases for analysis.

In many large survey programs, the data producer may perform imputation for key variables before the survey data set is released for public use. Typically, methods for *single imputation* are employed using techniques such as *hot deck imputation*, *regression imputation*, and *predictive mean matching*. Some survey programs may choose to provide data users with *multiply imputed* data sets (Schafer, 1996; Kennickell, 1998). When data producers perform imputation of item missing data, a best practice in data dissemination is to provide data users with both the imputed version of the variable (e.g., `I_INCOME_AMT`) and an indicator variable (e.g., `I_INCOME_FLG`) that identifies the values of the variables that have been imputed. Data users should expect to find general documentation for the imputations in the technical report that accompanies the survey data. The survey codebook should clearly identify the imputed variables and the imputation "flag" variables.

When imputations are not provided by the data producer (or the analyst chooses to employ their own imputation methods and models), the task of imputing item missing data will fall to the data user. Details on practical methods for user imputation of item missing data are provided later in [Chapter 12](#).

4.5 Preparing to Analyze Data for Sample Subpopulations

The analysis of complex sample survey data sets often involves separate estimation and inference for *subpopulations* or *subclasses* of the full population. For example, an analyst may wish to use the NHANES data to estimate the prevalence of diabetes separately for male and female adults, or compute HRS estimates of retirement expectations only for the population of the U.S. Census South Region. An NCS-R analyst may choose to estimate a separate logistic regression model for predicting the probability of past-year depression status for African-American women only. When analyses are focused in this way on these specific subclasses of the survey population, special care must be taken to correctly prepare the data and specify the subclass analysis in the command input to software programs. Proper analysis methods for subclasses of survey data have been well-established in the survey methodology literature (Kish, 1965; Cochran, 1977; Fuller et al., 1989; Korn

and Graubard, 1999; Lohr, 1999; Rao, 2003), and interested readers can consult these references for more general information on estimation of survey statistics and related variance estimation techniques for subclasses. A short summary of the theory underlying subclass analysis of survey data is also provided in Theory Box 4.1.

THEORY BOX 4.1 THEORETICAL MOTIVATION FOR UNCONDITIONAL SUBCLASS ANALYSES

To illustrate the importance of following the unconditional subclass analysis approach mathematically, we consider the variance of a sample total (the essential building block for variance estimation based on TSL). We denote design strata by h ($h = 1, 2, \dots, H$), first-stage PSUs within strata by α ($\alpha = 1, 2, \dots, a_h$), and sample elements within PSUs by i ($i = 1, 2, \dots, n_{h\alpha}$). The weight for element i , taking into account factors such as unequal probability of selection, nonresponse, and possibly poststratification, is denoted by $w_{h\alpha i}$. We refer to specific subclasses using the notation S . An estimate of the total for a variable Y in a subclass denoted by S is computed as follows (Cochran, 1977):

$$\hat{Y}_S = \sum_{h=1}^H \sum_{\alpha=1}^{a_h} \sum_{i=1}^{n_{h\alpha}} w_{h\alpha i} I_{S,h\alpha i} y_{h\alpha i}. \quad (4.2)$$

In this notation, I represents an indicator variable, equal to 1 if sample element i belongs to subclass S , and 0 otherwise. The closed-form analytic formula for the variance of this subclass total can be written as follows:

$$Var(\hat{Y}_S) = \sum_{h=1}^H \frac{a_h}{(a_h - 1)} \left[\sum_{\alpha=1}^{a_h} \left(\sum_{i=1}^{n_{h\alpha}} w_{h\alpha i} I_{S,h\alpha i} y_{h\alpha i} \right)^2 - \frac{\left(\sum_{\alpha=1}^{a_h} \sum_{i=1}^{n_{h\alpha}} w_{h\alpha i} I_{S,h\alpha i} y_{h\alpha i} \right)^2}{a_h} \right]. \quad (4.3)$$

This formula shows that the variance of the subclass total is calculated by summing the between-cluster variance in the subclass totals within strata, across the H sample strata. The formula also shows how the indicator variable is used to ensure that all sample elements (and their design strata and PSUs) are recognized in the variance calculation; this emphasizes the need for the software to recognize all of the original

design strata and PSUs. Analysts should note that if all $n_{h\alpha}$ elements within a given stratum denoted by h and PSU denoted by α do not belong to the subclass S (although elements from that subclass theoretically could belong to that PSU in any given sample), that PSU will still contribute to the variance estimation: The PSU helps to define the total number of PSUs within stratum h (a_h), and contributes a value of 0 to the sums in the variance estimation formula. In this way, sample-to-sample variability in the estimation of the total due to the fact that the subclass sample size is a random variable is captured in the variance calculation.

4.5.1 Subpopulation Distributions across Sample Design Units

Although most current survey data analysis software is programmed to correctly account for subclasses in analysis, a useful step in preparing for data analysis is to examine the distribution of the targeted subpopulation sample with respect to the sampling error strata and clusters that have been defined under the sampling error calculation model. [Figure 4.4](#) illustrates the different distributional patterns that might be observed in practice.

Design domains, or subclasses that are restricted to only a subset of the primary stage strata (e.g., adults in the Census South Region, or residents of urban counties), constitute a broad category of analysis subclasses. In

Schematic illustration of subclass types: Stratified, cluster sample design									
“Design domain”			“Mixed class”			“Cross-class”			
Str.	PSU 1	PSU 2	Str.	PSU 1	PSU 2	Str.	PSU 1	PSU 2	
1			1			1			
2			2			2			
3			3			3			
4			4			4			
5			5			5			

FIGURE 4.4

Subclass types in stratified cluster sample designs.

general, the analysis of design domain subclasses should not be problematic in most contemporary survey analysis software. Analysts should recognize that sampling errors estimated for domain subclasses will be based on fewer degrees of freedom than estimates for the full sample or cross-classes, given that design domains are generally restricted to specific sampling strata.

A second pattern that may be observed is a *mixed class*, or a population subclass that is not isolated in a subset of the sample design strata but is unevenly and possibly sparsely distributed across the strata and clusters of the sampling error calculation model. Experience has shown that many survey analysts often “push the limits” of sample designs, focusing on rare or highly concentrated subclasses of the population—for example, Hispanic adults with asthma in the HRS. While such analyses are by no means precluded by the sample design, survey analysts are advised to exercise care in approaching subclass analyses of this type for several reasons: (1) nominal sample sizes for mixed classes may be small but design effects due to weighting and cluster sampling may still be substantial; (2) a highly uneven distribution of cases to strata and clusters will introduce instability or bias in the variance estimates (especially those based on the TSL method); and (3) software approximations to the complex sample design degrees of freedom ($df = \# \text{ clusters} - \# \text{ strata}$) may significantly overstate the true precision of the estimated sampling errors and confidence intervals. Survey analysts who intend to analyze data for mixed classes are encouraged to consult with a survey statistician, but we would recommend that these subclasses be handled using unconditional subclass analysis approaches (Section 4.5.2).

We label the third pattern as a *cross-class* (Kish, 1987). Cross-classes are subclasses of the survey population that are broadly distributed across all strata and clusters of a complex sample design. Examples of cross-classes in a national area probability sample survey of adults might include males, or individuals aged 40 and above. Properly identified to the software, subclasses that are true cross-classes present very few problems in survey data analysis—sampling error estimation and degrees of freedom determination for confidence intervals and hypothesis tests should be straightforward.

We now consider two alternative approaches to subclass analysis that analysts of complex sample survey data sets could take in practice, and discuss applications where one approach might be preferred over another.

4.5.2 Unconditional Approach for Subclass Analysis

Recall from [Chapter 3](#) that the estimated standard error of an estimated survey statistic expresses the degree of variability in the statistic that we would expect from one hypothetical sample to another around the true population parameter of interest. If the subclass analysis were restricted only to sample cases that belonged to the subclass (sometimes referred to as the *conditional subclass analysis* approach, because it conditions subclass inference on the observed sample), sampling error estimates would in effect assume that each

hypothetical sample would have the *same* fixed number of subclass members (say m) and that the distribution of the fixed subclass sample size, m , across design strata and clusters would remain unchanged from sample to sample. When analyzing complex sample survey data sets in practice, this would only be the case when analyzing design domains (as defined above) with sample sizes that are fixed by design.

In all other applications, the subclass sample size is a *random variable*—varying both in its size and its distribution across the design strata and clusters. By performing an *unconditional subclass analysis* (i.e., one that does not condition on the observed distribution of subclass cases to particular strata and clusters of the full sample design, as described in West et al., 2008), we take into account these added sources of true sampling variability. Point estimates of population parameters will be identical under both subclass analysis approaches. However, because a conditional analysis does *not* incorporate this latter source of variance, it tends to result in *underestimates* of standard errors, which cause analysts to overstate the precision of estimated survey statistics for subclasses. Therefore, simply using the data management capabilities of statistical software to delete or filter out those cases that do not fall into the subclass of interest can produce biased inferences. This requires some additional preparation on the part of the data analyst (Section 4.5.3).

We note that this distinction between the conditional and unconditional subclass analysis approaches is only relevant when TSL is the technique being employed for variance estimation (see [Chapter 3](#) for details). This is due to the fact that linearization relies on the sampling error strata and clusters defined by the sampling error calculation model to compute variance estimates. When replication methods (e.g., JRR) are employed for variance estimation, only the weighted estimates from each replicate sample are used for variance estimation purposes, and the distribution of the subclass sample across the sampling error strata and clusters becomes irrelevant.

To make this distinction between the variance estimation methods in the case of subclass analysis clear, we consider an example. In a complex sample with a sampling error calculation model that defines two clusters per stratum, suppose that a subclass of analytic interest has no sample members in one of the two clusters in a particular stratum. If one were to employ linearization and attempt the *conditional* subclass analysis approach, deleting cases that did not belong to the subclass, this cluster would be deleted from the data set, and the software would encounter problems attempting to determine the contribution of between-cluster variance within this stratum to the overall variance estimate (given that it only has one cluster present for variance estimation, when at least two are required). The *unconditional* approach would allow linearization to proceed, as the cluster with no sampled elements from the subclass would now contribute totals of zero to the linearized variance estimates (reflecting sampling zeroes). If one were to employ replication approaches, the cluster in question would simply not contribute to any of the replicate sample estimates used for variance estimation.

We urge analysts to carefully consider the distinction between these two approaches, given that most software for the analysis of complex sample survey data uses linearization as the default variance estimation technique.

4.5.3 Preparation for Subclass Analyses

To properly prepare for a correct unconditional subclass analysis of a complex sample survey data set, data users should generate indicator variables for each subclass S that they are interested in analyzing:

$$I_{S,i} = \begin{cases} 1 & \text{if case } i \text{ is a member of the subclass of interest} \\ 0 & \text{if case } i \text{ is not a member of the subclass of interest} \end{cases}$$

Each case in the complete sample should be assigned a value of 1 or 0 for this indicator variable (if information used to define the subclass of interest is available for each case). This indicator variable will be used to identify the subclass members to the analysis software. Once these indicator variables have been created for subclasses of interest, data users need to utilize appropriate software options for unconditional subclass analyses. For example, Stata procedures offer the `subpop()` option, where the subclass indicator variable can be specified in the parentheses; SUDAAN offers the `SUBPOPN` keyword; SPSS (in the Complex Samples Module) offers the `SUBPOP` and `DOMAIN` subcommands; and SAS offers the `DOMAIN` keyword for `PROC SURVEYMEANS`, `PROC SURVEYREG`, `PROC SURVEYPHREG`, and `PROC SURVEYLOGISTIC` specifically, and allows users to indicate domains using the first variable listed in the `TABLES` statement of `PROC SURVEYFREQ`. Similar options and functions are available in other software, such as the `survey` package in R; see Appendix A for details.

4.6 Final Checklist for Data Users

We conclude this chapter with a summary of the important preparation steps that data users should follow prior to beginning the analysis of a complex sample survey data set.

1. Review the documentation for the data set provided by the data producer, specifically focusing on sections discussing the development of the final survey weights and sampling error (standard error) estimation. Contact the data producer if any questions arise.
2. Identify the correct weight variable for the analysis, keeping in mind that many survey data sets include separate weights for different

types of analyses. Perform simple descriptive analyses of the weight variable, noting the general distribution of the weights, whether the weights have been normalized, and whether there are missing or 0 weight values for some cases. Select a few key variables from the survey data set and compare weighted and unweighted estimates of descriptive parameters (e.g., means, proportions) for these variables.

3. Identify the variables in the data set containing the sampling error calculation codes (for strata and clusters) that define the sampling error calculation model. Examine how many clusters were selected from each sampling stratum (according to the sampling error calculation model), and whether particular clusters have small sample sizes. If only a single sampling error cluster is identified in a sampling stratum, contact the data producer or consult the documentation for the data set for guidance on recommended variance estimation methods. Determine whether replicate sampling weights are present if sampling error calculation codes are not available, and make sure that the statistical software is capable of accommodating replicate weights (Section 4.2.1).
4. Create a final analysis data set containing only the analysis variables of interest (including the survey weights, sampling error calculation variables, and case identifiers). Examine univariate and bivariate summaries for the key analysis variables to determine possible problems with missing data or unusual values on the individual variables.
5. Review the documentation provided by the data producer to understand the procedure (typically nonresponse adjustment) used to address unit nonresponse or nonresponse to a wave or phase of the survey data collection. Analyze the rates and patterns of item missing data for all variables that will be included in the analysis. Investigate the potential missing data mechanism by defining indicator variables flagging missing data for the analysis variables of interest. Use statistical tests (e.g., chi-square tests, two-sample t -tests) to see if there are any systematic differences between respondents providing complete responses and respondents failing to provide complete responses on important analysis variables (e.g., demographics). Choose an appropriate strategy for addressing missing data using the guidance provided in Section 4.4 and [Chapter 12](#).
6. Define indicator variables for important analysis subclasses. *Do not delete cases that are not a part of the primary analysis subclass.* Assess a cross-tabulation of the stratum and cluster sampling error calculation codes for the subclass cases to identify the distribution of the subclass across the strata and clusters defined by the sampling error calculation model. Consult a survey statistician prior to analysis of

subclasses that exhibit the “mixed class” characteristic illustrated in [Figure 4.4](#). Make sure to employ appropriate software options for unconditional subclass analyses if using TSL for variance estimation.

Based on many years of consulting on the analysis of survey data, the authors firmly believe that following these steps before performing any analyses of complex sample survey data sets will eliminate the most common mistakes that result in wasted time and effort or (even worse) unknowingly result in biased, incorrect analyses of the survey data.



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5

Descriptive Analysis for Continuous Variables

In May, average hourly earnings for all employees on private nonfarm payrolls increased by 5 cents to \$25.59, following an increase of 9 cents in April. Over the year, average hourly earnings have risen by 2.5 percent. Average hourly earnings of private-sector production and nonsupervisory employees increased by 3 cents to \$21.49 in May.

U.S. Bureau of Labor Statistics, Economic News Release, June 2016,
<http://www.bls.gov>.

5.1 Introduction

Estimation of totals, means, variances, and other distributional statistics for survey variables may be the primary objective of an analysis plan or possibly an exploratory step on a path to a more multivariate treatment of the survey data. Major reports of survey results can be filled with detailed tabulations of descriptive estimates. Scientific papers and publications that may emphasize a more analytical multivariate treatment of the data typically include initial descriptive estimation of population characteristics as part of the overall analysis plan.

This chapter describes techniques for generating population estimates of descriptive parameters for continuous survey variables. Section 5.2 examines features that distinguish descriptive analysis of complex sample survey data from more standard descriptive analyses of simple random samples or convenience samples. Basic methods and examples of estimating important descriptive parameters for univariate, continuous distributions are described in Section 5.3, followed in Section 5.4 by methods for studying simple bivariate relationships between two continuous survey variables. The chapter concludes with coverage of methods for descriptive estimation for subpopulations (Section 5.5) and estimation of simple linear functions of distributional statistics such as differences of means (Section 5.6).

5.2 Special Considerations in Descriptive Analysis of Complex Sample Survey Data

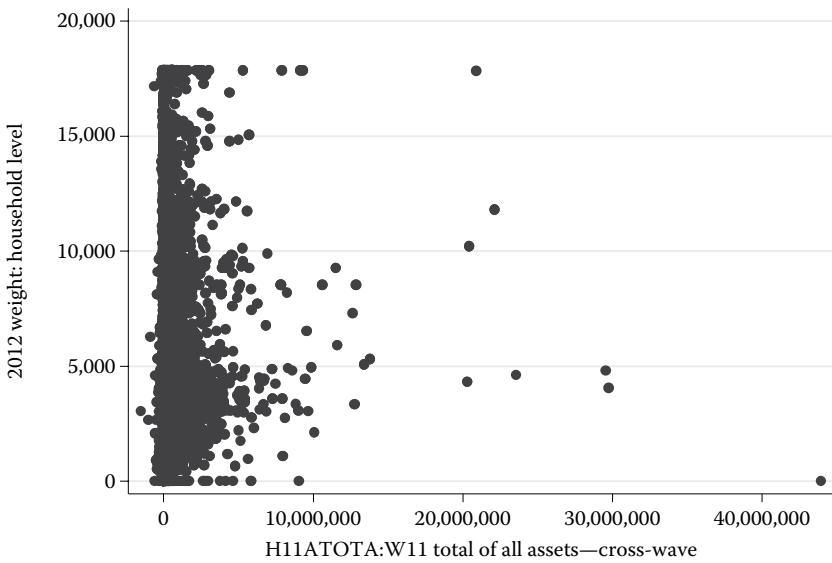
Descriptive analysis of complex sample survey data shares much in common with the standard statistical methods that are taught in any introductory statistics course, but there are several subtle differences that are important to keep in mind.

5.2.1 Weighted Estimation

Descriptive analysis of both continuous and discrete survey measures is intended to characterize the distributions of variables over the full survey population. If population elements have differing probabilities of inclusion in the sample (deliberately introduced by the sampling statistician or induced by a nonresponse mechanism), unbiased estimation for the population distribution requires weighting of the sample data. Depending on the distribution of the weights and the correlations between the weights and the survey variables of interest, unweighted sample estimates may yield a very biased picture of the true population distribution (Little and Vartivarian, 2005).

It is informative to plot the value of the survey weight against the value of the survey variable of interest. [Figure 5.1](#) illustrates a plot of this type, with the 2012 Health and Retirement Study (HRS) survey weight value on the vertical axis and the value of 2012 HRS total household wealth on the horizontal axis. Diagnostic plots of this type inform the user of the following important properties of the weights and their relationship to the variable of interest: (1) the variability of the weights, which can affect the sampling variability of descriptive estimates (Section 2.7.5); (2) any strong functional relationship between individual weight values and survey observations, signaling that the weights are highly “informative” for the estimation of population parameters; and (3) the potential for “weighted outliers”—points representing large values on both the survey variable and the survey weight that in combination will have a major influence on the estimated distributional statistics and their standard errors.

For example, [Figure 5.1](#) suggests that there is considerable variability in the 2012 HRS household weights, but there is little evidence of a functional (e.g., linear, quadratic) relationship of the weights to the measures of total household wealth. Therefore, for the total household wealth variable, weighted estimation will result in increased sampling variances for estimates, but the weighting may not have major impacts on the estimates of population parameters (Section 2.7). The plot also identifies eight HRS cases with exceptionally large values for total household wealth (e.g., >\$20,000,000). The survey weights for three of these “large net worth” cases are also large, each

**FIGURE 5.1**

Examining the relationship of a survey variable (total household wealth) and the survey weight in the 2012 HRS data set.

above the midpoint of the weight range and one close to the maximum for all HRS 2012 household weight values. These three points warrant investigation (Chapter 4) because they may have significant influence on the estimates of descriptive parameters in addition to substantial leverage in the estimation of multivariate models.

5.2.2 Design Effects for Descriptive Statistics

Estimates of descriptive parameters (or descriptive statistics) derived from complex sample survey data can be subject to substantial design effects, due to the stratification, cluster sampling and weighting associated with the design. Empirical research has consistently demonstrated that complex sample design effects are largest for weighted estimates of population means and totals for single survey variables, smaller for estimates of subpopulation means and proportions, and substantially reduced for regression coefficients and other statistics that are functions of two or more variables (Kish et al., 1976; Skinner et al., 1989). Throughout this chapter, the example analyses will include estimation of design effect ratios to provide the reader with a sense of the magnitude of the design effects and their variability across survey variables and estimated statistics.

5.2.3 Matching the Method to the Variable Type

Survey responses are recorded on a variety of scales, including simple binary choices (yes, no), nominal categories (Democrat, Republican, Independent), ordinal scales (1 = excellent, 2 = very good, 3 = good, 4 = fair, 5 = poor), ordinal counts (years of education, weeks not employed), interval scale variables (age in years), fully continuous variables (systolic blood pressure in mmHg), grouped or “interval censored” continuous variables (income categories, e.g., \$10,000–\$24,999), and censored or “semicontinuous” variables (the value of household wealth in stocks and bonds). With the obvious exception of nominal categorical variables and interval censored measures, it is common for survey analysts to apply descriptive analysis techniques appropriate for continuous data to survey variables that are measured on scales that are not strictly continuous.

The descriptive analytic methods described in this chapter may certainly be applied to ordinal, interval scale and semicontinuous survey measures; however, analysis results should be presented in a way that acknowledges the “noncontinuous” character of the underlying data. The classical interpretation of ordinal scales as a measure of an underlying continuous latent variable recognizes that the mapping of that construct to the ordinal metric may not be linear—moving from poor to fair on a health rating scale may not reflect the same degree of health improvement as moving from fair to good. The estimated 75th percentile of the distribution of household mortgage debt for HRS households may be a misleading statistic if the percent of households with no mortgage is not also reported. In short, as is true in all statistical summarization, it is the survey analyst’s responsibility to ensure that the reporting and interpretation of even the simplest descriptive analyses are accurate and transparent for the intended audience.

5.3 Simple Statistics for Univariate Continuous Distributions

This section outlines methods for estimating simple statistics that describe the population distributions of survey variables, including graphical tools and statistical estimators for population totals, means, variances, and percentiles. Weighted estimators of the most important distributional parameters for continuous survey variables are described in this section, and with a few exceptions, most of the major statistical software packages support weighted estimation for these statistics. When available, estimation of these univariate descriptive parameters and the corresponding standard errors is illustrated in Stata using the National Comorbidity Survey Replication (NCS-R), the 2011–2012 National Health and Nutrition Examination Survey (NHANES), and the 2012 HRS data sets. Examples of command syntax for estimating these same descriptive statistics using other software systems can be found on the book web site.

5.3.1 Graphical Tools for Descriptive Analysis of Survey Data

The authors' experience suggests that statistical graphics are currently underutilized as tools for the exploratory analysis of survey data (Tukey, 1977), which includes effective visual display of estimated population distributions of single variables or the population relationships among two or more independent variables (Tufte, 1983; Cleveland, 1993). A thorough treatment of the many graphical tools available to today's analysts would require a separate volume and, as a general subject, is well covered in any number of existing publications (Maindonald and Braun, 2007; SAS Institute Inc., 2002–2012; Mitchell, 2012). In this chapter, we will use selected tools in Stata to illustrate the concepts of graphical presentation and exploration of survey data.

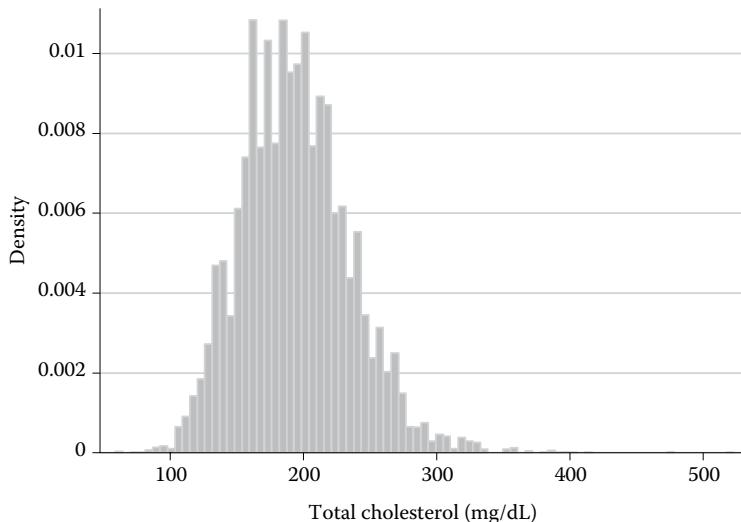
The key requirement in any graphical treatment of complex sample survey data is that the method and the software must enable the analyst to incorporate the influences of the survey weights in the construction of the final display. Just as an unweighted estimate of a mean may be biased for the true population value, a statistical graphic developed from unweighted survey data may present a misleading image of the true survey population that the analysis is intended to represent. The graphics programs in today's statistical software packages differ in their capability to incorporate weights in graphical analyses. Stata is one package that can incorporate the survey weights in the development of statistical graphics; however, as the examples in this chapter will illustrate, the different graphics programs may require specification of the survey weight as a standard probability weight (`pweight =`), a population frequency weight (`fweight =`), a relative weight (`aweight =`) that Stata proportionately scales to the sample size, or a flexible, user-defined weight (`iweight =`) designed for specific forms of estimation in Stata programs. Stata graphics include a number of options for displaying the estimated form of the population distribution for a single variable, including histograms, boxplots, spikeplots, and kernel density (`kdensity`) plots. The following two examples demonstrate Stata's capability to build histogram and boxplot graphics that incorporate survey weights.

EXAMPLE 5.1: A WEIGHTED HISTOGRAM OF TOTAL CHOLESTEROL (SOURCE: 2011–2012 NHANES)

After first opening the NHANES data set in Stata, we generate an indicator variable for adults (respondents with age greater than or equal to 18), for use in the analyses:

```
gen age18p = 1 if age >= 18 & age != .  
replace age18p = 0 if age < 18
```

The Stata software considers system missing values as being larger than the largest nonmissing value for a variable in a data set. This is the reason for the condition that the value on the AGE variable must be greater than or equal to 18 *and* not missing for the indicator variable

**FIGURE 5.2**

A weighted histogram of total cholesterol. (From 2011–2012 NHANES.)

to be equal to 1. System missing values are important to consider in *all* software packages when manually creating indicator variables, so that missing values are not mistakenly coded into either a 1 or 0.

The following Stata commands then generate the weighted histogram of NHANES total cholesterol measures presented in [Figure 5.2](#).

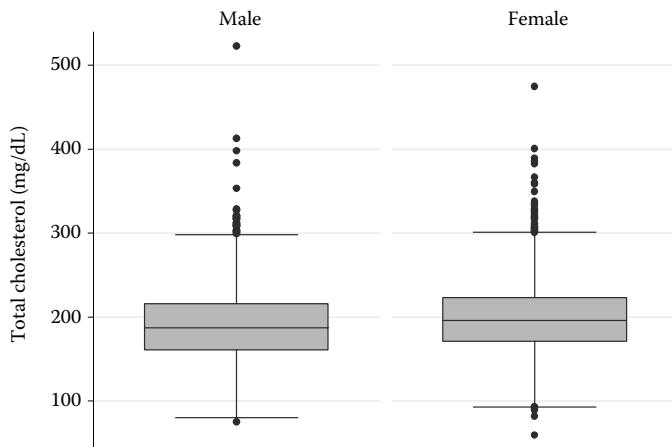
```
generate int_wtmec2yr = int(wtmec2yr)
histogram lbxtc if age18p [fweight = int_wtmec2yr]
```

Note that the Stata `histogram` command requires that the weight be specified as an integer `fweight` (frequency weight) value. Since these frequency weights must be integer values, a new weight is created by dropping the decimal places from the original values of the 2011–2012 NHANES mobile examination center (MEC) survey weight, `WTMEC2YR`. Since `WTMEC2YR` is a population scale weight, trimming the decimal places will have no significant effect on the graphical representation of the estimated distribution of total cholesterol.

[Figure 5.2](#) displays the histogram generated by Stata. Since the NHANES sample data inputs have been weighted, the distributional form of the histogram is representative of the estimated distribution for the NHANES survey population of U.S. adults aged 18 and older.

EXAMPLE 5.2: WEIGHTED BOXPLOTS OF TOTAL CHOLESTEROL FOR U.S. ADULT MEN AND WOMEN (SOURCE: 2011–2012 NHANES)

For scientific reports and papers, boxplots are a very useful tool for graphical presentation of the estimated (weighted) population distributions of single survey variables. The following Stata command requests a

**FIGURE 5.3**

Boxplots of the gender-specific weighted distributions of total serum cholesterol for U.S. adults. (From 2011–2012 NHANES.)

pair of boxplots that represent the estimated gender-specific population distributions of total serum cholesterol in the U.S. adults.

```
graph box lbxtc [pweight = wtmecc2yr] if age18p==1, ///
by(female)
```

Note that the Stata `graph box` command permits the specification of the analysis weight as a `pweight` (or probability weight) variable—no conversion to integer values is needed.

The pair of boxplots generated by the Stata command is displayed in [Figure 5.3](#). These boxplots suggest that male and female adults in the NHANES survey population have very similar distributions on this particular continuous variable.

5.3.2 Estimation of Population Totals

The estimation of a population total and its sampling variance has played a central role in the development of probability sampling theory. In survey practice, optimal methods for estimation of population totals are extremely important in government and academic surveys that focus on agriculture (e.g., acres in production), business (e.g., total employment), and organizational research (e.g., hospital costs). Acres of corn planted per year, total natural gas production for a 30-day period, and total expenditures attributable to a prospective change in benefit eligibility are all research questions that require efficient estimation of population totals. In those agencies and disciplines where estimation of population totals plays a central role, advanced “model-assisted” estimation procedures and specialized software are the norm. Techniques such as the *generalized regression (GREG) estimator* or *calibration estimators* integrate the survey data with known population controls on the distribution of

the population weighting factors to produce efficient weighted estimates of population totals (DeVille and Särndal, 1992; Valliant et al., 2000).

Most statistical software packages do not currently support advanced techniques for estimating population totals such as the GREG or calibration methods. Valliant et al. (2000) provide an extensive library of S-plus code implementing these estimation procedures, which can readily be translated into R code (Valliant et al., 2013). Stata and other software systems that support complex sample survey data analysis do provide the capability to compute simple weighted or *expansion estimates* of finite population totals, and also include a limited set of options for including population controls in the form of poststratified estimation (Theory Box 5.1).

In the case of a complex sample design including stratification (with strata indexed by $h = 1, \dots, H$) and cluster sampling (with clusters within stratum h indexed by $\alpha = 1, 2, \dots, a_h$), the simple weighted estimator for the population total can be written as follows:

$$\hat{Y}_w = \sum_{h=1}^H \sum_{\alpha=1}^{a_h} \sum_{i=1}^{n_{h\alpha}} w_{h\alpha i} y_{h\alpha i}. \quad (5.1)$$

A closed-form, unbiased estimate of the variance of this estimator is:

$$var(\hat{Y}_w) = \sum_{h=1}^H \frac{a_h}{(a_h - 1)} \left[\sum_{\alpha=1}^{a_h} \left(\sum_{i=1}^{n_{h\alpha}} w_{h\alpha i} y_{h\alpha i} \right)^2 - \frac{\left(\sum_{\alpha=1}^{a_h} \sum_{i=1}^{n_{h\alpha}} w_{h\alpha i} y_{h\alpha i} \right)^2}{a_h} \right]. \quad (5.2)$$

THEORY BOX 5.1 THE HORVITZ–THOMPSON ESTIMATOR OF A POPULATION TOTAL

The *H-T estimator* (Horvitz and Thompson, 1952) of the population total for a variable Y is written as follows:

$$\hat{Y} = \sum_{i=1}^N \frac{\delta_i Y_i}{p_i} = \sum_{i=1}^n \frac{y_i}{p_i}. \quad (5.3)$$

In Equation 5.3, $\delta_i = 1$ if element i is included in the sample and 0 otherwise, and p_i is the probability of inclusion in the sample for element i . The H-T estimator is an unbiased estimator for the population total Y , because the only random variable defined in the estimator is the indicator of inclusion in the sample (the y_i and p_i values are fixed in the population):

$$E(\hat{Y}) = E \sum_{i=1}^N \frac{\delta_i Y_i}{p_i} = \sum_{i=1}^N \frac{E(\delta_i) Y_i}{p_i} = \sum_{i=1}^N \frac{p_i Y_i}{p_i} = \sum_{i=1}^N Y_i = Y. \quad (5.4)$$

An unbiased estimator of the sampling variance of the H-T estimator is:

$$var(\hat{Y}) = \sum_{i=1}^n y_i^2 \frac{(1-p_i)}{p_i^2} + \sum_{i=1}^n \sum_{j \neq i}^n \frac{y_i y_j}{p_{ij}} \left(\frac{p_{ij} - p_i p_j}{p_i p_j} \right). \quad (5.5)$$

In this expression, p_{ij} represents the probability that both elements i and j are included in the sample; these joint inclusion probabilities must be supplied to statistical software to compute these variance estimates.

The H-T estimator weights each sample observation inversely proportionate to its sample selection probability, $w_{HT,i} = w_{sel,i} = 1/p_i$, and does not explicitly consider nonresponse adjustment or poststratification (Section 2.7). In fact, when the survey weight incorporates all three of these conventional weight factors, the variance estimator (5.2) does not fully reflect the stochastic sample-to-sample variability associated with the nonresponse mechanism, nor does it capture true gains in precision that may have been achieved through the poststratification of the weights to external population controls. Because survey nonresponse is a stochastic process that operates on the selected sample, the variance estimator could (in theory) explicitly capture this added component of sample-to-sample variability (Valliant, 2004). This method assumes that the data user can access the individual components of the survey weight, in addition to unique codes for the poststrata. Stata does provide the capability to directly account for the reduction in sampling variance due to the poststratification using the `poststrata()` and `postweight()` options for the `svyset` command.

The effects of nonresponse adjustment and poststratification weighting on the sampling variance of estimated population totals and other descriptive statistics may also be captured through the use of replicate weights, in which the nonresponse adjustment and the poststratification controls are separately developed for each BRR, JRR or Bootstrap replicate sample of cases (Valliant et al., 2013).

Recall from Section 3.6.2 that this simple estimator for the variance of a weighted total plays an important role in the computation of Taylor Series Linearization (TSL) estimates of sampling variances for more complex estimators that can be approximated as linear functions of estimated totals.

This simple weighted estimator of the finite population total is often labeled the *Horvitz–Thompson estimator* or “H-T” estimator (Horvitz and Thompson, 1952). Practically speaking, this labeling is convenient, but the estimator in Equation 5.1 and the variance estimator in Equation 5.2 make additional assumptions beyond those that are explicit in Horvitz and Thompson’s original derivation. Theory Box 5.1 provides interested readers with a short summary of the theory underlying the H-T estimator.

Two major classes of totals can be estimated using Equation 5.1. If y_{hai} is a binary indicator for an attribute (e.g., 1 = has the disease, 0 = disease free), the result is an estimate of the size of the subpopulation that shares that attribute:

$$\hat{Y}_w = \sum_{h=1}^H \sum_{\alpha=1}^{a_h} \sum_{i=1}^{n_{h\alpha}} w_{hai} y_{hai} = \hat{M} \leq \sum_{h=1}^H \sum_{\alpha=1}^{a_h} \sum_{i=1}^{n_{h\alpha}} w_{hai} \cdot 1 = \hat{N}.$$

Alternatively, if y is a continuous measure of an attribute of the sample case (e.g., acres of corn, monthly income, annual medical expenses), the result is an estimate of the population total of y , $\hat{Y}_w = \sum_{h=1}^H \sum_{\alpha=1}^{a_h} \sum_{i=1}^{n_{h\alpha}} w_{hai} y_{hai} = \hat{Y}$. Example 5.3 will illustrate the estimation of a subpopulation total, and Example 5.4 will illustrate the estimation of a population total of a variable Y .

EXAMPLE 5.3: ESTIMATING THE TOTAL COUNT OF U.S. ADULTS WITH A LIFETIME MAJOR DEPRESSIVE EPISODE (MDE)

The MDE variable in the NCS-R data set is a binary indicator (1 = yes, 0 = no) of whether an NCS-R respondent reported an MDE at any point in their lifetime. The aim of this example analysis is to estimate the total number of individuals who have experienced a lifetime MDE along with the standard error of the estimate (and the 95% confidence interval [CI]).

For this analysis, the NCS-R survey weight variable NCSRWTSH is selected to analyze all respondents completing the Part I survey ($n = 9,282$), where the lifetime diagnosis of MDE was assessed. Because the NCS-R data producers normalized the values of the NCSRWTSH variable so that the weights would sum to the sample size, the weight values must be expanded back to the population scale in order to obtain an unbiased estimate of the population total. This is accomplished by multiplying the Part I weight for each case by the ratio of the NCS-R survey population total ($N = 209,128,094$ U.S. adults aged 18+, Source: July 2001 Current Population Survey) divided by the count of sample observations ($n = 9,282$). The SECLUSTR variable contains the codes representing NCS-R sampling error clusters, while SESTRAT is the sampling error stratum variable.

```
gen ncsrwtsh_pop = ncsrwtsh * (209128094 / 9282)
svyset seclustr [pweight = ncsrwtsh_pop], strata(sestrat)
```

Once the complex design features of the NCS-R sample have been identified using the `svyset` command, the `svy: total` command is issued to obtain an unbiased weighted estimate of the population total along with a standard error for the estimate. The `mat list r(table)` post-estimation command then displays the actual estimates and confidence limits (rather than the default scientific notation that is used for large values), and the `estat effects` command computes an estimate of the design effect for this estimated total.

```
svy: total mde
mat list r(table)
estat effects
```

n	df	\hat{Y}_w	$se(\hat{Y}_w)$	$CI_{0.95}(\hat{Y}_w)$	$d^2(\hat{Y}_w)$
9,282	42	40,092,206	2,567,488	(34,910,806, 45,273,607)	9.03

The resulting Stata output indicates that 9,282 observations have been analyzed and that there are 42 design-based degrees of freedom. The weighted estimate of the total population of the U.S. adults who have experienced an episode of major depression in their lifetime is $\hat{Y} = 40,092,206$. The estimated value of the design effect for the weighted estimate of the population total is $d^2(\hat{Y}_w) = 9.03$, suggesting that the NCS-R variance of the estimated total is approximately nine times greater than that expected for a simple random sample of the same size.

Weighted estimates of population totals can also be computed for subpopulations. Consider subpopulations of NCS-R adults classified by marital status (married, separated/widowed/divorced, and never married). Under the complex NCS-R sample design, correct unconditional subpopulation analyses (Section 4.5.2) can be specified in Stata by adding the `over()` option to the `svy: total` command:

```
svy: total mde, over(mar3cat)
mat list r(table)
estat effects
```

Subpopulation	n	Estimated Total Lifetime MDE	Standard Error	95% CI	$d^2(\hat{Y})$
Married	5,322	20,304,190	1,584,109	(17,107,330, 23,501,051)	6.07
Sep./wid./div.	2,017	10,360,671	702,601	(8,942,723, 11,778,618)	2.22
Never married	1,943	9,427,345	773,137	(7,867,090, 10,987,600)	2.95

Note that the MAR3CAT variable is included in parentheses, to request estimates for each subpopulation defined by the levels of that variable.

We once again include the `mat list r(table)` postestimation command, which prints the full estimates of the totals and their confidence limits (rather than using scientific notation).

EXAMPLE 5.4: USING THE HRS DATA TO ESTIMATE TOTAL HOUSEHOLD WEALTH

Next, consider the example problem of estimating the total value of household wealth for the 2012 HRS target population (the U.S. households with adults born prior to 1960). The 2012 HRS constructed variable that measures total wealth for HRS household financial units is H11ATOTA. It is equal to the total value of reported household assets minus the household liabilities (debts), exclusive of assets/liabilities related to ownership of second homes.

To begin the analysis, we first identify the HRS variables containing the sampling error computation units (SECU), or ultimate clusters, and the sampling error stratum codes (STRATUM). We also specify the NWGTHH variable as the survey weight variable for the analysis, because we are performing an analysis at the level of the HRS household financial unit. The HRS data set includes an indicator variable (NFINR for 2012) that identifies the individual respondent who is the financial reporter for each HRS sample household. This variable is used to create a subpopulation indicator (FINR) that restricts the estimation to only sample members who are financial reporters for their HRS household unit. We then apply the `svy: total` command to the H11ATOTA variable, measuring the total value of household wealth.

```
gen finr = 1
replace finr = 0 if nfinr != 1
svyset secu [pweight = nwgthh], strata(stratum) ///
vce(linearized) singleunit(missing)
svy, subpop(finr): total H11ATOTA
```

<i>n</i>	<i>df</i>	\hat{Y}_w	$se(\hat{Y}_w)$	$CI_{0.95}(\hat{Y}_w)$
13,657	56	$\$2.53 \times 10^{13}$	$\$1.35 \times 10^{12}$	$(2.26 \times 10^{13}, 2.80 \times 10^{13})$

The Stata output indicates that the 2012 HRS target population includes approximately 58,970,000 households (not shown). In 2012, these 59 million estimated households owned household wealth valued at an estimated $\hat{Y}_w = \$2.53 \times 10^{13}$, with a 95% CI of $(\$2.26 \times 10^{13}, \$2.80 \times 10^{13})$.

5.3.3 Means of Continuous, Binary, or Interval Scale Data

The estimation of the population mean, \bar{Y} , for a continuous, binary or interval scale variable is a very common task for survey researchers seeking to describe the central tendencies of these variables in populations of interest. An estimator of the population mean, \bar{Y} , can be written as a nonlinear ratio of two estimated finite population totals:

$$\bar{y}_w = \frac{\sum_{h=1}^H \sum_{\alpha=1}^{a_h} \sum_{i=1}^{n_{h\alpha}} w_{h\alpha i} y_{h\alpha i}}{\sum_{h=1}^H \sum_{\alpha=1}^{a_h} \sum_{i=1}^{n_{h\alpha}} w_{h\alpha i}} = \frac{\hat{Y}}{\hat{N}}. \quad (5.6)$$

Note that if y is a binary variable coded 1 or 0, the weighted mean estimates the population proportion or prevalence, P , of “1s” in the population ([Chapter 6](#)):

$$\bar{y}_w = \frac{\sum_{h=1}^H \sum_{\alpha=1}^{a_h} \sum_{i=1}^{n_{h\alpha}} w_{h\alpha i} y_{h\alpha i}}{\sum_{h=1}^H \sum_{\alpha=1}^{a_h} \sum_{i=1}^{n_{h\alpha}} w_{h\alpha i}} = \frac{\hat{M}}{\hat{N}} = p. \quad (5.7)$$

Since \bar{y}_w is not a linear statistic, a closed-form formula for the variance of this estimator does not exist. As a result, variance estimation methods such as TSL, BRR, JRR, or the Bootstrap ([Chapter 3](#)) must be used to compute an estimate of the sampling variance of this estimator of the population mean. An application of TSL to the weighted mean in Equation 5.6 results in the following TSL variance estimator for the ratio mean:

$$var(\bar{y}_w) \doteq \frac{var(\hat{Y}) + \bar{y}_w^2 \times var(\hat{N}) - 2 \times \bar{y}_w \times cov(\hat{Y}, \hat{N})}{\hat{N}^2}. \quad (5.8)$$

Closed-form formulas are available to estimate the variances and covariances of the estimators of the population totals included in this TSL expression (Section 3.6.2), and BRR, JRR, and Bootstrap replicated variance estimation methods can also be used to estimate the standard errors of the estimated means (Section 3.6.3).

EXAMPLE 5.5: ESTIMATING THE MEAN VALUE OF HOUSEHOLD INCOME USING THE 2012 HRS DATA

In this example, we analyze the mean of the household income variable (H11ITOT) for the 2012 HRS survey population. Because this is a household-level measure, we once again apply the 2012 HRS household weight variable, NWGTHH.

```
svyset secu [pweight=nwgthh], strata(stratum) ///
vce(linearized) singleunit(missing)
```

The `svy: mean` command is then submitted in Stata to compute the weighted estimate of the mean household income in the 2012 HRS population:

```
svy, subpop(finr): mean h11itot
```

<i>n</i>	<i>df</i>	\bar{y}_w	$se(\bar{y}_w)$	$CI_{0.95}(\bar{y}_w)$
13,657	56	\$71,382	\$1,937	(\$67,502, \$75,263)

We see that the estimated mean of total household income for the HRS survey population is \$71,382, with an associated 95% CI of (\$67,502, \$75,263).

EXAMPLE 5.6: ESTIMATING MEAN SYSTOLIC BLOOD PRESSURE USING THE NHANES DATA

In this example, the 2011–2012 NHANES data are used to estimate the mean systolic blood pressure (mmHg) for the U.S. adult population aged 18 and older. The survey weight is the NHANES medical examination weight (WTMEC2YR). The following Stata command sequence declares the variables describing the complex sampling features of the 2011–2012 NHANES to Stata (where SDMVPSU contains masked PSU codes and SDMVSTRA contains masked stratum codes), generates the subpopulation indicator (AGE18P), and then computes the weighted estimate of the mean systolic blood pressure, the linearized estimate of the standard error of the weighted mean (based on an appropriate unconditional subclass analysis), a design-based 95% CI for the mean, and a design effect for the estimate:

```
svyset sdmvpsu [pweight = wtmecc2yr], strata(sdmvstra) ///
vce(linearized) singleunit(missing)
gen age18p = 1 if age >= 18 and age != .
replace age18p = 0 if age < 18
svy, subpop(age18p): mean bpxsy1
estat effects
```

<i>n</i>	<i>df</i>	\bar{y}_w	$se(\bar{y}_w)$	$CI_{0.95}(\bar{y}_w)$	$d^2(\bar{y}_w)$
5,132	17	122.03	0.62	(120.73, 123.33)	8.41

Based on the sample of $n = 5,132$ individual observations, the 2011–2012 NHANES estimate of mean systolic blood pressure for the U.S. adults aged 18 and older is $\bar{y}_w = 122.03$ mmHg. As observed in the examples of estimation of population totals, the design effect is fairly large when estimating a descriptive population parameter for the entire target population. For this estimate of mean systolic blood pressure, the estimated design effect ratio indicates that the variance of the estimated mean for the full NHANES sample is over eight times greater than would be expected from a simple random sample of the same size. For this estimate of mean systolic blood pressure in U.S. adults, the NHANES effective sample size is roughly $n_{eff} \sim 5132/8.41 = 610$.

EXAMPLE 5.7: ESTIMATING THE MEAN VALUE OF TOTAL HOUSEHOLD WEALTH USING THE HRS DATA

Next, the 2012 HRS data are used to compute an estimate of the mean of total household wealth for U.S. households with at least one adult born

prior to 1960. As in Example 5.4, the estimate is restricted to the subpopulation of HRS respondents who are the financial reporters for their household unit. The Stata commands required to perform this analysis follow:

```
svyset secu [pweight=nwgthh], strata(stratum)
svy, subpop(finr): mean H11ATOTA
estat effects
```

<i>n</i>	<i>df</i>	\bar{y}_w	$se(\bar{y}_w)$	$CI_{0.95}(\bar{y}_w)$	$d^2(\bar{y}_w)$
13,657	56	\$428,471	\$17,354	(\$393,707, \$463,234)	3.21

Based on this analysis of reports from $n = 13,657$ HRS financial units, the mean of 2012 household wealth in the HRS survey population is $\bar{y}_w = \$428,471$. The estimated design effect for the estimated mean, $d^2(\bar{y}_w) = 3.21$, indicates that while there is still a loss of precision in the HRS estimate relative to simple random sampling, the loss in effective sample size is not as severe as in the previous example based on the NHANES data.

5.3.4 Standard Deviations of Continuous Variables

Although experience suggests that it is not a common task, survey analysts may wish to compute an unbiased estimate of the population standard deviation of a continuous variable. Just as weights are required to obtain unbiased (or nearly unbiased) estimates of the population mean, weights must also be employed to obtain consistent estimates of the standard deviation of a random variable in a designated target population. A weighted estimator of the population standard deviation of a variable y can be written as follows:

$$s(y)_w = \sqrt{\frac{\sum_{h=1}^H \sum_{\alpha=1}^{a_h} \sum_{i=1}^{n_{h\alpha}} w_i (y_i - \bar{y}_w)^2}{\sum_{h=1}^H \sum_{\alpha=1}^{a_h} \sum_{i=1}^{n_{h\alpha}} w_i - 1}}. \quad (5.9)$$

In Equation 5.9, the estimate of the population mean for the variable y is calculated as in Equation 5.6. In Stata, analysts may use the `summary` command in combination with an “`aweight`” specification for the survey weight variable to generate this unbiased estimate of the population standard deviation.

EXAMPLE 5.8: ESTIMATION OF THE POPULATION STANDARD DEVIATIONS OF NHANES 2011–2012 MEASURES OF HIGH-DENSITY LIPOPROTEIN (HDL) AND TOTAL CHOLESTEROL LEVEL

The following Stata code illustrates the syntax for weighted estimation of the population standard deviation for continuous random variables. The variables used in this example are the NHANES 2011–2012 adult

sample measures of high-density lipoprotein (LBDHDD) and total cholesterol (LBXTC).

```
svyset sdmvpsu [pweight=wtmec2yr], strata(sdmvstra) ///
vce(linearized) singleunit(missing)
sum lbdhdd lbxtc [aweight=wtmec2yr] if age18p==1
```

Variable	<i>n</i>	Sum of Weights	\bar{y}_w	$s(y)_w$
High-density cholesterol	5,187	218,642,036	52.83	14.93
Total cholesterol	5,187	218,642,036	194.43	41.05

Users of the SAS software® can use PROC UNIVARIATE or PROC MEANS with a WEIGHT statement to generate this weighted estimate of the population standard deviation S_y .

5.3.5 Estimation of Percentiles, Medians, and Measures of Inequality in Population Distributions for Continuous Variables

5.3.5.1 Estimation of Distribution Quantiles

Estimation of quantiles, such as the median (Q_{50}) or the 95th percentile (Q_{95}) of the population distribution of a continuous variable, can play an important role in analyses of survey data. A sociologist may wish to compare sample estimates of percentiles of household income for a regional survey population to nationally defined poverty criteria. An epidemiologist may wish to estimate the 95th percentile of prostate-specific antigen (PSA) levels in a metropolitan sample of men over the age of 40.

The *ungrouped method* of quantile estimation (Loomis et al., 2005) builds on results related to the weighted estimator for totals presented earlier in this chapter (Section 5.3.2), employing a weighted sample estimate of the population *cumulative distribution function (CDF)* of a survey variable. Specifically, the CDF for a variable y in a given finite population of size N is defined as follows:

$$F(x) = \frac{\sum_{i=1}^N I(y_i \leq x)}{N}. \quad (5.10)$$

In Equation 5.10, $I(y_i \leq x)$ is an indicator variable equal to 1 if y_i is less than or equal to a specified value of y (denoted here by x), and 0 otherwise. The weighted estimator of the CDF from a complex sample of size n from this population is then written as follows:

$$\hat{F}(x) = \frac{\sum_{h=1}^H \sum_{\alpha=1}^{a_h} \sum_{i=1}^{n_{h\alpha}} w_{h\alpha i} I(y_{h\alpha i} \leq x)}{\sum_{h=1}^H \sum_{\alpha=1}^{a_h} \sum_{i=1}^{n_{h\alpha}} w_{h\alpha i}}. \quad (5.11)$$

The q -th quantile (e.g., $q = 0, 0.25, 0.50, 0.75, 1$) for a variable y is the smallest value of y such that the population CDF is greater than or equal to q . For example, the median would be the smallest value of y at which the CDF is greater than or equal to 0.5. The ungrouped method of estimating a quantile first considers the order statistics (the sample values of y ordered from smallest to largest), denoted by y_1, \dots, y_n , and finds the value of j ($j = 1, \dots, n$) such that:

$$\hat{F}(y_j) \leq q < \hat{F}(y_{j+1}). \quad (5.12)$$

Then, the estimate of the q -th population quantile Y_q is calculated as follows:

$$\hat{Y}_q = y_j + \frac{q - \hat{F}(y_j)}{\hat{F}(y_{j+1}) - \hat{F}(y_j)} (y_{j+1} - y_j). \quad (5.13)$$

Kovar et al. (1988) report results of a simulation study that suggests that Balanced Repeated Replication (BRR) performs well for variance estimation and construction of CIs when working with estimators of nonsmooth functions like quantiles. Both SAS and the WesVar PC software currently implement the BRR variance estimation approach for quantiles, and we recommend the use of this variance estimation approach for estimated quantiles in practice. Variance estimates for the estimated quantile in Equation 5.13 can also be computed using TSL (Binder, 1991). The SAS software currently uses the linearized variance estimator by default. The JRR approach to variance estimation is known to be badly biased for these types of estimators (Miller, 1974), but modifications to the Jackknife approach addressing this problem have been developed (Shao and Wu, 1989).

EXAMPLE 5.9: ESTIMATING POPULATION QUANTILES FOR TOTAL HOUSEHOLD WEALTH USING THE HRS DATA

This example considers the total household wealth variable collected from the 2012 HRS sample and aims to estimate the 0.25 quantile, the median, and the 0.75 quantile of household wealth in the HRS target population. The SAS software is used first in this example because the base Stata software (Version 14+) does not currently support commands specifically dedicated to the estimation of standard errors of weighted estimates of quantiles in complex sample survey data sets. Stata users can download and install the user-written `epctile` command (using `net install epctile.pkg` in web-aware Stata) to compute weighted estimates of quantiles along with estimated (linearized) standard errors and approximate 95% CIs.

The following SAS code generates the quantile estimates and standard errors, using an unconditional subclass analysis approach:

```
proc surveymeans data=to.hrs_sub_10jun2016 q1 median q3;
  weight nwghhh; stratum stratum; cluster secu;
  var h11atota;
  domain finrr12;
run;
```

TABLE 5.1

Estimation of Percentiles of the Distribution of Total Household Wealth

Percentile	SAS (TSL)		SAS (BRR)		Stata (TSL)	
	\hat{Q}_p	$se(\hat{Q}_p)$	\hat{Q}_p	$se(\hat{Q}_p)$	\hat{Q}_p	$se(\hat{Q}_p)$
Q_{25}	\$21,953	\$2,215	\$21,953	\$2,287	\$22,000	\$2,200
Q_{50} (median)	\$141,907	\$7,754	\$141,907	\$7,761	\$142,000	\$8,000
Q_{75}	\$439,965	\$18,652	\$439,965	\$19,940	\$440,000	\$18,869

Source: 2012 HRS.

Table 5.1 summarizes the results provided in the SAS output and compares the estimates with those generated using the BRR approach to variance estimation in the SAS software. In SAS, BRR variance estimation is requested by simply adding the VARMETHOD = BRR specification to the PROC SURVEYMEANS command statement.

The estimated median of the total household wealth for the HRS target population is \$141,907. The estimate of the mean total household wealth from Example 5.7 was \$428,471, suggesting that the distribution is highly skewed to the higher dollar value ranges.

From the side-by-side comparison in **Table 5.1**, SAS BRR estimates of the corresponding standard errors differ slightly from the TSL standard errors as expected. The resulting inferences about the population quantiles would not differ substantially in this example as a result.

The following Stata code can be used to perform the same analysis using the aforementioned user-written command:

```
svyset secu [pweight = nwgthh], strata(stratum)
epctile H11ATOTA, percentiles(25 50 75) ///
subpop(if nfinr==1) svy
```

We note how unconditional subpopulation analyses can also be performed using this command in Stata, where the subpopulation is specified as an option. We also note that the `svy` option is needed to refer to the complex sample design variables identified in the `svyset` command. The Stata results in **Table 5.1** indicate that while some rounding of the estimates is performed, the results are in agreement with those generated using TSL in SAS.

5.3.5.2 Estimation of Measures of Inequality in Population Distributions

Estimation of individual quantiles for the distribution of a continuous variable enables the survey analyst to address questions such as “What is the median value of total household wealth in the U.S. households with members aged 65 and older?” Furthermore, by estimating quantiles at multiple points over the (0, 1) range of $F(y)$, for example, $q = \{0.01, 0.05, 0.10, 0.25, 0.50, 0.75, 0.90, 0.95, 0.99\}$, the analyst can gain insight into how the variable of interest is distributed across the elements in the population. This is especially

important when the characteristic of interest is highly skewed across the survey population and simple measures of central tendency (means) and dispersion (standard deviation) may not be sufficient to describe the underlying distribution. This is true in household surveys where financial measures of income, wealth, debts and liabilities, and medical expenditures are highly skewed in the direction of small subpopulations with large unit values. It is also true in surveys of businesses and farms where small fractions of the full survey population account for a major share of the production of a good, service, or commodity (e.g., refined gasoline, mobile telephone service, livestock).

To answer questions regarding nonuniformity in the distribution of such variables across the elements of the target population, economists and other social scientists have developed a growing class of graphical displays and indices as tools to describe distributional inequality (Nygard and Sandstrom, 1981; Lorenz, 1905). Complex sample survey data are often used as the basis for deriving the statistical measures of inequality for target populations, and over the past 20 years there has been steady development in the theory for correctly producing weighted estimates and robust standard errors of these statistics (Binder and Kovacevic, 1995; Bhattacharya, 2007; Langel and Tille, 2013). Software procedures for estimating inequality statistics from complex sample survey data are also now available as user-written commands or functions (e.g., Stata .ado files or R packages) available for the major statistical software systems (Jenkins, 2006; Alfons and Templ, 2013).

**EXAMPLE 5.10: ESTIMATING THE LORENZ CURVE
AND GINI COEFFICIENT FOR THE 2012
HRS POPULATION DISTRIBUTION
OF TOTAL HOUSEHOLD WEALTH**

This example will illustrate an application of the user-written Stata command `svylorenz` (Jenkins, 2006) to estimate the Gini coefficient for the distribution of total household wealth in the HRS target population of the U.S. households. The Gini coefficient takes values in the (0, 1) range, and in this example measures the degree of inequality in the distribution of total wealth across the population of households that is studied in the 2012 HRS. A Gini coefficient value of $G = 0$ indicates perfect equality in the wealth distribution, with larger values signifying increasingly greater inequality in the wealth distribution.

Following the estimating equation formulation of Binder and Kovacevic (1995), an estimator of the Gini coefficient is:

$$\hat{G}(y) = \frac{2 \cdot \sum_{h=1}^H \sum_{\alpha=1}^{a_h} \sum_{i=1}^{n_{h\alpha}} w_{h\alpha i}^* \cdot \hat{F}_{h\alpha i} \cdot y_{h\alpha i} - 1}{\bar{y}_w}, \quad (5.14)$$

where:

$$w_{hai}^* = w_{hai} / \sum_h \sum_\alpha \sum_i w_{hei}.$$

\hat{F}_{hai} = the estimate of the CDF, $F(y)$, at the ordered value of y for case i in cluster α and stratum h .

\bar{y}_w = the weighted estimate of the mean of y .

After installing the svylorenz command, the following sequence of Stata commands will generate the estimates and standard errors for the Gini coefficient, the share (proportion) of the total wealth held by the quantile group, the cumulative share by quantile group, and the Lorenz curve ordinates for total household wealth based on the 2012 HRS.

```
svyset secu [pweight=nwgthh], strata(stratum)
gen posh1latota=h1latota
replace posh1latota=0 if h1latota<0
gen finr=1
replace finr=0 if nfinr!=1
svylorenz posh1latota, ngp(10) subpop(finr)
```

For this example analysis, all negative reported values of H11ATOTA are set to a minimum value of 0 since the svylorenz command requires that all values be greater than or equal to zero. Table 5.2 summarizes the results of this analysis of wealth inequality in the 2012 HRS household population. The estimated Gini coefficient is $\hat{G}(y) = 0.726$ ($SE = 0.009$), which suggests a high degree of concentration of total wealth among households in the upper deciles of the total asset distribution. The

TABLE 5.2

Estimation of Wealth Inequality Measures for the 2012 HRS Population of Households

Statistic	Estimate	Standard Error	95% Confidence Interval
Gini coefficient	0.726	0.009	(0.708, 0.745)
<i>Group Share (Percent) of Total Household Wealth</i>			
1st decile	0.00%	–	(0.00%, 0.00%)
2nd decile	0.06%	0.01%	(0.04%, 0.08%)
3rd decile	0.50%	0.05%	(0.43%, 0.62%)
4th decile	1.42%	0.08%	(1.25%, 1.60%)
5th decile	2.57%	0.13%	(2.30%, 2.83%)
6th decile	4.21%	0.18%	(3.86%, 4.57%)
7th decile	6.50%	0.24%	(5.99%, 6.92%)
8th decile	10.30%	0.34%	(9.60%, 10.90%)
9th decile	17.20%	0.48%	(16.29%, 18.18%)
10th decile	57.24%	1.39%	(54.52%, 59.97%)

Source: 2012 HRS.

degree of concentration is evident in the estimates of the group shares of total wealth for the 10 deciles of the household distribution. The upper decile is estimated to hold 57.2% ($SE = 1.4\%$) of all wealth owned by the 2012 HRS household population.

5.4 Bivariate Relationships between Two Continuous Variables

There are four basic analytic approaches that can be used to examine bivariate relationships between two continuous survey variables: (1) generation of a scatter plot; (2) computation of a pair-wise correlation coefficient, r ; (3) estimation of the ratio of two continuous variables, $\hat{R} = \hat{Y}/\hat{X}$; and (4) estimation of the coefficients of the simple linear regression of one variable on another, $\hat{Y} = \hat{\beta}_0 + \hat{\beta}_1 \cdot X$. The first three of these techniques are reviewed in this section. [Chapter 7](#) will address the estimation of linear regression models for continuous dependent variables in detail.

5.4.1 X–Y Scatter Plots

A comparison of the 2011–2012 NHANES MEC measures of HDL (the y variable) and total serum cholesterol (the x variable) illustrates how a simple scatter plot can be used to gain insight into the bivariate relationship of two survey variables. [Figure 5.4](#) presents an unweighted scatter plot examining

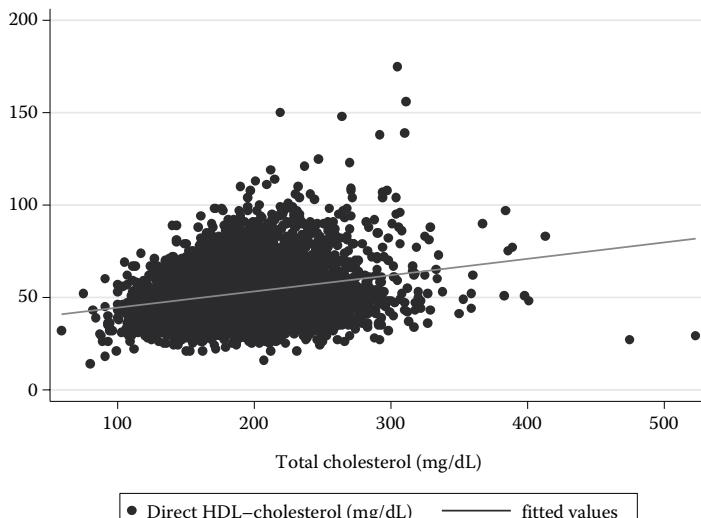


FIGURE 5.4

HDL versus total serum cholesterol (mg/dL) in U.S. adults (unweighted points, with the fit of a weighted regression line included). (From 2011–2012 NHANES.)

the relationship of these two variables. The figure not only suggests a positive relationship between HDL and total serum cholesterol but also illustrates considerable variability in the relationship and the presence of a few points that stand out as potential outliers. A drawback to the simple X-Y scatter plot summary is that there is no practical way to incorporate the population weights and the corresponding population frequency associated with each point in the two-dimensional X-Y space. Stata does provide a unique display in which the area of the dot representing an X-Y point is proportionate to its survey weight, and other packages (e.g., the survey package in R) offer these capabilities as well. Unfortunately, in survey data sets with hundreds and even thousands of data points, it is not possible to obtain the resolution needed to evaluate single points or to detect patterns in these types of weighted scatter plot displays.

One technique for introducing information on the effect of the weights in the plotted X-Y relationship is to overlay on the scatter plot the line representing the weighted regression of y on x , $\hat{y}_{wls} = \hat{\beta}_0 + \hat{\beta}_1 \cdot x$. To do this in the Stata software, we use the twoway graphing command, where the first command in parentheses defines the scatter plot and the second command overlays the weighted estimate of the simple linear regression model relating total cholesterol to HDL cholesterol (note that the probability weight variable is defined in square brackets for the second command).

```
twoway (scatter lbdhdd lbxtc if age18p==1) ///
(lfit lbdhdd lbxtc if age18p==1 [pweight=wtmec2yr])
```

5.4.2 Product Moment Correlation Statistic (r)

The product moment correlation (r) is a standard measure of the linear association between two continuous variables. Kish and Frankel (1974) included this pair-wise correlation statistic in their simulation studies and found that TSL, BRR, and JRR performed similarly in the estimation of standard errors for estimates of pair-wise correlation statistics. Unfortunately, few current software systems provide the capability to estimate single correlations (or weighted correlation matrices) and CIs for r that account for complex sample design features.

A weighted estimator of the product moment correlation statistic is written as follows:

$$\begin{aligned}
r_w &= \frac{s_{xy,w}}{s_{x,w} \cdot s_{y,w}} \\
&= \frac{\sum_{h=1}^H \sum_{\alpha=1}^{a_h} \sum_{i=1}^{n_{h\alpha}} w_{h\alpha i} (y_{h\alpha i} - \bar{y}_w)(x_{h\alpha i} - \bar{x}_w)}{\sqrt{\sum_{h=1}^H \sum_{\alpha=1}^{a_h} \sum_{i=1}^{n_{h\alpha}} w_{h\alpha i} (y_{h\alpha i} - \bar{y}_w)^2} \cdot \sqrt{\sum_{h=1}^H \sum_{\alpha=1}^{a_h} \sum_{i=1}^{n_{h\alpha}} w_{h\alpha i} (x_{h\alpha i} - \bar{x}_w)^2}}. \quad (5.15)
\end{aligned}$$

If a survey analyst does require weighted estimates and standard errors for the pair-wise correlation statistic, an alternative to direct estimation is to first standardize the two variables for which the correlation is desired, and then compute a weighted estimate of the slope parameter in a simple linear regression model relating the two standardized variables ([Chapter 7](#)).

**EXAMPLE 5.11: ESTIMATION OF THE CORRELATION OF
ADULTS' TOTAL AND HIGH-DENSITY
CHOLESTEROL MEASURES IN THE
2011–2012 NHANES**

In this example, we will use the 2011–2012 NHANES data and illustrate the indirect method of linear regression and standardized survey measures to estimate the correlation of total and high-density cholesterol levels in the U.S. adult population. To begin, we use the Stata `summary` command with the `[aweight =]` specification to obtain weighted estimates of the population mean and standard deviation for the two cholesterol measures (see Example 5.8 for estimation of the means and standard deviations):

```
sum lbdhdd lbxtc [aweight=wtmec2yr] if age18p==1
```

The Stata `correlate` command with the `[aweight =]` specification produces a weighted estimate of the population correlation, $r_w = 0.241$:

```
correlate lbdhdd lbxtc [aweight=wtmec2yr] if age18p==1
```

Next, the original values for the NHANES high-density (LBDHDD) and total (LBXTC) cholesterol measures are “standardized” by subtracting from each value the estimated mean and dividing that difference by the weighted estimate of the standard deviation.

```
gen stdlbxtc = (lbxtc - 194.4355) / 41.05184
gen stdlbdhdd = (lbdhdd - 52.83826) / 14.93157
summary stdlbdhdd stdlbxtc [aweight=wtmec2yr] if age18p==1
```

The `summary` command produces output that confirms (not shown) that the standardized cholesterol measures do, in fact, have a mean of zero and a standard deviation of 1.0.

Using Stata’s `svy: regress` command, the standardized measure for high-density cholesterol is regressed on the standardized value for total cholesterol. Using the standard `svyset` syntax, the regression is weighted by the NHANES MEC weight, and the estimated (linearized) standard error of the weighted estimate of the total cholesterol coefficient accounts for the primary stage stratification and cluster sampling in the complex sample design.

```
svyset sdmvpsu [pweight=wtmec2yr], strata(sdmvstra)
svy, subpop(age18p): regress stdlbdhdd stdlbxtc
```

Variable	<i>n</i>	$\hat{\beta}$	$se(\hat{\beta})$	<i>df</i>	$CI_{0.95,df}(\beta)$
STDLBXTC	5,187	0.241	0.014	17	(0.211, 0.271)

The coefficient, $\hat{\beta}$, in the weighted regression of std1bdhdd on std1bxtc is a population-weighted estimate of the correlation of the two cholesterol measures. The estimated value, $\hat{\beta} = r_w = 0.241$, matches the weighted estimate for the original (not standardized) variable generated above using the correlate command. The design-adjusted standard error of the correlation estimate is $se(\hat{\beta}) = se(r_w) = 0.014$, and the corresponding design-based 95% CI is $CI_{0.95,17}(\beta) = (0.211, 0.271)$.

5.4.3 Ratios of Two Continuous Variables

Occasionally, survey analysts need to estimate the ratio of two continuous survey variables (e.g., the ratio of HDL cholesterol level to total cholesterol). The ratio estimator of the population mean (5.6) of a single variable can be generalized to an estimator of the population ratio of two survey variables:

$$\hat{R} = \frac{\hat{Y}}{\hat{X}} = \frac{\sum_{h=1}^H \sum_{\alpha=1}^{\alpha_h} \sum_{i=1}^{n_{h\alpha}} w_{h\alpha i} y_{h\alpha i}}{\sum_{h=1}^H \sum_{\alpha=1}^{\alpha_h} \sum_{i=1}^{n_{h\alpha}} w_{h\alpha i} x_{h\alpha i}}. \quad (5.16)$$

The following TSL approximation provides estimates of the sampling variance of ratio estimates:

$$var(\hat{R}) \doteq \frac{var(\hat{X}) + \hat{R}^2 \cdot var(\hat{Y}) - 2 \cdot \hat{R} \cdot cov(\hat{Y}, \hat{X})}{\hat{X}^2}. \quad (5.17)$$

BRR and JRR estimation options now available in the major statistical software packages provide an appropriate alternative to TSL for estimating standard errors of R .

EXAMPLE 5.12: ESTIMATING THE POPULATION RATIO OF HIGH-DENSITY TO TOTAL CHOLESTEROL FOR U.S. ADULTS

A weighted estimate of this ratio based on 2011–2012 NHANES respondents aged 18+ is obtained in Stata using the svy: ratio command. Note that we once again define the subpopulation indicator (AGE18P) first before running the analysis, assuming that the variable has not been generated already:

```
svyset sdmvpsu [pweight=wtmec2yr], strata(sdmvstra)
gen age18p = 1 if age >= 18 and age != .
replace age18p = 0 if age < 18
svy, subpop(age18p): ratio (lbdhdd/lbxtc)
estat effects
```

<i>n</i>	<i>df</i>	\hat{R}	$se(\hat{R})$	$CI_{0.95}(\hat{R})$	$d^2(\hat{R})$
5,187	17	0.271	0.003	(0.265, 0.278)	8.030

THEORY BOX 5.2 RATIO ESTIMATORS OF POPULATION TOTALS

If two survey variables x and y are highly correlated and a control total for the variable x , X_{pop} , is known from an auxiliary data source, then the ratio estimator of the population total, $\hat{Y}_R = \hat{R} \cdot X_{pop}$, may provide a more precise estimate than the simple weighted estimator of the population total, \hat{Y}_w , described in Section 5.3.2. Because X_{pop} is assumed to be free of sampling variability, the standard error of the ratio estimator of the population total is $se(\hat{Y}_R) = se(\hat{R}) \cdot X_{pop}$.

Note that the two variables defining the numerator and denominator of the ratio are indicated in parentheses in the `svy: ratio` command, with the numerator variable listed before a forward slash (/), and the denominator variable listed after the slash.

Estimates of ratios may also be used to compute ratio estimates of population totals. See Theory Box 5.2.

5.5 Descriptive Statistics for Subpopulations

Section 4.5.3 discussed the important analytical differences between *conditional* and *unconditional* subpopulation analyses. Section 5.3.2 presented examples of unconditional subpopulation analyses in the estimation of totals. Stata's `svy` commands provide two options for correctly specifying subpopulation analyses. The `over()` option requests unconditional subclass analyses for subpopulations defined based on *all* levels of a categorical variable. This option is only available in Stata's descriptive analysis procedures. The more general `subpop()` option can be used with all `svy` commands in Stata. This option requests analysis for a specific subpopulation identified by an indicator variable, coded 1 if the case belongs to the subpopulation of interest and 0 otherwise. Procedures for survey data analysis in other software packages will have similar command options available for these subpopulation analyses (see the book web site for examples).

EXAMPLE 5.13: ESTIMATING THE PROPORTIONS OF MALES AND FEMALES AGE ≥ 70 WITH DIABETES USING THE HRS DATA

This first subpopulation analysis example uses the 2012 HRS data set to estimate the prevalence of diabetes for U.S. males and females aged 70 years and older. Because the HRS variable `DIABETES` is equal to 1 for respondents with diabetes and 0 otherwise, estimating the mean of this binary variable will result in the prevalence estimates of interest. The

following example command uses a logical condition in the `subpop()` option to specify the age range and then the `over()` option to perform separate subpopulation analyses for males and females.

```
svyset secu [pweight=nwgtr], strata(stratum) ///
vce(linearized) singleunit(missing)
svy: mean diabetes, subpop(if nage >= 70) over(gender)
```

We see that more elderly men (27.3%) are estimated to have diabetes

Gender	<i>df</i>	<i>n</i>	\bar{y}_w	$se(\bar{y}_w)$	$CI_{0.95}(\bar{y}_w)$
Male	54	3,495	0.273	0.007	(0.259, 0.289)
Female	54	4,369	0.227	0.009	(0.210, 0.244)

compared with elderly women (22.7%).

It might be tempting for an analyst to make the mistake of taking a *conditional* approach to these subpopulation analyses, using a Stata command like the following:

```
svy: mean diabetes if age > 70
```

Use of the subsetting `if` modifier to define a subpopulation for stratified samples is inappropriate because all cases not satisfying the condition are temporarily deleted from the analysis, along with their sample design information. This effectively fixes the stratum sample sizes for variance estimation calculations (when in fact the strata subpopulation sample sizes should be treated as random variables). See [Chapter 4](#) for more details.

EXAMPLE 5.14: ESTIMATING MEAN SYSTOLIC BLOOD PRESSURE FOR MALES AND FEMALES AGE >45 USING THE 2011–2012 NHANES DATA

Consider an example based on NHANES of estimating the mean systolic blood pressure for male and female adults over the age of 45. We once again illustrate a combination of options in Stata to set up this analysis, using a logical condition in the `subpop()` option to specify the age range and then the `over()` option to perform subpopulation analyses for males and females in this age range separately. We also request design effects for each subpopulation estimate using the `estat effects` postestimation command.

```
svy, subpop(if age > 45) : mean bpxsy1, over(gender)
estat effects
estat size
```

Gender	<i>n</i>	<i>df</i>	\bar{y}_w	$se(\bar{y}_w)$	$CI_{0.95}(\bar{y}_w)$	$d^2(\bar{y}_w)$
Male	1,329	17	128.30	0.87	(126.47, 130.13)	3.53
Female	1,343	17	128.12	0.95	(126.19, 130.18)	4.27

Survey analysts should be aware that restricting analysis to a subpopulation of the full sample may result in a reduction in the effective

degrees of freedom for variance estimation. Since Stata employs the variable degrees of freedom method discussed in Section 3.5.2, its programs ignore any original design strata that do not contain one or more observations from the subpopulation of interest. Stata signals that complete strata have been dropped by including a note in the output indicating that one or more design strata were “omitted because they contain no subpopulation members.” Approaches to this issue are not currently uniform across the different major statistical software packages.

The greatest reductions in effective degrees of freedom for variance estimation can occur when survey analysts are interested in estimation for rare subpopulations that comprise only a small percent of the survey population, or the subpopulation of interest is defined by a domain of sample strata, such as a single Census region. (Refer to [Figure 4.4](#) in [Chapter 4](#) for an illustration of how subpopulations may be distributed across the strata and clusters of a complex sample design.)

Software procedures for correct unconditional subpopulation analyses are currently also available in R (the *survey* package), SUDAAN, WesVar PC, Mplus, SPSS Complex Samples, and SAS (the SURVEY procedures). Examples of subpopulation analyses using these other software systems are available on the book web site.

5.6 Linear Functions of Descriptive Estimates and Differences of Means

The capability to estimate *functions* of descriptive statistics, especially differences of means or proportions, is an important feature of many survey analyses. In general, many important functions of descriptive statistics can be written as *linear combinations* of the descriptive statistics of interest. Examples of such linear combinations of estimates include differences of means, weighted sums of means used to build economic indices, or computation of a moving average of three monthly survey means:

$$\begin{aligned}\hat{\Delta} &= \bar{y}_1 - \bar{y}_2 \\ \hat{I} &= 0.25 \cdot \bar{y}_1 + 0.40 \cdot \bar{y}_2 + 1.5 \cdot \bar{y}_3 + 1.0 \cdot \bar{y}_4 \\ \bar{y}_{moving} &= (1/3) \cdot \bar{y}_{t1} + (1/3) \cdot \bar{y}_{t2} + (1/3) \cdot \bar{y}_{t3}.\end{aligned}$$

Consider the general form of a linear combination of $j = 1, \dots, J$ descriptive statistics (e.g., estimates of means for J subpopulations):

$$f(\theta_1, \dots, \theta_J) = \sum_{j=1}^J a_j \theta_j. \quad (5.18)$$

In Equation 5.18, θ_j represents the statistic of interest for the j -th subpopulation, while the a_j terms represent constants defined by the analyst. This function is estimated by simply substituting estimates of the descriptive statistics into the expression:

$$f(\hat{\theta}_1, \dots, \hat{\theta}_J) = \sum_{j=1}^J a_j \hat{\theta}_j. \quad (5.19)$$

The variance of this estimator is then calculated as follows:

$$\text{var}\left(\sum_{j=1}^J a_j \hat{\theta}_j\right) = \sum_{j=1}^J a_j^2 \text{var}(\hat{\theta}_j) + 2 \times \sum_{j=1}^{J-1} \sum_{k>j}^J a_j a_k \text{cov}(\hat{\theta}_j, \hat{\theta}_k). \quad (5.20)$$

Note that the variance of the linear combination incorporates the variances of the individual component estimates as well as the covariances of the estimated statistics.

Covariance between descriptive estimates can arise in several ways. First, the statistics of interest may represent overlapping subpopulations (Kish, 1987). An example would be a contrast comparing the mean systolic blood pressure for men to that for the total population, for example, $\hat{\Delta} = \bar{y}_{\text{total}} - \bar{y}_{\text{male}}$, or a longitudinal analysis in which the mean blood pressures of a sample panel of individuals are compared at two points in time, $\hat{\Delta} = \bar{y}_{\text{time}2} - \bar{y}_{\text{time}1}$. Due to the intraclass correlation among the sample elements within sample design clusters of complex sample designs, a degree of covariance is possible even when estimates are based on nonoverlapping samples, for example, $\hat{\Delta} = \bar{y}_{\text{female}} - \bar{y}_{\text{male}}$.

Under conditions where samples are overlapping or the complex design itself induces a covariance in the sample estimates, statistical software must compute and store the covariances of estimates in order to correctly compute the variance of a linear combination of means or other descriptive statistics. Stata's `lincom` command is one example of a postestimation command that enables analysts to correctly compute estimates and standard errors for linear combinations of estimates.

5.6.1 Differences of Means for Two Subpopulations

Analysts of survey data are frequently interested in making inferences about differences of descriptive statistics for two subpopulations. The inference can be based on a 95% CI for the difference of the two means, for example,

$$CI = (\bar{y}_{\text{female}} - \bar{y}_{\text{male}}) \pm t_{df, .975} \cdot se(\bar{y}_{\text{female}} - \bar{y}_{\text{male}}), \quad (5.21)$$

or it might employ a *two-sample t-test* based on the Student *t*-statistic,

$$t = (\bar{y}_{\text{female}} - \bar{y}_{\text{male}}) / se(\bar{y}_{\text{female}} - \bar{y}_{\text{male}}). \quad (5.22)$$

Applying the general formula for the variance of a linear combination (Equation 5.20 above), the standard error of the difference in the mean of the two subpopulation samples can be expressed as:

$$se(\bar{y}_1 - \bar{y}_2) = \sqrt{var(\bar{y}_1) + var(\bar{y}_2) - 2cov(\bar{y}_1, \bar{y}_2)}. \quad (5.23)$$

Under simple random sampling, the covariance of estimates from distinct subpopulation samples is zero; however, for clustered samples or samples that share elements, the covariance of the two sample means may be non-zero and generally positive in value. The following example estimates the contrast in the mean value of total household wealth for two subpopulations of HRS households: one subpopulation in which the household head has less than a high school education and a second subpopulation of households headed by a college-educated adult.

**EXAMPLE 5.15: ESTIMATING DIFFERENCES IN MEAN
TOTAL HOUSEHOLD WEALTH BETWEEN
HRS SUBPOPULATIONS DEFINED BY
EDUCATIONAL ATTAINMENT LEVEL**

Testing differences of subpopulation means using the svy: mean procedure in Stata is a two-step process. First, the mean of total household wealth is estimated for subpopulations defined by the levels of the EDCAT variable in the HRS data set. The estimates are further restricted to HRS household financial respondents (FINR = 1), and the 2012 HRS household weight (NWGTHH) is used to compute the estimated means.

```
gen finr = 1
replace finr = 0 if nfinr != 1
svyset secu [pweight = nwgthh], strata(stratum) ///
vce(linearized) singleunit(missing)
svy, subpop(finr): mean hilatota, over(edcat)
```

Education of Head (Years)	Stata Label	\bar{y}_w	$se(\bar{y}_w)$	$CI_{0.95}(\bar{y}_w)$
0–11	1	\$122,089	\$10,595	(\$100,863, \$143,314)
12	2	\$259,027	\$9,802	(\$239,390, \$278,664)
13–15	3	\$336,308	\$17,201	(\$301,849, \$370,768)
16+	4	\$834,141	\$46,478	(\$741,035, \$927,247)

Stata automatically saves these estimated means along with their estimated variances and covariances in memory until the next command is issued. Stata assigns the four subpopulations of household heads

with 0–11, 12, 13–15, and 16+ years of education to internal reference labels 1, 2, 3, and 4.

Following the computation of the subpopulation means, the `lincom` postestimation command is used to estimate the difference in means for household heads with 0–11 (subpopulation 1) versus 16+ years of education (subpopulation 4):

```
lincom [h11atota]1 - [h11atota]4
```

Education of Head	$\bar{y}_{0-11} - \bar{y}_{16+}$	$se(\bar{y}_{0-11} - \bar{y}_{16+})$	$CI_{0.95}(\bar{y}_{0-11} - \bar{y}_{16+})$
0–11 versus 16+	-\$712,052	\$48,886	(-\$809,983, -\$614,122)

After this postestimation command is submitted, Stata outputs the estimated difference of the two subpopulation means ($\hat{\Delta} = \bar{y}_{0-11} - \bar{y}_{16+} = -\$712,052$). The 95% CI for the population difference does not include 0, suggesting that households headed by a college graduate have a significantly higher mean total household wealth compared with households in which the head does not have a high school diploma.

To display the estimated variance–covariance matrix for the subpopulation estimates of mean household wealth, the Stata postestimation command `vce` is used:

`vce`

The output produced by this command is shown in the symmetric 4×4 matrix in [Table 5.3](#). Note that in this example, the covariance of the estimated means for the 0–11 and 16+ household heads is small and negative (-0.587×10^8).

Applying the formula for the standard error of the contrast:

$$\begin{aligned} se(\bar{y}_{0-11} - \bar{y}_{16+}) &= \sqrt{var(\bar{y}_{0-11}) + var(\bar{y}_{16+}) - 2 \cdot cov(\bar{y}_{0-11}, \bar{y}_{16+})} \\ &= \sqrt{[1.123 + 21.600 - 2 \times (-0.587)] \times 10^8} \\ &\doteq \$48,886. \end{aligned}$$

TABLE 5.3

Estimated Variance–Covariance Matrix for Estimated Subpopulation Means of Total Household Wealth (Estimates by Education Level of Household Head)

Subpopulation	1	2	3	4
1	1.123×10^8	0.257×10^8	0.564×10^8	-0.587×10^8
2		0.961×10^8	0.640×10^8	0.194×10^8
3			2.959×10^8	1.572×10^8
4				2.160×10^9

Source: 2012 HRS.

The result of this direct calculation exactly matches the output from the `lincom` command in Stata.

5.6.2 Comparing Means over Time

Analysts working with longitudinal survey data are often interested in comparing the means of a longitudinal series of survey measures. [Chapter 11](#) will address the various types of longitudinal data and introduce more sophisticated tools for longitudinal analysis of survey data.

When comparing means on single variables measured at two or more “waves” or points in time, an approach similar to that used in Section 5.6.1 can be applied. However, since longitudinal data are often released as a separate file for each time period with distinct weight values for each time point, special data preparation steps may be needed. We now consider an example of this approach using two waves of data from the HRS.

**EXAMPLE 5.16: ESTIMATING DIFFERENCES IN
MEAN TOTAL HOUSEHOLD WEALTH FROM
2010 TO 2012 USING DATA FROM THE HRS**

To estimate the difference in 2010 and 2012 mean household wealth for households in the HRS target population, the first step is to “stack” the 2010 and 2012 HRS data sets, combining them into a single data set. Provided that they responded to the survey in both HRS waves, each panel household has two records in the stacked data set—one for their 2010 observation and another for the 2012 interview. We provide more details on how to deal with attrition when analyzing longitudinal data in [Chapter 11](#).

Each pair of household records includes the wave-specific measure of total household wealth and the wave-specific survey weight. For this example, when stacking the data sets, we assigned these values to two new common variables, `TOTWEALTH` and `HHWEIGHT`. Each record also includes the permanently assigned stratum and cluster codes. As described in Example 5.4, the HRS public use data sets include an indicator variable for each wave of data that identifies the respondents who are the household financial reporters (`MFINR` for 2010, `NFINR` for 2012). Using the `over(year)` option, estimates of mean total household wealth are computed separately for 2010 and 2012. The `subpop(finx2010 _ 2012)` option restricts the estimates to the financial reporters for each of these two data collection years. The postestimation `lincom` statement then estimates the difference of means for the two time periods, its linearized standard error, and a 95% CI for the difference.

```
gen hhweight = mwgthh
replace hhweight = nwgthh if year == 2012
gen totwealth = h10atota
replace totwealth = h11atota if year == 2012
gen finr2010 = 0
replace finr2010 = 1 if (year == 2010 & mfinr == 1)
```

```

gen finr2012 = 0
replace finr2012 = 1 if (year == 2012 & nfinr == 1)
gen finr2010_2012 = 0
replace finr2010_2012 = 1 if finr2010 == 1 | finr2012 == 1
svyset secu [pweight=hhweight], strata(stratum) ///
vce(linearized) singleunit(missing)
svy, subpop(finr2010_2012): mean totwealth, over(year)

```

Total Wealth	\bar{y}_{year}	$se(\bar{y}_{year})$
2010	\$432,829	\$16,011
2012	\$437,807	\$17,016

lincom [totwealth]2010 - [totwealth]2012

Contrast	$\bar{y}_{2010} - \bar{y}_{2012}$	$se(\bar{y}_{2010} - \bar{y}_{2012})$	$CI_{0.95}(\bar{y}_{2010} - \bar{y}_{2012})$
2010 versus 2012	-\$4,978	\$7,936	(-\$20,877, \$10,921)

Note that the `svyset` command has been used again to specify the recoded survey weight variable (HHWEIGHT) in the stacked data set. The `svy: mean` command is then used to request weighted estimates and linearized standard errors (and the covariance of the estimates, which is saved internally) for each subpopulation defined by the YEAR variable. The resulting estimate of the difference of means is $\hat{\Delta} = \bar{y}_{2010} - \bar{y}_{2012} = -\$4,978$, with a linearized standard error of \$7,936. The analysis does not provide evidence that the mean total household wealth increased significantly from 2010 to 2012, a period in which the U.S. households were still recovering from the impacts of the global recession that began in 2008.

EXERCISES

- 5.1 Download the European Social Survey (ESS)—Russian Federation data set from the ASDA website. Using any statistical software, explore the data set by obtaining a list of variables and identify the complex sample design and weight (poststratification weight) variables. Answer these questions:
- What are the names of each variable?
 - How many strata and clusters does this data set have?
 - Examine the distributional characteristics of the weight variable. Fill in the table below. Does the weight sum to the sample size or a population total?

Summary of weight variable (PSPWGHT)

N	Sum	N Missing	Mean	Minimum	Maximum

- d. How many design degrees of freedom will be used during analysis and how did you calculate this number?
- 5.2 Identify the two survey variables measuring (1) Satisfaction with Life and (2) Trust in the Police. Next, answer the following questions:
- Prepare a weighted (if possible in your software of choice) histogram for each variable STFLIFE and TRSTPLC. What conclusions can be made based on the histograms?
 - What measurement scale is used for each variable and how can you justify use of a continuous variable analysis approach for these variables?
 - Use a statistical software procedure of your choice and fill in the table below. Ignore the complex sampling features for this initial descriptive analysis.

Variable Name	N	Mean	SE	Minimum	Maximum

- d. Perform a weighted analysis (with no design correction of the standard errors) for the same two variables. Obtain the same statistics as requested in part c, and complete the table below.

Variable Name	N	Mean	SE	Minimum	Maximum

- e. Repeat the analysis from part d, but perform a fully design-based analysis, using the weights and the stratum and cluster codes for variance estimation. Use both the TSL method and the JRR methods for variance estimation. Fill in the table below.

Variable Name	N	Mean	TSL SE	JRR SE	Minimum	Maximum

- f. How do the standard errors differ between the four analyses of parts c, d, and e? What impacts do the weights and the design variables have on the standard errors? Is there a difference between the standard errors using the TSL versus the JRR variance estimation method?
- g. Calculate the design effects and confidence limits for both means manually. Use the weighted mean and standard errors from the

TSL variance estimation in Part e. (*Hint:* use the weighted SE² for the SRS variance and the TSL SE² for the complex sampling variance.) What are the design effects and CIs for each mean? Verify your results by using a statistical software procedure and requesting design effects and CIs from a fully design-based analysis.

Variable Name	N	Mean	TSL SE	95% CI	Design Effect

- 5.3 Estimate the proportion of people in the Russian Federation target population who voted in the last election. Use the variable called VOTED_LASTELECTION, the TSL method for variance estimation, and the PSPWGHT variable for weighted estimation.
- What is the estimated proportion of people in the ESS Russian Federation who voted in the last election? What are the standard error and confidence limits for this proportion? Is this proportion of people who voted significantly different from a hypothesized proportion of 0.55?
 - Reestimate the proportion of voters among the subclasses of the variable called MALE (0 = Female, 1 = Male). Make sure to use an unconditional approach for this analysis.
 - Next, calculate the difference in proportions between men and women and discuss if the difference is significant at the alpha = 0.05 level. What conclusions would you make about the voting behavior among men and women?
- 5.4 Using a software procedure of your choice (remember that not all software enables percentile estimation in addition to estimation of standard errors for weighted estimates of percentiles) and the NHANES 2011–2012 data set, estimate the 25th percentile, the median, and the 75th percentile of Body Mass Index (BMXBMI) for U.S. adults aged 50 and older. You will need to create a subpopulation indicator of respondents aged 50+ for this analysis. Remember to perform an appropriate subpopulation analysis for this population subclass. Compute 95% CIs for each percentile.

6

Categorical Data Analysis

If the same group of individuals is classified in two or more different ways, as persons may be classified as inoculated and not inoculated, and also may be attacked and not attacked by disease, then we may require to know if the two classifications are independent.

R.A. Fisher
1925

6.1 Introduction

A casual perusal of the codebook and variable descriptions for most public-use survey data sets quickly leads to the observation that the responses to the majority of survey questions in the social sciences, public health, and related fields of research are measured as a binary choice (e.g., yes, no), a selection from multinomial response categories (e.g., ethnicity), a choice from an ordinal scale (e.g., strongly agree to strongly disagree) or possibly a discrete count of events. This chapter covers procedures for simple univariate, bivariate, and selected multivariate analyses for such categorical survey responses, focusing on the adaptation of established analytic techniques to complex sample survey data. For readers interested in a fuller discussion of these basic techniques of categorical data analysis, we recommend Agresti (2012).

The outline of this chapter parallels that of [Chapter 5](#). Section 6.2 highlights several important considerations in categorical data analysis for complex sample surveys. Basic methods for analyzing a single categorical variable are described in Section 6.3, including estimation of category proportions, goodness of fit (GOF) tests to compare the sample estimates with hypothesized population values, and graphical display of the estimated population distribution across the K categories of the single variable. Section 6.4 extends the discussion to bivariate analyses, including statistics that measure association and tests of hypotheses concerning independence of two categorical variables. The chapter concludes in Section 6.5 with coverage of two techniques for multivariate categorical data: the Cochran–Mantel–Haenszel (CMH) test and simple log-linear models for crosstabulated data. Multivariate regression modeling and related methods for categorical data will be introduced later in [Chapters 8 and 9](#).

6.2 Framework for Analysis of Categorical Survey Data

We begin this chapter by introducing a framework for the analysis of categorical data collected in complex sample surveys. We introduce methods for accommodating complex sample design features and important considerations for both univariate and bivariate analyses of categorical data. Sections 6.3 and 6.4 go into more detail about these analysis approaches.

6.2.1 Incorporating the Complex Design and Pseudo Maximum Likelihood

The simplicity of categorical survey responses can belie the range of sophistication of categorical data analysis techniques—techniques that range from the simplest estimation of category proportions to complex multivariate and even multilevel regression models. The majority of the standard estimators and test statistics for categorical data analysis are derived under the method of *maximum likelihood* and assume that the data are independent and identically distributed (i.i.d.) according to a discrete probability distribution. Under simple random sampling (SRS) assumptions, categorical variables are assumed to follow one of the several known probability distributions or *sampling models* (Agresti, 2012), that is, the binomial, the multinomial, the Poisson, the product-multinomial or, more rarely, a hypergeometric model. Unfortunately, due to sample weighting, cluster sampling, and stratification, the true likelihood of the sample survey data is generally difficult to specify analytically. Therefore, the simple elegance of maximum likelihood methods for estimation and inference does not easily transfer to complex sample survey data.

This chapter will introduce the methods and software that survey statisticians have developed to adjust standard analyses for complex sample design effects, including weighted estimates of proportions, design-based estimates of sampling variance, and generalized design effect corrections for key test statistics. Later, in [Chapters 8](#) and [9](#), different forms of the generalized linear model and *pseudo maximum likelihood* techniques will be discussed for regression modeling of categorical data that follow approximate binomial, multinomial, Poisson, or negative binomial distributions.

6.2.2 Proportions and Percentages

In Section 6.3, we discuss estimation of proportions and their standard errors. In this chapter, we denote estimates of population proportions as \hat{p} and population proportions as π . Many software packages choose to output estimates of proportions and standard errors on the percentage scale.

Translation between estimates and standard errors for proportions and percentages simply involves the following multiplicative scaling:

$$\text{percent} = 100 \cdot p, \quad \text{se}(\text{percent}) = 100 \cdot \text{se}(p), \quad \text{var}(\text{percent}) = 100^2 \cdot \text{var}(p).$$

While these relationships may be obvious to experienced analysts, our experience suggests that it is easy for mistakes to be made, especially in translating standard errors from the percentage to the proportion scale.

6.2.3 Crosstabulations, Contingency Tables, and Weighted Frequencies

Categorical data analysis becomes more complex (and also more interesting) when the analysis is expanded from a single variable to include two or more categorical variables. With two categorical variables, the preferred summary is typically a two-way data display with $r = 1, \dots, R$ rows and $c = 1, \dots, C$ columns, often referred to in statistical texts and literature as a *crosstabulation* or a *contingency table*. Crosstabs and contingency tables are not limited to two dimensions but may include a third (or higher) dimension, that is, $l = 1, \dots, L$ layers or subtables based on the categories of a third variable. For simplicity of presentation, the majority of the examples in this chapter will be based on the crosstabulation of two categorical variables (Section 6.4).

Consider the simple $R = 2$ by $C = 2$ (2×2) tabular display of observed sample frequencies shown in Figure 6.1. Under SRS, one-, two-, three-, or higher dimension arrays of unweighted sample frequencies like the 2×2 array illustrated in Figure 6.1 can be used directly to estimate statistics of interest, such as the proportion of individuals in category 1 of variable 2 that respond in category 1 of variable 1, $p_{1|1} = n_{11}/n_{1+}$, or derive tests of hypotheses for the relationships between categorical variables, for example, the Pearson chi-square (χ^2) test.

However, because individuals can be selected into a sample with varying probabilities, estimates and test statistics computed from the unweighted sample frequencies may be biased for the true properties of the survey

Variable 2	Variable 1		Row margin
	0	1	
0	n_{00}	n_{01}	n_{0+}
1	n_{10}	n_{11}	n_{1+}
Column margin	n_{+0}	n_{+1}	n_{++}

FIGURE 6.1

Bivariate distribution of observed sample frequencies.

Variable 2	Variable 1		Row margin
	0	1	
0	\hat{N}_{00}	\hat{N}_{01}	\hat{N}_{0+}
1	\hat{N}_{10}	\hat{N}_{11}	\hat{N}_{1+}
Column margin	\hat{N}_{+0}	\hat{N}_{+1}	\hat{N}_{++}

FIGURE 6.2

Bivariate distribution of weighted sample frequencies.

population. Therefore, it is necessary to translate from unweighted sample counts to weighted frequencies, as shown in Figure 6.2. For example, the weighted frequency (or estimated population count) in cell $(0, 1)$ is $\hat{N}_{01} = \sum_{h=1}^H \sum_{\alpha=1}^{a_h} \sum_{i \in (0,1)} w_{h\alpha i}$. The weighted proportions estimated from these weighted sample frequencies, for example, $p_{rc} = \hat{N}_{rc}/\hat{N}_{++}$, will reflect the relative size of the total population in the corresponding cell, row margin, or column margin of the crosstabulation.

We discuss bivariate analyses in more detail in Section 6.4.

6.3 Univariate Analysis of Categorical Data

Simple descriptive analyses of a single categorical variable in a survey data set can take a number of forms, including estimation of a simple population proportion π for binary responses; estimation of the vector of population proportions for each of the $k = 1, \dots, K$ categories of a multcategory nominal or ordinal response variable; and, with care, estimation of the means for ordinally scaled responses (Section 5.3.3). To draw inferences about the population parameters being estimated, analysts can construct $100(1 - \alpha)\%$ confidence intervals (CIs) for the parameters or perform Student t or simple χ^2 hypothesis tests. Properly weighted graphical displays of the frequency distribution of the categorical variable are also very effective tools for presentation of results.

6.3.1 Estimation of Proportions for Binary Variables

Estimation of a single population proportion, π , for a binary response variable requires only a straightforward extension of the ratio estimator (Section 5.3.3) for the population mean of a continuous random variable. By recoding the original response categories to a single indicator variable y_i with possible values 1 and 0 (e.g., yes = 1, no = 0), the ratio mean estimator estimates the proportion or *prevalence*, π , of “1s” in the population:

$$p = \frac{\sum_{h=1}^H \sum_{\alpha=1}^{a_h} \sum_{i=1}^{n_{h\alpha}} w_{h\alpha i} I(y_i = 1)}{\sum_{h=1}^H \sum_{\alpha=1}^{a_h} \sum_{i=1}^{n_{h\alpha}} w_{h\alpha i}} = \frac{\hat{N}_1}{\hat{N}}. \quad (6.1)$$

Most software procedures for survey data analysis provide the user with at least two alternatives for calculating ratio estimates of proportions. The first alternative is to use the single variable option in commands such as `svy: prop` and `svy: tab` in Stata, or PROC SURVEYFREQ in SAS. These programs are designed to estimate the univariate proportions for the discrete categories of a single variable as well as total, row, and column proportions for crosstabulations of two or more categorical variables. The second alternative for estimating single proportions is to first generate an indicator variable for the category of interest (with value 1 if a case falls into the category of interest, or 0 if a case does not fall into the category of interest) and then apply a procedure designed for estimation of means (e.g., `svy: mean` in Stata or PROC SURVEYMEANS in SAS). Both approaches will yield identical estimates of the population proportion and the standard error, but as explained below, estimated CIs developed by the different procedures may not agree exactly due to differences in the methods used to derive the lower and upper confidence limits.

An application of Taylor Series Linearization (TSL) to the ratio estimator of π in Equation 6.1 results in the following TSL variance estimator for the ratio estimate of a simple proportion:

$$v(p) \doteq \frac{V(\hat{N}_1) + p^2 \cdot V(\hat{N}) - 2 \cdot p \cdot \text{cov}(\hat{N}_1, \hat{N})}{\hat{N}^2}. \quad (6.2)$$

Replication techniques (JRR, BRR, Bootstrap) can also be used to compute estimates of the variances of these estimated proportions and the corresponding design-based CIs and test statistics.

If the analyst estimates a proportion as the mean of an indicator variable (e.g., using Stata's `svy: mean` procedure), a standard design-based CI is constructed for the proportion: $CI(p) = p \pm t_{1-\alpha/2, df} \cdot se(p)$. One complication that arises when proportions are viewed simply as the mean of a binary variable is that the true proportion, π , is constrained to lie in the interval $(0, 1)$. When the estimated proportion of interest is extreme (i.e., close to 0 or close to 1), the standard design-based confidence limits may be less than 0 or exceed 1. To address this problem, alternative computations of design-based CIs for proportions have been proposed, including (among others) the logit transformation procedure and the modified Wilson procedure (Rust and Hsu, 2007; Dean and Pagano, 2015).

Stata's `svy: tab` command uses the logit transformation procedure by default. Implementation of this procedure for constructing a CI is a two-step

process. First, using the weighted estimate of the proportion, one constructs a 95% CI for the logit transform of p :

$$\begin{aligned} \text{CI} [\text{logit}(p)] &= \{A, B\} \\ &= \left\{ \ln\left(\frac{p}{1-p}\right) - \frac{t_{1-\alpha/2, df} \cdot se(p)}{p \cdot (1-p)}, \quad \ln\left(\frac{p}{1-p}\right) + \frac{t_{1-\alpha/2, df} \cdot se(p)}{p \cdot (1-p)} \right\}, \end{aligned} \quad (6.3)$$

where:

p = the weighted estimate of the proportion of interest;

$se(p)$ = the design-based Taylor Series approximation to the standard error of the estimated proportion.

Next, the two confidence limits on the logit scale, A and B, are transformed back to the original (0, 1) scale:

$$\text{CI}(p) = \left\{ \frac{e^A}{1+e^A}, \frac{e^B}{1+e^B} \right\}. \quad (6.4)$$

Although procedures such as `svy: tab` in Stata and PROC CROSSTAB in SUDAAN default to the logit transformation formula for estimating $\text{CI}(p)$ for all values of p , the adjusted CIs generally do not differ from the standard symmetric CIs unless $p < 0.10$ or $p > 0.90$. Via empirical simulation studies, Dean and Pagano (2015) find support for use of adjusted CIs based on the Agresti–Coull and Clopper–Pearson methods of forming the intervals when $p < 0.10$ or $p > 0.90$, and these authors also find that the logit transformation and modified Wilson procedures tend to work well in these settings (assuming that the standard error of the estimated proportion is not zero). Interested readers can find a description of the modified Wilson Procedure in Theory Box 6.1.

More recently, Wu (2016) has advocated for the computation of *empirical likelihood CIs* for finite population proportions (Wu and Rao, 2006), demonstrating empirically that they have improved coverage relative to other competing methods when proportions are extremely large or small. Unfortunately, outside of R code provided by Wu (2005) in Appendix Section A4 of his article, this approach is not yet widely implemented in standard software for the analysis of complex sample survey data. We will provide any updates in this regard on the book's web site.

EXAMPLE 6.1: ESTIMATING THE PROPORTION OF THE U.S. ADULT POPULATION WITH AN IRREGULAR HEARTBEAT

In this example, data from the 2011–2012 National Health and Nutrition Examination Survey (NHANES) are used to estimate the proportion of U.S. adults with an irregular heartbeat (defined by BPXPULS = 2 in the NHANES data set). To enable a direct comparison of the results from

THEORY BOX 6.1 THE MODIFIED WILSON PROCEDURE FOR $CI(p)$

The modified Wilson procedure (Kott and Carr, 1997; Korn and Graubard, 1999; Dean and Pagano, 2015) for complex samples constructs the confidence limits for the proportion using the expression:

$$CI(p)_{\text{Wilson}} = \frac{(2n^* p + t^2) \pm \left(t \sqrt{(t^2 + 4p(1-p)n^*)} \right)}{2(n^* + t^2)},$$

where:

p = is the weighted estimate of the population proportion, π ;

$t = t_{1-\alpha/2, df}$ = the $(1 - \alpha/2)$ critical value of the Student t distribution with df design degrees of freedom; and

$n^* = p \cdot (1 - p) / var_{des}(p) = n/d^2(p)$ = the effective sample size for the estimate of π .

From the 2011–2012 NHANES data, the modified 95% Wilson CI for the proportion of U.S. adults with an irregular heartbeat (computed using PROC SURVEYFREQ) is equal to (0.0131, 0.0205), which is quite similar to the design-based CI in Table 6.1 computed by Stata using the logit transformation procedure. Interested readers can review Dean and Pagano (2015) for additional empirical evaluations of the performance of these alternative approaches to forming intervals for proportions using survey data.

analyses performed using svy: tab, svy: prop, and svy: mean in Stata, we generate a binary indicator, equal to 1 for respondents reporting an irregular heartbeat, and 0 otherwise. The recoding of the original response categories for BPXPULS would not be necessary for estimation performed using either svy: tab or svy: prop. Note that as in the Chapter 5 analysis examples, we create an indicator for the adult subpopulation aged 18 and older, enabling appropriate unconditional subpopulation analyses (Section 4.5.2). As in previous examples, during the recoding steps, missing data on the original variable are explicitly assigned to a missing data code on the recoded variable.

```
gen irregular = .
replace irregular = 1 if bpxpuls == 2
replace irregular = 0 if bpxpuls == 1

gen age18p = 1 if age >= 18 & age != .
replace age18p = 0 if age < 18
svyset sdmvpsu [pweight = wtme2yr], strata(sdmvstr) ///
vce(linearized) singleunit(missing)
```

svy, subpop(age18p): tab irregular, se ci col deff
 svy, subpop(age18p): proportion irregular
 svy, subpop(age18p): mean irregular

TABLE 6.1

Estimated Proportions of Adults in the U.S. with Irregular Heartbeats

Variable	n	Design df	Estimated Proportion	Linearized SE	95% CI	Design Effect
<i>Stata svy: tab, CI based on logit transform technique</i>						
Irregular	5,374	17	0.0164	0.0017	(0.0132, 0.0204)	1.21
<i>Stata svy: prop, CI based on logit transform technique</i>						
Irregular	5,374	17	0.0164	0.0017	(0.0132, 0.0204)	1.21
<i>Stata svy: mean, CI computed using the standard symmetric interval</i>						
Irregular	5,374	17	0.0164	0.0017	(0.0129, 0.0200)	1.21

Source: 2011–2012 NHANES.

Table 6.1 provides the weighted estimate of the proportion, the estimated standard error, the 95% CI, and the estimated design effect produced by each of these three command alternatives. [Note that *svy: tab* and *svy: prop* produce estimated proportions and standard errors for each category; only the results for IRREGULAR = 1 are shown.]

The results in **Table 6.1** suggest that for the period 2011–2012, 1.64% of U.S. adults were estimated to have irregular heartbeats, with a 95% CI of (1.32%, 2.04%) using the logit transform method in the *svy: tab* and *svy: prop* commands and a 95% CI of (1.29%, 2.00%) from the *svy: mean* command. Although the two CIs are not substantially different, due to the small value of *p*, the logit transform 95% CI for the proportion of adults with an irregular heartbeat is not symmetric about the point estimate of 1.64% prevalence.

6.3.2 Estimation of Category Proportions for Multinomial Variables

Estimation of multinomial proportions and standard errors for multicategory survey response variables (e.g., ethnicity, measured by 1 = Mexican, 2 = Other Hispanic, 3 = White, 4 = Black, 5 = Other) is a direct extension of the method for estimating a single proportion. The ratio estimator in Equation 6.1 is simply applied to indicator variables for each distinct category *k*:

$$p_k = \frac{\sum_{h=1}^H \sum_{\alpha=1}^{a_h} \sum_{i=1}^{n_{h\alpha}} w_{h\alpha i} I(y_i = k)}{\sum_{h=1}^H \sum_{\alpha=1}^{a_h} \sum_{i=1}^{n_{h\alpha}} w_{h\alpha i}} = \frac{\hat{N}_k}{\hat{N}}. \quad (6.5)$$

The result is a vector of estimated population proportions for each category: $\mathbf{p} = \{p_1, \dots, p_K\} = \{\hat{N}_1/\hat{N}, \dots, \hat{N}_K/\hat{N}\}$. Standard errors for the weighted

TABLE 6.2

Estimated Proportions of Adults in the U.S. Population by Race/Ethnicity

Race/Ethnicity	Estimated Proportion	Linearized SE	95% CI	Design Effect
Mexican	0.079	0.017	(0.050, 0.124)	29.36
Other Hispanic	0.066	0.015	(0.041, 0.106)	26.84
White	0.659	0.039	(0.573, 0.736)	48.44
Black	0.117	0.023	(0.076, 0.176)	37.98
Other	0.078	0.011	(0.058, 0.104)	11.92

Source: 2011–2012 NHANES ($n = 5,615$).

estimates of the individual category proportions can be computed using TSL (as presented in Equation 6.2) or by BRR, JRR, or Bootstrap (replication) methods. The most convenient method of simultaneously estimating the K category proportions for a multinomial categorical variable is through the use of the single variable option in programs such as svy: tab or svy: prop in Stata or PROC SURVEYFREQ in SAS.

EXAMPLE 6.2: ESTIMATING THE PROPORTIONS OF U.S. ADULTS BY RACE AND ETHNICITY

The following Stata commands estimate the proportions of the 2011–2012 NHANES adult survey population by self-reported race and ethnicity:

```
svyset sdmvpsu [pweight = wtmecc2yr], strata(sdmvstr)
svy, subpop(age18p): prop ridreth1
estat effects
```

Table 6.2 presents the estimated proportions of U.S. adults for the five NHANES race/ethnicity categories along with the standard errors of the estimates, the 95% CIs, and design effects for the estimated proportions.

As a brief aside, the large design effects for the sampling variance of the estimated proportions are due to the large cluster sizes in the primary stage of the 2011–2012 NHANES sample. However, the NHANES samples are not primarily designed to generate precise *overall* estimates of these types of proportions; they are designed to generate precise estimates for *subpopulations* of the U.S. population defined by demographic characteristics such as ethnicity and sex (Mohadjer and Curtin, 2008). NHANES design effects for estimates of subpopulation proportions are considerably smaller.

EXAMPLE 6.3: ESTIMATING THE PROPORTIONS OF U.S. ADULTS BY BLOOD PRESSURE CATEGORY USING THE 2011–2012 NHANES DATA

A common technique in survey data analysis is to classify the population into discrete categories based on the values of one or more continuous survey variables. This example illustrates the variable

recoding steps and use of the svy: tab command in Stata to estimate the proportions of U.S. adults falling into each of the following four categories of blood pressure status: (1) normal (systolic blood pressure [SBP] < 120 and diastolic blood pressure [DBP] < 80); (2) prehypertension (SBP 120–139, or DBP 80–89); (3) Stage 1 Hypertension (SBP 140–159, or DBP 90–99); and (4) Stage 2 Hypertension (SBP 160+, or DBP 100+).

The analysis begins with the data recoding steps. Based on the NHANES mean values of DBP and SBP (averaging several replicate measures), respondents are assigned to one of the four blood pressure categories:

```
generate bp_catr = .
replace bp_catr = 1 if (sbp < 120 & dbp < 80)
replace bp_catr = 2 if (missing(bp_catr) & ///
((sbp >= 120 & sbp < 140 ) | (dbp >= 80 & dbp < 90 )))
replace bp_catr = 3 if (missing(bp_catr) & ///
((sbp >= 140 & sbp < 160 ) | (dbp >= 90 & dbp < 100 )))
replace bp_catr = 4 if (missing(bp_catr) & ///
((160 <= sbp & sbp != .) | (dbp >= 100 & dbp !=. )))
```

The NHANES sample design is identified through the svyset command and the svy: tab command is then applied to generate weighted estimates of the proportions of the adult population (AGE18P = 1) falling into each of these four categories:

```
svyset sdmvpsu [pweight = wtmecc2yr], strata(sdmvstr)
svy, subpop(age18p): tab bp_catr, obs se ci col
svy, subpop(age18p): tab bp_catr, deff
```

The output generated by these commands is summarized in [Table 6.3](#). These results suggest that an estimated 47.2% of the adult population has “normal” blood pressure (95% CI = 44.0%, 50.5%), while roughly 43% of the adult population is at the prehypertension stage (95% CI = 40.3%, 45.4%). Approximately 10% of the adult population is estimated to have either Stage 1 or Stage 2 hypertension. As in Example 6.1, the asymmetry of the 95% CIs for the smaller estimated proportions is due to Stata’s use of the logit transform method to derive the CI limits.

TABLE 6.3

Estimated Proportions of U.S. Adults by Blood Pressure Status

Blood Pressure Category	Estimated Proportion	Linearized SE	95% CI	Design Effect
Normal	0.472	0.016	(0.440, 0.505)	6.70
Prehypertension	0.428	0.012	(0.403, 0.454)	4.10
Stage 1 hypertension	0.080	0.006	(0.068, 0.093)	3.19
Stage 2 hypertension	0.020	0.004	(0.013, 0.033)	6.79

Source: 2011–2012 NHANES; $n = 5,356$.

6.3.3 Testing Hypotheses Concerning a Vector of Population Proportions

To test a null hypothesis concerning multinomial proportions of the form $H_0: \{\pi_1 = 0.5, \pi_2 = 0.25, \pi_3 = 0.25\}$, the standard χ^2 GOF test statistic, $X^2 = n_{++} \cdot \sum_k (p_k - \pi_k)^2 / \pi_k$ (with degrees of freedom equal to the number of categories minus 1), can be considerably biased when applied to complex sample survey data. Jann (2008) has extended the GOF test to the complex sample survey data setting, and this procedure has been implemented in Stata's `mgof` command (we omit details of the approach here; interested readers can review the article).

EXAMPLE 6.4: A GOF TEST FOR PROPORTIONS OF RUSSIANS AGED 15+ BY MARITAL STATUS

Table 6.4 summarizes a descriptive analysis of the European Social Survey (ESS)-Russian Federation data set in which proportions for the multinomial distribution of the Russian population aged 15 years and older across marital status categories are estimated. Based on these same data, assume that the analyst wishes to test the null hypothesis that the true population proportions of Russian adults in the three categories are: married (50%), previously married (25%), and never married (25%).

After installing the user-written `mgof` command (web-aware Stata users can type `findit mgof` for help finding the command), a new variable, `pi`, is created using the `recode` command that contains the null hypothesis values for each category of the MARCAT variable:

```
recode marcat (1=.5) (2=.25) (3=.25), generate (pi)
```

Next, the `mgof` command is submitted to test the null hypothesis:

```
mgof marcat = pi, svy
```

Submitting this command produces the following test statistics and *p*-values for the GOF hypothesis test:

Goodness-of-fit Statistic	F	P($\mathcal{F}_{1,89,332} > F$)
Rao–Scott $X^2_{Pearson}$	1.68	0.19
$X^2_{LR, Jann}$	1.69	0.19

TABLE 6.4

Estimated Proportions of Russian Adults by Marital Status

Marital Status	Estimated Proportion	Linearized SE	95% CI	Design Effect
Married	0.504	0.013	(0.479, 0.529)	1.62
Previously married	0.230	0.011	(0.208, 0.254)	1.84
Never married	0.266	0.013	(0.241, 0.293)	2.25

Source: ESS Round 6 (2012)—Russian Federation ($n = 2,444$).

Interpreting the results of these tests, the null hypothesis is not rejected by either the design-adjusted Rao–Scott version of Pearson’s χ^2 test statistic (Section 6.4.4) or the likelihood ratio χ^2 statistic developed by Jann (2008). The weighted estimates computed using the collected sample data therefore appear to “fit” the hypothesized population distribution of category proportions.

6.3.4 Graphical Display for a Single Categorical Variable

Categorical survey variables naturally lend themselves to graphical display and analytic interpretation. As discussed in [Chapter 5](#), it is important that the software used to generate graphics for analysis or publication has the capability to incorporate the survey weights, so that the display accurately reflects the estimated distribution of the variable in the survey population.

**EXAMPLE 6.5: PIE CHARTS AND VERTICAL BAR CHARTS
OF THE ESTIMATED PROPORTIONS OF
RUSSIANS AGED 15+ BY MARITAL STATUS**

Using Stata graphics, simple weighted pie charts ([Figure 6.3](#)) or weighted vertical bar charts ([Figure 6.4](#)) produce an effective display of the estimated population distribution across categories of a single categorical variable. The Stata command syntax used to generate these

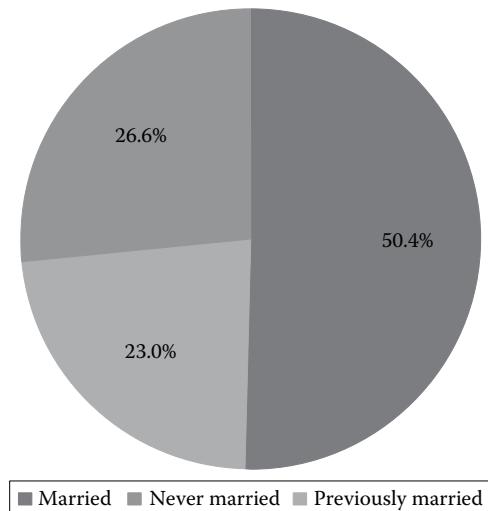
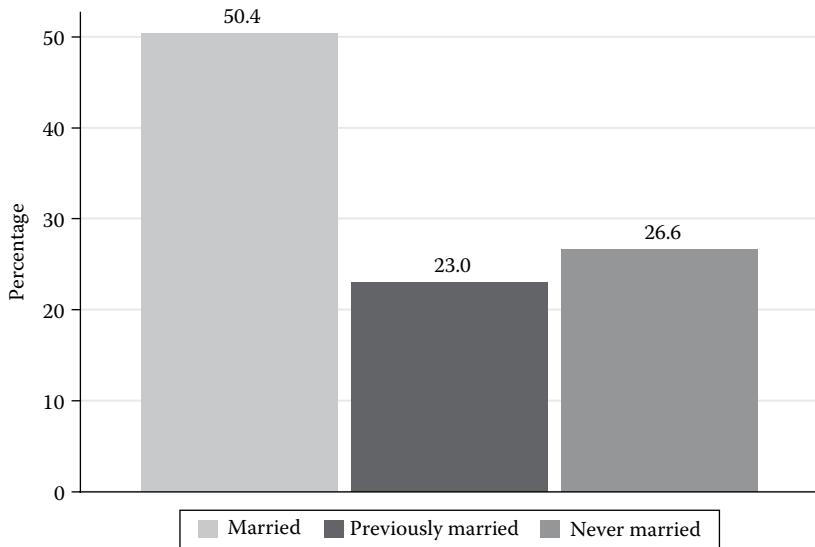


FIGURE 6.3

Pie chart of the estimated distribution of the marital status of Russian adults. (From ESS Round 6 (2012)—Russian Federation.)

**FIGURE 6.4**

Bar chart of the estimated distribution of the marital status of Russian adults. (From ESS Round 6 (2012)—Russian Federation.)

two figures follows. Note that both the graph pie and graph bar commands require the initial creation of indicator variables for the individual marital status categories (marcat1, marcat2, and marcat3). This is accomplished using the generate(marcat) option in the tabulate command:

```

tabulate marcat, generate(marcat)
label var marcat1 "Married"
label var marcat2 "Previously Married"
label var marcat3 "Never Married"

* Pie Chart (one long command).
graph pie marcat1 marcat2 marcat3 ///
[pweight=pspwght], plabel(_all percent, ///
format(%9.1f)) scheme(s2mono) legend ///
(label(1 "Married") label(2 "Previously Married") ///
label(3 "Never Married"))

* Vertical Bar Chart (one long command).
graph bar (mean) marcat1 marcat2 marcat3 ///
[pweight=pspwght], percentages ///
bar(1,color(gs12)) bar(2,color(gs4)) ///
bar(3,color(gs8)) blabel(bar, format(%5.1f)) ///
bargap(7) scheme(s2mono) ///
legend (label(1 "Married")) ///
label(2 "Previously Married") label(3 "Never Married"))///
ytitle ("Percentage")

```

6.4 Bivariate Analysis of Categorical Data

Bivariate analysis of categorical data may take a number of forms, ranging from estimation of proportions for the joint distribution of the two variables (total proportions) or estimation of “conditional” proportions based on levels of the second categorical variable (i.e., row proportions or column proportions) to techniques for measuring and testing bivariate association between two categorical variables. Bivariate categorical data analyses and reporting are important in their own right, and they are also important as exploratory tools in the development of more complex multivariate models (see the regression model building steps in Section 8.3).

6.4.1 Response and Factor Variables

Unlike simple linear regression for continuous survey variables, there is no requirement to differentiate variables by type (dependent or independent) or postulate a cause/effect relationship between two or more categorical variables that are being analyzed simultaneously. An example where assigning the variables to dependent or independent status is not necessary would be a bivariate analysis of the population distribution by education levels and Census region. Nevertheless, in many categorical data analysis problems it is natural to think of one categorical variable as the *response variable* and the other(s) as a *factor variable* that may be associated with the discrete outcome for the response variable. This section will introduce examples centered around the analysis of the joint distribution of U.S. adults’ experience with a lifetime episode of major depression (yes, no) and their gender (male, female), based on the National Comorbidity Survey Replication (NCS-R) data set. In these examples, it is convenient to label the NCS-R indicator variable for a lifetime major depression episode (MDE) as the response variable and the respondent’s gender (SEX) as the factor. Assigning response and factor labels to the categorical variables also sets up the transition to later discussion of regression modeling of categorical data where dependent and independent variables are clearly specified.

6.4.2 Estimation of Total, Row, and Column Proportions for Two-Way Tables

Based on the weighted frequencies illustrated in [Figure 6.2](#), estimates of population proportions can be computed as the ratio of the weighted sample frequency for the cell to the appropriate weighted total or marginal frequency value. For example, [Figure 6.5](#) illustrates estimation of the *total proportions* of the population in each cell and margin of the table. Note that the numerator of each estimated proportion is the weighted total frequency for the cell, for example, \hat{N}_{A1} , and the denominator is the weighted total population frequency, \hat{N}_{++} . Statistical software also enables the user to

Factor	Response		
	0	1	
A	$p_{A0} = \frac{\hat{N}_{A0}}{\hat{N}_{++}}$	$p_{A1} = \frac{\hat{N}_{A1}}{\hat{N}_{++}}$	$p_{A+} = p_{A0} + p_{A1}$
B	$p_{B0} = \frac{\hat{N}_{B0}}{\hat{N}_{++}}$	$p_{B1} = \frac{\hat{N}_{B1}}{\hat{N}_{++}}$	$p_{B+} = p_{B0} + p_{B1}$
	$p_{+0} = p_{A0} + p_{B0}$	$p_{+1} = p_{A1} + p_{B1}$	$p_{++} = 1.0$

FIGURE 6.5

Estimation of overall (total) population proportions (multinomial sampling model).

Factor	Response		
	0	1	
A	$p_{0 A} = \frac{\hat{N}_{A0}}{\hat{N}_{A+}}$	$p_{1 A} = \frac{\hat{N}_{A1}}{\hat{N}_{A+}}$	$p_{A+} = 1.0$
B	$p_{0 B} = \frac{\hat{N}_{B0}}{\hat{N}_{B+}}$	$p_{1 B} = \frac{\hat{N}_{B1}}{\hat{N}_{B+}}$	$p_{B+} = 1.0$

FIGURE 6.6

Estimation of row population proportions (product multinomial sampling model).

condition estimates of population proportions on the sample in particular rows or columns of the crosstabulation. Figure 6.6 illustrates the calculations of weighted estimates of *row proportions* for the estimated population distribution in Figure 6.2.

The following example uses the NCS-R data on lifetime MDE and SEX to illustrate the Stata syntax to estimate total proportions, row proportions, standard errors, and CIs.

**EXAMPLE 6.6: ESTIMATION OF TOTAL AND ROW
PROPORTIONS FOR THE CROSSTABULATION
OF GENDER AND LIFETIME MAJOR
DEPRESSION STATUS (SOURCE: NCS-R)**

The first of two svy: tab commands in Stata (shown below) requests the default estimates of the total proportions for the SEX × MDE crosstabulation along with the corresponding standard errors, 95% CIs, and design effects. The row option in the second svy: tab command specifies that the estimates, standard errors, CIs, and design effects will be for the row proportions.

```
svyset seclustr [pweight = ncsrwtlg], strata(sestrat)
svy: tab sex mde, se ci deff
svy: tab sex mde, row se ci deff
```

TABLE 6.5

Estimated Proportions of U.S. Adults by Gender and Lifetime Major Depression Status

Description	Parameter	Estimated Proportion	Linearized SE	95% CI	Design Effect
<i>Total Proportions</i>					
Male, no MDE	π_{A0}	0.406	0.007	(0.393, 0.421)	1.87
Male, MDE	π_{A1}	0.072	0.003	(0.066, 0.080)	1.64
Female, no MDE	π_{B0}	0.402	0.005	(0.391, 0.413)	1.11
Female, MDE	π_{B1}	0.120	0.003	(0.114, 0.126)	0.81
<i>Row Proportions</i>					
No MDE male	$\pi_{0 A}$	0.849	0.008	(0.833, 0.864)	2.08
MDE male	$\pi_{1 A}$	0.151	0.008	(0.136, 0.167)	2.08
No MDE female	$\pi_{0 B}$	0.770	0.006	(0.759, 0.782)	0.87
MDE female	$\pi_{1 B}$	0.230	0.006	(0.218, 0.241)	0.87

Source: NCS-R.

The estimated proportions, standard errors, 95% CIs, and design effect output from these two commands are summarized in [Table 6.5](#), where we see evidence of a higher prevalence of lifetime MDEs among females.

6.4.3 Estimating and Testing Differences in Subpopulation Proportions

Estimates of row proportions in two-way tables (e.g., $\hat{p}_{1|B} = 0.230$ in [Table 6.5](#)) are in fact subpopulation estimates in which the subpopulation is defined by the levels of the factor variable. Analysts interested in testing differences in response category proportions between two levels of a factor variable can use methodology similar to that discussed in Section 5.6 for comparison of subpopulation means.

EXAMPLE 6.7: COMPARING THE PROPORTIONS OF U.S. ADULT MEN AND WOMEN WITH LIFETIME MAJOR DEPRESSION

This example uses data from the NCS-R to test a null hypothesis that there is no difference in the proportions of U.S. adult men and women with a lifetime diagnosis of an MDE. To compare male and female row proportions for MDE = 1, the `svy: prop` command with the `over()` option is used to estimate the vector of row proportions ([Table 6.5](#)) and their design-based variance–covariance matrix. Internally, Stata labels the estimated row proportions for MDE = 1 as `_prop_2`. The `lincom` command is then executed to estimate the contrast of the male and female proportions and the standard error of this difference. The relevant Stata commands follow:

```

svyset seclustr [pweight=ncsrwtsh], strata(sestrat) ///
vce(linearized) singleunit(missing)

svy: proportion mde, over(sex)
lincom [_prop_2]Male - [_prop_2]Female

```

The output of the `lincom` command provides the following estimate of the male–female difference, its standard error, and a 95% CI for the contrast of proportions.

$\hat{\Delta} = p_{male} - p_{female}$	$se(\hat{\Delta})$	$CI_{95}(\Delta)$
-0.079	0.010	(-0.098, -0.059)

Because the design-based 95% CI for the difference in proportions does not include 0, the data suggest that the prevalence of lifetime MDE for women is in fact significantly higher than that for men.

6.4.4 χ^2 Tests of Independence of Rows and Columns

For a 2×2 table, the contrast of estimated subpopulation proportions examined in Example 6.7 is equivalent to a test of whether the response variable (MDE) is independent of the factor variable (SEX). More generally, under SRS, two categorical variables are independent of each other if the following relationship of the expected proportion in row r , column c of the crosstabulation holds:

$$\hat{\pi}_{rc} = \text{Expected proportion in row } r, \text{ column } c = \frac{n_{r+}}{n_{++}} \cdot \frac{n_{+c}}{n_{++}} = p_{r+} \cdot p_{+c}. \quad (6.6)$$

Under SRS, formal testing of the null hypothesis that two categorical variables are independent can be conducted by comparing the expected cell proportion under the independence assumption, $\hat{\pi}_{rc}$, to the observed proportion from the survey data, p_{rc} . Intuitively, if the differences $(\hat{\pi}_{rc} - p_{rc})$ are large, there is evidence that the independence assumption does not hold and that there is an association between the row and column variables. In standard practice, two statistics are commonly used to test the hypothesis of independence in two-way tables:

$$\text{Pearson's Chi-square Test Statistic: } X^2_{Pearson} = n_{++} \cdot \sum_r \sum_c (p_{rc} - \hat{\pi}_{rc})^2 / \hat{\pi}_{rc}. \quad (6.7)$$

$$\text{Likelihood Ratio Test Statistic: } G^2 = 2 \cdot n_{++} \cdot \sum_r \sum_c p_{rc} \times \ln\left(\frac{p_{rc}}{\hat{\pi}_{rc}}\right). \quad (6.8)$$

Under the null hypothesis of independence for rows and columns of a two-way table, these test statistics both follow a central χ^2 distribution with $(R - 1) \times (C - 1)$ degrees of freedom.

Ignoring the complex sample design that underlies most survey data sets can introduce bias in the estimated values of these test statistics. To correct the bias in the estimates of the population proportions used to construct the test statistic, weighted estimates of the cell, row, and column proportions are substituted, for example, $p_{rc} = \hat{N}_{rc}/\hat{N}_{++}$. To correct for the design effects on the sampling variances of these proportions, two general approaches have been introduced in the survey statistics literature. Both approaches involve scaling the standard $X_{Pearson}^2$ and G^2 test statistics by dividing them by an estimate of a *generalized design effect factor* (GDEFF). Theory Box 6.2 provides a mathematical explanation of how the generalized design effect adjustments are computed.

Fay (1979, 1985) and Fellegi (1980) were among the first to propose such a correction based on a generalized design effect. Rao and Scott (1984) and later Thomas and Rao (1987) extended the theory of generalized design effect corrections for these test statistics. The Rao–Scott method requires the computation of *generalized design effects* that are analytically more complicated than the Fellegi approach. The Rao–Scott corrections are now the standard in procedures for the analysis of categorical survey data in software systems such as Stata and SAS. The design-adjusted Rao–Scott Pearson and likelihood ratio χ^2 test statistics are computed as follows:

$$\begin{aligned} X_{R-S}^2 &= X_{Pearson}^2 / GDEFF, \\ G_{R-S}^2 &= G^2 / GDEFF. \end{aligned} \quad (6.9)$$

THEORY BOX 6.2 FIRST- AND SECOND-ORDER DESIGN EFFECT CORRECTIONS

The Fellegi (1980) method for a generalized design effect correction to the χ^2 test statistic is best summarized as a three-step process. First, the average of the design effects for the $R \times C$ (unweighted) proportions involved in the computation of the χ^2 statistic is computed. The standard Pearson or likelihood ratio χ^2 statistic computed under SRS is then divided by the average design effect. The resulting adjusted χ^2 test statistic is referred to a χ^2 distribution with degrees of freedom equal to $(R - 1) \times (C - 1)$ to test the null hypothesis of independence.

Rao and Scott (1984) built on this method by advocating the use of weighted estimates of the proportions in the construction of the standard χ^2 statistics. Under the Rao–Scott method, the *generalized design effect* is defined as the mean of the eigenvalues of the following matrix, D :

$$D = V_{Design} V_{SRS}^{-1}. \quad (6.10)$$

In Equation 6.10, V_{Design} is the matrix of design-based (e.g., linearized) variances and covariances for the $R \times C$ vector of estimated proportions used to construct the χ^2 test statistic, and V_{SRS} is the matrix of variance and covariances for the estimated proportions given a simple random sample of the same size. The Rao–Scott GDEFF for two-way tables can then be written as follows:

$$GDEFF = \frac{\sum_r \sum_c (1-p_{rc}) \cdot d^2(p_{rc}) - \sum_r (1-p_{r+}) \cdot d^2(p_{r+}) - \sum_c (1-p_{+c}) \cdot d^2(p_{+c})}{(R-1)(C-1)}. \quad (6.11)$$

The design-adjusted test statistics introduced in Equation 6.9 are computed based on *first-order design corrections* of this type.

Thomas and Rao (1987) derived *second-order design corrections* to the test statistics, which incorporate variability in the eigenvalues of the D matrix. These second-order design corrections can be implemented by dividing the adjusted test statistic based on the first-order correction (e.g., $X_{R-S}^2 = X_{Pearson}^2 / GDEFF$) by the quantity $(1 + a^2)$, where a represents the coefficient of variation of the eigenvalues of the D matrix. The F -transformed version of this second-order design-corrected version of the Pearson χ^2 statistic is currently the default test statistic reported by Stata's `svy: tab` command for analyses of two-way tables. Thomas and Rao (1987) used simulations to show that this second-order correction controls Type I error rates much better when there is substantial variance in the eigenvalues of D .

In theoretical terms, the aim in applying the first- or second-order complex sample design corrections to the standard χ^2 test statistic is to transform the test statistic such that under the null hypothesis of independence, H_0 , the moments (i.e., mean, variance) of its distribution will match those of the central χ^2 reference distribution with $(R - 1) \times (C - 1)$ degrees of freedom (Lohr, 1999).

Under the null hypothesis of independence of rows and columns, both of these adjusted test statistics can be referred to a χ^2 distribution with $(R - 1) \times (C - 1)$ degrees of freedom. Thomas and Rao (1987) showed that a transformation of the design-adjusted X_{R-S}^2 and G_{R-S}^2 values produced a more stable test statistic that under the null hypothesis closely approximated an \mathcal{F} distribution. Table 6.6 defines the F -transformed versions of these two χ^2 test statistics and the corresponding \mathcal{F} reference distributions to be used in testing the independence of rows and columns:

TABLE 6.6*F*-Transformations of the Rao–Scott Chi-square Test Statistics

<i>F</i> -Transformed Test Statistics	<i>F</i> Reference Distribution under H_0
$F_{R-S, Pearson} = X_{R-S}^2 / [(R-1)(C-1)]$	$\mathcal{F}_{(R-1)(C-1), (R-1)(C-1) df}$
$F_{R-S, LRT} = G_{R-S}^2 / (C-1)$, where C is the number of columns in the crosstab	$\mathcal{F}_{(C-1), df}$

A third form of the χ^2 test statistic that may be used to test the null hypothesis of independence of rows and columns in a crosstabulation of two categorical variables is the *Wald χ^2 test statistic* (Theory Box 6.3). We will see in later chapters that Wald statistics play an important role in hypothesis testing for linear and generalized linear models. However, simulation studies have shown that the standard Pearson χ^2 test statistic and its design-adjusted

THEORY BOX 6.3 THE WALD χ^2 TEST OF INDEPENDENCE FOR CATEGORICAL VARIABLES

The Wald χ^2 test statistic for the null hypothesis of independence of rows and columns in a two-way table is defined as follows:

$$Q_{Wald} = \hat{Y}'(\hat{H}\hat{V}(\hat{N})\hat{H}')^{-1}\hat{Y}, \quad (6.12)$$

where

$$\hat{Y} = (\hat{N} - E) \quad (6.13)$$

is a vector of $R \times C$ differences between the observed and expected cell counts, that is, $\hat{N}_{rc} - E_{rc}$, where under the independence hypothesis, $E_{rc} = \hat{N}_{r+} \cdot \hat{N}_{+c} / \hat{N}_{++}$. The matrix term $\hat{H}\hat{V}(\hat{N})\hat{H}'$ represents the estimated variance–covariance matrix for the vector of differences. In the case of a complex sample design, the variance–covariance matrix of the weighted frequency counts, $\hat{V}(\hat{N})$, is estimated using a TSL, BRR, or JRR approach that captures the effects of stratification, cluster sampling, and weighting. The matrix \hat{H} is the inverse of the matrix J defined in Theory Box 8.3 of Chapter 8 (see Equation 8.15).

Under the null hypothesis of independence, Q_{Wald} follows a χ^2 distribution with $(R-1) \times (C-1)$ degrees of freedom. An *F*-transformation of the Wald χ^2 test statistic reported in SUDAAN and other software programs is:

$$F_{Wald} = Q_{Wald} \times \frac{df - (R-1)(C-1)+1}{(R-1)(C-1)df} \sim \mathcal{F}_{(R-1)(C-1), df - (R-1)(C-1)+1} \text{ under } H_0. \quad (6.14)$$

forms proposed by Rao and Scott (1984) and Rao and Thomas (1988) perform best for both sparse and nonsparse tables (Sribney, 1998), and that these tests are more powerful than the Wald test statistic, especially for larger tables. As a result, Stata makes the $F_{R-S,Pearson}$ test statistic (with a second-order design correction incorporated) the default test statistic reported by its svy: tab command, and this is also the default test statistic reported by PROC SURVEYFREQ in SAS (with a first-order design correction incorporated).

**EXAMPLE 6.8: TESTING THE INDEPENDENCE OF
MDE AND GENDER IN U.S. ADULTS
USING THE NCS-R DATA**

In Example 6.7, based on the estimated 95% CI for the difference in proportions of males and females with a lifetime MDE, we concluded that U.S. adult women appear to have significantly higher rates of lifetime MDEs than their male counterparts. An equivalent way of interpreting that result is to say that adult prevalence of MDE is not independent of sex. A second approach to address the question of sex-specific differences in the prevalence of lifetime major depression is to perform the R-S χ^2 test of the null hypothesis H_0 : MDE prevalence is independent of sex. The following Stata command syntax can be used to perform a design-adjusted test of that hypothesis:

```
svyset seclustr [pweight=ncsrwtsh], strata(sestrat)
svy: tab sex mde, se ci deff
```

A summary of the results of this analysis is presented in [Table 6.7](#). By default, Stata reports the standard uncorrected Pearson χ^2 test statistic ($X^2_{Pearson} = 92.15$, $p < 0.0001$) and then reports the (second-order) design-adjusted Rao–Scott F -test statistic ($F_{R-S,Pearson} = 57.98$, $p < 0.0001$). In this case, both the unadjusted X^2 and the design-corrected Rao–Scott F -test statistics provide strong evidence to reject the null hypothesis and conclude that there is a significant association between MDE prevalence and gender.

As in the example, applying the design adjustment to the test statistic may not cause the analyst to alter their conclusion regarding the significance of an association between two categorical variables. However, as Example 6.9 will show, failure to properly account for complex sample

TABLE 6.7

Design-Based Analysis of the Association between Gender and Lifetime Experience of Major Depression

Tests of Independence

Unadjusted X^2	$P(X^2_{(1)} > X^2_{Pearson})$	Rao–Scott F	$P(F_{1,42} > F_{R-S})$
$X^2_{Pearson} = 92.15$	$p < 0.0001$	$F_{R-S,Pearson} = 57.98$	$p < 0.0001$

Parameters of the Rao–Scott Design-Adjusted Test

$n = 9,282$	Design $df = 42$	$GDEFF = 1.37$	$a = 0.00$
-------------	------------------	----------------	------------

Source: NCS-R.

design effects can lead to erroneous conclusions—the error almost always being to assume that an association exists when in fact correct treatment of the data does not support that finding.

**EXAMPLE 6.9: TESTING THE INDEPENDENCE OF
ALCOHOL DEPENDENCE AND EDUCATION
LEVEL IN YOUNG ADULTS (AGED
18–28) USING THE NCS-R DATA**

This example uses the `svy: tab` command in Stata to compute the Rao–Scott F -statistics and test the independence of two categorical variables that are available in the NCS-R data set (for Part II respondents, requiring use of the Part II weight NSCRWTLG): ALD, an indicator of receiving a diagnosis of alcohol dependence in the lifetime and ED4CAT, a categorical variable measuring educational attainment (1 = less than high school, 2 = high school, 3 = some college, 4 = college and above). The analysis is restricted to the subpopulation of NCS-R Part II respondents 18–28 years of age. After identifying the complex design features to Stata, we request the crosstabulation analysis and any related design-adjusted test statistics by using the `svy: tab` command:

```
svyset seclustr [pweight = ncsrwtlg], strata(sestrat)
svy, subpop(if 18 <= age & age < 29): tab ed4cat ald, ///
row se ci deff
```

ED4CAT is specified as the row (factor) variable and ALD as the column (response) variable. Weighted estimates of the row proportions are requested using the `row` option. Table 6.8 summarizes the estimated row proportions and standard errors for the ALD \times ED4CAT crosstabulation, along with the Rao–Scott F -test of independence.

TABLE 6.8

Design-Based Analysis of the Association between Alcohol Dependence and Education Level for Young Adults Aged 18–28

Education Level (Grades)	Alcohol Dependence (ALD) Row Proportions (Linearized SE)		
	0 = No	1 = Yes	Total
0–11	0.909 (0.029)	0.091 (0.029)	1.000
12	0.951 (0.014)	0.049 (0.014)	1.000
13–15	0.951 (0.010)	0.049 (0.010)	1.000
16+	0.931 (0.014)	0.069 (0.014)	1.000
Total	0.940 (0.009)	0.060 (0.009)	1.000

Tests of Independence

Unadjusted X^2	$P(\chi^2_{(3)} > X^2_{Pearson})$	Rao–Scott F	$P(F_{2.75, 115.53} > F_{R-S})$
$X^2_{Pearson} = 27.21$	$p < 0.0001$	$F_{R-S, Pearson} = 1.64$	$p = 0.19$

Parameters of the Rao–Scott Design-Adjusted Test

$n_{18-28} = 1,275$	Design $df = 42$	$GDEFF = 6.62$	$a = 0.56$
---------------------	------------------	----------------	------------

Source: NCS-R.

An estimated 9.1% of young adults in the lowest education group have been diagnosed with alcohol dependence at some point in their lifetime (95% CI = 4.7%, 17.0%), while an estimated 6.9% of young adults in the highest education group have been diagnosed with alcohol dependence (95% CI = 4.6%, 10.2%). By default, Stata reports the standard uncorrected Pearson χ^2 test statistic ($X^2_{Pearson} = 27.21$, $p < 0.0001$) and then reports the (second-order) design-adjusted Rao–Scott F -test statistic ($F_{R-S,Pearson} = 1.64$, $p = 0.19$) (Table 6.8). The standard Pearson χ^2 test rejects the null hypothesis of independence at $\alpha = 0.05$; however, when the corrections for the complex sample design are introduced, the Rao–Scott design-adjusted test statistic fails to reject a null hypothesis of independence between education and a lifetime diagnosis of alcohol dependence in this younger population. The appropriate inference in this case would thus be that there is no evidence of a bivariate association between these two categorical factors in this subpopulation. Multivariate analyses incorporating additional potential predictors of alcohol dependence could certainly be examined at this point (see Chapter 8 for examples).

We remind readers that Stata is using a second-order design correction for the test statistic, which is why the results of these analyses may differ from those found using other software packages (note the decimal degrees of freedom for the design-adjusted F -statistic, due to the second-order correction). If a user specifies the `deff` option in the `svy: tab` command, Stata also reports both the mean generalized design effect ($GDEFF = 6.63$) used in the first-order correction and the coefficient of variation of the generalized design effects ($a = 0.56$) used in the second-order correction.

Additional test statistics, including design-adjusted likelihood ratio and Wald test statistics, can be requested in Stata by using the `lr` and `wald` options for the `svy: tab` command. These options do not lead to substantially different conclusions in this illustration and will generally not lead to different inferences about associations between two categorical variables. As mentioned previously, Stata developers advocate the use of the second-order design-adjusted Pearson χ^2 statistic (or the Rao–Scott χ^2 statistic and its F -transformed version) in all situations involving crosstabulations of two categorical variables measured in complex sample surveys (Sribney, 1998).

6.4.5 Odds Ratios and Relative Risks

The *odds ratio*, which we denote by ψ , can be used to quantify the association between the levels of a *response variable* and a categorical factor. Figure 6.7 displays NCS-R weighted estimates (row proportions) of the prevalence of one or more lifetime episodes of major depression by gender.

The odds ratio compares the odds that the response variable takes a specific value across two levels of the factor variable. If the response variable is truly independent of the chosen factor, then $\psi = 1.0$. For

SEX	MDE		
	0	1	
A-male	$p_{0 A} = \frac{\hat{N}_{A0}}{\hat{N}_{A+}} = 0.849$	$p_{1 A} = \frac{\hat{N}_{A1}}{\hat{N}_{A+}} = 0.151$	$p_{A+} = 1.0$
B-female	$p_{0 B} = \frac{\hat{N}_{B0}}{\hat{N}_{B+}} = 0.770$	$p_{1 B} = \frac{\hat{N}_{B1}}{\hat{N}_{B+}} = 0.230$	$p_{B+} = 1.0$

FIGURE 6.7

Estimates of row proportions for MDE, by gender.

example, from [Figure 6.7](#), the estimated male (A)/female (B) odds ratio for MDE is:

$$\hat{\psi} = \frac{Odds(MDE = 1 | Male)}{Odds(MDE = 1 | Female)} = \frac{p_{1|A}/(1 - p_{1|A})}{p_{1|B}/(1 - p_{1|B})} = \frac{p_{1|A}/p_{0|A}}{p_{1|B}/p_{0|B}} = \frac{0.151/0.849}{0.230/0.770} = 0.595.$$

Note that although this estimate of ψ is computed using the estimated row proportions for the SEX \times MDE table, the same estimate would be obtained if the estimated total proportions had been used ([Table 6.4](#)):

$$\hat{\psi} = \frac{p_{A1}/p_{A0}}{p_{B1}/p_{B0}} = \frac{0.072/0.407}{0.120/0.402} = 0.595.$$

Since this odds ratio is estimated with no additional controls for other factors such as age or education, it would be labeled as an estimate of an *unadjusted odds ratio* in any scientific reports. Note that a correct description of this result is the following: "The odds that adult men experience major depression in their lifetime are estimated to be only 59.5% as large as the odds for women." A common mistake in reporting results for estimated odds ratios is to make a statement like the following: "The probability that a man experiences an episode of major depression in their lifetime is 59.5% of that for women."

The latter statement above is confusing the odds ratio statistic with a related, yet different, comparative measure, the *relative risk* (computed here using the estimates in [Table 6.5](#)):

$$\hat{RR} = \frac{\text{Prob}(MDE = 1 | Male)}{\text{Prob}(MDE = 1 | Female)} = \frac{p_{1|A}}{p_{1|B}} = \frac{0.151}{0.230} = 0.656.$$

The relative risk is the ratio of two conditional probabilities: the probability of MDE for males and the probability of MDE for females. Although both the odds ratio and the relative risk measure the association of a

categorical response and a factor variable, they should be distinguished. Only in instances where the prevalence of the response of interest is very small for all levels of the factor (i.e., $p_{1|A}$ and $p_{1|B} < 0.01$) will the odds ratio and relative risk statistics converge to similar numerical values.

A related quantity that is often of interest to epidemiologists is the population *attributable fraction* (AF) associated with a particular risk factor when analyzing categorical outcomes (e.g., disease status). The AF, which is a function of estimated relative risks associated with different levels of a categorical risk factor (all relative to some baseline category, usually representing no exposure to the risk factor), represents the proportional reduction in population disease (or mortality) that would occur if exposure to a risk factor were reduced to some baseline level, ideally representing no exposure to the risk factor. Heeringa et al. (2015) recently reviewed the literature on estimation of AFs, and presented straightforward approaches to estimating (and making inferences about) AFs based on complex sample survey data (Section 8.6).

If the response and factor variables are independent, then $\psi = 1.0$ (and $RR = 1.0$). Therefore, to test if categorical response and factor variables are independent, it would be reasonable to construct a CI of the form $\hat{\psi} \pm t_{1-\alpha/2, df} \cdot se(\hat{\psi})$, and establish whether (or not) the null value of $\psi = 1$ is contained within the interval. Although a TSL approximation to $se(\hat{\psi})$ can be derived directly, a CI for ψ is generally obtained from the technique of simple logistic regression (see below).

6.4.6 Simple Logistic Regression to Estimate the Odds Ratio

Logistic regression for binary dependent variables will be covered in depth in [Chapter 8](#). Here, the logit function and simple logistic regression models are briefly introduced to demonstrate their application to estimation of the unadjusted odds ratio and its CI.

The natural logarithm of the odds is termed a *logit function* (arising from the term “log-odds units”). Again, using the NCS-R MDE example in [Table 6.5](#), the logits of the probabilities of MDE for the male and female factor levels are:

$$\text{logit}(p_{1|A}) = \ln(Odds(MDE = 1 | Male)) = \ln\left(\frac{p_{1|A}}{1 - p_{1|A}}\right) = \ln\left(\frac{0.151}{0.849}\right) = -1.727.$$

$$\text{logit}(p_{1|B}) = \ln(Odds(MDE = 1 | Female)) = \ln\left(\frac{p_{1|B}}{1 - p_{1|B}}\right) = \ln\left(\frac{0.230}{0.770}\right) = -1.208.$$

Consider a single indicator variable, I_{male} , coded 1 = male and 0 = female, that distinguishes the two levels of SEX. The outcome MDE is coded

$1 = \text{yes}$, $0 = \text{no}$. A simple logistic regression model for these data is written as follows:

$$\text{logit}(P(MDE = 1 | SEX)) = \beta_0 + \beta_1 \cdot I_{\text{male}}.$$

Then, we can derive the following result:

$$\hat{\psi} = \frac{p_{1|A}/(1-p_{1|A})}{p_{1|B}/(1-p_{1|B})} = \frac{\exp(\text{logit}(p_{1|A}))}{\exp(\text{logit}(p_{1|B}))} = \frac{\exp(\hat{\beta}_0 + \hat{\beta}_1 \cdot 1)}{\exp(\hat{\beta}_0 + \hat{\beta}_1 \cdot 0)} = \exp(\hat{\beta}_1).$$

Therefore, given an estimate of the parameter β_1 that would be obtained by fitting the simple logistic regression model to the survey data, we can easily compute an estimate of the odds ratio. A $100(1-\alpha)\%$ CI for ψ can then be developed by exponentiating the lower and upper bounds of the standard CI for β_1 : $CI(\psi) = (\exp(\hat{\beta}_1 - t_{1-\alpha/2, df} \cdot se(\hat{\beta}_1)), \exp(\hat{\beta}_1 + t_{1-\alpha/2, df} \cdot se(\hat{\beta}_1)))$. The resulting CI is not symmetric about the estimated odds ratio but has been shown to provide more accurate coverage of the true population value for a specified level of Type I error (α).

EXAMPLE 6.10: SIMPLE LOGISTIC REGRESSION TO ESTIMATE THE NCS-R MALE/FEMALE ODDS RATIO FOR LIFETIME MDE

As mentioned previously, logistic regression will be covered in detail in later chapters. Here, a simple logistic regression of the NCS-R MDE variable on the indicator of male gender (SEXm) is used to illustrate the technique for estimating the unadjusted male/female odds ratio for MDE and a 95% CI for that odds ratio:

```
svyset seclustr [pweight = ncsrwtsh], strata(sestrat)
svy: logistic mde sexm
```

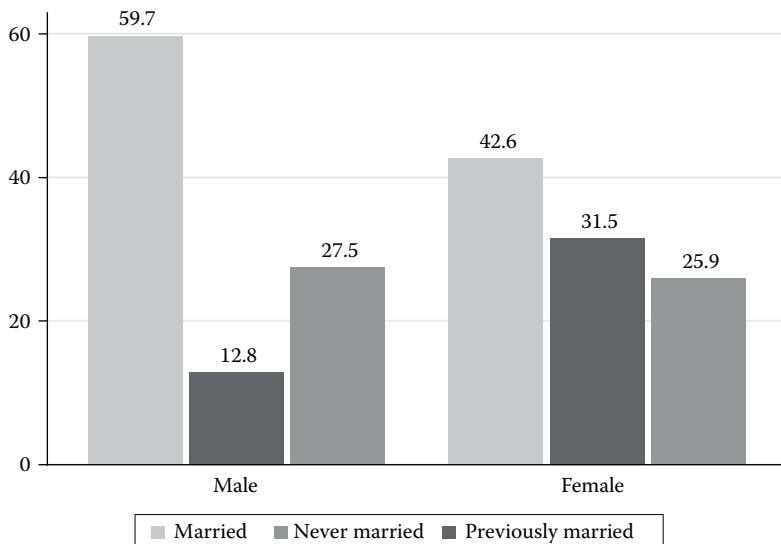
From the output provided by the `svy: logistic` command, the estimated odds ratio and a 95% CI for the population odds ratio are:

$\hat{\psi}_{MDE}$ (SE)	$CI_{95}(\psi)$
0.597 (0.041)	(0.520, 0.685)

Based on this analysis, the odds that an adult male has experienced a lifetime MDE are only 59.7% as large as the odds of MDE for adult females, which agrees (allowing for some rounding error) with the simple direct calculation above. Since the 95% CI does not include $\psi = 1$, we would reject the null hypothesis that MDE status is independent of gender.

6.4.7 Bivariate Graphical Analysis

Graphical displays are also useful tools to describe the bivariate distribution of two categorical variables. The Stata graphics command below generates gender-specific vertical bar charts for the ESS-Russia Federation

**FIGURE 6.8**

Bar chart of the estimated distributions of marital status of Russian adult men and women. (From ESS Round 6 (2012)—Russian Federation.)

MARCAT1—MARCAT3 variables generated in Example 6.3 (note that the pweight option is used to specify the survey weights, and the over() option is used to generate a plot for each level of gender). The output is shown in Figure 6.8.

```
graph bar (mean) marcat1 marcat2 marcat3 ///
[pweight=pspwght], percentages ///
bar(1,color(gs12)) bar(2,color(gs4)) ///
bar(3,color(gs8)) blabel(bar, format(%5.1f)) bargap(7) ///
scheme(s2mono) over(gndr) ///
legend (label(1 "Married") ///
label(2 "Previously Married") ///
label(3 "Never Married")) ytitle("Percentage")
```

6.5 Analysis of Multivariate Categorical Data

During the past 25 years, multivariate analysis involving three (or more) categorical variables has increasingly shifted to regression-based methods for generalized linear models ([Chapters 8](#) and [9](#)). The regression framework provides the flexibility to estimate the associations of categorical responses and factors as well as the ability to control for continuous covariates. In this

section, we briefly review the adaptation of two long-standing techniques for the analysis of multivariate categorical data to complex sample survey data: the Cochran-Mantel-Haenszel (CMH) test and simple log-linear modeling of the expected proportions of counts in multiway tables defined by cross-classifications of categorical variables.

6.5.1 Cochran–Mantel–Haenszel Test

Commonly used in epidemiology and related health sciences, the CMH test permits tests of the association between two categorical variables while controlling for the categorical levels of a third variable. For example, an analyst may be interested in testing the association between a lifetime diagnosis of MDE and gender while controlling for age categories. Although not widely available in software systems that support complex sample survey data analysis, design-based versions of the CMH test are available in SUDAAN's CROSSTAB procedure.

PROC CROSSTAB in SUDAAN supports two alternative methods for estimating the adjusted or *common odds ratio* and *common relative risk* statistics: the Mantel–Haenszel (M–H) method and the logit method. Both methods adjust for the complex sample design and generally result in very similar estimates of common odds ratios and relative risks.

EXAMPLE 6.11: USING THE NCS-R DATA TO ESTIMATE AND TEST THE ASSOCIATION BETWEEN GENDER AND DEPRESSION IN THE U.S. ADULT POPULATION WHEN CONTROLLING FOR AGE

In Examples 6.7, 6.8, and 6.10, we employed multiple approaches to analyzing the relationship of sex and MDE. In each case, we found evidence of a significant overall association between gender and a diagnosis of lifetime depression when analyzing the NCS-R data, where females had greater odds of receiving a diagnosis of depression at some point in their lives. This example is designed to test whether or not this association holds in the U.S. adult population when controlling for age. Given that the CMH test can be applied when the control variable is a categorical variable, a four-category age variable named AGECAT is constructed: 1 = ages 18–29, 2 = ages 30–39, 3 = ages 40–49, and 4 = ages 50+. The SUDAAN CROSSTAB procedure is then run to derive the CMH test and to use both the M–H and logit methods to estimate the common age-adjusted male/female odds ratio and relative risk for MDE.

```
title "ASDA2, Example 6.11: Test of Association between
Gender and MDE When Controlling for Age (NCSR)" ;
proc crosstab data=ncsr filetype=sas deft1 ;
nest sestrat seclustr ;
weight ncsrwtsh ;
class agecat mde sexm /nofreq ;
tables agecat*sexm*mde ;
risk mhor mhrrl lor lrrl ;
```

```

test cmh chisq ;
print nsum wsum rowper serow colper secol / stest=default
atest=default adjrisk=all style=nchs ;
run ;

```

Note that the sampling error codes (NEST statement) and the survey weights (WEIGHT statement) are identified first, with the cluster codes nested within the strata. Next, the CLASS statement specifies that all three variables are categorical. In the TABLES statement, the AGECAT variable is identified first, defining it as the categorical control variable for this analysis. We define SEXM as the row variable and MDE as the column variable. The RISK statement then requests estimates of the M–H common odds ratio and relative risk ratio, and the logit-based common odds and relative risk ratios. Finally, the TEST statement requests the overall design-adjusted CMH test, in addition to the Wald χ^2 tests which will be performed for each age stratum. Table 6.9 summarizes the key elements of the SUDAAN output.

The value of the design-adjusted CMH test statistic in this case is $X_{CMH}^2 = 94.26$, which has $p < 0.0001$ on one degree of freedom, suggesting that there is still a strong association between gender and lifetime depression after adjusting for age. This is supported by the design-adjusted Wald χ^2 statistics produced by SUDAAN for each age group (Equation 6.12). In each age stratum, there is evidence of a significant association of gender with lifetime depression. After adjusting for respondent's age, both the M–H and logit estimates of the common male/female odds ratio are about $\hat{\psi}_{MH|Age} \approx 0.60$. This can be compared to the estimated odds ratio, $\hat{\psi}_{Unadj} \approx 0.60$ from Example 6.10 when no adjustment for age is included. Males appear to have roughly 40% lower odds of having a lifetime diagnosis of depression compared to females, when adjusting for age. The M–H and logit method estimates of the common risk ratios also suggest a significant difference in the probability of depression for the two groups, with the expected probability about 10% lower for males when adjusting for age.

TABLE 6.9

SUDAAN Output for the Cochran–Mantel–Haenszel (CMH) Test of the MDE–SEX Association, Controlling for AGEAT

Cochran–Mantel–Haenszel Test Results

$X_{CMH}^2 = 94.26$	$df = 1$	$p < 0.0001$
---------------------	----------	--------------

Age Category-Specific Wald Tests of Independence for MDE and SEX

Age category	18–29	30–39	40–49	50+
Q_{Wald}	23.47	23.22	9.12	38.28
$P(\chi_1^2 > Q_{Wald})$	$p < 0.0001$	$p < 0.0001$	$p = 0.0043$	$p < 0.0001$

Age-Adjusted Estimates of Common Male/Female Odds Ratios and Relative Risks

Statistic	ψ_{M-H}	ψ_{Logit}	RR_{M-H}	RR_{Logit}
Point estimate	0.59	0.60	0.91	0.91
95% CI	(0.51, 0.67)	(0.52, 0.68)	(0.88, 0.93)	(0.89, 0.93)

6.5.2 Log-Linear Models for Contingency Tables

A text on the analysis of survey data would not be complete without a mention of log-linear models for multiway contingency tables (Bishop et al., 1975; Stokes et al., 2002; Agresti, 2012). Log-linear models permit analysts to study the *association structure* among categorical variables. In a sense, a log-linear model for categorical data is analogous to an ANOVA model for the cell means of a continuous dependent variable. The dependent variable in the log-linear model is the natural logarithm of the expected counts (or multinomial probabilities) for cells of a multiway contingency table. The model parameters are estimated effects associated with the categorical variables and their interactions.

For example, the following is the log-linear model under the null hypothesis of independence for three categorical variables X , Y , and Z :

$$\log(p_{ijk}) = \mu + \lambda_i^X + \lambda_j^Y + \lambda_k^Z, \quad (6.15)$$

where

p_{ijk} = the expected cell proportion under the model;

$\mu = \log(p_0) = 1/(\#cells)$.

A model that includes a first-order interaction between the X and Y variables would be written as:

$$\log(p_{ijk}) = \mu + \lambda_i^X + \lambda_j^Y + \lambda_k^Z + \lambda_{ij}^{XY}. \quad (6.16)$$

The cell proportions are assumed to follow a multinomial distribution and the model parameters are estimated using the method of maximum likelihood or iterative procedures such *iterative proportional fitting* (IPF) or the *Newton–Raphson method*. Tests of nested models (note that the model in Equation 6.15 is nested in the model in Equation 6.16) are performed using the *likelihood ratio test*.

Log-linear models for SRS data can be analyzed in virtually every major software package (e.g., PROC CATMOD in SAS). Presently, most software packages such as Stata, SAS, and SPSS do not include a program to perform the traditional log-linear modeling of complex sample survey data. The `svyloglin()` function in the R `survey` package (Lumley, 2010) does support log-linear modeling for complex sample survey data. The IVEware® (Raghunathan et al., 2001) %SASMOD command employs a generic JRR algorithm that in combination with PROC CATMOD can be used for log-linear model estimation and inference with data from complex sample surveys (Example 6.12).

There are two major explanations for why programs for log-linear modeling are not included in most software packages for survey data analysis. The first is that the common, general structure of the input data (grouped

cell counts of individual observations) does not lend itself readily to design-based estimation and inference where individual cases may have varying weights. In Skinner et al. (1989), Rao and Thomas discuss the extension of their design-based adjustment for χ^2 test statistics to the conventional likelihood ratio tests for log-linear models, but this technique would take on considerable programming complexity as the dimension and number of variations on the association structure in the model increases.

Grizzle et al. (1969) introduced the weighted least squares (GSK) method of estimating log-linear and other categorical data models. This generalized technique was programmed in the GENCAT software (Landis et al., 1976) and required the user to input a design-based variance–covariance matrix for the vector of cell proportions in the full crosstabular array. Under the GSK method, tests of hypotheses are performed using Wald statistics.

A second explanation for the scarcity of log-linear modeling software for complex sample survey data is that log-linear models for expected cell counts or multinomial proportions can be reparameterized as logistic regression models (Agresti, 2012) and all of the major software systems have more advanced programs for fitting logistic and other generalized linear models to complex sample survey data. These models will be considered in detail in [Chapters 8 and 9](#).

EXAMPLE 6.12: A SIMPLE LOG-LINEAR MODEL TO TEST THE ASSOCIATION BETWEEN LIFETIME MAJOR DEPRESSIVE EPISODE AND SEX

To illustrate an application of log-linear modeling to complex sample survey data, we return again to the now familiar question of whether the NCS-R data provide evidence of a significant association between sex and a lifetime experience of an episode of major depression. The log-linear model that we will estimate is:

$$\log(p_{ij}) = \mu + \lambda_i^{MDE} + \lambda_j^{SEX} + \lambda_{ij}^{MDE \times SEX}$$

where:

p_{ij} = the expected proportion in cell (i, j) under the model (multinomial sampling is assumed).

The IVEware %SASMOD program syntax used to fit the model (which requires running IVEware within the SAS software) is:

```
%sasmod(dir=P:\ASDA 2, setup=new, name=SASMOD_CATMOD2) ;
datain ncsr_a ;
cluster seclustr ;
stratum sestrat ;
weight ncsrwtsh;

proc catmod ;
model mde*sexm=_response_ ;
loglin mde sexm mde*sexm ;
run ;
```

Note that %SASMOD utilizes the NCS-R strata, cluster, and weight variables to form JRR replicates of the full sample. The program then calls PROC CATMOD in SAS to estimate the model for each replicate and the full sample. The standard JRR formula (Section 3.6.3.1) is then used to estimate the variances of the model parameter estimates.

Using the R survey package (Lumley, 2010), the following R code imports the NCS-R data from Stata, estimates the log-linear model, and generates a test of the interaction between gender and MDE:

```
# load the haven package
> library(haven)
> ncsr <- read_dta("P:/ASDA 2/ncsr_sub_13nov2015.dta")

> # load the survey package
> library(survey)
> ncsrvyp1 <- svydesign(strata=~sestrat, id=~seclustr,
weights=~ncsrwtsh, data=ncsr, nest=T)
> # run null model with mde and sexm
> null <- svyloglin(~mde+sexm, ncsrvyp1)
> summary(null)
```

Both %SASMOD and the R `svyloglin()` analysis produce identical estimates of the model parameters with only negligible differences in the standard errors and test statistics, due to the different default methods for complex sample variance estimation—JRR in %SASMOD and TSL in `svyloglin()`.

Table 6.10 summarizes the results of the analysis. For the 2×2 cross-classification of SEX \times MDE, the estimated log-linear model for the log of the multinomial proportions in each of the four cells includes: a row effects parameter, $\hat{\lambda}^{SEX}$; a column effects parameter, $\hat{\lambda}^{MDE}$, and a parameter for the interaction of row and column, $\hat{\lambda}^{SEX,MDE}$. Since there are four cell proportions and three parameters to estimate, this log-linear model is “saturated.” In this simple 2×2 example table, the null hypothesis of interest is whether the cell probabilities are solely a function of the margin variables $\hat{\lambda}^{SEX}$ and $\hat{\lambda}^{MDE}$ (i.e., the model of independence) or whether the interaction parameter, $\hat{\lambda}^{SEX,MDE}$, also plays a significant role. Therefore, in this simple 2×2 example, testing the null hypothesis of independence of MDE and sex is equivalent to testing $H_0: \hat{\lambda}^{SEX,MDE} = 0$. From [Table 6.10](#),

TABLE 6.10

IVEware® %SASMOD/SAS® CATMOD Log-Linear Model Analysis of the Association between Gender and Lifetime Experience of Major Depression

Description	Parameter	Parameter Estimate	JRR SE	t-Statistic ($H_0: \lambda = 0$)	Prob($t_{42} > t$)
MDE	λ^{MDE}	0.735	0.017	42.326	<0.0001
Gender	λ^{SEX}	0.123	0.012	10.551	<0.0001
MDE \times Gender	$\lambda^{MDE,SEX}$	-0.129	0.017	-7.439	<0.0001

Source: NCS-R.

$\hat{\lambda}^{SEX,MDE} = -0.129$ with standard error $se(\hat{\lambda}^{SEX,MDE}) = 0.017$, corresponding to a Student t -test statistic of $t = -7.439$ ($p < 0.0001$). Consistent with previous analyses, we would again reject the null hypothesis that the U.S. adults' lifetime experience of major depression is independent of their sex.

6.6 Summary

Variables for which responses are measured on a binary, multinomial, ordinal, or count scale are the predominant form of data collected in complex sample surveys. In this chapter, we have introduced methods for conducting basic univariate and bivariate analyses of categorical variables from complex sample survey data sets. By introducing the CMH Test, log-linear models, and the logistic regression model, we have opened the door to a larger discussion (Chapters 8, 9, and 13) of multivariate methods in the analysis of categorical data from complex sample surveys. The developments of these later chapters will focus on regression modeling of categorical responses using methods such logistic or probit regression, multinomial and ordinal regression, multinomial logit regression, and Poisson and negative binomial regression.

EXERCISES

- 6.1 Using the software procedure of your choice and the ESS-Russian Federation data set, *chapter_exercises_ess6rf* (see the ASDA website to download the data), estimate the row proportions in a two-way table where marital status (MARCAT, 1='MARRIED', 2='PREVIOUSLY MARRIED', 3='NEVER MARRIED') is the factor variable (or row variable) and Voted in the Last Election (VOTED_LASTELECTION, 1=YES, 0=NO) is the response variable (or column variable). Make sure to correctly identify and incorporate the sampling error stratum, sampling error cluster, and final survey weight variables in the ESS-Russian Federation data set. Use the weight that incorporates poststratification and design features. Then, answer the following questions:
 - a. What is the value of the Rao–Scott F -statistic for the overall test of the null hypothesis that marital status category and voting status are not associated? What are the degrees of freedom for this design-adjusted F -statistic?
 - b. Under this null hypothesis, what is the p -value for the F reference distribution?

- c. Based on this test, what is your statistical decision regarding the association between marital status and voting behavior in the ESS-Russian Federation survey population?
- 6.2 Repeat the analysis from 6.1 above, only performing unconditional subclass analyses for men and women separately (GNDR: 1 = Male 2 = Female). Do your inferences change when restricting the target population to only men or only women?
- 6.3 Create an indicator variable of high satisfaction with life (called HIGH_SAT) using the STFLIFE variable, coded so that 1 = (STFLIFE = 9 OR 10), 0 = (0 <= STFLIFE <= 8) and missing values are set to system missing in your software of choice. Then answer the following questions, while using the appropriate complex sample design variables and weights:
- What proportions of the total population, males, and females in the ESS-RF survey population are estimated to have high satisfaction with life? Make sure to provide three weighted estimates of proportions and design-adjusted standard errors to fully answer this question.
 - Compute design-based 95% CIs for each of the three proportions estimated in part a. Use your software of choice or calculate the CIs manually, and indicate which of the approaches discussed in the chapter were used to compute the intervals (and why).
 - Is there a significant association between Gender and High Satisfaction with Life? Provide statistical support for your inference.
- 6.4 Extend the analysis in 6.3 by conducting an analysis of the association between Gender and High Satisfaction with Life separately for each of the four age groups defined by the variable AGECAT. Then, answer these questions:
- When the age groups are analyzed separately, does the association (or lack thereof) between Gender and High Satisfaction with Life continue to hold?
 - Provide the design-adjusted F -statistic and p -value for each of the age-specific analyses to support your answer.
 - If the answer to part a. is "No," how do you explain this pattern of results in plain English?
- 6.5 *Extra-Credit Question (use SUDAAN or another software able to perform a design-based trend test):* Perform a CMH trend test of the association of Gender and High Satisfaction with Life, controlling for age groups.
- Prior to running the analysis, create a numeric version of the STRATIFY variable with values of 1–8 corresponding to the

eight character labels of STRATIFY and name the new variable NSTRAT. If using SUDAAN, sort the data by NSTRAT and PSU before use of a SUDAAN command.

- b. What are the values of the Wald F -test statistic, degrees of freedom, and p -value from the CMH general association Wald F -test?
- c. What is your conclusion regarding the significance of this association, controlling for the four age groups?



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7

Linear Regression Models

7.1 Introduction

Study regression. All of statistics is regression.

This quote came as a recommendation from a favorite professor to one of the authors while he was in the process of choosing a concentration topic for his comprehensive exam. The broader interpretation of the quote requires placing the descriptor in quotes, “regression”; but ask individuals with backgrounds as varied as social science graduate students or quality control officers in a paper mill to decipher the statement and they will think first of the linear regression model. Given the importance of the linear regression model in the history of statistical analysis, the emphasis that it receives in applied statistical training and its importance in real world statistical applications, the narrower interpretation is quite understandable.

This chapter introduces linear regression modeling for complex sample survey data—its similarities and how it differs (theoretically and procedurally) from standard ordinary least squares (OLS) regression analysis. We assume that the reader is familiar with the basic theory and methods for simple (single predictor) and multiple (multiple predictor) linear regression analysis for continuous dependent variables. Readers interested in a comprehensive reference on the topic of linear regression are referred to Draper and Smith (1981), Kleinbaum et al. (1988), Neter et al. (1996), DeMaris (2004), Faraway (2014), Fox (2008), or many other excellent texts on the subject.

Focusing on practical approaches for complex sample survey data, we emphasize “aggregated” *design-based approaches* to the linear regression analysis of survey data (sometimes referred to as *population-averaged modeling*), where design-based variance estimates for weighted estimates of regression parameters in *finite* populations are computed using nonparametric methods such as the Taylor series linearization (TSL) method, balanced repeated replication (BRR), jackknife repeated replication (JRR), or bootstrapping. *Model-based approaches* to the linear regression analysis of

complex sample survey data, which may explicitly include fixed effects of sampling strata and/or random effects of sampling clusters in the regression models and may or may not utilize the sampling weights (e.g., Skinner et al., 1989; Pfeffermann et al., 1998; Little, 2003; Pfeffermann, 2011), are introduced in [Chapter 13](#). Over the years, there have been many contributions to the survey methodology literature comparing and contrasting these two approaches to the regression analysis of survey data, including papers by DuMouchel and Duncan (1983), Hansen et al. (1983), and Kott (1991).

We present a brief history of important statistical developments in linear regression analysis of complex sample survey data to begin this chapter. Kish and Frankel (1974) were two of the first to empirically study and discuss the impacts of complex sample designs on inferences related to regression coefficients. Fuller (1975) derived a linearization-based variance estimator for multiple regression models with unequal weighting of observations and introduced variance estimators for estimated regression parameters under stratified and two-stage sampling designs. Shah et al. (1977) further discussed the violations of standard linear model assumptions when fitting linear regression models to complex sample survey data, discussed appropriate methods for making inferences about linear regression parameters estimated using survey data, and presented an empirical evaluation of the performance of variance estimators based on TSL.

Binder (1983) focused on the sampling distributions of estimators for regression parameters in finite populations and defined related variance estimators. Skinner et al. (1989, Sections 3.3.4 and 3.4.2) summarized estimators of the variances for regression coefficients that allowed for complex sample designs (including linearization estimators) and recommended the use of linearization methods or other robust methods (such as JRR) for variance estimation. Kott (1991) further discussed the advantages of using variance estimators based on TSL for estimates of linear regression parameters: protection against correlated random errors within primary sampling units (PSUs), protection against possible nonconstant variance of the random errors, and the fact that a within-PSU correlation structure does not need to be identified to have a nearly unbiased estimator. Fuller (2002) provided a modern summary of regression estimation methods for complex sample survey data, and Pfeffermann (2011) discussed the relative merits of a variety of possible design-based and model-based approaches to fitting linear regression models to complex sample survey data, presenting empirical support for the use of a “q-weighted” method. In this method, the modified sampling weights used to compute estimates of the regression coefficients are the original probability weights divided by the *expectations* of the weights as a function of the covariates in the model of interest (i.e., predicted values of the weights based on a model regressing the weights on the predictor variables in the model of interest). We consider this approach in the illustration presented later in this chapter.

7.2 Linear Regression Model

Regression analysis is a study of the relationships among variables: a *dependent variable* and one or more *independent variables*. Figure 7.1 illustrates a simple linear regression model of the relationship of a dependent variable, y , and a single independent variable x . The regression relationship among the observed values of y and x is expressed as a regression model, for example, $y = \beta_0 + \beta_1 x + \varepsilon$, where y is the dependent variable, x is the independent variable, β_0 and β_1 are model parameters, and ε is an error term that reflects the difference between the observed value of y and its conditional expectation under the model, $\varepsilon = y - \hat{y} = y - \beta_0 - \beta_1 x$.

In statistical practice, a fitted regression model may be used to simply predict the expected outcome for the dependent variable based on a vector of independent variable measurements x , $E(y | x) = \hat{\beta}_0 + \hat{\beta}_1 x_1 + \dots + \hat{\beta}_p x_p$, or to explore the functional relationship of y and x . Across the many scientific

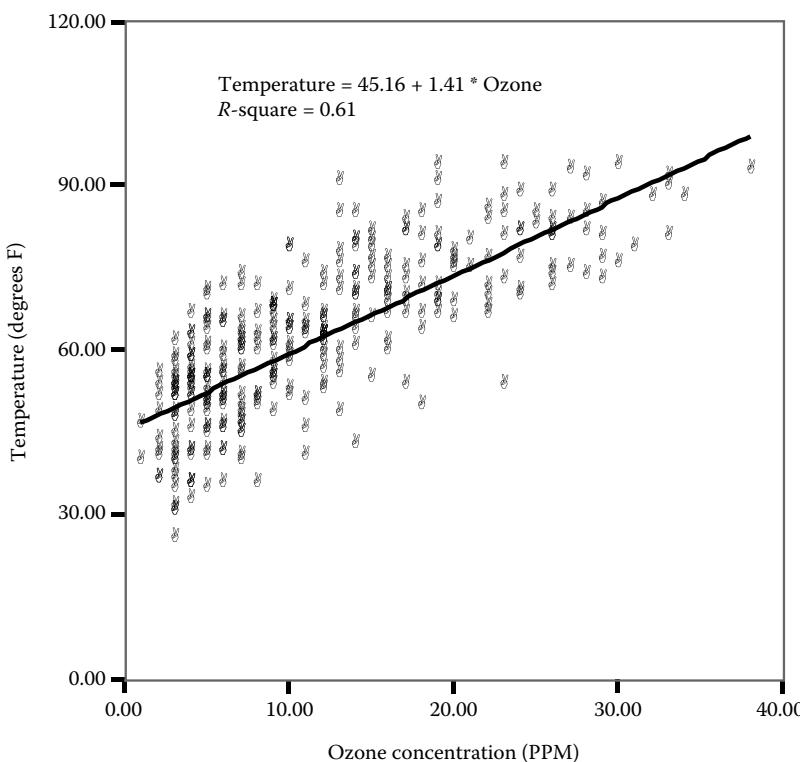


FIGURE 7.1

Linear regression of air temperature on ozone level. (From Breiman and Friedman, 1985).

disciplines that use regression analysis methods, dependent variables may also be referred to as response variables, regressands, outcomes, or even “left-hand side variables.” Independent variables may be labeled as predictors, regressors, covariates, factors, cofactors, explanatory variables, or “right-hand side variables.” We primarily refer to response variables and predictor variables in this chapter, but other terms can be used interchangeably.

This chapter will focus on the broad class of regression models known as *linear models*, or models for which the conditional expectation of y given x , $E(y|x)$, is a linear function of the unknown parameters. Consider the following three specifications of linear models:

$$y = \beta_0 + \beta_1 x + \varepsilon. \quad (7.1)$$

Note in this model that the dependent variable, y , is a linear function of the unknown parameters and the independent variable x .

$$y = \beta_0 + \beta_1 x + \beta_2 x^2 + \varepsilon. \quad (7.2)$$

In this model (7.2), the response variable y is still a linear function of the β parameters for x and x^2 ; however, the linear model defines a *nonlinear* relationship between y and x .

$$\begin{aligned} y &= \mathbf{x}\boldsymbol{\beta} + \varepsilon \\ &= \sum_{j=0}^p \beta_j x_j + \varepsilon \\ &= \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \cdots + \beta_p x_p + \varepsilon. \end{aligned} \quad (7.3)$$

Here, the linear model is first expressed in *vector notation*. Vector notation may be used as an abbreviation to represent a complex model with many parameters and to facilitate computations using the methods of matrix algebra.

When specifying linear regression models, it is useful to be able to reference specific observations on the subjects in a survey data set:

$$y_i = \mathbf{x}_i \boldsymbol{\beta} + \varepsilon_i, \quad (7.4)$$

where:

$$\mathbf{x}_i = [1 \quad x_{1i} \quad \dots \quad x_{pi}] \text{ and } \boldsymbol{\beta}^T = [\beta_0 \quad \beta_1 \quad \dots \quad \beta_p].$$

In this notation, i refers to sampled element (or respondent) i in a given survey data set.

7.2.1 Standard Linear Regression Model

Standard procedures for unbiased estimation and inference for the linear regression model involve the following assumptions:

1. The model for $E(y|x)$ is linear in the parameters (Equation 7.2).
2. Correct model specification—in short, the model includes the predictor variables and regression coefficients that accurately reflect the true model under which the data were generated.
3. $E(\varepsilon_i|x_i) = 0$, or the expected value of the residuals given a set of values on the predictor variables is equal to 0.
4. Homogeneity of Variance— $\text{var}(\varepsilon_i|x_i) = \sigma_{y,x}^2$, or the variance of the residuals given values on the predictor variables is a constant parameter equal to $\sigma_{y,x}^2$.
5. Normality of residuals (and also y): for continuous outcomes, we assume that $\varepsilon_i | x_i \sim N(0, \sigma_{y,x}^2)$, or that given values on the predictor variables, the residuals are independently and identically distributed (i.i.d.) as normal random variables with mean 0 and constant variance $\sigma_{y,x}^2$.
6. Independence of residuals: As a consequence of (5), $\text{cov}(\varepsilon_i, \varepsilon_j | x_i, x_j) = 0$, $i \neq j$, or residuals on different subjects are *uncorrelated* given values on their predictor variables.

There are several implications of these standard model assumptions. First, we can write:

$$\hat{y} = E(y | x) = E(x\beta) + E(\varepsilon) = x\beta + 0 = x\beta = \beta_0 + \beta_1 x_1 + \cdots + \beta_p x_p. \quad (7.5)$$

This equation for the predicted value of y is the *regression function*, or the expected value of the dependent variable y conditional on a set of values on the predictor variables (of which there are p). Further, we can write

$$\text{var}(y_i | x_i) = \sigma_{y,x}^2. \quad (7.6)$$

$$\text{cov}(y_i, y_j | x_i, x_j) = 0. \quad (7.7)$$

These assumptions, therefore, imply that the dependent variable has constant variance given values on the predictors and that no two values on the dependent variable are correlated given values on the predictors. Putting all of the implications together, we have

$$y_i \sim N(x_i\beta, \sigma_{y,x}^2). \quad (7.8)$$

Values on the dependent variable, y , are therefore assumed to be i.i.d. normally distributed random variables with a mean defined by the linear combination of the regression parameters and the predictor variables and a constant variance.

7.2.2 Survey Treatment of the Regression Model

Since the late 1940s and early 1950s, when economists and sociologists (Kendall and Lazarsfeld, 1950; Klein and Morgan, 1951) first applied regression analysis to complex sample survey data, survey statisticians have sought to relate design-based estimation of regression relationships to the standard linear model. The result was the linked concepts of a finite population and the superpopulation model, which are described in more detail in [Chapter 3](#) and also Theory Box 7.1.

THEORY BOX 7.1 FINITE POPULATIONS AND SUPERPOPULATION MODELS

In theory, weighted estimation of a linear regression model, $y = \beta_0 + \beta_1 x + \varepsilon$ from complex sample survey data results in unbiased estimates of the regression function, $E(y|x) = B_0 + B_1 x$, where $B = [B_0, B_1]$ are *finite population regression parameters*. If instead of observing a sample of size n of the N population elements a complete census had been conducted, the finite population regression parameter B_1 for this simple “line” could be computed algebraically as follows:

$$B_1 = \frac{\sum_{i=1}^N (X_i - \bar{X})(Y_i - \bar{Y})}{\sum_{i=1}^N (X_i - \bar{X})^2}.$$

The theory suggests that we distinguish between the true regression model parameters, β , and the particular values, B , that characterize the current finite survey population that was sampled for the survey. For example, consider a simple linear regression model of the effect of years of education on adults’ earned income. The model can be interpreted as:

$$E(\text{Income} | \text{Education}) = \beta_0 + \beta_1 \cdot \text{Education(years)}$$

or

$$\text{Income} | \text{Education} \sim N(\beta_0 + \beta_1 \cdot \text{Education(years)}, \sigma_{I:E}^2).$$

In contrast, a strict finite population regression interpretation is that for the particular population that has been sampled, the best prediction of adult income, given their education level, is found on the line $E(\text{Income}|\text{Education}) = B_0 + B_1 \cdot \text{Education}(\text{years})$. The concept of a *superpopulation* links these two interpretations by introducing the assumption that although the surveyed population is finite (size N), the individual relationship between income and education in that finite population conforms to an underlying superpopulation model. Therefore, the fixed set of pairs of income and education values in the finite population of N elements is itself a sample from an infinite number of possible data pairs that could be generated by a stochastic superpopulation model, denoted by ζ : $\text{Income} = \beta_0 + \beta_1 \cdot \text{Education}(\text{years}) + \varepsilon$.

Under the superpopulation model, the finite population parameters B will vary about the true model parameters β . However, the bias of making inferences for β based on estimates, \hat{B} (which are unbiased for B), is small, and of the order $O(N^{-1/2})$ (meaning that the bias is a function of $N^{-1/2}$, and will thus become small as the population size becomes larger). Therefore, for large populations, an unbiased estimate of B (generally computed using weighted least squares [WLS]) can serve as an unbiased estimate of β . Model diagnostics can then be used to question the hypothesized superpopulation model or the suitability of B as a summary measure of the relationships.

When survey analysts conduct a regression analysis using complex sample survey data, they choose between two targets—the finite population or a more universal superpopulation model—for their estimation and associated inference. Sometimes this is a conscious choice, and sometimes the choice is less conscious and only implicit in the analyst's presentation of the results and the inferences that are drawn.

In theory, weighted, design-based estimation of a regression equation permits the survey analyst to make unbiased inferences concerning values of the regression relationship as it exists within the finite population that corresponds to the geographic, demographic, and temporal definition of the survey population. To extend this inference beyond the survey population requires the analyst to make generalizing assumptions about the relationship of the finite population that has been studied to an overarching superpopulation model that may govern the relationships of the variables of interest. Theory Box 7.1 discusses the relationship of the superpopulation model and the finite population regression function in more detail. In practice, if the survey population is large and the regression model is correctly specified, then the survey data analyst may treat these two conceptual approaches as virtually equivalent (Skinner et al., 1989; Korn and Graubard, 1999).

7.3 Four Steps in Linear Regression Analysis

There are four basic steps that analysts should follow when fitting regression models to complex sample survey data: specification, estimation, evaluation (diagnostics), and inference. These steps apply to all types of regression models and not just those discussed in this chapter for continuous response variables. The following sections describe each step, considering the standard approach first, followed by the adaptation of the step for complex sample survey data.

7.3.1 Step 1: Specifying and Refining the Model

Survey data are typically observational data. The process of initial specification and subsequent refinement of a regression model for survey data involves multiple iterations of the four-step process. At the beginning of each cycle in this iterative process, it is important for the survey analyst to step back from the “number crunching” and critically evaluate the scientific interpretation and the plausibility of the emerging model.

A model is initially postulated based on subject matter knowledge and empirical investigation of the data. The specific aims of the analysis will often determine the choice of the dependent variable, y , and one or more independent variables of particular interest, x . Scientific subject matter knowledge and information gleaned from prior studies and publications can be used to identify additional independent variables (i.e., covariates that are known predictors of the dependent variable) or variables that may *mediate* or *moderate* (DeMaris, 2004) the relationships of the independent variables of primary interest with the dependent variable y . For example, an epidemiologist aiming to model the effect of obesity on systolic blood pressure (BP, in mmHg) decides to include age, gender, and race of the respondent as additional covariates. Based on prior research conducted by a colleague, she has evidence that advanced age moderates the relationship between systolic BP level and obesity. She will test for an interaction between age and the obesity measure (as well as other potential interactions—Section 7.4).

Empirical results from simple descriptive and graphical statistical analysis of the survey data itself can also be used to identify independent variable candidates for the model. The epidemiologist in our example might conduct an exploratory analysis, plotting systolic BP against respondent age. At older ages, the resulting scatter plot shows a curvilinear relationship to systolic BP, suggesting the addition of a quadratic term to the initial model. See Cleveland (1993) for a good resource on data exploration.

Contemporary survey data sets may contain hundreds of variables, and there is a temptation to bypass the scientific review and empirical investigations and “see what works.” Regression programs in statistical software

packages often include variable selection algorithms such as *stepwise regression*, *forward selection*, and *backward selection* that are capable of culling a set of significant predictors from a large input of independent variable choices. These algorithms may prove useful in the model exploration and fitting process, but they are numerical tools and should not substitute for the survey analyst's own scientific and empirical assessment of the model and its final form. Careless use of such techniques leaves the analyst exposed to problems of *confounding* or *spurious relationships* that can distort the model and its interpretation.

A variety of variable selection and model-building approaches have been proposed for linear regression models. One such model-building “recipe” commonly used in our teaching and consulting practice is described in Section 7.4.5.

7.3.2 Step 2: Estimation of Model Parameters

After the survey data analyst has specified a linear regression model (Step 1), the next step in the modeling process involves computation of estimates of the regression parameters in the specified model. This section describes mathematical methods that can be used for estimation of those parameters.

7.3.2.1 Estimation for the Standard Linear Regression Model

By far, the most popular method of estimating unknown parameters in linear regression models is *ordinary least squares (OLS) estimation*. This method focuses on estimating the unknown set of regression parameters β in a specified model by minimizing the residual sum of squares (or sum of squared errors, SSE) based on the model:

$$SSE = \sum_{i=1}^n (y_i - \hat{y}_i)^2 = \sum_{i=1}^n (y_i - x_i \beta)^2. \quad (7.9)$$

Once the estimate of β has been obtained analytically (7.11), an estimate of the variance of the random errors in the model, σ_{y-x}^2 , is obtained as follows:

$$\hat{\sigma}_{y-x}^2 = \frac{\sum_{i=1}^n (y_i - x_i \hat{\beta})^2}{n-p}. \quad (7.10)$$

Here, p is the number of regression parameters in the specified model.

The least squares estimate has several important properties. First, parameter estimates and their variances and covariances are analytically simple

to compute, requiring only a single noniterative algebraic or matrix algebra computation:

$$\begin{aligned}\hat{\boldsymbol{\beta}} &= (\mathbf{X}^T \mathbf{X})^{-1} \mathbf{X}^T \mathbf{y} \\ \text{var}(\hat{\boldsymbol{\beta}}) &= \hat{\Sigma}(\hat{\boldsymbol{\beta}}) = (\mathbf{X}^T \mathbf{X})^{-1} \hat{\sigma}_{yx}^2.\end{aligned}\tag{7.11}$$

Second, the estimator is unbiased:

$$E(\hat{\boldsymbol{\beta}} | \mathbf{X}) = \boldsymbol{\beta}.\tag{7.12}$$

Third, the estimator has the lowest variance among all other unbiased estimators that are also linear functions of the response values, making it the *best linear unbiased estimator* (BLUE). Finally, assuming normally distributed errors, the least squares estimates are equal to estimates derived based on maximum likelihood estimation (MLE).

As described in Section 7.2, one key assumption of the standard linear regression model is homogeneity of the error variance:

$$\text{var}(\varepsilon) = \text{var}(y_i | \mathbf{x}_i) = \sigma_{yx}^2 = \text{constant}.\tag{7.13}$$

In practice, it is common to find that the variance of the residuals is heterogeneous—varying over the $i = 1, \dots, n$ cases with differing values of y and \mathbf{x} . For OLS estimation, the consequence of heterogeneity of variance is loss of efficiency (larger standard errors) in the estimation of the regression coefficients. *Weighted least squares* (WLS) estimation of the regression coefficients addresses this inefficiency by weighting each sample observation's contribution to the sums of squares by the reciprocal of its residual variance, $W_i = 1/\sigma_{yx,i}^2$. In matrix notation, the WLS estimator of the linear regression coefficients is:

$$\hat{\boldsymbol{\beta}} = (\mathbf{X}^T \mathbf{W} \mathbf{X})^{-1} \mathbf{X}^T \mathbf{W} \mathbf{y}.\tag{7.14}$$

Here, \mathbf{W} is an $n \times n$ diagonal matrix (with zeroes off the diagonal) and the n values of the inverse variance weights on the diagonal.

The standard linear regression model and the OLS estimator are statistically elegant, but the underlying assumptions are easily violated when analyzing real world data. To minimize the mean square error of estimation, techniques such as transformation of the dependent variable, WLS estimation, and other approaches such as ridge regression (Hoerl and Kennard, 1970) and robust variance estimation (Judge et al., 1985; Fuller et al., 1989) have been developed to address problems of non-normality, heterogeneity of variances, collinearity of predictors, and correlated errors.

7.3.2.2 Linear Regression Estimation for Complex Sample Survey Data

Estimation of regression relationships for complex sample survey data alters the standard approach to estimation of coefficients and their standard errors. We first discuss what changes with estimation of the parameters, and then address what changes in terms of variance estimation.

7.3.2.2.1 Estimation of Parameters

The observed data from a complex sample survey are typically not “identically distributed.” Due to variation in sample selection and sample inclusion probabilities, survey weights must generally be employed to develop unbiased estimates of the population regression parameters. Recall that in standard methods of regression analysis, WLS estimation incorporates a weight for each sample element inversely proportional to the residual variance. In the context of fitting regression models to complex sample survey data sets, where final survey weights have been calculated to compensate for unequal probability of selection, unit nonresponse, and possibly poststratification (Section 2.7), the survey weights can be incorporated into the estimation of the regression parameters via the use of WLS estimation. The contribution of each case to the residual sum of squares is made proportional to its population weight. This results in the following analytic formula for the WLS estimate of the finite population regression parameters:

$$\hat{\mathbf{B}} = (\mathbf{X}^T \mathbf{W} \mathbf{X})^{-1} \mathbf{X}^T \mathbf{W} \mathbf{y}. \quad (7.15)$$

Here, \mathbf{W} is an $n \times n$ diagonal matrix (with zeroes off the diagonal) and the n values of the survey weights on the diagonal. Theory Box 7.2 provides mathematical motivation for the weighted survey estimator of \mathbf{B} , and Theory Box 7.3 further considers the decision of whether to use analysis weights when estimating regression parameters from complex sample survey data.

Although the motives for conventional WLS estimation (heterogeneity of residual variances) and weighted survey estimation (unbiased population representation) are very different, the WLS computational algorithms that have been built into regression software for several decades serve perfectly well for weighted survey estimation of the finite population regression model. Consequently, analysts who naively specified the survey weight as the weight variable in a standard linear regression program (e.g., SAS PROC REG, regress in Stata, and SPSS Linear Regression) have obtained the correct design-based estimates of the population regression parameters. Unfortunately, the naïve use of weighted survey estimation in standard linear regression programs generally results in biased estimates of standard errors for the parameter estimates (see below). Stata explicitly recognizes the differences in weighting concepts and requires the user to declare probability weights, or “pweights.” Stata also uses a robust estimator of variance when a “pweight” is specified.

THEORY BOX 7.2 A “WLS” ESTIMATOR FOR FINITE POPULATION REGRESSION MODELS

When fitting regression models to complex sample survey data collected from a finite population, we compute estimates of the finite population parameters \mathbf{B} that minimize the following objective function:

$$f(\mathbf{B}) = \sum_{i=1}^N (y_i - \mathbf{x}_i \mathbf{B})^2.$$

We can think of this objective function $f(\mathbf{B})$ as a finite population “residual” sum of squares, SSE_{pop} . An unbiased sample estimate of this total incorporating the survey weights can be written as follows:

$$\hat{WSSSE}_{pop} = \sum_h^H \sum_{\alpha}^{a_h} \sum_{i=1}^{n_{h\alpha}} w_{h\alpha i} (y_{h\alpha i} - \mathbf{x}_{h\alpha i} \mathbf{B})^2.$$

In this expression, h is a stratum index, α is a cluster (or primary sampling unit) index, and i is an index for elements within the α -th cluster. WLS estimation is used to derive estimates of \mathbf{B} that minimize this sample estimate of the actual objective function for the finite population.

Correct interpretation of estimated regression parameters is essential for effectively communicating the results of investigations involving regression analyses in scientific publications. In a simple linear regression model for a continuous dependent variable, after obtaining estimates of the regression parameters, we can calculate the following expected values on the response variable, associated with a one-unit change in a given predictor variable x :

$$E(y | x = x_0) = \hat{B}_0 + \hat{B}_1 x_0. \quad (7.16)$$

$$E(y | x = x_0 + 1) = \hat{B}_0 + \hat{B}_1 x_0 + \hat{B}_1. \quad (7.17)$$

We can therefore write the following about the estimate of the regression parameter β_1 :

$$\hat{B}_1 = E(y | x = x_0 + 1) - E(y | x = x_0). \quad (7.18)$$

THEORY BOX 7.3 SHOULD SURVEY WEIGHTS BE USED TO ESTIMATE REGRESSION MODELS?

This is an important question that statisticians and data analysts working with complex sample survey data need to answer when fitting regression models. When employing the design-based approaches that we illustrate in this chapter and attempting to make inferences about finite populations, the use of survey weights ensures that the estimates of regression parameters will be unbiased with respect to the sample design. Weighted estimation does not, however, protect analysts from model misspecification; if an analyst is fitting a poorly specified model using survey weights, they will simply be computing unbiased estimates of the regression parameters in a model that does a poor job of describing relationships in the larger target population.

Statisticians and data analysts who advocate *model-based* approaches emphasize the importance of sound model specification. Those following this approach will generally argue that the use of survey weights in estimation should not be necessary if a model has been correctly specified; in these cases, the use of weights in estimation introduces the risk of computing inefficient estimates, with standard errors larger than they need to be (Korn and Graubard, 1999). If the computed survey weights are informative about a dependent variable of interest, then the variables used to compute the weights (or the weights themselves!) should be included in the model as covariates. Pfeffermann (2011) discusses alternative model-based and design-based approaches to fitting regression models to survey data, clarifying the differences between these approaches and finding general support (via simulation) for a variant of probability-weighted estimation.

Given that this is an area of healthy debate in the survey statistics literature (Gelman, 2007; Heeringa et al., 2015), we encourage data analysts to not choose a side, *per se*, but rather to consider the sensitivity of their inferences to alternative choices of estimation approaches. Today's statistical software makes it very easy to fit a carefully specified regression model with and without survey weights (holding the variance estimation approach constant), and examine the sensitivity of the results to the use of weights in estimation. In short, if the use of weights leads to substantially different parameter estimates and inferences, a model may be misspecified (e.g., Korn and Graubard, 1999), and the weighted estimates should be reported (as they will be unbiased). However, if the use of weights in estimation does not change parameter estimates substantially and only results in large increases in the standard errors of the estimates, a model may indeed be well-specified, and the use of weights in estimation may be unnecessary. One can also

formally compare weighted and unweighted regression parameters to assess the significance of the differences using a method described by Fuller (1984) and outlined on the web page for this book. Bollen et al. (2016) provide a comprehensive review of related methods for comparing weighted and unweighted regression parameters to assess the need for using weights in regression analysis.

Overall, we feel that the design-based approaches illustrated in this and later chapters, where the use of weights in estimation results in unbiased population estimates of regression parameters, generally work well in practice and are easier to defend as having favorable properties. We are usually never certain that regression models have been correctly specified, despite our best efforts, and we are willing to accept slight losses in the efficiency of estimates as long as they are unbiased. See Heeringa et al. (2015), Binder (2011), Pfeffermann (2011), or Korn and Graubard (1999) for more perspective on this issue. We consider the “q-weighted” approach for increasing the efficiency of weighted survey estimates of regression parameters that was proposed and evaluated by Pfeffermann (2011) in our illustration later in this chapter.

The parameter estimate therefore describes, on average, the expected change in the continuous response variable y for a one-unit change in the predictor variable x .

When an additional predictor variable z is added to the model, representing a theoretical control variable or possibly a confounding variable, a portion of the relationship between x and y is attributable to the variable z , and the interpretation of the regression parameter for the predictor variable x requires that the predictor variable z be fixed at a constant value, z_0 :

$$E(y | x = x_0, z = z_0) = \hat{B}_0 + \hat{B}_1 x_0 + \hat{B}_2 z_0. \quad (7.19)$$

$$E(y | x = x_0 + 1, z = z_0) = \hat{B}_0 + \hat{B}_1 x_0 + \hat{B}_1 + \hat{B}_2 z_0. \quad (7.20)$$

$$\hat{B}_1 = E(y | x = x_0 + 1, z = z_0) - E(y | x = x_0, z = z_0). \quad (7.21)$$

We therefore interpret the estimate of the parameter B_1 in this case as the expected difference in y associated with a one-unit increase in x , holding the value of the predictor variable z constant. When multiple control variables are added to a linear regression model, we hold all of them at fixed values when interpreting the regression parameter for a primary predictor of interest. The interpretation of estimated regression parameters does not change

at all when analyzing sample survey data sets collected from finite populations, aside from the fact that the regression parameters are describing relationships in a finite population of interest. We will consider interpretations of regression parameters in detail in all examples presented in this chapter.

7.3.2.2 Estimation of Variances of Parameter Estimates

As described in [Chapter 3](#), the complex designs of most large probability samples (stratification, cluster sampling, unequal selection probabilities) preclude the use of conventional variance estimators that can be derived for MLE for data that are presumed to be i.i.d. draws from a probability distribution (i.e., normal, binomial, Poisson). Instead, robust, nonparametric methods based on the TSL of the estimator or replication variance estimation methods (BRR, JRR, bootstrapping) are employed (Wolter, 2007).

The general approach to variance estimation using TSL for linear regression coefficients can be illustrated for the simple linear regression model (which involves a single predictor variable). Extension of the method to multiple linear regression is straightforward but algebraically more complex. In the case of a simple linear regression model with a single predictor x , an analytic formula for the calculation of the associated finite population regression parameter B (given all data for the finite population with size N) can be written as follows:

$$B_1 = \frac{\sum_{i=1}^N (X_i - \bar{X})(Y_i - \bar{Y})}{\sum_{i=1}^N (X_i - \bar{X})^2} = \frac{T_{xy}}{T_{x^2}}. \quad (7.22)$$

This formula can be written as a ratio of two totals: T_{xy} and T_{x^2} . We can calculate an estimate of this ratio by applying the survey weights to the observed sample data:

$$\hat{B}_1 = \frac{\sum_h \sum_{\alpha}^{a_h} \sum_{i=1}^{n_{h\alpha}} w_{h\alpha i} (y_{h\alpha i} - \bar{y}_w)(x_{h\alpha i} - \bar{x}_w)}{\sum_h \sum_{\alpha}^{a_h} \sum_{i=1}^{n_{h\alpha}} w_{h\alpha i} (x_{h\alpha i} - \bar{x}_w)^2} = \frac{\hat{T}_{xy}}{\hat{T}_{x^2}}. \quad (7.23)$$

Note that the sample estimate \hat{B} is also a ratio of sample totals. Under the TSL approximation method, an estimate of the sampling variance of this ratio of two sample totals can be written as follows:

$$var(\hat{B}) \equiv \frac{var(\hat{T}_{xy}) + \hat{B}^2 var(\hat{T}_{x^2}) - 2\hat{B} cov(\hat{T}_{xy}, \hat{T}_{x^2})}{(\hat{T}_{x^2})^2}. \quad (7.24)$$

In multiple linear regression, TSL approximation methods require weighted sample totals for the squares and cross-products of all of the y and $x = \{1 \ x_1 \ \dots \ x_p\}$ combinations. The computations are more complex but the approach is a direct extension of the technique shown here for a simple linear regression model. Replication methods like JRR or BRR (Section 3.6.3) can also be used to estimate sampling variances of estimated regression parameters (Kish and Frankel, 1974).

Statistical software designed for regression analysis of complex sample survey data applies the TSL, BRR, JRR, or bootstrapping methods to estimate the sampling variance of each parameter estimate, $\text{var}(\hat{\beta}_j)$, $j = 1, \dots, p$, as well the $p(p + 1)/2$ unique covariances, $\text{cov}(\hat{\beta}_j, \hat{\beta}_k)$, between the parameter estimates. These estimates of sampling variances and covariances are then assembled into the estimated *variance–covariance matrix* of the parameter estimates:

$$\text{var}(\hat{\beta}) = \hat{\Sigma}(\hat{\beta}) = \begin{bmatrix} \text{var}(\hat{\beta}_0) & \text{cov}(\hat{\beta}_0, \hat{\beta}_1) & \dots & \text{cov}(\hat{\beta}_0, \hat{\beta}_p) \\ \text{cov}(\hat{\beta}_0, \hat{\beta}_1) & \text{var}(\hat{\beta}_1) & \dots & \text{cov}(\hat{\beta}_1, \hat{\beta}_p) \\ \vdots & \vdots & \ddots & \vdots \\ \text{cov}(\hat{\beta}_0, \hat{\beta}_p) & \text{cov}(\hat{\beta}_1, \hat{\beta}_p) & \dots & \text{var}(\hat{\beta}_p) \end{bmatrix}. \quad (7.25)$$

The estimated variances and covariances can then be used to develop Student t -statistics and Wald chi-square or Wald F -statistics required to test hypotheses concerning the population values of the regression parameters (Section 7.3.4).

A variety of software procedures exist in statistical software packages for fitting linear regression models to survey data using the methods discussed in this section; we consider procedures in some of the more common general-purpose statistical software packages here. In SAS, PROC SURVEYREG can be used; IBM SPSS Statistics offers the General Linear Model procedure in the Complex Samples Module (CSGLM); Stata offers the `svy: regress` command, which will be considered in this book; SUDAAN offers PROC REGRESS; the `survey` package in R offers the `svyglm()` function. See Appendix A for more details on software options for linear regression analysis of complex sample survey data.

7.3.3 Step 3: Model Evaluation

The standard linear regression model is an “elegant” statistical tool, but its simplicity and “best” properties hinge on a number of model assumptions (Section 7.2). Standard texts on linear regression modeling (e.g., Neter et al., 1996) provide detailed coverage of procedures designed to evaluate the model *goodness of fit* (GOF), examine how closely the data match the basic model assumptions, and determine if certain observations are unduly influencing

the fit of the model. The process does not change substantially when fitting finite population models to complex sample survey data sets. In this section, we briefly consider some of the model diagnostics that can be used to evaluate the model and discuss some current work on model diagnostics adapted for regression models fitted to complex sample survey data (see also Theory Box 7.4):

1. *Explained variance and GOF:* A standard measure of the “fit” of the regression model to the data is the *coefficient of multiple determination* or the *R² statistic*, which is interpreted as the proportion of variance in the dependent variable explained by regression on the independent variables:

$$R^2 = 1 - \frac{SSE}{SST}. \quad (7.26)$$

In Equation 7.26, SST refers to the total sum of squares, or the sum of squared differences between the response values and the mean of the response variable, and SSE is given in Equation 7.9 above. The use of R^2 as a measure of explained variance carries forward to regression modeling of complex sample survey data, although the statistic that is output by the analysis software is generally a *weighted* version, where each squared difference contributing to the sums is weighted by the corresponding survey weight:

$$R_{\text{weighted}}^2 = 1 - \frac{WSSE}{WSST}. \quad (7.27)$$

Although in theory it could be argued that this weighted R^2 statistic estimates the proportion of population variance explained by the population regression of y on x , in practice it is safe to simply view it as the fraction of explained variance in y attributable to the regression on x . Analysts who are new to regression modeling of social science, education, or epidemiological data should not fret if the achieved R^2 values are lower than those seen in their textbook training. Physicists may be disappointed with $R^2 < 0.98–0.99$ and chemists with $R^2 < 0.90$, but social scientists and others who work with human populations will find that their best regression model will often explain only 20%–40% of the variation in the dependent variable.

2. *Residual diagnostics:* In the standard regression context, analysis of the distributional properties of the residual terms, $\varepsilon_i = (y_i - \hat{y}_i)$, is used to evaluate how well the assumptions of the normal linear model are met (Section 7.2). Despite the theoretical distinction between the

THEORY BOX 7.4 MODEL EVALUATION FOR COMPLEX SAMPLE SURVEY DATA

When fitting regression models to complex sample survey data collected from a finite population, outlier statistics used for model evaluation are simply adapted by replacing unweighted values with weighted values. This theory box presents mathematical expressions for some of these adaptations, which again are not yet widely implemented in general purpose statistical software packages. To keep the expressions as general as possible, we use notation from generalized linear model theory. Generalized linear models will be discussed in more detail in [Chapters 8 and 9](#).

First, we consider computation of *Pearson residuals*:

$$r_{pi} = (y_i - \mu_i(\hat{B}_w)) \sqrt{\frac{w_i}{V(\hat{\mu}_i)}}.$$

In this notation, μ_i refers to the expected value of the outcome (y) for sampled case i , computed as a function of the weighted estimates of the regression parameters. The term w_i refers to the survey weight for the i -th case based on the complex sample design, and the term $V(\mu_i)$ refers to the *variance function* for the outcome, which partly defines the variance of the outcome variable in a generalized linear model as a function of the expected value of the outcome.

The *hat matrix* is computed as

$$H = W^{1/2} X (X' W X)^{-1} X' W^{1/2},$$

where:

$$W = \text{diag} \left\{ \frac{w_1}{V(\mu_1)[g'(\mu_1)]^2}, \dots, \frac{w_n}{V(\mu_n)[g'(\mu_n)]^2} \right\}.$$

This matrix is used for the computation of various diagnostic statistics, and specifically, measures of leverage. This matrix is an $n \times n$ diagonal matrix, with zeroes off the diagonal and diagonal elements defined by the survey weights divided by a term that is a function of the variance function for the observation and the derivative of the *link function* g for the specific generalized linear model (in a linear regression model, the link function is the identity function). Note that the derivative of the link function is computed for the diagonal elements and is evaluated as a function of the expected value of the outcome

according to the model. If a *canonical link* is used to define the generalized linear model (which is often the case in practice), the diagonal elements simplify to

$$\mathbf{W} = \text{diag}(w_1 V(\mu_1), \dots, w_n V(\mu_n)).$$

Diagonal elements of the hat matrix (denoted by h_{ii}) updated with the survey weights are used to identify influential cases with high leverage, and a common rule of thumb is to identify diagonal elements larger than $2(p + 1)/n$, or to identify large gaps in leverage values. Removing cases with high leverage will generally have little impact on estimates of regression parameters, but will have a large impact on the uncertainty of the estimates (i.e., standard errors).

Next, we consider computation of *Cook's Distance (D) statistic* in the complex sample design setting. Cook's D statistic can be useful for identifying observations that have a large impact on estimates of the regression parameters when they are removed from the estimation, taking the precision of the estimates into account. Cook's D statistic is computed for an individual sample observation i as follows:

$$c_i = \frac{w_i^* w_i e_i^2}{p \phi V(\hat{\mu}_i) (1 - h_{ii})^2} \mathbf{x}_i' [\hat{V}\text{ar}(U_w(\hat{\mathbf{B}}_w))]^{-1} \mathbf{x}_i,$$

where:

w_i^* = survey weight.

w_i = remainder of the diagonal element in the hat matrix (e.g., $V(\hat{\mu}_i)$ for a canonical link).

e_i = residual.

p = number of parameters in the regression model.

ϕ = dispersion parameter in the generalized linear model.

$\hat{V}\text{ar}(U_w(\hat{\mathbf{B}}_w))$ = linearized variance estimate of the *score equation*, which is used for pseudo MLE in generalized linear models fitted to complex sample survey data ([Chapter 9](#)).

Once the value of Cook's D has been determined for an individual sample element, the following test statistic can be computed to assess the significance of the D statistic:

$$\frac{(df - p + 1) \cdot c_i}{df} \sim F(p, df - p),$$

where:

df = number of PSUs—number of strata (design-based degrees of freedom).

This test statistic is approximately F -distributed, and can be used to identify any unusual elements that are having a significant impact on the estimates of the regression parameters when taking the complex design features into account.

When computation of these various diagnostic statistics becomes available in the statistical software packages discussed in this book, we will provide updates on the book web site.

concept of a finite population regression model and a broader super-population model, we recommend using standard residual analysis to evaluate regression models that are fitted to complex sample survey data. Li and Valliant (2015) describe recent advances in the study of residual diagnostics for regression models fitted to data from complex samples. These advances have been implemented in a new contributed package for the R software (*svydiags*), and we illustrate use of the functions in this package later in this chapter (Section 7.5.4).

3. *Model specification and homogeneity of variance:* Two-way scatter plots of the residuals for the estimated model against the predicted values, \hat{y} , and the independent variables, x , can identify problems with lack of correct functional form (e.g., omitting a squared term for age when modeling blood pressure) or where a moderating variable or interaction has not been correctly included in the model.

These same plots may be used to diagnose a problem with heterogeneity of residual variances. A pattern of residuals that spreads out in a fan-shaped pattern with increasing values for the predicted y or increasing values of an independent variable is a common observation. To address the problem of heterogeneity of variance and reduce standard errors for the estimated β coefficients, a standard approach in regression analysis is to employ WLS, weighting each observation's contribution to the SSE inversely proportional to its residual variance, that is, $w_i^{(hv)} = 1/\sigma_{y,x_i}^2$. With complex sample survey data, this becomes complicated, because weighted estimating equations for finite population regression parameters, B , already include the survey weights, say $w_i^{(survey)}$. While it is possible to create a composite weight, $w_i^* = w_i^{(survey)} \cdot w_i^{(hv)}$ (see Little, 2004 for a suggested approach), in cases of serious heterogeneity of variance it may be possible to identify a transformation of the dependent or independent variables

(see below) that eliminates much of the residual variance heterogeneity but still permits the use of the survey weights in the estimation of the regression function.

4. *Normality of the residual errors:* This assumption can be assessed using standard diagnostic plots for the model-based residuals (e.g., normal quantile–quantile [Q–Q] plots or histograms). The Q–Q plot is a plot of quantiles for the observed residuals against those computed from a theoretical normal distribution having the same mean and variance as the distribution of observed residuals. A straight 45° line in this plot would therefore suggest that normality is a reasonable assumption for the random errors in the model. We present examples of these Q–Q plots in the application later in this chapter.

In large survey data sets, formal tests of the normality of the residuals (e.g., the Kolmogorov–Smirnov and Shapiro–Wilks tests) tend to be extremely “powerful” and the null hypothesis of normality will be rejected due to the slightest deviation from normality. Our recommendation is to use the more informal visual methods illustrated in Section 7.5. Empirical research has provided evidence that as long as the residuals display symmetry about $E(e_i) = 0$, the regression estimates are quite robust against failure of strict normality. If the residual distribution is highly skewed or irregular (e.g., bimodal), the analyst should first determine that the model has been correctly specified (Section 7.4.1), and no important predictor variables or interaction terms have been omitted in error.

Transformation of the dependent variable is a common method to address serious problems of non-normality of residuals and also heterogeneity of residual variances. Analysts should be careful when making transformations, however, because they can destroy the straightforward interpretation of the parameters discussed above. A common transformation that is often used when violations of normality are apparent and residual distributions appear to be right-skewed is the natural (base e) log transformation of the response variable:

$$\ln(y) = B_0 + B_1 x + e. \quad (7.28)$$

When this particular transformation is used, the regression parameters still have a somewhat straightforward interpretation:

$$\frac{E(y | x = x_0 + 1)}{E(y | x = x_0)} = \frac{e^{(B_0 + B_1 x_0 + B_1)}}{e^{(B_0 + B_1 x_0)}} = e^{B_1}. \quad (7.29)$$

That is, a one-unit change in a given predictor variable will *multiply* the expected response by $\exp(B_1)$. The important issue to keep

in mind when transforming the dependent variable is that predicted values on the response variable need to be back-transformed to the original scale of the response. For example, square root transformations are often used to stabilize variance of the residuals, and predicted values based on this type of model would need to be squared to return to the original scale of the response.

5. *Collinearity diagnostics:* When specifying linear regression models, analysts need to be careful not to include predictor variables that are highly correlated with each other in the same model. This type of model misspecification can lead to problems of *multicollinearity*, which can have an adverse effect on the properties of the estimated regression parameters: standard errors of the estimated coefficients become inflated, due to *variance inflation factors* (which are a function of the amount of variance in a given predictor explained by the other predictors), and the signs of estimated coefficients may even change artificially relative to what their values would be in the absence of multicollinearity. Analysts should always first examine the correlations of the different predictor variables that they are considering, and make sure that none of them are excessively high in absolute value (say, greater than 0.7). In addition, *condition indices* for fitted linear regression models should not exceed 30 in value, and variance inflation factors greater than 2 warrant consideration and further analysis. In these cases, analysts should consider either combining correlated predictors (e.g., using principal components analysis or factor analysis) or omitting redundant predictors. See Faraway (2014) for more discussion of problems with multicollinearity.

Recent research in this area has considered the computation of these important diagnostic statistics for assessing multicollinearity when fitting linear regression models to complex sample survey data. Liao and Valliant (2012a,b) have led the way in this area, developing the underlying theory for determining these diagnostic statistics in a manner that accounts for the complex sampling features and illustrating practical examples of their implementation. Unfortunately, at the time of this writing, these diagnostic tools have not yet been implemented in any major statistical software packages. Liao and Valliant are currently developing a contributed package for the R software (mentioned earlier) that will include these collinearity diagnostics. We will provide updates in this area on the web page for the second edition of this book.

6. *Outliers and influence statistics:* Finally, analysts should determine if the sample data include *outlier values* (observations poorly fitted by a given model) or *influential points* (observations that have a strong impact on the fit of a model). Tools such as standard residual plots, *studentized residuals*, *hat statistics* (measures of leverage), and

Cook's Distance (D) statistics have been developed for this purpose. Regression models can be fitted with and without potential outliers and influential points, in order to assess whether the fit of the model (i.e., the significance of regression parameters) is changing substantially depending on the points in question. For more detail on these diagnostic methods in the standard linear regression case, we refer readers to Neter et al. (1996) or Faraway (2014).

Influential points should still be investigated for their impact on the fit of a model when fitting linear regression models to complex sample survey data sets. What changes is the way that complex sampling features are incorporated when calculating the various statistics (e.g., Cook's D statistics) used for residual diagnostics. Li and Valliant (2009, 2011a) were the first to discuss the identification of influential points when sampling weights are involved in the estimation of linear regression models, and these authors also discussed how to adapt the forward search method for identifying influential cases to the complex sampling context (Li and Valliant, 2011b). More recent work by Li and Valliant (2015) discussed extensions of the adjustments to diagnostic statistics for samples involving stratification and cluster sampling. Collectively, the current literature in this area suggests that the survey weights are most important for assessing the influence of individual observations on model fit.

Unfortunately, these promising methods for producing weighted versions of commonly used diagnostic statistics have not yet been widely implemented in general-purpose statistical software packages containing procedures for linear regression analysis of complex sample survey data. At the time of this writing, Rick Valliant has communicated that these tools will eventually be available in the aforementioned contributed R package *svydiags*, which is currently under development. We demonstrate use of the functions for regression diagnostics that are currently available in this package in the example analyses later in this chapter. It is our hope that the very near future will bring additional software advances in this area, and we will continue to provide readers with updates in this regard on the book web site.

This evaluation step of regression analysis may lead to a modification of the model structure. One then cycles back through the model-fitting and model diagnostics process, with careful consideration of model structure and parsimony.

7.3.4 Step 4: Inference

After following the three steps above, the final step in the model-building process is making inferences about the regression parameters in the finite population of interest. This section describes that process.

7.3.4.1 Inference Concerning Model Parameters

After rigorously evaluating the fit of a model, an analyst can use the estimated parameters and their standard errors to characterize or infer about the conditional distribution of y given the predictor variables x . The analyst can perform a variety of hypothesis tests concerning the parameters being estimated, ranging from tests for a single regression parameter to tests for multiple regression parameters. We begin this section by considering tests for single regression parameters.

In the standard linear regression context, when the residuals follow a normal distribution, hypothesis tests for a single regression parameter associated with predictor variable k employ a t -test statistic:

$$t = \frac{\hat{\beta}_k - \beta_k}{se(\hat{\beta}_k)} \sim t_{n-p}. \quad (7.30)$$

Therefore, when performing a test of the null hypothesis $H_0: \beta_k = 0$ versus the alternative hypothesis $H_A: \beta_k \neq 0$, one can calculate a t -statistic by dividing the estimate of the regression parameter β_k by its standard error. For reasonably large samples, when H_0 is true, this test statistic is distributed as a variate from a Student t distribution with $n - p$ degrees of freedom, where p is the number of parameters being estimated in the regression model (including the intercept). The analyst (or their software) refers the computed t -statistic to a Student t distribution with $n - p$ degrees of freedom. If the absolute value of the test statistic, t , exceeds a critical value of the Student t distribution (e.g., $t_{1-\alpha/2, n-p}$ for a two-sided test), H_0 is rejected with a Type I error probability of α . Pivoting on the value of t for the two-sided test, a $100(1 - \alpha)\%$ confidence interval for the true model parameter can be constructed as $\hat{\beta}_k \pm t_{1-\alpha/2, df} \cdot se(\hat{\beta}_k)$.

When constructing the confidence interval (or the pivotal hypothesis test statistic) for a single regression parameter estimated from complex sample survey data, two aspects of the inferential process change: (1) $se(\hat{\beta})$, or the correct standard error of the estimated regression parameter, is *estimated* using a nonparametric technique like TSL, BRR, or JRR; and (2) the degrees of freedom for the Student t reference distribution must be adjusted to reflect the reduced degrees of freedom for the complex sample estimate of $se(\hat{\beta})$. Recall from [Chapter 3](#) that the design degrees of freedom are approximated as $df = \sum_h a_h - H$, or the number of primary stage ultimate clusters minus the number of primary stage strata. For example, in the National Comorbidity Survey Replication (NCS-R) data set, the approximation to the design degrees of freedom is $84 - 42 = 42$. The correct estimate of the standard error and degrees of freedom for the Student t reference distribution can be used to develop a design-based $100(1 - \alpha)\%$ confidence interval (corresponding to a Type I error rate of α) for the regression parameter of interest, as follows:

$$\hat{B} \pm t_{1-\alpha/2, df} \cdot se(\hat{B}). \quad (7.31)$$

The t -statistic for the comparable two-sided hypothesis test of $H_0: B = 0$ can be developed as: $t = \hat{B}/se(\hat{B})$. This is the form of the t -test statistic that is routinely printed in tables of regression model output. The “ p -values” generally printed alongside the test statistics are the probability that $t_{df} \geq t$.

In standard linear regression, F -tests are often used to test hypotheses about multiple parameters in the model. The *overall F-test* typically reported in the analysis of variance (ANOVA) table output generated by software procedures for fitting regression models using standard OLS methods tests the null hypothesis $H_0: \beta_1 = \beta_2 = \dots = \beta_p = 0$, that is, the fitted model predicts $E(y|x)$ no better than a model that only includes the intercept ($\beta_0 = \bar{Y}$). *Partial F-tests* can be used to test whether selected subsets of parameters in the model are not significantly different from 0. In this case, a “full” model is compared with a nested “reduced” model that contains a subset of the predictor variables in the “full” model. This type of hypothesis test is essentially a test of the null hypothesis that multiple parameters (the parameters omitted in the “reduced” model) are all equal to 0. This multiparameter test can be extremely useful for testing hypotheses about categorical predictor variables represented by several indicator variables in a regression model (Section 7.4.2.1). More formally, we can use the following notation to indicate the $p = p_1 + p_2$ predictor variables of interest:

$$\begin{aligned} x &= (x_1, x_2) \\ x_1 &= p_1 \text{ predictors} \\ x_2 &= p_2 \text{ predictors.} \end{aligned}$$

Then, we can write the full model as follows:

$$full: y = x\beta + \varepsilon. \quad (7.32)$$

The reduced model then omits the p_2 predictor variables:

$$reduced: y = x_1\beta_1 + \varepsilon. \quad (7.33)$$

Then, to test the null hypothesis that the regression parameters associated with the p_2 predictor variables are all equal to 0, that is, $H_0: \beta_2 = 0$, we can calculate the following partial F -test statistic:

$$F = \frac{\frac{SSE_{reduced} - SSE_{full}}{(n-p_1)-(n-p_1-p_2)}}{\frac{SSE_{full}}{n-p_1-p_2}} = \frac{\frac{SSE_{reduced} - SSE_{full}}{p_2}}{\frac{SSE_{full}}{n-p}}. \quad (7.34)$$

Under the null hypothesis and assuming normally distributed residuals, this F -statistic follows an \mathcal{F} distribution with numerator degrees of freedom equal to p_2 and denominator degrees of freedom equal to $n - p$. This general result allows one to perform a variety of multiparameter tests when comparing nested linear regression models, at least in the simple random sample setting. This F -statistic is also fairly robust to slight deviations from normality in the residuals.

In the complex sample survey data setting, these multiparameter tests must be adapted to the complex design features of the sample. *Wald test statistics* (Judge et al., 1985) replace the overall F -test and the partial F -test. The equivalent multiparameter Wald test statistics can be calculated as follows:

$$\begin{aligned} \text{Overall: Modified } X_{W,\text{overall}}^2 &= \frac{\hat{\mathbf{B}}^T \hat{\boldsymbol{\Sigma}}(\hat{\mathbf{B}})^{-1} \hat{\mathbf{B}}}{p} = F_{W,\text{overall}} \\ \text{Partial: Modified } X_{W,\text{partial}}^2 &= \frac{\hat{\mathbf{B}}_2^T \hat{\boldsymbol{\Sigma}}(\hat{\mathbf{B}}_2)^{-1} \hat{\mathbf{B}}_2}{p_2} = F_{W,\text{partial}}, \end{aligned} \quad (7.35)$$

where:

$\hat{\mathbf{B}}, \hat{\mathbf{B}}_2$ are vectors of estimated regression parameters.

$\hat{\boldsymbol{\Sigma}}(\hat{\mathbf{B}}), \hat{\boldsymbol{\Sigma}}(\hat{\mathbf{B}}_2)$ are the estimated variance–covariance matrices.

Under the null hypothesis $H_0: \mathbf{B} = \mathbf{0}$, the overall modified Wald test statistic, $F_{W,\text{overall}}$, follows an \mathcal{F} distribution with numerator degrees of freedom equal to p and denominator degrees of freedom equal to the design degrees of freedom (df). Likewise, to test $H_0: \mathbf{B}_2 = \mathbf{0}$, or the null hypothesis that the p_2 parameters are all equal to 0 in the nested model, the modified Wald partial test statistic is referred to the critical value of the F distribution with p_2 and df degrees of freedom.

Wald tests can also be used to test more general hypotheses regarding linear combinations of regression model parameters. Consider the null hypothesis $H_0: \mathbf{C}\mathbf{B} = \mathbf{0}$, where \mathbf{C} is a matrix that defines specific linear combinations of the regression parameters in the vector \mathbf{B} . In this case, a version of the Wald test statistic that follows a chi-square distribution with degrees of freedom equal to the rank of the matrix \mathbf{C} under the specified null hypothesis can be written as follows:

$$X_W^2 = [\mathbf{C}\hat{\mathbf{B}}]'[\mathbf{C}\hat{\boldsymbol{\Sigma}}(\hat{\mathbf{B}})\mathbf{C}]^{-1}[\mathbf{C}\hat{\mathbf{B}}] \approx \frac{\text{contrast "squared"}}{\text{variance of contrast}}. \quad (7.36)$$

We consider one example of this more general type of hypothesis test for linear combinations of multiple parameters. First, suppose that a specified linear regression model includes three parameters of interest, that is, $\mathbf{B}' = [B_1, B_2, B_3]$. Using this more general framework for the Wald test statistic, if one

wished to test the null hypothesis $H_0: B_2 - B_3 = 0$ (or equivalently $H_0: B_2 = B_3$), the C matrix would take the following form:

$$C = \begin{bmatrix} 0 & 0 & 0 \\ 0 & 1 & -1 \\ 0 & 0 & 0 \end{bmatrix}.$$

Then, the Wald test statistic specified in Equation 7.36 above would follow a chi-square distribution with one degree of freedom (because the rank of the C matrix is 1). These more general hypothesis tests are available in a variety of software packages that can fit regression models to complex sample survey data sets, including SAS and Stata. Dividing these more general chi-square test statistics by the number of parameters being tested will result in test statistics that follow F distributions, similar to Equation 7.35. We consider examples of how to specify these tests for multiple parameters in Section 7.5.

7.3.4.2 Prediction Intervals

Predicting expected outcomes for populations and single individuals is an important scientific application of regression modeling (Neter et al., 1996). Even in the social and health sciences, where regression models are more often used to explore relationships among dependent and independent variables, prediction from fitted regression models still has a role. In the standard linear regression case, given a set of predictor values, $\mathbf{x}_{obs,i}$, the estimated regression model can be used to calculate a predicted value for y , in addition to *confidence intervals* and *prediction intervals* for the predicted value. First, we consider the expected value of the response variable y given an estimated model and a known vector of values on the predictor variables, $\mathbf{x}_{obs,i}$:

$$\hat{E}(y_i | \mathbf{x}_{obs,i}) = \mathbf{x}_{obs,i}'\hat{\beta}. \quad (7.37)$$

Given this expected value, we can calculate a confidence interval for the expected value once the variance of the expected value is calculated:

$$var(\hat{E}(y_i | \mathbf{x}_{obs,i})) = \mathbf{x}_{obs,i}'cov(\hat{\beta})\mathbf{x}_{obs,i}. \quad (7.38)$$

A $100(1 - \alpha)\%$ confidence interval for the expected value of y given $\mathbf{x}_{obs,i}$ (i.e., the average expected outcome for a population of cases with covariates $\mathbf{x}_{obs,i}$) can then be calculated as follows:

$$\mathbf{x}_{obs,i}\hat{\beta} \pm t_{1-\alpha/2, n-p} \sqrt{var(\hat{E}(y_i | \mathbf{x}_{obs,i}))}. \quad (7.39)$$

Note that the confidence interval above does not take into account the variance of the random errors that are also a part of the linear regression model. A *prediction interval* for a *single future value* of y does take this estimated variance ($\hat{\sigma}_{yx}^2$) into account:

$$x_{obs,i}\hat{\beta} \pm t_{1-\alpha/2,n-p}\sqrt{var(\hat{E}(y_i | x_{obs,i})) + \hat{\sigma}_{yx}^2}. \quad (7.40)$$

Prediction intervals, therefore, are wider than more standard confidence intervals for the expected value because they also include variance in the prediction due to random error. Both intervals can give analysts a notion of the precision of the predicted values based on the fitted model if prediction of future values is an important objective of the modeling process.

Confidence intervals for predicted values can also be computed in the context of regression models for complex sample survey data. Standard errors for the predicted values can be computed using the *delta method* (essentially linearization), which is a technique that can accommodate a wide variety of general predictions, based on fixed values of the predictors and the estimated regression parameters. For computational details on this technique, which is an approximate method based on large samples, interested readers can refer to the Stata (Version 14) Survey Data Reference Manual (SVY; StataCorp, 2015). The intervals change in that the degrees of freedom used to calculate the critical t -statistic are now based on the design degrees of freedom, and the variance–covariance matrix of the parameter estimates is estimated using approximate methods like TSL or replicated methods like JRR and BRR. Correct computation of these confidence intervals for predicted values when fitting regression models to complex sample survey data is currently implemented in Stata's `predictnl` postestimation command.

One can also compute different forms of *marginal predicted values* based on regression models fitted to complex samples (along with confidence intervals for the marginal predicted values). Heuristically, the marginal predicted value of a dependent variable for a given value of a covariate of interest is computed by first obtaining predicted values of the dependent variable using design-based estimates of the regression parameters of interest, and assuming that every case in the data set has the same value of the covariate of interest. The values of the other covariates (aside from the covariate of interest) are either left unchanged or fixed to constant values (e.g., their means) when computing these predicted values for each case. These predicted values are then averaged across all cases to compute the marginal predicted value, and a standard error for this marginal predicted value can be computed using the delta method. *Average marginal effects* of specific changes in the covariate of interest on the dependent variable can then be computed for any given values of the other covariates by comparing marginal predicted values for different values of the covariate of interest with selected

other covariates fixed to particular values (Bauer, 2015). These approaches are currently implemented in the Stata software via the `margins` command, and marginal predicted values computed using this command (and corresponding confidence intervals for the predicted values) can then be plotted using the subsequent `marginsplot` command. We illustrate the use of these commands in our illustration later in this chapter.

7.4 Some Practical Considerations and Tools

In this section, we discuss important considerations for data analysts fitting regression models to complex sample survey data sets in practice, and provide practical guidance on steps to avoid potential pitfalls when fitting regression models and making inferences based on the fitted models.

7.4.1 Distribution of the Dependent Variable

We specifically focus our discussion in this chapter on linear regression models for *continuous dependent variables* (e.g., weight in kilograms, blood pressure in millimeters of mercury to the second decimal place, weekly household expenditures on food items). Surprisingly, many survey data sets include very few variables that are measured on a truly continuous scale. Many response variables may be *semicontinuous*, *censored*, or *grouped* (or “coarsened”) in nature. We do not consider models for semicontinuous, censored, or grouped dependent variables in this chapter; Tobit regression models, Heckman selection models, and other forms of latent variable models might be considered by analysts for these types of response variables (Skrondal and Rabe-Hesketh, 2004). The Stata software (Version 14) currently provides versions of commands designed to handle dependent variables of this type in the setting of complex sample survey data.

Many survey variables of interest are measured as ordinal scale variables. Examples include age in years and education in years. Survey questions such as “On a scale of 1–5, where 1 is excellent and 5 is poor, please rate your overall health” produce a response on an ordinal scale. Over the years, it has been common practice to fit linear regression models to ordinal scale-dependent variables. DeMaris (2004) describes an ordinal scale variable as *approximately continuous* if it meets the following conditions: the number of sample observations, n , is large; measurement is at least on an ordinal scale; the response has at least five-ordered levels; and the distribution of responses to the ordered categories is not skewed and ideally is approximately normal in appearance. We agree that there are obvious cases where it may be acceptable to apply linear regression to an ordinal dependent variable; however, analysts will generally have a difficult time satisfying the

underlying statistical assumptions for the models discussed in this chapter when working with ordinal outcomes. This could lead to highly inefficient or faulty inferences. Especially for ordinal variables with small numbers of levels, a better choice is to choose a regression model that is more appropriate for the measurement scale of the dependent variable. Several regression models appropriate for ordinal and categorical response variables are discussed in detail in [Chapter 9](#).

7.4.2 Parameterization and Scaling for Independent Variables

An extremely important aspect of fitting linear regression models is the treatment and coding of categorical *predictor* variables, which can definitely be considered in the linear regression models discussed in the chapter. See also Theory Box 7.5 for a discussion of fitting analysis of variance (ANOVA) and analysis of covariance (ANCOVA) models as linear regression models for categorical predictors. When analysts consider nominal categorical predictor variables (e.g., race/ethnicity, region of the country) in linear

THEORY BOX 7.5 ANOVA AND ANCOVA AS LINEAR REGRESSION ANALYSIS

Statistical texts on linear models often include separate chapters for linear regression models for continuous outcomes, ANOVA models (where all predictors are categorical) and analysis of covariance (ANCOVA) models (involving a mix of categorical and continuous predictors). ANOVA and ANCOVA models for normal data are generally discussed in the context of experimental designs (e.g., full factorial, randomized block) and experimental hypotheses are tested using F -statistics and multiple comparisons that are functions of expected mean squares. Historically, the distinction between ANOVA, ANCOVA, and linear regression analysis was reinforced in statistical software systems that included separate programs adapted for ANOVA and standard linear regression modeling. Other programs such as SAS PROC GLM integrated these two analyses in a linear model framework.

In fact, ANOVA- and ANCOVA-type analyses can be performed through proper specification of a linear regression model (e.g., main effects, interactions, nesting); see Neter et al. (1996). Analysts who wish to apply ANOVA-type procedures to complex sample survey data can do so using regression analysis programs with indicator variable parameterization of categorical independent variables and interactions appropriate for the ANOVA-type model that they wish to fit to the data (e.g., indicator variables for levels of the main effects and interactions for a full factorial model).

regression models, they often generate *indicator variables* (a.k.a. “dummy” variables) to represent levels of the categorical predictor variables in the models. Regression parameters associated with these indicator variables (which are equal to 1 for cases falling into a specific category and 0 otherwise) represent changes in the expected value of the continuous outcome for a specific category relative to a *reference category*, which does *not* have an indicator variable included in the model. Alternative dichotomous specifications of these indicator variables are possible (e.g., 1/-1 “effect” coding, where estimated regression parameters represent changes in the expected value of the outcome relative to the *overall mean*), but we focus on the (1, 0) coding in this book for ease of interpretation.

Consider a categorical predictor variable measuring race/ethnicity with three possible values in a survey of a human population: 1 = Caucasian, 2 = African-American, and 3 = Other race/ethnicity. Analysts need to choose one of these three categories to be a reference category, and this choice is generally guided by contrasts of interest and research objectives (e.g., comparing African-Americans and other groups to Caucasians). In cases where the choice of the reference category is not clear, choosing the most prevalent group in the sample data will suffice. In the case of the race/ethnicity variable, an analyst choosing “Caucasian” to be the reference category would need to create two indicator variables to include as predictors in a regression model: a variable indicating African-Americans (1 = African-American, 0 = Caucasian or Other race/ethnicity), and a variable indicating the Other race/ethnicity group (1 = Other race/ethnicity, 0 = Caucasian/African-American). Most modern statistical software capable of fitting regression models to survey data will perform this “dummy” coding automatically for categorical predictors, requiring the analyst to simply choose the reference category for the analysis.

Continuing with the race/ethnicity example, suppose that a regression model was fitted to a continuous response variable y , where race/ethnicity was the only predictor variable. The dummy coding described above would lead to the following regression function:

$$E(y | x) = B_0 + B_1x_1 + B_2x_2. \quad (7.41)$$

In this model, $x_1 = 1$ for African-Americans and 0 otherwise, while $x_2 = 1$ for other racial/ethnic groups and 0 otherwise. The expected value on the continuous outcome variable y for African-Americans would therefore be calculated as

$$E(y | x) = B_0 + B_1 \times 1 + B_2 \times 0 = B_0 + B_1, \quad (7.42)$$

and the expected value for individuals in other racial/ethnic groups would be calculated as

$$E(y | x) = B_0 + B_1 \times 0 + B_2 \times 1 = B_0 + B_2. \quad (7.43)$$

Because both indicator variables would be equal to 0 for Caucasians, the expected value on the outcome variable for Caucasians would simply be B_0 . The regression parameters B_1 and B_2 therefore represent differences in the expected outcomes between African-Americans or Other racial/ethnic groups and Caucasians, and hypothesis tests about differences between the groups could therefore be conducted by testing whether these parameters are equal to 0. Similarly, the difference in expected outcome values between the nonreference groups (African-Americans and Others) would be equal to $B_1 - B_2$, or the difference in expected outcomes between these two groups.

When using statistical software to fit regression models to complex sample survey data, analysts have two choices: they can create indicator variables manually, or use special options in the different procedures to have the software automatically create indicator variables for the levels of categorical variables, given knowledge about a reference category. Users of the Stata software can define the reference category of a given categorical predictor variable when specifying a regression command, using *factor variable coding*. For example, one could fit a linear regression model using the command:

```
regress depvar ib1.catvar,
```

where *depvar* refers to the dependent variable in a linear regression model (fitted using the *regress* command), *catvar* refers to a categorical predictor variable, and *ib1.* refers to the specific value of *catvar* that is to be set as the reference category (in this case, the indicator variable (*i*) that will be omitted from the model as the baseline (*b*) category is 1). In general, when fitting any type of regression model, Stata users can include *i.* before the names of any categorical predictor variables, and Stata will by default set the *lowest alphanumeric category* as the reference category (if the user does not specify some form of *ib#.*). The following code presents an example of this, once again considering the race/ethnicity example (where *OUTCOME* is the continuous outcome variable and *ETHNIC* is the race/ethnicity variable):

```
regress outcome i.ethnic
```

We will consider several additional examples of factor variable coding in Stata later in this chapter.

Analysts should also exercise caution when interpreting intercept parameters (β_0) in linear regression models. The intercept, or the expected value of the response variable y when all of the predictor variables are fixed at value 0, is often not of much interest, because it may represent an expectation that is well outside the range of the collected data on the predictor variables. As a result, reformulation (or *centering*) of the continuous predictor variables in the model can make the intercept more interpretable:

$$y = \beta_0^* + \beta_1(x - \bar{x}) + \beta_2(z - \bar{z}) + \varepsilon. \quad (7.44)$$

By subtracting the means of the predictor variables x and z from the observed values on each variable, and then using the “centered” predictors in the model, the reformulated intercept (denoted by an asterisk) now has the interpretation of the expected value on the response variable y when the predictors are equal to their *means*. One can think of this term as representing a *centercept*, or the overall average value on the response variable y .

We note that the choice of omitting the intercept in a regression model forces the expected value of y to be 0 when all of the predictor variables in the model are set to 0. This might be done when preliminary knowledge of the subject matter being studied dictates that the expected value of the response be 0 when all predictor variables are set to 0.

7.4.3 Standardization of the Dependent and Independent Variables

Analysts can also *standardize* all of the variables being considered in a linear regression model (including indicator variables). One can standardize any variable by subtracting the mean for the variable, similar to centering, and then also dividing by the standard deviation of the variable:

$$x_{i,\text{std.}} = \frac{x_i - \bar{x}}{sd(x)}. \quad (7.45)$$

This is often done in practice when predictor variables are measured on very different scales (e.g., income and grade point average), and rescales all of the variables so that they are on the same scale (changes of one unit in standardized variables correspond to changes of one standard deviation in the unstandardized variables). The estimates of the regression parameters in a model where *all* variables have been standardized are often referred to as *standardized regression coefficients*, and these can be used to determine which predictor variable has the largest relative impact on the expected value of the response variable. Nothing changes about this process when analyzing complex sample survey data, but an analyst should note whether weighted estimates or unweighted sample estimates of the mean and standard deviation were used to standardize the variables.

7.4.4 Specification and Interpretation of Interactions and Nonlinear Relationships

Analysts should also exercise caution when interpreting regression parameters associated with predictor variables that define nonlinear relationships between predictors and the outcome, or predictor variables that define interactions between two or more predictors. Consider the following linear

regression model defining a nonlinear (and specifically quadratic) relationship between x and y :

$$y = \beta_0 + \beta_1 x + \beta_2 x^2 + \varepsilon. \quad (7.46)$$

In this model, the regression parameters β_1 and β_2 are *linked*, because they involve different transformations of the same predictor x , and β_1 alone in the presence of β_2 has no interpretation. Instead, the parameter β_2 measures the extent of the nonlinearity in the relationship between x and y . If the estimate of β_2 suggests that the parameter is not different from 0, one can assume (unless higher order polynomial terms are significant) that the relationship between x and y is linear.

The same issue arises when considering linear regression models that involve interactions between predictors. Consider the following linear regression model:

$$y = \beta_0 + \beta_1 x + \beta_2 z + \beta_3 xz + \varepsilon. \quad (7.47)$$

In this model, the three regression parameters β_1 , β_2 , and β_3 are once again *linked*, and one cannot interpret the regression parameter β_1 as being the relationship of the predictor variable x with the response variable y . The full relationship of x with y depends on the values of z (and therefore the value of β_3), and different values of z will result in different relationships of x with y .

In general, interactions between two or more predictor variables are computed for entry into a regression model by saving the product of two or more variables as a new variable. Interactions can be easily computed for two or more continuous predictor variables, for two or more categorical predictor variables, or for combinations of both types of variables. When working with categorical predictor variables, relevant products of *all* dummy variables to be included in the model for a given categorical variable must be computed for all other predictor variables that are specified to interact with the categorical predictor. For example, to include the interaction of a three-category predictor with a continuous variable, two product terms must be computed and included in the regression model: the product of the continuous variable with each of the indicators for the two nonreference categories of the categorical predictor. Most software procedures will perform these tasks automatically, but analysts need to be extremely careful when including interaction terms in a regression model.

Plotting predicted values in linear regression models with significant interactions can be extremely helpful when attempting to interpret significant regression parameters (i.e., regression parameters statistically different from zero) associated with the interactions. Social scientists often think of one of the variables involved in an interaction (e.g., z in the example above)

as a *moderator variable*, because that variable moderates the relationship of the other variable(s) involved in the interaction with the response variable (i.e., the relationship of x with the response variable depends on the value of z). The plot in Figure 7.2 illustrates the predicted values of a continuous response variable y based on the parameter estimates in two different regression models, showing two possible interactions between a continuous predictor variable x and a binary moderator variable z , taking on values of 1 and 0 for two different groups.

In the left panel of Figure 7.2, there appears to be an interaction of x with z ; the relationship of x with the continuous outcome y clearly depends on the value of z . The right panel shows no interaction, because the relationship of x with y in both groups defined by z is essentially the same. Analysts often make the mistake of interpreting regression parameters associated with single predictors in models that include interactions between that predictor and other predictors as “main effects.” For example, in the first model fitted in Figure 7.2 (left panel), an analyst may be tempted to interpret the regression parameter associated with the predictor x as being the “main effect” of x . In truth, the relationship of x depends on the value of z , even if

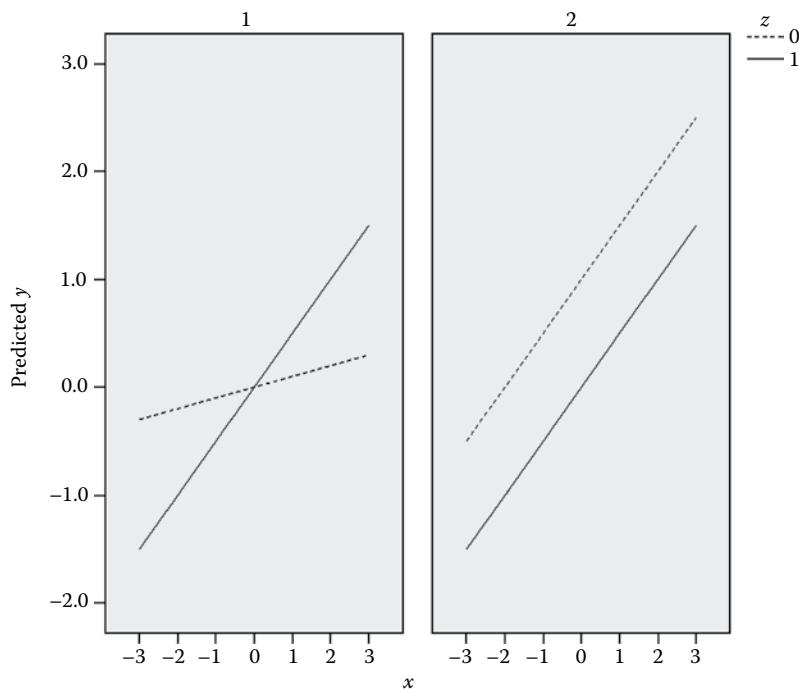


FIGURE 7.2

Hypothetical fits of two linear regression models, one with a significant interaction between x and z (left panel), and one without (right panel).

the interaction between x and z is *not significant*, so there is no “main effect” of x . This problem can be eliminated by eliminating regression parameters representing interactions from the model if they are not significantly different from zero, which will be discussed in the next section. Nothing about the interpretation of interactions changes when fitting models to complex sample survey data.

7.4.5 Model-Building Strategies

A universal set of model-building steps that is widely acknowledged and will always lead to the best fitting linear regression model does not exist. Many statisticians have proposed practical guidelines for model fitting, keeping in mind the four steps in regression modeling discussed in Section 7.3. Out of many quality choices, we consider the model-building steps proposed by Hosmer et al. (2013). These steps are summarized below:

1. Conduct exploratory bivariate analyses (e.g., two-sample t -tests, chi-square tests, tests of correlations, one-way ANOVA, etc.) to get a sense of candidate predictors that appear to have a significant relationship with the response variable.
2. Include those predictor variables that are *scientifically relevant* and have a bivariate relationship of significance $p < 0.25$ with the response variable in the initial multivariate model, and possibly consider variable selection techniques (e.g., backward selection), with discretion. Be wary of *multicollinearity*, which could arise from including predictors that are highly correlated with each other in the same model (Section 7.3.3).
3. Verify the importance of the predictor variables retained in the model, using t -tests for individual coefficients and Wald tests for multiple coefficients (Section 7.3.4), and assess whether or not the coefficients of *all* of the predictor variables change substantially in the multivariate model (relative to the bivariate case); this represents the preliminary “main” model.
4. Examine the forms of the predictor variables: if they are categorical, are sample sizes in each category large enough to use the categories as they are in the model? If they are continuous, do they have linear relationships with the response variable? Or do the relationships appear to be nonlinear? Residual diagnostics are useful as a part of this step.
5. Consider adding *scientifically relevant* interactions between the predictor variables to the model, one at a time, and do not retain them if they are not significant.
6. If any continuous or ordinal predictor variable has a large number of zeroes, include an indicator variable that is equal to 1 for nonzero

values and 0 for zero values in the model, in addition to the predictor variable in question, and see if the fit of the model has been improved.

The idea behind this last step (6) is that if we have a semicontinuous predictor with many zero values and also continuous values, it is unlikely that we would have a true linear relationship passing through the mass of points at 0 and continuing through the range of nonzero values. If we create the indicator variable and also include the predictor variable in the model, this introduces a discontinuity, modeling the effect of being zero or nonzero and then for nonzero values the linear relationship of the predictor with the response variable.

We remind readers that there are many possible model-fitting strategies that one can follow; in particular, Harrell (2015) also provides a comprehensive critique of alternative strategies.

7.5 Application: Modeling Diastolic Blood Pressure with the 2011–2012 NHANES Data

In this practical application of linear regression analysis for complex sample survey data, we consider building a predictive model of diastolic BP (DBP) (a continuous response variable) based on the sample of data collected from the U.S. adult population (age ≥ 18) in the 2011–2012 National Health and Nutrition Examination Survey (NHANES). After exploring the bivariate relationships of the predictors of interest with DBP, we perform a naïve linear regression analysis that completely ignores the complex design features of the NHANES sample. Next, we perform a weighted regression analysis that ignores the stratification and cluster sampling of the NHANES sample design. Finally, we take all of the important design features of the NHANES sample (stratification, cluster sampling, and weighting for unequal probability of selection, nonresponse, and poststratification) into account at each step of the model-building process.

Specifically, the design variables that the online documentation for the 2011–2012 NHANES data set states should be used for variance estimation* include SDMVPSU (which contains masked versions, or approximations, of the true primary sampling unit codes for each respondent for the purposes of variance estimation; Section 4.3.1) and SDMVSTRA (which contains the “approximate” sampling stratum codes for each respondent, for variance estimation purposes). In addition, the appropriate survey weight to be used to generate finite population estimates of the regression parameters

* http://www.cdc.gov/nchs/data/nhanes/analytic_guidelines_11_12.pdf

for the U.S. adult population for the years of 2011 and 2012 is WTMEC2YR. This survey weight variable was selected for analysis purposes instead of WTINT2YR because variables that will be used in the regression analyses were collected as a part of the physical examination, and the NHANES physical examination was performed on a *subsample* of all respondents (which required adjustments to the survey weights to account for the subsampling and nonresponse to the mobile examination center (MEC) follow-up phase of the NHANES data collection).

7.5.1 Exploring the Bivariate Relationships

In this application, we follow the regression modeling strategies recommended by Hosmer et al. (2013) to build a model for DBP (Section 7.4.5). We will describe each of the steps explicitly as a part of the example. First, we consider a set of predictors of DBP that are scientifically relevant: age, gender, ethnicity, and marital status. We begin by identifying the relevant design variables for the NHANES sample in Stata, requesting TSL for variance estimation, and indicating that identified strata with single PSUs should result in missing standard errors (see [Chapters 3](#) and [4](#) for more on this issue):

```
svyset sdmvpsu [pweight = WTMEC2YR], strata(sdmvstra) ///
vce(linearized) singleunit(missing)
```

An initial descriptive summary of the DBP variable in the NHANES data set (BPXDI1) revealed several values of 0, and we set these values to missing in Stata before proceeding with the analysis:

```
gen bpxdi1_1 = BPXDI1
replace bpxdi1_1 = . if BPXDI1 == 0
```

We also generate an indicator variable for the subpopulation of adults (respondents with age greater than or equal to 18), for use in the analyses:

```
gen age18p = 1 if age >= 18 & age != .
replace age18p = 0 if age < 18
```

With the subpopulation indicator defined, we now consider a series of simple bivariate regression analyses, to get an initial exploratory sense of the relationships of the candidate predictor variables with DBP. We make use of the `svy: regress` command to take the survey weights, stratum codes, and cluster codes into account when fitting these simple initial regression models, so that parameter estimates will be unbiased and variance estimates will reflect the complex design features of the NHANES sample. We first compute a weighted estimate of the mean age for the adult subpopulation,

and then center the AGE variable at the weighted mean age based on the NHANES sample (46.36):

```
svy, subpop(age18p): mean age
gen agec = age - 46.36
```

Next, the continuous dependent variable, BPXDI1_1, is regressed separately on each of the candidate predictors. For the categorical predictor variables (i.e., race/RIDRETH1, gender/RIAGENDR, and marital status/MARCAT), we consider multiparameter Wald tests in Stata (Section 7.3.4) to assess the significance of the bivariate relationships. The Stata software allows users to perform these multiparameter Wald tests by using `test` commands immediately after the models have been estimated:

```
svy, subpop(age18p): regress bpxdil_1 i.RIDRETH1
test 2.RIDRETH1 3.RIDRETH1 4.RIDRETH1 5.RIDRETH1

svy, subpop(age18p): regress bpxdil_1 i.marcat
test 2.marcat 3.marcat

svy, subpop(age18p): regress bpxdil_1 i.riagendr
test 2.riagendr

svy, subpop(age18p): regress bpxdil_1 agec
test agec
```

Note in the four Stata commands above how the indicator for the adult subpopulation (AGE18P) is explicitly specified for the analysis, via the use of the `subpop()` option. This ensures that Stata will perform an unconditional subclass analysis, treating the adult subpopulation sample size as a random variable and taking the full complex design of the NHANES sample into account.

We note also that after the dependent variable has been specified first following the `regress` command, the categorical predictor variables in the regression models are identified with the `i.` modifier, initiating dummy variable (or indicator) coding. In the example commands above, we use the default factor variable coding, where the lowest alphanumeric value of a given categorical variable will be set as the reference category, with no corresponding indicator variable included in the model. The terms indicated in the `test` commands above (e.g., `2.RIDRETH1`) then refer to the specific regression parameters for each of the nonreference indicator variables temporarily generated by Stata to fit the model, and the labels for the parameters can be clearly identified in the model output. The `test` commands are used to test the null hypothesis that all of the listed regression parameters are equal to zero (or, in other words, the mean DBP does not vary as a function of a given predictor variable). [Table 7.1](#) presents the results of these initial bivariate analyses.

TABLE 7.1

Initial Design-Based Bivariate Regression Analysis Results Assessing Potential Predictors of Diastolic Blood Pressure for the 2011–2012 NHANES Adult Sample

Predictor Variable	Parameter Estimate (Linearized SE)	Test Statistic	p-Value
Race/ethnicity (n = 5,112)		Wald F(4,14) = 3.93	0.02
Mexican-American	—	—	—
Other Hispanic	−0.15 (1.46)	t(17) = −0.11	0.92
Non-Hispanic White	2.18 (0.74)	t(17) = 2.94	<0.01
Non-Hispanic Black	2.29 (0.70)	t(17) = 3.26	<0.01
Other race	1.31 (0.70)	t(17) = 1.85	0.08
Age (cent.) (n = 5,112)	0.04 (0.02)	t(17) = 2.09	0.05
Gender (n = 5,112)		Wald F(1,17) = 15.01	<0.01
Male	—	—	—
Female	−2.20 (0.57)	t(17) = −3.87	<0.01
Marital status (n = 4,845)		Wald F(2,16) = 0.85	0.45
Married	—	—	—
Previously married	−0.15 (0.70)	t(17) = −0.21	0.84
Never married	−1.12 (0.84)	t(17) = −1.33	0.20

Note: — denotes reference category.

Stata presents *adjusted Wald tests* for the parameters in each of these models by default, where the standard Wald F-statistic (Section 7.3.4) is multiplied by $(df - k + 1)/df$, with df = the design-based degrees of freedom, and k = the number of parameters being tested (Korn and Graubard, 1990). Under the null hypothesis, the resulting test statistic follows an F distribution with k and $df - k + 1$ degrees of freedom. For example, in the Wald test for the ethnicity predictor, there are $k = 4$ parameters being tested, and the design-based degrees of freedom are equal to 31 (ultimate clusters) minus 14 (strata), or 17. The denominator degrees of freedom for the adjusted test statistic are therefore $17 - 4 + 1 = 14$.

Note the different subpopulation sample sizes in Table 7.1; over 250 of the adult cases appear to have missing data on the marital status variable. The design-based multiparameter Wald tests and t -tests for the single parameters suggest that race/ethnicity, age, and gender each have potentially significant relationships with the response variable (DBP). Specifically, investigating the weighted parameter estimates in these simple models, males, non-Hispanic whites, non-Hispanic blacks, and older adults appear to have the highest DBPs at first glance, while marital status does not appear to be related to DBP. Following the guidelines of Hosmer et al., we therefore include the first three predictors in an initial model for the response variable measuring DBP.

7.5.2 Naïve Analysis: Ignoring Sample Design Features

In the first regression analysis, we *ignore* the sample weights, stratification, and cluster sampling inherent to the NHANES sample design, we do not consider any interactions between the predictors, and we use standard OLS estimation to calculate the parameter estimates for the adult subpopulation:

```
regress bpxdi1_1 i.ridreth1 i.riagendr agec if age18p == 1
```

When fitting regression models in Stata, the first variable listed after the main command is the response variable (BPXDI1_1), and the variables listed after the response variable represent the predictor variables in the model. The variable list is then generally followed by options (after a comma). In this example, we do not include any options; however, we do restrict the analysis conditionally to those subjects with age ≥ 18 by using the *if* modifier. We also once again use the *i.* modifiers to have Stata automatically generate indicator variables for selected levels of the categorical predictor variables (recall that Stata, by default, treats the lowest valued level of a categorical predictor as the reference category; see Section 7.4.2 for syntax to manually choose the reference category). Table 7.2 presents OLS estimates of the regression parameters in this preliminary model, along with their standard errors and associated test statistics.

TABLE 7.2

Unweighted OLS Estimates of the Regression Parameters in the Initial Diastolic Blood Pressure Model

Predictor	Parameter Estimate	Standard Error	t-Statistic (df)	p-Value	95% CI
Intercept	70.784	0.548	129.20 (5105)	<0.001	(69.709, 71.858)
<i>Ethnicity</i>					
Other Hispanic	0.255	0.738	0.35 (5105)	0.730	(-1.192, 1.702)
Non-Hispanic White	1.193	0.597	2.00 (5105)	0.046	(0.021, 2.364)
Non-Hispanic Black	2.205	0.615	3.58 (5105)	<0.001	(0.999, 3.412)
Other race	2.013	0.662	3.04 (5105)	0.002	(0.716, 3.310)
Mexican-American	-	-	-	-	-
<i>Gender</i>					
Female	-2.404	0.331	-7.25 (5105)	<0.001	(-3.054, -1.754)
Male	-	-	-	-	-
Age (centered)	0.041	0.009	4.58 (5105)	<0.001	(0.024, 0.059)

Note: $n = 5,112$, $R^2 = 0.018$, F-test of null hypothesis that all parameters are 0: $F(6, 5105) = 15.58$, $p < 0.001$. – denotes the reference category.

These initial parameter estimates suggest that age has a positive linear relationship with DBP, females tend to have significantly lower mean DBP, and Mexican-American respondents tend to have the lowest mean BPs (significantly lower than whites, blacks, and other ethnicities). These parameter estimates may be biased, however, because the NHANES survey weights for respondents given a physical examination were not used to calculate nationally representative finite population estimates. In addition, the standard errors are likely understated, because the weights and the stratified cluster sample design of the NHANES sample were not taken into account. We therefore consider these results only for illustration purposes.

7.5.3 Weighted Regression Analysis

Next, we consider WLS estimation for calculating the parameter estimates in the initial model. Note that we explicitly indicate in the Stata command (with the pweight option) that the NHANES survey weights for respondents given a physical examination (WTMEC2YR) should be included in the estimation to calculate unbiased estimates of the regression parameters:

```
regress bpxdi1_1 i.RIDRETH1 i.riagendr agec ///
if age18p == 1 [pweight = WTMEC2YR]
```

Table 7.3 below presents weighted estimates of the regression parameters, in addition to *robust standard errors* automatically calculated by Stata's standard

TABLE 7.3

Weighted Least Squares (WLS) Estimates of the Regression Parameters in the Initial Diastolic Blood Pressure Model

Predictor	Parameter Estimate	Robust Standard Error	t-Statistic (df)	p-Value	95% CI
Intercept	71.149	0.566	125.66 (5105)	<0.001	(70.039, 72.259)
<i>Ethnicity</i>					
Other Hispanic	-0.141	0.721	-0.20 (5105)	0.845	(-1.555, 1.272)
Non-Hispanic White	1.904	0.611	3.12 (5105)	0.002	(0.707, 3.102)
Non-Hispanic Black	2.302	0.645	3.57 (5105)	<0.001	(1.037, 3.567)
Other race	1.262	0.705	1.79 (5105)	0.074	(-0.121, 2.644)
Mexican-American	-	-	-	-	-
<i>Gender</i>					
Female	-2.291	0.432	-5.31 (5105)	<0.001	(-3.138, -1.444)
Male	-	-	-	-	-
Age (centered)	0.037	0.012	3.17 (5105)	0.002	(0.014, 0.060)

Note: $n = 5,112$, weighted $R^2 = 0.017$, F-test of null hypothesis that all parameters are 0: $F(6, 5105) = 10.41$, $p < 0.001$. – denotes the reference category.

regression command (`regress`) when sampling weights are explicitly specified with the `pweight` option. Recall from earlier chapters that this option generally refers to a “probability” weight; the full NHANES survey weights are the base “probability” weights, adjusted for nonresponse and calibrated to population control totals (Section 2.7). The “robust” standard errors are “sandwich-type” standard errors (see Freedman, 2006, for an introduction) that are considered robust to possible misspecification of the correlation structure of the observations. In this part of the example, there is some misspecification involved: we have once again *ignored* the stratification and cluster sampling inherent to the NHANES sample design when calculating the standard errors, meaning that they will likely be understated. Stata’s automatic calculation of robust standard errors for the parameter estimates in the presence of analysis weights is therefore an effective type of “safeguard” against this failure to incorporate the sample design features in the analysis (meaning that standard errors will not be understated), but we do not recommend following this approach in practice. Readers should be aware that not all software packages capable of survey data analysis perform this type of calculation automatically when standard regression commands are used with survey weights specified. We only present this part of the analysis for illustrative purposes.

In [Table 7.3](#), we note fairly large differences in some of the parameter estimates relative to the OLS case ([Table 7.2](#)), especially in terms of the race/ethnicity parameters. When failing to incorporate the survey weights ([Table 7.2](#)), the differences between the ethnic groups were either being overstated (note that the difference in means between those with other ethnicities and Mexican-Americans is smaller and no longer significant at the 0.05 level) or understated (the difference between Mexican-Americans and whites is larger when accounting for the weights, with stronger evidence of a significant difference). The estimates in [Table 7.3](#) are nationally representative parameter estimates, and use of the OLS estimates in [Table 7.2](#) would have painted an incorrect picture of the relationships of these variables with DBP; the weights definitely appear to be informative about these relationships (see Theory Box 7.3 for more discussion of whether to use weights in regression modeling). We also note that the robust standard errors tend to be larger than the understated standard errors from [Table 7.2](#), where no adjustments to the standard errors were made to account for the complex design features of the NHANES sample.

To emphasize the differences that analysts might see when specifying the survey weights but failing to specify the sampling error codes (stratum and cluster codes) correctly in specialized software procedures for regression analysis of survey data, we include output from a similar analysis using SAS PROC GLM with a `WEIGHT` statement below:

```
proc glm data = nhanes1112;
  class ridreth1 (ref = "1") riagendr (ref = "1");
```

```

model bpxdil_1 = ridreth1 riagendr agec / solution;
where age18p = 1;
weight wtmecc2yr;
run;
quit;

```

Parameter	Estimate	Standard Error	t-Value	Pr > t
Intercept	71.14869684	0.59156886	120.27	<0.0001
RIDRETH1 2	-0.14141197	0.84161219	-0.17	0.8666
RIDRETH1 3	1.90419899	0.60771827	3.13	0.0017
RIDRETH1 4	2.30195323	0.73448786	3.13	0.0017
RIDRETH1 5	1.26178602	0.80523230	1.57	0.1172
RIDRETH1 1	0.00000000	.	.	.
RIAGENDR 2	-2.29113574	0.31815963	-7.20	<0.0001
RIAGENDR 1	0.00000000	.	.	.
agec	0.03682344	0.00928946	3.96	<0.0001

Readers should note in the SAS output above that the weighted parameter estimates are identical to those found in Stata, but the standard errors are computed differently (using standard WLS calculations). A more appropriate approach for SAS users would be to use PROC SURVEYREG and specify the NHANES stratum and cluster variables, enabling appropriate variance estimation. We now consider this more appropriate form of the analysis.

7.5.4 Appropriate Analysis: Incorporating All Sample Design Features

We now use the `svy: regress` command in Stata to fit the initial finite population regression model to the adult subpopulation and take *all* of the NHANES complex sample design features into account, calculating weighted estimates of the regression parameters and linearized estimates of the standard errors for the parameter estimates (incorporating the stratification and cluster sampling of the NHANES sample). Note how an unconditional subpopulation analysis is requested by specifying the binary AGE18P indicator in the `subpop()` option, similar to the bivariate analyses performed previously:

```

svyset sdmvpsu [pweight = WTMEC2YR], strata(sdmvstra) ///
vce(linearized) singleunit(missing)

svy, subpop(age18p): regress bpxdil_1 i.RIDRETH1 ///
i.riagendr agec

estat effects, deff

```

We also use the postestimation command `estat effects, deff` to request calculation of design effects for the estimated regression parameters. Table 7.4 presents the estimated parameters in this initial “main” model:

TABLE 7.4

Design-Based Estimates of the Regression Parameters in the Initial “Main” Model for Diastolic Blood Pressure, Linearized Standard Errors for the Estimates, Design-Adjusted Test Statistics and Confidence Intervals for the Parameters, and Design Effects for the Parameter Estimates

Predictor	Est.	Linearized SE	t-Statistic (df)	p-Value	95% CI	DEFF
Intercept	71.149	0.518	137.4 (17)	<0.001	(70.056, 72.241)	1.06
<i>Ethnicity</i>						
Other Hispanic	-0.141	1.375	-0.10 (17)	0.919	(-3.042, 2.759)	3.86
Non-Hispanic White	1.904	0.809	2.35 (17)	0.031	(0.197, 3.611)	2.47
Non-Hispanic Black	2.302	0.665	3.46 (17)	0.003	(0.900, 3.704)	1.00
Other race	1.262	0.707	1.79 (17)	0.092	(-0.229, 2.753)	1.09
Mexican-American	-	-	-	-	-	-
<i>Gender</i>						
Female	-2.291	0.548	-4.18 (17)	<0.001	(-3.448, -1.134)	3.97
Male	-	-	-	-	-	-
Age (centered)	0.037	0.021	1.77 (17)	0.095	(-0.007, 0.081)	6.02

Note: Subclass $n = 5,112$, weighted $R^2 = 0.017$, adjusted Wald test for all parameters: $F(6,12) = 10.13$, $p < 0.001$. – denotes the reference category.

The estimated parameters and tests of significance presented in Table 7.4 confirm most of the simple relationships observed in the initial design-based bivariate analyses, and suggest that the relationships remain similar when taking other predictor variables into account in a multivariate analysis (with the exception of the linear relationship of age with DBP). When holding the other predictor variables in this model fixed, non-Hispanic Whites and Blacks have significantly higher expected DBP values than Mexican-Americans, females have significantly lower DBP than males, and interestingly, age does not appear to have a significant linear relationship with DBP. Age is, therefore, the only predictor that does not appear to be important, but we have only considered a linear relationship thus far. None of the sample sizes for the groups defined by the categorical variables appear to be extremely small, so we do not consider further recoding of these variables. Readers should note that the weighted parameter estimates in Table 7.4 are exactly equal to those in Table 7.3; differences arise in how the estimated standard errors for the parameter estimates are being calculated.

There are several important observations regarding the test statistics for the regression parameters in Table 7.4. First, the degrees of freedom for the t-statistics based on the complex sample design of the NHANES (17) are calculated by subtracting the number of strata (14) from the number of sampling error computation units, or ultimate clusters (31). These degrees of freedom are substantially different from those noted in Tables 7.2 and 7.3 ($df = 5105$), where the complex design was not taken into account when performing the

estimation; this shows how the primary sampling units (rather than the unique respondents) are providing the independent contributions to the estimation of distributional variance when one accounts for the complex sample design. In addition, Stata presents an adjusted Wald test for all of the parameters in the model (see the discussion of the [Table 7.1](#) results). The numerator degrees of freedom for this adjusted statistic are equal to k (6 in this example, because six parameters are being tested; the “null” or “reduced” model still contains the intercept parameter), and the denominator degrees of freedom are calculated as $df - k + 1$ ($17 - 6 + 1 = 12$ in this example). This adjusted Wald test definitely suggests that a null hypothesis that all of the regression parameters are equal to 0 would be strongly rejected.

The design effects presented in [Table 7.4](#) (DEFF) are nearly all greater than 1, suggesting that the complex design of the NHANES sample is generally resulting in a decrease in the precision of the parameter estimates relative to the precision that would have been achieved under a simple random sampling design with the same sample size (Section 2.4). The effects of the complex design on the standard errors are apparent.

We now consider some initial model diagnostics to assess the fit of this preliminary model. We start by saving the residuals in a new variable (RESIDS) in Stata, and then plotting the residuals against the values of the continuous mean-centered age (AGEC) variable. The left-hand panel of [Figure 7.3](#) presents this plot.

```
predict resids, resid
scatter resids agec
```

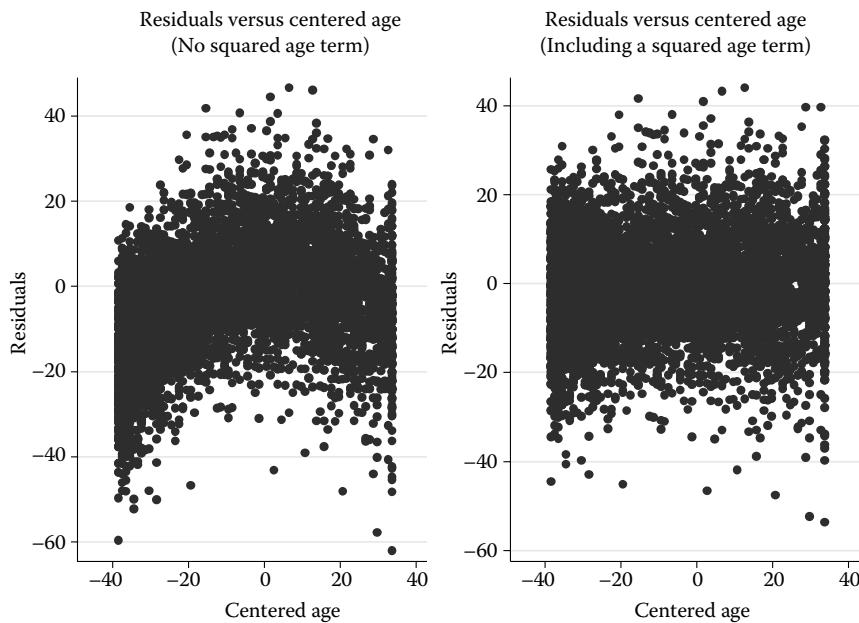
The first plot in [Figure 7.3](#) indicates a fairly well-defined curvilinear pattern of the residuals as a function of age, suggesting that the structure of the model has been misspecified; there is evidence that age actually has a quadratic relationship with DBP that has not been adequately captured by including a linear relationship of age with the response variable. We therefore add a squared version of age (AGECSQ) to the model to capture this relationship:

```
gen agecsq = agec * agec

svy, subpop(age18p): regress bpxdil_1 i.RIDRETH1 ///
i.riagendr agec agecsq
estat effects

predict resids2, resid
scatter resids2 agec
```

In the new model ([Table 7.5](#)), the regression parameters for both the centered age predictor and the squared version of the age predictor are significantly different from 0 ($p < 0.001$), confirming that the relationship of age with DBP is in fact nonlinear and quadratic in nature. The weighted R -squared of the

**FIGURE 7.3**

Plots of residuals versus centered age for the diastolic blood pressure application, before and after the addition of the squared AGE variable to the model.

TABLE 7.5

Estimates of the Regression Parameters in the Intermediate Model for the Diastolic Blood Pressure Response Variable, Prior to Inclusion of Interaction Terms

Predictor	Est.	Linearized SE	t-Statistic (df)	p-Value	95% CI	DEFF
Intercept	74.462	0.565	131.73 (17)	<0.001	(73.270, 75.655)	0.65
<i>Ethnicity</i>						
Other Hispanic	0.218	1.217	0.18 (17)	0.860	(-2.350, 2.786)	1.22
Non-Hispanic White	2.084	0.857	2.43 (17)	0.026	(0.276, 3.893)	1.31
Non-Hispanic Black	2.511	0.734	3.42 (17)	0.003	(0.963, 4.059)	1.16
Other race	1.410	0.687	2.05 (17)	0.056	(-0.041, 2.860)	1.20
Mexican-American	-	-	-	-	-	-
<i>Gender</i>						
Female	-2.169	0.489	-4.43 (17)	<0.001	(-3.202, -1.137)	1.16
Male	-	-	-	-	-	-
Age (centered)	0.075	0.016	4.80 (17)	<0.001	(0.042, 0.108)	1.59
Age (cent.) squared	-0.012	0.001	-16.28 (17)	<0.001	(-0.013, -0.010)	1.77

Note: Subclass $n = 5,112$, weighted $R^2 = 0.114$, adjusted Wald test for all parameters: $F(7,11) = 159.86$, $p < 0.001$. – denotes the reference category.

new model becomes 0.114, suggesting an improved fit by allowing the relationship of age with DBP to be nonlinear. The right-hand panel of Figure 7.3 shows the improved distribution of the residuals as a function of age after adding the squared term, where there is no pattern evident in the residuals as a function of age.

Now, we consider testing specific interactions of interest, one at a time: the interactions between age (both predictors) and race/ethnicity, and the interactions between age (both predictors) and gender. This step essentially allows for testing whether the nonlinear relationship of age with DBP tends to be moderated by these two demographic factors; for example, is the quadratic trend in DBP as a function of age flatter (i.e., more stable) for certain ethnic groups than others? We first add the interaction between age and ethnicity to the model, and then investigate a design-adjusted Wald test of the null hypothesis that all eight parameters associated with this first order interaction are simultaneously equal to zero:

```
svy, subpop(age18p): regress bpxdi1_1 i.RIDRETH1 ///
i.riagendr agec agecsq ///
i.RIDRETH1#c.agec i.RIDRETH1#c.agecsq

test 2.RIDRETH1#c.agec 3.RIDRETH1#c.agec ///
4.RIDRETH1#c.agec 5.RIDRETH1#c.agec 2.RIDRETH1#c.agecsq ///
3.RIDRETH1#c.agecsq 4.RIDRETH1#c.agecsq 5.RIDRETH1#c.agecsq
```

Note in the `svy: regress` command how the interactions are specified: the term `i.RIDRETH1#c.agec` indicates that an interaction (#) between the categorical predictor RIDRETH1 (i.) and the *continuous* predictor AGEC (indicated with c.) should be included in the model. The subsequent `test` command then simply lists all eight parameters defining the two interaction terms, exactly as they are labeled in the output (including the c. notation for the continuous predictors).

We remind readers that when using the `test` commands in conjunction with survey regression commands, Stata performs an adjusted Wald test by default. The `nosvyadjust` option can be added to a `test` command if a user does not desire the additional adjustment to the test statistic. The multi-parameter Wald test for all of the newly added interaction parameters essentially amounts to a design-based test of *change in R-squared* for comparing nested models (where in this case, one model includes the interactions, and one does not). The adjusted Wald test performed by Stata indicates that we can reject this null hypothesis ($F(8,10) = 7.00, p < 0.01$), which suggests that adding the interactions between both age terms and ethnicity is significantly improving the fit of the model (we will return to their interpretation shortly).

Next, we add the two-way interactions between the two age terms and gender (RIAGENDR) to the model, and again test the associated parameters using an adjusted Wald test:

```
svy, subpop(age18p): regress bpxdil_1 i.RIDRETH1 ///
i.riagendr agec agecsq ///
i.RIDRETH1#c.agec i.RIDRETH1#c.agecsq ///
i.riagendr#c.agec i.riagendr#c.agecsq

test 2.riagendr#c.agec 2.riagendr#c.agecsq
```

This Wald test once again suggests that at least one of the two regression parameters associated with the interactions between the age terms and gender is significantly different from zero ($F(2,16) = 4.83, p = 0.03$), so we have evidence in favor of the model including these interactions as well. Readers can use similar methods to test interactions between two (or more) categorical predictors.

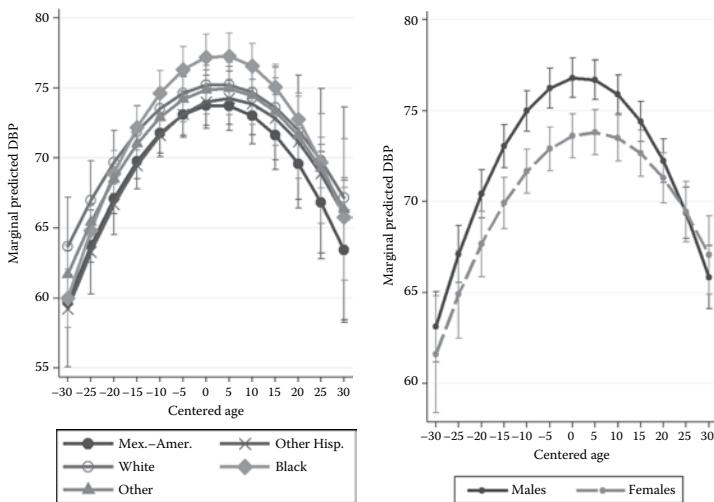
After fitting this latest model including the new interaction terms, we can plot *marginal predicted values* for DBP based on the fitted model to assess variability in the relationship of age with DBP depending on race/ethnicity and gender. In order to do this, we first refit the model specifying an “interaction” between the original centered age variable and itself, so that Stata does not simply interpret the squared age term from the previous syntax as an arbitrary additional predictor, and instead knows that there is a curvilinear relationship between centered age and the outcome:

```
svy, subpop(age18p): regress bpxdil_1 i.RIDRETH1 ///
i.riagendr agec c.agec#c.agec ///
i.RIDRETH1#c.agec i.RIDRETH1#c.agec#c.agec ///
i.riagendr#c.agec i.riagendr#c.agec#c.agec
```

While this syntax may seem tedious, it is essential for correctly plotting curvilinear relationships involving continuous predictor variables. We generate the plots of marginal predicted values for DBP using the following syntax:

```
margins RIDRETH1, at (agec=(-30(5)30))
marginsplot
margins riagendr, at (agec=(-30(5)30))
marginsplot
```

This margins syntax indicates that we wish to display marginal predicted values of DBP for each level of RIDRETH1 (plot 1) and RIAGENDR (plot 2), separately at all possible increments of five units in centered age (from -30 to 30; i.e., -30, -25, -20, ..., 25, 30). The marginal predicted values are computed by default in Stata by: (1) assuming that everyone in the data set has a particular value of RIDRETH1 (or RIAGENDR) and centered age, (2) computing the predicted values based on the fitted model for each case in the data set, and then (3) averaging the predictions. We then plot these marginal predicted values (including 95% confidence intervals for the predictions) using the marginsplot command. The resulting plots are displayed in [Figure 7.4](#).

**FIGURE 7.4**

Plots of marginal predicted values based on the regression model, including interactions between age and race/ethnicity as well as age and gender, illustrating differences in the curvilinear relationship of centered age with diastolic blood pressure depending on race/ethnicity and gender.

[Figure 7.4](#) shows that African-Americans have a higher acceleration in DBP as a function of age, up until about middle age. The same can be said for males, where the gap between males and females in marginal predicted values widens approaching middle age, and then narrows in older ages. While these differences are subtle, they are significant (as shown earlier).

We now carefully consider diagnostics for this latest model. We first refit the model, and then save variables containing residuals (EHAT1) and predicted values (YHAT1) based on the fitted model. Next, we generate a series of diagnostic plots to assess the assumptions underlying the model:

```
svy, subpop(age18p): regress bpxdi1_1 i.RIDRETH1 ///
i.riagendr agetc c.agec#c.agec ///
i.RIDRETH1#c.agec i.RIDRETH1#c.agec#c.agec ///
i.riagendr#c.agec i.riagendr#c.agec#c.agec

predict ehat1, resid

symplot ehat1, name(sym_ehat1_1, replace) ///
title(Symplot of Residuals)

histogram ehat1, normal name(h_ehat1, replace) ///
title(Histogram of Residuals)

qnorm ehat1, name(qnorm_ehat1, replace) ///
```

```

title(Normal Q-Q Plot of Residuals)

predict yhat1, xb

scatter ehat1 yhat1, name(ehat1xyhat1, replace) ///
title(Residuals vs. Predicted Y)

graph combine sym_ehat1_1 h_ehat1 qnorm_ehat1 ///
ehat1xyhat1, rows(2)

```

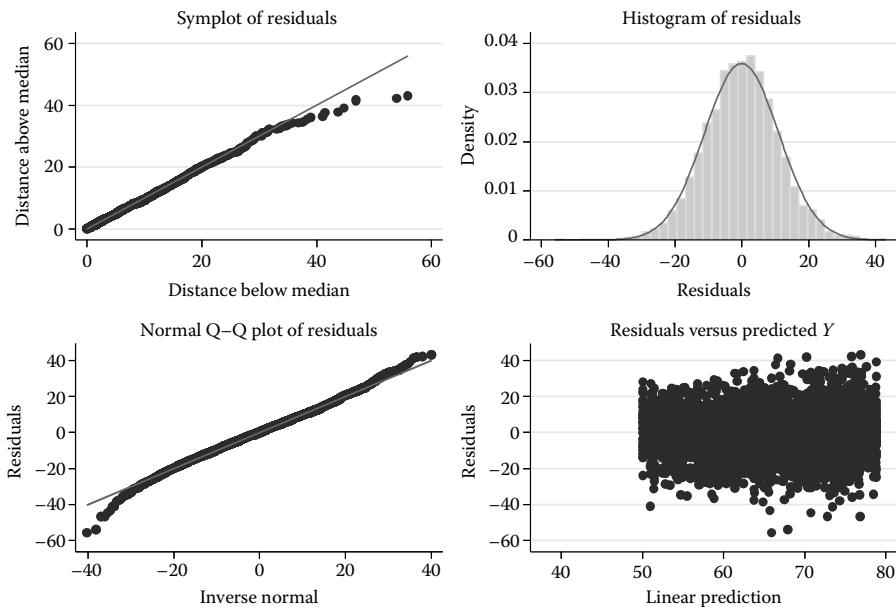
We introduce one additional diagnostic plot that can be helpful for assessing model fit. The `symplot` command in Stata produces a symmetry plot, which is useful for determining whether the distribution of values on a given continuous variable appears to be symmetric in nature. Specifically, the distance below the median of the first-ordered value in the distribution is plotted against the distance above the median of the last-ordered value; the distance below the median of the second-ordered value is plotted against the distance above the median of the second-to-last-ordered value; and so forth. If the values in the symmetry plot lie on the straight diagonal line, there is evidence that the distribution is symmetric. The resulting plot in the upper-left panel of [Figure 7.5](#) suggests that the distribution of the residuals based on the final fitted model is nearly symmetric around 0 (allowing for a handful of outliers), alleviating possible concerns about slight deviations from normality.

Collectively, the diagnostic plots presented in [Figure 7.5](#) suggest that the residuals follow a symmetric distribution, and that assumptions of normality and constant variance for the residuals definitely seem reasonable. Given any apparent violations of normality in the distribution of the residuals, the symmetry of the residuals around the expected value of 0 gives us confidence in the inferences that we are making. However, the diagnostic assessments that we have performed so far have neglected to account for the complex sampling features.

We now examine the residuals and check for the possibility of influential points and outliers in a manner that accounts for the complex sampling features. We do this using state-of-the-art diagnostic techniques for linear regression models fitted to complex sample survey data, which were discussed earlier in Section 7.3.3. Several of these diagnostic tools have been implemented in the contributed R package `svydiags`, which at the time of this writing is available upon request in .zip format from Rick Valliant (rvalliant@survey.umd.edu). We will provide updates on the book web page when this contributed package is available on the Comprehensive R Archive Network (CRAN). First, we load the contributed survey package in R, assuming that it has already been installed from a CRAN mirror:

```
library(survey)
```

Next, we install the local .zip file containing the `svydiags` functions, which can be done using the Packages menu in the R GUI (given that the .zip

**FIGURE 7.5**

Diagnostic plots for the “final” regression model fitted to the diastolic blood pressure response variable in the 2011–2012 NHANES data set.

archive has been saved in some working directory), and load the `svydiags` package. We then load the 2011–2012 NHANES data, recode the dependent variable, compute the centered age variable, create a survey design object describing the complex sampling features, refit the final regression model discussed above using the `svyglm()` function, and then generate the parameter estimates, standard errors, and tests of significance for the parameters, using the same approximate degrees of freedom method (number of clusters minus number of strata) employed by Stata:

```
library(svydiags)

load("C:\\\\nhanes1112.rdata")

nhanes1112$bpxdi1.1 <- nhanes1112$BPXDI1
nhanes1112$bpxdi1.1[nhanes1112$BPXDI1 == 0] <- NA
nhanes1112$agec <- nhanes1112$age - 46.36
nhanes1112$agec2 <- nhanes1112$agec ^ 2

dnhanes <- svydesign(id =~ sdmvpsu, strata =~ sdmvstra,
weights =~ WTMEC2YR, nest = TRUE, data = nhanes1112)

finmod <- svyglm(bpxdi1.1 ~ as.factor(RIDRETH1) +
as.factor(riagendr) + agec + agec2 + as.factor(RIDRETH1):agec
```

```
+ as.factor(RIDRETH1):agec2 + as.factor(riagendr):agec +
as.factor(riagendr):agec2, subset = (age18p == 1), design =
dnhanes)

summary(finmod, df.resid = degf(dnhanes))
```

Now that we have replicated the model-fitting process in R and created an object named `finmod` containing all of the relevant information about the model, we can first employ the `svyCooksD()` function in the `svydiags` package to generate the modified Cook's D statistic for each case, measuring the influence of that case on the parameter estimates in the final model:

```
mcook <- svyCooksD(mobj = finmod, stvar = "sdmvstra", clvar =
"sdmvpsu", doplot = TRUE)
```

The plot of the modified Cook's D statistics for each case generated by the `doplot = TRUE` argument is shown in [Figure 7.6](#). The two horizontal lines indicate rules of thumb for which cases have overly large influence on the parameter estimates in the model (values of 2 or 3). We see that several cases fall above the highest horizontal line, which warrants refitting the model excluding some of these extreme cases.

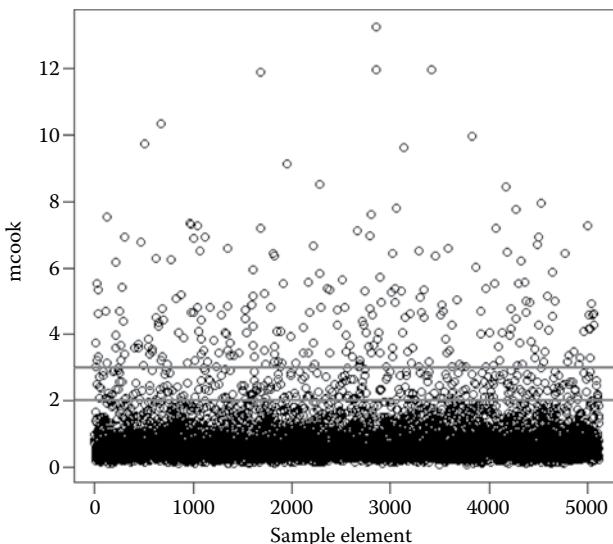


FIGURE 7.6

Plot of modified Cook's D statistics for the $n = 5112$ cases analyzed in the final model, demonstrating the influence of each individual case and accounting for the complex sampling features of the 2011–2012 NHANES.

We specifically identify the four cases with the largest modified Cook's D statistics, and create a temporary data frame object excluding these specific rows:

```
mcook [mcook > 11]
      3257      5529      5543      6624
11.88683 11.97656 13.26392 11.97656
nhanes1112a <- nhanes1112[-c(3257,5529,5543,6624),]
```

We then create a new survey design object using this new data frame, and refit the model excluding these cases:

```
dnhanes2 <- svydesign(id =~ sdmvpsu, strata =~ sdmvstra,
weights =~ WTMEC2YR, nest = TRUE, data = nhanes1112a)

finmod2 <- svyglm(bpxdi1.1 ~ as.factor(RIDRETH1) +
as.factor(riagendr) + agec + agec2 + as.factor(RIDRETH1):agec
+ as.factor(RIDRETH1):agec2 + as.factor(riagendr):agec +
as.factor(riagendr):agec2, subset = (age18p == 1), design =
dnhanes2)

summary(finmod2, df.resid = degf(dnhanes2))
```

The results of this analysis (not shown) suggest slight shifts in the resulting parameter estimates, but none large enough to cause us to change our inferences. One could explore the impact of removing additional cases with large values of Cook's statistic at this point, but we do not consider these further. In practice, if the exclusion of a small number of influential points results in different inferences, a sound argument would be needed for why those individual cases should be removed from the analysis (e.g., extreme values for particular variables).

Next, we examine design-based calculations of dfbetas, which indicate the influence of individual observations on the parameter estimates in the final model. Using the original model fit object, we compute these values using the following function in the *svydiags* package:

```
dfbetas <- svydfbetas(mobj = finmod, stvar = "sdmvstra", clvar =
"sdmvpsu")
```

The resulting object shows, for each case used to fit the model, the changes in each of the parameter estimates that would occur if a given case was excluded from the analysis. We examine these changes for the case in row 5543, which was found above to have the largest modified Cook's D statistic:

```
b <- data.frame(dfbetas$Dfbetas)
b$X5543
```

```
[1] -0.0012526839  0.0015667514  0.0015432959  0.0013492664
0.0014159274
[6] -0.0007269432 -0.0163536130 -0.0118780945  0.0125492120
0.0118395900
[11]  0.0162467031  0.0127952869  0.0055352874  0.0113366512
0.0099378641
[16]  0.0066420863  0.0019866268  0.0021669724
```

The two boldfaced values above correspond to the changes in the estimates of the centered age and centered age squared parameters (the 7th and 8th parameters in the model output) that would occur from dropping this one case. These examinations can therefore be used to quantify the impacts that individual cases are having on the parameter estimates, fully accounting for the complex sampling features in the calculations. We recommend performing these analyses alongside an examination of the Cook's D statistics to describe the impact that a given case is having on the parameter estimates if that case is being considered for exclusion from the analysis.

Finally, we compute standardized residuals based on the final fitted model, or residuals divided by the standard deviation of the residuals based on the fitted model (again accounting for the complex sampling features in the calculations). We can generate the standardized residuals by using the `svystdres()` function in the `svydiags` package:

```
st.resids <- svystdres(mobj = finmod, stvar = "sdmvstra",
clvar = "sdmvpstu", doplot = TRUE)
```

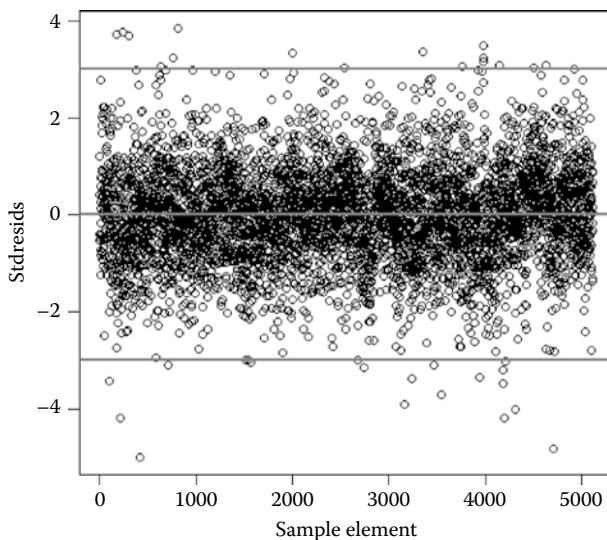
The plot of the standardized residuals that is automatically generated when using the `doplot = TRUE` argument ([Figure 7.7](#)) draws horizontal lines at values of -3 and 3 for the standardized residuals, where cases with residuals outside of this range would normally be considered outliers.

We identify those cases with standardized residuals less than -4:

```
st.resids$stdresids [st.resids$stdresids < -4]
 2735        3732        3138        1158        5815
-4.183308 -4.995978 -4.182579 -4.000169 -4.817674
```

These are cases that are not being fitted adequately by the final model. For example, the case in row 3732 was 80 years old and had a recorded DBP of 10 (!). Careful assessment of these outliers (accounting for the complex sampling features) can lead to the identification of situations like this, where there may have been data entry errors. If a value of 10 is unrealistic or not possible, this case could be dropped from the analysis moving forward.

After assessing the model diagnostics carefully (accounting for the complex sampling features if possible) and possibly making changes to the model specification or dropping overly influential cases or extreme outliers (with discretion), the focus can turn to interpretation of the parameter

**FIGURE 7.7**

Plot of standardized residuals for the $n = 5112$ cases analyzed in the final model, accounting for the complex sampling features of the 2011–2012 NHANES.

estimates in the final model. Table 7.6 presents the parameter estimates and associated tests of significance in the “final” model for this example. The estimates in Table 7.6 provide strong evidence of the quadratic relationship of age with DBP when adjusting for other sociodemographic features, and also show how there are still strong ethnicity and gender effects on BP. We once again note the substantial improvement in the model R -squared values (from 0.017 to 0.120) due to the inclusion of the squared age term and the additional interactions. In addition, while most of the design effects are greater than 1, suggesting losses in the efficiency of the estimates given the complex sampling employed by NHANES, there are examples of estimates with *increased* efficiency due to the complex sampling features (likely due to effective stratification). Clear interpretation of the estimated parameters is essential, however, to understand these design effects further.

If we wish to describe our “final” interpretation of the parameter estimates in this model, we need to be very careful with the estimated interaction coefficients. Importantly, the estimated coefficients for ethnicity, gender, and the two age predictors are *not* main effects for the entire population. Instead, because of the interactions included in the final model, these coefficients correspond to subgroups defined by the *reference categories* (or “0” values) of other variables involved in the interaction. So, the four estimated coefficients for the nonreference race/ethnicity categories correspond to race/ethnicity effects specifically for individuals with a value of 0 on the two age variables (or individuals with age equal to the population mean, given the centered age variable). It would therefore be erroneous to say, based on Table 7.6,

TABLE 7.6

Estimates of the Regression Parameters in the Final Model for the Diastolic Blood Pressure Response Variable, Including Significant Interaction Terms (Estimates and Standard Errors Based on the “q-Weighted” Approach Outlined by Pfeffermann (2011) are in Parentheses)

Predictor	Est.	Linearized SE	t-Statistic (df)	p-Value	95% CI	DEFF
Intercept	75.346 (75.41)	0.819 (0.772)	91.99 (17)	<0.001	(73.618, 77.075)	1.43
<i>Ethnicity</i>						
Other Hispanic	0.271 (0.25)	0.921 (0.954)	0.29 (17)	0.772	(−1.672, 2.215)	0.91
Non-Hispanic White	1.461 (1.50)	0.910 (0.895)	1.60 (17)	0.127	(−0.460, 3.382)	1.70
Non-Hispanic Black	3.450 (3.57)	0.961 (0.989)	3.59 (17)	0.002	(1.422, 5.478)	1.16
Other race	1.144 (1.24)	0.895 (0.892)	1.28 (17)	0.218	(−0.744, 3.032)	0.98
Mexican-American	—	—	—	—	—	—
<i>Gender</i>						
Female	−3.195 (−3.43)	0.759 (0.633)	−4.21 (17)	0.001	(−4.797, −1.593)	4.19
Male	—	—	—	—	—	—
Age (centered)	0.039 (0.05)	0.040 (0.040)	0.99 (17)	0.332	(−0.045, 0.123)	1.20
Age (cent.) squared	−0.015 (−0.02)	0.002 (0.002)	−8.43 (17)	<0.001	(−0.019, −0.011)	0.82
<i>Age × ethnicity</i>						
Age × Other Hisp.	0.050 (0.05)	0.050 (0.047)	1.00 (17)	0.332	(−0.055, 0.154)	1.07
Age × White	−0.004 (−0.01)	0.053 (0.051)	−0.08 (17)	0.934	(−0.117, 0.108)	2.07
Age × Black	0.035 (0.036)	0.039 (0.037)	0.89 (17)	0.385	(−0.047, 0.116)	0.78
Age × Other	0.015 (0.01)	0.049 (0.046)	0.30 (17)	0.766	(−0.089, 0.119)	1.13
<i>Age sq. × ethnicity</i>						
Age sq. × Other Hisp.	0.001 (0.001)	0.003 (0.003)	0.24 (17)	0.811	(−0.006, 0.008)	1.57
Age sq. × White	0.003 (0.003)	0.002 (0.002)	1.55 (17)	0.139	(−0.001, 0.006)	0.71
Age sq. × Black	−0.002 (−0.01)	0.002 (0.002)	−1.19 (17)	0.249	(−0.007, 0.002)	0.66
Age sq. × Other	0.001 (0.001)	0.001 (0.003)	0.48 (17)	0.634	(−0.005, 0.008)	1.31
<i>Age × gender</i>						
Age × female	0.045 (0.034)	0.023 (0.026)	1.94 (17)	0.069	(−0.004, 0.095)	2.37
<i>Age Sq. × gender</i>						
Age Sq. × female	0.003 (0.003)	0.002 (0.002)	2.04 (17)	0.058	(−0.001, 0.007)	3.46

Note: Subclass $n = 5,112$, weighted $R^2 = 0.120$, adjusted Wald test for all parameters: $F(17,1) = 176.18$, $p = 0.059$. — denotes the reference category.

that African-Americans have a mean DBP that is higher by 3.45 units than Mexican-Americans *in general*; this interpretation is only true *for individuals with age equal to the population mean*.

In the same manner, one would interpret the estimated coefficients for age and age-squared not as main effects for the entire population, but rather effects of age *for the reference categories of race/ethnicity and gender*. That is, for Mexican-American males, the relationship of age with DBP is defined by a quadratic equation with intercept 75.35, linear age coefficient 0.039 (not significantly different from zero), and quadratic age coefficient -0.015 (significantly different from zero). The estimated interaction coefficients then represent *changes* in these age coefficients corresponding to the nonreference categories of race/ethnicity and gender. So why did we find in the Wald test that the overall interaction terms involving race/ethnicity were significant, given that none of these "change" coefficients seem to be different from zero in Table 7.6? Keep in mind that we are looking at changes in relationships relative to *specific* reference categories. It would appear that the difference in the quadratic age coefficients for whites and African-Americans is largest, but we are not getting a test of this difference (given that Mexican-American is the reference category). If we were to change the reference category to white, the change coefficient for African-Americans would now be positive and significant (at the 5% level).

In general, if one finds significant interactions in a linear regression model (or any regression model for that matter), very interesting insights are possible regarding subgroup differences in the relationships of interest. Great care is simply needed in interpreting these relationships.

Finally, we conclude this illustration by applying the "q-weighted" approach proposed by Pfeffermann (2011) to our "final" model, to determine whether we can generate similar weighted estimates with increased efficiency. This approach proceeds as follows:

1. Fit a regression model to the final survey weights using the predictor variables in the regression model of substantive interest. [We note that under mild regularity conditions, this "q-weighted" approach will ultimately yield consistent estimates of the finite population regression parameters even if this initial regression model for the weights is misspecified in some way; see Pfeffermann (2011, p. 124).] In our example:

```
regress WTMEC2YR i.RIDRETH1 i.riagendr agec
```

2. Save the expected values (i.e., predicted values) of the survey weights for each case as a function of the predictor variables in the data set:

```
predict w_hat, xb
```

3. Divide the final analysis weights by their expected values as a function of the predictor variables:

```
gen q_WTMEC2YR = WTMEC2YR / w_hat
```

4. Use the new “q-weights” as the survey weights in estimating the final regression model:

```
svyset sdmvpsu [pweight = q_WTMEC2YR], ///
strata(sdmvstra) vce(linearized) singleunit(missing)

svy, subpop(age18p): regress bpxdi1_1 i.RIDRETH1 ///
i.riagendr agec c.agec#c.agec ///
i.RIDRETH1#c.agec i.RIDRETH1#c.agec#c.agec ///
i.riagendr#c.agec i.riagendr#c.agec#c.agec
```

We compare weighted estimates and standard errors based on this approach with those based on the original weights in [Table 7.6](#). We note that these estimates tend to have higher efficiency than those based on the original weights, but the differences in this example are not substantial. Given the ease of implementing this approach and its demonstrated empirical benefits in terms of efficiency (Pfeffermann, 2011), we recommend that analysts fitting regression models to complex sample survey data consider applying it before presenting any final estimates.

EXERCISES

7.1 Regression Model Building:

- Briefly outline and describe the four model-building steps recommended in this chapter.
- Describe how each of the four steps changes when analyzing complex sample survey data.

7.2 Linear Regression Analysis Project Using ESS6 Russian Federation Data:

This exercise asks you to perform a linear regression analysis using the ESS Round 6 Russian Federation data. Exercise 7.2 contains many parts and emphasizes model-building and correct analysis of data collected from a complex sample survey. The data set, *chapter_exercises_ess6ru*, is available for download from the ASDA web site, in SAS or Stata format.

- Perform data exploration of the Satisfaction with Government (STFGOV) variable through use of a weighted frequency table, weighted bar chart, or a weighted histogram. This will be the dependent variable in the linear regression exercises to follow. Discuss the distribution of the variable and explain how this variable can function as a continuous outcome despite consisting of 10 distinct levels.
- Consider three possible predictors of the dependent variable Satisfaction with the Government (STFGOV): (1) a left-to-right

political scale collapsed into three categories, from the 0–10 scale LRSCALE (LR3CAT, 1 = left to moderately left, 2 = moderate, 3 = moderately right to right); (2) gender (GNDR, 1 = Male, 2 = Female); and (3) Self-rated health status (HEALTH, 1 = Very good, 2 = Good, 3 = Fair, 4 = Bad, 5 = Very bad). Describe how each predictor variable should be handled in the regression model (continuous or categorical).

- c. Fit a set of bivariate models where STFGOV is predicted by each possible predictor listed in part b (one at a time), while incorporating the complex sample design features (STRATIFY and PSU) and the final survey weights (PSPWGHT). Based on these results, what are the F -test statistics, degrees of freedom, and p -values for each possible predictor variable?
- d. Fit the “preliminary” model with the retained predictors (from part c), fully accounting for the complex sampling features. Request design effects for the estimated coefficients, and produce a residual versus predicted plot and a histogram with a superimposed normal curve of the residuals. Based on these results, answer the following questions:
 - i. Do these plots indicate acceptable model fit?
 - ii. What other techniques might be used to assess model fit?
 - iii. What do the design effects indicate about the relationships of each predictor?
 - iv. How many degrees of freedom are used for the significance tests, and how are they calculated?
 - v. What is the R -squared for this model and what does this mean?
- e. Test the interaction of gender and left/right political orientation (three category variables) in the “preliminary” model. Then, answer these questions:
 - i. What are the F -test statistic, degrees of freedom, and p -value for the interaction?
 - ii. Is the interaction term significant at the $\alpha = 0.05$ level?
 - iii. Should the interaction be retained in your final model?
- f. Fit your “final” model, and based on these results, prepare a table similar to [Table 7.5](#). Be sure to either exclude or include your interaction terms depending on the decision you made in part e. Include variable labels, design effects, and descriptive columns in the table.
- g. Fit your “final” model using the final survey weights, but without applying the complex sample design adjustments to the standard errors (i.e., ignoring PSU and STRATIFY in the variance

- estimation). Based on these results, prepare a table similar to [Table 7.3](#). Make sure to label the standard error column as either “robust standard error” or “standard error” depending on how your software of choice handles weighted but non-design-based standard error calculations. Do any of your inferences change? Would any of your inferences change if you ignored the weights as well?
- h. Write a brief paragraph (as you might for a research article) explaining the methods that you used to estimate the model parameters and estimate the standard errors of the estimated parameters in a way that accounts for the complex sample design of the ESS6 Russian Federation data. Also, discuss how your conclusions might have changed had you not performed a correct design-based analysis incorporating the complex sample design features and the survey weights.



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8

Logistic Regression and Generalized Linear Models for Binary Survey Variables

8.1 Introduction

Perusal of the electronic codebook for any major survey data set quickly reveals that many key survey questions require only a simple “yes” or “no” answer. Consider these questions from three of the studies used for the examples in this book:

HRS	“Are you currently covered by Medicare health insurance?”
NHANES	“Have you ever been told by a doctor or health professional that you have diabetes or sugar diabetes?”
NCS-R	“Did you ever use drugs or alcohol so often that it interfered with your responsibilities at work, at school or at home?”

The responses to such questions are coded as *binary variables* (or *dichotomous variables*). This chapter is devoted to *generalized linear models* (GLMs) for a binary survey variable—focusing primarily on the application of *logistic regression* analysis to complex sample survey data. There are many excellent texts on standard simple random sample methods for logistic regression analysis, including comprehensive introductions to the theory, methods, and applications provided in texts by Hosmer et al. (2013), Agresti (2012), and Allison (1999). Readers wanting a full mathematical treatment of GLMs are referred to McCullagh and Nelder (1989) and McCulloch et al. (2008).

The general aims of this chapter are to: (1) introduce the fundamental concepts of regression for categorical data based on GLMs that are important to understand for effective application of the techniques to survey data; (2) provide a systematic review of the stages in fitting the logistic regression model to complex sample survey data; and (3) present example logistic regression analyses based on the Health and Retirement Study (HRS) and National Comorbidity Survey Replication (NCS-R) data that illustrate typical applications of the model-building steps to actual survey data sets.

Section 8.2 will touch on the important underlying concepts of GLMs as they apply to *logistic regression* and *probit regression* but will leave much of the underlying theory and detailed development to specialized texts on the topic. Sections 8.3 through 8.6 describe the theory and methods that are important in the four stages of building and interpreting a logistic regression model: specification, estimation, evaluation, and interpretation/inference for complex sample survey data. Section 8.7 takes the reader through an example analysis in which a logistic regression model is fit to the binary indicator of having had a major depressive episode (MDE) at some point in the lifetime in the NCS-R data set. The chapter concludes in Section 8.8 with a comparative application of the logistic, probit, and complementary-log-log (C-L-L) regression techniques to the problem of modeling the probability of alcohol dependency in U.S. adults.

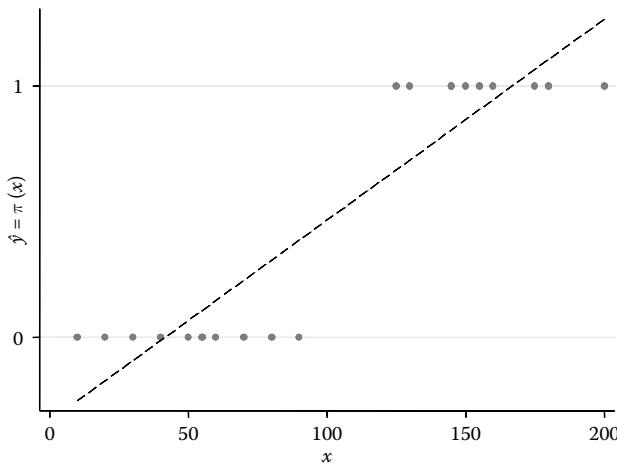
8.2 GLMs for Binary Survey Responses

In principle, GLMs for a binary dependent variable and linear regression models for a continuous variable (Chapter 7) share a common aim—to estimate a regression equation that relates the expected value of the dependent variable y to one or more predictor variables, denoted by x . In linear regression for a continuous dependent variable, the expected value of y is the conditional mean of y given a vector of covariates, x , and is estimated by an equation that is linear in the regression parameters:

$$\hat{Y} = E(y | x) = B_0 + B_1x_1 + \cdots + B_p x_p. \quad (8.1)$$

When y is a binary variable with possible values 0 and 1 ($y = \{0, 1\}$), $E(y|x) = \pi(x)$ is the conditional probability that $y = 1$ given the covariate vector x . Throughout this chapter, the notation $\pi(x)$ will be used to represent this probability that $y = 1$ conditional on a vector of observed predictors, x .

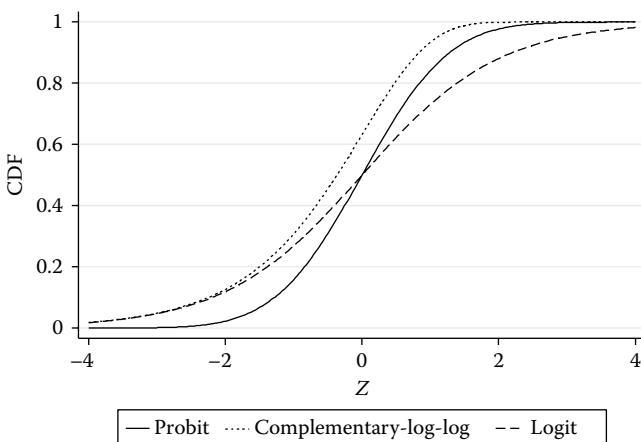
A naive approach to regression analysis of a binary dependent variable is to model the $\pi(x)$ as a linear function of x . There are several problems with this approach. First, as we will see in Section 8.4, the sample of observations on the dependent variable y is assumed to follow a binomial distribution—a severe violation of the normality and homogeneity of variance assumptions required for efficient least squares estimation of the coefficients of the linear regression model. Second, as shown in Figure 8.1, a naive linear regression model for $\pi(x)$ does not accurately capture the relationship between y and x —and it may even produce predicted values for $\pi(x)$ that are outside the permissible range of 0–1.

**FIGURE 8.1**

Naïve use of linear regression for a binary dependent variable.

The alternative would be to identify a nonlinear function of $\pi(x)$, say $g(\pi(x))$, that yields a fitted regression model that is linear in the coefficients for the model covariates, x . Ideally, the estimated function, $g(\pi(x))$, should also be chosen so that, when it is transformed back [i.e., $\pi(x) = g^{-1}(g(\pi(x)))$], the resulting values of the estimated $\pi(x)$ will fall in the range between 0 and 1.

In the terminology of GLMs, functions like $g(\pi(x))$ are termed *link functions*. The two most common link functions used to model binary survey variables are the logit and the probit. The functional relationships of the logit and probit to the values of $\pi(x)$ are illustrated in Figure 8.2, where one can see

**FIGURE 8.2**

Cumulative distribution functions (CDFs) for the Logit, Probit, and C-L-L links.

THEORY BOX 8.1 A LATENT VARIABLE INTERPRETATION OF THE LOGIT MODEL

In specifying a logistic (or probit) regression model for a binary outcome variable, the observed response on the binary outcome variable y can be viewed as determined by the value of a *latent* (or unobserved) continuous variable z . If the true value of the link function (or logit), z_i , for a survey respondent is less than or equal to some threshold value Z , the respondent answers with a $y = 1$; if the value of $z_i > Z$, the respondent is expected to answer with $y = 0$. Since z_i is a latent variable and is never directly observed, its value for each respondent must be modeled as a function of observed survey variables.

The intercept parameter B_0 may be interpreted as a “cutpoint” along the distribution of the logit (or probit) values. Changes in the predictor variables shift this “cutpoint,” therefore changing the probability of a response of 1; thinking about the logistic regression model in this way will be useful for understanding ordinal logistic regression models in Section 9.3.

the value of $\pi(x)$ that would result from a given value of the logit or probit. Theory Box 8.1 presents a latent variable interpretation of the logit and probit link functions and a mechanism for relating these linear functions in x to the $\pi(x)$ that are the quantities of true interest in the model estimation.

8.2.1 Logistic Regression Model

For a logistic regression model, the link function is the *logit*:

$$g(\pi(x)) = \text{logit}(\pi(x)) = z = \ln\left(\frac{\pi(x)}{1 - \pi(x)}\right) = B_0 + B_1x_1 + \dots + B_px_p. \quad (8.2)$$

The logit is nonlinear in $\pi(x)$ but is presumed to be linear in the regression parameters, $B = \{B_0, B_1, \dots, B_p\}$. Based on the fitted regression model for the logit, the estimated value of $\pi(x)$ can be recovered by applying the inverse logit function:

$$\hat{\pi}(x) = g^{-1}(g(\hat{\pi}(x))) = \frac{\exp(\hat{B}_0 + \hat{B}_1x_1 + \dots + \hat{B}_px_p)}{1 + \exp(\hat{B}_0 + \hat{B}_1x_1 + \dots + \hat{B}_px_p)}. \quad (8.3)$$

The inverse function $g^{-1}()$ is the cumulative distribution function (CDF) for the logistic probability distribution. Under the logistic model (8.2), $\hat{\pi}(x)$ is the

logistic CDF evaluated at the estimated logit corresponding to the covariate vector \mathbf{x} .

Unlike the linear regression model for normally distributed y , there is no direct solution such as the method of least squares to estimate the regression coefficients in the logit model. Instead, an iterative estimation procedure such as the Newton–Raphson or Fisher Scoring algorithm (Agresti, 2012) is used to determine the values of estimated coefficients that maximize the following weighted pseudo-likelihood function:

$$PL(\mathbf{B} | \mathbf{X}) = \prod_{i=1}^n \{\pi(\mathbf{x}_i)^{y_i} \cdot [1 - \pi(\mathbf{x}_i)]^{1-y_i}\}^{w_i}. \quad (8.4)$$

It is important to note that the link function is not an explicit transformation of the variable y but rather a transformation of the $E(y|\mathbf{x}) = \pi(\mathbf{x})$. Also note that evaluation of the pseudo-likelihood (8.4) requires both the original observations, y_i , the modeled values of $\hat{\pi}(\mathbf{x}_i)$, and in the case of complex sample survey data, the final survey weights w_i . We discuss this function in more detail in Section 8.4.

Each cycle in the iterative estimation of the logistic regression model requires four operations:

1. The value of the logit (8.2) is estimated for each survey respondent i based on the current iteration values of the estimated parameters:

$$z_i = \hat{B}_0 + \hat{B}_1 x_{1i} + \cdots + \hat{B}_p x_{pi}.$$
2. The logit for each case is then transformed back to the probability scale by evaluating the logistic CDF at the value of z_i as illustrated in 8.3.
3. The value of the likelihood (8.4) is then evaluated at the $i = 1, \dots, n$ values of the estimated $\hat{\pi}(\mathbf{x}_i)$ and observed y_i values.
4. The algorithm then adjusts the values of the individual parameter estimates \hat{B}_j to maximize the likelihood function, and returns to repeat the cycle.

The iterative algorithm stops when the change in the estimates of the vector of \mathbf{B} values no longer increases the value of the likelihood function. The values of the individual \hat{B}_j at the final iteration are the final estimates.

8.2.2 Probit Regression Model

The probit regression model is an alternative to logistic regression for modeling a binary dependent variable. Probit regression models are also GLMs, and the procedures for estimating the models parallel those illustrated in

Section 8.2.1 for logistic regression. The difference in the two approaches is that the link function changes to the *probit* (inverse Normal):

$$g(\pi(x)) = \Phi^{-1}(\pi(x)) = z = B_0 + B_1x_1 + \cdots + B_px_p. \quad (8.5)$$

In contrast to logistic regression, where z is assumed to follow the logistic probability distribution, the probit is assumed to follow a standard normal distribution. Again, as in logistic regression, transforming back from the probit scale to the quantities of interest $\pi(x)$ requires an evaluation of the standard Normal CDF at the estimated value of the probit, $z_i = \hat{B}_0 + \hat{B}_1x_{1i} + \cdots + \hat{B}_px_{pi}$:

$$\begin{aligned} \hat{\pi}(x_i)_{\text{probit}} &= \Phi(z_i) = \text{Prob}(Z \leq z_i) \\ &= \int_{-\infty}^{\hat{B}_0 + \hat{B}_1x_{1i} + \cdots + \hat{B}_px_{pi}} \frac{1}{\sqrt{2\pi}} \cdot \exp\{-Z^2\} dZ. \end{aligned} \quad (8.6)$$

With the probit link (8.5) replacing the logit and the normal probability transform (8.6) replacing the logistic CDF transform (8.3), the steps in estimating the probit regression model are identical to those outlined above for logistic regression. In general, inferences derived under logistic and probit regressions do not differ significantly.

8.2.3 Complementary-Log-Log Model

A third less commonly used link function in regression analysis of a binary dependent variable is the C-L-L link. Most software packages for survey data analysis that support logistic and probit regression modeling also permit the user the option to choose the C-L-L link. The C-L-L link function is related to the Gompertz distribution, and the link may be referred to as the “gom-pit.” The primary distinction for the C-L-L link is that unlike the logit or probit, the CDF is not required to be symmetric about the midpoint $\pi(x) = 0.5$ ([Figure 8.2](#)). Its most common application is in situations where $\pi(x)$ is either very close to 0 or close to 1 (at one or the other extreme). Interested readers are referred to Allison (1999) for applications of the C-L-L link function to both binary regression models and survival analysis.

Section 8.8 will provide a parallel comparison of a model fitted under all three links: the logit, the probit, and the C-L-L.

8.3 Building the Logistic Regression Model: Stage 1—Model Specification

The four stages in logistic regression modeling of survey data are identical to those presented in [Chapter 7](#) for linear regression: (1) model specification;

(2) estimation of model parameters and their standard errors; (3) model evaluation and diagnostics; and (4) interpretation of results and inference based on the final model. As in all statistical model-building processes, stages 1–3 define an iterative process designed to sequentially refine and test the model. Several cycles of the model specification, estimation, and evaluation sequence are usually required before a final model is identified and inferences can be made concerning the modeled relationship in the larger survey population.

The logistic regression model is a flexible modeling tool that can simultaneously accommodate both categorical and continuous predictors as well as terms for the interactions among the predictors. As in all regression modeling, identification of a best logistic regression model for the survey data should follow a systematic, scientifically governed process whereby important candidate predictors are identified and evaluated, first individually and then in the multivariate context of other potentially important explanatory variables. Our recommendation is that survey analysts follow Hosmer et al.'s (2013) incremental process for specifying the initial model, refining the set of predictors, and then determining the final form of the logistic regression model:

- Perform initial bivariate analyses of the relationship of y to individual predictor variable candidates.
- Select the predictors that have a bivariate association with y at significance $p < 0.25$ as *candidates* for main effects in a multivariate logistic regression model (Harrell [2015] argues that one should simply begin with *all* predictors of scientific interest in a multivariate model).
- Evaluate the contribution of each predictor to the multivariate model using the Wald test.
- Check the linearity assumption for continuous predictors.
- Check for scientifically justified interactions among predictors.

Hosmer et al. (2013) advocate a final step involving the application of polynomial functions and smoothing splines to test that the logistic model is truly linear in the logit. Interested readers are referred to that text for a description of this final step in the evaluation of the fit of a logistic regression model.

8.4 Building the Logistic Regression Model: Stage 2— Estimation of Model Parameters and Standard Errors

Given the specification of a logistic regression model of the form $\text{logit}(\pi(x)) = B_0 + B_1x_1 + \dots + B_px_p$, the second step in the model-building

process is to compute estimates of the regression parameters in the model along with their standard errors. For simple random samples, the logistic regression model parameters and standard errors can be estimated using the method of maximum likelihood. The likelihood function for a simple random sample of n observations on a binary variable y with possible values 0 and 1 is based on the binomial distribution:

$$L(\boldsymbol{\beta} | \mathbf{x}) = \prod_{i=1}^n \pi(x_i)^{y_i} [1 - \pi(x_i)]^{1-y_i}, \quad (8.7)$$

where $\pi(x_i)$ is linked to the regression model coefficients through the logistic CDF:

$$\pi(x_i) = \frac{\exp(x_i\boldsymbol{\beta})}{1 + \exp(x_i\boldsymbol{\beta})}. \quad (8.8)$$

When the survey data have been collected under a complex sample design, straight-forward application of maximum likelihood estimation (MLE) procedures is no longer possible, for several reasons. First, the probabilities of selection (and responding) for the $i = 1, \dots, n$ sample observations are generally no longer equal. Survey weights (Section 2.7) are thus required to estimate the finite population values of the logistic regression model parameters. Second, the stratification and clustering of complex sample observations violates the assumption of independence of observations that is crucial to the standard MLE approach to estimating the sampling variances of the model parameters and choosing a reference distribution for the likelihood ratio test statistic (see Lumley and Scott, 2014, 2015 for more discussion of this testing issue).

Two general approaches have been developed to estimate the logistic regression model parameters and standard errors for complex sample survey data. Grizzle et al. (1969) first formulated an approach based on weighted least squares (WLS) estimation. The WLS estimation method was originally programmed for logistic regression in the GENCAT software package (Landis et al., 1976) and still remains available as an option in programs such as SAS PROC CATMOD. Later, Binder (1981, 1983) presented a second general framework for fitting logistic regression models and other GLMs to complex sample survey data. Binder proposed *pseudo-maximum likelihood estimation* (PMLE) as a technique for estimating the model parameters. The PMLE approach to parameter estimation was combined with a linearized estimator of the variance–covariance matrix for the parameter estimates, taking complex sample design features into account. Further development and evaluation of the PMLE approach was presented in Roberts et al. (1987), Morel (1989), and Skinner et al. (1989). The PMLE approach is now the standard

method for logistic regression modeling in all of the major software systems that support analysis of complex sample survey data.

In theory, the finite population regression parameters for a GLM of interest are those values that maximize a likelihood function for the $i = 1, \dots, N$ elements in the survey population. For a binary dependent variable y (with possible values 0 or 1), the population likelihood can be defined as

$$L(\mathbf{B} | \mathbf{x}) = \prod_{i=1}^N \pi(x_i)^{y_i} [1 - \pi(x_i)]^{1-y_i}, \quad (8.9)$$

where under the logit link, $\pi(x_i)$ is evaluated using the logistic CDF and the parameters in the specified logistic regression model: $\pi(x_i) = \exp(x_i \mathbf{B}) / [1 + \exp(x_i \mathbf{B})]$. Note that as in [Chapter 7](#), the finite population model parameters are denoted by the standard alphabetic B to distinguish them from the superpopulation model parameters denoted by β . Here, as in linear regression, the distinction is primarily a theoretical one.

Estimates of these finite population regression parameters are obtained by maximizing the following unbiased estimate of the population likelihood, which is a weighted function of the observed sample data and the $\pi(x_i)$ values:

$$\begin{aligned} PL(\mathbf{B} | X) &= \prod_{i=1}^n \{\pi(x_i)^{y_i} \cdot [1 - \pi(x_i)]^{1-y_i}\}^{w_i} \\ \text{with: } \pi(x_i) &= \frac{\exp(x_i \mathbf{B})}{[1 + \exp(x_i \mathbf{B})]}. \end{aligned} \quad (8.10)$$

Like the standard MLE procedure, this weighted pseudo-likelihood function can be maximized using the iterative Newton–Raphson method or related algorithms. (See Theory Box 8.2 for more detail.)

The next hurdle in analyzing logistic regression models for complex sample survey data is to estimate the sampling variances and covariances of the parameter estimates. Binder (1983) proposed a solution to this problem that applied a multivariate version of Taylor Series Linearization (TSL). The result is a *sandwich-type variance estimator* of the form

$$\text{var}(\hat{\mathbf{B}}) = (\mathbf{J}^{-1}) \text{var}[S(\hat{\mathbf{B}})] (\mathbf{J}^{-1}), \quad (8.11)$$

where \mathbf{J} is a matrix of second derivatives with respect to the \hat{B}_j of the pseudo-log-likelihood for the data (derived by applying the natural log function to the likelihood defined in Equation 8.10) and $\text{var}[S(\hat{\mathbf{B}})]$ is the variance–covariance matrix for the sample total of the weighted *score functions* for

THEORY BOX 8.2 PSEUDO-MAXIMUM LIKELIHOOD ESTIMATION FOR COMPLEX SAMPLE SURVEY DATA

For a binary dependent variable and binomial data likelihood, the pseudo-maximum likelihood approach to the estimation of the logistic regression parameters and their variance–covariance matrix requires the solution to the following vector of estimating equations:

$$S(\mathbf{B}) = \sum_h \sum_{\alpha} \sum_i w_{hai} D'_{hai} [(\pi_{hai}(\mathbf{B})) \cdot (1 - \pi_{hai}(\mathbf{B}))]^{-1} (y_{hai} - \pi_{hai}(\mathbf{B})) = \mathbf{0}. \quad (8.12)$$

where D_{hai} is the vector of partial derivatives, $\delta(\pi_{hai}(\mathbf{B})) / \delta B_j; j = 0, \dots, p$.

In Equation 8.12, h is a stratum index, α is a cluster (or SECU) index within stratum h , and i is an index for individual observations within cluster α . The term w_{hai} is the survey weight for observation i . The term $\pi_{hai}(\mathbf{B})$ refers to the probability that the outcome variable is equal to 1 as a function of the parameter estimates and the observed data according to the specified logistic regression model. For a logistic regression model of a binary variable, this reduces to a system of $p + 1$ estimating equations (where p is the number of predictor variables, and there is one additional parameter corresponding to the intercept in the model):

$$S(\mathbf{B})_{\text{logistic}} = \sum_h \sum_{\alpha} \sum_i w_{hai} (y_{hai} - \pi_{hai}(\mathbf{B})) \mathbf{x}'_{hai} = \mathbf{0}. \quad (8.13)$$

where \mathbf{x}'_{hai} = a column vector of the $p + 1$ design matrix elements for case $i = [1 \ x_{1,hai} \ \cdots \ x_{p,hai}]'$.

For the probit regression model, the estimating equations reduce to:

$$S(\mathbf{B})_{\text{probit}} = \sum_h \sum_{\alpha} \sum_i w_{hai} \frac{(y_{hai} - \pi_{hai}(\mathbf{B})) \cdot \phi(\mathbf{x}'_{hai}\mathbf{B})}{\pi_{hai}(\mathbf{B}) \cdot (1 - \pi_{hai}(\mathbf{B}))} \mathbf{x}'_{hai} = \mathbf{0}. \quad (8.14)$$

where $\phi(\mathbf{x}'_{hai}\mathbf{B})$ is the standard normal probability density function evaluated at $\mathbf{x}'_{hai}\mathbf{B}$.

The weighted parameter estimates are computed by using the Newton–Raphson method to derive a solution for $S(\mathbf{B}) = \mathbf{0}$ (Agresti, 2012). Binder showed that the vector of weighted parameter estimates based on PMLE is *consistent* for \mathbf{B} even when the sample design is complex; that is, the bias of this estimator is of order $1/n$, so that, as the sample size gets larger (which is often the case with complex samples), the bias of the estimator approaches 0.

THEORY BOX 8.3 TAYLOR SERIES ESTIMATION OF $\text{VAR}(\hat{\mathbf{B}})$

The computation of variance estimators for the pseudo-maximum likelihood estimates of the finite population parameters in the logistic regression model makes use of the J matrix of second derivatives:

$$\begin{aligned} J &= -\left[\frac{\partial^2 \ln PL(\mathbf{B})}{\partial^2 \mathbf{B}} \right] \Big| \mathbf{B} = \hat{\mathbf{B}} \\ &= \sum_h \sum_{\alpha} \sum_i x'_{h\alpha i} x_{h\alpha i} w_{h\alpha i} \hat{\pi}_{h\alpha i}(\mathbf{B}) (1 - \hat{\pi}_{h\alpha i}(\mathbf{B})). \end{aligned} \quad (8.15)$$

Due to the weighting, stratification, and cluster sampling inherent to complex sample designs, J^{-1} is not equivalent to the variance–covariance matrix of the pseudo-maximum likelihood parameter estimates, as is the case in the SRS setting (Section 8.4). Instead, a *sandwich-type variance estimator* is used, incorporating the matrix J and the estimated variance–covariance matrix of the weighted score equations from Equation 8.13:

$$\hat{\text{Var}}(\hat{\mathbf{B}}) = (J^{-1}) \text{var}[S(\hat{\mathbf{B}})] (J^{-1}). \quad (8.16)$$

The symmetric matrix $\text{var}[S(\hat{\mathbf{B}})]$ is the variance–covariance matrix for the $p + 1$ estimating equations in Equation 8.12 above. Each of these $p + 1$ estimating equations is a summation over strata, clusters, and elements of the individual “scores” for the n survey respondents. Since each estimating equation is a sample total of respondents’ scores, standard formulae for stratified sampling of ultimate clusters (Chapter 3) can be used to estimate the variances and covariances of the $p + 1$ sample totals. In vector notation:

$$\text{var}[S(\hat{\mathbf{B}})] = \frac{n-1}{n-(p+1)} \sum_{h=1}^H \frac{a_h}{(a_h-1)} \sum_{\alpha=1}^{a_h} (\mathbf{s}_{h\alpha} - \bar{\mathbf{s}}_h)' (\mathbf{s}_{h\alpha} - \bar{\mathbf{s}}_h)$$

which for n large is:

$$\text{var}[S(\hat{\mathbf{B}})] \cong \sum_{h=1}^H \frac{a_h}{(a_h-1)} \sum_{\alpha=1}^{a_h} (\mathbf{s}_{h\alpha} - \bar{\mathbf{s}}_h)' (\mathbf{s}_{h\alpha} - \bar{\mathbf{s}}_h)$$

where for the logistic link:

$$\mathbf{s}_{h\alpha} = \sum_{i=1}^{n_\alpha} \mathbf{s}_{h\alpha i} = \sum_{i=1}^{n_\alpha} w_{h\alpha i} (y_{h\alpha i} - \hat{\pi}_{h\alpha i}(\mathbf{B})) x'_{h\alpha i}; \text{ and } \bar{\mathbf{s}}_h = \frac{1}{a_h} \sum_{\alpha=1}^{a_h} \mathbf{s}_{h\alpha}. \quad (8.17)$$

The estimator of $\text{var}[\hat{\beta}]$ for the probit or C-L-L link is obtained by substituting the appropriate expressions for the individual score functions in the calculation of the s_{ho} . For more details, interested readers should refer to Binder (1983).

the individual observations used to fit the model. Interested readers can find a more mathematical treatment of this approach in Theory Boxes 8.2 and 8.3. Binder's linearized variance estimator, $\text{var}(\hat{\beta})$, is the default variance estimator in most major software packages for survey data analysis. However, most systems also provide options to select a Jackknife Repeated Replication (JRR) or Balanced Repeated Replication (BRR) method to estimate the variance–covariance matrix, $\text{var}(\hat{\beta})_{\text{rep}}$, for the estimated model coefficients.

8.5 Building the Logistic Regression Model: Stage 3—Evaluation of the Fitted Model

The next step in building the logistic regression model is to test the contributions of the individual model parameters and evaluate the overall goodness of fit (GOF) of the model.

8.5.1 Wald Tests of Model Parameters

When fitting logistic regression models to data collected from simple random samples, the statistical significance of one or more logistic regression parameters can be evaluated using a *likelihood ratio test*. Under the null hypotheses $H_0: \beta_j = 0$ (single parameter) or $H_0: \beta_q = 0$ (with q parameters), the following test statistic G follows a chi-square distribution with either 1 (for a single parameter) or q degrees of freedom:

$$G = -2 \ln \left[\frac{L(\hat{\beta}_{\text{MLE}})_{\text{reduced}}}{L(\hat{\beta}_{\text{MLE}})_{\text{full}}} \right], \quad (8.18)$$

where $L(\hat{\beta}_{\text{MLE}})$ is the likelihood under the model evaluated at the maximum likelihood estimates of β .

The *reduced* model in this case is the model excluding the q regression parameters to be tested, while the *full* model is the model including the q

regression parameters. Both models should be fitted using *exactly* the same set of observations for this type of test to be valid.

As described in Section 7.3.4 for the linear regression model, complex sample designs invalidate the key assumptions that underlie the F -tests or likelihood ratio tests used to compare alternative models in simple random samples; we describe recent developments in this area for GLMs fitted to data from complex samples below. Instead, Wald-type tests are often used to test hypotheses concerning the parameters of a specified logistic regression model. The default output from software procedures enabling analysts to fit logistic regression models to complex sample survey data provides a table of the estimated model coefficients, the estimated standard errors, and the test statistic and a “ p -value” for the simple hypothesis test, $H_0: B_j = 0$. (See, e.g., [Table 8.1](#) in Section 8.6.) Different software applications may report the test statistic as a Student t -statistic, $t = \hat{B}_j/se(\hat{B}_j)$, or as a Wald X^2 . If the former of the two tests is output, the test statistic is referred to a Student t distribution with nominal design-based degrees of freedom ($df = \#clusters - \#strata$) to determine and report the p -value. If the output is in the form of the Wald X^2 , the reference distribution for determining the p -value is χ^2_1 , or a central chi-square distribution with 1 degree of freedom. The two tests are functionally equivalent. In fact, the absolute value of the Student t -test statistic is simply the square root of the Wald X^2 test statistic for this single parameter hypothesis test.

More generally, software procedures enabling analysts to fit logistic regression models to complex sample survey data provide convenient syntax to specify Wald tests for a variety of hypotheses concerning the full vector of regression parameters. The general form of the null hypothesis for a Wald Test is defined by $H_0: CB = 0$, where C is a matrix of constants that defines the hypothesis being tested (see Section 7.3.4.1 for examples). The Wald test statistic is computed as

$$X_{Wald}^2 = (\hat{CB})' [C(\text{var}(\hat{B}))C']^{-1} (\hat{CB}), \quad (8.19)$$

where $\text{var}(\hat{B})$ is a design-consistent estimate of the variance–covariance matrix of the estimated logistic regression coefficients (see Equation 8.11 for an example based on TSL). Under the null hypothesis, this Wald test statistic follows a chi-square distribution with q degrees of freedom, where q is the rank, or number of independent rows, of the matrix C . This test statistic can also be converted into an approximate F -statistic by dividing the Wald X^2 test statistic by the degrees of freedom.

In Stata, the `test` postestimation command is used to specify a multi-parameter hypothesis test after fitting a model. Section 7.5 has already illustrated the application of the `test` command for constructing hypothesis tests for parameters in the linear regression model. The syntax is identical for constructing hypothesis tests for the parameters of the logistic model or other GLMs estimated in Stata. For example, after fitting a logistic regression

model which includes two indicator variables to represent the effects of two of the three NHANES race/ethnicity categories (1 = White, 2 = Black, 3 = Other, with White considered as a reference category), the command

```
test 2.race 3.race
```

tests the overall importance of race, that is, $H_0: \{B_{\text{Black}} = 0, B_{\text{Other}} = 0\}$, while the command

```
test 2.race - 3.race
```

tests the hypothesis $H_0: \{B_{\text{Black}} - B_{\text{Other}} = 0\}$ or equivalently $H_0: \{B_{\text{Black}} = B_{\text{Other}}\}$.

It is important to emphasize here again that survey analysts must be cautious about interpreting single parameter hypothesis tests when the estimated coefficient applies to an indicator variable for a multicategory predictor (e.g., levels of education) or when the model also includes an interaction term that incorporates the predictor of interest. In the former case, a significant result indicates that the category expectation (for the outcome) is significantly different from that of the *reference category*, but not necessarily other levels of the multicategory predictor. Tests of parameters for main effects in a model with interactions involving that same variable are confounded and not easily interpreted (see Section 8.6 for an example of interpretation of interaction terms).

More recently, Lumley and Scott (2014) and Lumley and Scott (2015) have developed design-adjusted likelihood ratio tests for the regression parameters in logistic regression models fitted to complex sample survey data. In addition, these authors have developed design-adjusted *Akaike Information Criteria (AIC)* and *Bayesian Information Criteria (BIC)* that can be used to compare the fits of competing logistic regression models that do not necessarily have a nested relationship (i.e., where one model contains a subset of the parameters in a larger model). At the time of this writing, these design-adjusted tools have been implemented in the contributed R package *survey*. We will provide readers with updates regarding implementation of these tools in other software on the book web site, and we present examples of performing these tests and computing the design-adjusted information criteria in R in Section 8.7.

8.5.2 GOF and Logistic Regression Diagnostics

Summary statistics to measure overall *GOF* and methods for diagnosing the fit of a logistic regression model for individual cases or specific patterns of covariates have been developed for simple random samples. These GOF statistics and diagnostic tools have been included in the standard logistic regression procedures in most major statistical software packages. Chapter 5 in Hosmer et al. (2013) reviews these summary statistics and diagnostic methods in detail.

Included in the summary techniques are: (1) two test statistics based on the Pearson and deviance residuals for the fitted model; (2) the Hosmer–Lemeshow

GOF test; (3) classification tables comparing observed values of y to discrete classifications formed from the model's predicted values, $\hat{\pi}(x)$; and (4) the area under the receiver operating characteristic (ROC) curve. Several *pseudo-R²* measures have also been proposed as summary measures of the fit of a logistic regression model. However, since these measures tend to be incorrectly confused with the R^2 values (explained variability) in linear regression, we agree with Hosmer et al. (2013) that while they may be used by the analyst to compare the fits of alternative models, they should not be cited as a measure of fit in scientific papers or reports.

Archer and Lemeshow (2006) and Archer et al. (2007) have extended the standard Hosmer and Lemeshow GOF test for application to complex sample survey data. The A-L procedure is a modification of the standard Hosmer–Lemeshow test for GOF that takes the survey weights and the stratification and cluster sampling features of the complex sample design into account when assessing the residuals ($y_i - \hat{\pi}(x_i)$) based on the fitted model. Archer and Lemeshow's paper should be consulted for more details, but Stata has implemented this design-adjusted approach for assessing GOF in the post-estimation command `estat gof`. We present examples of the use of this command in Section 8.7.

At the time that this second edition is being written, survey analysis software is still in a phase where summary measures of GOF are being translated or newly developed for application to logistic regression modeling of complex sample survey data. Furthermore, it may be some time before the major software systems routinely incorporate robust GOF evaluation procedures in the software procedures for complex sample survey data analysis. In lieu of simply bypassing the GOF evaluation entirely (outside of Stata), we recommend:

1. Applying the Archer and Lemeshow GOF test and other available summary GOF measures when they are available in the software system.
2. If the logistic regression procedure for complex sample survey data in the chosen software system does not provide capabilities to generate summary GOF measures, reestimate the model using the survey weights in the system's standard logistic regression program. The weighted estimates of parameters and predicted probabilities will be identical, and serious lack of fit should be quantifiable even though the standard program tools do not correctly reflect the variances and covariances of the parameter estimates given the complex sample design.

Summary measures such as the Archer and Lemeshow test statistic have the advantage that they yield a single test of the overall suitability of the fitted model. However, even when a summary GOF measure suggests that the model provides an acceptable fit to the data, a thorough evaluation of the fit

of a model may also include examination of the fit for specific patterns of covariates. Does the model fit well for some patterns of covariates x_j , but not for others? The number and statistical complexity of diagnostic tools that have been suggested in the literature preclude a detailed discussion here. We encourage survey analysts to consult Hosmer et al. (2013) for a description of the diagnostic options and guidance on how these computational and graphical methods may be applied using Stata, SAS, and other software systems.

Regarding regression diagnostics for logistic regression models fitted to complex sample survey data, we can offer the following recommendations at the time of this second edition:

1. Use one or more of the techniques described in [Chapter 5](#) of Hosmer et al. (2013) to evaluate the fit of the model for individual patterns of covariates. If the complex sample logistic regression modeling procedure in your chosen software system (e.g., SAS PROC SURVEYLOGISTIC) does not include the full set of diagnostic capabilities of the standard programs, use the standard programs (e.g., SAS PROC LOGISTIC) with a weight specification (see Ryan et al., 2015 for details). As mentioned before, the weighted estimates of parameters and predicted probabilities will be identical and serious breakdowns in the model for specific covariate patterns should be identifiable even though the standard program does not correctly reflect the variances and covariances of the parameter estimates given the complex sample design.
2. Remember that regression diagnostics serve to inform the analyst of specific cases where the model provides a poor fit or cases that exert extreme influence on the overall fit of the model. They are useful in identifying improvements in the model or anomalies that warrant future investigation, but small numbers of “predictive failures” occur in almost all regression modeling and do not necessarily invalidate the entire model.

8.6 Building the Logistic Regression Model: Stage 4—Interpretation and Inference

In logistic regression modeling, one can make inferences concerning the significance and importance of individual predictor variables in several ways. As described in Section 8.5.1, Wald X^2 tests or likelihood ratio tests may be employed to test the null hypothesis that a single coefficient is significantly different from zero, $H_0: B_j = 0$, or more complex hypotheses concerning

multiple parameters in the fitted model. Confidence intervals (CIs) for individual model coefficients may also be used to draw inferences concerning the significance of model predictors, and also provide information on the potential magnitude and uncertainty associated with the estimated effects of individual predictor variables.

Recall from Section 6.4.5 that an estimated logistic regression coefficient is the natural logarithm of the odds ratio comparing the odds that $y = 1$ for a predictor with value $x + 1$ to the odds that $y = 1$ when that predictor has a value x . In addition, the estimated coefficient for an indicator variable associated with a level of a categorical predictor is the natural logarithm of the odds ratio comparing the odds that $y = 1$ for the level represented by the indicator to the odds that $y = 1$ for the reference level of the categorical variable. Consequently, the estimated coefficients are often labeled the *log-odds* for the corresponding predictor in the model. A design-based CI for a logistic regression parameter is computed as

$$CI_{1-\alpha}(B_j) = \hat{B}_j \pm t_{df, 1-\alpha/2} \cdot se(\hat{B}_j). \quad (8.20)$$

Typically, $\alpha = 0.05$ is used (along with the design-based degrees of freedom, df) and the result is a 95% CI for the parameter. In theory, the correct inference to make is that over repeated sampling, 95 out of 100 CIs computed in this way are expected to include the true population value of B_j . If the estimated CI includes $\ln(1) = 0$, analysts may choose to infer that $H_0: B_j = 0$ is accepted with a Type I error rate of $\alpha = 0.05$.

Inference concerning the significance/importance of predictors can be performed directly for the \hat{B}_j s (on the log-odds scale). However, to quantify the magnitude of the effect of an individual predictor, it is more useful to transform the inference to a scale that is easily interpreted by scientists, policy makers, and the general public. As discussed in Section 6.4.5, in a logistic regression model with a single predictor, x_1 , an estimate of the odds ratio corresponding to a one-unit increase in the value of x_1 can be obtained by exponentiating the estimated logistic regression coefficient:

$$\hat{\psi} = \exp(\hat{B}_1). \quad (8.21)$$

If the model contains only a single predictor, the result is an estimate of the *unadjusted odds ratio*. If the fitted logistic regression model includes multiple predictors, that is,

$$\text{logit}(\hat{\pi}(x)) = \ln \left[\frac{\hat{\pi}(x)}{1 - \hat{\pi}(x)} \right] = \hat{B}_0 + \hat{B}_1 x_1 + \cdots + \hat{B}_p x_p, \quad (8.22)$$

the result $\hat{\psi}_j | \hat{B}_{k\neq j} = \exp(\hat{B}_j)$ is an *adjusted odds ratio*. In general, the adjusted odds ratio represents the *multiplicative* impact of a one-unit increase in the predictor variable x_j on the odds of the outcome variable being equal to 1, holding all other predictor variables constant. Confidence limits can also be computed for adjusted odds ratios:

$$CI(\hat{\psi}_j) = \exp(\hat{B}_j \pm t_{df, 1-\alpha/2} \cdot se(\hat{B}_j)). \quad (8.23)$$

Software procedures for logistic regression analysis of survey data generally offer the analyst the option to output parameter estimates and standard errors on the log-odds scale (the original \hat{B}_j s) or transformed estimates of the corresponding adjusted odds ratios and CIs.

The adjusted odds ratios and CIs can be estimated and reported for any form of a predictor variable, including categorical variables, ordinal variables, and continuous variables. To illustrate, consider a simple logistic regression model (based on the 2006 wave of HRS data collection) of the probability that a U.S. adult aged 50+ has arthritis. The predictors in this main effects only model are gender, education level (with levels less than high school, high school, and more than high school), and age:

$$\text{logit}(\pi(x)) = B_0 + B_1 I_{Male} + B_2 I_{Educ,<HS} + B_3 I_{Educ,HS} + B_4 X_{Age(yrs)}$$

where:

I_{Male} = indicator variable for male gender (female is reference).

$I_{Educ,<HS}, I_{Educ,HS}$ = indicators for education level (>high school is reference).

$X_{Age(yrs)}$ = respondent age in years.

The results from fitting this simple model in Stata (using the following commands) are summarized in [Tables 8.1](#) and [8.2](#).

```
svyset secu [pweight = kwgtr], strata(stratum)
svy: logit arthritis male ib3.edcat3 kage
svy: logit arthritis male ib3.edcat3 kage, or
```

Interpreting the output from this simple example, we can make the following statements:

- The estimated ratio of odds of arthritis for men relative to women is $\hat{\psi} = 0.55$.
- The estimated odds of arthritis for persons with less than a high school education are $\hat{\psi} = 1.56$ times the odds of arthritis for persons with more than a high school education.

TABLE 8.1

Estimated Logistic Regression Model for Arthritis

Predictor ^a	Category	\hat{B}	$se(\hat{B})$	t	$P(t_{56} > t)$
INTERCEPT	Constant	-2.753	0.138	-20.0	<0.01
GENDER	Male	-0.595	0.045	-13.34	<0.01
ED3CAT	<12 years	0.456	0.056	8.12	<0.01
	12 years	0.267	0.042	6.41	<0.01
AGE (years)	Continuous	0.047	0.002	22.11	<0.01

Source: 2006 HRS. $n = 18,375$.^a Reference categories for categorical predictors are: GENDER (female); ED3CAT (>12 years).**TABLE 8.2**

Estimates of Adjusted Odds Ratios in the Arthritis Model and 95% CIs for the Odds Ratios

Predictor ^a	Category	$\hat{\psi}$	$CI_{.95}(\psi)$
GENDER	Male	0.552	(0.505, 0.603)
ED3CAT	<12 years	1.558	(1.410, 1.766)
	12 years	1.306	(1.202, 1.420)
AGE	Continuous	1.050	(1.044, 1.053)

Source: 2006 HRS. $n = 18,375$.^a Reference categories for categorical predictors are: GENDER (female); ED3CAT (>12 years).

- The estimated odds of arthritis increase by a factor of $\hat{\psi} = 1.05$ for each additional year of age.

Note that for continuous predictors, the increment x to $x + 1$ can be a relatively small step on the full range of x . For this reason, analysts may choose to report odds ratios for continuous predictors for a greater increment in x . A common choice is to report the odds ratio for a one standard deviation increase in x . For example, the standard deviation of 2006 HRS respondents' age is approximately 10 years. The estimated odds ratio and the 95% CI for the odds ratio associated with a one standard deviation increase in age are computed as follows:

$$\begin{aligned}\hat{\psi}_{10yrs} &= e^{\hat{B}_4 \cdot 10} = e^{0.047 \times 10} = \exp(0.047 \times 10) = 1.60 \\ CI_{.95}(\psi_{10yrs}) &= (\exp(\hat{B}_4 \times 10 - t_{56,0.975} \times 10 \times se(\hat{B}_4)), \\ &\quad \exp(\hat{B}_4 \times 10 + t_{56,0.975} \times 10 \times se(\hat{B}_4))) \\ &= \exp(0.47 \pm 2.003 \times 10 \times 0.002) = (1.54, 1.67).\end{aligned}$$

When interactions between predictor variables are included in the specified model, analysts need to carefully consider the interpretation of the parameter estimates. For example, consider an extension of the 2006 HRS model for the logit of the probability of arthritis that includes the two-way interaction between education level and gender. The estimated coefficients and standard errors for this extended model reported by Stata (using the command below) are shown in Table 8.3.

```
svy: logit arthritis male ib3.edcat3 kage c.male#ib3.edcat3
```

Note that when the interaction between gender and education is added to the model, the parameter estimates for age, gender, and less than high school education change slightly, but the estimated parameter for high school education is substantially reduced, from $\hat{B}_{HS} = 0.267$ to $\hat{B}_{HS} = 0.177$. This is due to the fact that this parameter now represents the contrast in log-odds between high school education and greater than high school education for *females only* (the reference level for gender), and is combined with the parameter for the (12 years \times Male) product term to define the same contrast in log-odds for males. The parameter associated with the product term therefore represents a *change* in this contrast for males relative to females.

Apparently linked to this decrease in “main effect” size for high school education is a significant positive interaction between a 12th grade education and male gender. The estimated change in log-odds for males with 12th grade education relative to males with greater than 12th grade education is thus computed as $0.177 + 0.201 = 0.378$. (Although the results are not shown, the two-way interaction between GENDER and AGE was tested in a separate model and was not significant.)

TABLE 8.3

Estimated Logistic Regression Model for Arthritis, Including the Two-Way Interaction between Education and Gender

Predictor ^a	Category	\hat{B}	$se(\hat{B})$	t	$P(t_{42} > t)$
INTERCEPT	Constant	-2.728	0.135	-20.22	<0.01
GENDER	Male	-0.659	0.061	-10.81	<0.01
ED3CAT	<12 years	0.454	0.063	7.20	<0.01
	12 years	0.177	0.050	3.56	<0.01
AGE	Continuous	0.047	0.002	22.11	<0.01
ED3CAT \times	<12 years \times Male	0.004	0.102	0.04	0.970
GENDER	12 years \times Male	0.201	0.087	2.20	0.026

Source: 2006 HRS. $n = 18,375$.

^a Reference categories for categorical predictors are: GENDER (female); ED3CAT(>12 years).

TABLE 8.4

Covariate Patterns, Logits, and Odds Ratios for the Arthritis Model

Pattern (j)	Gender	Education	Age	Logit: z_j	Odds Ratio ^a
1	Male	<HS	65	0.190	0.82
2	Male	HS	65	0.111	0.75
3	Male	>HS	65	-0.267	0.52
4	Female	<HS	65	0.845	1.57
5	Female	HS	65	0.569	1.19
6	Female	>HS	65	0.392	1.00

^a Relative to joint reference of Female with > High School Education.

To explore the impact of the interaction of GENDER and ED3CAT on the estimated logits and odds ratios, assume that AGE is fixed at 65 years. Consider the possible patterns of covariates shown in columns (2)–(4) of **Table 8.4**. To estimate the value of the logit for each covariate pattern, the estimated coefficients in **Table 8.3** are applied to the corresponding values of the predictor variables:

$$\begin{aligned} \text{logit}(\pi(x)) = & -2.728 - 0.659I_{\text{Male}} + 0.454I_{\text{Educ},<\text{HS}} + 0.177I_{\text{Educ},\text{HS}} + 0.047X_{\text{Age}(yrs)} \\ & + 0.004(I_{\text{Male}} \times I_{\text{Educ},<\text{HS}}) + 0.201(I_{\text{Male}} \times I_{\text{Educ},\text{HS}}). \end{aligned}$$

Table 8.4 shows the estimated logits for the six unique covariate patterns (with age fixed at 65). To evaluate the ratio of odds of arthritis for men and women of different education levels, a general technique to compare the estimated odds for two different patterns of covariates is used. Consider two “patterns” of covariate values x_1 and x_2 . Using the example in **Table 8.4**, x_1 might be pattern 1, 65-year-old males with <HS education, and x_2 might be the reference category for the GENDER \times ED3CAT interaction, which would be 65-year-old women with >HS education. To obtain the estimated odds ratio that compares x_1 with x_2 , the following five steps are required:

1. Based on the estimated model, compute the values of the logit function for the two sets of covariates: $\text{logit}_1 = \sum_{j=0}^p \hat{B}_j x_{1j}$; $\text{logit}_2 = \sum_{j=0}^p \hat{B}_j x_{2j}$. These are shown for the six example covariate patterns in **Table 8.4**. For example, $\text{logit}_1 = 0.190$ and $\text{logit}_2 = 0.392$ for the two patterns chosen for this illustration.
2. Compute the difference between the two logits, $\hat{\Delta}_{1:2} = \text{logit}_1 - \text{logit}_2 = 0.190 - 0.392 = -0.202$.
3. Exponentiate the difference in the two logits to estimate the odds ratio comparing x_1 with x_2 , $\hat{\psi}_{1:2} = e^{\hat{\Delta}_{1:2}} = e^{-0.202} = 0.817$.
4. To reflect the uncertainty in the estimated odds ratios, the estimates should be accompanied by an estimated CI. The CI of an

odds ratio comparing two arbitrary covariate patterns, x_1 and x_2 , takes the general form of expression (8.23) above. The standard error estimate requires the derivation of the standard error of the difference in the two logits:

$$se(\hat{\Delta}_{1:2}) = \sqrt{\sum_{j=0}^p (x_{1j} - x_{2j})^2 var(\hat{B}_j) + 2 \sum_{j < k} (x_{1j} - x_{2j})(x_{1k} - x_{2k}) cov(\hat{B}_j, \hat{B}_k)}. \quad (8.24)$$

Note that any common values for x_j in logit_1 and logit_2 can be ignored in evaluating this standard error. The calculation of the standard error of the difference in logits requires the values of $\text{var}(\hat{B}_j)$ and $\text{cov}(\hat{B}_j, \hat{B}_k)$. These may be obtained in Stata by issuing the `estat vce` command after the model has been estimated.

5. Exponentiate the CI limits for the difference in logits to estimate the 95% CI for the odds ratio: $CI(\psi_{1:2}) = \exp[\hat{\Delta}_{1:2} \pm t_{df=975, 0.975} \cdot se(\hat{\Delta}_{1:2})]$.

Assuming that the sample design variables have already been specified using the `svyset` command, we include Stata commands below that facilitate the execution of these five steps, along with the Stata output generated:

* First, use svy: logit to estimate the model.

svy: logit arthritis male ib3.edcat3 kage c.male#ib3.edcat3

```
* men age 65 with < HS education vs. women age 65 with > HS
* education: odds ratio computation

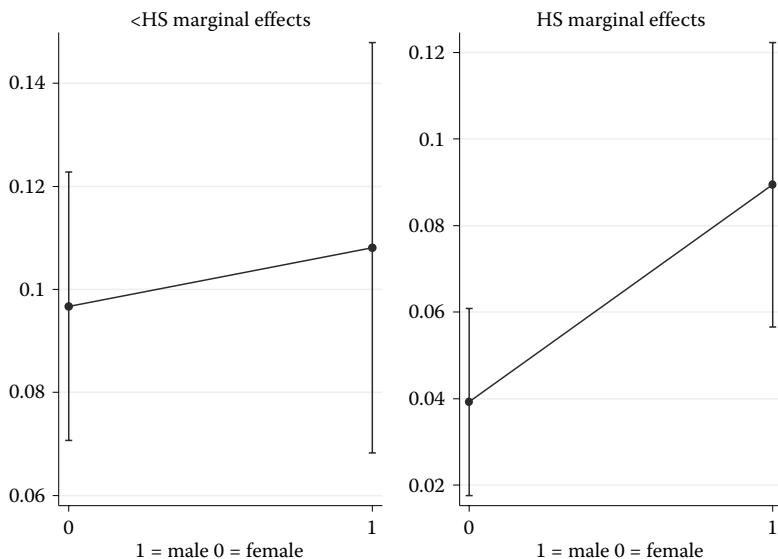
nlcom exp((65*_b[kage] + 1*_b[male] + 1*_b[1.edcat3] ///
+ 0*_b[2.edcat3] + 1*_b[1.edcat3#c.male] ///
+ 0*_b[2.edcat3#c.male] + _b[_cons]) - (65*_b[kage] ///
+ 0*_b[male] + 0*_b[1.edcat3] + 0*_b[2.edcat3] + ///
0*_b[1.edcat3#c.male] + 0*_b[2.edcat3#c.male] + _b[_cons]))
```

	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
_nl_1	.8168955	.0729445	11.20	0.000	.6739268 .9598642

We see above how the `nlcom` command can be used to estimate the odds ratio of interest (referring to the parameter estimates saved in memory from the most recent fitted model) and compute a 95% CI for the odds ratio. We would conclude (based on the 95% CI for this odds ratio that does not include a value of 1) that men aged 65 with less than high school education have significantly reduced odds of arthritis compared with women aged 65 with more than high school education (the estimated odds are about 18% lower).

The technique described above for estimating odds ratios applies generally to *any* observed patterns of covariates x_1 and x_2 . The final column in [Table 8.4](#) shows the estimated odds ratios comparing each of the six covariate patterns based on the estimated logistic regression model including the interaction of gender and education level. Holding age constant at 65 years, the coding of gender (female reference) and education level (>High School is the reference) results in 65-year-old women with >HS education as the natural reference group.

A convenient way to visualize and interpret significant interactions using Stata is to plot *average marginal effects* of one covariate as a function of another covariate, as shown in [Figure 8.3](#). These effects show changes in the *marginal predicted values* of the binary dependent variable for one category of a predictor of interest (e.g., education) relative to the reference category, separately for the levels of the other variable involved in the interaction (e.g., gender). Marginal predicted values are computed by default in Stata by (1) setting all cases in the analytic sample to have the same value on the covariate of interest (e.g., fixing all cases to have the same value of education), and then (2) computing predicted values for each case based on the fitted model and averaging the predictions. This can also be done separately for different subpopulations (e.g., males and females) when examining interactions. In addition to computing average marginal effects based on these marginal predicted values, one can also compute design-adjusted standard errors of the average marginal effects by using the *delta method*, which is similar in principle to the TSL approximation method described in [Chapter 3](#). Computing these marginal predicted values, computing average marginal effects, and then

**FIGURE 8.3**

Plots of estimated marginal effects of less than high school and high school education (relative to more than high school education) on the probability of arthritis for males and females separately. (From 2006 HRS.)

plotting the average marginal effects (in addition to CIs for the effects based on their standard errors) is facilitated by the `margins` and `marginsplot` postestimation commands in Stata.

We provide an example of using these commands below. First, after fitting the model above that includes the interaction between education and gender, we compute the average marginal effect of the second nonreference category of education (using the `dydx()` option), separately for males and females, and then plot the marginal effects using the `marginsplot` command. We then repeat this for the third nonreference category of education, and combine the plots:

```
* Fit model including interaction of gender and education.
svy: logit arthritis male ib3.edcat3 kage c.male#ib3.edcat3

* Compute marginal effects of less than high school
* education (vs. more than high school) on predicted
* probability of arthritis for males and females.
margins, dydx(1.edcat3) by(male)
marginsplot
graph save Graph "S:\edcat1.gph", replace

margins, dydx(2.edcat3) by(male)
marginsplot
```

```
graph save Graph "S:\edcat2.gph", replace
graph combine "S:\edcat1.gph" "S:\edcat2.gph"
```

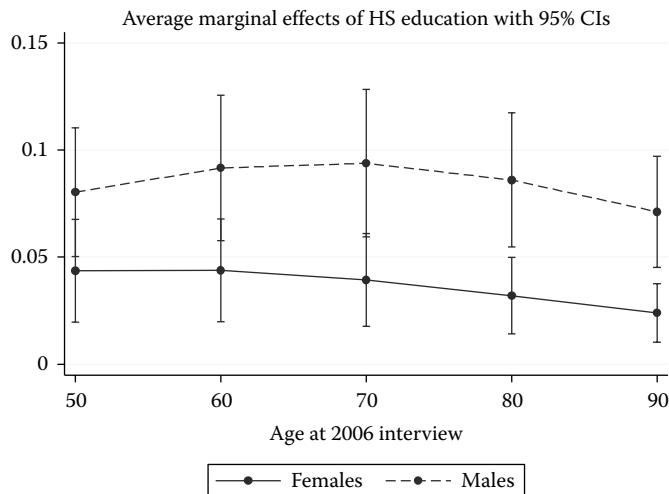
If one was looking at the average marginal effects corresponding to a one-unit change in the value of a continuous predictor, that variable would simply be included in the `dydx()` function. If one was looking to plot the effects of a categorical predictor as a function of selected values of a continuous predictor, one would use `at()` instead of `by()` in the commands above (see example below).

[Figure 8.3](#) shows the plots that result from running the commands above, which include 95% CIs for the average marginal effects by default. We see very clearly that the effect of high school education (vs. more than high school education) on the predicted probability of arthritis is much stronger for males than for females, while this is not the case for the effect of less than high school education. We recommend visualizing significant interactions in this way, not just when fitting logistic regression models but when fitting any types of regression models where significant interactions emerge. Stata makes it especially easy to do this using the commands illustrated above.

Finally, we emphasize to readers that the relationships of predictor variables with the expected value of the outcome in regression models where the expected value is a nonlinear function of the predictors (including logistic regression models) *depend on* the values of other covariates, *even if the model does not include interaction terms* (Ai and Norton, 2003). For this reason, when interpreting the relationships of a covariate with the predicted probability that a given survey variable is equal to 1, we recommend always plotting average marginal effects associated with that covariate (or with a given interaction) as a function of other covariates included in the model. This will allow the analyst to get a sense of whether the relationship of interest is robust to changing values of the other covariates included in the model. For example, given the significant interaction noted above, we can plot the average marginal effects of high school education (vs. more than high school education) for males and females separately at different possible values of age, looking at 10-year increments:

```
margins, dydx(2.edcat3) by(male) at(kage=(50(10)90))
marginsplot
```

The resulting plot of average marginal effects (in addition to 95% CIs for the effects) is displayed in [Figure 8.4](#), and shows how the difference in this effect between males and females does change slightly depending on a person's age, with the difference in this effect becoming larger as a function of age. Regardless, we see consistent evidence of this effect being larger for males than for females. We will consider additional examples of the use of these types of plots for interpretation in the next section.

**FIGURE 8.4**

Plots of estimated marginal effects of high school education (relative to more than high school education) on the probability of arthritis for males and females separately, considering different possible values of age. (From 2006 HRS.)

As mentioned in the Section 6.4.5 discussion of the relative risk statistics, logistic regression and other generalized models are often used with complex sample survey data to estimate the “risk” of an outcome (e.g., risk of diabetes, risk of crime victimization, risk of successfully graduating from college) as a function of the model covariates. In this “risk estimation” context, the analysis of average marginal effects (expressed as the change in the average probability of the outcome if the risk factor is present, given the specified covariate levels) is closely tied to the estimation of the *attributable fraction* (*AF*) of the outcome that is associated with a specific exposure to a risk factor covariate (Graubard et al., 2007). For example, an epidemiologist may use a logistic or Poisson regression model to study the risk of emphysema as a function of lifetime smoking status. Based on the risk model, the Stata margins and margin-splot commands illustrated above could be used to compute and display the average marginal effect for lifetime smoking behavior, that is, the change in the population average probability of developing emphysema associated with lifetime smoking versus no lifetime smoking. The AF for lifetime smoking is an estimate of the fraction of all incident cases of emphysema that would not occur if lifetime smoking behavior was eliminated from the population.

Heeringa et al. (2015) provide an in-depth review of best practices for estimating AFs from complex sample survey data and provide a general four step algorithm for: (1) estimating the logistic regression or Poisson risk model; (2) computing weighted estimates of the AF statistics; (3) using JRR and bootstrap methods to estimate design-based standard errors; and (4) applying special methods for constructing CIs for the AF population value (Greenland, 2004).

Analysts interested in a detailed review of AF estimation based on complex sample survey data are referred to this 2015 publication. An R function and documentation as well as SAS code showing how to implement these four steps in design-based estimation and inference for the AF statistic are available on the book web site.

8.7 Analysis Application

This section presents an example logistic regression analysis that follows the four general modeling stages described in Sections 8.3 through 8.6.

EXAMPLE 8.1: EXAMINING PREDICTORS OF A LIFETIME MDE IN THE NCS-R DATA

The aim of this example is to build a logistic regression model for the probability that an U.S. adult has been diagnosed (DSM-IV) with an MDE in their lifetime. The dependent variable is the NCS-R variable MDE, which takes a value of 1 for persons who meet lifetime criteria for major depression and 0 for all others. The following predictors are considered: AG4CAT (a categorical variable measuring age brackets, including 18–29, 30–44, 45–59, and 60+), SEX (1 = male, 2 = female), ALD (an indicator of any lifetime alcohol dependence), ED4CAT (a categorical variable measuring education brackets, including 0–11, 12, 13–15, and 16+ years), and MAR3CAT (a categorical variable measuring marital status, with values 1 = “married,” 2 = “separated/widowed/divorced,” and 3 = “never married”). The primary research question of interest is whether MDE is related to alcohol dependence after adjusting for the effects of the demographic factors listed above.

8.7.1 Stage 1: Model Specification

The analysis session begins by specifying the complex design features of the NCS-R sample in the Stata `svyset` command. Note that we specify the “long” or Part 2 NCS-R survey weight (NCSRWTLG) in the `svyset` command. This is due to the use of the alcohol dependence variable in the analysis, which was measured in Part 2 of the NCS-R survey. Recall that the NCS-R Part 2 questionnaire was only administered to a subsample of the NCS-R Part 1 respondents.

```
svyset seclustr [pweight = ncsrwtlg], strata(sestrat) ///
vce(linearized) singleunit(missing)
```

There are 42 sampling error strata and 84 sampling error computation units (two per stratum) in the NCS-R sampling error calculation model, resulting in 42 design-based degrees of freedom.

Following the recommendations of Hosmer et al., the model building begins by examining the bivariate associations of MDE with each of the potential predictor variables. Since the candidate predictors are all categorical variables, the bivariate relationship of each predictor with MDE is analyzed in Stata by using the svy: tab command and requesting row percentages (as discussed in [Chapter 6](#)).

```
svy: tab ag4cat mde, row se
svy: tab sex mde, row se
svy: tab ald mde, row se
svy: tab ed4cat mde, row se
svy: tab mar3cat mde, row se
```

[Table 8.5](#) presents the results of these bivariate analyses, including the Rao–Scott *F*-tests of association. The table also presents estimates of the percentages of each predictor category that received the lifetime MDE diagnosis, along with the linearized standard errors of these weighted estimates.

Based on these initial tests of association, all of the predictor variables appear to have significant bivariate associations with MDE, including ALD, the indicator of lifetime alcohol dependence, and all of the predictors appear to be good candidates for inclusion in the initial multivariate logistic regression model.

TABLE 8.5

Initial Bivariate Design-Based Tests of Association Assessing Potential Predictors of Lifetime Major Depressive Episode (MDE) Based on the NCS-R Adult Sample

Predictor	Rao–Scott <i>F</i> -Test ^a	Category	% with MDE (SE)
AG4CAT	$F(2.76,115.97) = 26.39$ $p < 0.01$	18–29	18.4% (0.9)
		30–44	22.9% (1.1)
		45–59	22.3% (1.3)
		60+	11.1% (1.0)
SEX	$F(1,42) = 44.83$ $p < 0.01$	Male	15.3% (0.9)
		Female	22.6% (0.7)
ALD	$F(1,42) = 120.03$ $p < 0.01$	Yes	45.2% (0.3)
		No	17.7% (0.7)
ED4CAT	$F(2.90,121.93) = 4.30$ $p < 0.01$	<12 years	16.3% (1.2)
		12 years	18.6% (0.8)
		13–15 years	21.3% (1.0)
		16+ years	19.7% (1.1)
MAR3CAT	$F(1.90,79.74) = 11.08$ $p < 0.01$	Married	17.3% (0.7)
		Previously	23.9% (1.5)
		Never	19.4% (1.2)

Source: NCS-R, $n = 5,692$.

^a See [Chapter 6](#) for more details on the derivation of this test statistic, which can be used to test the null hypothesis of no association between the predictor variable and the outcome variable (MDE).

8.7.2 Stage 2: Model Estimation

The next step in the Hosmer–Lemeshow model-building procedure is to fit the “initial” multivariate model, examining the main effects for all five predictors. Stata provides two commands for fitting the multivariate logistic regression model: `svy: logistic` and `svy: logit`. The default output for the `svy: logistic` command is estimates of adjusted odds ratios and 95% CIs for the adjusted odds ratios. Note the use of the `i.` modifier, which indicates those predictor variables that should be considered categorical in the logistic regression model. When using this modifier, indicator variables will be created for each of the categories of the predictors, and the indicator for the lowest-valued category will be omitted from the model (by default). To change this default, one can use the `ib#.` modifier, which sets the category with value # as the reference category. We use this to set the reference category of SEX to 2 (females).

```
svy: logistic mde i.ag4cat ib2.sex ald i.ed4cat ///
i.mar3cat
```

In `svy: logistic`, estimates of the parameters and standard errors for the logit model can be requested by using the `coef` option:

```
svy: logistic mde i.ag4cat ib2.sex ald i.ed4cat ///
i.mar3cat, coef
```

Stata users who wish to see the estimated logistic regression coefficients and standard errors may also use the companion program, `svy: logit`:

```
svy: logit mde i.ag4cat ib2.sex ald i.ed4cat i.mar3cat
```

Estimated odds ratios and 95% CIs can be generated in `svy: logit` by adding the `or` option:

```
svy: logit mde i.ag4cat ib2.sex ald i.ed4cat i.mar3cat, or
```

Other software systems (e.g., SAS PROC SURVEYLOGISTIC) will output both the estimated logistic regression coefficients (and standard errors) and the corresponding odds ratio estimates. (Readers should be aware that the `svy: logit` and `svy: logistic` commands differ slightly in the procedures for calculation of the standard errors for odds ratios.)

In each form of the Stata `svy: logistic` or `svy: logit` command, the dependent variable, MDE, is listed first, followed by the predictor variables (and their interactions, if applicable). Because the ALD variable is already coded as either 0 or 1, it does not require use of the `i.` modifier like the other categorical predictors.

TABLE 8.6

Estimated Logistic Regression Model for the Lifetime MDE Outcome (Output Generated by Using the svy: logit Command)

Predictor ^a	Category	\hat{B}	$se(\hat{B})$	t	$P(t_{42} > t)$
INTERCEPT		-1.583	0.121	-13.12	<0.001
AG4CAT	30–44	0.256	0.094	2.71	0.010
	45–59	0.206	0.092	2.26	0.029
	60+	-0.676	0.141	-4.78	<0.001
SEX	Male	-0.577	0.077	-7.48	<0.001
ALD	Yes	1.424	0.154	9.24	<0.001
ED4CAT	12	0.079	0.097	0.82	0.418
	13–15	0.231	0.093	2.48	0.017
	16+	0.163	0.111	1.47	0.148
MAR3CAT	Previously	0.486	0.085	5.69	<0.001
	Never	0.116	0.108	1.07	0.290

Source: NCS-R, $n = 5,692$, adjusted Wald test for all parameters: $F(10,33) = 28.07, p < 0.001$.

^a Reference categories for categorical predictors are: AG4CAT (18–29); SEX (female); ALD (no); ED4CAT (<12 years); MAR3CAT (married).

Tables 8.6 and 8.7 summarize the output generated by fitting the MDE logistic regression model. The initial model includes main effects for the chosen predictor variable candidates but at this point does not include any interactions between the predictors.

8.7.3 Stage 3: Model Evaluation

The adjusted Wald tests in Stata for the AG4CAT, ED4CAT, and MAR3CAT categorical predictors in this initial model are generated by using the `test` command:

```
test 2.ag4cat 3.ag4cat 4.ag4cat
test 2.mar3cat 3.mar3cat
test 2.ed4cat 3.ed4cat 4.ed4cat
```

Note that we do not request these multiparameter Wald tests for the SEX and ALD predictor variables, because they are represented by single indicator variables in the regression model and the overall Wald test for each predictor is equivalent to the t -test reported for the single estimated parameter for that predictor. Further, note in each of the `test` statements that we include the $K - 1$ indicator variables generated by Stata for each of the categorical predictors (e.g., `2.ag4cat`) when the `i.` modifier is used to identify categorical predictor variables. Stata users can find the names of these indicators in the Stata Results window once the model has been fitted. Table 8.8 provides

TABLE 8.7

Estimates of Adjusted Odds Ratios for the Lifetime MDE Outcome

Predictor ^a	Category	$\hat{\psi}$	95% CI for ψ
AG4CAT	30–44	1.29	(1.067, 1.562)
	45–59	1.23	(1.022, 1.479)
	60+	0.51	(0.383, 0.677)
SEX	Male	0.56	(0.480, 0.656)
ALD	Yes	4.15	(3.042, 5.668)
ED4CAT	12	1.08	(0.890, 1.316)
	13–15	1.26	(1.044, 1.519)
	16+	1.18	(0.941, 1.471)
MAR3CAT	Previously	1.63	(1.369, 1.932)
	Never	1.12	(0.903, 1.396)

Source: NCS-R, $n = 5,692$, adjusted Wald test for all parameters: $F(10,33) = 28.07$, $p < 0.001$.

^a Reference categories for categorical predictors are: AG4CAT (18–29); SEX (female); ALD (no); ED4CAT (<12 years); MAR3CAT (married).

the design-adjusted Rao–Scott F versions of the resulting Wald test statistics and associated p -values.

Two of the three design-adjusted Wald tests are significant at the 0.01 level. The exception is the Wald test for education [$F(3,40) = 2.13$, $p = 0.112$], which suggests that the parameters associated with education in this logistic regression model are not significantly different from zero and that education may not be an important predictor of lifetime MDE when adjusting for the relationships of the other predictor variables with the outcome. If the objective of the model-building process is the construction of a parsimonious model, education could probably be dropped as a predictor at this point. For the purposes of this illustration (and because of the marginal significance), we will retain education in the model moving forward.

TABLE 8.8

Design-Adjusted Rao–Scott F -Tests for the Parameters Associated with the Categorical Predictors in the Initial MDE Logistic Regression Model

Categorical Predictor	F -Test Statistic	$P(\mathcal{F} > F)$
AG4CAT	$F_{(3,40)} = 19.03$	<0.001
ED4CAT	$F_{(3,40)} = 2.13$	0.112
MAR3CAT	$F_{(2,40)} = 16.60$	<0.001

8.7.4 Stage 4: Model Interpretation/Inference

Based on the results in Tables 8.6 and 8.8, it appears that each of the predictors in the multivariate model has a significant (or marginally significant) relationship with the probability of MDE after adjusting for the relationships of the other predictor variables. Focusing on the primary predictor variable of interest, we see that the odds of having had an MDE at some point in the lifetime are multiplied by 4.15 when a person has had a diagnosis of alcohol dependence at some point in their lifetime, when adjusting for the relationships of age, sex, education, and marital status. Of course, this model does not allow for any kind of causal inference, given that time ordering of the events is not available in the NCS-R data set; we can, however, conclude that there is strong evidence of an association between the two disorders in this finite population when adjusting for other demographic covariates. We visualize the average marginal effects of alcohol dependence on the predicted probability of having a lifetime MDE for different possible age categories by executing the postestimation commands below and producing the plot shown in Figure 8.5.

```
margins, dydx(alcohol) by(ag4cat)
marginsplot
```

Figure 8.5 shows that alcohol dependence is expected to increase the probability of a lifetime major depressive episode by anywhere from 0.1 to 0.3, depending on the age category.

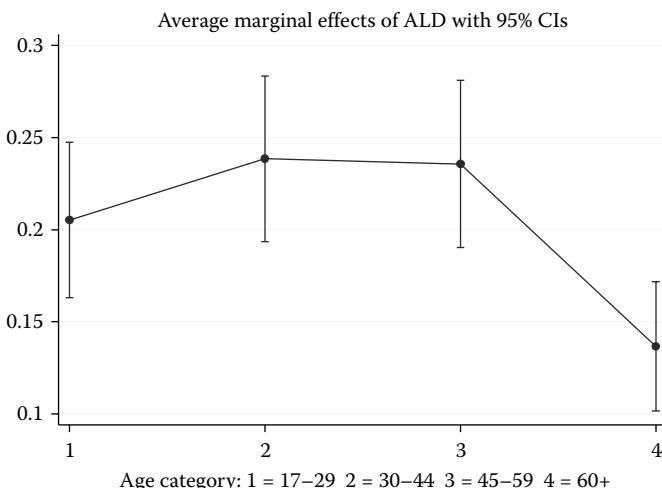


FIGURE 8.5

Plots of estimated average marginal effects of alcohol dependence on the probability of having a lifetime major depressive episode for different age categories.

We also note that relative to married respondents, respondents who were previously married have significantly higher (63% higher) odds of having had an MDE in their lifetime when adjusting for the other covariates. Further, middle-age respondents have significantly higher odds of lifetime MDE (relative to younger respondents), while older respondents and males have significantly reduced odds of lifetime MDE (again relative to younger respondents and females). Each of these effects could be visualized as a function of other covariates included in the model by using the margins and marginsplot commands demonstrated above.

Respondent age is represented in the model as four grouped categories of age. Including grouped categories for age (or recoded categories of any continuous predictor, more generally) in a logistic regression model will result in estimates of the expected contrasts in log-odds for respondents in each of the defined categories, relative to the reference category. Since the model parameters are estimated separately for each defined age group (with age 18–29 as the reference), the model will capture any nonlinearity of effect in the ordered age groupings. Inspecting the estimated coefficients and odds ratios for the grouped age categories in [Tables 8.6](#) and [8.7](#), it appears that there is significant nonlinearity in the effect of age on the probability of MDE. Relative to the 18–29-year-old group, the odds of MDE increase by factors of 1.29 (age 30–44) and 1.23 (age 45–59) for the middle age ranges but decrease by a factor of 0.51 in the age 60 and older group. Such nonlinear effects of age are common in models of human disorders, and are possibly attributable to normal processes of aging and selective mortality. If the example model was estimated with age (in years) as a continuous predictor variable, at this stage in the model-building process the analyst would reestimate the model including both the linear and quadratic terms for age.

At this stage in the model-building process, we have chosen to retain all of the candidate main effects. Next, we apply Archer and Lemeshow's (2006) design-adjusted test to assess the GOF of this initial model:

```
estat gof
```

The design-adjusted *F*-statistic reported in the Stata Results window is $F_{A-L}(9,34) = 1.23$, with a *p*-value of 0.31. This suggests that the null hypothesis that the model fits the data well is not rejected. We therefore have confidence moving forward that the fit of this initial model is acceptable. (Note: the estat gof command currently does not work if a subpop() option has been used to fit the model. A work-around is to fit the model using the if modifier instead of the subpop() option, but we would only recommend doing this if the conditional analysis that results does not arbitrarily delete sampled clusters. See [Chapter 4](#) for details.)

Next, we consider testing some scientifically relevant two-way interactions between the candidate predictor variables. For illustration purposes, we suppose that possible two-way interactions of sex with the other four covariates

measuring age, lifetime alcohol dependence, education, and marital status are of interest, if sex is posited by an NCS-R analyst as being a possible moderator of the relationships of these other four covariates with lifetime MDE. We fit a model including these two-way interactions in Stata using the following command:

```
svy: logistic mde ag4cat ib2.sex ald i.ed4cat i.mar3cat ///
i.ag4cat#ib2.sex ib2.sex#c.ald i.ed4cat#ib2.sex ///
i.mar3cat#ib2.sex, coef
```

Note how the interactions are specified in this command: after all of the predictor variables are listed, a # sign is used to specify two-way interactions of the relevant variables, and any variables not indicated as categorical need to be specified as c. variables (or continuous variables) in the interaction terms (Stata will assume that variables included in the interaction terms are categorical by default). [Table 8.9](#) presents the estimates of the regression parameters in this model generated by executing the command above in Stata.

At this point, the statistical question is whether these two-way interactions are making a significant additional contribution or improvement to the fit of this model to the NCS-R data. That is, are any of the parameters associated with the two-way interaction terms significantly different from 0? We can test this hypothesis by once again using design-adjusted Wald tests. The terms in the `test` commands below can be easily determined from the Stata Results window:

```
test 2.ag4cat#1.sex 3.ag4cat#1.sex 4.ag4cat#1.sex
test 1.sex#c.ald
test 2.ed4cat#1.sex 3.ed4cat#1.sex 4.ed4cat#1.sex
test 2.mar3cat#1.sex 3.mar3cat#1.sex
```

The results of these four Wald *F*-tests are displayed in [Table 8.10](#). Based on these results, we fail to reject the null hypotheses for all four of the tests, suggesting that these two-way interactions are actually not making a significant contribution to the fit of the model. We therefore do not consider these two-way interactions any further, and would proceed with making inferences based on the estimates from the model presented in [Table 8.6](#).

We also illustrate calculation of the design-adjusted AIC that has been implemented in the `survey` package of R (Lumley and Scott, 2015) for comparing the fits of competing models. First, we import the Stata data set into a data frame object using the `read.dta()` function of the `foreign` package, and keep only those cases given the longer NCS-R interview (as no missing data are allowed on the design variables). Then, we load the newest version of the contributed `survey` package, declare an NCS-R design object containing the complex sampling features and the survey data, fit the MDE models

TABLE 8.9

Estimated Logistic Regression Model for Lifetime MDE, Including Two-Way Interactions of the Other Predictor Variables with SEX

Predictor ^a	Category	\hat{B}	$se(\hat{B})$	t	$P(t_{42} > t)$
INTERCEPT	Constant	-1.600	0.134	-11.94	<0.001
AG4CAT	30–44	0.220	0.114	1.94	0.059
	45–59	0.215	0.102	2.09	0.042
	60+	-0.646	0.175	-3.68	0.001
SEX	Male	-0.546	0.357	-1.53	0.134
ALD	Yes	1.553	0.211	7.36	<0.001
ED4CAT	12	0.131	0.084	1.56	0.126
	13–15	0.297	0.117	2.54	0.015
	16+	0.242	0.152	1.59	0.118
MAR3CAT	Previously	0.418	0.111	3.78	<0.001
	Never	0.017	0.130	0.13	0.894
AG4CAT × SEX	30–44 × Male	0.097	0.201	0.48	0.633
	45–59 × Male	0.003	0.213	0.01	0.990
	60+ × Male	-0.038	0.302	-0.13	0.901
ALD × SEX	Yes × Male	-0.200	0.242	-0.83	0.413
ED4CAT × SEX	12 × Male	-0.138	0.271	-0.51	0.614
	13–15 × Male	-0.169	0.269	-0.63	0.534
	16+ × Male	-0.194	0.344	-0.56	0.576
MAR3CAT × SEX	Previously × Male	0.182	0.208	0.88	0.385
	Never × Male	0.232	0.212	1.09	0.280

Source: NCS-R. $n = 5,692$, adjusted Wald test for all parameters: $F(19,24) = 17.15$, $p < 0.001$.

^a Reference categories for categorical predictors are: AG4CAT (18–29 years); GENDER (female); ALD (no); ED4CAT(<12 years); MAR3CAT (married); SEX(female).

TABLE 8.10

Design-Adjusted Wald Tests of First-Order Interactions of Sex and Other Categorical Predictors in the MDE Logistic Regression Model

Interaction Term	F-Test Statistic	$P(F > F)$
AG4CAT × SEX	$F_{(3,40)} = 0.25$	0.863
ALD × SEX	$F_{(1,42)} = 0.68$	0.413
ED4CAT × SEX	$F_{(3,40)} = 0.13$	0.944
MAR3CAT × SEX	$F_{(2,41)} = 0.77$	0.472

without and with the interactions, and compute the design-adjusted AIC values for each of the models:

```

library(foreign)
ncsr <- read.dta("S:\\chapter_exercises_ncsr.dta")

ncsr$racec <- factor(ncsr$racecat, levels = 1:4, labels
=c("Other", "Hispanic", "Black", "White"))
ncsr$marcatc <- factor(ncsr$mar3cat, levels = 1:3, labels
=c("Married", "Previously Married", "Never Married"))
ncsr$edcatc <-factor(ncsr$ed4cat, levels = 1:4, labels
=c("0-11", "12", "13-15", "16+"))
ncsr$sexc <- factor(ncsr$sex, levels = 1:2,
labels=c("Male", "Female"))
ncsr$agcatc <- factor(ncsr$ag4cat, levels = 1:4,
labels=c("18-29", "30-44", "45-59", "60+"))

ncsr.lg <- ncsr[!is.na(ncsr$ncsrwtlg),]

library(survey)

# design object
ncsrsrvyp2 <- svydesign(strata=~sestrat, id=~seclustr,
weights=~ncsrwtlg, data=ncsr.lg, nest=T)
# fit first model
ex81 <- svyglm(mde ~ factor(agcatc) + factor(sexc) + ald +
factor(edcatc) + factor(marcatc), family=quasibinomial,
design=ncsrsrvyp2)
# compute design-adjusted AIC
AIC(ex81)

# fit model with interactions
ex81.1 <- svyglm(mde ~ factor(agcatc) + factor(sexc) + ald +
factor(edcatc) + factor(marcatc) +
factor(sex):factor(agcatc) + factor(sexc):ald +
factor(sexc):factor(edcatc) + factor(sexc):factor(marcatc),
family=quasibinomial, design=ncsrsrvyp2)
# compute design-adjusted AIC
AIC(ex81.1)

```

The design-adjusted AIC for the first model is 5288.08, while the design-adjusted AIC for the second model is 5303.89. We would therefore select the first model as having a better fit given the number of parameters being estimated. We can also consider a design-adjusted likelihood ratio test comparing the fits of these two models (which is also only currently available in the *survey* package of R):

```
# design-adjusted Likelihood Ratio Test
anova(ex81, ex81.1, test="Chisq", method="LRT")

Working (Rao-Scott) LRT for factor(agcatc):factor(sex)
factor(sexc):ald factor(sexc):factor(edcatc)
factor(sexc):factor(marcatc)
  in svyglm(formula = mde ~ factor(agcatc) + factor(sexc) +
ald + factor(edcatc) + factor(marcatc) +
factor(sex):factor(agcatc) +
  factor(sexc):ald + factor(sexc):factor(edcatc) +
factor(sexc):factor(marcatc),
family = quasibinomial, design = ncsrsvyp2)
Working 2logLR = 3.412191 p = 0.90812
(scale factors: 3 1.5 1.1 0.84 0.78 0.65 0.57 0.34 0.23)
```

We see from the result of the design-adjusted likelihood ratio test ($p = 0.90812$) that we would fail to reject the (smaller) nested model that does not include the interactions as the preferable model. Using multiple approaches that account for the complex sampling features, we do not have any evidence of the interactions improving the fit of this model.

8.8 Comparing the Logistic, Probit, and C-L-L GLMs for Binary Dependent Variables

This chapter has focused on logistic regression techniques for modeling $\pi(x)$ for a binary dependent variable. As discussed in Section 8.2, alternative GLMs for a binary dependent variable may be estimated using the probit or C-L-L link function. In discussing these alternative GLMs, we noted that inferences derived from logistic, probit, and C-L-L regression models should generally be consistent.

To illustrate this claim, consider the results in [Table 8.11](#) for a side-by-side comparison of estimated logistic, probit, and C-L-L regression models. The example used for this comparison is a model of the probability that a U.S. adult is alcohol dependent (ALD). The data are from the NCS-R long interview (or Part 2 of the survey) and each model includes the same demographic main effects considered in Section 8.7 for the model of MDE: SEX, AG4CAT, ED4CAT, and MAR3CAT. The Stata commands for the estimation of the three models follow:

```
svy: logit ald i.ag4cat ib2.sex i.ed4cat i.mar3cat
test 2.ag4cat 3.ag4cat 4.ag4cat
test 2.mar3cat 3.mar3cat
test 2.ed4cat 3.ed4cat 4.ed4cat
```

```

svy: probit ald i.ag4cat ib2.sex i.ed4cat i.mar3cat
test 2.ag4cat 3.ag4cat 4.ag4cat
test 2.mar3cat 3.mar3cat
test 2.ed4cat 3.ed4cat 4.ed4cat

svy: cloglog ald i.ag4cat ib2.sex i.ed4cat i.mar3cat
test 2.ag4cat 3.ag4cat 4.ag4cat
test 2.mar3cat 3.mar3cat
test 2.ed4cat 3.ed4cat 4.ed4cat

```

Table 8.11 presents a summary of the estimated coefficients, standard errors, and p -values for simple hypothesis tests of the form $H_0: B_j = 0$. **Table 8.12** presents the results for the Wald tests of the overall age, education, and marital status effects. Note that although the coefficients and standard errors for the

TABLE 8.11

Comparison of Logistic, Probit, and C-L-L Models of Alcohol Dependency in U.S. Adults

Predictor ^a	Category	Logistic			Probit			C-L-L		
		\hat{B}	$se(\hat{B})$	p	\hat{B}	$se(\hat{B})$	p	\hat{B}	$se(\hat{B})$	p
Intercept		-3.124	0.225	<0.01	-1.719	0.105	<0.01	-3.148	0.218	<0.01
SEX	Male	0.997	0.119	<0.01	0.471	0.056	<0.01	0.965	0.115	<0.01
AG4CAT	30–44	0.146	0.178	0.416	0.065	0.084	0.444	0.143	0.171	0.408
	45–59	-0.051	0.144	0.726	-0.034	0.067	0.609	-0.045	0.140	0.748
	60+	-1.120	0.212	<0.01	-0.531	0.093	<0.01	-1.083	0.209	<0.01
ED4CAT	12 years	-0.268	0.194	0.173	-0.124	0.095	0.200	-0.260	0.185	0.167
	13–15 years	-0.264	0.176	0.141	-0.124	0.085	0.152	-0.256	0.169	0.137
	16+ years	-0.736	0.197	<0.01	-0.339	0.092	<0.01	-0.713	0.190	<0.01
MAR3CAT	Previously	0.517	0.142	<0.01	0.255	0.069	<0.01	0.494	0.136	<0.01
	Never	0.065	0.169	0.0701	0.039	0.077	0.616	0.060	0.164	0.713

Source: NCS-R. $n = 5,692$.

^a Reference categories for categorical predictors are: AG4CAT (60+ years); SEX (female); ED4CAT(<12 years); MAR3CAT (married).

TABLE 8.12

Design-Adjusted Wald Tests of Categorical Predictors in the ALD Models

Categorical Predictor	Wald F-Test Statistic (p -Value = $P(F > F)$)		
	Logistic	Probit	C-L-L
AG4CAT	$F_{(3,40)} = 12.06$ (<0.001)	$F_{(3,40)} = 15.26$ (<0.001)	$F_{(3,40)} = 11.52$ (<0.001)
ED4CAT	$F_{(3,40)} = 4.80$ (0.006)	$F_{(3,40)} = 4.79$ (0.006)	$F_{(3,40)} = 4.77$ (0.006)
MAR3CAT	$F_{(2,41)} = 6.54$ (0.003)	$F_{(2,41)} = 6.66$ (0.003)	$F_{(2,41)} = 6.50$ (0.004)

probit model show the expected difference in scale from those of the logistic and C-L-L models, the three models produce similar p -values for the test of each parameter and would not lead to significant differences in inferences concerning the effects of the individual parameters. Given the similarity in these results, we recommend using the logit model for general applications. Faraway (2016) points out three advantages of this approach: simpler mathematical formulation of the models, ease of interpretation via odds ratios, and easier analysis of retrospectively sampled data.

EXERCISES

- 8.1 Consider what changes during logistic regression analysis when analyzing complex sample survey data, as compared to data assumed to be collected using a simple random sample. With that in mind, answer the following questions:
- Why is MLE not appropriate for logistic regression using data derived from a complex sample design? What method is used instead and why is this needed?
 - What are the model-building steps used when estimating logistic, probit, or C-L-L models? Are they different than those covered in [Chapter 7](#) (linear regression)?
 - List three methods used to evaluate logistic model fit and explain how each helps in evaluation of model fit. What strategy might you employ if your software of choice does not include any design-based diagnostic tests, such as ROC curves?
- 8.2 Question 8.2 extends an analysis from [Chapter 6](#) where we examined the relationship between gender and satisfaction with life, using the ESS6 Russian Federation data set (see the ASDA web site to download the data). This question adds to the previous analysis by predicting a binary variable representing high satisfaction with life (HIGH_SAT, 1 = Yes, 0 = No), with age, gender, an indicator of very good health, and marital status, using design-based logistic regression (with the TSL variance estimation method). Using a software package of your choosing, answer the following questions:
- First, create an indicator variable of high satisfaction with life called HIGH_SAT using the STFLIFE variable coded so that 1 = (STFLIFE = 9 OR 10), 0 = (0 <= STFLIFE <= 8), and missing values are set to system missing in your software.
 - Create an indicator of very good health called GOOD_HEALTH. Code this as GOOD_HEALTH = 1 (YES) if the variable HEALTH = 1, GOOD_HEALTH = 0 if HEALTH is equal to (2,3,4,5), and GOOD_HEALTH = . if HEALTH is any other value,

including missing. Examine the distribution of the HEALTH variable. Based on this distribution, why is it important to collapse some of the cells in the HEALTH variable prior to performing a logistic regression analysis?

- c. Using logistic regression models that account for the complex sample design variables and the survey weight, perform bivariate tests of the associations between HIGH_SAT and each predictor variable mentioned above: AG4CAT, GNDR, MAR3CAT, and GOOD_HEALTH. Prepare a table similar to [Table 8.5](#) and identify which predictors are retained when using $p < 0.25$ as a cutoff.
 - d. Fit a “preliminary” model with the retained predictors from part c. Make sure to use the design variables and the survey weight for design-based variance estimation. Based on these results, which predictors will you retain for the “final” model?
 - e. Fit the “final” model with main effects and the two-way interactions of very good health (GOOD_HEALTH) and each additional predictor in your “final” model. Prepare a table similar to [Table 8.9](#), and use these results to support your decision to either include or exclude the two-way interaction terms. What predictors will remain in your final model?
 - f. Using your “final” model from part e., prepare a summary table similar to [Table 8.11](#) (with just the logistic regression part) and write a short discussion (1–2 paragraphs) describing the results of your analyses. Make sure to interpret the estimated coefficient for each predictor, and discuss the overall approach used (method of estimation, method of variance estimation) to incorporate the complex sample design features.
 - g. To illustrate how one might use your estimated model in practice, include a detailed computation of the predicted probability of having high satisfaction in life for someone with a specified set of values on the covariates included in the model. Clearly state the set of values and explain what the results mean.
- 8.3 Fit a logistic regression model to the ESS6 Russian Federation data, where the probability of having voted in the last election is predicted by gender and marital status, among the subpopulation of those aged 25–35 (young adult voters). Follow these steps:
- a. Prior to fitting the model, create a subpopulation indicator called AGE25_35 that is equal to 1 if $25 \leq \text{AGEA} \leq 35$, and 0 otherwise (if AGEA is not missing). Perform a cross-tabulation analysis to ensure that this variable is set to 1 only if age is 25–35, inclusive, and zero otherwise. What is the unweighted subpopulation sample size, and what percentage of respondents fall into this subpopulation?

- b. Fit a logistic model with having voted in the last election as a binary outcome, using an *unconditional* (rather than conditional) approach with the subpopulation indicator created in part a, and examine the significance of the predictors gender (GNDR) and marital status (MARCAT, use MARCAT = 1 or MARRIED as the reference group). Answer these questions:
- Why is the unconditional approach important for correct subpopulation estimation ([Chapter 4](#))? What is the risk of using a conditional or “subsetting” approach?
 - Are both gender and marital status significant predictors of having voted within the subpopulation of interest? Provide statistical support for your conclusions.
 - Prepare a table similar to [Table 8.6](#) and discuss/interpret your findings. Be sure to state that the results are for the subpopulation of interest and that a proper unconditional approach was used for subpopulation analysis.

8.4 Question 8.4 focuses on interpretation of logistic regression results with main effects and a significant interaction term. The table in part a. (below) presents results from a logistic regression model where the probability of having alcohol dependence during the lifetime (1 = Yes, 0 = No) is regressed on gender (SEX, 1 = M, 2 = F) and an indicator of being age 45 and older, plus the interaction of these two terms. The NCS-R data is used in this example and complex sample design features and the Part 2 weight are incorporated in the analysis through use of the correct statements in SAS PROC SURVEYLOGISTIC:

```
proc surveylogistic data=ncsr ;
strata sestrat ; cluster seclustr ; weight ncsrwtlg ;
class sex (ref='F') /param=ref ;
model ald (event='1')= sex age45p sex*age45p ;
format sex sf. ;
run ;
```

- a. Estimated Logistic Regression Model for Lifetime Alcohol Dependence

Parameter	Estimate	SE	t-Value	Pr > t
Intercept	-3.0588	0.1063	-28.77	<0.0001
Male	0.6948	0.1240	5.60	<0.0001
Age 45+	-0.9572	0.1842	-5.20	<0.0001
Age 45+ × Male	0.7655	0.2358	3.25	0.0023

Source: NCS-R, $n = 5,692$, adjusted Wald test for all parameters: $F(3,42) = 21.85$, $p < 0.0001$. Reference groups: female and those aged 44 and younger. (Output generated by SAS PROC SURVEYLOGISTIC.)

- b. Based on the results from the part (a) table, prepare a short paragraph (as for publication) interpreting the results provided. Make sure to discuss what the main effects and the interaction term now mean in the presence of the interaction term.

9

Generalized Linear Models for Multinomial, Ordinal, and Count Variables

9.1 Introduction

[Chapter 8](#) covered generalized linear models (GLMs) for survey variables that are measured on a binary or dichotomous scale. The aim of this chapter is to introduce generalized linear modeling techniques for three other types of dependent variables that are common in survey data sets: *nominal categorical variables*, *ordinal categorical variables*, and *counts* of events or outcomes. [Chapter 8](#) laid the foundation for generalized linear modeling, and this chapter will emphasize specific methods and software applications for three principal methods. Section 9.2 will introduce the “baseline” *multinomial logit regression model* for a survey variable with three or more nominal response categories. The *cumulative logit model* for dependent variables that are measured on an ordinal scale will be covered in Section 9.3. Regression methods for dependent variables that are counts (i.e., number of events, attributes, etc.), including *Poisson regression models* and *negative binomial regression models*, are presented in Section 9.4. Stata software will be used to illustrate the applications of these methods, but the reader is encouraged to visit the companion web site for this book to find each example replicated in the other major software systems that support these advanced modeling procedures.

9.2 Analyzing Survey Data Using Multinomial Logit Regression Models

9.2.1 Multinomial Logit Regression Model

The *multinomial logit regression model* is the natural extension of the simple binary logistic regression model to survey responses that have three or more distinct categories. This technique is most appropriate for survey variables with nominal response categories; we present examples of these variables

(a) NHANES HUQ.040

What kind of place do you go to most often: is it a clinic, doctor's office, emergency room, or some other place?

1. CLINIC OR HEALTH CENTER.....
2. DOCTOR'S OFFICE OR HMO.....
3. HOSPITAL EMERGENCY ROOM.....
4. HOSPITAL OUTPATIENT DEPARTMENT...
5. SOME OTHER PLACE.....
6. REFUSED.....
7. DON'T KNOW.....

(b) NCS-R EM7.1

What about your current employment situation as of today—are you?

1. EMPLOYED.....
2. SELF-EMPLOYED.....
3. LOOKING FOR WORK; UNEMPLOYED.....
4. TEMPORARILY LAID OFF.....
5. RETIRED.....
6. HOMEMAKER.....
7. STUDENT.....
8. MATERNITY LEAVE.....
9. ILLNESS/SICK LEAVE.....
10. DISABLED.....
11. OTHER (SPECIFY).....

FIGURE 9.1

Survey questions with multinomial response categories.

from the National Health and Nutrition Examination Survey (NHANES) and the National Comorbidity Survey Replication (NCS-R) in [Figure 9.1](#). It is common practice in surveys to use a fairly detailed set of response categories to code the respondent's answer and then recode the multiple categories to a smaller but still scientifically useful set of nominal groupings. For example, the NCS-R public-use data set contains a recoded labor force status variable, WKSTAT3, which combines the 11 questionnaire responses for current work force status into three grouped categories: 1 = Employed (EMP); 2 = Unemployed (UN); and 3 = Not in the labor force (NLF). The multinomial logit regression model is ideally suited for multivariate analysis of dependent variables like WKSTAT3.

Multinomial logit regression may also be applied to survey variables measured on Likert-type scales (e.g., 1 = strongly agree, ..., 5 = strongly disagree) or other ordered categorical response scales (e.g., self-rated health status: 1 = excellent, ..., 5 = poor), but the cumulative logit regression model covered in Section 9.3 may be the more efficient technique for modeling such ordinal dependent variables.

To understand the multinomial logit regression model for a dependent variable y with K nominal categories, assume that category $y = 1$ is chosen as

the *baseline category*. Multinomial logit regression is a method of simultaneously estimating a set of $K - 1$ simple logistic regression models that model the odds of being in category $y = 2, \dots, K$ versus the baseline category $y = 1$. Consider the example of the NCS-R recoded variable for labor force status, WKSTAT3, with three nominal categories: 1 = employed (EMP); 2 = unemployed (UN); 3 = not in the labor force (NLF). To fit the multinomial logit regression model to this “trinomial” dependent variable, two *generalized logits* are needed:

$$\begin{aligned}\text{logit}(\pi(\text{"UN"} | \mathbf{x})) &= \text{logit}(\pi_2) = \ln\left(\frac{\pi(y = 2 | \mathbf{x})}{\pi(y = 1 | \mathbf{x})}\right) = B_{2:0} + B_{2:1}x_1 + \dots + B_{2:p}x_p. \\ \text{logit}(\pi(\text{"NLF"} | \mathbf{x})) &= \text{logit}(\pi_3) = \ln\left(\frac{\pi(y = 3 | \mathbf{x})}{\pi(y = 1 | \mathbf{x})}\right) = B_{3:0} + B_{3:1}x_1 + \dots + B_{3:p}x_p.\end{aligned}\quad (9.1)$$

A natural question to ask at this point is, “Is it possible to simply estimate the multinomial logit regression model as a series of binary logistic regression models that consider only the response data for two categories at a time?” Strictly speaking, the answer is no. The parameter estimates for what Agresti (2012) labels the “separate-fitting” approach will be similar but not identical to those for simultaneous estimation of the multinomial logits. Standard errors for the former will be greater than those for the simultaneous estimation and only the latter yields the full variance–covariance matrix that is needed to test hypotheses concerning the significance or equivalence of parameters across the estimated logits. Fortunately, almost all software systems that support analysis of complex sample survey data now include the capability for simultaneous estimation of the multinomial logit regression model.

9.2.2 Multinomial Logit Regression Model: Specification Stage

The specification stage of building a multinomial logit model parallels that described in detail in Section 8.3 for specifying a logistic regression model for a binary dependent variable. However, there are two aspects of the model specification that require special emphasis.

1. *Choice of the baseline category:* In the example model formulation for the two distinct logits in Equation 9.1, category $y = 1$ is the selected baseline category. The survey analyst is free to choose which of the K categories they prefer to use as the baseline. This choice will not affect the overall fit of the multinomial logit model or overall tests of significance for the parameters associated with predictors included in the model. However, interpretation of the parameter estimates will depend on the selected baseline category, given how the generalized

logits are defined. By default, Stata will use the lowest numbered category as the baseline category for estimating the logits and corresponding odds ratios. To choose a different category as the baseline for the multinomial logits, the Stata analyst can use the baseoutcome(#) option, where # represents the value of the desired baseline category. In general, when a choice of a baseline category is not clear based on research objectives, we recommend using the most common category (or mode) of the nominal dependent variable.

2. *Parsimony*: Because each of the $K - 1$ logits that form the multinomial logit model will include the identical design vector of covariates, $\mathbf{x} = \{1, x_1, \dots, x_p\}$, and each estimated logit will have $B_k = \{B_{k0}, B_{k1}, \dots, B_{kp}\}$ parameters, the total number of parameter estimates will be $(K - 1) \times (p + 1)$. Consequently, to ensure efficiency in estimation and accuracy of interpretation, the final specification of the model should attempt to minimize the number of predictors that are either not significant or are highly collinear with other significant covariates. Analysts can use design-adjusted multiparameter Wald tests to determine the overall importance of predictors across the $K - 1$ logit functions, and we will consider an example of this in Section 9.2.6.

9.2.3 Multinomial Logit Regression Model: Estimation Stage

The principal difference in estimation for the multinomial logit model versus the simple binary logit model of Chapter 8 is that the pseudo likelihood function for the data is based on the multinomial distribution (as opposed to the binomial) and the number of parameters and standard errors to be estimated increases from $p + 1$ for the binary logit model to $(K - 1) \times (p + 1)$ for the multinomial logit regression model. When survey data are collected from a sample with a complex design, the default in most current software systems is to employ a multinomial version of Binder's Taylor Series Linearization estimator, $\hat{V}\text{ar}(\hat{\mathbf{B}})_{TSL}$, to derive the estimated variance–covariance matrix of the model parameter estimates. Most software systems also provide a Balanced Repeated Replication (BRR) or Jackknife Repeated Replication (JRR) option to compute replication variance estimates, $\hat{V}\text{ar}(\hat{\mathbf{B}})_{rep}$. Theory Box 9.1 provides a more mathematically oriented summary of the estimation of the multinomial logit regression parameters and their variance–covariance matrix when working with complex sample survey data.

In Stata, the `svy: mlogit` command is used to estimate the multinomial logit regression coefficients and their standard errors. In SAS, analysts employ the standard PROC SURVEYLOGISTIC procedure with the GLOGIT option to perform a multinomial logit regression analysis. We introduce other software that can be used to fit multinomial logit models to complex sample survey data on the book's companion web site.

THEORY BOX 9.1 ESTIMATION FOR THE MULTINOMIAL LOGIT REGRESSION MODEL

Estimation of the model parameters involves maximizing the following multinomial version of the pseudo likelihood function:

$$PL_{Mult}(\hat{\mathbf{B}} | \mathbf{X}) = \prod_{i=1}^n \left\{ \prod_{k=1}^K \hat{\pi}_k(\mathbf{x}_i)^{y_{i(k)}} \right\}^{w_i}, \quad (9.2)$$

where:

$y_{i(k)} = 1$ if $y = k$ for sampled unit i , 0 otherwise.

$\hat{\pi}_k(\mathbf{x}_i)$ is the estimated probability that $y_i = k | \mathbf{x}_i$.

w_i is the survey weight for sampled unit i .

The maximization involves application of the Newton–Raphson algorithm to solve the following set of $(K - 1) \times (p + 1)$ estimating equations, assuming a complex sample design with strata indexed by h and clusters within strata indexed by α :

$$S(\mathbf{B})_{Mult} = \sum_h \sum_{\alpha} \sum_i w_{h\alpha i} (y_{h\alpha i}^{(k)} - \pi_k(\mathbf{B})) \mathbf{x}'_{h\alpha i} = \mathbf{0}, \quad (9.3)$$

where:

$\mathbf{x}'_{h\alpha i}$ = a column vector of the $p + 1$ design matrix elements for case i

$$= [1 \quad x_{1,h\alpha i} \quad \dots \quad x_{p,h\alpha i}]';$$

$\mathbf{B} = \{B_{2,0}, \dots, B_{2,p}, \dots, B_{K,0}, \dots, B_{K,p}\}$ is a $(K - 1) \times (p + 1)$ vector of parameters;

$$\pi_k(\mathbf{B}) = \frac{\exp(\mathbf{x}' \mathbf{B}_k)}{1 + \sum_{k=2}^K \exp(\mathbf{x}' \mathbf{B}_k)};$$

$$\text{and } \pi_{1(base)}(\mathbf{B}) = 1 - \sum_{k=2}^K \pi_k(\mathbf{B}).$$

The variance–covariance matrix of the estimated parameters takes the now familiar sandwich form, based on Binder's application of Taylor Series Linearization to estimates derived using pseudo maximum likelihood estimation:

$$\hat{Var}(\hat{\mathbf{B}}) = (\mathbf{J}^{-1}) \text{var}[S(\hat{\mathbf{B}})] (\mathbf{J}^{-1}). \quad (9.4)$$

The matrices J and $\text{var}[S(\hat{B})]$ are derived as illustrated in Theory Box 8.3 for simple logistic regression, with the important change that both are now $(K - 1) \times (p + 1)$ symmetric matrices, reflecting the full dimension of the parameter vector for the multinomial logit regression model.

9.2.4 Multinomial Logit Regression Model: Evaluation Stage

Like simple logistic regression and all other forms of GLMs, the evaluation stage in building the multinomial logit regression model begins with Wald tests of hypotheses concerning the model parameters. With $(K - 1) \times (p + 1)$ parameter estimates, the number of possible hypothesis tests is almost limitless. However, there are a series of hypothesis tests that should be standard practice for evaluating these complex models. Standard t -tests for single parameters and Wald tests for multiple parameters should be used to evaluate the significance of the covariate effects in individual logits, that is, $H_0: B_{k,j} = 0$, or across all estimated logits, that is, $H_0: B_{2,j} = \dots = B_{K,j} = 0$. Example questions that could drive hypothesis tests include: Is gender a significant predictor of the odds that a U.S. adult is unemployed versus employed? Is gender a significant predictor in determining the labor force status of U.S. adults regardless of category? Other multiparameter Wald tests can be readily constructed to test custom hypotheses that are relevant for interpretation of a given model. If gender significantly alters the odds that an adult is unemployed or not in the labor force (NLF) relative to employed, is the gender effect equivalent for unemployment and NLF status? Examples of these general forms of hypothesis tests will be provided in the analytical example in Section 9.2.6.

Fagerland and Hosmer (2012) have developed a general purpose goodness-of-fit test for assessing the consistency of predictions based on a fitted multinomial logit model with the observed nominal data for the dependent variable. While their article does not specifically address accounting for complex sampling features, they have developed an add-on Stata postestimation command entitled `mlogitgof` that performs the goodness-of-fit test after using `svy: mlogit` to fit a model accounting for complex sampling features (including survey weights). We illustrate the use of this command in Stata for assessing the quality of fit for a multinomial logit model in our example below (Section 9.2.6).

9.2.5 Multinomial Logit Regression Model: Interpretation Stage

The interpretation of the parameter estimates in a multinomial logit regression model is a natural extension of the interpretation of effects in the simple logistic regression model. Simply exponentiating a parameter estimate results

in an adjusted odds ratio, corresponding to the multiplicative impact of a one-unit increase in the predictor variable, x_j , on the odds that the response is equal to k relative to the odds of a response in the baseline category:

$$\begin{aligned}\hat{\psi}_{k:j} &= \exp(\hat{B}_{k:j}) \\ CI(\hat{\psi}_{k:j}) &= \exp[\hat{B}_{k:j} \pm t_{df,1-\alpha/2} \cdot se(\hat{B}_{k:j})],\end{aligned}\tag{9.5}$$

where:

$\hat{B}_{k:j}$ = the parameter estimate corresponding to predictor j in logit equation k .

If the survey analyst is interested in the impact of a one-unit increase in predictor x_j on the odds of belonging to one of two nonbaseline categories, the following odds ratio estimates the multiplicative effect of a one-unit change in x_j on the odds of being in category k compared with category k' :

$$\begin{aligned}\hat{\psi}_{k,k':j} &= \exp(\hat{B}_{k:j} - \hat{B}_{k':j}) \\ CI(\hat{\psi}_{k,k':j}) &= \exp[(\hat{B}_{k:j} - \hat{B}_{k':j}) \pm t_{df,1-\alpha/2} \cdot se(\hat{B}_{k:j} - \hat{B}_{k':j})],\end{aligned}\tag{9.6}$$

where:

$\hat{B}_{k:j}, \hat{B}_{k':j}$ = the parameter estimates corresponding to predictor j in logit equations k and k' .

More generally, the technique outlined in Section 8.6 can be applied to evaluate the relative odds of being in category k versus the baseline category for any selected multivariate covariate patterns x_1 and x_2 or to compare the odds of being in category k versus k' for any common covariate pattern, x . We illustrate these techniques with examples in the following section.

9.2.6 Example: Fitting a Multinomial Logit Regression Model to Complex Sample Survey Data

In this example, we fit a multinomial logit regression model to the NCS-R response variable WKSTAT3C, which takes on three values: 1 = employed (EMP), 2 = unemployed (UN), and 3 = not in the labor force (NLF). [Figure 9.2](#) is a simple bar graph that illustrates a weighted estimate of the population distribution for the WKSTAT3C variable.

We consider as predictor variables AG4CAT, SEX, ALD (a lifetime diagnosis of alcohol dependence), MDE (a lifetime diagnosis of a major depressive episode), ED4CAT (1 = 0–11, 2 = 12, 3 = 13–15, and 4 = 16+ years.), and MAR3CAT (1 = married, 2 = previously married, 3 = never married). This example does not formally follow through with all of the recommended

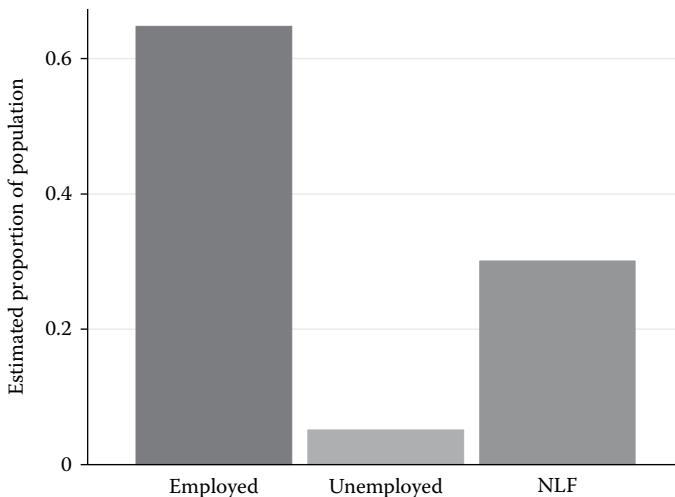


FIGURE 9.2
Weighted distribution of WKSTAT3. (From NCS-R.)

model-fitting steps proposed by Hosmer et al. (2013); however, Table 9.1 does show the results from a preliminary analysis of the bivariate associations between WKSTAT3C and each of the six categorical predictors that are considered in the initial model specification.

The results for the Rao–Scott F -tests (see Chapter 6 for more details on these tests) suggest that the four demographic predictors (AG4CAT, SEX, ED4CAT, and MAR3CAT) all have a significant bivariate association with work force status, and that the two diagnosis variables (ALD, MDE) have a somewhat weaker association.

To determine if these marginal associations remain significant when controlling for the other predictors, the following Stata command sequence can be used to fit the multinomial logit regression model taking the complex design of the NCS-R sample into account.

TABLE 9.1
Initial Bivariate Design-Based Tests Assessing Potential Predictors of WKSTAT3 for the NCS-R Adult Sample

Categorical Predictor	F-Test Statistic	$P(F > F)$
AG4CAT	$F_{4.96,208.51} = 113.49$	<0.001
SEX	$F_{1.87,78.75} = 27.33$	<0.001
ALD	$F_{1.72,72.44} = 3.12$	0.057
MDE	$F_{1.73,72.86} = 4.67$	0.016
ED4CAT	$F_{5.15,216.12} = 27.64$	<0.001
MAR3CAT	$F_{3.20,134.34} = 23.12$	<0.001

```
svyset seclustr [pweight = ncsrwtlg], strata(sestrat) ///
vce(linearized) singleunit(missing)

svy: mlogit WKSTAT3C ib2.sex ald mde i.ED4CAT i.ag4cat ///
i.MAR3CAT, rrr
```

Note that the `svy: mlogit` command is used to fit the model to the `WKSTAT3C` outcome (we use `///` to indicate a command that continues on to the next line). The nominal categorical dependent variable `WKSTAT3C` is listed first, followed by a list of the predictor variables in the model (which could be in any order), with categorical predictors indicated by the “`i.`” prefix. The `rrr` option is used in the `svy: mlogit` command to request output of the estimated odds ratios (which Stata interprets as *relative risk ratios*) and 95% confidence intervals (CIs). (This option can be omitted to generate the estimated coefficients on the logit scale.) The default baseline category for the multinomial logit regression model in Stata will be the lowest-valued category, which in this example would be 1 = “Employed.” Alternative baseline categories can be identified by using the `baseoutcome(#)` option in the `svy: mlogit` command, where `#` represents the value of the reference outcome category. For example, consider the following command:

```
svy: mlogit WKSTAT3C ib2.sex ald mde i.ED4CAT i.ag4cat ///
i.MAR3CAT, rrr baseoutcome(3)
```

This command would fit the multinomial logit model to `WKSTAT3C` with 3 = “Not in Labor Force” as the baseline category.

[Table 9.2](#) provides the detailed Stata output for the estimated model, including coefficient estimates, linearized standard errors, *t*-statistics, and *p*-values for each of the (two) generalized logits. [Table 9.3](#) presents the estimated coefficients transformed into odds ratios and 95% CIs for the odds ratios. We recommend the more concise display of the estimated odds ratios and CIs in [Table 9.3](#) for reporting the results of a multinomial logit regression model in scientific publications (e.g., Kavoussi et al., 2009).

To evaluate the fitted model, we perform multiparameter Wald tests of the overall significance of each of the predictors: AG4CAT, SEX, ALD, MDE, MAR3CAT, and ED4CAT:

```
test 2.ag4cat 3.ag4cat 4.ag4cat
test 1.sex
test ald
test mde
test 2.MAR3CAT 3.MAR3CAT
test 2.ED4CAT 3.ED4CAT 4.ED4CAT
```

The Wald tests specified in these `test` statements are testing the null hypothesis that *all* parameters associated with each individual predictor (e.g., age, education level) in the two logits are not significantly different from zero.

TABLE 9.2

Estimated Multinomial Logit Regression Model for WKSTAT3

Logit 2: Unemployed versus Employed					
Predictor ^a	Category	$\hat{B}_{2:j}$	$se(\hat{B}_{2:j})$	t	$P(t_{42} > t)$
INTERCEPT		-0.643	0.296	-2.17	0.035
AG4CAT	30–44	-0.852	0.294	-2.89	0.006
	45–59	-0.838	0.258	-3.25	0.002
	60+	1.828	0.295	6.20	<0.001
SEX	Male	-1.393	0.198	-7.05	<0.001
ALD	Yes	-0.164	0.357	-0.46	0.649
MDE	Yes	-0.140	0.157	-0.89	0.379
ED4CAT	12	-0.847	0.235	-3.60	0.001
	13–15	-1.365	0.258	-5.30	<0.001
	16+	-1.731	0.310	-5.57	<0.001
MAR3CAT	Previously	-0.589	0.225	-2.62	0.012
	Never	-2.785	0.380	-7.32	<0.001

Logit 3: Not in Labor Force versus Employed					
Predictor ^a	Category	$\hat{B}_{3:j}$	$se(\hat{B}_{3:j})$	t	$P(t_{42} > t)$
INTERCEPT		-3.790	0.173	-2.19	0.034
AG4CAT	30–44	-0.316	0.129	-2.46	0.018
	45–59	0.065	0.171	0.38	0.706
	60+	2.381	0.173	13.78	<0.001
SEX	Male	-0.640	0.110	-5.82	<0.001
ALD	Yes	0.333	0.130	2.56	0.014
MDE	Yes	0.098	0.088	1.12	0.269
ED4CAT	12	-0.651	0.141	-4.62	<0.001
	13–15	-0.917	0.146	-6.26	<0.001
	16+	-1.229	0.160	-7.70	<0.001
MAR3CAT	Previously	-0.052	0.105	-0.50	0.621
	Never	0.553	0.132	4.18	<0.001

Source: NCS-R, $n = 5,692$, adjusted Wald test for all parameters: $F(22,21) = 73.91 p < 0.001$.

^a Reference categories for categorical predictors are: 18–29 (AG4CAT); Female (SEX); No (ALD); No (MDE); <12 years (ED4CAT); Married (MAR3CAT).

Table 9.4 provides the design-adjusted Rao–Scott F -test statistics and the associated p -values for these overall tests of the individual effects.

Inspection of these overall test results shows that, as might be expected, the covariates AG4CAT, SEX, ED4CAT, and MAR3CAT are all strongly significant determinants of the relative odds that an adult is employed, unemployed, or not in the labor force. Focusing on the effects of alcohol dependence (ALD) and major depression (MDE), we note an interesting pattern. Controlling for the demographic variables, MDE ($p = 0.330$) does not

TABLE 9.3

Estimates of Adjusted Odds Ratios for the Work Force Status Outcome (WKSTAT3)

Predictor ^a	Category	Unemployed: Employed		NLF: Employed	
		$\hat{\psi}_{2j}$	95% CI for $\hat{\psi}_{2j}$	$\hat{\psi}_{3j}$	95% CI for $\hat{\psi}_{3j}$
AG4CAT	30–44	0.43	(0.24, 0.77)	0.73	(0.56, 0.94)
	45–59	0.43	(0.26, 0.73)	1.07	(0.76, 1.51)
	60+	6.22	(3.43, 11.28)	10.81	(7.62, 15.34)
SEX	Male	0.25	(0.17, 0.37)	0.53	(0.42, 0.66)
ALD	Yes	0.85	(0.41, 1.74)	1.40	(1.07, 1.82)
MDE	Yes	0.87	(0.63, 1.19)	1.10	(0.92, 1.32)
ED4CAT	12	0.43	(0.27, 0.69)	0.52	(0.39, 0.69)
	13–15	0.26	(0.15, 0.43)	0.40	(0.30, 0.54)
	16+	0.18	(0.10, 0.33)	0.29	(0.21, 0.40)
MAR3CAT	Previously	0.55	(0.35, 0.87)	0.95	(0.77, 1.17)
	Never	0.06	(0.03, 0.13)	1.74	(1.33, 2.70)

^a Reference categories for the categorical predictors are: 18–29 (AG4CAT); Female (SEX); No (ALD); No (MDE); <12 years (ED4CAT); Married (MAR3CAT).

appear to have a significant effect, while ALD ($p = 0.011$) appears to have a significant relationship with work force status. Referring back to the t -tests of the individual logit parameters in Table 9.2, the ALD relationship becomes clearer. It appears that ALD significantly affects the odds of being NLF relative to employed, but is not significant in explaining unemployment status (relative to being employed).

Consider another example of a design-adjusted postestimation Wald test: a test of the null hypothesis that the three education parameters in logit(2) are equivalent to those in logit(3) (i.e., the effect of education in the two logits is equivalent). We would use the following command in Stata to test this null hypothesis:

```
test [NLF=unemployed] : 2.ED4CAT 3.ED4CAT 4.ED4CAT
```

TABLE 9.4

Overall Wald Tests for the Predictors in the Multinomial Model for WKSTAT3

Categorical Predictor	F-Test Statistic	P($F > F$)
AG4CAT	$F_{(6,37)} = 83.59$	0.001
SEX	$F_{(2,41)} = 35.75$	0.001
ALD	$F_{(2,41)} = 5.05$	0.011
MDE	$F_{(2,41)} = 1.14$	0.330
ED4CAT	$F_{(6,37)} = 13.68$	0.001
MAR3CAT	$F_{(4,39)} = 24.81$	0.001

The F -test statistic and associated p -value for this Wald test are: $F_{3,40} = 1.25$, $P(\mathcal{F} > F) = 0.30$. The design-adjusted Wald test statistic suggests a failure to reject the null hypothesis that these three pairs of coefficients are equal to each other. Note that we use value labels for the outcome categories in square brackets after the `test` command; if value labels were not entered in the data set, one would just use the numeric values for the two outcome categories.

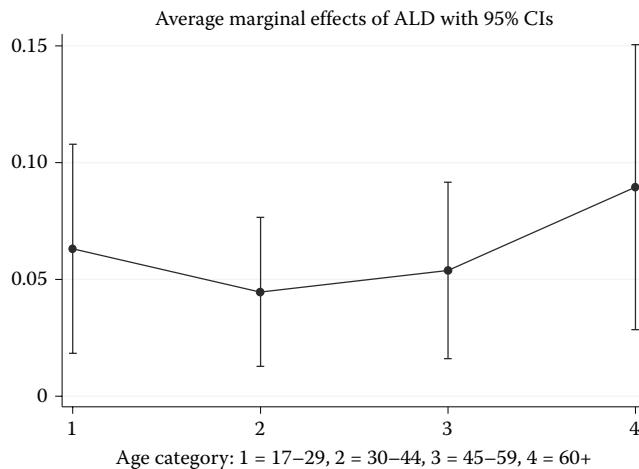
As described in Section 9.2.5, the magnitudes and directions of significant effects can be interpreted as odds ratios—odds for unemployed versus employed for logit(2) and odds for NLF versus employed for logit(3). Consider first the results for logit(2) comparing unemployed to employed work force status. From [Table 9.3](#), the odds of being unemployed versus employed are significantly lower for middle-aged persons ($\hat{\psi}_{2:30-44} = \hat{\psi}_{2:45-59} = 0.43$) relative to younger persons and men ($\hat{\psi}_{2:male} = 0.25$) relative to women. The odds of unemployment (vs. being employed) decrease with level of education ($\hat{\psi}_{2:12yrs} = 0.43$; $\hat{\psi}_{2:13-15yrs} = 0.26$; $\hat{\psi}_{2:16+yrs} = 0.18$), where less than high school education is the reference category, and are lower for previously married ($\hat{\psi}_{2:prev} = 0.55$) and never married persons ($\hat{\psi}_{2:male} = 0.06$) as compared with married persons. All of these interpretations are population estimates of these relationships when holding the other predictor variables in the model at fixed values.

Now, consider the results for the “Not in Labor Force” (NLF) outcome. Relative to younger persons between the ages of 18 and 29, the odds of being NLF decrease significantly for 30–44-year olds ($\hat{\psi}_{3:30-44} = 0.73$) and then rise to a significant increase in NLF odds in the age 60+ retirement years ($\hat{\psi}_{3:60+} = 10.81$). As observed for unemployment, the odds of being NLF versus employed are significantly lower for men ($\hat{\psi}_{3:male} = 0.53$) and decrease with level of education ($\hat{\psi}_{3:12yrs} = 0.52$; $\hat{\psi}_{3:13-15yrs} = 0.40$; $\hat{\psi}_{3:16+yrs} = 0.29$). All else being equal, persons who were never married had higher odds of being NLF ($\hat{\psi}_{3:never} = 1.74$) than their married counterparts. Finally, alcohol dependency is associated with significantly increased odds ($\hat{\psi}_{3:ALD} = 1.40$) of being out of the labor force. For an example of reporting the results of a multinomial logit regression analysis of complex sample survey data in a scientific publication, we refer readers to Kavoussi et al. (2009).

Analysts can also display marginal predicted probabilities of having particular outcome categories as a function of selected covariates, as discussed in [Chapter 8](#). For example, we can visualize the average marginal effects of alcohol dependency on the probability of not being in the labor force (outcome 3) for different age categories by using the following postestimation commands:

```
margins, dydx(alcohol) by(ag4cat) predict(pr outcome(3))
marginsplot
```

The average marginal effects and 95% CIs for the effects shown in [Figure 9.3](#) illustrate a consistent tendency of alcohol dependence to increase the

**FIGURE 9.3**

Average marginal effects of alcohol dependence on the probability of not being in the labor force, for different age categories.

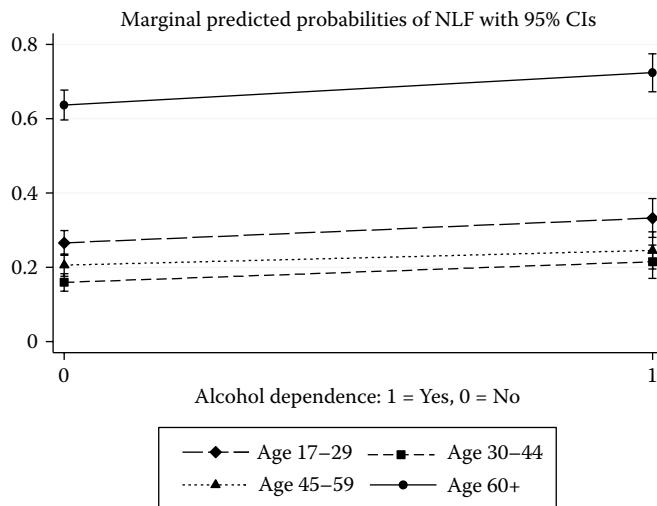
probability of not being in the labor force in a significant fashion (a value of 0 for the average marginal effect would mean that the probability did not change as the covariate changed from 0 to 1), regardless of age. We also note that the effects, while significant, do in fact depend on the values of other covariates, despite the absence of interaction terms in this model (as was discussed in Chapter 8). We can also plot marginal predicted probabilities of not being in the labor force as a function of alcohol dependence and age by using the following postestimation commands:

```
margins, by(ald ag4cat) predict(pr outcome(3))
marginsplot
```

Figure 9.4 presents the resulting marginal predicted probabilities of not being in the labor force for each combination of values on these two variables. We feel that these types of visual displays enhance the presentation of multinomial logit regression results, and these postestimation commands in Stata make it especially easy to generate these plots.

Finally, we assess the goodness-of-fit of this example multinomial logit model using the procedure described by Fagerland and Hosmer (2012). After installing the add-on command in web-aware Stata (users can type `findit mlogitgof`), an analyst simply needs to fit the model and then submit the `mlogitgof` command after fitting the model:

```
svy: mlogit WKSTAT3C ib2.sex ald mde i.ED4CAT i.ag4cat ///
i.MAR3CAT, rrr
mlogitgof
```

**FIGURE 9.4**

Marginal predicted probabilities of not being in the labor force, for different categories of alcohol dependence and age.

The resulting output suggests that we would reject the null hypothesis that the fitted model is the correct model:

Goodness-of-fit test for a multinomial logistic regression model

Dependent variable: WKSTAT3C

```

number of observations = 5679
number of outcome values = 3
base outcome value = 1
number of groups = 10
chi-squared statistic = 34.979
degrees of freedom = 16
Prob > chi-squared = 0.004

```

This test suggests that the model does not fit the data well; recall, however, that this test does not fully account for the complex sampling features, meaning that the *p*-value is likely too small. We may revisit the specification of the model and whether certain important predictor variables were omitted. In this simple illustration, we only considered the main effects of a small number of predictors. We could, for example, examine whether there were any interactions between the predictors that we did include (in the absence of any theory suggesting that other important predictors of employment status should have been included). We leave this as an exercise at the end of the chapter.

9.3 Logistic Regression Models for Ordinal Survey Data

Ordinal response questions like the two examples in [Figure 9.5](#) are common in survey practice. The Health and Retirement Study (HRS) health rating question shown in [Figure 9.5](#) part (a) exemplifies a question type in which the respondent is asked to assign discrete rankings to attributes—their own or those of others. A more subtle form of ordinal response arises in questions like the NHANES activity question shown in part (b) of [Figure 9.5](#). In that question, the ordinality of the response is not explicitly incorporated in a rating-type response scale but the response categories do implicitly capture ever-increasing levels of physical activity.

As discussed in [Chapter 5](#), survey analysts have historically treated descriptive analysis of ordinal response data in a number of different ways. The same is true in regression modeling for ordinal categorical data. At one extreme, the ordinal responses are treated as continuous random variables. Many survey analysts do not hesitate to fit a standard linear regression model to ordinal response data. Others completely ignore the natural ordering of the response categories and analyze the ordinal data as though it were nominal in nature (i.e., apply multinomial logit regression as in Section 9.2). In practical terms, neither approach is necessarily wrong. DeMaris (2004) identifies conditions under which he feels that a linear regression treatment leads to robust analysis—enough levels (5 or more), large n and a response

(a) HRS

Would you say your health is excellent, very good, good, fair, or poor?

1. EXCELLENT
2. VERY GOOD
3. GOOD
4. FAIR
5. POOR

8. DK (don't know); NA (not ascertained)
9. RF (refused)

(b) NHANES

Please tell me which of these four sentences *best* describes your usual daily activities:

1. You sit during the day and do not walk about very much
2. You stand or walk about quite a lot during the day, but do not have to carry or lift things very often
3. You lift or carry light loads, or have to climb stairs or hills often; or
4. You do heavy work or carry heavy loads

7. Refused
9. Don't know

FIGURE 9.5

Ordinal response questions from the HRS and the NHANES.

distribution that is not highly skewed across the ordinal range. Analysts who ignore the ordinality of such responses and apply the general multinomial logit regression technique of Section 9.2 are also certainly not wrong in their approach. However, such models require the estimation of many parameters [recall that one estimates $(K - 1) \times (p + 1)$ parameters when fitting a multinomial logit model] and therefore may not be the most efficient modeling option.

9.3.1 Cumulative Logit Regression Model

A special class of logistic regression models has been developed for regression analysis of ordinal survey variables. These models differ from multinomial logit regression models for nominal categorical response variables in that they acknowledge the ordering of the response categories when estimating the relationships of the predictor variables with the probabilities of having certain responses. Ordinal models involve fewer parameters than multinomial logit regression models and are more parsimonious as a result. Standard statistical texts describe several approaches to specifying (parameterizing) an ordinal logistic regression model (Agresti, 2012; Hosmer et al., 2013). Here our focus will only be on the most common form, the *cumulative logit model*.

A *cumulative logit* is defined for the probability of having an ordinal response less than or equal to k , relative to the probability of having a response greater than k :

$$\begin{aligned} \text{logit}[P(y \leq k) | \mathbf{x}] &= \ln \left[\frac{P(y \leq k) | \mathbf{x}}{P(y > k | \mathbf{x})} \right] \\ &= \ln \left[\frac{P(y = 1 | \mathbf{x}) + \dots + P(y = k | \mathbf{x})}{P(y = k + 1 | \mathbf{x}) + \dots + P(y = K | \mathbf{x})} \right] \quad (9.7) \\ &= B_k - (B_1 x_1 + B_2 x_2 + \dots + B_p x_p). \end{aligned}$$

For an ordinal variable with K categories, $K - 1$ cumulative logit functions are defined. Each cumulative logit function includes a unique intercept or “cut point,” B_k , but all share a common set of regression parameters for the p predictors, $\mathbf{B} = (B_1, \dots, B_p)$. Consequently, a cumulative logit model for an ordinal response variable with K categories and $j = 1, \dots, p$ predictors requires the estimation of $(K - 1) + p$ parameters—far fewer than the $(K - 1) \times (p + 1)$ parameters for a multinomial logit model.

By using logits defined by cumulative probability, the cumulative logit model captures trends across the adjacent categories of an ordinal response variable. By using a single set of regression parameters for the predictors, the model provides true parsimony in estimating the relationship between predictors and the profile of responses over the ordinal response categories. The concept

of a “cumulative logit” is certainly more complex than that of a baseline category logit that is employed in the parameterization of simple logistic regression or even multinomial logit regression models. In actuality, though, it is simply just an alternative way of parameterizing the model for estimating the probability that a response will fall in ordinal category $y = 1, \dots, K$.

Consider the cumulative logit model in Equation 9.7. If the cumulative logit is estimated for a covariate pattern $\mathbf{x} = \{x_1, x_2, \dots, x_p\}$, then the transform

$$\hat{\phi}(y \leq k | \mathbf{x}) = \frac{\exp(x\hat{\mathbf{B}})}{1 + \exp(x\hat{\mathbf{B}})} = \frac{\exp[\hat{B}_k - (\hat{B}_1x_1 + \hat{B}_2x_2 + \dots + \hat{B}_px_p)]}{1 + \exp[\hat{B}_k - (\hat{B}_1x_1 + \hat{B}_2x_2 + \dots + \hat{B}_px_p)]} \quad (9.8)$$

estimates the cumulative probability (denoted here by $\hat{\phi}(y \leq k | \mathbf{x})$) that the response, y , is less than or equal to ordinal category k . To “recover” estimates of the individual response category probabilities, $\hat{\pi}_k(\mathbf{x})$, from the estimated cumulative probabilities simply requires taking the difference in the estimated cumulative probability through response categories k and $k - 1$:

$$\hat{\pi}_k(\mathbf{x}) = \hat{\phi}(y \leq k | \mathbf{x}) - \hat{\phi}(y \leq k - 1 | \mathbf{x}), \quad (9.9)$$

where:

$$\hat{\phi}(y \leq 0 | \mathbf{x}) = 0.$$

9.3.2 Cumulative Logit Regression Model: Specification Stage

The cumulative logit model is a specialized model that is applicable to true ordinal response variables such as a health satisfaction ratings and satisfaction scores, where the categorized response (excellent, very good, good, fair, poor) can be viewed as the observed representation of an underlying continuous measure of a latent attribute, belief or attitude. The general steps in specifying and building a final cumulative logit regression model—variable selection, evaluation of potential nonlinearity for continuous predictors, tests of interaction of main effects, and so on—are identical to those applied in other regression models.

9.3.3 Cumulative Logit Regression Model: Estimation Stage

Procedures for pseudo maximum likelihood estimation of the parameters of the cumulative logit regression model are identical to those described in Section 9.2.3 for the multinomial logit regression model. The final parameter estimates are obtained by application of the Newton–Raphson algorithm to maximize the weighted multinomial likelihood given by Equation 9.2.

At each iteration, the values of $\hat{\pi}_k(x_i)$ are obtained through the probability calculation sequence similar to that described in Equations 9.8 and 9.9. Like multinomial logit regression, the default variance estimator in most current software systems is the multinomial version of Binder's Taylor Series Linearization estimator (9.4), with most major software packages also providing analysts the options to use BRR or JRR to compute replication variance estimates, $\hat{Var}(\hat{B})_{rep}$.

Analysts should be aware that different software packages use different parameterizations of the cumulative logit model. For example, the Stata svy: ologit procedure fits these models using the parameterization described in Equation 9.7, in which the covariate adjustment, $\Delta_i = \sum_{j=1}^p B_j x_{ij}$, is subtracted from the cut point B_k for the k -th cumulative logit. Positive values for estimates of the regression parameters in the model will thus signify increases in the probability of higher-valued responses categories for higher values for the corresponding predictor variables. The SURVEYLOGISTIC procedure in the SAS software uses the following parameterization of the model:

$$\text{logit}[P(Y \leq k) | \mathbf{x}] = B_k + (B_1 x_1 + B_2 x_2 + \cdots + B_p x_p), \quad (9.10)$$

with the covariate adjustment *added* to the cut point for cumulative logit k —reversing the sign on the regression parameters compared with the Stata default. Use of the DESCENDING option in the SAS SURVEYLOGISTIC procedure will yield results that are identical to the Stata default. Analysts need to carefully check how these models are being parameterized by the software procedures that they are using prior to interpreting the results from these types of analyses.

9.3.4 Cumulative Logit Regression Model: Evaluation Stage

Procedures (Student t tests, Wald tests) described for testing the significance of individual model parameters or multiparameter predictors in the simple logistic model (Section 8.5.1) apply directly to the evaluation of fitted cumulative logit models. Unfortunately, goodness-of-fit measures and diagnostic tools like those available for binary logistic regression (Section 8.5.2) or multinomial logistic regression (Section 9.2.6) have not yet been developed for the more complex logistic regression models for ordinal response data and therefore are not yet available in statistical software procedures for complex sample survey data analysis.

Analysts are able to perform one type of diagnostic for the cumulative logit model. The literature occasionally labels the cumulative logit model as the *proportional odds model*. This alternate label derives from a property of the model which results from the fact that each of the $K - 1$ cumulative logits are assumed to share a common set of regression coefficients, \mathbf{B} , for the model predictors. When analyzing complex sample survey data, tests of

this assumption require the estimation of an alternative *generalized cumulative logit model* (Peterson and Harrell, 1990), where the regression parameters identified in Equation 9.7 are allowed to vary depending on the choice of k (i.e., $B_{k:1}$ instead of $B_{1:1}$). The “proportional odds” or “equal slopes” assumption can be formally tested by fitting this alternative model (also using design-based methods) and performing a design-adjusted Wald test of the null hypothesis that all pairwise contrasts of the regression parameters for each predictor across the $K - 1$ logit functions in the generalized model are equal to zero (e.g., $B_{1:1} - B_{2:1} = 0$; $B_{1:1} - B_{3:1} = 0$; etc.). This design-based test is currently implemented in the user-written Stata command `gologit2` (Stata users can submit the command `findit gologit2` for more details) and the CSORDINAL procedure of the SPSS Complex Samples module. Additional implementations will be noted on the companion web site for this book when they become available.

In cases where this formal test rejects the null hypothesis of equal slopes, the survey analyst should first extend their model-building investigation to evaluate whether the current predictor set should be modified (adding new predictors, interaction terms or nonlinear effects) in order for the equal slopes assumption to hold. If this extended investigation fails to resolve the problem of apparent inequality in the slope parameters of the cumulative logit model, the analyst can ignore the ordinality of the response and revert back to a generalized multinomial logit model for categorical response variables (Section 9.2), or consider more parsimonious generalized forms of the cumulative logit model (which are currently implemented in the Stata command `gologit2`). Often, despite the formal rejection of the equal slopes test, the interpretations of the results from the two models—cumulative and generalized logit—may be consistent and the analyst may still choose the cumulative logit model for its simplicity of form and interpretation.

9.3.5 Cumulative Logit Regression Model: Interpretation Stage

Like most regression models, the interpretation of results from a cumulative logit regression model can occur at two different levels. At the evaluation stage (see above), t -tests of single-parameter predictors or Wald tests of multiparameter predictors will identify those predictors that have a significant relationship with the ordinal response variable. Examination of the estimated coefficients for the cumulative logits can inform the analyst about the directional nature of the relationships between the response variable and the predictors. For example, under the Stata default parameterization, positive values for estimates of the regression parameters for a continuous predictor correspond to increased probability of higher-valued response categories as the predictor value itself increases. Likewise, positive coefficients for parameters representing a level of a categorical predictor (e.g., males relative to females) suggest that, relative to the reference category,

the distribution of ordinal responses for the predictor category is shifted toward the higher values of the response distribution (in SAS, the interpretation would be reversed unless the DESCENDING option is used in PROC SURVEYLOGISTIC.).

While estimates of the “cut point” intercept terms of the cumulative logit model are critical to model fit, they typically are of little further interest in the analysis and interpretation of the results. For interpretation and summarization of the model results, survey analysts may choose to go beyond simply establishing the significance and directionality of predictor effects. Following Agresti (2012), a more quantitative presentation of the direction and magnitude of significant effects of predictors in cumulative logit regression models can be based on one of two related sets of statistics.

The first is the set of cumulative odds ratios that can be estimated directly from the fitted model. If the k th cumulative logit is estimated for two covariate patterns, x_1 and x_2 , the following exponential function estimates a *cumulative odds ratio*:

$$\hat{\psi}_{y \leq k} = \exp[\hat{B}'(x_1 - x_2)] = \exp[\hat{B}_1(x_{11} - x_{12}) + \dots + \hat{B}_p(x_{p1} - x_{p2})]. \quad (9.11)$$

The interpretation of the cumulative odds ratio statistic is slightly different from the standard odds ratio. For the given covariate patterns x_1 and x_2 , the cumulative odds that the ordinal response, y , is less than or equal to category k are $\hat{\psi}_{y \leq k}$ times greater for x_1 than the odds for x_2 . Cumulative odds ratios and CIs are readily generated as output from software procedures for fitting cumulative logit models to complex sample survey data. In scientific reports and publications, they can be summarized in standard tables (Table 9.6) or by using graphical displays of the type illustrated in Section 9.2.6.

The second (and related) set of statistics that can be used to quantify the effects of individual predictors are estimates of cumulative probabilities of the form in Equation 9.8. For example, holding all other predictors constant, expression (9.8) could be used to estimate men’s and women’s cumulative probability of response in category $y = 1, \dots, K$. Estimated values and standard errors (or CIs) for $\hat{\phi}(y \leq k | x)$ for men and women could then be compared side-by-side in a tabular format or in a graph. To compare distributions of the estimated cumulative probabilities across the range of a continuous variable (e.g., age or blood pressure), Agresti (2012) recommends evaluating the cumulative logit for each category at the quartiles of that predictor’s distribution (Q_{25}, Q_{50}, Q_{75}). We consider Stata commands for calculation and display of these types of marginal predicted probabilities in our example below.

Readers are encouraged to reference Agresti (2012), Hosmer et al. (2013), Allison (1999), and Long and Freese (2006) for additional tips on evaluating and interpreting the results of cumulative logit regression models.

9.3.6 Example: Fitting a Cumulative Logit Regression Model to Complex Sample Survey Data

This section considers an example of fitting a cumulative logit model to a recoded version of the satisfaction with life variable (STFLIFE) in the 2012 European Social Survey (ESS) Russian Federation data set. The original variable was measured on a 0 to 10 scale, with 0 representing extremely dissatisfied and 10 representing very satisfied. For purposes of this example, this variable was recoded into a variable with five categories: 0–1, 2–4, 5, 6–8, and 9–10. We begin with a simple descriptive analysis, and run the Stata commands below to generate the weighted bar chart presented in [Figure 9.6](#).

```
tabulate stflife2, gen(sat)

graph bar sat* [pweight=pspwght] , ///
ytitle("Proportions") legend(row(1) lab(1 "0-1") ///
lab(2 "2-4") lab(3 "5") lab(4 "6-8") lab(5 "9-10"))
```

Before beginning the model-building process, analysts should examine simple frequency distributions for ordinal response variables. If the majority of responses on a discrete ordinal outcome are grouped in single categories or highly skewed to the highest or lowest possible values, the cumulative logit model may not be the best choice, and simple binary or multinomial logit regression models would be more appropriate for a recoded version of the ordinal response variable. In this case, we see that most of the individuals in Russia are estimated to respond in the 6–8 range on the original variable.

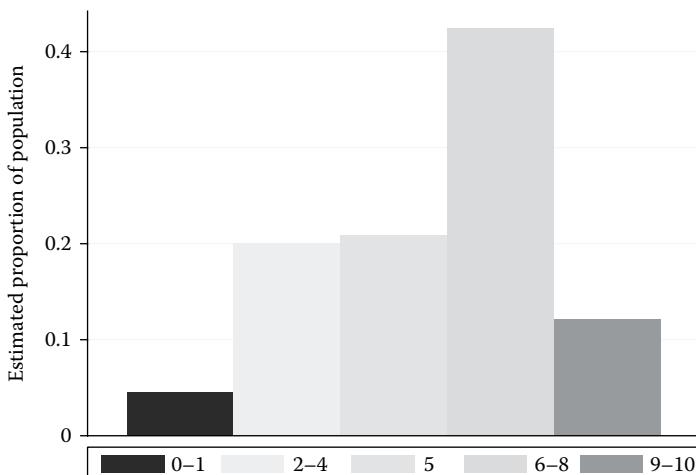


FIGURE 9.6

Bar chart (weighted) of the recoded version of the 2012 ESS Russia variable STFLIFE (where 0 = extremely dissatisfied and 10 = very satisfied).

This weighted population distribution across the life satisfaction categories and the implicit continuum of satisfaction that underlies this response scale suggest that this categorical variable would be a reasonable choice for a dependent variable in an ordinal regression model.

The objective in this simple example is to model the life satisfaction for Russian adults as a function of age, gender, and marital status. We remind readers that the Hosmer et al. steps discussed in [Chapter 8](#) are always recommended when building a regression model. For purposes of brevity, we only consider fitting a single simple model using these three demographic variables and do not illustrate the full sequence of model-building steps.

After specifying the complex sampling features of the ESS Russia data set using the `svyset` command (the cluster variable PSU, the final survey weight variable PSPWGHT, and the stratum variable STRATIFY), we use the `svy: ologit` command to fit the cumulative logit regression model in Stata:

```
svyset psu [pweight = pspwght], strata(stratify)

svy: ologit stflife2 i.agecat i.marcat male
svy: ologit, or
```

Similar to other regression commands in Stata, the response variable (STFLIFE2) is listed first, followed by a list of the predictor variables (no interactions are included in this model). The model is reestimated with the `or` option to request that Stata provide output in the form of the estimated cumulative odds ratios and 95% CIs.

[Table 9.5](#) summarizes the estimated “cut point” parameters (or B_k values from Equation 9.7) for the logistic distribution in this model, along with the weighted estimates of the regression parameters for the nonreference categories of age, marital status, and gender. [Table 9.6](#) presents the corresponding estimates of the cumulative odds ratios and design-based 95% CIs for the odds ratios (with standard errors computed using Taylor Series Linearization).

In [Table 9.5](#), first note the estimates of the four intercept parameters. As described above, these parameter estimates are rarely of real analytic interest but are used by the analysis software to calculate predicted probabilities of being in one of the five ordered response categories for STFLIFE2.

Consider next the regression parameter estimates ([Table 9.5](#)) and estimated cumulative odds ratios ([Table 9.6](#)) for the nonreference categories of age, marital status, and gender. First, the t -test results for the three age coefficients suggest that the three oldest age categories (30–44, 45–59, and 60+) all have significantly different distributions on the ordinal outcome compared with the youngest age category (15–29). These three coefficients are all negative and significant at the 0.001 level. Given the parameterization that Stata is using (9.7), these estimates suggest that increasing age is negatively related to life satisfaction (where older age increases the probability

TABLE 9.5

Estimated Cumulative Logit Regression Model for STFLIFE2

Predictor	Category	\hat{B}	$se(\hat{B})$	t	$P(t_{176} > t)$
INTERCEPT	Cut 1	-3.711	0.214	-17.31	<0.001
	Cut 2	-1.793	0.167	-10.75	<0.001
	Cut 3	-0.835	0.159	-5.24	<0.001
	Cut 4	1.384	0.154	9.01	<0.001
AGECAT ^a	2 = 30–44	-0.529	0.136	-3.89	<0.001
	3 = 45–59	-0.746	0.143	-5.20	<0.001
	4 = 60+	-0.808	0.166	-4.88	<0.001
MARCAT ^a	2 = Previous	-0.209	0.105	-1.98	0.049
	3 = Never	-0.137	0.132	-1.04	0.300
GENDER ^a	1 = Male	-0.110	0.095	-1.15	0.251

Source: 2012 (Round 6) ESS Russian Federation data set, $n = 2,415$. Adjusted Wald test for all parameters: $F(6,171) = 7.65$, $p < 0.001$.

^a Reference categories: AGECAT = 15–29, MARCAT = Married, GENDER = Female.

of being in *lower* valued categories, indicating less satisfaction). The estimated cumulative odds ratios for these three age categories suggest that the odds of being in higher satisfaction categories are decreased by 41%, 53%, and 55%, respectively (holding marital status and gender fixed). From Table 9.6, we also see that the odds of being in higher satisfaction categories for previously married individuals are decreased by about 19% relative to married individuals. Finally, we note that males and females do not differ significantly in terms of distributions on life satisfaction when holding age and marital status fixed.

TABLE 9.6

Estimated Cumulative Odds Ratios in the Cumulative Logit Regression Model for STFLIFE2

Predictor	Category	Cumulative Odds Ratio	
		$\hat{\psi}_{y \leq k;j}$	95% CI for $\hat{\psi}_{y \leq k;j}$
AGECAT ^a	2 = 30–44	0.589	(0.450, 0.771)
	3 = 45–59	0.474	(0.358, 0.630)
	4 = 60+	0.446	(0.321, 0.618)
MARCAT ^a	2 = Previous	0.811	(0.659, 0.999)
	3 = Never	0.872	(0.672, 1.131)
GENDER ^a	1 = Male	0.896	(0.743, 1.081)

Source: 2012 (Round 6) ESS Russian Federation data set; $n = 2415$.

^a Reference categories: AGECAT = 15–29, MARCAT = Married, GENDER = Female.

To test the proportional odds or “equal slopes” assumption that underlies the cumulative logit model, we first install the `gologit2` command in web-aware Stata, and then execute the following commands:

```
tabulate agecat, gen(agecat)
tabulate marcat, gen(marcat)

gologit2 stflife2 agecat2 agecat3 agecat4 marcat2 ///
    marcat3 male, svy autofit
```

We note that the `gologit2` command does not allow for factor variable notation, so we needed to create indicator variables for the nonreference categories of age and marital status first. We also note that the `gologit2` command accommodates complex sample design features that have already been set using the `svyset` command via the `svy` option. This command fits the original cumulative logit model, and then (via the `autofit` option) fits a series of models that relax the proportional odds assumption (which requires estimation of more parameters). The fits of these models are compared automatically, and the command then yields results of these comparisons with explicit instructions for how to interpret these results:

Testing parallel-lines assumption using the 0.05 level of significance...

```
Step 1: Constraints for parallel lines imposed for agecat2
(P Value = 0.7570)
Step 2: Constraints for parallel lines imposed for agecat3
(P Value = 0.8772)
Step 3: Constraints for parallel lines imposed for marcat2
(P Value = 0.4898)
Step 4: Constraints for parallel lines imposed for marcat3
(P Value = 0.2593)
Step 5: Constraints for parallel lines imposed for male (P
Value = 0.1235)
Step 6: Constraints for parallel lines imposed for agecat4
(P Value = 0.2091)
Step 7: All explanatory variables meet the pl assumption
```

Wald test of parallel-lines assumption for the final model:

Adjusted Wald test

```
( 1) [1]agecat2 - [2]agecat2 = 0
( 2) [1]agecat3 - [2]agecat3 = 0
( 3) [1]marcat2 - [2]marcat2 = 0
( 4) [1]marcat3 - [2]marcat3 = 0
( 5) [1]male - [2]male = 0
( 6) [1]agecat4 - [2]agecat4 = 0
( 7) [1]agecat2 - [3]agecat2 = 0
( 8) [1]agecat3 - [3]agecat3 = 0
```

```
( 9) [1] marcat2 - [3]marcat2 = 0
(10) [1] marcat3 - [3]marcat3 = 0
(11) [1] male - [3]male = 0
(12) [1] agecat4 - [3]agecat4 = 0
(13) [1] agecat2 - [4]agecat2 = 0
(14) [1] agecat3 - [4]agecat3 = 0
(15) [1] marcat2 - [4]marcat2 = 0
(16) [1] marcat3 - [4]marcat3 = 0
(17) [1] male - [4]male = 0
(18) [1] agecat4 - [4]agecat4 = 0

F( 18,    159) =      1.01
Prob > F =      0.4566
```

The *F*-test *does not* reject the null goodness-of-fit hypothesis. We can therefore safely conclude that the assumption of proportional odds holds for our example model, and proceed with our interpretations as stated above.

If the null hypothesis of equal slopes/proportional odds/parallel lines had been rejected, we would be left with the difficult question of whether to ignore the apparent violation of this key model assumption in exchange for the simplicity of interpretation offered, or to opt instead for a generalized form of the model (Peterson and Harrell, 1990) or other modeling alternative that relaxes the equal slopes assumption but is far more complex and difficult to interpret. Agresti (2012) points out that for large sample sizes, this test is extremely powerful against the null hypothesis that the proportional odds assumption is met. Agresti advises that even when the test rejects the assumption, the parsimony of the cumulative logit model parameterization may still make it a practical choice relative to the much more complex alternatives. We recommend comparing results from alternative models and using more flexible models if there are substantial differences in the resulting inferences.

9.4 Regression Models for Count Outcomes

9.4.1 Survey Count Variables and Regression Modeling Alternatives

Regression models for dependent variables that are discrete counts of events or outcomes are also important in the analysis of survey data. Figure 9.7 provides an example of a survey question from the HRS that produces a count of falls that respondents aged 65 and older have experienced in the past 2-year period. The example question sequence illustrates a typical convention in survey measurement of counts. Respondents are initially queried as to whether any events occurred during the reference period. If the respondent answers “yes,” a follow-up question captures a count of events (>0), which is recorded by the interviewer in the boxes. Respondents who answer “no” to the initial screening question are presumed to have a zero count of events.

[If aged 65 or older]	
Have you fallen down in the last 2 years?	
1	Yes
2	No
8	Don't know
9	Refused
Blank	inapplicable, respondent is <65 years
How many times have you fallen in the last 2 years?	
<input type="checkbox"/>	Number of times
<input type="checkbox"/>	Don't know
<input type="checkbox"/>	Refused

FIGURE 9.7

Example of a survey question sequence producing a count variable. (From 2012 HRS.)

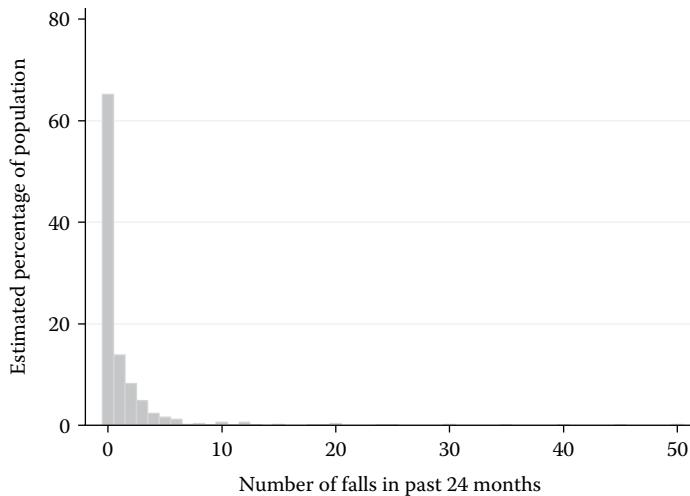
It is clear that the question sequence encodes two pieces of information: a count of events (y) and the “exposure” time, t , during which the reported events occurred. The length of the observation period can be fixed (e.g., the 2 years) or may vary from one sample respondent to another (e.g., since you last saw a doctor). Regression models for these types of counts aim to model the relationship between the count response y and predictor variables of theoretical interest x , or equivalently, the relationship of x with the rate $\lambda = y/t$ at which the event occurred. The regression models described in this section model *rates*, or event counts per unit of time. [Chapter 10](#) will introduce regression techniques for survival analysis or event history analysis that model the time to an event, where time itself is the dependent variable.

[Figure 9.8](#) illustrates the estimated population distribution of counts that results from the 2012 HRS question on number of falls in the past 2 years, generated using the following command in Stata:

```
histogram numfalls24 [fweight = nwgr], discrete percent
```

This figure illustrates two common properties of distributions of count-type survey variables. Often, the event of interest occurs rarely in the population and the distribution of counts is dominated by a very high proportion of zero values. The distribution is also highly skewed with declining frequencies for “1,” “2,” “3,” and so on falls. The survey analyst can choose from a number of alternative approaches to regression modeling of these types of count variables.

Linear regression techniques are frequently used by survey analysts to model count data. Theory Box 9.2 discusses the pros and cons of trying to apply linear regression in the analysis of survey counts. Today, the preferred

**FIGURE 9.8**

Histogram (weighted) of 2012 HRS counts of falls in the past 24 months.

THEORY BOX 9.2 LINEAR REGRESSION FOR COUNT VARIABLES

One alternative for modeling a count response might be to fit a standard linear regression model to a log-transformed version of the rate, denoted by $\lambda = y/t$. However, two problems can arise with this approach: the normality assumption for the residuals rarely holds for the counts or transformed rates, and the variance of $\log(\lambda_i)$ is by definition heterogeneous:

$$\text{var}[\log(\lambda_i)] \doteq \frac{\text{var}(\lambda_i)}{\lambda_i^2} = \frac{(1 - \lambda_i)}{\lambda_i}. \quad (9.12)$$

If the event of interest is fairly common and the distribution of counts is symmetrically (if not normally) distributed over the possible range, then a standard linear regression model of the form $y = B_0 + B_1x_1 + \dots + B_p x_p$ may be a practical approach. Initial graphical analyses can be very helpful in making this choice, and residual diagnostics also play an important role (Chapter 7).

alternatives for regression modeling of count data are GLMs based in full or in part on the Poisson and negative binomial distributions.

9.4.2 Generalized Linear Models for Count Variables

This section considers four related GLMs for regression modeling of count data: the Poisson regression model, the negative binomial regression model, and “zero-inflated” versions of both the Poisson and negative binomial models. The presentation here is deliberately simplified and will focus on the most important concepts for survey analysts, along with an application to the 2012 HRS data on falls. For a more in-depth mathematical treatment of these models, we encourage readers to see Chapter 8 of Long and Freese (2006) or Hilbe (2007).

9.4.2.1 Poisson Regression Model

The simplest of the GLMs for count data is the *Poisson regression model*. The Poisson distribution, $y_i \sim \text{Poisson}(t_i\lambda_i)$, is a natural statistical distribution for describing counts of events, y_i , that randomly occur at some expected rate, λ_i , over a period of time, t_i . In the Poisson regression model, the natural *log link* function is employed to model this rate as a linear function of the predictors, x :

$$\log(\lambda_i) = B_0 + B_1x_{1i} + \dots + B_px_{pi}. \quad (9.13)$$

A Poisson random variable y_i has the unique property that its mean is equal to its variance: $E(y_i | x_i) = \text{var}(y_i | x_i) = t_i\lambda_i$, or $E(\text{count} | x) = \text{time} \times E(\text{rate} | x)$. Hence, given the model for the log of the rate in Equation 9.13, we have:

$$\begin{aligned} E(y_i | x_i) &= t_i\lambda_i \\ &= t_i \exp(B_0 + B_1x_{1i} + \dots + B_px_{pi}) \\ &= \exp[\log(t_i) + B_0 + B_1x_{1i} + \dots + B_px_{pi}]. \end{aligned} \quad (9.14)$$

When formulating a linear model for the expected value of the response variable, the natural log link transformation can be applied to the expected value for y_i defined in Equation 9.14 to produce a convenient linear combination of predictor variables and regression parameters:

$$g[E(y_i | x_i)] = \log[E(y_i | x_i)] = \log(t_i) + B_0 + B_1x_{1i} + \dots + B_px_{pi}. \quad (9.15)$$

This is the standard Poisson regression model, incorporating an exposure time *offset variable*, $\log(t_i)$, which represents the observation period for individual i .

9.4.2.2 Negative Binomial Regression Model

A key assumption of the Poisson regression model is that the mean and variance of the observed counts are equal: $E(y_i|x_i) = \text{var}(y_i|x_i) = t_i\lambda_i$. In practice, the variance of the count variable may differ from the mean. The *negative binomial regression model* is an extension of the Poisson regression model that relaxes this assumption by introducing a dispersion parameter, α , that allows the variance of the count to differ from the mean by a factor of $(1 + \alpha)$: $\text{var}_{NB}(y_i|x_i) = E(y_i|x_i) \cdot (1 + \alpha) = t_i\lambda_i(1 + \alpha)$. If the dispersion parameter is equal to 0, the negative binomial model reduces to the Poisson model.

Both the Poisson and negative binomial GLMs share the natural log link and “log rate” form of the GLM, $\log(\lambda_i) = B_0 + B_1x_{1i} + \dots + B_px_{pi}$, and an identical expression for the expected count, $E(y_i|x_{1i}) = \exp[\log(t_i) + B_0 + B_1x_{1i} + \dots + B_px_{pi}]$. Pseudo maximum likelihood estimation of the Poisson regression model will be based on a weighted Poisson likelihood function, while the extended negative binomial model will employ a weighted version of the negative binomial likelihood in the estimation of the regression model parameters and the additional dispersion parameter, α (Theory Box 9.3).

In general, the Poisson and negative binomial regression models should yield very similar estimates of the regression parameters and rate ratios (RRs). However, if the variance of the count data differs from the mean of the counts by a significant amount ($\alpha \neq 0$), fitting the regression model with the simpler Poisson likelihood will result in biased estimates of standard errors and test statistics.

9.4.2.3 Two-Part Models: Zero-Inflated Poisson and Negative Binomial Regression Models

A *two-part model* is an appropriate alternative if the count variable of interest arises through a mixture of processes. Zero-inflated and zero-truncated versions of the Poisson and negative binomial regression models (Long and Freese, 2006) include a Part 1 logistic regression model, such as (8.2), of the probability that the count is zero and a Part 2 Poisson or negative binomial regression model (9.13) for the actual counts (Theory Box 9.3). An example is the analysis of y = number of alcoholic drinks consumed per week, where the model that predicts abstinence ($y = 0$) is very likely to differ from the model that predicts frequency and consumption in that segment of the population that may drink alcohol either occasionally or often, as the case may be.

The two-part model allows the survey analyst to specify one set of predictors, z , for the logistic model that predicts the probability of a zero count and a second set of predictors, x , for the Poisson or negative binomial regression function for predicting positive counts, $y > 0$. Stata offers two commands for fitting these two-part models to count variables from complex sample designs: `svy: zip` (zero-inflated Poisson) and `svy: zinb` (zero-inflated negative binomial). The output from each of these programs will provide

two sets of estimated coefficients. The first will be the estimated coefficients, standard errors, and test statistics for the Part 1 logistic model of the probability that $y = 0$:

$$\log \left[\frac{P(y = 0)}{P(y > 0)} \right] = A_0 + A_1 z_1 + \cdots + A_q z_q. \quad (9.16)$$

Stata labels this part of the model the “inflation,” because it will account for the excess of 0 counts that could not be properly modeled using only a one-part Poisson or negative binomial model. The second set of output produced by Stata for the zero-inflated models is the Part 2 estimates in the Poisson or negative binomial regression model for cases with positive counts, $y > 0$:

$$\log[E(y_i | x_i)] = \log(t_i) + B_0 + B_1 x_{1i} + \cdots + B_p x_{pi}. \quad (9.17)$$

THEORY BOX 9.3 PSEUDO LIKELIHOOD FOR THE POISSON AND NEGATIVE BINOMIAL REGRESSION MODELS

The weighted pseudo likelihood for estimating the parameters of the Poisson regression model (9.13) is:

$$\begin{aligned} PL(\mathbf{B} | y_i, \mathbf{x}_i) &= \prod_{i=1}^n \left\{ \frac{(t_i \lambda_i)^{y_i} \exp(-t_i \lambda_i)}{y_i!} \right\}^{w_i} \\ &= \prod_{i=1}^n \left\{ \frac{[t_i \exp(\mathbf{x}'_i \mathbf{B})]^{y_i} \exp[-t_i \exp(\mathbf{x}'_i \mathbf{B})]}{y_i!} \right\}^{w_i}. \end{aligned} \quad (9.18)$$

The pseudo likelihood that is maximized to estimate the regression parameters, \mathbf{B} , of the negative binomial regression model and the dispersion parameter, α , is:

$$\begin{aligned} PL(\mathbf{B}, \alpha | y_i, \mathbf{x}_i) &= \prod_{i=1}^n \left\{ \frac{\Gamma(y_i + \alpha^{-1})}{y_i! \Gamma(\alpha^{-1})} \cdot \left(\frac{\alpha^{-1}}{\alpha^{-1} + t_i \lambda_i} \right)^{\alpha^{-1}} \cdot \left(\frac{t_i \lambda_i}{\alpha^{-1} + t_i \lambda_i} \right)^{y_i} \right\}^{w_i} \\ &= \prod_{i=1}^n \left\{ \left(\frac{\Gamma(y_i + \alpha^{-1})}{y_i! \Gamma(\alpha^{-1})} \cdot \frac{\alpha^{-1}}{\alpha^{-1} + t_i \exp(\mathbf{x}'_i \mathbf{B})} \right)^{\alpha^{-1}} \cdot \left(\frac{t_i \exp(\mathbf{x}'_i \mathbf{B})}{\alpha^{-1} + t_i \exp(\mathbf{x}'_i \mathbf{B})} \right)^{y_i} \right\}^{w_i}. \end{aligned} \quad (9.19)$$

9.4.3 Regression Models for Count Data: Specification Stage

As outlined in Section 9.4.2, the model specification stage in regression analysis of count variables requires the analyst to apply scientific reasoning and quantitative evaluation in choosing between a one- and two-part model. The first question to ask is “Can the count variable be viewed as resulting from a mixture of processes that creates two groups, one that always responds with a zero and one that sometimes responds with a zero?” If the answer is “No: depending on x , events may occur at different rates, but the underlying process (e.g., accidents, bouts of flu, etc.) is common across the survey population,” then a one-part Poisson (svy: poisson) or negative binomial regression model (svy: nbreg) is preferred. If the answer is “Yes,” then either the zero-inflated Poisson model (svy: zip) or the zero-inflated negative binomial model (svy: zinb) may provide a better fit to the count data.

The choice between the simpler Poisson regression model and the extended negative binomial regression model will depend on whether the survey data satisfy the Poisson assumption, $E(y_i|x_i) = \text{var}(y_i|x_i) = t_i\lambda_i$, which is an assumption that can be formally evaluated by estimating the dispersion parameter α and its design-based 95% CI (Section 9.4.4). Once the survey analysts have selected the appropriate GLM for their count data, the steps in variable selection, tests of nonlinearity, and adding interaction terms can proceed as described previously for other forms of regression analysis.

9.4.4 Regression Models for Count Data: Estimation Stage

Estimation of the parameters in regression models for count data follows the general method of maximizing a weighted Poisson or negative binomial pseudo likelihood function (Theory Box 9.3). Section 8.4 has described the basic steps of the Newton–Raphson maximization algorithm for the example case of simple logistic regression.

The default variance estimator in most current software systems is again a version of Binder’s Taylor Series Linearization estimator (9.4) that is appropriate to the data likelihood (Poisson, negative binomial). As is true for all regression models covered in Chapters 7 through 10, most major software packages also provide analysts the option to use BRR or JRR to compute replication variance estimates, $V\hat{\text{ar}}(\hat{\boldsymbol{B}})_{\text{rep}}$.

In Stata, the following programs are available to estimate the various forms of regression models for count variables: svy: poisson (Poisson), svy: nbreg (negative binomial), svy: zip (zero-inflated Poisson), and svy: zinb (zero-inflated negative binomial). Outside of the Stata software package, programs for fitting the zero-inflated regression models to complex sample survey data are not widely available; however, Long and Freese (2006) outline how to fit these and other two-part models using separate programs for logistic regression and the standard Poisson or negative binomial regression program.

9.4.5 Regression Models for Count Data: Evaluation Stage

The evaluation stage in building regression models for count data closely parallels that for other forms of GLMs. As described in Section 9.4.1, an important evaluation step in modeling count data is to ascertain whether the Poisson or the negative binomial form of the model best fits the data. When the two models are estimated for the same set of predictors, x , the Poisson model is “nested” in the extended negative binomial model. For complex sample survey data, Stata does not provide a likelihood ratio test of the null hypothesis that α is 0, but instead outputs a point estimate of α and the design-based 95% CI for the true value. If the 95% CI for α includes 0, one can use the simpler Poisson regression model.

Once the analyst has chosen the type of model, evaluation of the significance of parameters proceeds in standard fashion. Student t -tests for the significance of single parameters are routinely included along with the parameter estimates in the output from Poisson and negative binomial regression procedures in statistical software packages enabling survey data analysis. In Stata, design-adjusted Wald tests for multiple-parameter predictors or custom hypotheses for linear combinations of parameters can be obtained through the use of the `test` postestimation command.

Unfortunately, at the time of this writing, goodness-of-fit tests available for Poisson and negative binomial regression models fitted to simple random samples of data (e.g., the `estat gof` postestimation command in Stata) have not yet been adapted for applications involving complex sample survey data. However, when analyzing complex sample survey data, graphical techniques that compare the modeled distribution of counts (0, 1, 2, etc.) to the observed distribution from the survey can be extremely useful in gauging the quality of the model fit over the range of responses. Here again, readers are referred to Long and Freese (2006) for examples and Stata program syntax. We aim to provide readers with any updates in this area on the book web site.

9.4.6 Regression Models for Count Data: Interpretation Stage

The interpretation of the results of regression models for counts is generally based on estimates and CIs for a statistic termed the *rate ratio* (RR). Based on the identical log(rate) forms of the Poisson and negative binomial models in Equation 9.15, some simple algebra yields:

$$\log[E(y_i/t_i|x_i)] = B_0 + B_1x_{1i} + \cdots + B_px_{pi}. \quad (9.20)$$

This formulation of the Poisson regression model enables exponentiated versions of the regression parameters associated with the predictor variables of interest to be interpreted as RR statistics. Consider the ratio of two expected rates when one predictor, x_j , is increased by one unit:

$$\begin{aligned}
 E(y_i/t_i | x_{ji} + 1) &= \exp[B_0 + B_1x_{1i} + B_2x_{2i} + \dots + B_j(x_{ji} + 1) + \dots + B_px_{pi}] \\
 E(y_i/t_i | x_{ji}) &= \exp[B_0 + B_1x_{1i} + B_2x_{2i} + \dots + B_jx_{ji} + \dots + B_px_{pi}] \\
 \Rightarrow \exp(B_j) &= \frac{E(y_i/t_i | x_{ji} + 1)}{E(y_i/t_i | x_{ji})} \\
 &= \frac{\text{Expected rate at } (x_{ji} + 1)}{\text{Expected rate at } x_{ji}} = \hat{RR}_j.
 \end{aligned} \tag{9.21}$$

Holding all other variables constant, a one-unit increase in the predictor variable x_j will therefore multiply the expected rate at which the event occurs by $RR_j = \exp(B_j)$.

In a similar fashion to odds ratios from logistic regression models, one can estimate $100(1 - \alpha)\%$ CIs for RRs as:

$$CI_{(1-\alpha)}(\hat{RR}_j) = \exp\left[\hat{B}_j \pm t_{df, 1-\alpha/2} \cdot se(\hat{B}_j)\right]. \tag{9.22}$$

9.4.7 Example: Fitting Poisson and Negative Binomial Regression Models to Complex Sample Survey Data

To illustrate the use of Stata procedures for regression modeling of count survey data, Poisson and negative binomial regression models were fitted to a recoded variable, NUMFALLS24, derived from two variables measured in the 2012 HRS (have you fallen in the past 2 years? 1 = yes, 5 = no; and if you have fallen in the past 2 years, how many times have you fallen?). Because only 2012 HRS respondents aged 65 and older were asked about falls, we also generate a subpopulation indicator, AGE65P:

```
gen age65p = .
replace age65p = 1 if nage >= 65 & nage != .
replace age65 = 0 if nage < 65
```

We also generate an offset variable, OFFSET24 (measured in units of months, so that estimated rates represent falls per month):

```
gen offset24 = 24
```

Note that for the 2012 HRS falls measure, the reference period is fixed at 24 (months), enabling us to model the rate of falls per month. In other applications, the exposure time for individual respondents could vary. In such cases, the value of the exposure variable would be set equal to the exposure time recorded for each case.

[Figure 9.8](#) from Section 9.4.1 presents the weighted distribution of the recoded variable NUMFALLS24. [Table 9.7](#) provides a simple (unweighted)

TABLE 9.7

Distribution (Unweighted) of the NUMFALLS24 Variable

Variable	n	Median	Mean	SD	Var	Min.	Max.
NUMFALLS24 (All)	10,594	0	1.2	3.3	11.0	0	50
NUMFALLS24 (>0)	3,835	2	3.3	4.8	23.5	1	50

Source: 2012 HRS.

statistical summary of the distribution of this variable—both for all cases and cases where the count is greater than 0.

```
sum numfalls24 if age65p == 1, detail
sum numfalls24 if numfalls24 >= 1 & age65p == 1, detail
```

The output generated by submitting these initial commands in Stata (summarized in Table 9.7) gives us a sense of the distribution of this count outcome. First, we note that 10,594 adults provided a nonmissing response to this question. We also note that the variance is substantially greater than the mean, which suggests that the Poisson distribution may not be the best choice of a distribution for this outcome measure. As a result, we will also fit a negative binomial regression model to this count response in Stata. Because nearly two-thirds of the observed counts are 0, a two-part zero-inflated version of the negative binomial regression model will also be estimated.

To keep the illustration simple, respondent reports of the number of falls in the past 24 months are modeled as a function of five predictors: GENDER, AGE, ARTHRITIS, DIABETES, and BMI. We begin by centering AGE and BMI at the weighted estimates of their means for individuals aged 65 and above, so that the estimated intercepts in our regression models can be meaningfully interpreted:

```
svyset secu [pweight = nwgtr], strata(stratum)
svy, subpop(age65p): mean nage
svy, subpop(age65p): mean R11BMI
gen nage_c = nage - 74.5
gen bmi_c = R11BMI - 27.7
```

For illustration purposes, we do not take the example analysis through all of the Hosmer et al. steps discussed in previous chapters. But we remind readers that the same steps of identifying key main effects, testing nonlinearity of relationships of continuous predictors, and investigating potential first-order interactions (Section 8.3) would apply in regression modeling of count data.

The three commands below, which follow the use of svyset to declare the essential complex sampling features of the 2012 HRS to Stata, are used to fit

the Poisson, negative binomial and zero-inflated negative binomial models to the generated count variable, NUMFALLS24:

```
svyset secu [pweight = nwgtr], strata(stratum)
svy, subpop(age65p): poisson numfalls24 ib2.gender ///
nage_c arthritis diabetes bmi_c, irr exposure(offset24)

svy, subpop(age65p): nbreg numfalls24 ib2.gender ///
nage_c arthritis diabetes bmi_c, irr exposure(offset24)

svy, subpop(age65p): zinb numfalls24 ib2.gender nage_c ///
arthritis diabetes bmi_c, inflate(ib2.gender nage_c) ///
arthritis) irr exposure(offset24)
```

Note that in each model command, the Stata syntax includes two options: `irr` and `exposure()`. The `irr` option requests that Stata report the results in terms of estimated RRs associated with each of the predictors and CIs for the RRs. The `exposure()` option specifies the exposure time offset for each sample case (fixed to 24 months in this case).

In this example, we elect to use a smaller set of predictors z for the Part 1 logistic model of the zero-inflated negative binomial model. We provide the names of these variables (GENDER, AGE, and ARTHRITIS), which would normally be selected based on theoretical considerations as predictors of never falling, as arguments for the `inflate()` option in the `svy: zinb` command. Another key feature of the commands is the use of `subpop(age65p)` for an appropriate unconditional analysis of the subpopulation of adults 65 years and older.

The remainder of each command is structured like all other regression commands for survey data in Stata. The recoded count response variable (NUMFALLS24) is listed first, followed by the predictor variables of interest. The `ib2.` coding used for GENDER indicates that we wish to treat females (GENDER = 2) as the reference group for GENDER when fitting the models.

[Table 9.8](#) compares the estimates and 95% CIs for the RRs for the Poisson and negative binomial regression models. The results in [Table 9.8](#) suggest that the one-part Poisson and negative binomial regression models would lead to nearly identical conclusions concerning the significance and nature of the effects of the chosen predictors on the rate of falls in the HRS subpopulation aged 65 and above. The estimated CIs for the RRs suggest that males, older adults, and those with arthritis or diabetes experience falls at a significantly higher rate. We would also infer that BMI does not predict the rate of falling when adjusting for all of the other predictors. The estimate of the dispersion parameter in the negative binomial model is $\hat{\alpha} = 3.8$, $CI_{0.95}(\alpha) = (3.5, 4.2)$, indicating that the variance of the observed counts of falls is roughly 4.8 times the mean. This, in turn, implies that the negative binomial is the preferred model for this example.

[Table 9.9](#) contains the Part 2 estimates of these same RRs from the zero-inflated negative binomial model as well as the Part 1 estimates of the odds ratios in the logistic regression model for the probability that the reported

TABLE 9.8

Estimated Rate Ratios from the Poisson and Negative Binomial Regression Models for NUMFALLS24

Predictor ^a	Category	Poisson		Negative Binomial	
		\hat{RR}_j	$CI_{0.95}(RR_j)$	\hat{RR}_j	$CI_{0.95}(RR_j)$
SEX	Male	1.29	(1.101, 1.520)	1.27	(1.076, 1.492)
AGE (Cent.)	Continuous	1.01	(1.006, 1.024)	1.02	(1.008, 1.025)
ARTHRITIS	Yes	2.09	(1.788, 2.438)	2.10	(1.793, 2.459)
DIABETES	Yes	1.28	(1.113, 1.474)	1.30	(1.131, 1.488)
BMI (Cent.)	Continuous	1.00	(0.987, 1.021)	1.00	(0.988, 1.015)

Source: 2012 HRS.

Note: Estimated dispersion parameter in the negative binomial model is $\hat{\alpha} = 3.8$, $CI_{0.95}(\alpha) = (3.5, 4.2)$. $n = 10,026$. Adjusted Wald tests for all parameters. Poisson: $F(5,51) = 30.51$, $p < 0.001$; negative binomial: $F(5,51) = 26.91$, $p < 0.001$.

^a Reference categories for categorical predictors are: Female (SEX), No (ARTHRITIS), No (DIABETES).

TABLE 9.9

Estimated Rate Ratios and Odds Ratios from the Zero-Inflated Negative Binomial Regression Model for NUMFALLS24

Predictor	Category	Part 2: NB Regression ^a		Part 1: Logistic Zero Inflation [#]	
		\hat{RR}_j	$CI_{0.95}(RR_j)$	$\hat{\psi}_j$	$CI_{0.95}(\psi)$
SEX	Male	1.58	(1.31, 1.91)	4.53	(1.68, 12.30)
AGE (Cent.)	Continuous	1.00	(0.99, 1.01)	0.91	(0.89, 0.93)
ARTHRITIS	Yes	1.75	(1.41, 2.16)	0.40	(0.25, 0.64)
DIABETES	Yes	1.31	(1.13, 1.51)	—	—
BMI (Cent.)	Continuous	1.00	(0.99, 1.01)	—	—

Source: 2012 HRS.

^a Estimate of dispersion parameter is $\hat{\alpha} = 3.0$, $CI_{0.95}(\alpha) = (2.6, 3.4)$.

[#] Stata output for svy: zinb with the irr option is in the form of $\hat{B}_j = \ln(\hat{\psi}_j)$ for the Part 1 logistic model. Estimates and CIs shown here are based on the standard transformation in Equations 8.21 and 8.23.

count = 0. The results for the Part 1 logistic regression model confirm that older persons have significantly lower odds of zero falls in a 2-year (24-month) period. After the Part 1 adjustment for the probability of zero falls, the estimated RRs from the Part 2 negative binomial regression model suggest that age does not have further significance in predicting the rate at which falls occur. Interestingly, after controlling for age and arthritis, men ($\hat{\psi} = 4.53$) have much higher odds of zero falls than women—a result that was not evident in the one-part Poisson and negative binomial regression models, where being male appeared to increase the rate at which falls occurred. Although

women are more likely than men to experience at least one fall, men who are prone to experience falls appear to do so at a significantly higher rate than women of the same age and health status ($\hat{RR} = 1.58$).

The results in Table 9.9 also point out that all else being equal, persons with arthritis have reduced odds of zero falls ($\hat{\psi} = 0.40$) and higher adjusted overall rates of falls ($\hat{RR} = 1.75$). We also note that having diabetes continues to significantly increase the rate at which falls occur among those experiencing at least one fall. Controlling for the other predictors, BMI is not significant in predicting the rate of falling.

In the complex sample survey data context, there is currently no statistical test to aid in choosing between the standard negative binomial regression model and the zero-inflated alternative. Based on the results in Tables 9.8 and 9.9, the zero-inflated negative binomial regression model appears to offer scientific insights into the complexity of this simple count measure for falls among older adults that are not evident from the simpler one-part model.

EXERCISES

- 9.1 Using the NCS-R data set and a software procedure of your choice, continue with model fitting for the multinomial logistic regression example presented in Section 9.2.6. Recall that the results of the goodness-of-fit test (from the Fagerland and Hosmer `mlogitgof` command) indicated a poor model fit ($p = 0.004$). For this test, a p -value less than 0.05 indicates poor model fit for our multinomial logistic model predicting work status. This exercise extends the example by adding additional predictors to the model in an attempt to improve model fit.
- Begin by setting the complex sample design variables (Stata) or use an equivalent approach in your chosen software. Then, replicate the model results presented in Section 9.2.6, using the following model specification (Stata syntax):

```
svy: mlogit WKSTAT3C ib2.sex ald mde ///
i.ED4CAT i.ag4cat i.MAR3CAT, rrr
```

If you are using Stata, download and use the `mlogitgof` command after fitting the above model. Make sure your results match those presented previously in this chapter.

- Next, add two main effects to the above model: 1. an indicator of a social phobia diagnosis (DSM_SO, 1 = Yes, 5 = No), and 2. race/ethnicity in four categories (RACECAT, 1 = Other/Asian, 2 = Hispanic/Mexican, 3 = Black, 4 = White):

```
svy: mlogit WKSTAT3C ib2.sex ald mde i.ED4CAT ///
i.ag4cat i.MAR3CAT i.racecat 1.DSM_SO, rrr
```

- c. Fit the model detailed in part b and perform postestimation Wald tests for each predictor variable. Based on these results, which variables are significant in their contribution to the model? Should any variables be dropped from the model?
 - d. If you are using Stata, repeat the `mlogitgof` postestimation command and examine the results. What is the *p*-value for the goodness-of-fit test? What does this indicate about the model in question?
 - e. Prepare a table of results similar to [Table 9.3](#) and write a short paragraph describing the key findings. Make sure to discuss how you incorporated the complex sample design effects in the analysis.
 - f. (*Extra Credit, using Stata or other software that is able to produce plots of marginal predicted values*): Produce a plot of marginal predicted probabilities of not being in the labor force as a function of alcohol dependence and age, similar to [Figure 9.4](#). How would you interpret the plot? Does the addition of race and social phobia as predictors in the model change the interpretation of the plot, and if so, how?
- 9.2 Generate a weighted bar chart examining the estimated distribution of the OBESE6CA outcome in the NCS-R population. Use the NCSRWTSH survey weight, or the Part 1 NCS-R weight. If an analyst were interested in predicting responses on this outcome for a member of this population, would ordinal (cumulative logit) regression be a reasonable analytic approach?
- 9.3 Fit an ordinal (cumulative logit) regression model to the OBESE6CA outcome in the NCS-R data (1 = BMI less than 18.5, 2 = 18.5–24.9, 3 = 25–29.9, 4 = 30–34.9, 5 = 35–39.9, 6 = 40+). Be careful to recognize the parameterization of the model given the software procedure that you choose to fit the model. Make sure to incorporate the complex features of the sample design and the Part 1 NCS-R weight (NCSRWTSH) in the analysis, and consider the following candidate predictors: age, gender, education, region, and race. Be careful with how you handle the categorical predictors. Complete the following exercises based on the estimated coefficients in this model:
- a. Write the ordinal logit model that you are estimating in detail, including the regression parameters and the predictor variables, and using a general specification for the cut point k .
 - b. (*Extra Credit, Stata software*): Install the `gologit2` command and use this command postestimation to test the proportional odds assumption. Be sure to create indicator variables for the test as the “factor” coding is not available in this

command. What would you conclude about the proportional odds assumption for this model? If the assumption is violated, why might you still choose to use ordinal logistic regression?

- c. What is the interpretation of the relationship of age with the ordinal OBESE6CA outcome? Does age appear to have an impact on obesity level? Justify your answer.
 - d. What is the interpretation of the relationship of gender with the OBESE6CA outcome? Does gender appear to have an impact on obesity level? Justify your answer.
 - e. Which variables appear to have a significant relationship with obesity level? Are the directions of the relationships positive or negative (in terms of the actual labels for the values on the OBESE6CA outcome)?
 - f. Based on the estimated parameters in this model, compute the predicted probability that a 50-year-old white male in the East region with 0–11 years of education will report that their obesity level is <18.5.
- 9.4 This exercise uses the HRS 2012 data set and focuses on identifying predictors of a count of the number of days per week respondents drank alcohol (averaged over the previous 3-month period), given ever drinking. The analysis is performed in the subpopulation of those aged 65+. The outcome variable, DAYSDRKPERWK, was created from two variables from HRS 2012 Section C—Physical Health: NC128 and NC129. For example, NC128 asks “Do you ever drink any alcoholic beverages such as beer, wine, or liquor?” and if NC128 = 1 or “yes,” the next question, NC129, asks “In the last three months, on average, how many days per week have you had any alcohol to drink? (For example, beer, wine, or any drink containing liquor.)” The coding for the outcome variable DAYSDRKPERWK ranges from 0 (never drank or drank <1 day per week) to 7 (drank every day in average week during past 3 months). See Section 9.4.7 for a review of similar syntax for creating a variable measuring the number of falls during the past 2 years. In addition, an offset variable used in Poisson regression, OFFSET, was set to 7 (representing 7 days of exposure for all respondents).
- a. Using an appropriate software procedure, prepare a weighted bar chart of the response variable DAYSDRKPERWK, in the subpopulation of those aged 65+ (AGE65P). Based on the graph, provide a short description of the distribution.
 - b. Perform an unweighted descriptive analysis of the response variable, within the subpopulation of interest. What is the

mean and variance of the response variable? What might this comparison suggest in terms of alternate analysis techniques?

- c. Fit a design-based Poisson regression model to the DAYSDRKPERWK response variable, treating the number of days drank per week, on average, during the past 3 months as a count variable. Consider the predictor variables NAGE, GENDER, DIABETES, and MARCAT. Be sure to use AGE65P for a correct subpopulation analysis for those aged 65 and older, include the offset variable (OFFSET) in the model, and use correct factor coding for categorical variables. Finally, account for the complex sample design of the HRS (stratum codes = STRATUM, sampling error computation units = SECU) when estimating standard errors for the parameter estimates, and compute unbiased estimates of the regression parameters using the final survey weights (NWGTR). Generate a table similar to [Table 9.8](#) (with just the Poisson regression section) presenting the results of the analysis, including weighted parameter estimates displayed as rate ratios (defined as the exponent of the parameter estimate), design-adjusted standard errors, and 95% CIs for the parameters.
- d. Use a postestimation `test` statement (Stata command) or equivalent for each predictor in the model and prepare a table of results similar to [Table 8.8](#) (from [Chapter 8](#)). Based on these results, what decisions would you make about the inclusion of these predictors in the model?
- e. Refit the model using the same design-based approach, only assuming a negative binomial distribution for the count of days drank per week for the pseudo maximum likelihood estimation. What is the estimate of the dispersion parameter in this model? What does this suggest about the Poisson regression approach?
- f. Compare the estimates of the parameters and the estimated risk ratios obtained using each approach, and discuss whether any of your inferences would differ depending on the assumed distribution for the counts.

10

Survival Analysis of Event History Survey Data

10.1 Introduction

Survival analysis, or *event history analysis* as it is often labeled in the social sciences, includes statistical methods for analyzing the time at which “failures” or events of interest occur. Common examples of *event times* of interest in the survival analysis literature include motor longevity (engineering), time of death, time to disease incidence or recovery (medicine and public health), time to unemployment, time to divorce, or time to retirement (social sciences). Survival analysis is an important statistical topic that when treated in its full depth and breadth fills entire volumes. This chapter will only scratch the surface of this topic, focusing on basic theory (Section 10.2) and application for three survival analysis techniques that are commonly used with complex sample survey data. Section 10.3 will introduce nonparametric Kaplan–Meier (K–M) analysis of the survivorship function. The Cox Proportional Hazards (CPH) model will be covered in Section 10.4, and Section 10.5 presents a description and application of logit and complementary-log-log (C–L–L) models for discrete time event history data. Readers interested in the general theory and applications of survival analysis methods are referred to classic texts including Kalbfleisch and Prentice (2002), Lee (1992), and Miller (1981). Newer texts on applied methods (Hosmer et al., 2008) and several excellent user guides are also available that illustrate procedures for survival analysis in SAS (Allison, 1995) and Stata (Cleves et al., 2016).

10.2 Basic Theory of Survival Analysis

10.2.1 Survey Measurement of Event History Data

In the context of population-based survey research, survival analysis problems arise in three primary ways: (1) through longitudinal observations

on individuals in a panel survey; (2) by administrative record follow-up of survey respondents; and (3) from retrospective survey measurement of events and times that events occurred. The Health and Retirement Study (HRS) and other longitudinal panel studies prospectively follow and reinterview sample members over time. In this *prospective cohort design*, dates of events such as retirement, institutionalization, morbidity, and mortality are captured in the longitudinal data record. Administrative follow-up of a sample of survey participants using vital statistics, medical records, or other record-keeping systems also generates a prospective measurement of events of interest and the dates on which they occurred. The NHANES III-linked mortality file (<http://www.cdc.gov/nchs/data-linkage/index.htm>) is an excellent example where U.S. Vital Statistics records were used to prospectively detect and record the death of an NHANES III respondent for a period of years after the survey was conducted.

The third means of generating “survival data” in the survey context is through the use of retrospective measurement of event histories. [Figure 10.1](#) is an illustration of a question sequence from the National Comorbidity Survey Replication (NCS-R) that uses retrospective recall to report and date events over the course of the respondent’s lifetime (or other relevant observation

*D37. Think of the very first time in your life you had an episode lasting (several days or longer/two-weeks or longer) when most of the day nearly every day you felt (sad/or/discouraged/or/uninterested) and also had some of the other problems (you cited earlier). Can you remember your exact age?
YES.....1
NO.....5 GO TO *D37b
DON'T KNOW.....8 GO TO *D37b
REFUSED.....9 GO TO *D37b
 *D37a. (How old were you?) _____ YEARS OLD GO TO *D37b.1
DON'T KNOW.....998 GO TO *D37b.1
REFUSED.....999 GO TO *D37b.1
 *D37b. About how old were you (the first time you had an episode of this sort)? IF “ALL MY LIFE” OR “AS LONG AS I CAN REMEMBER,” PROBE: Was it before you first started school? IF NOT YES, PROBE: Was it before you were a teenager? _____ YEARS OLD
BEFORE STARTED SCHOOL 4
BEFORE TEENAGER 12
NOT BEFORE TEENAGER..... 13
DON'T KNOW..... 998
REFUSED..... 999

FIGURE 10.1

Example of NCS-R retrospective event recall questions.

period). Survey methodologists are well aware of recall, telescoping, and non-random censoring errors that may be associated with such retrospective measurements (Groves et al., 2009). Techniques such as Event History Calendars that use key lifetime events and dates are often employed to anchor the retrospective recall measurement of events and times (Belli, 2000).

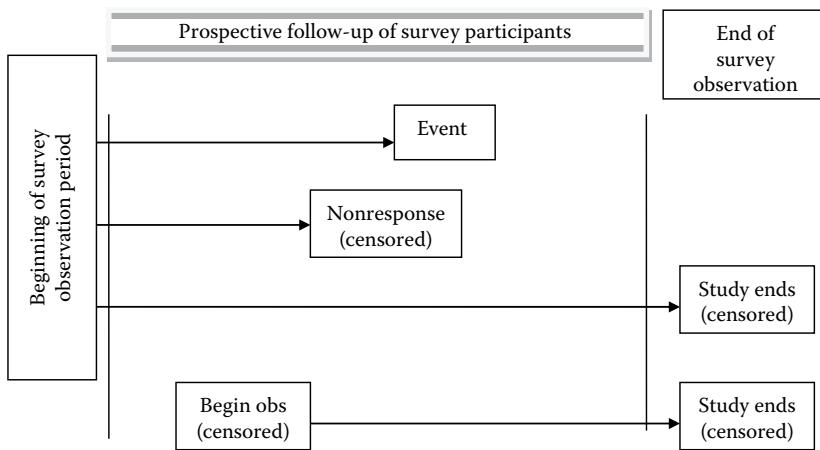
10.2.2 Data for Event History Models

Time itself is at the heart of survival analysis—time to occurrence of an event, T , or the time at which the observation on the survey subject is censored, C . Only one of these two times is directly measured. T is measured if the event of interest occurs during the survey observation or follow-up period. The censoring time, C , is measured in cases where the respondent is *lost to follow-up* (due to noncontact, refusal, or other reasons) or if the survey observation period has ended and no event has yet occurred. Estimation of the survival analysis model requires assumptions concerning the relationship of T and C —the most common being that time to event and censoring time distributions are independent of each other after controlling for any covariates in the model.

The majority of survival analysis problems deal with time to a single event or the first occurrence of the event. Often the transition is to an *absorbing state* (e.g., mortality). This is the class of applications that we will consider in this chapter. However, readers should be aware that event history methods have been extended to include models of repeated events (e.g., heart attacks, marriages) or *spells* of time between events (e.g., unemployment episodes, or events that may be due to multiple causes or *competing risks*; see Yamaguchi, 1991 and Allison, 1995).

In the literature and in applications, survival models are often referred to as *continuous time* or *discrete time* models. The dependent variables T and C may be measured on a continuous scale (e.g., number of milliseconds until failure) or a discrete scale (e.g., number of years of marriage until divorce). Discrete survival times often arise in longitudinal survey designs where observations occur on a periodic basis (e.g., every 2 years for the HRS) and it is difficult to precisely pinpoint the date and time that the event occurred.

Figure 10.2 illustrates the general nature of the observational data that are available for a survival analysis of survey data. The figure illustrates the *observational window* spanning the time period at which survey observations begin to the point in time when the survey observations end. In the figure, the first horizontal “time” arrow illustrates the case where an event occurs and the time to the event, T , is recorded. The second arrow represents a case that is followed from the beginning of the survey observation window but is lost to follow-up (censored) before the study is complete. A second form of censored observation is represented by the third arrow in the figure. This case is successfully monitored from the beginning to the end of the observation window but the event of interest does not occur. In cases 2 and 3, the

**FIGURE 10.2**

Prospective view of event history survey data.

time that is recorded in the data set is the censoring time, C ; an event time is never observed. The censoring mechanism that is illustrated by cases 2 and 3 in Figure 10.2 is termed *right censoring*. Survey observations may also be *left censored* as illustrated by the fourth and final horizontal arrow in Figure 10.2. Left censoring of survey observations can occur for several reasons including ineligibility in the initial period of survey observation or initial nonresponse.

“Censored” observations such as these are important in survival analysis since they remain representative of the *population at risk* up to the point that further observation is censored. In the analysis examples presented in this chapter, we will assume *Type 1 Censoring*, where any censoring is random over the fixed period of observation.

10.2.3 Important Notation and Definitions

Prior to examining survival analysis models in more detail, several important statistical definitions are required. The *probability density function* for the event time is denoted by $f(t)$, and is defined as the probability of the event at time t (for continuous time), or by π_m denoting the probability of failure in the interval $(m, m + 1)$ for discrete time. The corresponding cumulative distribution functions (CDFs) are defined in the standard fashion:

$$\begin{aligned}
 F(t) &= \int_0^t f(t) dt \text{ for continuous } t; \text{ or} \\
 F(m) &= \sum_{k \leq m} \pi(k) \text{ for } t \text{ measured in discrete intervals of time.}
 \end{aligned} \tag{10.1}$$

The CDFs for survival time measure the probability that the event occurs at or before time t (continuous) or before the close of time period m (for discrete time).

The *survivor function* or *survivorship function*, $S(t)$, is the complement to the CDF and is defined as follows:

$$\begin{aligned} S(t) &= 1 - P(T \leq t) = 1 - F(t) \text{ for continuous time; or} \\ S(m) &= 1 - F(m) \text{ for discrete time.} \end{aligned} \quad (10.2)$$

The value of the survivor function for an individual is the probability that the event has *not yet occurred* at time t (continuous) or prior to the close of observation period m (discrete time).

The concept of a *hazard* or *hazard function* plays an important role in the interpretation of survival analysis models. A hazard is essentially a conditional probability. For continuous time models, the hazard is $h(t) = f(t)/S(t)$, or the conditional probability that the event will occur at time t given that it has not occurred prior to time t . In discrete time models, this same conditional probability takes the form $h(m) = \pi(m)/S(m - 1)$.

10.2.4 Models for Survival Analysis

Survival analysis models are classified into four major types, based on the assumptions that are made concerning the probability distributions of survival times. We briefly discuss these four types of survival analysis models in this section.

Parametric survival models assume a parametric distribution for the probability density function $f(t)$. A very common example is the exponential distribution with rate parameter 1. In this case, $f(t) = e^{-t}$, $F(t) = 1 - e^{-t}$, and $S(t) = e^{-t}$. This distribution is characterized by a constant hazard function, $h(t) = f(t)/S(t) = e^{-t}/e^{-t} = 1$. Additional common examples of parametric models for survival times include the Weibull distribution (often used for human mortality), the log-normal distribution, and the gamma distribution. For more details on parametric models for survival data, we refer readers to Kalbfleisch and Prentice (2002) or Miller (1981). Software procedures for fitting parametric survival models to complex sample survey data are not yet widely available. Stata currently provides the `svy: streg` command for users interested in fitting these models to survey data, but similar procedures have not yet been widely implemented in other statistical packages. As a result, our focus in this chapter will be on nonparametric and semiparametric survival models that can currently be fitted in several major software packages while taking complex sample designs into account.

Nonparametric survival models make no assumptions concerning the probability density functions of survival times, and include approaches like *K-M estimation* and *life table methods*. These empirically-based methods estimate

survivor functions and hazards solely using the observed survey data, and do not rely on any parametric assumptions (i.e., assumed probability models). We present examples of applying these methods to survey data in Section 10.3.

The popular *Cox Proportional Hazards (CPH) model* is labeled as a *semiparametric survival model*. The CPH model makes no strong assumptions concerning the underlying probability distribution for event times but does make an assumption of proportionality in the regression parameterization of the individual hazard associated with the covariate vector, \boldsymbol{x} . We consider an example of fitting a CPH model to survey data in Section 10.4.

Finally, a special class of survival models exists for *discrete time event history data*. The models and methods introduced above are largely applicable for survival times that are roughly continuous in nature, taking on many possible values on a continuum. Some survival times may be measured in terms of discrete units of time only; for example, in a panel survey covering 5 years, a researcher might wish to analyze the number of years until a person loses their job (1, 2, 3, 4, or 5) as a function of selected covariates. Because these failure times are measured in terms of a small number of discrete values, alternative methods are needed. Section 10.5 introduces *discrete time logit models* and *C-L-L models* for discrete time event history data.

In each of the following sections, the example applications will be based on a survival analysis of the age of onset for a major depression episode (MDE) from the NCS-R ([Figure 10.1](#)). The event of interest for the survival analysis is thus the first MDE that the respondent experiences. The event time is the age that they report experiencing their first MDE. Individuals who have never in their life prior to interview had an MDE are assumed to provide right-censored data; that is, we analyze their ages at interview, but the ages are considered to be right-censored for the purposes of the survival analysis. In Sections 10.4 and 10.5, we illustrate the fitting of CPH and discrete time logit regression models to the NCS-R data using Stata, considering gender (SEX), age at interview (INTWAGE), marital status (MAR3CAT), education (ED4CAT), and ethnicity (RACECAT) as possible predictors of the hazard of having a first MDE at a given age. Note that in this analysis, each NCS-R respondent's observation window ([Figure 10.2](#)) begins at birth and continues until: (1) the age at which they first experience an MDE or (2) the age at which they are interviewed for NCS-R.

10.3 (Nonparametric) K-M Estimation of the Survivor Function

The *K-M* or *product limit estimator* is a nonparametric estimator of the survivorship function, $S(t)$. It can be applied to event times that are measured on a

continuous time (t) basis or as counts of events measured over discrete time periods, $m = 1, \dots, M$.

10.3.1 K-M Model Specification and Estimation

A general form of the K-M estimator for complex sample survey data applications can be expressed as

$$\hat{S}(t) = \prod_{t(e) \leq t} \left(1 - \frac{\hat{D}_{t(e)}}{\hat{N}_{t(e)}} \right), \quad (10.3)$$

where:

$t(e)$ = times at which unique events $e = 1, \dots, E$ are observed.

$$\hat{D}_{t(e)} = \sum_{i=1}^n I[t_i = t(e)] \cdot \delta_i \cdot w_i; \quad \hat{N}_{t(e)} = \sum_{i=1}^n I[t_i \geq t(e)] \cdot w_i,$$

where:

$I[\cdot]$ = indicator = 1 if [expression] is true, 0 otherwise;

δ_i = 1 if the observed time for case i is a true event, 0 if a censored time; and

w_i = the survey weight for observation i .

The survivorship at any point in time t is estimated as a product over unique event times, where $t(e) \leq t$, of the estimated conditional survival rates at each event time $t(e)$. Note how at each unique event time the rate of events is a ratio of the weighted estimate of total events at $t(e)$ to the estimated population "at risk" at time $t(e)$. Note also that the survey weights (possibly incorporating adjustments for nonresponse and poststratification/calibration) for the observations are incorporated into the estimation of the survivorship function.

Unlike the regression-based methods described later in this chapter, the K-M estimator of survivorship does not permit adjustment for individual covariates. However, the K-M estimates of survivorship can be computed separately for subgroups, $h = 1, \dots, H$, of the survey population (e.g., separately for men and women). PROC KAPMEIER in SUDAAN and the SPSS Complex Samples Cox Regression program (product limit estimator option) provide the capability to conduct a full K-M analysis for complex sample survey data including estimation for subpopulations. Stata provides the capability to compute and plot weighted estimates of the survivor function, but currently does not permit design-based estimation of the standard errors of the estimates or confidence intervals (CIs). At present, PROC PHREG in SAS permits survey-weighted K-M estimation and display of the survival function for different subgroups (in conjunction with PROC SGPlot; Gardiner,

2015), but this procedure does not support design-adjusted estimates of standard errors and CIs nor does it allow the use of noninteger weights. Any changes in terms of the capabilities of these software procedures will be reported on the book web site.

Under complex sample designs, SUDAAN employs a Taylor Series Linearization (TSL), Balanced Repeated Replication (BRR), or Jackknife Repeated Replication (JRR) estimator of the standard error of $\hat{S}(t)$. SUDAAN's TSL estimates of $se(\hat{S}(t))$ require the generation of a large matrix of derivative functions that may lead to computational difficulties. SUDAAN allows users to circumvent this problem by estimating the K-M survivorship and standard errors for a subset of points (e.g., deciles) of the full survivorship distribution. Another alternative that we recommend is to employ the JRR option in SUDAAN to estimate the full survivorship distribution and CIs for the individual $\hat{S}(t)$. Using the TSL or JRR estimates of standard errors, confidence limits for individual values of $\hat{S}(t)$ are then derived using a special two-step transformation/inverse transformation procedure (see Kalbfleisch and Prentice, 2002 and Theory Box 10.1 for details).

THEORY BOX 10.1 CONFIDENCE INTERVALS USING KAPLAN-MEIER ESTIMATES OF $\hat{S}(t)$

A two-step (transformation, inverse transformation) procedure can be used to estimate CIs for the survivorship at time t , $S(t)$.

In the first step, the $100(1 - \alpha)\%$ CI is estimated on the $\log(-\log(\hat{S}(t)))$ scale:

$$CI_{g(S(t))} = g(\hat{S}(t)) \pm t_{df,1-\alpha/2} \cdot se(g(\hat{S}(t))),$$

where:

$$\begin{aligned} g(\hat{S}(t)) &= \log(-\log(\hat{S}(t))); \text{ and} \\ se(g(\hat{S}(t))) &= \sqrt{\frac{var(\hat{S}(t))}{[\hat{S}(t) \cdot \log(\hat{S}(t))]^2}}. \end{aligned} \quad (10.4)$$

For simple random sample (SRS) data, $var(\hat{S}(t))$ is based on Greenwood's (1926) estimator. For complex samples, $var(\hat{S}(t))$ is estimated by TSL (RTI, 2012) or through JRR methods.

The inverse transformation, $\exp(-\exp())$, is then applied to the lower and upper limits of $CI_{1-\alpha}(g(S(t)))$ to construct the $100(1 - \alpha)\%$ CI for $S(t)$.

10.3.2 K-M Estimator: Evaluation and Interpretation

Since the K-M estimator is essentially “model free,” the evaluation phase of the analysis is limited to careful inspection and display of the estimates of $\hat{S}(t)$ and the associated standard errors. Interpretation and display of the results is best done using plots of the estimated survivorship functions against time. Such plots are an effective way to display the overall survivorship curves and to compare the survival outcomes for the distinct groups (Figure 10.3).

Under SRS assumptions, two quantitative tests (a Mantel-Haenszel test and a Wilcoxon test) comparing observed and expected “failures” over time can be used to evaluate whether the survivorship curves for two groups are equivalent (i.e., test a null hypothesis defined as $H_0: S_1(t) = S_2(t)$). Analogous Wald-type X^2 test statistics could be developed for complex sample applications, but to the best of our knowledge these have not been implemented in the current software programs that support K-M estimation for complex sample survey data. In this chapter, we will focus on the graphical display of the K-M estimates of the survivorship function, using these plots to inform decisions about predictors to use in CPH and discrete time regression models of survival.

10.3.3 K-M Survival Analysis Example

We begin our analysis example for this chapter by computing and plotting weighted K-M estimates of the survivor functions (10.3) for four NCS-R

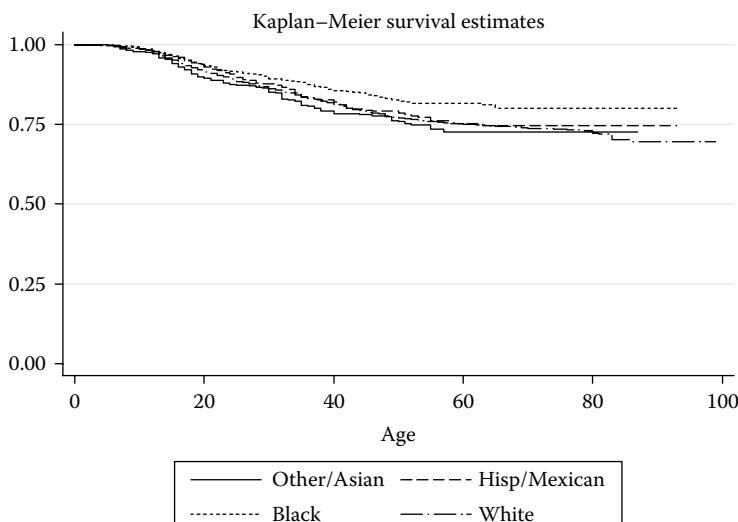


FIGURE 10.3

Weighted Kaplan-Meier estimates of the survivor functions for lifetime major depressive episode for four ethnic groups. (From NCS-R.)

subgroups defined by the race variable (RACECAT). Even if a full K-M analysis is not the goal, this initial step is useful to visually examine the survivor functions for different groups, and determine whether (a) the functions appear to differ substantially and (b) the survival functions appear to be roughly parallel (one of the assumptions underlying the Cox model, discussed in Section 10.4).

We first define a new variable AGEONSETMDE as being equal to the age of first MDE (MDE_OND), if a person has had an MDE in their lifetime, or the age of the respondent at the interview (INTWAGE) if a person has not had an MDE in their lifetime:

```
gen ageonsetmde = intwage
replace ageonsetmde = mde_ond if mde == 1
```

The recoded variable, AGEONSETMDE, will serve as the time-to-event variable in this example. Next, we declare the structure of the NCS-R time-to-event data in Stata using the `stset` command. This is a required specification step that must be run before invoking a Stata survival analysis command.

```
stset ageonsetmde [pweight = ncsrwtsh], failure(mde==1)
```

With the initial `stset` command, we define AGEONSETMDE as the variable containing the survival times (ages of first MDE onset, or right-censored ages at NCS-R interview for those individuals who had not yet experienced an MDE in their lifetime), and the indicator of whether an event actually occurred or whether the data should be analyzed as right-censored. This indicator is simply the indicator of lifetime MDE in the NCS-R data set (MDE), equal to 1 if the individual has ever had an MDE, and 0 otherwise (the censored cases). Note that we also define a “pweight” (or survey weight) for the time-to-event data with the `[pweight = ncsrwtsh]` addition. Once the `stset` command has been submitted, Stata displays the following output:

```
failure event: mde == 1
obs. time interval: (0, ageonsetmde]
exit on or before: failure
    weight: [pweight=ncsrwtsh]

-----
9282 total obs.
      0 exclusions

-----
9282 obs. remaining, representing
1829 failures in single record/single failure data
385696 total analysis time at risk, at risk from t =
earliest observed entry t =          0
last observed exit t =            99
```

We see that there are 1,829 recorded “failure events” or individuals having experienced an MDE in their lifetime (with MDE = 1). Stata also processes the total number of observations at risk at each age starting with age 0, and the last observed exit from the risk set (an individual was interviewed at age 99 and reported never having an episode of MDE in his lifetime). Stata saves these variables in memory for any subsequent survival analysis commands, similar to how `svyset` works for identification of complex design variables (strata, clusters, weights).

Stata allows users to plot weighted population estimates of the survivor functions (provided that survey weights were specified in the `stset` command) for different groups by using the `sts graph` command with a `by()` option, and we now apply this command to the NCS-R data:

```
sts graph, by(racecat) legend(lab(1 "Other/Asian") ///
lab(2 "Hisp/Mexican") lab(3 "Black") lab(4 "White"))
```

This command generates the plot in [Figure 10.3](#).

The resulting plot in [Figure 10.3](#) is very informative. First, by age 90, only about 25% of the persons in each race group will have had a major depressive episode. Further, the black race group consistently has a smaller percent of persons that have experienced a major depressive episode by each age considered. We also note that there is no strong evidence of distinct crossing of the estimated survival functions across ages; an assumption of parallel lines would seem fairly reasonable for these four groups.

Stata users can also use the `sts list` command to display estimates of the overall survivor function at specified time points (or ages in this example). The command below requests estimates of the survivor function at seven unique time points:

```
sts list, at(10 20 30 40 50 60 70)
```

Submitting this command results in the following Stata output:

Time	Total	Fail	Survivor
			Function
10	9171.84	139.004	0.9850
20	8169.95	632.016	0.9165
30	6390.66	401.574	0.8659
40	4736.49	327.113	0.8155
50	2997.27	186.745	0.7760
60	1779.61	59.0606	0.7568
70	949.309	22.2811	0.7438

Note: survivor function is calculated over full data and evaluated at indicated times; it is not calculated from aggregates shown at left.

We note that design-adjusted standard errors for these estimates of the survivor function are not presently available in Stata. At present, PROC KAPMEIER in SUDAAN does provide the capability to compute weighted estimates of the survivor function along with design-based standard errors and 95% CIs for the survival estimates. Example SUDAAN syntax required to conduct this descriptive analysis for the NCS-R MDE data is as follows:

```
proc kapmeier;
nest sestrat seclustr ;
weight ncsrwtsh ;
event mde ;
class racecat ;
strhaz racecat ;
time ageonsetmde ;
setenv decwidth=4 ;
output/kapmeier=all filename="c10_km_out" filetype=sas ;
replace ;
run ;
```

Table 10.1 contains an extract from the complete set of results produced by this analysis. The table displays the total population K-M estimates of the survivor function, along with the standard errors and 95% CIs for the values of the survivor function at ages $t = 10, 20, 30, \dots, 70$. Note that the weighted estimates of $\hat{S}(t)$ at these ages match those obtained in the weighted analysis using Stata's sts list syntax. The full output includes age-specific estimates of the survivor function for the total population and separately for each of the four race/ethnic groups defined by RACECAT. In PROC KAPMEIER, the stratified K-M analysis is invoked by the use of the STRHAZ varname; statement. SUDAAN

TABLE 10.1

Selected Results from the Kaplan–Meier Analysis of the NCS-R Age of Onset for MDE Data in SUDAAN

Age of Onset	$\hat{S}(t)$	SUDAAN $se(\hat{S}(t))$	SUDAAN $CI_{0.95}(S(t))$
10	0.985	0.001	(0.982, 0.988)
20	0.917	0.004	(0.908, 0.924)
30	0.866	0.005	(0.855, 0.876)
40	0.816	0.005	(0.804, 0.826)
50	0.776	0.006	(0.764, 0.787)
60	0.757	0.006	(0.745, 0.769)
70	0.744	0.007	(0.730, 0.757)

does not provide the capability to plot the estimated curves and CIs for the survivorship at each age of onset; however, the analysis output can be saved using SUDAAN's OUTPUT statement and exported to a software package that has a general graphics capability to produce the desired plots.

10.4 The Cox Proportional Hazards (CPH) Model

The CPH model (Cox, 1972) is one of the most widely used methods for survival analysis of continuous time event history data. CPH regression provides analysts with an easy-to-use and easy-to-interpret multivariate tool for examining impacts of selected covariates on expected hazard functions. Despite its widespread use and the semiparametric nature of the underlying model, survey analysts must be careful to examine the critical "proportional hazards" assumption and to ensure that the model is fully and correctly identified. Focusing largely on clinical trials, Freedman (2008) cautions against blind use of Cox regression models without performing some initial descriptive analyses of the survival data.

10.4.1 CPH Model: Specification

The Cox model for proportional hazards is specified as follows:

$$h(t | \mathbf{x}_i) = h_0(t) \exp\left(\sum_{j=1}^P B_j x_{ij}\right). \quad (10.5)$$

In 10.5, $h(t | \mathbf{x}_i)$ is the expected hazard function for an individual i with vector of covariates \mathbf{x}_i at time t . The model includes a baseline hazard function for time t , $h_0(t)$, that is common to all population members. The individual hazard at time t is the product of the baseline hazard and an individual-specific factor, $\exp\left(\sum_{j=1}^P B_j x_{ij}\right)$, that is a function of the regression parameters, $B = \{B_1, \dots, B_p\}$ and the individual covariate vector, $\mathbf{x}_i = \{x_{i1}, \dots, x_{ip}\}$. Individual hazards are therefore a proportional scaling of the baseline hazard: $h(t | \mathbf{x}_i) \propto h_0(t)$. There is no separate intercept parameter in the CPH model specification; the baseline expectation (i.e., the hazard when all covariates are equal to 0) is absorbed into $h_0(t)$.

The CPH model is most applicable to continuous or nearly continuous measurement of event and censoring times. Available software for estimating the CPH model anticipates the possibility that multiple events/censoring may occur at any time point t and incorporates rules for handling such ties.

For example, Stata assumes that events occur before censoring if there are ties—censored cases at time t remain in the risk set for events at time t . If the time scale for the survey observations is very coarse (e.g., years in a study of children age 5–18) or explicitly discrete (e.g., the 2-year period between consecutive HRS survey interviews), many events and censorings may occur at time period t . If the measurement of time is coarse and ties are common, analysts might consider the C-L-L discrete time model of Section 10.5 as an alternative to CPH regression.

The values of covariates in the CPH model may be fixed (e.g., gender, race) or they may be *time-varying covariates*, meaning that the values of the covariates can change depending on the time at which the set of sample units “at risk” is being evaluated. Stata allows users to set up time-varying covariates for use in the svy: stcox command for estimating the CPH model. If the desired model includes a large number of time-varying covariates, an alternative to the CPH model is to recode the event and censoring times into discrete time units and apply the discrete time logistic or C-L-L models described in Section 10.5.

10.4.2 CPH Model: Estimation Stage

The CPH regression parameters B_j are estimated using a *partial likelihood* procedure, based on the conditional probability that an event occurred at time t (see Freedman [2008] for a nice primer, or Lee [1992] for more details). For estimation, the E observed event times are ordered such that $t_{(1)} < t_{(2)} < \dots < t_{(E)}$. The *risk set* at a given time t , $t = 1, \dots, E$, is the set of respondents who: (1) have not experienced the event prior to time t and (2) were not randomly censored prior to time t . The probability of an event that occurs at time t for the i -th respondent, conditional on the risk set R_t , is defined as follows:

$$P(t_i = t | \mathbf{x}_i, R_t) = \frac{\exp\left(\sum_{j=1}^P B_j x_{ij,t}\right)}{\sum_{l \in R_t} \exp\left(\sum_{j=1}^P B_j x_{lj,t}\right)}. \quad (10.6)$$

where:

$$R_t = \{\text{set of cases still “at risk” at time } t\}.$$

This conditional probability is computed for every event that occurs. The partial likelihood function for the survey observations of event times is then defined as the product of these probabilities (Theory Box 10.2). An iterative mathematical algorithm is then applied to derive estimates of the regression parameters that maximize the partial likelihood function.

THEORY BOX 10.2 PARTIAL LIKELIHOOD FOR THE COX PROPORTIONAL HAZARDS MODEL

The partial likelihood that forms the basis for estimating the regression parameters of the CPH model is the product of conditional probabilities—one for each distinct event, $e = 1, \dots, E \leq n$ that is recorded in the survey period. Each conditional probability component of this partial likelihood is the ratio of the time $t(e)$ hazard for the case experiencing the event (case i) to the sum of hazards for all sample cases remaining in the risk set at $t(e)$:

$$L(B) = \prod_{i=1}^n \left[\frac{h(t(e)_i | \mathbf{x}_i)}{\sum_{j=1}^n I[t(0)_j < t(e)_i \leq t(e)_j] \cdot h(t(e)_j | \mathbf{x}_j)} \right]^{\delta_i \cdot w_i},$$

where:

$t(0)_j$ is the observation start time for respondent j .

$t(e)_i$ and $t(e)_j$ are the respective event (censoring) times for respondents i and j .

$I[t(0)_j < t(e)_i \leq t(e)_j]$ is the 0, 1 indicator that respondent i is in the risk set when unit j experiences an event.

$\delta_i = 1$ if unit i experiences the event, 0 if unit i is censored.

w_i = the survey weight for unit i .

In the partial likelihood for complex sample survey applications, the contribution of the i -th case to the partial likelihood is raised to the power of its survey weight, w_i . Censored cases that remain in the risk set contribute to the denominator of the conditional probabilities for events that occur to other cases; however, the direct contributions of censored cases to the product likelihood are factors of 1 (due to the $\delta_i = 0$ exponent).

Binder (1992) describes the TSL approach for estimating $\text{var}(\hat{\mathbf{B}})_{TSL}$ that accounts for the complex sample design. BRR, JRR, or bootstrap methods can also be used to compute replicated estimates of the variances and covariances of the model coefficients, $\text{var}(\hat{\mathbf{B}})_{Rep}$. Routines capable of fitting proportional hazards models and computing design-based estimates of standard errors for the parameter estimates are currently implemented in Stata, SAS, the SPSS Complex Samples module, SUDAAN, the survey package in R, MPlus, and IVEware (Appendix A).

10.4.3 CPH Model: Evaluation and Diagnostics

Procedures for constructing CIs and testing hypotheses for the estimated parameters of the CPH model parallel those described in previous chapters for the parameters of other linear and generalized linear regression models (see Section 7.5 for example).

Diagnostic tool kits for CPH models fitted to complex sample survey data sets are still in the early stages of development. Inspection of the K-M estimates of the survivor functions for different groups can be helpful as an initial step, to see if the survival functions are approximately parallel. A better graphical check of the proportional hazards assumption that is currently implemented in Stata is a plot of $-\ln(-\ln(\hat{S}_h(t)))$ against $\ln(t)$, where $\hat{S}_h(t)$ is a weighted estimate of the survival function for group h . Based on the specified Cox model, the transformed versions of the survival functions should be parallel as a function of $\ln(t)$.

At the time of the writing of this second edition, only selected software systems have incorporated standard residual diagnostics for CPH models into the CPH model programs for complex sample survey data. For example, it is possible to generate *partial Martingale residuals* (e.g., in SUDAAN) for the purpose of checking the functional forms of continuous covariates in the Cox model. These residuals are computed as

$$M_i = \delta_i - \hat{H}_i(t), \quad (10.7)$$

where δ_i represents an indicator variable for whether or not a given sample case i had the event of interest occur (1 = event, 0 = censored), and $\hat{H}_i(t)$ represents a weighted estimate of the *cumulative hazard function* based on the fitted model (or the cumulative sum of all instantaneous probabilities of failure up until time t ; one can also think of this function as the “total rate” of experiencing an event up to time t). These residuals can be plotted against the values of individual continuous covariates to check for the possibility of nonlinear relationships, which would indicate that the functional forms of continuous covariates may have been misspecified.

Any additional developments allowing users to generate these residuals and further evaluate the goodness of fit of Cox models will be highlighted on the companion web site for the book. For additional discussion of fitting Cox models to complex sample survey data sets, we refer interested readers to Cleves et al. (2016, Section 9.5).

10.4.4 CPH Model: Interpretation and Presentation of Results

Interpretation of results and population inference from the CPH model is typically based on comparisons of *hazards*—the conditional probabilities that the event will occur at time t given that it has not occurred prior to time t . Given estimates of the regression parameters in the model, consider the ratio

of estimated hazards if predictor variable x_j is incremented by one unit and all other covariates remain fixed:

$$\begin{aligned}\hat{HR}_j &= \frac{h_0(t)\exp(\hat{B}_1(x_1) + \cdots + \hat{B}_j(x_j + 1) + \cdots + \hat{B}_p(x_p))}{h_0(t)\exp(\hat{B}_1(x_1) + \cdots + \hat{B}_j(x_j) + \cdots + \hat{B}_p(x_p))} \\ &= \exp(\hat{B}_j).\end{aligned}\quad (10.8)$$

The one-unit change in x_j will multiply the expected hazard by $\hat{HR}_j = \exp(\hat{B}_j)$. This multiplicative change in the hazard function is termed the *hazard ratio*. If x_j is an indicator variable for a level of a categorical predictor, then $\hat{HR}_j = \exp(\hat{B}_j)$ is the relative hazard compared to the hazard for the reference category used to parameterize the categorical effect.

The procedure for developing a $100(1 - \alpha)\%$ CI for the population hazard ratio parallels that used to build a CI for the odds ratio statistic in simple logistic regression:

$$\text{CI}(HR_j) = \exp(\hat{B}_j \pm t_{df, 1-\alpha/2} \cdot se(\hat{B}_j)). \quad (10.9)$$

10.4.5 Example: Fitting a CPH Model to Complex Sample Survey Data

We now turn to fitting the CPH model to the NCS-R age of MDE onset data. The appropriate data structure for this type of analysis features one row per sampled individual, with that row containing measures on the survival time, a censoring indicator, covariates of interest, and complex sample design features (stratum and cluster codes and survey weights). Prior to fitting the Cox model to the NCS-R data, we once again declare the variables containing the relevant NCS-R sampling error codes to Stata (note that we use the sampling weight variable NCSRWTSH and request a TSL approach [Binder, 1992] for variance estimation):

```
svyset seclustr [pweight=ncsrwtsh], strata(sestrat) ///
vce(linearized) singleunit(missing)
```

Next, we submit the `stset` data preparation command required by Stata for survival analysis. Note that a common `pweight` variable must be specified in the `svyset` and `stset` commands:

```
stset ageonsetmde [pweight = ncsrwtsh], failure(mde==1)
```

After defining the complex design variables and the `stset` coding of the dependent variable AGEONSETMDE, the Cox model is fit using the `svy: stcox` command (note that value 2 [female] for the predictor variable SEX is explicitly set as a reference category):

```
svy: stcox intwage ib2.sex i.mar3cat i.ed4cat i.racecat
```

Note that we use the “i.” prefix to declare certain predictor variables (SEX, MAR3CAT, ED4CAT, and RACECAT) as categorical, so that Stata includes the appropriate dummy variables in the model. The syntax of the svy: stcox command is fairly simple and similar to other regression analysis commands for survey data within Stata, provided that the two previous steps (declaring the time-to-event data and the complex design variables) have been followed carefully. What makes the command unique is the fact that a dependent variable (AGEONSETMDE in this case) is *not* specified; the first variable listed in the command, INTWAGE, is a predictor variable in the Cox model. The initial use of the stset command directs Stata to set up the appropriate Cox model, and Stata reads the list of variables in the svy: stcox command as the predictors to be included in the model. Submitting this command produces the estimated hazard ratios in [Table 10.2](#).

The design-adjusted *F*-test of the null hypothesis that all of the regression parameters in the Cox model are equal to zero strongly suggests that some of the predictors have a significant impact on the hazard of MDE onset at any given age, and the design-based 95% CIs for the hazard ratios also support this finding. Specifically, Hispanic and Black respondents have marginally

TABLE 10.2

Estimated Hazard Ratios for the NCS-R Cox Proportional Hazards Model of Age to Onset of a Major Depression Episode

Predictor ^a	Estimated Hazard Ratio	Estimated SE	<i>t</i> -Statistic (<i>df</i>)	<i>p</i> -Value	95% CI
<i>Education</i>					
12 years	0.95	0.06	-0.85 (42)	0.40	(0.82, 1.08)
13–15 years	1.05	0.06	0.79 (42)	0.44	(0.93, 1.18)
16+ years	0.91	0.06	-1.42 (42)	0.16	(0.80, 1.04)
<i>Ethnicity</i>					
Hispanic	0.78	0.10	-1.86 (42)	0.07	(0.59, 1.02)
Black	0.62	0.09	-3.22 (42)	0.003	(0.46, 0.84)
White	1.08	0.12	0.66 (42)	0.51	(0.85, 1.37)
<i>Marital Status</i>					
Previously married	1.65	0.099	8.37 (42)	<0.001	(1.46, 1.87)
Never married	1.08	0.096	0.91 (42)	0.37	(0.91, 1.30)
<i>Gender</i>					
Male	0.64	0.040	-7.28 (42)	<0.001	(0.56, 0.72)
Age	0.95	0.002	-20.80 (42)	<0.001	(0.94, 0.96)

Note: *n* = 9,282, Design-adjusted *F*-test of null hypothesis that all parameters are 0: *F*(10, 33) = 53.02, *p* < 0.001.

^a Reference categories for categorical predictors are: <12 years (education); Asian/Other (ethnicity); Married (marital status); Female (gender).

($p < 0.10$) and significantly ($p < 0.01$) reduced hazards of onset of MDE at any given age holding the other covariates fixed, relative to the Asian/Other ethnic group; this agrees with the initial evidence provided by the K–M estimates of the survival functions for the four ethnic groups. Further, with every 1-year increase in age at the time of interview (a birth cohort predictor), the hazard of MDE onset is multiplied by 0.95, or decreased by about 5%, holding the other covariates fixed; this suggests that younger individuals at the time of the interview are at higher hazard of MDE onset at any given age than older individuals. Finally, previously married individuals have a hazard of MDE onset that is about 65% higher at any given age compared to currently married individuals at that age, and males have a hazard of MDE onset that is about 36% lower at any given age than females, holding the other covariates fixed.

We now consider the graphical check of the proportional hazards assumptions described in Section 10.4.3. Recall that this graphical check involves a plot of $-\ln(-\ln(\hat{S}_h(t)))$ against $\ln(t)$, where $\hat{S}_h(t)$ is a weighted estimate of the survival function for group h and t represents the time variable. Based on the specified Cox model, the transformed versions of the survival functions should be parallel as a function of $\ln(t)$. Remember that the `stset` command specification of the dependent variable and the `pweight` value remains in effect. The `stphplot` command is used to generate this special diagnostic plot:

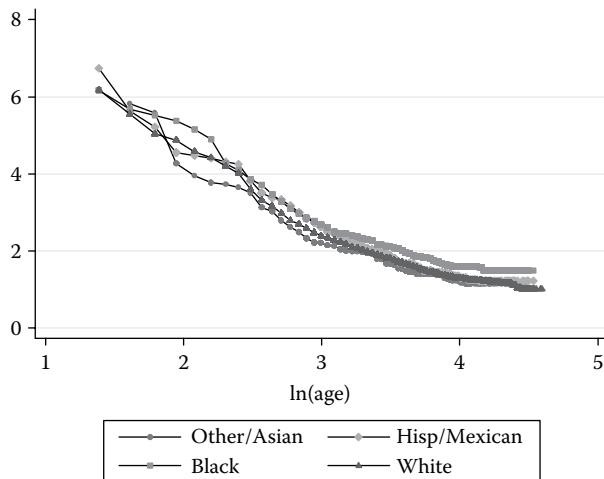
```
stphplot, by(racecat) legend(lab(1 "Other/Asian") ///
lab(2 "Hisp/Mexican") lab(3 "Black") lab(4 "White"))
```

This command generates the plot in [Figure 10.4](#).

From [Figure 10.4](#), we see minimal evidence of the transformed survival curves crossing during the ages when the majority of the data were collected, suggesting that an assumption of proportional hazards would be reasonable for the four race groups. If the transformed survival curves were not approximately parallel (e.g., there is evidence at the highest ages of a possible cross between the White ethnic group and the Hispanic/Mexican and Other/Asian groups), one could fit a model allowing for the effects of ethnicity to vary depending on the age at which a risk set is being formed for estimation. This could be done by including interactions of race with age in this model, which would be time-varying covariates. For more on how to do this when using `svy: stcox`, Stata users can see `help tvc_note`.

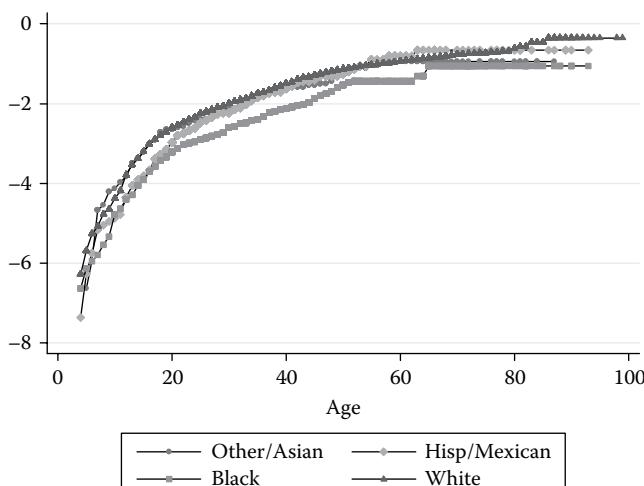
Optionally, Stata users could also plot $-\ln(-\ln(\hat{S}_h(t)))$ against t (a variation of the parallel lines check) and/or adjust the estimates for mean values of covariates using the `adj()` option:

```
stphplot, by(racecat) adj(intwage sexf swd nevermarried ///
ed12 ed1315 ed16 ) nonnegative nolntime ///
legend(lab(1 "Other/Asian") lab(2 "Hisp/Mexican") ///
lab(3 "Black") lab(4 "White"))
```

**FIGURE 10.4**

Graphically examining the proportional hazards assumption for the fitted Cox model of onset of major depression episode (MDE), with no adjustment for covariates. (From NCS-R.)

The resulting plot in [Figure 10.5](#) shows that when adjusting for the means of the covariates (and using the alternative specification of the plot enabled by the nonnegative and nolntime options), we still do not have convincing evidence against an assumption of proportional hazards.

**FIGURE 10.5**

Graphically examining the proportional hazards assumption for the fitted Cox model of onset of major depression episode (MDE), with adjustment for covariates. (From NCS-R.)

10.5 Discrete Time Survival Models

Survival models for events measured in discrete time are needed only when events are reported in discrete time units. For a dependent variable representing a discrete survival time, there are $m = 1, \dots, M$ observed intervals, such as time periods between waves of a longitudinal survey, or time measured in years (year 1, year 2, etc.). In some cases, the “discrete” nature of the survival data may be due to *coarsening* in the dating of events (within the past 4 weeks, did you ...?) or even deliberate grouping of times to provide disclosure protection for individual survey respondents.

10.5.1 Discrete Time Logistic Model

A popular choice for modeling hazard functions when working with discrete survival outcomes is the *discrete time logit model* (Yamaguchi, 1991; Singer and Willett, 1993; Allison, 1995). This model is defined as follows:

$$\begin{aligned} \ln\left(\frac{h_{i,m}}{1-h_{i,m}}\right) &= B_{0,m} + \mathbf{x}_{i,m}\mathbf{B} \\ &= B_{0,m} + B_1x_{1,m} + \dots + B_px_{p,m}. \end{aligned} \quad (10.10)$$

In Equation 10.10, $h_{i,m}$ refers to the hazard of failure at discrete time m for respondent i , $B_{0,m}$ is a time-specific intercept term that applies to all individuals at time m , $\mathbf{x}_{i,m}$ is a row vector of values of covariates (possibly time varying) for respondent i , and \mathbf{B} is the vector of regression parameters. It is important to note that Equation 10.10 models the logit of the individual hazard, $h_{i,m}$. To recover the estimated hazard from the estimated logit model requires the inverse logit transformation:

$$\hat{h}_{i,m} = \frac{\exp(\hat{B}_{0,m} + \mathbf{x}_{i,m}\hat{\mathbf{B}})}{1 + \exp(\hat{B}_{0,m} + \mathbf{x}_{i,m}\hat{\mathbf{B}})}. \quad (10.11)$$

Once the discrete time logit model has been estimated, estimates of the individual hazards, standard errors, and CIs can be readily generated using Stata’s `predict` postestimation command.

Allison (1995) describes an alternative discrete time model that is based on the C-L-L link:

$$\log[-\log(1-h_{i,m})] = \alpha_m + B_1x_{1,m} + \dots + B_px_{p,m}. \quad (10.12)$$

The C-L-L version of the discrete time model is most applicable when the true model for the underlying continuous time process that generates the

discrete time measures is the CPH model of Section 10.4. An advantage of the C-L-L discrete time model is that $H\hat{R}_j = \exp(\hat{B}_j)$. Exponentiating the estimated \hat{B}_j yields an estimate of the *hazard ratio* corresponding to a one unit change in x_j , which is identical to the interpretation for the CPH model.

The regression parameters from the two discrete time models do have slightly different interpretations—log(odds) for the logit version, log(hazard) for the C-L-L—however, both models share the following features:

- Identical *person-time* data set formats are required to fit the two models.
- Both models permit direct estimation of the effect of time on the hazard, through the $\hat{B}_{0,m}$ in the logit form and the $\hat{\alpha}_m$ in the C-L-L model.
- Both models permit the use of time-varying covariates, $x_{i,m}$.
- For complex sample survey data, pseudo maximum likelihood estimation is used to estimate the regression parameters in each model (Section 8.2).

In most cases, the choice of the logit or the C-L-L form of the discrete time survival model will not affect the survey analyst's interpretation of the significance and nature of the relationship of the model covariates to the hazard function.

10.5.2 Data Preparation for Discrete Time Survival Models

Discrete time survival models require a special data input structure that is labeled a *person-time* data format. The person-time data input format contains multiple records for each respondent: one record to represent each discrete time interval during which the respondent was observed, *up to and including* the time interval when the event of interest actually occurred or the observation was censored. A respondent who experiences the event at the third ($m = 3$) discrete time point will have three records in the data set. Another respondent whose observation period is censored at time $m = 5$ will have five person-time data records in the data set.

Each person-time record will contain a value for a binary dependent variable, Y_{imr} , taking on value 1 if the event occurred to respondent i at time period m , or value 0 if no event occurred or the respondent was censored at time m . The sequence of person-time records extends from the first discrete time point, $m = 1$, until the time period when an event actually occurred (i.e., until the dependent variable is equal to 1), or until time M (the last possible discrete time period) if no event occurred (all records for this type of censoring will have the dependent variable equal to 0). If a respondent drops out of the sample or leaves the study for some other reason prior to the end of the time period, they will have a person-time record for each time point at which

they were observed, plus one additional record for the time point at which they were lost. All of their records will have the dependent variable $Y_{im} = 0$.

The discrete time models offer an advantage in that they directly model the effect of time on the hazard of the event. Each person-time record therefore requires one or more variables to indicate the time period. There are several ways to parameterize the effect of time in the discrete time model. The method we recommend is to create a set of indicator variables—one for each time period, $I = \{I_1, \dots, I_M\}$. Each person-time record will contain all M indicator variables, but only the indicator corresponding to the time period m will have $I_m = 1$. All other time indicators (for times $m' \neq m$) for that record will be set to $I_{m' \neq m} = 0$. When this parameterization is used, the logit or C-L-L model should be estimated without the overall intercept term. (If the overall intercept is modeled, one time indicator variable should be dropped.) We illustrate the implications of this coding for the specification of a discrete time model in Equation 10.13:

$$\begin{aligned}\ln\left(\frac{h_{i,m}}{1-h_{i,m}}\right) &= B_0 \cdot I + B_1 x_{1,m} + \dots + B_p x_{p,m} \\ &= B_{0,1} \cdot 0 + \dots + B_{0,m} \cdot 1 + \dots + B_{0,M} \cdot 0 + B_1 x_{1,m} + \dots + B_p x_{p,m} \\ &= B_{0,m} + B_1 x_{1,m} + \dots + B_p x_{p,m}.\end{aligned}\tag{10.13}$$

There are two advantages to this “time indicator” parameterization of the discrete time models. First, no functional relationship (e.g., linear, quadratic) is imposed on the relationship between the hazard and time. Second, if time periods are not of equal length or must be collapsed (if event times are sparse), the individual time period intercepts will adjust for the variability in the size of the time units and the regression parameters for the covariates will not be biased.

An alternative parameterization is to model the sequential discrete time unit indices ($m = 1, 2, 3, \dots, M$) as linear or quadratic predictors. For the discrete time logit model:

$$\ln\left(\frac{h_{i,m}}{1-h_{i,m}}\right) = B_0 + \gamma_1 m + \gamma_2 m^2 + B_1 x_{1,m} + \dots + B_p x_{p,m}.\tag{10.14}$$

This is a much more parsimonious parameterization of time and may be preferred if the total number of discrete times is large (say, $M > 15$). (For simplicity of presentation and comparability to the CPH model results in [Table 10.2](#), this parameterization is used in the analysis example in Section 10.5.5.) One practical analysis strategy is to first fit the discrete time model using the unconstrained time indicator parameterization (10.13). If the estimated coefficients show a linear or quadratic trend, the model could be reestimated more parsimoniously using the model in Equation 10.14.

In addition to the binary dependent variable and the indicators representing the time period, each person-time record in the input data set will include the vector of p covariates, $\mathbf{x}_m = \{x_{1,m}, \dots, x_{p,m}\}$. Individual variables in the covariate vector may be time invariant (e.g., gender) or may be time varying (e.g., body weight in kilograms).

Finally, in survey data sets, a survey weight and the sampling error stratum and cluster codes are assigned to each person-time record. In most cases, the weight value assigned to each time point will be the baseline weight ($m = 1$) assigned to the sample cases at the start of the observation period. However, in cases such as longitudinal surveys where there may be substantial panel attrition due to nonresponse over the multiple waves in the observation period, the time t weight for each observed case may provide a better weighted representation of the population risk set at time t . The person-time input structure for discrete time models allows the user this flexibility to adjust the time-specific weight for prior nonresponse.

The following examples should help to clarify the required person-time data structure. Assume that a sample of individuals is observed for five waves of survey data collection, and a discrete survival time T is recorded for each individual, equal to 1 for events that occur in a fixed interval of time prior to Wave 1, equal to 2 for events that occur between the Wave 1 and Wave 2, and so forth ($T = 1, 2, 3, 4, 5$). [Table 10.3](#) illustrates the person-time data inputs for two hypothetical respondents who experience the event of interest: the first at the second wave ($m = 2$), and the second at the fourth wave ($m = 4$).

In [Table 10.3](#), note the presence of a time-invariant survey weight (which may be time varying depending on the design of the sample), and stratum and cluster codes for sampling error estimation (also time invariant). In this hypothetical example, time is represented in the model as a single integer-value covariate, making this input consistent with model parameterization (10.14) above. If the time-period indicator parameterization of the model (10.13) was chosen, each person-time record would include five indicator variables (one for each of the $M = 5$ possible observation times in

TABLE 10.3

Example Data Structure for Discrete Time Survival Models, for ($n = 2$) Individuals Experiencing an Event of Interest

ID	Weight	Stratum	Cluster	Time (t)	Y_{im}	X_{im}	Z_i
1	1.56	1	1	1	0	23	1
1	1.56	1	1	2	1	25	1
2	0.82	1	2	1	0	14	0
2	0.82	1	2	2	0	16	0
2	0.82	1	2	3	0	17	0
2	0.82	1	2	4	1	17	0

TABLE 10.4

Example Data Structure for Discrete Time Survival Models, for Censored Individuals

ID	Weight	Stratum	Cluster	Time (t)	Y_{im}	X_{im}	Z_i
3	1.25	2	1	1	0	19	1
3	1.25	2	1	2	0	19	1
3	1.25	2	1	3	0	18	1
3	1.25	2	1	4	0	21	1
3	1.25	2	1	5	0	22	1

this hypothetical example). Since the two example cases in [Table 10.3](#) experienced the event of interest, the value of the dependent variable is coded as $Y_{im} = 1$ for the event time, and $Y_{im} = 0$ for all person-year records preceding the event. The X_{im} variable (e.g., body mass index) is a time-varying covariate, and the Z_i variable (e.g., indicator of female gender) is a time-invariant covariate.

[Table 10.4](#) illustrates an example of the person-time data structure for a censored respondent who did not experience the event of interest by the fifth and final wave of data collection. Note in [Table 10.4](#) that the person-time records for this right-censored case include the same input variables as the event cases in [Table 10.3](#); however, the values of the dependent variable including the final time point are coded $Y_{im} = 0$.

10.5.3 Discrete Time Models: Estimation Stage

Mathematically, estimation of the regression parameters for the discrete time logit and C-L-L models for complex sample survey data is a direct application of the pseudo maximum likelihood methods described in Section 8.3 for the simple logistic and C-L-L models for a binary dependent variable. Likewise, procedures for estimation of $\text{var}(\hat{\boldsymbol{B}})_{\text{TSL}}$ or alternatively $\text{var}(\hat{\boldsymbol{B}})_{\text{Rep}}$ are identical to those for the standard logit and C-L-L generalized linear models. Provided that the data are structured correctly in the person-time input format described above, any statistical software procedure capable of fitting logistic or C-L-L regression models to complex sample survey data can be used to fit these models.

As pointed out by Allison (1995, [Chapter 7](#)), some analysts' natural intuition leads them to believe that because the required person-time data structure involves multiple observations for the same person, an extra level of clustering may be introduced in the data that is similar to the clustering that occurs in repeated measures data ([Chapter 11](#)). Fortunately, as explained in Theory Box 10.3, this is actually not a concern in the estimation of sampling variances for the parameters in discrete time models. In modeling event history data, the issue of correlation among the person-time records arises only

THEORY BOX 10.3 THE LACK OF A CLUSTERING EFFECT IN PERSON-TIME DATA

The explanation for absence of a “clustering effect” in the person-time data is that the pseudo likelihood for the complete set of observed event and censoring times can be factored into separate pseudo likelihoods for the individual event times, $m = 1, \dots, M$. Consequently, estimation for each component of the factored likelihood can be treated as if its set of person-time records were independent of those used to estimate the hazard probabilities for other discrete time points. See Allison (1982) for a mathematical proof that the full likelihood for the discrete time models can be factored into time-period-specific likelihoods.

when working with discrete event time models that permit individuals to have multiple events.

10.5.4 Discrete Time Models: Evaluation and Interpretation

As described above, procedures for CI construction, hypothesis testing, and general model evaluation for the discrete time models follow directly from those described in [Chapter 8](#) for the logit and C-L-L models for a binary dependent variable:

1. *Discrete time logit model.* The regression coefficients in the discrete time logit model are estimated on the log-odds scale, where the odds in question pertain to the conditional hazard probabilities. Exponentiating the estimated regression coefficients yields the estimated odds ratio: $\hat{\psi}_j = \exp(\hat{B}_j)$. CIs for these estimated odds ratios are constructed in the now familiar fashion, $\text{CI}(\psi_j) = \exp(\hat{B}_j \pm t_{df, 1-\alpha/2} \cdot se(\hat{B}_j))$. Given pseudo maximum likelihood estimates of the regression parameters and a vector of covariates, $x_{i,m}$, the estimated hazard at time m can be computed as follows:

$$\hat{h}_{i,m} = \frac{\exp(\hat{B}_{0,m} + x_{i,m}\hat{B})}{1 + \exp(\hat{B}_{0,m} + x_{i,m}\hat{B})}. \quad (10.15)$$

Note that this is mathematically identical to the computation of a predicted probability based on a fitted logistic regression model.

2. *Discrete time C-L-L model.* An advantage of the C-L-L model for discrete time data is that population inferences and discussions of results use the *hazard ratio* statistic $H\hat{R}_j = \exp(\hat{B}_j)$. Procedures for

constructing CIs and interpreting the hazard ratio statistics generated from the C-L-L model for discrete time data are identical to those presented for the CPH model in Section 10.4.4.

With this background, we now consider fitting the discrete time logit and discrete time C-L-L models to the NCS-R data on age of onset for major depression.

10.5.5 Fitting a Discrete Time Model to Complex Sample Survey Data

An important first step in fitting the discrete time hazard model is to transform the NCS-R input data into the appropriate person-time format. The following Stata commands “expand” the NCS-R data set from a one record per person file to a multiple record per person file, with records from year = 1 to year at age of interview (INTWAGE). The use of the “gen pyr = _n” command below creates a new variable called PYR which represents person-years of life ranging from 1 to year at age of interview (INTWAGE).

```
expand intwage
bysort caseid: gen pyr = _n
```

The NCS-R data set now includes one “person-year” time record for each year of life for a given individual (e.g., 45 rows for a 45-year old). Next, the indicator variable MDETV is generated for each person-year record. The variable MDETV = 1 if the value of time (PYR) corresponding to the person-year record is equal to the age of onset of MDE, and MDETV = 0 otherwise:

```
gen mde_tv = 1 if pyr == mde_ond
replace mde_tv = 0 if pyr != mde_ond
```

The variable MDETV will be the dependent variable when fitting the logit and C-L-L regression models to these data. The following example Stata list output for the *first respondent* in the NCS-R data set shows the person-year data for this discrete time modeling example:

```
list caseid intwage ncsrwtsn sestrat seclustr pyr mde_tv ///
ageonsetmde if caseid == 1
```

	caseid	intwage	ncsrwtsh	sestrat	seclustr	pyr	mde_tv	ageons~e
1.	1	41	2.02426	1	2	1	0	34
2.	1	41	2.02426	1	2	2	0	34
3.	1	41	2.02426	1	2	3	0	34
4.	1	41	2.02426	1	2	4	0	34
5.	1	41	2.02426	1	2	5	0	34

6.	1	41	2.02426	1	2	6	0	34
7.	1	41	2.02426	1	2	7	0	34
8.	1	41	2.02426	1	2	8	0	34
9.	1	41	2.02426	1	2	9	0	34
10.	1	41	2.02426	1	2	10	0	34
<hr/>								
11.	1	41	2.02426	1	2	11	0	34
12.	1	41	2.02426	1	2	12	0	34
13.	1	41	2.02426	1	2	13	0	34
14.	1	41	2.02426	1	2	14	0	34
15.	1	41	2.02426	1	2	15	0	34
<hr/>								
16.	1	41	2.02426	1	2	16	0	34
17.	1	41	2.02426	1	2	17	0	34
18.	1	41	2.02426	1	2	18	0	34
19.	1	41	2.02426	1	2	19	0	34
20.	1	41	2.02426	1	2	20	0	34
<hr/>								
21.	1	41	2.02426	1	2	21	0	34
22.	1	41	2.02426	1	2	22	0	34
23.	1	41	2.02426	1	2	23	0	34
24.	1	41	2.02426	1	2	24	0	34
25.	1	41	2.02426	1	2	25	0	34
<hr/>								
26.	1	41	2.02426	1	2	26	0	34
27.	1	41	2.02426	1	2	27	0	34
28.	1	41	2.02426	1	2	28	0	34
29.	1	41	2.02426	1	2	29	0	34
30.	1	41	2.02426	1	2	30	0	34
<hr/>								
31.	1	41	2.02426	1	2	31	0	34
32.	1	41	2.02426	1	2	32	0	34
33.	1	41	2.02426	1	2	33	0	34
34.	1	41	2.02426	1	2	34	1	34

Note that the sampling error stratum and cluster codes and sampling weight values are included on each person-year record for the respondent. This respondent was 41 years old when interviewed and first had an MDE at age 34. Although there are more data records for this individual (ages 35–41), only the records from ages 1–34 (the event time) should be analyzed when we fit the model.

Next, we fit the standard design-based logit regression model ([Chapter 8](#)) to the person-year data. The `svy: logistic` command assumes that the complex design features of the NCS-R data set have already been declared to Stata (see the `svyset` command in Section 10.4.5). However, unlike the CPH model, Stata's `stset` command is *not* required. The following predictors of the event are included in the discrete time model: PYR (person-year), INTWAGE (age at interview), SEX, ED4CAT, RACECAT, and MAR3CAT. We note that including INTWAGE in the model serves to introduce a cohort effect in the model; in other words, do persons of different ages at the time of the interview have different hazards?

```
svy: logistic mdetv pyr intwage ib2.sex i.ed4cat ///
i.racecat i.mar3cat if pyr<=ageonsetmde
```

TABLE 10.5

Estimated Odds Ratios for the NCS-R Discrete Time Logit Model of Age to Onset of Major Depression Episode

Predictor ^a	Estimated Odds Ratio	Estimated SE	t-Statistic (df)	p-Value	95% CI
<i>Education</i>					
12 years	0.98	0.06	-0.30 (42)	0.76	(0.86, 1.12)
13–15 years	1.11	0.06	1.62 (42)	0.11	(0.98, 1.23)
16+ years	0.98	0.06	-0.31 (42)	0.76	(0.86, 1.11)
<i>Ethnicity</i>					
Hispanic	0.78	0.10	-1.84 (42)	0.07	(0.59, 1.02)
Black	0.63	0.10	-3.05 (42)	0.004	(0.47, 0.86)
White	1.08	0.13	0.63 (42)	0.54	(0.85, 1.37)
<i>Marital Status</i>					
Previously married	1.64	0.10	8.10 (42)	<0.001	(1.45, 1.85)
Never married	0.97	0.08	-0.40 (42)	0.69	(0.81, 1.15)
<i>Gender</i>					
Male	0.64	0.04	-7.14 (42)	<0.001	(0.57, 0.73)
Person-year	1.03	0.002	15.82 (42)	<0.001	(1.03, 1.04)
Age	0.94	0.002	-23.82 (42)	<0.001	(0.94, 0.95)

Note: Design-adjusted F-test of null hypothesis that all parameters are 0: $F(11, 32) = 53.63$, $p < 0.001$.

^a Reference categories for categorical predictors are: <12 years (education); Asian/Other (ethnicity); Married (marital status); Female (gender).

The use of the if modifier is especially important in the model commands; we only want to analyze those person-years for times equal to or less than the age of MDE onset (or age of interview for right-censored individuals never having experienced an MDE). Fitting the logit version of the model results in the estimates of odds ratios presented in Table 10.5.

Focusing on the results for the discrete time logit model, we see that the estimated odds ratios in this discrete time hazard model are remarkably similar to the estimated hazard ratios found for the CPH model fitted in Section 10.4.5, which suggests that the two approaches result in similar estimates of the impacts of these sociodemographic predictors on the risk of MDE onset at any given age. For example, the discrete time hazard model suggests that holding all other covariates fixed (including person-year, or the age at which a person might be at risk), males have 36% lower odds of having an MDE for the first time than females.

Given that the discrete time modeling approach can be implemented using standard design-based logistic regression modeling techniques, any of the diagnostics discussed in Chapter 8 could be applied when evaluating the fit of this model.

TABLE 10.6

Estimated Hazard Ratios for the NCS-R Discrete Time C-L-L Model of Age to Onset of Major Depression Episode

Predictor ^a	Estimated Hazard Ratio	Estimated SE	t-Statistic (df)	p-Value	95% CI
<i>Education</i>					
12 years	0.98	0.06	-0.30 (42)	0.77	(0.86, 1.12)
13–15 years	1.10	0.06	1.61 (42)	0.11	(0.98, 1.23)
16+ years	0.98	0.62	-0.30 (42)	0.76	(0.86, 1.11)
<i>Ethnicity</i>					
Hispanic	0.78	0.10	-1.84 (42)	0.07	(0.60, 1.02)
Black	0.78	0.10	-3.04 (42)	0.004	(0.47, 0.86)
White	1.08	0.13	0.63 (42)	0.54	(0.85, 1.37)
<i>Marital Status</i>					
Previously married	1.64	0.10	8.11 (42)	<0.001	(1.45, 1.85)
Never married	0.97	0.08	-0.41 (42)	0.69	(0.81, 1.15)
<i>Gender</i>					
Male	0.64	0.04	-7.14 (42)	<0.001	(0.57, 0.73)
Person-year (time)	1.03	0.002	15.82 (42)	<0.001	(1.03, 1.04)
Interview age	0.94	0.002	-23.83 (42)	<0.001	(0.94, 0.95)

Note: Design-adjusted F-test of null hypothesis that all parameters are 0: $F(11, 32) = 53.65$, $p < 0.001$.

^a Reference categories for categorical predictors are: <12 years (education); Asian/Other (ethnicity); Married (marital status); Female (gender).

Finally, the comparable discrete time C-L-L model is fit to the person-time data using Stata's svy: cloglog command:

```
svy: cloglog mde tv pyr intwage ib2.sex i.ed4cat ///
i.racecat i.mar3cat if pyr <= ageonsetmde, eform
```

Table 10.6 presents the results for the C-L-L model in the form of estimates and CIs for the hazard ratios (note the use of the eform option in the command above).

Compared to the results in Table 10.4 for the CPH model (hazard ratios) and the discrete time logit model results in Table 10.5 (odds ratios), we again see a similar pattern of results in the estimated hazard ratios for the C-L-L discrete time model for age of onset of major depression. Controlling for the other predictors and a linear time effect, education level does not appear to have a significant impact on the hazard of MDE. Black respondents have a significantly lower hazard for MDE relative to persons of Asian and Other race/ethnicities. Controlling for the other predictors in the model, previously married persons

have a greater hazard of MDE than married adults, and the estimated hazard for men is about 64% of that for women (all else being equal).

EXERCISES

- 10.1 This exercise considers the data from the NCS-R. The objective of this analysis is to model the gender-specific hazard of first onset of Alcohol Abuse (ALCABUSE, 1 = yes, 0 = no); in other words, do males and females in the NCS-R population have different hazards of onset of Alcohol Abuse? Begin the analysis by generating an age of first onset of Alcohol Abuse variable, equal to age of onset of Alcohol Abuse (ALA_OND) if DSM_ALA is equal to 1 (or yes), or equal to age at interview (INTWAGE) if DSM_ALA equals 5 (or no) and ALA_OND equals missing. Note that cases not qualifying for Alcohol Abuse are *right-censored* cases in terms of age of Alcohol Abuse onset, so you should also compute an indicator variable for the censored cases. Present the code that you used to compute these variables, which will serve as the “time-to-event” variable and the right-censoring variable in this analysis.
- 10.2 Generate weighted (using the NCS-R Part 2 survey weight = NCSRWTLG) K-M estimates of the survival curves for each gender by using the indicator variable SEXM (1 = male, 0 = female). What do the survival curves suggest about the hazards of initial Alcohol Abuse diagnosis as a function of gender?
 - a. (*Extra Credit*) Use a software procedure capable of producing design-based standard errors and confidence limits (e.g., SPSS Complex Samples or SUDAAN) for K-M estimates. Generate weighted (using NCSRWTLG) survival curves with correct standard errors and confidence limits for the two groups defined by the variable SEXM. Again, what do the survival curves suggest about the hazards of initial Alcohol Abuse diagnosis as a function of respondent gender?
- 10.3 Fit a CPH model to the age of onset of Alcohol Abuse, recognizing the right-censoring and the complex sample design features of the NCS-R (stratum codes = SESTRAT, cluster codes = SECLUSTR, NCS-R Part 2 survey weight = NCSRWTLG). Consider as predictors of the hazard function the categorical education variable representing highest education level attained (ED4CAT: 1 = 0–11 years, 2 = 12 years, 3 = 13–15 years, and 4 = 16+ years) and the indicator variable for males (SEXM). Use the education variable as though it is time invariant in the model. Based on the weighted estimates of the regression parameters in this model and their estimated standard errors:

- a. Is there evidence of significant differences between gender categories and the education categories in terms of the hazard functions? If so, what are the differences?
 - b. Compute the estimated hazard ratio of initial Alcohol Abuse onset for females compared to males, holding the education variables constant, and compute a 95% CI for this hazard ratio. How would you interpret these results?
- 10.4 (*Using Stata or other software capable of a design-based test*) Test the assumption of proportional hazards for the two gender groups using the graphical methods discussed in this chapter. Does this assumption seem justified? What would be an alternative analytic approach if this assumption seems violated?
- 10.5 Using the data management methods discussed in this chapter, construct an expanded version of the NCS-R data set that could be used to fit a discrete time logit model to the age of onset of Alcohol Abuse. Generate a table showing the data structure for the first two respondents in the NCS-R data set.
- 10.6 Fit a discrete time logit model to the expanded data set considering the same predictors of first onset of Alcohol Abuse used to fit the Cox model, ED4CAT and SEXM. Make sure to recognize the complex design features when fitting the model, and do not forget to include interview age (INTWAGE) as a predictor in the model (Section 10.5.5). Also, make sure to limit the records analyzed to include the records up to and including the age of onset or censoring. Based on the data structure and output from this model, answer the following questions:
- a. Why do we include the interview age as a predictor in this model?
 - b. What mistake would occur if you skipped the limiting of observations to up to and including the age of onset/censoring?
 - c. Would we make the same inferences as from the Cox model about the differences in the hazards for the four education groups and for males compared to females?
 - d. Prepare a table comparing the estimated odds ratios from the discrete time logit approach to the estimated hazard ratios from the Cox modeling approach and write a short paragraph interpreting these results.

11

Analysis of Longitudinal Complex Sample Survey Data

11.1 Introduction

In this chapter, we review current thinking on appropriate analytic techniques for *longitudinal data* collected in a *panel survey*, where the initial sample design was complex in nature (possibly featuring stratification, cluster sampling, and weighting for unequal probability of selection, as discussed in prior chapters), and attempts were made to repeatedly measure the initially sampled units at multiple follow-up waves. Many different patterns of missing data can emerge in panel surveys featuring repeated measurement of the same units over time; for example, some cases may provide complete data at every measurement occasion, others may choose not to participate at particular waves, and others may drop out of the panel survey permanently at a particular time point. This introduces the possibility of several alternative design-based and model-based approaches that simultaneously account for: (1) the correlation of the repeated measurements on a given individual; (2) the complex sampling features; and (3) the different patterns of nonresponse (Thompson, 2015). With this chapter, we attempt to describe and illustrate those methods that are advocated in the current literature as being most appropriate for a particular analytic objective.

A variety of survey designs can be used to study changes in selected population phenomena over time. *Repeated cross-sectional surveys* such as the National Health and Nutrition Examination Survey (NHANES), which are defined by the cross-sectional measurement of repeated independent samples from a given population over time, enable researchers to study marginal changes in the features of a population over time. *Rotating panel designs* such as the Current Population Survey and true *panel survey* designs such as the Panel Study of Income Dynamics (PSID; Hill, 1992) and the Health and Retirement Survey (HRS; Juster and Suzman, 1995) all play an important role in understanding both societal and *individual-level* change over time. Binder (1998) and Kalton and Citro (1993) provide sound overviews of the key issues associated with longitudinal sample designs, both at the design and analysis

stages. Menard (2008) and Lynn (2009) address design, measurement, and analysis for longitudinal surveys. In this chapter, we focus on appropriate techniques for the analysis of data collected from panel surveys, where the same individuals are measured repeatedly over time and estimates of expected trajectories in measures of interest for individuals in selected population subgroups are of scientific interest.

We first consider the possible analytic objectives that analysts of panel survey data may have in mind in Section 11.2. For each of these objectives, we consider potential analytic techniques proposed in the literature that one might employ, and describe their implementation in detail. Finally, we consider several example analyses of real longitudinal survey data from the HRS in Section 11.3, illustrating use of the alternative methods with existing software and comparing the results for particular analytic objectives across the competing methods that have been proposed in the extant literature. We conclude with some thoughts on directions for future research in Section 11.4.

11.2 Alternative Analytic Objectives with Longitudinal Survey Data

This section reviews possible analytic objectives that those working with longitudinal survey data may have in mind. A clear analytic objective is essential for choosing an appropriate method for analyzing the longitudinal survey data.

11.2.1 Objective 1: Descriptive Estimation at a Single Time Point

Analysts with this objective in mind are interested in making descriptive inferences about a specific target population at a particular point in time. For example, an analyst of the HRS data may be interested in describing the mean total household assets of the HRS target population in 2012, or estimating the proportion of individuals in the HRS target population who chose to pursue part-time employment in 2012. These objectives involve a desire to make descriptive inference in a *single wave* from the overall panel survey, and therefore rely on methods quite similar to those discussed in [Chapters 5 and 6](#).

The key complication of these approaches is how to account for the fact that many of the individual elements initially sampled for the panel survey may not respond in the specific wave of interest. For this type of *wave non-response*, three primary approaches are generally advocated in the literature (Kalton, 1986; West and McCabe, 2017):

1. *Weight adjustment.* Adjust the final survey weights from the initial wave of the panel survey, which likely reflect (a) unequal probabilities

of selection, (b) differential unit nonresponse in the initial wave, and (c) calibration adjustments given population controls from the initial wave, for the conditional probability of responding at the follow-up wave in question (given that a sampled case responded in the initial wave). This approach assumes that nonresponse in the current wave is occurring at random *conditional on the observed measures recorded in earlier waves* and that wave nonresponse does *not* depend on the measures being recorded in the current wave of interest.

2. *Multiple imputation.* Impute the values of the measures of interest in the current wave multiple times using measures recorded in previous waves, including the initial wave, and then apply multiple imputation combining rules (Little and Rubin, 2002) to the results of analyses of the imputed data sets to make overall inferences (see [Chapter 12](#) for more details regarding multiple imputation). The analyses of the multiple imputed data sets would account for the final survey weights from the initial wave of the panel survey, in addition to any available stratification codes, cluster codes, or replicate weights for variance estimation. Like the weight adjustment method, this method assumes that wave nonresponse is occurring at random *conditional on the predictors used in the imputation models*.
3. *Methods for nonignorable missing data.* This class of methods does *not* assume that wave nonresponse is occurring at random conditional on measures observed in previous waves, but rather allows the wave nonresponse to depend on some arbitrary function of the measures of interest in the current wave. Popular approaches to making descriptive inferences in this case include *pattern-mixture models* and *selection models* (Little and Rubin, 2002; West and McCabe, 2017), but these approaches all rely on assumptions regarding the relationship of wave nonresponse with the measures of interest in the current wave. For this reason, *sensitivity analyses* define a critical component of analyses assuming that the wave nonresponse is not ignorable, where the sensitivity of inferences to different assumptions about the wave nonresponse mechanism is carefully examined.

Simple complete case analyses of the data in a current wave that only account for complex sampling features from the initial wave of data collection assume that the wave nonresponse is occurring *completely at random*, independent of measures collected in earlier waves or the measures collected in the current wave. This is an extremely strong assumption, and one that often proves to be incorrect. We encourage analysts of longitudinal survey data with these descriptive objectives in mind to employ each of the approaches outlined above and examine the sensitivity of their inferences to the assumptions underlying each approach. We illustrate this approach in Section 11.3.

11.2.2 Objective 2: Estimation of Change across Two Waves

Analysts with this objective in mind are interested in making inference about the change in a descriptive parameter of interest over a time period defined by two waves of the larger panel survey. For example, an HRS analyst may be interested in making inference about the mean change in total household assets in the HRS target population from 2010 to 2012. If all panel survey respondents initially sampled were to provide complete information for the measures of interest at each of the two waves, this analysis would be straightforward: one would compute the change measure of interest for each respondent, save the change measure in a new variable, and apply the standard descriptive techniques discussed in [Chapters 5 and 6](#), accounting for the complex sampling features from the initial wave of data collection.

More specifically, the simplest type of analysis is the analysis of individual change over two points in time denoted by t and $t - k$, for example,

$$\bar{\delta}_{t-k,t} = \frac{\sum_i w_i \cdot (y_{t,i} - y_{t-k,i})}{\sum_i w_i}, \quad (11.1)$$

where w_i is a survey weight for sample element i ; or, $\hat{y}_{t,i} = \hat{\beta}_0 + \hat{\gamma} y_{t-k,i} + \hat{\beta}_1 x$; where $\hat{\gamma}$, $\hat{\beta}$ are weighted estimates of regression parameters. We considered an example of analyzing the mean change between two points in time in Example 5.16 from [Chapter 5](#).

In real panel surveys, this ideal scenario is seldom realized, and analysts need to account for the differential attrition that produced the ultimate survey respondents in each of the two waves of interest. Analysts will likely encounter one of two scenarios in this case:

1. *If the measure of change is relative to the initial wave of data collection*, one of the three methods outlined for Objective 1 in Section 11.2.1 can be employed, where the weights for cases with complete data at both time points are adjusted for wave nonresponse at the follow-up wave, or missing values at the follow-up wave are first imputed assuming that wave nonresponse is either occurring at random or not at random, and then the resulting complete cases are analyzed further accounting for the complex sampling features at the initial wave. These approaches are illustrated in detail by West and McCabe (2017), and considered further in Section 11.3.
2. *If the measure of change is based on two waves aside from the initial wave of data collection*, where differential wave nonresponse in each of the two waves of interest is a real possibility, approaches based on imputation are generally recommended (Kalton, 1986). In these

cases, one can impute missing values in both waves of interest multiple times using measures recorded in earlier waves, and then analyze the measures of change in the imputed data sets accounting for the complex sampling features from the initial wave of data collection.

We once again reiterate here that analyses of change across two waves that do not account for the possibility of differential attrition over time run the risk of being substantially biased, as respondents providing complete data over time may represent a selected subset of the full initial sample of elements with unique properties. We encourage analysts to use one of the methods outlined above when estimating measures of change across two waves, and we illustrate these methods in Section 11.3.

11.2.3 Objective 3: Trajectory Estimation Based on Three or More Waves

In this third case, analysts have explicit interest in estimating expected within-person trajectories for particular outcomes over time, using three or more waves of information to estimate the trajectories (where some individuals may only be able to contribute fewer than three waves). This is the most complicated scenario, where different individuals may respond in different combinations of waves, and there may be many different patterns of attrition to account for. We now consider five general classes of approaches that have been proposed in the literature for fitting models to these types of longitudinal survey data.

11.2.3.1 Approach 1: Weighted Multilevel Modeling

Following this first approach, one would begin by creating a vertical data set, containing multiple measurements (or rows) per survey respondent (across the waves) and multiple respondents per sampling cluster (if applicable), and then employ approaches for weighted estimation of multilevel models (Pfeffermann et al., 1998) to estimate both (a) the overall expected trajectories of interest, and (b) between-subject variance in the trajectories of interest (Skinner and Holmes, 2003). The complication in this case is how the appropriate weights should be computed for weighted estimation of the multilevel models. This approach would proceed as follows:

1. The baseline survey weight represents the subject-specific survey weight, where subjects would generally define Level 2 of the multilevel model.
2. The Level 1 weights are generally the wave-specific weights associated with each individual responding in a given wave, incorporating

different adjustments for attrition in each wave. The calculations of these wave-specific weights for each responding individual need to reflect appropriate adjustments to the initial survey weights for each individual for differential attrition patterns at each wave, so that they effectively recover the original representative sample in each wave. These wave-specific weights also need to be appropriately scaled so that their sum is equal to the available number of data points within each individual; a failure to do this can introduce bias in the weighted estimates of multilevel model parameters (Pfeffermann et al., 1998; Rabe-Hesketh and Skrondal, 2006; Carle, 2009).

3. Primary sampling units (PSUs; if available) then define the third level of the multilevel model, and if PSU-level weights are available, they need to be accounted for in the estimation. The subject-specific weights at Level 2 need to be *conditional* weights, reflecting probabilities of selection conditional on a given PSU being selected. Stratification effects are generally accounted for via the inclusion of fixed stratum effects in the third level of the multilevel model (Pfeffermann et al., 1998).

Multilevel models can extend the simple “two-point” change models discussed in Section 11.2.2 to examine trends in repeated measures or growth curves based on multiple observations collected from the individual sampled persons (or units of analysis more generally). In this section, we present a synthesis of the existing literature on suggested approaches to using multilevel models for longitudinal analysis of complex sample survey data. We then consider examples of these approaches using available software in Section 11.3.

We first describe general notation for multilevel models that can be fitted to longitudinal survey data arising from complex sample designs. Let y_{it} be the response for individual i at time t , which may vary randomly over time. We assume that the randomly sampled individual i has some “permanent” status that partly defines the observed responses, which can be denoted by b_i . These values for the randomly sampled individuals are assumed to arise from a normal distribution with a fixed mean (for the population) of 0 and a variance of τ^2 (see McCulloch and Neuhaus, 2011, for more discussion about this assumption). Then, observed values for y_{it} , conditional on a randomly sampled value of b_i , are assumed to arise from a normal distribution with mean $\beta_t + b_i$ (where β_t is the population mean of the response at time t) and variance σ^2 . More succinctly,

$$\begin{aligned} b_i &\sim N(0, \tau^2) \\ y_{it} | b_i &\sim N(\beta_t + b_i, \sigma^2). \end{aligned} \tag{11.2}$$

Thinking in a multilevel modeling context, τ^2 represents between-individual variance, while σ^2 represents within-individual variance over time. The variance of y_{it} is thus partitioned into variance across individuals and transitory variance, and can be written as $\tau^2 + \sigma^2$.

A simple model for an outcome y measured over time can then be written as follows:

$$y_{it} = \beta_t + b_i + e_{it}. \quad (11.3)$$

In this model, $t = 1, \dots, T$, where T represents the total number of waves, $i = 1, \dots, n$ (persons), β_t is the population mean of the outcome at time t , b_i is a long-term difference from β_t for person i (a random variable corresponding to a random individual effect), and e_{it} is a transitory effect at time t for person i (each individual will randomly vary around their “permanent” state at time t). It is important to note that the e_{it} values may be correlated over time. One possible model expressing this correlation could be the first-order autoregressive [AR(1)] model:

$$e_{it} = \rho e_{i(t-1)} + \varepsilon_{it}. \quad (11.4)$$

The model in Equation 11.3 can thus be rewritten as follows, using the AR(1) model for the transitory effects:

$$y_{it} = \beta_t + b_i + \rho e_{i(t-1)} + \varepsilon_{it}. \quad (11.5)$$

In this specification, ε_{it} represents random measurement error, and the b_i and ε_{it} are assumed to be independent. We also assume that $E(b_i) = E(\varepsilon_{it}) = 0$, $var(b_i) = \tau^2$, $var(\varepsilon_{it}) = \sigma^2_\varepsilon$, and that the e_{it} and ε_{it} are mutually independent and stationary. We can then write:

$$var(e_{it}) = \frac{\sigma^2_\varepsilon}{(1 - \rho^2)}. \quad (11.6)$$

In this section, we focus on a multilevel modeling approach that has been developed to fit models of this form to longitudinal data from complex sample surveys (Skinner and Holmes, 2003). To fit this model, we must first address the question of how the longitudinal survey weights should be incorporated in the model estimation. Pfeffermann et al. (1998) laid the groundwork for appropriate methods of incorporating survey weights into the estimation of parameters in multilevel models for complex sample survey data. They also proposed appropriate variance estimators for the estimated parameters (based on the delta method, which is similar to linearization). The methods proposed by these authors can be used to estimate two-level multilevel

models for longitudinal survey data given survey weights computed for *both* the Level 2 units (individuals) and the Level 1 units (repeated observations). Theory Box 11.1 describes the procedure for constructing the weights for the individual levels in detail.

Unfortunately, the multilevel modeling approach proposed by Pfeffermann et al. (1998) does not allow for autocorrelation of transitory effects within persons, as described in Equation 11.5. The original approach was described for the case where Level 2 units were PSUs and Level 1 units were sampled individuals, and autocorrelated errors from different individuals within the same cluster would not be expected or realistic. Skinner and Holmes (2003) developed a method to circumvent this problem and enable the methods proposed by Pfeffermann et al. (1998) to be applied, but this method has yet to be programmed in any general purpose statistical software packages. Veiga et al. (2014) further expanded on this approach, and have developed Stata software implementing it. We provide descriptions of these alternative approaches for modeling serially correlated observations in Section 11.3.2.2.

Rabe-Hesketh and Skrondal (2006) further investigated methods of fitting multilevel models to complex sample survey data (and specifically binary outcomes). Based on their research, these authors stressed the importance in pseudo maximum likelihood (PML) estimation (Chapter 8) of incorporating appropriately scaled weights at *all* levels of a multilevel study (e.g., school-level, or Level 2, weights and student-level, or Level 1, weights, and not simply student-level weights). Addressing a limitation of the approaches proposed by Pfeffermann et al. (1998) and Skinner and Holmes (2003), these authors also discussed the computation of “sandwich” estimates of standard errors (based on a Linearization approach) to incorporate stratification and primary stage clustering of a complex sample into the calculation of design-based standard errors for the parameter estimates derived using the PML approach.

Their proposed method is implemented in the **gllamm** (Generalized Linear Latent and Mixed Models) program that these authors developed for the Stata system (visit <http://www.gllamm.org>), in addition to the mixed-effects modeling procedures in Stata (e.g., the `mixed` command). The underlying assumption of this approach is that the primary stage clusters represent the highest-level units in the multilevel design (e.g., students at Level 1 nested within schools at Level 2, and schools at Level 2 nested with primary stage clusters at Level 3). Via simulation, these authors found good coverage for confidence intervals based on the robust standard errors. Thinking about multilevel models for longitudinal survey data, we can apply the same models, where the repeated observations across waves define the Level 1 observations, the sampled individuals defined Level 2, and the PSUs define Level 3 of the data hierarchy. We consider an example of this type later in Section 11.3.

Skinner and Vieira (2007) specifically focused on the impacts of cluster sampling on variance estimation when analyzing longitudinal survey data

**THEORY BOX 11.1 WEIGHTED ESTIMATION
IN TWO-LEVEL MULTILEVEL MODELS**

Following Pfeffermann et al. (1998), the sampling weights for individuals at Level 2 and repeated observations at Level 1 are computed as follows. In general, given a longitudinal study design with these two levels, the appropriate weight for the data from individual i at time t , w_{it} , is computed as

$$w_{it} = \frac{1}{\pi_i \pi_{t|i}}, \quad (11.7)$$

where π_i represents individual i 's original probability of inclusion in the sample, and $\pi_{t|i}$ represents the probability that individual i responds at time t . The $\pi_{t|i}$ values might be estimated using a propensity modeling approach (e.g., Lepkowski and Couper, 2002), where the probability of responding at time t is predicted using a logistic regression model with predictors from previous waves. We assume that some reasonable methodology has been used for estimation of these response probabilities in this discussion.

For purposes of the multilevel modeling approach discussed in this section, define the *Level 2 weight* as

$$w_i = \frac{1}{\pi_i}, \quad (11.8)$$

and define the *Level 1 weight* as

$$w_{t|i} = \frac{1}{\pi_{t|i}}. \quad (11.9)$$

Then, we have

$$w_{it} = w_i w_{t|i}, \quad (11.10)$$

and

$$w_{t|i} = \frac{w_{it}}{w_i}. \quad (11.11)$$

A reasonable approach suggested by Skinner and Holmes (2003) is to let $w_i = w_{il}$, or to let the Level 2 weight for individual i be the inverse of the probability of being selected for the sample *and* responding at the baseline wave. Then, $w_{1|i} = w_{il}/w_{\bar{i}} = 1$. This procedure will result in less variance in the Level 1 weights denoted by $w_{t|i}$.

The computed Level 1 weights can then be scaled, as recommended by Pfeffermann et al. (1998) and Skinner and Holmes (2003) to minimize small-sample estimation bias. Scaling weights (e.g., normalizing weights; Chapter 4) generally does not have an impact on the estimates of parameters in *multivariate* models, but this is not the case when fitting *multilevel* models to complex sample survey data. Skinner and Holmes (2003, p. 212) suggest rescaling the Level 1 weights described above as follows:

$$w_{t|i}^* = \frac{t^*(i)w_{t|i}}{\sum_{t=1}^{t^*(i)} w_{t|i}}. \quad (11.12)$$

In this notation, $t^*(i)$ represents the last wave at which individual i provides a response. Note that this method ensures that the average rescaled weight for a given individual i is equal to 1. Rabe-Hesketh and Skrondal (2006) outline additional options for scaling the Level 1 weights, one of which we consider in the example in this section. Carle (2009) examines the performance of these various scaling methods via empirical simulations, and arrives at the general conclusion that the choice of the weight-scaling method does not have a significant impact on inferences; it simply needs to be done in one way or another. The main point is that some form of scaling needs to be employed to reduce potential biases in the estimates of the multilevel model parameters.

with multilevel models. They concluded that the simple method of including a random cluster effect in a three-level multilevel model for longitudinal survey data (where again, PSUs define Level 3 of the multilevel study design, individuals define Level 2, and the repeated measurements define Level 1) has the potential to seriously underestimate effects of clustering on the standard errors of parameter estimates. In a practical application, model-based standard errors for key parameter estimates in the three-level model were nearly identical to those found in a two-level model *excluding* the random cluster effects, clearly suggesting that attempting to incorporate the effects of cluster sampling via random cluster effects and relying on model-based standard errors would be erroneous. These authors showed that calculation

of “robust” standard errors (Goldstein, 2003, p. 80) in a three-level multilevel model including random cluster effects at Level 3 resulted in standard errors that most closely resembled those computed by applying the classical linearization approach to the computation of design-based standard errors (incorporating clustering, and considered by the authors to be a “gold standard”) for parameter estimates in a *two-level* model for the longitudinal data, including random individual effects only (a method similar to that proposed by Rabe-Hesketh and Skrondal). The example provided by these authors, however, did not consider the effects of weighting or stratification, and the authors acknowledged that additional work was needed (and ongoing) in this area.

Additional work by Vieira and Skinner (2008) found that point estimators for the regression parameters and variance–covariance parameters in a model for longitudinal survey data based on PML estimation, when combined with a variance estimator based on Taylor Series Linearization (allowing for clustering of the sample), had the best performance overall, providing more support for the work of Rabe-Hesketh and Skrondal (2006). However, their simulations only considered respondents at all possible waves of a panel survey (“complete” respondents, meaning respondents with any wave non-response were dropped), and once again ignored survey weights that might be adjusted for other types of attrition or wave nonresponse. We note that the general PML estimation method and linearization variance estimation method proposed by these authors can accommodate single survey weights for the individuals, possibly adjusted for other forms of nonresponse, which varies from the multilevel modeling approach accommodating weights at both Level 2 (sampled individuals) and Level 1 (repeated observations) of the longitudinal hierarchy.

Critical to the success of the weighted multilevel modeling approach is the calculation of appropriate adjustments for attrition in each of the waves. This approach makes use of all available information collected in the panel survey, representing an attractive alternative to only analyzing cases with complete data. In the monotone missing data case, if one were to analyze only cases with complete data in all of the waves of interest, the risk of bias is again strong if those individuals represent a selected subset of the full sample in terms of the outcomes of interest. Some type of adjustment would seemingly be needed for the initial survey weights when following this type of complete case approach and throwing out the information for cases without complete data, but clear guidance regarding that adjustment is not presently available in this literature. The existing literature has examined how to account for stratified cluster sampling in variance estimation when fitting multilevel models to complete cases in longitudinal survey data sets (Feder et al., 2000), but guidance on appropriate weight adjustments in these cases is an open area for future research. We explore different possible approaches in Section 11.3, in hopes of motivating additional research in this area.

11.2.3.2 Approach 2: Covariance Structure Modeling

This second approach employs marginal covariance structure modeling to fit models to longitudinal data collected from complex sample surveys. Recall the basic model specified in Equation 11.5, using the AR(1) model for the transitory effects:

$$y_{it} = \beta_t + u_i + \rho v_{i(t-1)} + \varepsilon_{it}. \quad (11.13)$$

Now, let $y_i = (y_{i1}, \dots, y_{iT})'$ be a vector of observations on the dependent variable of interest collected on the i -th individual, assuming no nonresponse. Then, we have

$$E(y_i) = \beta = (\beta_1, \dots, \beta_T)' \quad (11.14)$$

and

$$\text{var}(y_i) = \tau^2 J_T + \sigma^2 V_T(\rho), \quad (11.15)$$

where J_T is a $T \times T$ matrix of 1's, and $V_T(\rho)$ is a $T \times T$ matrix with the (t, t') and (t', t) elements defined by $\rho^{(t'-t)}$, for $1 \leq t \leq t' \leq T$.

This model therefore has T parameters for the mean of the outcome, but only three parameters for the variance of the outcome (σ_e^2 , σ_u^2 , and ρ). Denote this set of three parameters by ϕ , and define the sample estimator of the variance–covariance matrix of the vector of observations on a given individual i as

$$\hat{S} = \frac{\sum_{i \in s} w_i (y_i - \bar{y})(y_i - \bar{y})'}{\sum_{i \in s} w_i}. \quad (11.16)$$

The mean in Equation 11.16 is actually a vector of weighted estimates of means at the T time points. Then, let $\hat{A} = \text{vech}(\hat{S})$, or a vector containing the $T(T+1)/2$ distinct elements of \hat{S} , and let $A(\phi) = \text{vech}(\text{var}(y_i))$, or a vector containing the $T(T+1)/2$ distinct elements of the variance–covariance matrix for y_i defined in Equation 11.15. Estimation of the parameters defining the variance–covariance matrix then proceeds by obtaining a generalized least squares (GLS) estimator of ϕ , denoted by $\hat{\phi}_{\text{GLS}}$, as the iterative solution that minimizes

$$[\hat{A} - A(\phi)]' \hat{V}^{-1}(\hat{A}) [\hat{A} - A(\phi)], \quad (11.17)$$

where $\hat{V}(\hat{A})$ is a design-consistent estimator of the variance–covariance matrix of \hat{A} , possibly obtained using linearization or replication methods for variance estimation.

Given the GLS estimate of the set of variance–covariance parameters denoted by φ , a goodness-of-fit statistic is readily obtained as

$$X_W^2 = [\hat{A} - A(\hat{\varphi}_{GLS})]^\top \hat{V}^{-1}(\hat{A}) [\hat{A} - A(\hat{\varphi}_{GLS})], \quad (11.18)$$

where provided that the model is correct and the sample is large enough for $\hat{V}(\hat{A})$ to be a good approximation to the variance–covariance matrix of \hat{A} , then the goodness-of-fit statistic in Equation 11.17 will be distributed as a chi-squared statistic with $k - 3$ degrees of freedom, with $k = T(T + 1)/2$. It is important to note that $\hat{V}(\hat{A})$ may be unstable with a small number of PSUs in the design, and Skinner and Holmes (2003) present alternatives.

Skinner and Holmes (2003, pp. 209–210) also discuss two possible approaches to dealing with nonresponse due to attrition when using the covariance structure modeling approach. One approach involves only considering the attrition sample who responded at all points up to time T , and developing adjusted weights denoted by w_{it} that incorporate both the probability of selection and the probability of responding until time T . The procedure described above can then be applied using the adjusted weights. These authors also describe a more sophisticated approach that we do not describe in detail here; interested readers can refer to the text of their paper for more details.

The covariance structure modeling approach offers the advantage of easily handling serial correlation and provides users with a goodness-of-fit test. Unfortunately, the covariance structure approach described here has yet to be readily implemented in any general purpose statistical software packages. Further, Skinner and Holmes (2003) report evidence of bias in estimates of variance components when using the GLS approach described above with the V matrix estimated from the data.

Veiga et al. (2014) presented an alternative approach that combined the ideas of multilevel modeling and covariance structure modeling. Following this approach, we once again recognize longitudinal survey data collected from complex samples as having a three-level structure. At Level 3, we have the PSUs (or ultimate clusters/SECUs; Chapter 4), potentially having associated sampling weights. At Level 2, we have survey respondents nested within clusters, each with their own *conditional* survey weights. At Level 1, we have the repeated measures across waves, nested within the survey respondents. Veiga et al. (2014) propose fitting a multilevel model to data with this structure that includes random PSU effects (to capture within-PSU correlations), and *wave-specific* random effects of individuals (essentially, the random errors at each time point associated with the survey responses from individuals are allowed to have unique variances and covariances).

To ensure that the proposed model is identified and all parameters are estimable, the model does not include a fixed overall intercept or fixed effects of time-varying covariates (outside of time itself). This approach therefore enables estimation of changes in the means of a particular outcome variable over time for individuals in a target population, along with the fixed effects of time-invariant covariates and changes in the variances (and covariances) of the outcome measures over time, but prevents estimation of the fixed effects of other time-varying covariates.

Veiga et al. (2014) present an example of fitting this model (accounting for PSU-specific weights and conditional survey weights at the individual level) using an *unstructured* variance–covariance matrix for the random errors, allowing for unique variances of the errors at each of eight waves, and unique covariances of the errors for each pair of waves. They note that other more constrained covariance structures are possible, and find that the *Toeplitz* structure resulted in the most parsimonious model. They use the method of *probability-weighted iterative generalized least squares* (*PWIGLS*) to fit the models and employ a linearization-based variance estimation approach that is both design- and model-consistent, similar to Pfeffermann et al. (1998). However, they only consider the weights of respondents who have provided *complete data* at all of the waves (where these base sampling weights might be adjusted for differential probabilities of providing complete data to account for those respondents who did not provide complete data). Extensions of this approach that incorporate all available information for cases that have responded in at least one wave are still needed. These authors implemented this model-fitting procedure using the Stata programming language Mata, and a link to this software can be found in Veiga et al. (2014). We consider an application of this approach in Section 11.3.3.1.

11.2.3.3 Approach 3: Weighted GEE Estimation

In this third approach, extensions of the generalized estimating equation (GEE) technique originally proposed by Liang and Zeger (1986) that use either case-specific or observation-specific weights to account for complex sampling features and different patterns of attrition over time (Fitzmaurice et al., 1995; Robins et al., 1995; Sutradhar and Kovacevic, 2000; Roberts et al., 2009; Carrillo et al., 2010) are used to estimate the parameters in a model of interest (which presumably would include, at a minimum, time as a predictor of interest). In this approach, which enables an analyst to model changes in the marginal mean of a dependent variable over time while also accounting for one of several possible correlation structures for the repeated measurements over time, baseline sampling weights (possibly adjusted for unit nonresponse in the initial wave) are adjusted by weights that account for the probability of having a particular *response pattern* over time, and individuals are treated as clusters for variance estimation purposes.

The general case-specific weighted GEE approach assumes that the initial wave includes the entire baseline sample of individuals (with corresponding base sampling weights that may be adjusted for the probability of responding at the initial wave), and proceeds as follows (Fitzmaurice et al., 1995; Raghunathan, 2016):

1. Create a vertical data set (with multiple rows per sampled case), including a response indicator for each wave following the initial wave, the response pattern in previous waves, time-invariant auxiliary variables for each case, and the values of any available lagged survey information from previous waves ([Table 11.1](#)).
2. Use a well-specified logistic regression model to estimate the probability of responding for case i at wave t , denoted by p_{it} , conditional on the response pattern in previous waves (i.e., based on a model fitted to only those cases that have the same pattern of response indicators in previous waves as case i). Use the auxiliary variables and the lagged survey responses available in the vertical data set (not shown in [Table 11.1](#)) as predictors, and save the predicted probabilities. A failure to carefully specify the response propensity model for a given wave conditioning on prior wave information (under the assumption that missing responses are *missing at random*, conditional on the prior wave information) will lead to bias in the weighted GEE estimates.
3. Compute the probability of having a particular response pattern as the product of the estimated probabilities of responding (or not responding) in each wave, up until the final wave. For cases that do not respond in all waves, some of the estimated probabilities used to compute this product will be $(1 - p_{it})$, or the probability of *not responding* in a particular wave conditional on information from previous waves. (We note that the probability of dropping out permanently in a particular wave that is *not* the final wave can be represented as the product of all conditional probabilities of *not responding* from that wave forward.)
4. Invert the final case-specific probabilities of having a particular response pattern, and adjust the base sampling weights by these inverted predictions. Proceed to estimate the parameters in the model of interest using GEE with each case's contribution to the estimating equation multiplied by the adjusted case-specific weight.

We note that cases 1, 2, and 3 in the hypothetical example in [Table 11.1](#) have a *monotone pattern of missing data*, while case 4 has a *nonmonotone pattern of missing data*. In longitudinal surveys with several waves, many nonmonotone patterns could be possible. Raghunathan (2016, pp. 138–139) argues that a multiple imputation approach may be more effective in

TABLE 11.1
 An Illustration of the Data Preparation Required to Compute Case-Specific Weights for the Weighted GEE Approach,
 Considering a Longitudinal Study with Four Waves

Case ID	Wave	Response Indicator (Outcome)	Predicted Probability	Cumulative Probability	Lagged Cumulative Probability	Response Pattern in Prior Waves ^a	Final Case-Specific Weight Adjustment
			of Outcome				
1	2	1	p_{12}	p_{12}	—	—	—
1	3	1	p_{13}	$p_{12} \times p_{13}$	p_{12}	1	—
1	4	1	p_{14}	$p_{12} \times p_{13} \times p_{14}$	$p_{12} \times p_{13}$	1, 1	$1/(p_{12} \times p_{13} \times p_{14})$
2	2	1	p_{22}	p_{22}	—	—	—
2	3	0	$1 - p_{23}$	$p_{22} \times (1 - p_{23})$	p_{22}	1	—
2	4	0	$1 - p_{24}$	$p_{22} \times (1 - p_{23}) \times (1 - p_{24})$	$p_{22} \times (1 - p_{23})$	1, 0	$1/[p_{22} \times (1 - p_{23}) \times (1 - p_{24})]$
3	2	1	p_{32}	p_{32}	—	—	—
3	3	1	p_{33}	$p_{32} \times p_{33}$	p_{32}	1	—
3	4	0	$1 - p_{34}$	$p_{32} \times p_{33} \times (1 - p_{34})$	$p_{32} \times p_{33}$	1, 1	$1/[p_{32} \times p_{33} \times (1 - p_{34})]$
4	2	1	p_{42}	p_{42}	—	—	—
4	3	0	$(1 - p_{43})$	$p_{42} \times (1 - p_{43})$	p_{42}	1	—
4	4	1	p_{44}	$p_{42} \times (1 - p_{43}) \times p_{44}$	$p_{42} \times (1 - p_{43})$	1, 0	$1/[p_{42} \times (1 - p_{43}) \times p_{44}]$

^a The response pattern in prior waves is used to define the subset of cases that will be used to fit the logistic regression model predicting the probability of responding in the current wave for this particular case. In Wave 2, all cases will be used to estimate the probability of responding.

these nonmonotone scenarios, given the difficulty of estimating the probabilities of responding in particular waves conditional on unique patterns of response outcomes in previous waves that are necessary for this case-specific weighting approach. The difficulty arises from the number of unique patterns of response outcomes in previous waves that would arise in these nonmonotone scenarios, meaning that some of the logistic regression models would be fitted to small subsets of cases. We discuss this recommended type of multiple imputation approach for nonmonotone patterns of missing data in Section 11.2.3.4.

Notably, weighted GEE is a *marginal modeling approach*, enabling inference about the average trajectories of interest in the target population, but not inference about subject-specific variability in the trajectories of interest. If an analyst of longitudinal survey data with a monotone missing data pattern is interested in estimating between-subject variability in trajectories of interest, the weighted multilevel modeling approaches discussed earlier in Section 11.2.3.1 need to be employed. This approach also assumes that the missing data are arising at random, conditional on the covariates included in the response propensity models underlying the weighted GEE method. We consider examples of the weighted GEE approach using case-specific weights later in Section 11.3.

Extensions of the weighted GEE approach allowing for time-varying weights (rather than the case-specific weights described above) have also been developed and are currently implemented in the SAS and SUDAAN software (Carrillo and Karr, 2013; Thompson, 2015). SAS implements this approach in the GEE procedure, available in releases 9.4 and above, which allows users to model the conditional probabilities of response using the MISSMODEL keyword. SUDAAN uses GEE when fitting regression models with weights by default, and requires users to compute their own time-varying weights as input (Table 11.1). This approach is especially convenient for accommodating different patterns of attrition. Following this approach, the time-varying weights for *cases responding at a particular wave* would simply be the survey weights from the initial wave, multiplied by the inverted value of the cumulative product of the conditional probabilities of responding (or not responding) up to a particular time point where a case responded (see the “Cumulative Probability” column in Table 11.1, where only cases with the response indicator equal to 1 would be analyzed). The weighted estimating equations then simply allow each individual contribution from a responding sample case at each time point to be weighted by this wave-specific weight.

11.2.3.4 Approach 4: Multiple Imputation Analysis

This fourth approach begins with all available longitudinal survey data in a wide format, with one row per panel survey respondent, and uses sequential regression imputation techniques (Raghunathan et al., 2001; Raghunathan,

2016; see [Chapter 12](#) for details) to impute missing values for respondents that did not provide information in particular waves. Missing values on key variables are imputed multiple times based on well-specified models for the variables with missing data, which are generally fitted using the respondents providing complete data in all of the waves. These imputation models take advantage of the fact that the same variables are measured in different waves, where an imputation model for a key outcome in a later wave would likely benefit from having a measure of that same outcome in a previous wave as a predictor. After this imputation process has been repeated multiple times, resulting in multiple complete wide data sets, one would fit the model of interest to each imputed data set (possibly a weighted GEE model using the Wave 1 survey weights for each individual, or a multilevel model with the baseline survey weights serving as Level 2 weights and the Level 1 weights for each individual set to 1.0, given the “complete” data), and then combine the estimates from each imputed data file into a single set of estimates and design-adjusted standard errors (Little and Rubin, 2002; Sikkel et al., 2009).

This approach clearly relies on well-specified imputation models, and may be limited if the individuals providing complete data in all of the waves represent a very specific subpopulation (where the imputation models being used may not apply to everyone in the population of interest). Careful assessment of the quality and fit of the imputation models is key to the performance of this approach, and existing software tools now allow analysts to impute missing values based on assumed nonignorable missing data mechanisms (e.g., West and Little, 2013; West and McCabe, 2016) to examine the sensitivity of multiple imputation estimates to assumptions made about the mechanism underlying the wave nonresponse. We consider an example of this multiple imputation approach in Section 11.3.

11.2.3.5 Approach 5: Calibration Adjustment for Respondents with Complete Data

Following this fifth approach (Sikkel et al., 2009), we would use the ideas of poststratification adjustment discussed in [Chapter 2](#) to calibrate the baseline survey weights of individuals providing *complete data* in all of the waves of interest to reflect the original population represented by the *full sample* of respondents in the first wave. Suppose, for example, that the sample in the first wave of a five-wave panel survey represents a population that is 50% male and 50% female (after applying the Wave 1 survey weights in estimation). In subsequent waves, males respond at lower rates. When examining the individuals who provided complete data in the first five waves of the panel survey and the population that they represent, we might find that the population represented is 35% male and 65% female (after applying the baseline survey weights). Clearly some adjustment of the baseline survey weights is needed (presumably to give more weight to those males

who responded in all five waves), and this is where one can consider this calibration approach.

The calibration approach proceeds as follows:

1. Identify auxiliary variables in the first wave that are measured for the full sample of respondents and are generally predictive of both (1) key survey measures and (2) the probability of responding in future waves.
2. Compute weighted estimates of population distributions across subgroups defined by cross-classifications of these auxiliary variables, based on the respondents in the first wave. These weighted estimates serve as the benchmark population features for the calibration approach.
3. Compute weighted estimates of population distributions across the same subgroups based on those respondents that provided complete data in all of the waves of interest.
4. Based on the ratios of population percentages in the different subgroups defined by (2) and (3) above, compute calibration adjustments for the Wave 1 survey weights of the respondents who provided complete data in all of the waves of interest. For example, if 5% of the population appears in a certain subgroup (based on the benchmark estimate) and 2.5% of the population is estimated to come from that same subgroup based on the respondents with complete data across the waves, those respondents would have their weights adjusted by a factor of 2.

This approach clearly relies on the measurement of good auxiliary variables in the first wave, which is a definite advantage of panel surveys where the same measures are collected over time. This approach also discards potentially useful information that would otherwise be analyzed when following some of the approaches described in earlier subsections. We evaluate the quality of estimates based on this approach relative to estimates found when using the other approaches in Section 11.3.

11.3 Alternative Longitudinal Analyses of the HRS Data

We now consider illustrations of each of the approaches outlined in Section 11.2 using current software procedures. In each of these illustrations, we analyze data from the 2006, 2008, 2010, and 2012 waves of the HRS, treating the sample of responding financial reporters with nonzero weights in 2006 as the “full sample” in the initial wave. Our variable of interest measured

for financial reporters in each of these waves is the total annual household income, which was computed based on the income of the respondents and their spouse only (if applicable). Given a handful of extreme reports (including zeroes) and general evidence of a right skew in the distribution of the reported annual income values in each of these four waves, we consider a natural log transformation of the reported income value (plus \$1, to enable analysis of the zero reports) in each wave as our outcome variable of interest.

We start with a merged HRS data set in the “wide” (or “horizontal”) format, with one row per responding financial reporter. This data file (available on the book web site) contains the sample design information in the baseline wave (2006), including the survey weight, KWGTR, the stratum variable, STRATUM, and the sampling error computation unit variable, SECU. Also available for responding financial reporters in each of the four waves are measures of age (in years), arthritis (yes/no), diabetes (yes/no), years of education (0–11, 12, 13–15, 16+), race/ethnicity (Hispanic, Non-Hispanic White, Non-Hispanic Black, Non-Hispanic Other), marital status (married/ previously married/never married), number of falls in the past 2 years, and self-rated health (1 = Excellent, 2 = Very Good, 3 = Good, 4 = Fair, 5 = Poor). We consider these variables as possible covariates when illustrating each of the different types of analyses discussed above.

We first create the four log-transformed income variables using the available responses in each wave, and assess histograms for these four transformed measures. All of these histograms (not shown) suggest that the log-transformed income values are roughly normally distributed, with the exception of some outliers:

```
gen ln_inc06 = ln(H8ITOT + 1)
gen ln_inc08 = ln(H9ITOT + 1)
gen ln_inc10 = ln(H10ITOT + 1)
gen ln_inc12 = ln(H11ITOT + 1)

hist ln_inc06
hist ln_inc08
hist ln_inc10
hist ln_inc12
```

11.3.1 Example: Descriptive Estimation at a Single Wave

Our analytic objective in these illustrations of descriptive estimation at a single wave is to estimate the mean total household income in 2008 in the HRS target population. Of the baseline sample of 11,789 participating financial reporters in 2006 with a valid value for log-transformed annual household income, 10,574 (89.7%) also provided valid income reports in 2008. We wish to estimate the mean total household income in 2008 in a manner that repairs possible nonresponse bias in the estimates due to financial reporters who did not participate in the 2008 wave. We consider a simple

TABLE 11.2

Descriptive Estimates of Mean Total Household Income in 2008 for the HRS Target Population Following Alternative Estimation Approaches

Approach	<i>n</i>	Estimated Mean	95% CI
Complete case analysis	10,574	34,223.97	32,467.83, 36,075.10
Response propensity adjustment	10,574	33,309.15	31,580.11, 35,132.86
Multiple imputation	11,789 ^a	33,281.21	31,568.93, 35,086.35

^a After imputation (total number of complete cases in 2006).

complete case analysis, in addition to the three approaches outlined above in Section 11.2.1: weighting, multiple imputation, and methods for non-ignorable missing data (imputation based on a selection model):

1. *Complete Case Analysis.* Following this approach, we simply perform a design-based descriptive analysis of the available log-transformed household income values in 2008, and back-transform the weighted estimate and the 95% confidence limits to the original dollar scale. The results from this initial analysis are reported in Table 11.2.

```
* Complete case analysis for 2008 log-income.
svyset secu [pweight = kwgtr], strata(stratum)
svy: mean ln_inc08
matrix list r(table)
matrix a = r(table)
di exp(a[1,1])
di exp(a[5,1])
di exp(a[6,1])
```

2. *Weight Adjustment.* Following this second approach, we first fit a response propensity model, predicting response in the 2008 wave with selected covariates in 2006, including the total household income in 2006. We only include main effects of these covariates in the model (after imputing modal values for small counts of cases with missing data on the covariates) for illustration purposes. In a real analysis, we may want to consider interactions between covariates, provided that they are predictive of both response propensity and the key variable(s) of interest in the later wave. We use the 2006 survey weights to estimate the response propensity model parameters (Wun et al., 2007), and then compute predicted probabilities of response based on the weighted parameter estimates. The 2006 survey weights are then multiplied by the inverses of the mean estimated response propensities within deciles of the response propensities, which is a technique that is used to minimize variability in the ultimate adjusted sampling weights that result from these

nonresponse adjustments (Valliant et al., 2013). Here is the code that one can use in Stata to do this:

```
* Weight adjustment approach for 2008 log-income.

* Compute response indicator for 2008.
gen resp08 = 1 if ln_inc08 != .
replace resp08 = 0 if ln_inc08 == .
tab resp08, miss

* Modal imputation of missing covariate values.
replace selfrhealth_06 = 3 if selfrhealth_06 == .
replace marcat_06 = 2 if marcat_06 == .
replace diabetes_06 = 0 if diabetes_06 == .
replace arthritis_06 = 1 if arthritis_06 == .
replace racecat = 2 if racecat == .
replace edcat = 2 if edcat == .

* Response propensity model, with predictions.
svyset secu [pweight = kwgtr], strata(stratum)
svy: logit resp08 ln_inc06 i.selfrhealth_06 age_06 ///
i.marcat_06 diabetes_06 arthritis_06 i.racecat i.edcat
predict phat, p

* Form deciles of response propensity, and compute means
* within each decile for weight adjustment.
xtile dec = phat, nq(10)
egen mean_phat = mean(phat), by(dec)
gen adj_kwgt = kwgtr * (1 / mean_phat)

* Estimation using adjusted weights.
svyset secu [pweight = adj_kwgt], strata(stratum)
svy: mean ln_inc08
matrix a = r(table)
di exp(a[1,1])
di exp(a[5,1])
di exp(a[6,1])
```

Of the covariates used in the response propensity model, only self-rated health, age, and marital status are significantly associated with both the response indicator and log-transformed income in 2008 (results not shown), meaning that some of the covariates have the desired properties for reduction of nonresponse bias (see [Chapter 2](#) for discussion). Some of the covariates (e.g., log-transformed 2006 income and education category) are strong predictors of log-transformed income in 2008 only, which should help to reduce the variance in the weighted estimates. We note in [Table 11.2](#) that the adjusted estimate of the mean total household income in 2008 has been reduced by nearly \$1000 after the adjustment; respondents in 2008 tended to be those with higher incomes.

3. *Multiple Imputation.* Following this third approach, which like the weight adjustment approach above assumes that the missing data in 2008 are *missing at random* (or, in other words, the missing data mechanism is ignorable conditional on the covariates used in the imputation model), we first predict missing values for 2008 log-transformed income multiple (five) times, reflecting the variability in the predictive distribution for this variable, and then we analyze each data set and combine the results into a single set of estimates and standard errors (see Chapter 12 for more discussion of the multiple imputation analysis approach). Here is the code that we can use in Stata to do this, employing the same covariates used in the weighting adjustments. Per recommendations of Reiter et al. (2006), note that we also include deciles of the 2006 sampling weights and the sampling strata as predictors in the imputation models, to account for the complex sampling features when imputing the missing income values:

```
* Create deciles of the 2006 sampling weights.
xtile wgt_dec = kwgtr, nq(10)

* Set data structure and register both complete "regular"
* variables and variables with missing data to be imputed.
mi set flong
mi register imputed ln_inc08
mi register regular ln_inc06 selfrhealth_06 age_06 ///
    marcat_06 diabetes_06 arthritis_06 racecat edcat ///
    stratum wgt_dec
mi describe

* Implement regression imputation after setting a seed.
set seed 41279

mi impute chained (regress) ln_inc08 = ln_inc06 ///
    i.selfrhealth_06 age_06 i.marcat_06 diabetes_06 ///
    arthritis_06 i.racecat i.edcat i.wgt_dec i.stratum, ///
    noisily augment add(5) burnin(5)

* Set complex sampling features in MI framework.
mi svyset secu [pweight = kwgtr], strata(stratum)

* Multiple Imputation estimation.
mi estimate, vartable: svy: mean ln_inc08
matrix list r(table)
matrix a = r(table)
di exp(a[1,1])
di exp(a[5,1])
di exp(a[6,1])
```

We note that the overall inference that we would make regarding mean income in 2008 is very similar to that produced by the weighting

adjustment for nonresponse. The estimated fraction of missing information (FMI) value for the multiple imputation estimate (produced by the vartable option above) is 3.5%, which is well below the unweighted item-missing data rate of 10.3% for this income variable. We were therefore able to effectively recover missing information on income in 2008 using the covariates in the imputation model, and we do not see immediate evidence of a nonignorable missing data mechanism for income (which would be suggested if the FMI value was larger than the item-missing data rate; Nishimura et al., 2016).

4. *Imputation Using a Selection Model.* Finally, we fit a probit selection model, which enables us to initially assess the correlation of the residuals in a substantive model for income with the residuals in a probit model for an indicator of providing a valid income measure in 2008. If these residuals are positively correlated, it could mean, for example, that someone providing a higher-than-expected income value (a positive residual unexplained by the covariates in the substantive model) has a higher-than-expected value on the 2008 response indicator (a positive residual, once again unexplained by the covariates in the selection model). Such a mechanism would suggest that missingness on income is nonignorable, given that those with larger income in 2008 are more likely to respond. To fit this type of selection model, we do need to identify good *instrumental variables*, which are variables that are predictive of the response indicator in 2008 but not the substantive variable of interest (log-transformed income in 2008). From the analysis above, we know that diabetes and arthritis serve this role well, as they were significant predictors in the response propensity model but not the regression model for income in 2008. We therefore include these predictors in the selection (response) equation of the probit selection model, but not in the substantive equation. See West and McCabe (2017) for more discussion of this issue.

We first fit the selection model to the original data set (prior to imputation, and using the original HRS sample design variables), and then examine the correlation of the residuals in the substantive and selection equations:

```
svyset secu [pweight = kwgtr], strata(stratum)
svy: heckman ln_inc08 ln_inc06 selfrhealth_06 age_06 ///
    i.marcat_06 i.edcat, ///
    select(resp08 = diabetes_06 arthritis_06 ///
    selfrhealth_06 age_06 i.marcat_06)
```

The estimated residual correlation parameter is denoted as rho in the Stata output. This weighted estimate is 0.017, with a design-based 95% confidence interval of (-0.018, 0.053). The fact that 0 is included in this interval suggests that there is a negligible correlation between

the unique residuals associated with the income reports in 2008 (given the predictors in the substantive model) and the unique residuals associated with the probability of responding (again given the predictors in the selection model). This means that the weighting and imputation methods above (which assumed ignorable missing data mechanisms) should provide sufficient bias correction. The imputation model used for income would therefore apply for both respondents and nonrespondents in 2008, meaning that the imputation model fitted to respondents would not be biased in any way (where the selection model approach would provide estimates of a substantive model corrected for nonignorable selection bias). For more details on imputation approaches using fitted selection models if this correlation were to be non-negligible, see West and McCabe (2017).

11.3.2 Example: Change across Two Waves

We now consider examples of possible approaches when the analytic objective involves estimation of the mean change in a variable of interest across two waves for a given individual in the target population. We consider measures of total household income provided by financial reporters in 2006 and 2010, and our objective is to estimate the mean change in household income (in dollars) for an individual from the HRS target population across these 4 years. In this example, the variable of interest that we would ideally like to compute for each financial reporter in the sample is the difference in actual income between 2010 and 2006. However, we do not have income reports from 2010 for financial reporters who did not respond in both of these waves; only 9402 (79.75%) of the 11,789 responding financial reporters in 2006 also provided income information in 2010. We therefore consider the same weighting and imputation approaches discussed in Section 11.3.1 to address potential bias in estimates of this mean change due to wave nonresponse in 2010.

1. *Complete Case Analysis.* Following this approach, we first compute the change in income from 2006 to 2010 for each financial reporter who provided values of income in both waves. We then perform a

TABLE 11.3

Descriptive Estimates of Mean Change in Total Household Income from 2006 to 2010 for Those Individuals in the HRS Target Population, Following Alternative Estimation Approaches

Approach	<i>n</i>	Estimated Mean Change	95% CI
Complete case analysis	9,402	-6,551.40	-10,289.72, -2,813.09
Response propensity adjustment	9,402	-6,115.54	-9,526.65, -2,704.43
Multiple imputation	11,789 ^a	-3,455.83	-9,656.79, 2,745.13
Calibration	9,402	-6,341.66	-9,908.63, -2,774.69

^a After imputation (total number of complete cases in 2006).

simple design-based descriptive analysis of the changes in income, only for those “complete case” individuals who responded in both waves. The results from this initial complete case analysis, generated using the Stata code below, are reported in Table 11.3.

```
* Complete case analysis: mean change in income,
* 2006 to 2010.
gen incdiff_06_10 = H10ITOT - H8ITOT
svyset secu [pweight = kwgtr], strata(stratum)
svy: mean incdiff_06_10
```

The 95% confidence interval for the mean change clearly does not include 0, and the estimated mean change is negative. This suggests that on average, individuals in the HRS target population experienced a significant decline in total household income from 2006 to 2010, a decline that is not unexpected given the impact of the global financial recession of 2008.

2. *Weight Adjustment.* For this second approach, we adjust the base sampling weights of individuals providing valid income reports at each of these two waves to account for those individuals who reported income in 2006 but not 2010 (who would be dropped from the complete case analysis, potentially introducing bias in the estimate of mean change). We compute the adjusted weights exactly as described in Section 11.3.1, only using an indicator of response in 2010, and then estimate the mean change in income from 2006 to 2010 using the adjusted weights for each of the financial reporters who responded in both waves:

```
* Compute response indicator for 2010.
gen resp10 = 1 if ln_inc10 != .
replace resp10 = 0 if ln_inc10 == .
tab resp10, miss

* Modal imputation of missing covariate values.
replace selfrhealth_06 = 3 if selfrhealth_06 == .
replace marcat_06 = 2 if marcat_06 == .
replace diabetes_06 = 0 if diabetes_06 == .
replace arthritis_06 = 1 if arthritis_06 == .
replace racecat = 2 if racecat == .
replace edcat = 2 if edcat == .

* Response propensity model.
svyset secu [pweight = kwgtr], strata(stratum)
svy: logit resp10 ln_inc06 i.selfrhealth_06 age_06 ///
    i.marcat_06 diabetes_06 arthritis_06 i.racecat i.edcat
predict phat, p

* Form deciles of response propensity, and compute means
* within each decile for weight adjustment.
```

```

xtile dec = phat, nq(10)
egen mean_phat = mean(phat), by(dec)
gen adj_kwgt = kwgt * (1 / mean_phat)

* Estimation of mean change using adjusted weights.
svyset secu [pweight = adj_kwgt], strata(stratum)
svy: mean incdiff_06_10

```

We note in Table 11.3 that our inferences would hardly be affected at all relative to the complete case analysis, and that the 95% confidence interval for the mean change once again does not include 0. This confidence interval is also slightly narrower than that for the complete case analysis, which reflects some gains in efficiency due to the use of covariates in the response propensity model that are strongly predictive of income in 2010.

3. *Multiple Imputation.* We now apply the same regression imputation approach from Section 11.3.1 to impute missing values on reported income in 2010 multiple (five) times. Given that the imputed values are on the natural-log scale, we first back-transform the imputed values to the original dollar scale (by exponentiating the imputed values), and then compute the difference in income between 2006 and 2010 for each responding financial reporter in each of the five imputed data sets. We also place bounds on the imputed values of these changes in income from 2006 to 2010 for nonrespondents in 2010, ensuring that the imputed change values fall within the range of the original observed data:

```

* Multiple imputation of 2010 log-income.

* Create deciles of the 2006 sampling weights.
xtile wgt_dec = kwgt, nq(10)

* Set data structure and register both complete "regular"
* variables and variables with missing data to be imputed.
mi set flong
mi register imputed ln_inc10
mi register regular ln_inc06 selfrhealth_06 age_06 ///
    marcat_06 diabetes_06 arthritis_06 racecat edcat ///
    stratum wgt_dec
mi describe

* Implement regression imputation
set seed 41279

mi impute chained (regress) ln_inc10 = ln_inc06 ///
    i.selfrhealth_06 age_06 i.marcat_06 diabetes_06 ///
    arthritis_06 i.racecat i.edcat ///
    i.wgt_dec i.stratum, ///
    noisily augment add(5) burnin(5)

```

```

* Compute bounded change scores in each imputed data set.
sum incdiff_06_10 if _mi_m == 0
sum ln_inc10 if _mi_m == 0
replace ln_inc10=14.92 if ln_inc10 > 14.92 & ln_inc10 != .
gen new_chg0610 = exp(ln_inc10) - exp(ln_inc06)
replace new_chg0610 = -12300000 if new_chg0610 < -12300000
replace new_chg0610 = 2062968 if new_chg0610 > 2062968 ///
& new_chg0610 != .

* Set complex sampling features for MI analysis.
mi svyset secu [pweight = kwgtr], strata(stratum)

* Multiple Imputation estimation.
mi estimate, vartable noisily: svy: mean new_chg0610

```

We note in Table 11.3 that our estimate of the mean change in income has been reduced, and would no longer be considered significant after multiple imputation of the missing income values. Closer inspection of the design-based estimates from each imputed data set reveals smaller (negative) estimates of mean changes and larger within-imputation variance than was observed for the complete cases, meaning that nonrespondents likely had smaller changes in general. This provides an example where multiple imputation, which imputes missing values for specific variables of interest rather than relying on global nonresponse adjustments that are “variable-agnostic,” is picking up additional information for the missing cases that the weighting adjustments may not have been fully capturing. We also note that the FMI value for the mean change in income is 9.5%, which once again is much smaller than the unweighted nonresponse rate of 20.25% for income in 2010. We are therefore recovering much of the missing information using the available covariates, and we no longer have a strong evidence of a significant negative change in total household income.

After fitting a selection model to these data using the same approach described in Section 11.3.1, we once again find evidence of a negligible correlation between the residuals in the substantive model and the residuals in the selection model (estimated value of $\rho = 0.033$, 95% CI = 0.003, 0.063), suggesting that this is minimal evidence of a nonignorable missing data mechanism at work here, and the multiple imputation estimates assuming an ignorable missing-at-random mechanism should be considered reasonable.

We note that the multiple imputation approach illustrated here could be extended to more complex models and more waves, using the same basic syntax. In some cases, imputed data sets may need to be restructured into vertical formats before being analyzed (e.g., when fitting a multilevel model to the imputed data), but this process is straightforward (Section 11.3.3), and facilitated by the

mi reshape command in Stata. In general, when imputing missing values in longitudinal survey data sets, we recommend that users first impute the missing values in a wide-format data set (using information from adjacent waves in the imputation models, as we have done here), and then fit the models of interest, which may require restructuring the data. We provide additional examples of multiple imputation analyses in [Chapter 12](#).

4. *Calibration.* Finally, we apply the calibration approach outlined in Section 11.2.3.5 to estimate the mean change in income from 2006 to 2010. Starting with the wide-format data set and the full sample in 2006, we first compute the sums of the 2006 survey weights (i.e., estimates of the population sizes) within each of the 32 cross-classes defined by gender, race, and education category (selected simply for illustration purposes as significant predictors of income), and we then save these sums in an independent data set:

```
use "S:\chapter11_hrs.dta", clear
* Modal imputation of missing covariate values.
replace racecat = 2 if racecat == .
replace edcat = 2 if edcat == .

* Compute sums of 2006 weights in cross-classes
* defined by sex, race, and education.
egen cal_class = group(racecat edcat gender)
collapse (sum) kwgtr, by(cal_class)
rename kwgtr popsize

save "S:\cal_pop_sizes.dta", replace
```

Next, we repeat this process, but only for those cases with complete data in 2006 and 2010. We then merge the two independent data sets by calibration class, and compute the calibration adjustments for each class as the ratios of the estimated population sizes based on the 2006 (baseline) sampling weights for the full sample to the estimated population sizes based on the cases with complete data in 2006 and 2010:

```
* Repeat process for cases with complete data.
use "S:\chapter11_hrs.dta", clear
* Modal imputation of missing covariate values.
replace racecat = 2 if racecat == .
replace edcat = 2 if edcat == .

gen ln_inc10 = ln(H10ITOT + 1)

* Compute response indicator for 2010.
gen resp10 = 1 if ln_inc10 != .
replace resp10 = 0 if ln_inc10 == .
tab resp10, miss
```

```

* Only keep cases with complete data.
keep if resp10 == 1

* Compute sums of 2006 weights in cross-classes
* defined by sex, race, and education.
egen cal_class = group(racecat edcat gender)
collapse (sum) kwgtr, by(cal_class)
rename kwgtr sumrespwghts

save "S:\cal_resp_sizes.dta", replace

* Merge the two data sets of estimated population sizes.
merge 1:1 cal_class using "S:\cal_pop_sizes.dta"

* Compute calibration adjustments for each cross-class.
gen cal_adj = popsize / sumrespwghts

save "S:\cal_resp_sizes.dta", replace

```

Finally, we re-open the original wide data set, merge the calibration adjustments into the data set (matching by cross-class), multiply the 2006 sampling weights by the calibration adjustments, and verify that the sums of the calibrated weights in each cross-class for respondents with complete data are equal to the sums of the baseline weights in each cross-class for the full sample:

```

* Open original data set and merge calibration adjustments.
use "S:\chapter11_hrs.dta", clear

* Modal imputation of missing covariate values.
replace racecat = 2 if racecat == .
replace edcat = 2 if edcat == .

egen cal_class = group(racecat edcat gender)
sort cal_class
gen ln_inc06 = ln(H8ITOT + 1)
gen ln_inc10 = ln(H10ITOT + 1)

merge m:1 cal_class using "S:\cal_resp_sizes.dta"

* Compute response indicator for 2010.
gen resp10 = 1 if ln_inc10 != .
replace resp10 = 0 if ln_inc10 == .
tab resp10, miss

* Compute calibrated weights for cases with complete data.
gen kwgtr_cal = kwgtr * cal_adj if resp10 == 1

* Verify that sums of calibrated weights for cases
* with complete data are equal to sums of base weights
* for full sample.
total kwgtr, over(cal_class)
total kwgtr_cal if resp10 == 1, over(cal_class)

```

After this verification, we estimate the mean change based on the cases with complete data in 2006 and 2010, using the calibrated weights for

estimation and estimating variance accounting for the other complex sampling features:

```
* Estimate mean change using complete cases.  
gen incdiff_06_10 = H10ITOT - H8ITOT  
svyset secu [pweight = kwgtr_cal], strata(stratum)  
svy: mean incdiff_06_10
```

We note in [Table 11.3](#) that our inference based on the calibration approach would largely be similar to that based on the complete case analysis and the response propensity adjustment: there is a significant reduction in mean income from 2006 to 2010. The above approach could be repeated with other possible cross-classes (e.g., based on 2006 income) to assess the sensitivity of the inference to the choice of the cross-classes for calibration.

11.3.2.1 Accounting for Refreshment Samples When Estimating Mean Change

In many panel surveys that employ rotating panel designs (e.g., the U.S. Current Population Survey), estimates of mean changes in particular measures from one wave to the next are not based entirely on panel respondents, but include refreshment samples that are specific to particular waves. In these cases, imputation of missing values for the refreshment sample cases in waves where they are not included would not make logical sense. In these settings, one should employ the approaches described for making inference about differences in estimates between subgroups in [Chapter 5](#), treating the two waves being compared as separate subgroups and making sure to use the final weight computed for respondents in each wave in the analysis. The covariance of these two estimates would then need to account for the fact that individuals from the same sampling cluster may appear in both waves. However, should the fact that the same *individual* might also appear in both waves also be accounted for when estimating this covariance? In our experience with several empirical studies, treating the individual as a lower stage of multistage cluster sampling when estimating the variance of this type of difference in means across waves of a panel study does not make a substantial difference in the covariance of the estimates.

Consider this hypothetical example using a stacked version of the 2006 and 2008 HRS data sets, where individuals responding in both waves would have two rows in the resulting data set and a common household ID code (HHID, nested within the HRS sampling clusters), and the final weight variables would be specific to each wave. We consider the approach outlined in [Chapter 5](#) for comparing estimates from the two waves, using two different specifications of the sample design: one that only accounts for common sampling clusters across the two waves when estimating the covariance of the two estimated means, and one that accounts for the

common sampling clusters as first-stage sampling units (with a small sampling fraction within strata of 0.01), along with individuals as second-stage sampling units within the clusters (again with a small sampling fraction of 0.01):

```
* Ignore individuals as second-stage clusters.
svyset secu [pweight = weight], strata(stratum)
svy: mean income, over(wave)
lincom [income]2008 - [income]2006

* Account for individuals (HHID) as second-stage clusters,
* incorporating small FPCs.
gen samprate = 0.01

svyset secu [pweight = weight], strata(stratum) ///
    fpc(samprate) || hid, fpc(samprate)
svy: mean income, over(wave)
lincom [income]2008 - [income]2006
```

Both approaches produce nearly identical inferences, where the standard error of the weighted estimate of the difference in the means accounts for the single-stage or multistage cluster sampling. The standard error of the weighted estimate of the mean difference (\$3,749.24) in the first case is \$8,431.68, while the standard error of the same weighted estimate in the second case (accounting for individuals as second-stage sampling clusters, given the repeated measurements on some individuals) is \$8,432.23. Assuming slightly larger FPCs (e.g., 0.05 at either level) does not make a difference. When sampling fractions are generally small (either for the ultimate clusters at the first stage or individuals at the second stage), the contributions of lower stage clusters (individuals in this case) to the covariance of estimates from different waves in a panel study are generally quite small, meaning that the simple approach of accounting for the common sampling clusters across both waves would be sufficient in practice.

11.3.3 Example: Weighted Multilevel Modeling

We now consider an example of fitting a multilevel model to the 2006, 2008, 2010, and 2012 waves of the HRS data, using both wave-specific survey weights at Level 1 and respondent-specific survey weights at Level 2 in the estimation. We have two objectives in this example: (1) using all available information from the respondents across the four waves, estimate trajectories in annual income for both males and females, and compare the trajectories statistically; and (2) estimate any remaining between-respondent variance in the intercepts and trajectories among individuals in the HRS target population during this time period. Per the HRS documentation (Heeringa and Connor, 1995), survey weights representing inverses of the products of the probability of being sampled and the probability of responding at a given

wave were computed for responding households at each wave, to account for wave nonrespondents.

We first illustrate the necessary data management syntax to go from a “wide” format data set with one row per respondent to the required “vertical” format with multiple rows per respondent. We start by computing log-transformed versions of all available annual income reports from the four waves, select the variables of interest, and set the 2006 survey weight as the respondent-specific (baseline) sampling weight at Level 2. We then use the reshape command in Stata to transform the HRS data set from wide to long format, and scale the wave-specific sampling weights per the recommended “normalizing” method discussed by Chambers and Skinner (2003).

```

* Reshape the original wide data.
gen ln_inc1 = ln(H8ITOT + 1)
gen ln_inc2 = ln(H9ITOT + 1)
gen ln_inc3 = ln(H10ITOT + 1)
gen ln_inc4 = ln(H11ITOT + 1)

* Initial wave-specific survey weights.
gen wgt1 = kwgtr
gen wgt2 = lwgtr
gen wgt3 = mwgtr
gen wgt4 = nwgtr

* Baseline survey weight for respondents from 2006.
gen basewgt = kwgtr

* Keep variables of interest.
keep hhid pn gender ln_inc1-ln_inc4 wgt1-wgt4 ///
secu stratum basewgt

* Reshape data set from wide to vertical format.
reshape long ln_inc wgt, i(hhid pn) j(year)

* Drop missing income values (wave nonresponse).
drop if ln_inc == .

* Form a unique ID variable.
egen newid = concat(hhid pn)
destring newid, gen(newid_num)

* Compute conditional Level 1 weights
* (Skinner and Holmes 2003), and rescale weights.
gen level1wgt = wgt / basewgt
gen level2wgt = basewgt

* "Method 2" rescaling (normalizing weights).
egen sumw = sum(level1wgt), by(newid)
egen nj = count(ln_inc), by(newid)
gen level1wgt_r = level1wgt * nj/sumw

```

The data now have the appropriate vertical structure for the weighted multi-level modeling analysis, and we illustrate this structure below for the first 20 rows in the newly restructured vertical data set:

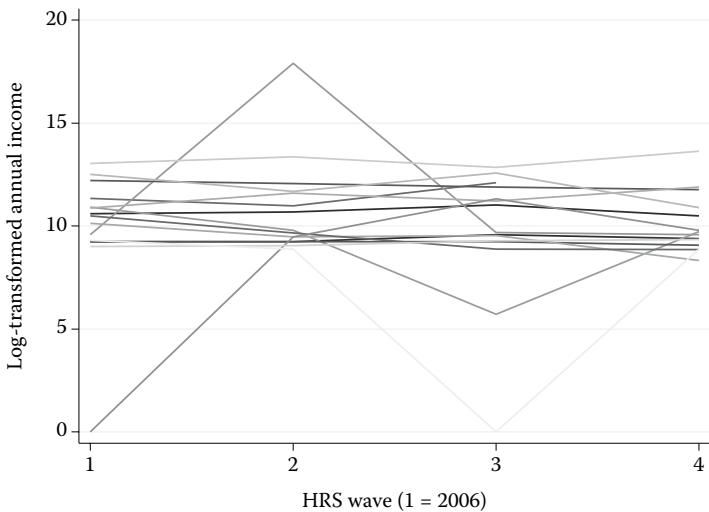
	newid	year	level1wgt_r	level2wgt	ln_inc	gender
1.	000003010	1	.9055811	4093	10.59636	1
2.	000003010	2	.9485039	4093	10.69197	1
3.	000003010	3	1.063333	4093	11.01484	1
4.	000003010	4	1.082582	4093	10.4913	1
5.	010001010	1	1.181266	7434	9.229064	1
6.	010001010	2	1.320145	7434	9.236106	1
7.	010001010	3	.7501688	7434	9.575053	1
8.	010001010	4	.7484209	7434	9.392745	1
9.	010004010	1	.9737449	5217	11.34865	1
10.	010004010	2	.9731849	5217	10.98191	1
11.	010004010	3	1.05307	5217	12.1168	1
12.	010013010	1	.9750476	5373	9.569203	1
13.	010013010	2	.9623446	5373	17.9101	1
14.	010013010	3	1.010979	5373	9.675646	1
15.	010013010	4	1.051629	5373	9.585827	1
16.	010013040	1	.9386594	5440	10.91874	2
17.	010013040	2	1.063756	5440	9.785154	2
18.	010013040	3	.9560866	5440	5.70711	2
19.	010013040	4	1.041498	5440	9.72466	2
20.	010038010	1	.9557571	5217	12.21305	1

Note that there are up to four rows per respondent (financial reporter) in this restructured data set, containing a unique respondent identifier, a year identifier (1 = 2006, 2 = 2008, etc.), the scaled wave-specific weights (with mean 1.0 for each respondent), the respondent-specific 2006 weights, the wave-specific log-transformed income values, and the subject-specific gender codes.

For analysis purposes, we recode the YEAR variable to represent number of years since 2006 (YRSSINCE06), taking on values 0, 2, 4, and 6:

```
gen yrssince06 = 0 if year == 1
replace yrssince06 = 2 if year == 2
replace yrssince06 = 4 if year == 3
replace yrssince06 = 6 if year == 4
```

After this initial data management, we can make use of Stata's graphical capabilities for panel data to examine an initial *multiple line plot* for a small subsample of HRS respondents. We generate the plot in [Figure 11.1](#) using the following two commands (additional editing was performed using Stata's graph editor):

**FIGURE 11.1**

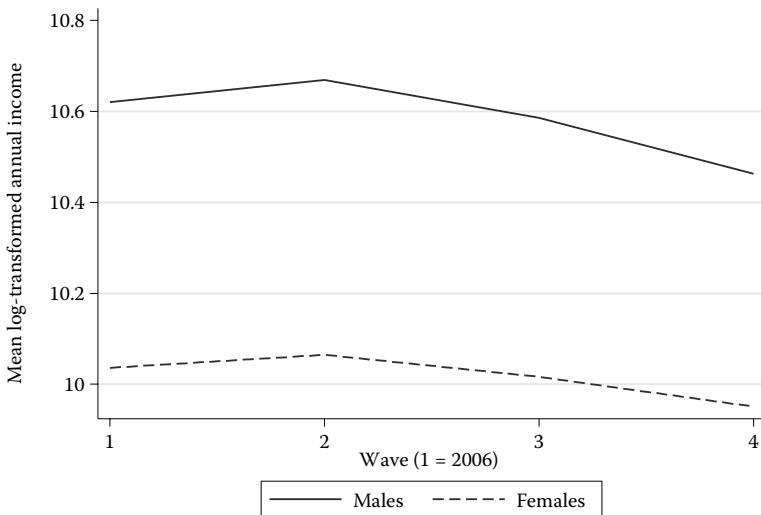
Multiple line plot showing trends in log-transformed annual income from 2006 to 2012 for a small subsample of HRS financial reporters.

```
* Plot data for small subsample of subjects.
xtset newid_num year
xtline ln_inc if newid_num <= 10200000, overlay ///
legend(off) ytitle(Log-Transformed Annual Income) ///
tttitle(HRS Wave (1 = 2006))
```

From this small subsample of respondents, we definitely see substantial between-respondent variance in the mean values of log-transformed annual income (suggesting the inclusion of a random intercept in a multilevel model for the data). We do not see evidence of substantial variability among the respondents in their trajectories, although there are clearly some unusual respondents experiencing substantial variation over time. We also look at a plot of unweighted mean values for males and females (one should save the restructured vertical data file first under a new name before collapsing the data set for purposes of this plot):

```
* Plot means across waves for males and females.
collapse (mean) ln_inc, by(gender year)
xtset gender year
xtline ln_inc, overlay ///
ytitle(Mean Log-Transformed Annual Income) ///
tttitle(Wave (1 = 2006))
```

In [Figure 11.2](#), we note that males tend to have a higher (unweighted) mean than females in each wave, and we also detect a possible curvilinear trend in mean log-transformed annual income. Our models will allow for this

**FIGURE 11.2**

Multiple line plot showing trends in mean log-transformed annual income from 2006 (Wave 1) to 2012 (Wave 4) for males and females.

possibility, but we do not see strong evidence of different trends for males and females.

We are now ready to fit the weighted multilevel model of interest using the `mixed` command in Stata. We first compute a squared version of the new rescaled year variable, enabling us to fit a model that includes fixed effects of years since 2006, years since 2006 squared, gender, and interactions between gender and each of the year variables. Next, we compute a variable containing a unique code for each of the HRS sampling error computation units (which are coded 1 or 2 for each of the HRS sampling strata), for the purpose of computing robust standard errors reflecting the intra-cluster correlations arising from the cluster sampling (Rabe-Hesketh and Skrondal, 2006). The effects of the sampling strata will be accounted for by including fixed stratum effects in the model. Finally, we also include random intercepts, random effects of years since 2006, and random effects of years since 2006 squared for each respondent, allowing these three random effects to have a general variance-covariance structure:

```
* Fit multilevel model of interest.
gen yrs06sq = yrssince06*yrssince06
egen unique_secu = group(stratum secu)
mixed ln_inc c.yrssince06##i.gender c.yrs06sq##i.gender ///
    i.stratum [pweight = level1wgt_r] ///
    || newid_num: yrssince06 yrs06sq, ///
    variance cov(unstruct) ///
    pweight(level2wgt) pwscale(size) ///
    vce(cluster unique_secu)
```

We carefully note important options used in this syntax to fit the multilevel model accounting for the respondent-specific and (scaled) wave-specific survey weights. The [pweight = level1wgt_r] option specifies the conditional, scaled wave-specific weights at Level 1, while the pweight(level2wgt) option specifies the respondent-specific weights in 2006 at Level 2. Although this is unnecessary given the earlier data management, we also include the pwscale(size) option, which would automatically normalize the Level 1 weights within each Level 2 respondent. The cov(unstruct) option allows the three random effects to have unique variances and covariances. Finally, the vce(cluster unique_secu) option requests that robust, sandwich-type standard errors be computed reflecting the intra-cluster correlations.

Given the complexity of these models and the resulting Stata output, we include the actual Stata output from fitting this model below:

Obtaining starting values by EM:									
Performing gradient-based optimization:									
Iteration 0: log pseudolikelihood = -3.022e+08									
Iteration 1: log pseudolikelihood = -3.020e+08									
Iteration 2: log pseudolikelihood = -3.019e+08									
Iteration 3: log pseudolikelihood = -3.019e+08									
Iteration 4: log pseudolikelihood = -3.019e+08									
Computing standard errors:									
Mixed-effects regression				Number of obs = 40,325					
Group variable: newid_num				Number of groups = 11,789					
Obs per group:									
min = 1									
avg = 3.4									
max = 4									
Log pseudolikelihood = -3.019e+08 Wald chi2(60) = 5134.15									
Prob > chi2 = 0.0000									
(Std. Err. adjusted for 112 clusters in unique_secu)									

ln_inc		Robust							
		Coef.	Std. Err.	z	P> z	[95% Conf. Interval]			
yrssince06		.0240185	.0150499	1.60	0.111	-.0054787 .0535158			
2.gender		-.5619222	.0354198	-15.86	0.000	-.6313439 -.4925006			
gender#c.yrssince06									
2		.0053894	.0220435	0.24	0.807	-.0378151 .048594			
yrs06sq		-.0094561	.0028249	-3.35	0.001	-.0149928 -.0039193			
gender#c.yrs06sq									
2		.0012008	.0036437	0.33	0.742	-.0059407 .0083423			
stratum									
2		.1688801	.1066258	1.58	0.113	-.0401026 .3778629			
3		.3205789	.0595461	5.38	0.000	.2038708 .4372871			
4		.4617349	.0456192	10.12	0.000	.3723229 .5511469			
5		.2687635	.0929799	2.89	0.004	.0865264 .4510007			
6		.2377024	.1813596	1.31	0.190	-.1177559 .5931606			
7		.7435081	.0893011	8.33	0.000	.5684811 .9185352			

	8	.3798766	.0447116	8.50	0.000	.2922436	.4675097
	9	.5331056	.1310302	4.07	0.000	.2762911	.78992
	10	.8097707	.1514721	5.35	0.000	.5128909	1.106651
	11	.2496312	.2342885	1.07	0.287	-.2095659	.7088282
	12	.2918107	.122146	2.39	0.017	.0524089	.5312125
	13	.6212048	.0965329	6.44	0.000	.4320038	.8104057
	14	.4835137	.0452381	10.69	0.000	.3948487	.5721786
	15	.5270103	.0804145	6.55	0.000	.3694008	.6846199
	16	.2257717	.0735858	3.07	0.002	.0815462	.3699972
	17	.5952817	.0961691	6.19	0.000	.4067938	.7837696
	18	.7651221	.1399946	5.47	0.000	.4907378	1.039506
	19	.6316019	.1115861	5.66	0.000	.4128972	.5803067
	20	-.1454788	.1675017	-0.87	0.385	-.4737762	.1828186
	21	.4390896	.1013933	4.33	0.000	.2403624	.6378168
	22	.8055653	.1827756	4.41	0.000	.4473317	1.163799
	23	.6225997	.0432332	14.40	0.000	.537866	.7073334
	24	.4333461	.0686031	6.32	0.000	.2988864	.5678057
	25	.5283591	.0798621	6.62	0.000	.3718321	.684886
	26	.482608	.0969039	4.98	0.000	.2926797	.6725362
	27	.5894716	.0470894	12.52	0.000	.497178	.6817651
	28	.4051973	.0730532	5.55	0.000	.2620156	.5483789
	29	.5262572	.0470189	11.19	0.000	.4341018	.6184125
	30	.4670825	.0444934	10.50	0.000	.3798771	.554288
	31	.464193	.0497094	9.34	0.000	.3667643	.5616216
	32	.2108956	.1077358	1.96	0.050	-.0002627	.4220538
	33	.1931331	.1164993	1.66	0.097	-.0352014	.4214676
	34	-.0059096	.269963	-0.02	0.983	-.5350274	.5232082
	35	.3609932	.1165093	3.10	0.002	.1326391	.5893473
	36	.0170487	.1874262	0.09	0.928	-.3503	.3843974
	37	.168937	.0842175	2.01	0.045	.0038738	.3340003
	38	.4454747	.0547952	8.13	0.000	.338078	.5528713
	39	.4070119	.0440516	9.24	0.000	.3206725	.4933514
	40	.6901032	.0896625	7.70	0.000	.5143679	.8658385
	41	.5353654	.0989309	5.41	0.000	.3414644	.7292664
	42	.3910658	.0430351	9.09	0.000	.3067186	.475413
	43	.3842676	.1073781	3.58	0.000	.1738104	.5947247
	44	.3769977	.0595536	6.33	0.000	.2602749	.4937205
	45	.5021343	.0583944	8.60	0.000	.3876834	.6165852
	46	.4560482	.049509	9.21	0.000	.3590122	.5530841
	47	.1898394	.0471173	4.03	0.000	.0974913	.2821875
	48	.3858483	.0685417	5.63	0.000	.251509	.5201877
	49	.1357135	.1524849	0.89	0.373	-.1631514	.4345784
	50	.197195	.0916388	2.15	0.031	.0175862	.3768037
	51	.272965	.1546447	1.77	0.078	-.030133	.576063
	52	-.7738671	.1884314	-4.11	0.000	-.143186	-.4045483
	53	.4938157	.0796057	6.20	0.000	.3377914	.64984
	54	-.5024009	.3015392	-1.67	0.096	-.1093407	.0886051
	55	.0630471	.1286935	0.49	0.624	-.1891876	.3152818
	56	.7020623	.2148519	3.27	0.001	.2809604	1.123164
	_cons	10.3206	.0478293	215.78	0.000	10.22685	10.41434

Interpreting this output, we note the following:

1. Stata computes robust “sandwich-type” standard errors for the parameter estimates, adjusting for the clustering of observations by sampling error computation unit (of which there are 112) and also accounting for the survey weights at each level. These standard errors therefore reflect the complex sampling features and the model being fitted (i.e., variances are estimated with respect to the model and the sample design; see Rabe-Hesketh and Skrondal (2006) for details).
2. Stata is attempting to maximize a pseudo-likelihood function, incorporating the sampling weights at each level in the estimation.
3. Interpreting the weighted estimates of the fixed effects, we see clear evidence of a substantial gender gap, with males tending to have a significantly higher mean. We also see strong evidence of an “upside-down U-shaped” curvilinear pattern in log-transformed annual income for both males and females, given the significant negative fixed effect of years since 2006 squared and the nonsignificant fixed effect of years since 2006; this is entirely consistent with [Figure 11.2](#). The interaction terms are both nonsignificant, suggesting similar trajectories for males and females.
4. Based on the weighted estimates of the variances of the random effects and the approximate confidence intervals for these variance components, we see substantial evidence of variance in the intercepts among respondents, and less evidence of variance among respondents in the trajectories. The unexplained variance in the intercepts might be explained by including fixed effects of other subject-level covariates (e.g., education).

We now fit the same model ignoring the complex sampling features, to assess the impact of this approach on the parameter estimates and the standard errors of the estimates:

```
* Model-based approach ignoring complex sampling features.
mixed ln_inc c.yrssince06##i.gender c.yrs06sq##i.gender ///
|| newid_num: yrssince06 yrs06sq, ///
variance cov(unstruct)
```

In the abbreviated excerpt of the output for this model below, we see that our inferences related to the general trajectories would in fact change somewhat, as the fixed effect of years since 2006 is now significant (suggesting a nonzero initial rate of growth starting in 2006). We also note that there is now marginal ($p < 0.10$) evidence of different curvilinear trends for males and females when ignoring the weights, when there was no evidence of such a difference at all when computing the unbiased (weighted) estimates. Finally, the estimate of the variance of the intercepts (0.786; not shown) is reduced by nearly

one-third when ignoring the weights. Under these circumstances, we would definitely report the weighted estimates, as the sampling weights do appear to be informative about these trajectories.

Performing EM optimization:						
Performing gradient-based optimization:						
Iteration 0: log likelihood = -65361.059						
Iteration 1: log likelihood = -65309.095						
Iteration 2: log likelihood = -65301.992						
Iteration 3: log likelihood = -65300.801						
Iteration 4: log likelihood = -65300.565						
Iteration 5: log likelihood = -65300.387						
Iteration 6: log likelihood = -65300.346						
Iteration 7: log likelihood = -65300.304						
Iteration 8: log likelihood = -65300.298						
Iteration 9: log likelihood = -65300.295						
Iteration 10: log likelihood = -65300.295						
Iteration 11: log likelihood = -65300.294						
Iteration 12: log likelihood = -65300.294						
Computing standard errors:						
Mixed-effects ML regression						
Number of obs = 40,325						
Group variable: newid_num						
Number of groups = 11,789						
Obs per group:						
min = 1						
avg = 3.4						
max = 4						
Wald chi2(5) = 955.51						
Prob > chi2 = 0.0000						
Log likelihood = -65300.294						
<hr/>						

ln_inc Coef. Std. Err. z P> z [95% Conf. Interval]						

yrssince06 .0244253 .0112526 2.17 0.030 .0023707 .0464799						
2.gender -.5854596 .0238333 -24.56 0.000 -.6321719 -.5387473						
gender#c.yrssince06						
2 -.0123405 .0149538 -0.83 0.409 -.0416494 .0169684						
yrs06sq -.0104752 .0018938 -5.53 0.000 -.0141869 -.0067635						
gender#c.yrs06sq						
2 .0042591 .0025152 1.69 0.090 -.0006707 .0091888						
_cons 10.62496 .0179009 593.54 0.000 10.58988 10.66005						
<hr/>						

11.3.3.1 Example: Veiga et al. (2014)

We now consider an illustration of fitting a multilevel model to these data using the alternative approach described by Veiga et al. (2014). Doing this requires downloading, modifying, and running a Mata program from the web site for this article, and then running this program in Stata.* Before we do this, we start by opening the original HRS data set in wide format (with one row per individual), creating four new measures of log-transformed

* http://onlinelibrary.wiley.com/journal/10.1111/%28ISSN%291467-9876/homepage/63_1.htm

income in preparation for the generation of a vertical data file, and creating an indicator variable identifying cases with complete data on income:

```
gen ln_inc1 = ln(H8ITOT + 1)
gen ln_inc2 = ln(H9ITOT + 1)
gen ln_inc3 = ln(H10ITOT + 1)
gen ln_inc4 = ln(H11ITOT + 1)

* Identify cases with complete data.
gen comp = (ln_inc1!=. & ln_inc2!=. & ln_inc3!=. & ///
ln_inc4!=.)
```

Next, we fit a response propensity model to these data, modeling the probability of having complete data across the four waves as a function of covariates in the baseline wave (2006) and accounting for the complex sampling features:

```
* Fit a response propensity model predicting the
* probability of providing income data at all 4 waves.

* Modal imputation of missing covariate values.
replace selfrhealth_06 = 3 if selfrhealth_06 == .
replace marcat_06 = 2 if marcat_06 == .
replace diabetes_06 = 0 if diabetes_06 == .
replace arthritis_06 = 1 if arthritis_06 == .
replace racecat = 2 if racecat == .
replace edcat = 2 if edcat == .

svyset secu [pweight = kwgtr], strata(stratum)
svy: logit comp ln_inc1 i.selfrhealth_06 age_06 ///
    i.marcat_06 diabetes_06 arthritis_06 i.racecat i.edcat
predict phat, p
```

As an alternative to the response propensity modeling approach, one could also consider the calibration approach described in Section 11.2.3.5, which is designed to make cases with complete data across the waves representative of the target population.

Next, we adjust the baseline survey weights in 2006 for cases with complete data by the inverse of the predicted probability of having complete data across the four waves (accounting for the cases that did not have complete data). We then create a new unique cluster ID variable that combines the HRS stratum and cluster codes, create a unique ID variable for each respondent, and reshape the wide data set of cases with complete data into a vertical format after keeping only the variables of interest. We note that the cluster-specific weights required by the Veiga et al. approach are set to 1 in this case, given that weights for each of the HRS clusters are not provided in the public-use data files:

```
* Adjust baseline sampling weights in 2006 by inverse of
* predicted probability of complete data.
gen indwgt = kwgtr * (1 / phat)
```

```

* Set cluster-specific weight equal to 1 (HRS SECU weights
* not provided in the public-use data).
egen newclust = group(stratum secu)
gen clustwgt = 1

* Create unique person ID.
egen newid = concat(hhid pn)
destring newid, gen(newid_num)

* Only keep cases with complete data.
keep if comp == 1

* Only keep variables of interest.
keep newid_num newclust gender ln_inc1-ln_inc4 indwgt ///
clustwgt

* Reshape data to vertical format.
reshape long ln_inc, i(newid_num) j(wave)

```

Now, in the vertical data set, we create unique indicator variables for each wave (required by the Veiga et al. approach), in addition to an indicator of being a male respondent and a constant variable equal to 1 for all cases:

```

* Create unique indicators for each wave.
gen wave1 = (wave == 1)
gen wave2 = (wave == 2)
gen wave3 = (wave == 3)
gen wave4 = (wave == 4)

* Compute constant variable for Veiga et al. macro.
gen cons = 1

* Recode gender.
gen male = (gender == 1)

```

We are now ready to modify the Mata program provided by Veiga et al. (2014) so that it recognizes the number of HRS waves (four) and the covariance structure for the repeated income measures that we wish to estimate in our model (Toeplitz). Following this approach, we will be estimating the variance of the random cluster intercepts, in addition to the constant variance and three covariance parameters defining the Toeplitz covariance structure for the four waves of data (constant variance among individuals over time, and common covariances for all measures one, two, and three waves apart). In total, there are therefore $s = 5$ variance–covariance parameters that we wish to estimate, and we need to modify two lines of the Veiga et al. Mata program that define s (near the beginning and near the end; see the program `pwigls_genlin_adcv_modAV1.do` on the book web site):

```
s = 5
```

The next modification that we need to make is the definition of the five “delta” matrices that will be combined to define the Toeplitz covariance structure, as described in the Veiga et al. (2014) paper. There are actually five symmetric 4×4 matrices (for the four waves) that need to be defined, but the first matrix is all zeroes:

```

delta_matrix=J(s,16,0)

delta_matrix[2,]=
(1,0,0,0,
 0,1,0,0,
 0,0,1,0,
 0,0,0,1)

delta_matrix[3,]=
(0,1,0,0,
 1,0,1,0,
 0,1,0,1,
 0,0,1,0)

delta_matrix[4,]=
(0,0,1,0,
 0,0,0,1,
 1,0,0,0,
 0,1,0,0)

delta_matrix[5,]=
(0,0,0,1,
 0,0,0,0,
 0,0,0,0,
 1,0,0,0)

rowshape(delta_matrix[1,],4)
rowshape(delta_matrix[2,],4)
rowshape(delta_matrix[3,],4)
rowshape(delta_matrix[4,],4)
rowshape(delta_matrix[5,],4)

name1 = tokens(varlist)

name3 = ("Sigma_u_2","Genlin(1)","Genlin(2)", ///
"Genlin(3)","Genlin(4)","Genlin(5)")

```

Following the notation of this program, “Sigma_u_2” is the variance of the random cluster intercepts, and the remaining “Genlin” parameters (1 through 4) are the variance and covariance parameters describing the Toeplitz structure (5 is not relevant here).

Finally, we need to modify each line of the Mata program defining the Toeplitz covariance structure, given the number of waves. We note that

we refer to the four nonzero “delta” matrices defined above in these expressions:

```
theta_genlin=theta[2,]*rowshape(delta_matrix[2,],4)+  
theta[3,]*rowshape(delta_matrix[3,],4)+  
theta[4,]*rowshape(delta_matrix[4,],4)+  
theta[5,]*rowshape(delta_matrix[5,],4)  
  
theta0_genlin=theta0[2,]*rowshape(delta_matrix[2,],4)+  
theta0[3,]*rowshape(delta_matrix[3,],4)+  
theta0[4,]*rowshape(delta_matrix[4,],4)+  
theta0[5,]*rowshape(delta_matrix[5,],4)
```

These modifications are needed in five places in the Mata program, and these are clearly commented in the file pwigls_genlin_adcv_modAV1.do on the book web site.

Once these modifications have been made and the updated Mata program has been saved, we can run the Mata program in Stata to define the function that will be used to fit the model, and sort the data set by cluster ID, individual ID, and wave:

```
/* Running the .do file with the mata function ***/  
do "pwigls_genlin_adcv_modAV1.do"  
  
sort newclust newid_num wave
```

Next, we declare two global macro variables, one (“wav”) containing the four wave indicators and a second (“x”) containing the covariates of interest in the model (the four wave indicators and the male indicator). Recall that we are fitting a model with no intercept, and estimating the means for each of the four waves:

```
gl wav wave1 wave2 wave3 wave4  
gl x wave1 wave2 wave3 wave4 male
```

Finally, we fit the model of interest using the function defined by the Mata program. For illustration purposes, we fit the model to a random subset of HRS financial reporters with numeric IDs less than 20,000,000. (Fitting the model to the entire data set simply takes longer for convergence.) In order, the arguments to the function are: the covariates, the dependent variable, the wave indicators, the constant term, the cluster ID, the cluster weights, and the individual weights (the program will automatically scale the individual weights so that they are normalized within clusters):

```
keep if newid_num < 20000000  
  
mata: pwigls_genlin_adcvw4toep1("$x","ln_inc", "$wav",  
"cons", "newclust" , "clustwgt", "indwgt")
```

The output generated by the model fitting function is shown below:

Probability Weighted Iterative Generalized Least Squares							
General Information							
Response Variable =	ln_inc						
Weight at Level 2 =	clustwgt						
Weight at Level 1 =	indwgt						
Start running on 10 Aug 2016 at	22:59:41						
Number of Iterations =	7						
Number of Time points =	4						
Number of Level 1 units =	666						
Number of Level 2 units =	67						
Fixed Effects							
	Coef.	Std.Err.	z	P> z	[95%Conf. Interval]	Init.Val.	
wave1	10.2636	.064375	159.43	0.000	10.1374	10.3898	10.2732
wave2	10.2596	.06362	161.26	0.000	10.1349	10.3843	10.2693
wave3	10.1561	.068067	149.21	0.000	10.0226	10.2895	10.1657
wave4	9.95694	.067421	147.68	0.000	9.82479	10.0891	9.96659
male	.427748	.08468	5.05	0.000	.261778	.593717	.425256
Variance Components							
	Coef.	Std.Err.	z	P> z	[95%Conf. Interval]	Init.Val.	
Sigma_u_2	.059156	.025703	2.30	0.021	.016878	.101435	.5
Genlin(1)	1.36033	.217148	6.26	0.000	1.00315	1.7175	1.30586
Genlin(2)	.70801	.174523	4.06	0.000	.420944	.995075	.5
Genlin(3)	.710341	.175359	4.05	0.000	.421902	.99878	.5
Genlin(4)	.629109	.17227	3.65	0.000	.34575	.912469	.5
General Linear Matrix							
[symmetric]							
	1	2	3	4			
1	1.360328393				+-----+		
2	.7080096706	1.360328393					
3	.7103411129	.7080096706	1.360328393				
4	.6291093613	.7103411129	.7080096706	1.360328393			
	+-----+						
Total Variance							
[symmetric]							
	1	2	3	4	+-----+		
1	1.419484785						
2	.7671660627	1.419484785					
3	.769497505	.7671660627	1.419484785				
4	.6882657534	.769497505	.7671660627	1.419484785			
	+-----+						
Note: Robust Standard Errors							

In the output above, we see the number of sampled financial reporters (666), the number of HRS sampling error computation units, or clusters (67), the cluster and individual weight variables, the dependent variable, and then weighted population estimates of the fixed effects and the covariance parameters. In addition, we see robust standard errors for the weighted estimates that are estimated with respect to both the model and the sample design (as described earlier). Examining the weighted estimates of the fixed effects and the corresponding 95% confidence intervals, we see evidence of similar mean income in the first three waves, followed by a more substantial decline

in the fourth wave (2012). The gender gap is once again apparent, with males tending to have significantly higher mean income.

We also note weak evidence of unexplained variance between HRS sampling error computation units (or clusters), denoted by Σ_u . However, recall that we assumed that each cluster had an equal probability of selection (which may be resulting in a biased estimate of this variance component). In other applications where cluster-specific survey weights are available, these weights should certainly be used in estimation. Finally, we note the weighted estimates of the between-individual variance at each wave (1.36) and the covariances of the individual effects at each wave (e.g., adjacent observations have an estimated covariance of 0.71). These covariances seem to be similar regardless of the time between a given pair of waves. Other covariance structures could certainly be considered, as discussed by Veiga et al. (2014); for example, the between-individual variance could be allowed to vary depending on the wave.

Finally, we examine the sensitivity of our estimates to the use of weights in estimation by simply setting both the cluster- and individual-specific weights to 1:

```
gen indwgtone = 1

mata: pwigls_genlin_adcvw4toep1("$x", "ln_inc", "$wav",
"cons", "newclust" , "clustwgt", "indwgtone" )
```

The resulting estimates and inferences (not shown) are quite similar, suggesting that the (adjusted) individual survey weights in 2006 are not very informative about the population means at each time point, the gender effect, or the covariance parameters. A failure to use the weights in estimation would not be introducing substantial bias in our parameter estimates in this example, but we would recommend examining weighted and unweighted estimates in general and reporting weighted estimates if differences in inference arise.

11.3.4 Example: Weighted GEE Analysis

We now consider an example of the weighted GEE approach discussed earlier, using case-specific weights accounting for the different patterns of wave nonresponse in the HRS. Preparation for a weighted GEE analysis of this type requires fitting several logistic regression models to wave-specific response indicators for an outcome variable of interest, each time conditioning on the response pattern in the prior waves. We therefore fit a series of design-based logistic regression models, predicting response to the income question in 2008, 2010, and 2012, each time using respondents with different patterns of responses in the prior waves as the subpopulations of interest (note that for purposes of this illustration, all 11,789 panel cases were considered respondents in the baseline wave of 2006). As covariates in these logistic

regression models, we consider the reported income value (log-transformed) in 2006, along with several nonmissing baseline covariates from 2006. We fit these models to the original HRS data set in the wide format:

```

* Modal imputation of missing covariate values.
replace selfrhealth_06 = 3 if selfrhealth_06 == .
replace marcat_06 = 2 if marcat_06 == .
replace diabetes_06 = 0 if diabetes_06 == .
replace arthritis_06 = 1 if arthritis_06 == .
replace racecat = 2 if racecat == .
replace edcat = 2 if edcat == .

gen ln_inc06 = ln(H8ITOT + 1)
gen ln_inc08 = ln(H9ITOT + 1)
gen ln_inc10 = ln(H10ITOT + 1)
gen ln_inc12 = ln(H11ITOT + 1)

* Compute response indicator for 2008.
gen resp08 = 1 if ln_inc08 != .
replace resp08 = 0 if ln_inc08 == .
tab resp08, miss

* Response propensity model (2008).
svyset secu [pweight = kwgtr], strata(stratum)
svy: logit resp08 ln_inc06 i.selfrhealth_06 age_06 ///
    i.marcat_06 diabetes_06 arthritis_06 i.racecat i.edcat
predict phat08, p

* Compute response indicator for 2010.
gen resp10 = 1 if ln_inc10 != .
replace resp10 = 0 if ln_inc10 == .
tab resp10, miss

* Response propensity model (2010), respondents in 2008.
svyset secu [pweight = kwgtr], strata(stratum)
svy, subpop(if resp08 == 1): logit resp10 ln_inc06 ///
    i.selfrhealth_06 age_06 ///
    i.marcat_06 diabetes_06 arthritis_06 i.racecat i.edcat
predict phat10_11, p

* Response propensity model (2010), nonrespondents in 2008.
svyset secu [pweight = kwgtr], strata(stratum)
svy, subpop(if resp08 == 0): logit resp10 ln_inc06 ///
    i.selfrhealth_06 age_06 ///
    i.marcat_06 diabetes_06 arthritis_06 i.racecat i.edcat
predict phat10_10, p

* Compute response indicator for 2012.
gen resp12 = 1 if ln_inc12 != .

```

```

replace resp12 = 0 if ln_inc12 == .
tab resp12, miss

* Response propensity model (2012), 111 pattern.
svyset secu [pweight = kwgtr], strata(stratum)
svy, subpop(if resp08 == 1 & resp10 == 1): logit resp12 ///
    ln_inc06 i.selfrhealth_06 age_06 ///
    i.marcat_06 diabetes_06 arthritis_06 i.racecat i.edcat
predict phat12_111, p

* Response propensity model (2012), 110 pattern.
svyset secu [pweight = kwgtr], strata(stratum)
svy, subpop(if resp08 == 1 & resp10 == 0): logit resp12 ///
    ln_inc06 i.selfrhealth_06 age_06 ///
    i.marcat_06 diabetes_06 arthritis_06 i.racecat i.edcat
predict phat12_110, p

* Response propensity model (2012), 101 pattern.
svyset secu [pweight = kwgtr], strata(stratum)
svy, subpop(if resp08 == 0 & resp10 == 1): logit resp12 ///
    ln_inc06 i.selfrhealth_06 age_06 ///
    i.marcat_06 diabetes_06 arthritis_06 i.racecat i.edcat
predict phat12_101, p

* Response propensity model (2012), 100 pattern.
svyset secu [pweight = kwgtr], strata(stratum)
svy, subpop(if resp08 == 0 & resp10 == 0): logit resp12 ///
    ln_inc06 i.selfrhealth_06 age_06 ///
    i.marcat_06 diabetes_06 arthritis_06 i.racecat i.edcat
predict phat12_100, p

```

Next, we compute the cumulative probabilities of responding at each wave for each individual case:

```

* Compute cumulative response probabilities

gen cumprob1 = 1

gen cumprob2 = phat08 if resp08 == 1
replace cumprob2 = 1-phat08 if resp08 == 0

gen cumprob3 = phat08 * phat10_11 ///
    if resp08 == 1 & resp10 == 1
replace cumprob3 = phat08 * (1-phat10_11) ///
    if resp08 == 1 & resp10 == 0
replace cumprob3 = (1-phat08) * phat10_10 ///
    if resp08 == 0 & resp10 == 1
replace cumprob3 = (1-phat08) * (1-phat10_10) ///
    if resp08 == 0 & resp10 == 0

```

```

gen cumprob4 = phat08 * phat10_11 * phat12_111 ///
    if resp08 == 1 & resp10 == 1 & resp12 == 1
replace cumprob4 = phat08 * phat10_11 * (1-phat12_111) ///
    if resp08 == 1 & resp10 == 1 & resp12 == 0
replace cumprob4 = phat08 * (1-phat10_11) * phat12_110 ///
    if resp08 == 1 & resp10 == 0 & resp12 == 1
replace cumprob4 = phat08 *(1-phat10_11)*(1-phat12_110) ///
    if resp08 == 1 & resp10 == 0 & resp12 == 0
replace cumprob4 = (1-phat08)*phat10_10 *phat12_101 ///
    if resp08 == 0 & resp10 == 1 & resp12 == 1
replace cumprob4 = (1-phat08)*phat10_10*(1-phat12_101) ///
    if resp08 == 0 & resp10 == 1 & resp12 == 0
replace cumprob4 = (1-phat08)*(1-phat10_10)*phat12_100 ///
    if resp08 == 0 & resp10 == 0 & resp12 == 1
replace cumprob4=(1-phat08)*(1-phat10_10)*(1-phat12_100)///
    if resp08 == 0 & resp10 == 0 & resp12 == 0

```

Next, we compute the overall cumulative probability of having a particular response pattern for each case (CUMPROB4), reshape the data set into the required vertical format, and multiply the base sampling weight for each panel respondent in 2006 by the inverse of the overall cumulative probability of having a particular response pattern:

```

* Compute overall probability of response pattern.
gen cumprob_case = cumprob4

* Reshape data set, keeping variables of interest.
gen ln_inc1 = ln(H8ITOT + 1)
gen ln_inc2 = ln(H9ITOT + 1)
gen ln_inc3 = ln(H10ITOT + 1)
gen ln_inc4 = ln(H11ITOT + 1)

* Baseline sampling weight for individual from 2006.
gen basewgt = kwgtr

keep hhid pn gender marcat_06 diabetes_06 arthritis_06 ///
    racecat edcat ln_inc1-ln_inc4 secu stratum basewgt ///
    cumprob_case

reshape long ln_inc wgt, i(hhid pn) j(year)

* Form a unique ID variable.

egen newid = concat(hhid pn)
destring newid, gen(newid_num)

* Compute the case-specific weights for weighted GEE.
gen casewt = basewgt * (1 / cumprob_case)

```

```
* Compute measure of years since 2006, and squared version.
gen yrssince06 = 0 if year == 1
replace yrssince06 = 2 if year == 2
replace yrssince06 = 4 if year == 3
replace yrssince06 = 6 if year == 4

gen yrs06sq = yrssince06*yrssince06
```

We then employ the weighted GEE approach to examine population estimates of the marginal change over time in log-transformed income for males and females. We treat individuals as clusters, include fixed stratum effects, set the correlation structure to be unstructured (given the unbalanced data set, where some cases do not have complete responses), and test the interactions between both years since 2006 and years since 2006 squared with gender:

```
* Fit weighted GEE model.
xtset newid_num year
xtgee ln_inc c.yrssince06##i.gender c.yrs06sq##i.gender ///
    i.stratum [pweight = casewt], corr(uns)
estat wcorrelation
```

Examining the output, we no longer see strong evidence of a nonlinear trend over time when using this marginal modeling approach (unlike the multi-level modeling approach in Section 11.3.3, where we were explicitly conditioning on random subject effects):

Iteration 1: tolerance = .24071225						
Iteration 2: tolerance = .00511372						
Iteration 3: tolerance = .00025702						
Iteration 4: tolerance = .00001743						
Iteration 5: tolerance = 1.379e-06						
Iteration 6: tolerance = 1.222e-07						
GEE population-averaged model						
Group and time vars: newid_num year						
Link: identity						
Family: Gaussian						
Correlation: unstructured						
Scale parameter: 2.28706						
Wald chi2(60) = 247.93						
Prob > chi2 = 0.0000						
(Std. Err. adjusted for clustering on newid_num)						

ln_inc		Robust				
		Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
yrssince06		-.0837022	.0480113	-1.74	0.081	-.1778026 .0103982
2.gender		-.6217098	.100058	-6.21	0.000	-.8178199 -.4255998
gender#c.yrssince06						
2		.0742509	.0827539	0.90	0.370	-.0879438 .2364456
yrs06sq		.0050879	.0081957	0.62	0.535	-.0109753 .0211512
gender#c.yrs06sq						

2	-.0076464	.013348	-0.57	0.567	-.0338081	.0185152
stratum						
2	.3158994	.5143065	0.61	0.539	-.6921227	1.323922
3	.7467036	.5242659	1.42	0.154	-.2808386	1.774246
4	-.444524	1.262352	-0.35	0.725	-2.918689	2.029641
5	.7898456	1.618421	0.49	0.626	-2.382201	3.961892
6	.8542305	.6791201	1.26	0.208	-.4768205	2.185282
7	1.507295	.5454734	2.76	0.006	.4381867	2.576403
8	.9551998	.5094052	1.88	0.061	-.0432159	1.953616
9	.6773107	.5429146	1.25	0.212	-.3867823	1.741404
10	1.467586	.492562	2.98	0.003	.5021822	2.43299
11	.3092727	.7823276	0.40	0.693	-1.224061	1.842607
12	1.187935	.5730078	2.07	0.038	.0648601	2.311009
13	1.005892	.5650043	1.78	0.075	-.1014961	2.11328
14	.97375	.4982294	1.95	0.051	-.0027617	1.950262
15	.8222744	.5416592	1.52	0.129	-.2393582	1.883907
16	.8456724	.4881629	1.73	0.083	-.1111093	1.802454
17	1.276917	.5145329	2.48	0.013	.2684507	2.285383
18	1.397814	.5267904	2.65	0.008	.3653236	2.430304
19	1.055951	.6977541	1.51	0.130	-.3116214	2.423524
20	1.124006	.7815293	1.44	0.150	-.4077634	2.655775
21	1.154815	.484176	2.39	0.017	.2058479	2.103783
22	1.13661	.5241062	2.17	0.030	.1093804	2.163839
23	.5672964	.5454186	1.04	0.298	-.5017043	1.636297
24	.9702661	.5499848	1.76	0.078	-.1076842	2.048216
25	.9441888	.486515	1.94	0.052	-.0093632	1.897741
26	1.251989	.559142	2.24	0.025	.156091	2.347887
27	1.247647	.4964189	2.51	0.012	.2746839	2.22061
28	1.012526	.4951085	2.05	0.041	.0421316	1.982921
29	1.282404	.5053575	2.54	0.011	.2919212	2.272886
30	.9693431	.5034691	1.93	0.054	-.0174383	1.956124
31	1.161934	.4981921	2.33	0.020	.1854952	2.138372
32	.9680243	.6344909	1.53	0.127	-.2755551	2.211604
33	.9476448	.5865529	1.62	0.106	-.2019777	2.097267
34	.423263	.4873485	0.87	0.385	-.5319225	1.378448
35	1.167646	.5390566	2.17	0.030	.1111144	2.224177
36	.7535923	.6609817	1.14	0.254	-.541908	2.049093
37	.7030033	.4860949	1.45	0.148	-.2497252	1.655732
38	1.383805	.5762668	2.40	0.016	.2543423	2.513267
39	.9507585	.4916987	1.93	0.053	-.0129532	1.91447
40	1.437053	.4904077	2.93	0.003	.4758718	2.398235
41	1.322208	.53213	2.48	0.013	.2792521	2.365164
42	.6620029	.503468	1.31	0.189	-.3247763	1.648782
43	1.071578	.517171	2.07	0.038	.0579411	2.085214
44	1.174418	.4946859	2.37	0.018	.2048518	2.143985
45	1.382111	.4885863	2.83	0.005	.4244997	2.339723
46	1.071244	.507519	2.11	0.035	.0765251	2.065963
47	.693522	.4855557	1.43	0.153	-.2581497	1.645194
48	.9355299	.4909906	1.91	0.057	-.0267939	1.897854
49	.4250969	.6258578	0.68	0.497	-.801562	1.651756
50	.8213465	.4904102	1.67	0.094	-.1398399	1.782533
51	.9867888	.5205207	1.90	0.058	-.033413	2.006991
52	.0818238	.5202392	0.16	0.875	-.9378264	1.101474
53	1.028963	.50682	2.03	0.042	.0356143	2.022312
54	.3523894	.5920819	0.60	0.552	-.8080697	1.512849
55	.3059683	.550127	0.56	0.578	-.7722608	1.384197
56	1.381775	.504372	2.74	0.006	.3932245	2.370326
<i>_cons</i>	9.808905	.4726353	20.75	0.000	8.882557	10.73525
<hr/>						
Estimated within-newid_num correlation matrix R:						
	c1	c2	c3	c4		
r1	1					
r2	.4357663	1				
r3	.5732002	.5657337	1			
r4	.3024913	.3282373	.463225	1		

We note marginal evidence of a negative linear trend over time, where income appears to be decreasing slightly, and this is consistent with our initial descriptive analyses. The overall gender gap in expected income remains strongly significant when employing the weighted GEE approach. Finally, we see evidence of varying correlations of the repeated measures over time when examining the weighted estimates of the correlations in the unstructured working correlation matrix.

11.4 Concluding Remarks

We have presented a variety of state-of-the-art approaches to the analysis of longitudinal survey data in this chapter. In general, we recommend that readers carefully define the objective(s) of their longitudinal analysis, and determine whether simple descriptive approaches would suffice, or more complicated modeling approaches might be needed. In particular, if trajectory estimation is of interest, readers need to decide whether they are interested in estimating between-cluster or between-subject variance in trajectories (which would require a weighted multilevel modeling approach). If estimation of marginal trajectories is the only objective, weighted GEE approaches would likely suffice.

Other weighting approaches for longitudinal surveys have been proposed in the literature. One is the *generalized weight share method* described by Lavallée (1995, 2007). This method mainly has applications in longitudinal household surveys where the composition of households is frequently changing over time, and measures are collected from individuals within the households. For example, adult children may move out of households, households may be combined (via marriage, possibly), and so on. This approach also has applications in longitudinal surveys where refreshment samples are added at later waves. Notably, this approach does not primarily address issues related to nonresponse adjustment and adjustment for attrition over time, but rather what happens when the sample composition is changing and the individuals introduced into the sample may not necessarily have a direct link with the target population of interest. For more details on these approaches, we refer readers to Lavallee (2007).

We anticipate continued software development in these areas in the near future, but this chapter demonstrates that many of these approaches are readily implemented in existing software packages.

EXERCISES

- 11.1 Briefly describe the main analytic objectives outlined in this chapter and provide a list of suggested analysis methods, given a particular

objective. Make sure to clarify what each objective addresses analytically and discuss key assumptions of each analysis method.

- 11.2 Open the 2006–2012 HRS longitudinal data set (available from the book web site) and obtain a list of variables contained in this data set. If needed, review the data set description provided in Section 11.3. Consider two options to perform descriptive analysis for a single time point: (1) complete case analysis with design variables/weights, and (2) weight adjustments similar to those of Section 11.3.1. Now, carry out these steps:
- a. Use a software package of your choice, and restrict the data set to those that were financial respondents in 2006 and also had a nonzero respondent level weight in 2006 (Stata code: `if kfinr == 1 & kwgtr != 0`).
 - b. Next, create a series of log-transformed variables from the H8ITOT to H11ITOT variables, representing total household income for each year: 2006, 2008, 2010, 2012. Use the same names as in the example: LN_INC06, LN_INC08, LN_INC10, LN_INC12. (Note, the actual names should be lowercase but we use upper case to highlight variable names in the text.) Make sure to follow the coding logic presented just before Section 11.3.1 when creating these variables, and check the distributions of the variables using a series of histograms. Do they appear to be relatively normal?
 - c. The analytic goal is to estimate mean household income in 2010. With that in mind, how many financial respondents provided income information in 2006, and how many financial respondents did the same in 2010? What percentage of the 2006 baseline respondents also gave information about household income in 2010?
 - d. Perform a complete case analysis using a design-based approach, and obtain the number of observations, back-transformed (exponentiated) weighted estimates, and 95% confidence limits for the mean 2010 income. Place those results in the first row of a table similar to [Table 11.2](#) and label this row “Complete Case Analysis.”
 - e. Next, perform a weight adjustment to account for the missing data on the 2010 income variable, using the logic of the Stata code presented in the example given in Section 11.3.1. Be sure to include the modal assignments of missing data on the model covariates. Fit a design-based logistic regression model using these same covariates, and then output the predicted values for use with the decile “smoothing” approach/weight adjustment. This process creates an adjusted weight called ADJ_KWGTR that accounts for possible bias due to wave nonresponse in 2010.

- f. Using the adjusted weight from part e, reset the survey variables to use this adjusted weight (rather than the original weight) and perform design-based estimation of mean income in 2010. Place these results in the 2nd row of the table created in part d, and label this row “Response Propensity Adjustment.” Title this table with a meaningful title similar to [Table 11.2](#), and make sure the rows and columns have understandable labels.
 - g. Finally, write a short paragraph describing your results. Be sure to describe the two methods used in this analysis and how the weight adjustment improves upon a complete case analysis.
 - h. (*Extra Credit*) Implement the multiple imputation method for estimated mean total household income in 2010 by following the code and logic from the example given in Section 11.3.1. Use statistical software of your choice that is capable of performing multiple imputation and analyzing imputed data sets with correct combining rules (see [Chapter 12](#) for details on imputation). Add these results to the table you created for parts a–g of this question. How do the MI results compare to the other methods used?
- 11.3 Open the HRS 2006–2012 longitudinal data set (available from the book web site) and obtain a list of variables contained in this data set. If needed, review the data set description provided in Section 11.3. This exercise examines change in total HH income between 2006 and 2012, using weight adjustments similar to those of Section 11.3.2. Use the logic of the Stata code from this section as a guide for answering this question. With that in mind, carry out these steps:
- a. As in Question 2, use a software package of your choice and restrict the data set to those that were financial respondents in 2006 and also had a nonzero respondent level weight in 2006 (Stata code: `if kfinr == 1 & kwgtr != 0`).
 - b. Create a series of log-transformed variables from the H8ITOT to H11ITOT variables representing total income for each year: 2006, 2008, 2010, 2012. Use the same names as in the example and Question 2: LN_INC06, LN_INC08, LN_INC10, LN_INC12. (Note, the actual names should be lowercase but we use uppercase to highlight variable names in the text.)
 - c. Generate a variable called INCDIFF_06_12, representing the difference in total household income from 2006 to 2012. Use the original variables for this step rather than the log-transformed versions (sample Stata code: `gen incdiff_06_12 = H11ITOT - H8ITOT`).

- d. Set or use the sample design variables: the original 2006 individual weight (KWGTR) and the stratum and cluster variables (STRATUM, SECU). Obtain the design-based estimate of the mean difference in total household income, 2006–2012. What is the mean difference in total household income for 2006–2012, and what is the estimated standard error?
 - e. Compute a response indicator for income in 2012 using the variable LN_INC12 and the logic presented in Section 11.3.2 (weight adjustment method). Also, use modal imputation of missing covariate values, again as presented in Section 11.3.2.
 - f. Fit a response propensity model for the log-transformed income variable for 2012 with the same predictors as in Section 11.3.2, and output the predicted probabilities from this model. Create deciles of response propensity, compute means per decile, and finally, create an adjusted weight called ADJ_KWGTR1, as demonstrated in the example (and similar to the weight adjustment from Question 2).
 - g. Perform a design-based analysis of the mean difference in total household income (2006–2012) using the adjusted weight, ADJ_KWGTR1, and compare the results with those without a weight adjustment. What is the mean and standard error from the analysis using the adjusted weight? How does the weight adjustment help “repair” the wave nonresponse?
- 11.4 This exercise asks you to replicate the analysis presented in Section 11.3.3, using the weighted multilevel modeling method. The analysis objective is to examine change in total household income over four waves of HRS data (2006, 2008, 2010, and 2012). The example works through data management steps, including variable construction, weight adjustments/rescaling, and reshaping the data from wide to long format. (Make sure to save the “long” file prior to graphing since collapsing of data is done in the graphing!) Following data management, you will generate some graphics and finally fit a set of weighted multilevel models. Use the logic of the Stata code from this section as a guide for replicating the example outputs in a software package of your choice (note: not all software packages will have procedures enabling you to fit weighted multilevel models!). Your task is to perform all steps of the process and provide the following results and code based on your own work (from the software that you select for this task). Make sure that your outputs match those below or from Section 11.3.3:
- a. Reproduce this output:

```
. sum level1wgt_r
Variable |       Obs        Mean      Std. Dev.          Min          Max

```

```

-----+
level1wgt_r |      40,325          1   .2649942          0          4
. list newid year level1wgt_r level2wgt ln_inc gender in 1/20

+-----+
|   newid    year   level1-r   level2-t     ln_inc   gender |
|-----|
1. | 000003010     1   .9055811     4093   10.59636     1 |
2. | 000003010     2   .9485039     4093   10.69197     1 |
3. | 000003010     3   1.063333    4093   11.01484     1 |
4. | 000003010     4   1.082582    4093   10.4913      1 |
5. | 010001010     1   1.181266    7434   9.229064     1 |
|-----|
6. | 010001010     2   1.320145    7434   9.236106     1 |
7. | 010001010     3   .7501688    7434   9.575053     1 |
8. | 010001010     4   .7484209    7434   9.392745     1 |
9. | 010004010     1   .9737449    5217   11.34865     1 |
10. | 010004010    2   .9731849    5217   10.98191     1 |
|-----|

```

- b. Reproduce Figure 11.1: Change the title for the Y Axis to “<Your Last Name>” plus the original title.
- c. Reproduce Figure 11.2: Change the title for the Y Axis to “<Your Name>” plus the original title.
- d. Reproduce the full output from the weighted multilevel model accounting for the design features, with your name inserted into the code using a comment. For example (Stata code):

```

. mixed ln_inc c.yrssince06##i.gender c.yrs06sq##i.gender i.stratum ///
>   [pweight = level1wgt_r] ///
>   /* Output produced by <YOUR NAME> on <DATE> */ ///
>   || newid_num: yrssince06 yrs06sq, variance cov(unstruct) ///
>   pweight(level2wgt) pwscale(size) vce(cluster unique_secu)

```

- e. Reproduce the full output from the weighted multilevel model without accounting for the cluster sampling with your name inserted into the code using a comment. For example (Stata code):

```

. mixed ln_inc c.yrssince06##i.gender c.yrs06sq##i.gender ///
>   [pweight = level1wgt_r] ///
>   /* Output produced by <YOUR NAME> on <DATE> */ ///
>   || newid_num: yrssince06 yrs06sq, variance cov(unstruct) ///
>   pweight(level2wgt) pwscale(size)

```

- f. Write a brief paragraph describing how the weighting methods used and inclusion of complex sample design features in the design-based model improve the quality of the analysis. How do the results from the two models differ and would your overall conclusions change? What other analysis methods might be used given the analysis objective of this exercise?

12

Imputation of Missing Data: Practical Methods and Applications for Survey Analysts

12.1 Introduction

In the 7 years that have elapsed since the publication of the first edition of this book, there have been many published advances in missing data theory, methods, and tools for use with complex sample survey data, including the method of fractional imputation (FI; Kim and Fuller, 2004; Kim and Shao, 2014), the Finite Population Bayesian Bootstrap (IVEware®, 2016; Zhou et al., 2016a,b), multiple imputation (MI; Van Buuren, 2012; Carpenter and Kenward, 2013; Berglund and Heeringa, 2014; Stata Corp, 2015; Raghunathan, 2016), and maximum likelihood methods (Chambers et al., 2012). The sheer volume of recently published articles, new texts, and how-to guides on the subject testify to the pace of new developments and the importance that missing data play in everyday statistical estimation and inference. The overall aim of this chapter is to bring the problem of item missing data forward and focus on it, examine its nature, assess its potential impact on estimation and inference, and offer practical solutions for dealing with “item missingness” in the course of survey data analysis.

Missing data are ubiquitous problems in the analysis of survey data. *Statistical imputation procedures* are techniques for assigning analyzable values to item missing data on survey variables. Although major Federal statistical programs such as the Current Population Survey (CPS) were employing imputation of item missing data as early as the late 1940s (Ono and Miller, 1969), it was rare to see applications of imputation to item missing data prior to the early 1970s. Further, when imputation methods were applied, the techniques were often combined with postsurvey editing, were very ad hoc in nature, and paid little attention to the theoretical implications of the methods for analysis and inference.

The U.S. National Academy of Sciences Panel on Incomplete Data (Madow and Olkin, 1983) brought together leading survey statisticians to consider

item missing data as a true statistical problem and to lay the foundation for a more theoretically justified treatment of missing data in survey analysis. Since that time, the statistical science of imputation and other methods of analysis that address the missing data problem have flourished. A taste of the variety of methods that have been proposed can be found in the colorful names of the techniques: mean imputation, predictive mean matching (PMM), nearest neighbor, regression imputation, the hot deck, row and column method, MI, and FI. Kalton and Kasprzyk (1986), Little and Rubin (2002), and Durant (2005) review the wide range of techniques, the methods and applications, and the relative strengths and weaknesses of these techniques.

Throughout the preceding discussion of statistical methods and examples in Chapters 5 through 11 of this book, the problem of *item missing data* for otherwise complete cases was allowed to remain in the background. As a case in point, recall the example analysis in Section 9.4 in which a negative binomial regression model was fit to the Health and Retirement Study (HRS) data for number of falls in the past 2 years. In addition to the dependent variable (count of falls), the model included six predictor variables. Table 12.1 summarizes the item missing data rates for the count of falls and the six predictors in that model. The interviewed respondents in the 2012 HRS panel included $n = 10,283$ adults aged 65+ who were eligible to be asked this question. After listwise deletion, Stata used only $n = 10,026$ complete data observations to estimate the regression model parameters and the standard errors of the parameter estimates—a 2.6% reduction in the nominal sample size. The example analysis incorporated the 2012 HRS weighting adjustments for baseline sample unit nonresponse and panel attrition, but did not attempt to compensate for the otherwise complete cases that were lost in the analysis due to the presence of item missing data on one or more of the analysis variables.

This chapter begins with an overview of important missing data concepts in Section 12.2. Section 12.3 then provides an overview of imputation approaches to analysis with missing data, outlining the general framework of method choice, model specification (where applicable), and practical methods for imputation, estimation, and inference for complex sample survey data. This is followed in Section 12.4 by an introduction to the MI method, including selection of the imputation model, multivariate MI methods and software, and estimation and inference with multiply imputed data. An introduction to Fractional Imputation (FI) theory, methods, and software

TABLE 12.1

Item Missing Data Rates for Variables Included in the 2012 HRS Falls Model ($n = 10,283$ Eligible Respondents Aged 65 and Older, $n_{com} = 10,026$ with Complete Data for All Six Variables)

Variable	Falls	Age	Gender	Arthritis	Diabetes	BMI
%Missing	1.3	<0.01	0.0	0.2	0.1	1.1

then follows in Section 12.5. The chapter concludes in Section 12.6 with applications of the MI and FI methods to a missing data problem encountered in an analysis of the 2011–2012 National Health and Nutrition Examination Survey (NHANES) data on diastolic blood pressure (DBP) and hypertension.

12.2 Important Missing Data Concepts

12.2.1 Sources and Types of Missing Data

Respondents' participation in surveys is almost always a voluntary decision. Even in "mandatory" government survey programs such as the American Community Survey (ACS), some sampled units may not provide an interview. *Unit nonresponse* is the term commonly used by survey methodologists to refer to situations in which sampled units either refuse or are unable to participate in the survey interview (Groves et al., 2009). *Wave nonresponse* occurs when a panel member is not reinterviewed in 1 or more follow-up waves of a longitudinal survey program.

Increasingly, population-based studies such as NHANES or HRS have added supplemental components to collect biomarker data (saliva, blood, and body measurements), work histories, medical records information, and other information that requires special respondent consent and different data collection procedures. Failure to obtain respondent consent or cooperation in a phase of the study (*Phase nonresponse*) results in missing data for variables from that entire phase of the study. For example, approximately 4.3% of adults who participated in the initial 2011–2012 NHANES interview did not agree to participate in a subsequent medical (mobile examination center [MEC]) examination. HRS requests special consent of respondents to link U.S. Social Security earnings records and Medicare records (for panel members aged 65+) to their survey data. At any given wave, approximately 20% of respondents do not provide consent to this special record linkage.

Unit nonresponse or nonresponse to a longitudinal wave (or phase) of a survey data collection can be a major source of missing information in sample surveys, but they are not the only source. To ensure high levels of overall survey cooperation and to guarantee that basic human subject protections are met, respondents are often read or provided a statement to the following effect at the start of the interview: "Your participation is voluntary. If we come to a question that you do not wish to answer, you may skip it." Categories of "Don't Know" or "Refused" are often explicitly included in the response options for individual survey items. Missing data for individual variables can also occur due to mistakes in interview administration, although, in today's world, computer-assisted interviewing (CAI) and web-based survey administration minimize many of the missing data problems

associated with incorrect skips or missed item follow-ups. In the survey literature and throughout this text, the term *item missing data* is used to refer to missingness on one or more variables in a survey record that is otherwise complete.

12.2.2 Patterns of Item Missing Data in Surveys

If we consider a rectangular file of survey data with rows representing sample cases and columns representing the survey variables of interest, unit nonresponse produces a pattern of missing data that is illustrated in [Figure 12.1](#).

Section 2.7.3 introduced the concept of unit nonresponse weighting adjustments to compensate for potential bias due to completely missing data for significant fractions (e.g., 10%, 20%, 30%, or more) of the probability sample that was selected to represent the survey population.

Complete nonresponse to an entire wave of a longitudinal survey or phase of a multiphase survey produces a *monotonic pattern* of item missing data ([Figure 12.2](#))—core data are present for interviewed cases but data for

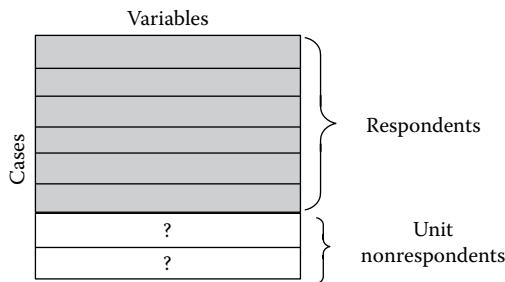


FIGURE 12.1
Unit nonresponse missing data pattern.

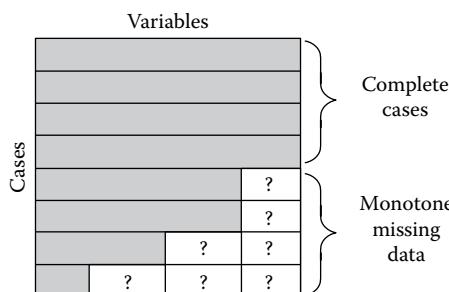


FIGURE 12.2
Monotonic pattern of missing data.

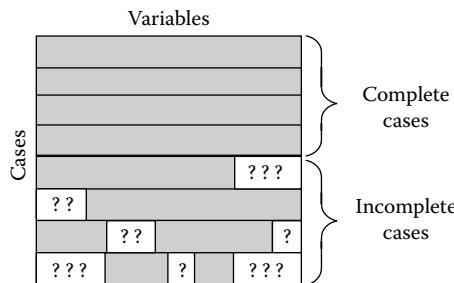


FIGURE 12.3
Generalized pattern of missing data.

subsequent waves/phases may be missing. Although imputation methods may be used to address monotonic patterns of item missing data including complete phase nonresponse (Schafer et al., 1996), it is common in survey practice to see nonresponse weighting adjustments applied to repair this problem.

As noted in the example of the HRS falls analysis (above), many variables measured in surveys are subject to low rates of item missing data, and more sensitive or difficult items (e.g., income measures) may have higher missing data rates ranging from 5% to 15%. The arbitrary nature of these response outcomes typically produces a *generalized pattern* of item missing data, in which there is no particular hierarchical or monotonic trend in the missing data structure (Figure 12.3).

Survey designers may also deliberately decide to use randomized procedures to permit item missing data on selected variables for subsets of respondents. The technique of *matrix sampling* or “missing by design” sampling can be employed with modularized sets of survey questions (Raghunathan and Grizzle, 1995; Thomas et al., 2006; Chipperfield and Steel, 2011). In these designs, a battery of core questions is asked of all respondents and more in-depth modularized questionnaire components are randomly assigned to subsamples of survey participants. Matrix sampling designs tend to produce a nonmonotonic missing data structure such as that illustrated in Figure 12.4, and the technique of MI (to be discussed later in this chapter) has typically been used to analyze these data.

12.2.3 Item Missing Data Mechanisms

In describing the MI method and other imputation techniques, notation introduced by Little and Rubin (2002) will be employed. Let Y denote a complete data matrix (i.e., the matrix of true values of some variable y , where there are no missing data). This is illustrated below for a simple data set of $i = 1, \dots, 4$ cases and $j = 1, \dots, 4$ variables. Note in the illustration below that

		Variables	
		???	???
		???	???
Cases		???	???
		???	???
		???	
		???	

Missing by design

FIGURE 12.4

Matrix sampling (missing by design).

the values ($y_{12}, y_{23}, y_{31}, y_{44}$) are in bold font, to signify that these true underlying values will *not* be observed in the survey.

$$\mathbf{Y} = \begin{bmatrix} y_{11} & \mathbf{y}_{12} & y_{13} & y_{14} \\ y_{21} & y_{22} & \mathbf{y}_{23} & y_{24} \\ \mathbf{y}_{31} & y_{32} & y_{33} & y_{34} \\ y_{41} & y_{42} & y_{43} & \mathbf{y}_{44} \end{bmatrix}.$$

This underlying set of true values of the variables of interest is decomposed into two subsets of values, $\mathbf{y} = \{\mathbf{y}_{obs}, \mathbf{y}_{mis}\}$, where \mathbf{y}_{obs} are the values that are observed and \mathbf{y}_{mis} are the values that are not observed and replaced by item missing values (e.g., a “.” code in Stata or SAS). Readers should note that the “data” matrix \mathbf{Y} can include design variables such as stratum and cluster codes and weights, which generally do not have any missing data.

Let \mathbf{M} denote a missing data indicator matrix of the same dimensions as \mathbf{Y} , where the value in row i and column j is equal to 1 if the corresponding value in \mathbf{Y} is recorded as missing in an actual survey, and 0 if the value is observed. Returning to the simple example of four cases and four variables, the matrix of missing data indicators would look like this:

$$\mathbf{M} = \begin{bmatrix} 0 & \mathbf{1} & 0 & 0 \\ 0 & 0 & \mathbf{1} & 0 \\ \mathbf{1} & 0 & 0 & 0 \\ 0 & 0 & 0 & \mathbf{1} \end{bmatrix}.$$

A *missing data pattern* describes the distribution of the values in \mathbf{M} . A *missing data mechanism* defines the conditional distribution of the values in \mathbf{M} given the values in \mathbf{Y} , $P(\mathbf{M}|\mathbf{Y})$. The missing data mechanism can be thought of as a probability model for the missing data indicator. In other words, why are the missing data arising? Are reasons for missing data related to the study variables in any way? Survey analysts need to have a basic understanding of

missing data mechanisms in order to evaluate the models and methods that are applied in compensating for missing data.

The missing data mechanism is defined to be *missing completely at random (MCAR)* if the probability that a respondent does not report an item value is completely independent of the true underlying values of all of the observed and unobserved variables; that is, $P(M|Y) = P(M)$ for all Y . Complete case analysis (listwise deletion) requires the assumption that the missing data are MCAR.

The mechanism is termed *missing at random (MAR)* if missingness depends only on the observed values of the variables in the survey, that is, $P(M|Y) = P(M|Y_{obs})$. In other words, the probability of a value being recorded as missing depends on *observed values of other variables*, but not on the missing values themselves. Using an example, the probability of having a missing value on height might depend on the observed value of the individual's fully observed age, but *not* on the unobserved value of height. Finally, the mechanism is *not missing at random (NMAR)* if missingness depends on the unobserved values of the variables with missing data (in addition to the observed values) in the survey data set; that is, $P(M|Y) = P(M|Y_{obs}, Y_{mis})$. Again, using the example, the probability of having a missing value on height does depend on the actual height, and possibly also depends on the age of the respondent.

From the standpoint of being able to effectively and practically address item missing data in a survey data set, most imputation methods and software assume that the missing data mechanism is in fact MAR. Certainly, the MAR assumption may not strictly apply for all missing items. It is reasonable to expect that the probability of item missing data on survey variables such as personal income may depend, at least in part, on the underlying value even when other factors are accounted for. In applying imputation methods that assume MAR, the resulting imputations may not completely compensate for an NMAR missing data mechanism. Unfortunately, missing data problems where the mechanism is strongly NMAR may not be easily addressed in a simple and straightforward manner. Techniques for analyzing data subject to nonignorable missingness such as *selection models* (Heckman, 1979) or *pattern mixture models* have been proposed (Little and Rubin, 2002; West and Little, 2013), but they typically require either independent assessment of the missing data model or interpretation based on a sensitivity analysis (Scharfstein et al., 1999) conducted over a set of reasonable models postulated for the complete data and the NMAR mechanism.

12.2.4 Review of Strategies to Address Item Missing Data in Surveys

Before turning specifically to the subject of best practices for imputation of item missing data from complex sample surveys, it is useful to review the full range of options that are available to survey analysts.

Option 1: Complete case analysis—The simplest approach to handling item missing data is to do nothing and analyze only the available set of complete cases. Software that defaults to listwise deletion will automatically strike

any case with item missing data on one or more variables from the analysis. Implicit in this approach is the assumption that the missing data are MCAR. Practically, if the individual and aggregate rates of item missing data for variables included in the analysis are very low (say <2% of cases have missing values), analysis based on complete cases only should be acceptable. However, even when item missing data rates are low, the listwise deletion of cases with item missing data may result in small losses of sample precision, irregular counts of case inputs over different analyses, and potentially small biases if the missing data mechanism is MAR or NMAR.

Option 2: Use full information maximum likelihood (FIML) methods—This alternative approach generally involves the use of all available information in a given survey data set (including values from cases with incomplete data), and applies maximum likelihood estimation techniques given all of the observed information to compute parameter estimates of interest. The FIML technique assumes that the missing data are MAR. Applications of the FIML technique for complex sample survey data are not common, primarily due to the challenge of incorporating informative sample design features (stratification, cluster sampling, weighting) into the maximum likelihood analysis and the corresponding inferential techniques. Chambers et al. (2012) and Allison (2012) are excellent references for statistically sophisticated analysts who wish to explore the application of maximum likelihood methods to complex sample survey data with missing values.

Option 3: Use the expectation–maximization (EM) algorithm—This approach to handling missing data, which is described in extensive detail in Little and Rubin (2002), is an iterative procedure defined by a two-step algorithm. The algorithm is initiated by a model of interest that the analyst wishes to fit to a data set that might include missing values on the variables of interest. First, in the expectation (E) step, the *EM algorithm* computes the expected value of the complete data log-likelihood function (given the model) based on the cases with *complete* data and the algorithm's estimates of the sufficient statistics for the missing data (given the model and the available data points for the incomplete cases). Then, in the maximization (M) step, the algorithm substitutes the expected values for the missing data obtained from the E step into the complete data likelihood and maximizes the likelihood function *as if no data were missing* to obtain new parameter estimates. The new parameter estimates are substituted back into the E step and the EM cycle repeats. The procedure iterates through these two steps until prespecified convergence criteria for the parameter estimates are satisfied (i.e., there is little change in the estimates at subsequent steps). This approach is currently employed by the Missing Values Analysis (MVA) module in the SPSS software, but is limited in that standard errors and associated test statistics (e.g., *t*-tests) do not reflect the complex sample design or the uncertainty in estimating the missing values. Because of this limitation, imputation methods described below are generally considered more appropriate for survey data.

Option 4: Analyze complete cases, but introduce additional weighting adjustments to compensate for item missing data on a key variable—The use of weighting to compensate for missing data is generally limited to monotonic patterns of missing data, in which large numbers of variables are associated with each “step” in the pattern. As described in Section 12.2.1, unit nonresponse, phase nonresponse, and longitudinal attrition in panel surveys produce missing data patterns where a weighting adjustment is the practical choice.

There is no theoretical barrier to employing a reweighting approach to compensate for item missing data on key survey variables. Practically, though, attempting to adjust the base weight variables to address item missing data on single variables leads to difficulties. If the pattern of missing data is generalized (Figure 12.3), different weighting adjustment factors would be needed for each target variable with missing data. Analytically, the weight-by-variable approach would work for univariate analyses, but which of the variable-specific weights would be chosen for a multivariate analysis? Simply put, imputation is the better strategy for addressing multivariate, generalized patterns of item missing data.

Option 5: Perform a single imputation of missing values, creating a “complete” data set—Public-use survey data sets are often released with a single imputed value replacing missing data on key survey variables. Ideally, the data producers who performed the imputation also include a companion imputation flag variable that distinguishes actual from imputed values in the data set (Section 4.4). When missing values are “flagged” in a survey data set, data users may also choose to perform their own single imputations using an established stochastic imputation method such as the *hot deck* (Theory Box 12.1), *regression imputation*, or *PMM* (Little and Rubin, 2002). SAS and other software systems include programs that allow data users to perform imputations using these techniques. Use of deterministic procedures such as single mean, median, or modal value imputation is not encouraged unless the imputation is simply serving to fill in a small handful of missing values of an otherwise nearly complete survey variable.

The advantage to a singly imputed data set is that it is “complete,” with missing values replaced by analyzable data entries. Provided that the imputation technique is multivariate and retains the stochastic properties in the observed data, a single imputation may address potential bias for a MAR missing data mechanism. The principal shortcoming in the standard design-based analysis of a singly imputed data set is that it precludes estimation and inference that fully reflects the variance attributable to the item missing data imputations. Here again, if rates of item missing data for individual variables and in the aggregate are low, the resulting slight underestimation of variance may not be a true problem. For imputations performed using the hot deck method, Rao and Shao (1992) proposed a Jackknife technique for estimating variances from singly imputed data sets that include missing data flags,

THEORY BOX 12.1 EXPLICIT VERSUS IMPLICIT MODELS FOR IMPUTATION OF ITEM MISSING DATA

Imputations of missing values for survey variables may be based on explicit distributional models or they may be based on techniques that “imply” an underlying model or set of assumptions concerning the missing data. In the example described in Section 12.4, the joint distribution for the three continuous variables (DBP, age, and BMI) is assumed to be multivariate normal: $f(y|\theta) = \text{MVN}(\mu, \Sigma)$. This is an example of an *explicit imputation model*. A modification of this explicit model might be to assume that DBP, age, and BMI follow multivariate normal distributions that are conditioned on gender. This modified model is an example of the *general location* model (Schafer, 1999).

An example of an imputation procedure that incorporates an *implicit imputation model* is *hot deck imputation*, in which cases are grouped into cells based on common values for observed categorical variables (e.g., age category \times gender), and within these cells missing values of another variable (e.g., DBP) are imputed by randomly drawing a replacement value from an observed “donor” in the same hot deck cell (Kalton and Kasprzyk, 1986). Although this simple hot deck method does not impute based on an explicit regression model for y , the model that is implied by the method might be the general location model or an analysis of variance (ANOVA) model.

but the method has not been widely incorporated into survey data analysis programs in the major software systems.

Option 6: Perform MI or FI for estimation and inference—A final alternative to address the problems of generalized patterns of missing data in survey analysis is to conduct the analysis in the model-based *MI* framework or alternatively using the design-based method of *FI*. The MI and FI methods will be explored in detail in Sections 12.4 through 12.6. Like single imputation approaches, MI and FI produce completed data sets for analysis. Although theoretically distinct in their approach, both MI and FI use repetition of the imputation process or multiple possible outcomes for y_{mis} to enable estimation and inference that reflects the uncertainty due to imputation of missing values.

12.3 Factors to Consider in Choosing an Imputation Method

There is no single imputation method or statistical modeling technique that is optimal for all forms of item missing data problems. Survey analysts

have a range of options to consider depending on the missing data pattern, the missing data mechanism, and rates of item missing values. Imputation techniques ranging from the simplest univariate mean substitution to a full application of MI or FI analysis share some basic attributes—for example, all imputation techniques produce a *completed* data set that can then be analyzed using standard software procedures for the analysis of complex sample survey data. However, in cases where the missing data problem is nontrivial, the goals of the imputation process should be more ambitious. The following is a list of those goals.

Goal 1: Stochastic—The imputation procedure should be stochastic—based on *random draws* of donor values from observed cases (as in the *hot deck* or *predictive mean matching*), or of model parameters and error terms from the predictive distribution of y_{mis} . For example, in linear regression imputation of the missing values of a continuous variable y_k , the function used to impute missing values based on the conditional predictive distribution for y_k may be written as $\hat{y}_{k,mis} = \hat{B}_0 + \hat{B}_{j\neq k} \cdot y_{j\neq k} + e_i$. In forming the imputed values of $y_{k,mis}$, the individual predictions should incorporate random draws of the coefficients and independent draws of the errors (e_i) from their respective estimated distributions. In a hot deck imputation procedure or procedures such as predictive mean or propensity score matching imputation, the donor value for $y_{k,mis}$ is drawn at random from observed values in the same hot deck cell or in a matched “neighborhood” of the missing data case.

Goal 2: Multivariate—To preserve associations among the many variables that may be included in the analysis model, the imputation procedure should be multivariate in nature. The MI algorithms included in today’s major statistical software packages preserve the multivariate properties of the data, through a sequence of conditional imputations (given monotonic missing data patterns) or through the use of iterative methods that are designed to simulate draws of missing values from the joint posterior distribution of the multivariate set of survey items. Donor-based methods such as the FI hot deck can also be adapted to jointly impute missing data for multiple variables conditional on the observed data for the case.

Goal 3: Model based—The procedure for imputing missing values should be explicitly or implicitly based on a model for the data to ensure the statistical transparency and integrity of the imputation process. A process of arbitrary assignment of imputations, even if based on expert judgement, is not replicable in the scientific sense and will not preserve the statistical properties (means, variances, covariances) of the survey data. The model that underlies the imputation process is often an explicit distributional model, but good results may also be obtained using techniques where the imputation model is implicit (Theory Box 12.1).

Goal 4: “Congenial” to intended analyses—In the words of Meng (1994), we should avoid the mistake of choosing an imputation model such that “... a procedure for analyzing the imputed data sets cannot be derived from the model adopted for the imputation.” This concept of *congeniality* between the

model used for imputation and the analysis model/methods has been the main theme in critiques of MI as a general solution to item missingness in survey data (Fay, 1996; Kim et al., 2006). This concern is especially relevant in MI applications for public-use data sets where the imputer and analyst are generally not the same individual. In imputing generalized patterns of missing data in a large survey data set, the imputer may have the advantage of being able to access data that may not be available to the analyst (e.g., detail on the structure of the sample design, or data from the sample frame or an external administrative source). Including added information in the imputations that is not available to analysts may result in *super-efficiency* (Rubin, 1996) in the analysis of imputed data.

However, the general purpose imputer is also disadvantaged in that they cannot know in advance all of the analytic applications (Which variables? Which subpopulations? What are the true functional forms of the models?) for which the completed data sets will be used. To address the bias that can result if imputations are “uncongenial” to the ultimate analyses, this chapter will recommend two practical solutions. First, compared to the analysts’ model, the imputation model should: (1) be broader in terms of variables; (2) include controls for major subpopulations or potential domains of analysis; and (3) to the extent possible, reflect the true nonlinearities and interactions among the variables included in the imputation model (see [Figure 12.6](#) later in this chapter). Second, and maybe most effective in preventing imputations that are not congenial with the analyst’s model, if the survey data include appropriate codes for missing values, recent software developments permit the analyst to perform MIs directly as part of the analysis session, thereby reducing the prospect of serious uncongeniality between the imputation model and the analytic method/model.

A special issue of congeniality of the imputation model and analysis methods/models for survey data is how informative features of the complex sample design, including stratification, cluster sampling and weighting, are factored into the imputation of missing values (Reiter et al., 2006). Guidance on this issue will be provided under the general overview of MI provided in [Section 12.4](#). The Finite Population Bayesian Bootstrap (FPBB) method (Zhou et al., 2016a,b) is also specifically designed to solve the problem of multiply imputing missing values in data collected under an informative complex sample design.

Goal 5: Enable analysis (estimation and inference) that incorporates the imputation uncertainty—As noted above, the primary disadvantage of a single imputation approach to analysis with item missing data is that it does not provide an accessible means to incorporate the imputation uncertainty into the standard errors and confidence intervals (CIs) that are critical to making correct inferences about population statistics. MI and FI are two theoretically distinct approaches to the imputation of missing survey data that share the common feature that multiple imputed values are assigned to each missing data point. In replicating the imputation over multiple possible values of y_{mis} ,

both MI and FI enable estimation of the added variance that is due to the imputation process.

Goal 6: Robust—No imputation model or procedure will ever exactly match the true distributional assumptions for the underlying random variables or the assumed missing data mechanism. Imputation procedures applied to survey data sets by data producers or data users should be reasonably robust against modest departures from the underlying assumptions. Fortunately, empirical research has demonstrated that if the more demanding theoretical assumptions underlying MI are relaxed, applications to survey data can produce estimates and inferences that remain valid and robust (Herzog and Rubin, 1983). Likewise, Kim (2011) provides similar evidence of the robustness of the FI method, even under conditions in which the analysis model includes parameters that were omitted from the imputation model.

Goal 7: Usable—For applied survey data analysis, usability and software support are always criteria that should be used in selecting a statistical procedure. In the most mathematically rigorous representations, the theory of MI or the FI method can be highly complex (Rubin, 1987; Schafer, 1997; Kim, 2011). For highly specific problems with complex missing data patterns or mechanisms, survey analysts who lack the mathematical sophistication are encouraged to consult with a survey statistician prior to conducting and publishing their analysis. However, for general missing data problems of the type illustrated in Section 12.7, today's software provides a usable platform for conducting an MI or FI analysis that when appropriately applied should generate robust inferences for the target population.

12.4 Multiple Imputation

12.4.1 Overview of MI and MI Phases

The ideas that underlie MI methods for missing data were formulated by Donald Rubin in the early 1970s (Rubin, 1976). Since that time, MI theory and methods have been advanced by Rubin and his students (Rubin, 1999; Yucel, 2011). MI is not simply a technique for imputing missing data. It is also a method for obtaining estimates and inferences for statistics ranging from simple descriptive statistics to the population parameters of complex multivariate models.

As illustrated in [Figure 12.5](#), three distinct phases comprise a complete *MI analysis* of a survey data set. The first phase is the definition of the data and the distributional components of the *imputation model*. The second phase applies specific methods and algorithms to generate the MIs of the missing values. The third and final phase is the calculation of MI estimates and

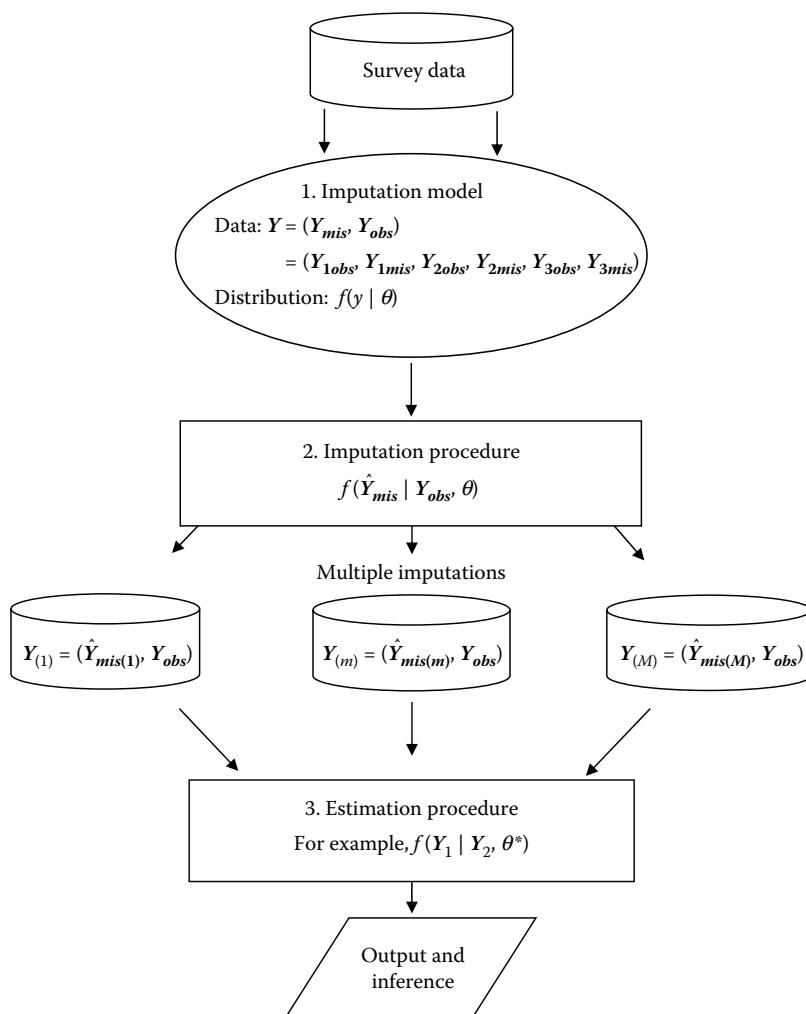


FIGURE 12.5
Stages of multiple imputation.

standard errors, and the construction of CIs and hypothesis test statistics for making inferences regarding population parameters and relationships.

12.4.2 Models for Multiply Imputing Missing Data

The actual process of imputing item missing values is governed by the *imputation model*, which is defined by the set of values that are available to the imputation process, $\mathbf{y} = \{\mathbf{y}_{obs}, \mathbf{y}_{miss}\}$, and the distributional assumptions, $f(\mathbf{y} | \theta)$, for the multivariate relationships among the elements of \mathbf{y} . As noted in the goals that we outlined for imputation methods (Section 12.3), to ensure

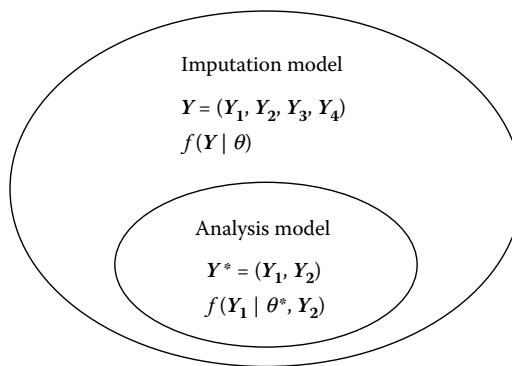
congeniality with a future analyst's modeling of the imputed data, the imputation model should:

- Include a broader set of variables than the eventual analytic model
- Control for variables representing major subpopulations or domains of analysis
- Reflect to the degree possible the true nonlinearities and interactions among the variables included in the imputation model
- Utilize conditional predictive methods that conform to methods (e.g., logistic regression) that analysts will use to analyze the imputed data

Consider a problem in which there are three continuous variables of interest in a 2011–2012 NHANES analysis of adult diastolic blood pressure (DBP): $y_1 = \text{DBP (mmHg)}$; $y_2 = \text{age (years)}$; and $y_3 = \text{body mass index (BMI; kg/m}^2)$. Further, let us assume that the item missing data rate is 9% for DBP and 2% for BMI, and that following rigorous edit checks, cleaning and follow-up by NHANES staff, age is observed for every case. One possible imputation model would be to include all three variables in the imputation process and to assume that the joint distribution for these three continuous variables is multivariate normal: $f(\mathbf{y} | \boldsymbol{\theta}) = \text{MVN}(\boldsymbol{\mu}, \boldsymbol{\Sigma})$. Under this model, MIs of the missing data for DBP and BMI are easily performed using methods described in Schafer (1997). The imputations performed under this imputation model would serve for univariate MI estimation of the mean DBP, μ_1 , or mean BMI, μ_3 , and they would also serve for the MI estimation of the regression of DBP on age and BMI, for example, $E(y_1 | y_2, y_3) = B_0 + B_1 \cdot y_2 + B_2 \cdot y_3$. Van Buuren and Oudshoorn (1999) illustrate the process of imputation model selection for an MI analysis of blood pressure in a cohort of persons aged 85+ from Leiden in the Netherlands.

12.4.2.1 Choosing the Variables to Include in the Imputation Model

The choice of variables to include in the imputation model should not be limited to only variables that have item missing data or variables that are expected to be used in a subsequent analysis. As a general rule of thumb, the set of variables included in the *imputation model* for an MI analysis should be much larger and broader in scope than the set of variables required for the *analytic model*. For example, if age and BMI are the chosen predictors in the analytic model for DBP, the imputation of item missing data for DBP and BMI might include many additional variables such as gender, race/ethnicity, marital status, height, weight, and systolic BP. [Figure 12.6](#) is a schematic representation of the desired relationship between the imputation model and the analytic model. The large outer oval represents the broad set of imputation model variables and joint distribution model that can contribute to the derivation of imputed values for missing items. Nested within this broad set

**FIGURE 12.6**

Relationship of the imputation and analysis models.

of imputation model variables is the smaller set of variables and the conditional model that will be the focus of the analysis.

Obviously, it is not feasible to define an imputation model and perform MIs using every possible variable in the survey data set. Based on recommendations from Schafer (1999) and Van Buuren (2012), some practical guidelines for choosing which variables to include in the imputation model are the following:

- All analysis variables (Y_1 and Y_2 in Figure 12.6)
- Other variables that are correlated or associated with the analysis variables (Y_3)
- Variables that predict item missing data on the analytic variables (Y_4)

Failure to include one or more analysis variables (Y_1 and Y_2) in the imputation model can result in bias in the subsequent MI estimation and inference. Including additional variables that are good predictors of the analytic variables (e.g., Y_3) improves the precision and accuracy of the imputation of item missing data. For example, when analyzing longitudinal data from a panel survey, Y_1 , Y_2 , and Y_3 might represent measures of the same characteristic across three waves. An analytic model may be focused on estimating the relationship of Y_2 and Y_3 , but an analyst imputing missing values for Y_3 could certainly use Y_1 to improve the imputation model. Finally, under the assumption that item missing data are MAR, incorporating variables (Y_4) that predict the propensity for response reduces bias associated with the item missing data mechanism.

Imputation of missing data collected under a complex sample design must also consider this question: How can informative design features such as stratification, cluster sampling, and weighting be incorporated into the imputation model? Published work (Rubin, 1996; Reiter et al., 2006) has emphasized the importance of including variables identifying complex sample design features

into imputation models. In particular, recent work by Reiter et al. (2006) demonstrates that ignoring complex sample design variables in the imputation models can lead to bias in MI estimates when the design variables are *informative*, or related to the survey variable of interest (which is often the case in practice). Including design variables in the imputation models when they are *not* related to the survey variable of interest can at worst lead to inefficient (and thus conservative) MI estimates. Even more recently, Zhou et al. (2016a,b) have demonstrated the benefits of simulating synthetic populations based on informative complex sample design features, and then imputing missing values in the synthetic populations under simple random sampling assumptions, eliminating any further need to account for the complex sampling features in analysis.

Theoretically, the effects of sample design strata and randomly sampled clusters may be modeled using a multilevel model that includes fixed effects of the strata, γ_{str} , and random effects of the clusters randomly sampled within strata, $u_{cl(str)}$:

$$y_i = \beta x_i + \gamma_{str,i} + u_{cl(str),i} + \varepsilon_{(str,cl),i}.$$

A hierarchical Bayes approach would be a flexible choice of method to multiply impute missing values of y under this mixed-effects regression model. Research on these methods is ongoing (Van Buuren, 2012; Gelman et al., 2013), and the only software package of which we are currently aware that implements this highly sophisticated approach to MI of complex sample survey data is the *pan* package in the R software (Schafer and Yucel, 2002).

Following Reiter et al. (2006) and Berglund and Heeringa (2014), the approach that we employ in the MI examples (Section 12.6) in this text is to include the complex sample design strata, clusters, and weights as fixed effects in the imputation model. Empirically, the following reduced model (with only a fixed effect for the weight and the stratum \times cluster indicator) performs well and generally avoids the instability problems encountered in employing the full hierarchical mixed-effects model for design parameters:

$$y_i = \beta x_i + \delta w_i + \gamma_{strat \times cluster, i} + \varepsilon_i.$$

In Stata, the following command creates the composite stratum \times cluster indicator variable, DESCODE, for the 2011–2012 NHANES data set:

```
gen descod = sdmvstra*10+sdmvpsu
```

Unfortunately, for complex sample designs with many strata and two or more clusters per stratum (e.g., the Health and Retirement Study, $H = 56$), this full “fixed effects” specification with indicator variables for the strata \times cluster combinations may require estimation of too many parameters and result in an unstable model fit or convergence failure. In such cases, it may be

necessary to use fixed characteristics that differentiate strata and primary sampling unit (PSU) population characteristics (e.g., geographic region, urban/rural, PSU size), and form groups of strata or combine similar PSUs to form pseudo-PSUs.

As noted earlier, research on MI for complex sample survey data is ongoing. Zhou et al. (2016a,b) apply FPBB to simulate “bootstrapped” target populations, and then perform imputations and MI analyses on the simulated population data sets. The FPBB method has now been implemented in the most recent release of the %IMPUTE command in the IVEware software package. The ASDA web site will continue to provide updates on this and other developments related to best practices for applying MI to complex sample data.

12.4.2.2 Distributional Assumptions for the Imputation Model

Once the set of variables for the imputation model has been chosen, a decision must be made concerning the joint distributional model for the chosen variables. In theoretical discussions of MI methods, convenient choices of multivariate models for the joint distribution of the broad set of imputation variables might be multivariate normal (continuous), multinomial (categorical), or *general location* (mixed categorical and continuous) models. As described in Section 12.4.2.3, many of the current software programs explicitly assume that the variables in the imputation model follow one of these standard multivariate data models.

Because the chosen imputation model may include many variables of different types (continuous, categorical, count, and semicontinuous mixtures of zeroes and continuous values), it may be difficult if not impossible to specify an analytical form for the joint posterior distribution of these variables. In such cases, several authors (Van Buuren and Oudshoorn, 1999; Raghunathan et al., 2001) have proposed using iterative *sequential regression* (SR) methods to approximate imputation draws from the unknown *joint posterior distribution* of the imputation model variables (Schafer, 1997). In these cases, the joint posterior distribution of the data is assumed to exist but its exact form is never truly observed. A potential vulnerability of this technique is that the target distribution that is being simulated in the SR process may not in fact exist for some missing data problems. Fortunately, empirical tests and simulation studies suggest that, when applied to large survey data sets with moderate rates of item missing data, these generalized methods of multivariate imputation do in fact yield reasonable results even when the number and diversity of variables included in the imputation model is large.

12.4.3 Creating the MIs

The second phase of an MI analysis is to generate $m = 1, \dots, M$ completed data sets in which the missing values, y_{mis} , have been imputed. The $m = 1, \dots, M$ independently imputed versions of the data set are termed *repetitions*. As described below, Bayesian MI imputes missing values by performing

stochastic draws from the posterior predictive distribution, $f(y_{mis}|y_{obs})$, averaging over possible values of θ . Using various algorithms, MI employs a sequence of imputation (I) and prediction (P) steps to approximate the posterior predictive distribution. After convergence of the algorithm, MI generates $m = 1, \dots, M$ independent imputations of the y_{mis} through stochastic draws from the constructed posterior predictive distribution.

A variety of algorithms, often tailored to the specific missing data pattern and mechanism, is used to generate the imputations. Readers are referred to the comprehensive texts by Rubin (1987), Schafer (1997), and Gelman et al. (2013) and articles by Tanner and Wong (1997), Gelfand and Smith (1990), Gelfand et al. (1990), and King et al. (2001) for more in-depth coverage of specific algorithms for addressing missing data under explicit data models and theoretically exact Bayesian methods.

Here, we consider the more typical survey data context where the imputation model is multivariate, the model includes variables of all types, and there is a generalized pattern of missing data across the variables in the model. In such cases of a “messy” pattern of missing data where exact methods do not strictly apply, the authors of MI software have generally followed one of the three general approaches described in the following sections.

12.4.3.1 Transforming the Imputation Problem to Monotonic Missing Data

The first approach is to transform the pattern of item missing data to a monotonic pattern by first using simple imputation methods or a *Markov Chain Monte Carlo* (MCMC) posterior simulation approach to fill in the missing values for variables in the model that have very low rates of item missing data (Berglund and Heeringa, 2014). Under a specified model for the data, imputation of a true monotonic pattern of item missing data is greatly simplified: the imputation of missing data is reduced to a sequence of imputations for single variables. Each imputation requires only a single step—no iteration is required as in the MCMC approach described below. This approach works best when the generalized pattern of missing data is dominated by missing data for one or two variables. Through inspection of the pattern of missing data across individual cases, it would be possible to use simple methods to “fill in” selected missing values for the variables with small amounts of missing data, creating a monotonic pattern of missing data (Little and Rubin, 2002) and simplifying the imputation problem. Solas 3.0 (Statistical Solutions) and PROC MI in SAS offer the analyst this option.

12.4.3.2 Specifying an Explicit Multivariate Model and Applying Exact Bayesian Posterior Simulation Methods

A second algorithmic approach to generating imputations for a generalized pattern of item missing data is to declare an explicit probability model for the data, for example, $f(\mathbf{y}|\boldsymbol{\theta}) = \text{MVN}(\boldsymbol{\mu}, \boldsymbol{\Sigma})$ or $f(\mathbf{y}|\boldsymbol{\theta}) = \text{general location model}$

(Schafer, 1997). Individual imputations are then generated by random draws from the correct posterior distribution of the missing values $f(\hat{Y}_{\text{miss}} | \mathbf{Y}_{\text{obs}}, \theta)$ under the explicit probability model.

Early versions of multivariate imputation programs, such as NORM (Schafer, 1997), assumed a multivariate normal distribution for all variables. Actual imputations for the multivariate model employed *data augmentation*, a form of the general class of MCMC posterior simulation algorithms. Later updates such as MIX (Schafer, 1997) incorporated the option of a general location model, more suitable to a mix of continuous and categorical variables. SAS PROC MI is another general purpose MI program that offers the option to employ the MCMC methods of Schafer (1997) and can accommodate both continuous and categorical variables.

12.4.3.3 SR or “Chained Regressions”

The third alternative for multiply imputing item missing data for large mixed sets of continuous, nominal, ordinal, count, and semicontinuous variables is a method that is variously labeled the *SR algorithm*, the *chained equations* (CEs) technique, or the *fully conditional specification* (FCS) method. The SR algorithm forms the basis for the %IMPUTE command in the IVEware software system (Raghunathan et al., 2001). The CEs algorithm (Van Buuren and Oudshoorn 1999) has been extended and enhanced (Royston, 2005; Carlin et al., 2008) and is available in the `mi_impute_chained` command of Stata. SAS PROC MI now includes an SR algorithm specified with an “`fcs ...;`” statement. Appendix A provides an updated inventory of the features of these and other MI software.

Each of these SR algorithms is based on an iterative *Gibbs Sampler-like* algorithm. Each iteration ($t = 1, \dots, T$) of the algorithm moves one by one through the sequence of variables in the imputation model, $\mathbf{Y} = \{Y_1, \dots, Y_k, \dots, Y_p\} = \{Y_1, Y_2, Y_3, Y_4\}$. In the very first iteration, the variable with the *smallest* amount of missing data is regressed on variables in the imputation model with complete data, using an appropriate model (e.g., logistic regression for a binary variable). Imputations for the missing values on the first variable are generated by stochastic draws from the predictive distribution defined by the regression model. Next, the variable with the second smallest amount of missing data is regressed on the first imputed variable and all other variables in the imputation model with complete data, and imputed values are generated. This algorithm proceeds until the variable with the most missing data is regressed on all other variables (some having imputed values) in the imputation model to develop the predictive distribution for the last variable.

Subsequent iterations use some or all of the variables in the imputation model (depending on the software) to reimpute the values that were originally missing for each of the variables. Based on the current (iteration t) values of the observed and imputed values for the imputation model variables, regression models are once again estimated for each target variable that originally had missing data, and as mentioned above, the regression models

can be tailored to each specific variable. For example, the IVEware software uses linear regression (continuous variables), multinomial logistic regression (nominal/ordinal variables), Poisson regression (count variables), or two-stage logistic/linear regression (semicontinuous variables) to model the conditional predictive distributions of individual variables Y_k , $f(\hat{Y}_k^{(t)} | \hat{Y}_{j \neq k}^{(t)}, \theta^{(t)})$. Updated imputations, $\hat{Y}_k^{(t)}$, are then generated by stochastic draws from the predictive distribution defined by the updated regression model. Once the last variable in the sequence has been imputed, the algorithm again cycles through each variable. The iteration of the cycles stops when a user-defined convergence criterion is met (e.g., $T = 10$ iterations in the Stata mi programs).

Under an explicitly defined imputation model, $f(Y|\theta)$, and a suitable prior distribution, $g(\theta)$, for the distributional parameters, the SR algorithm will, in theory, converge to the Bayesian joint posterior distribution for the data. Since the SR method never explicitly defines $f(Y|\theta)$, the assumption must be made that the posterior distribution does exist and that the final imputations generated by the iterative algorithm do represent draws from the actual, albeit unknown, posterior distribution. Although the exact theoretical properties of the resulting imputations remain somewhat of an unknown, in most applications the SR approach with its application of the Gibbs Sampler algorithm does converge to a stable joint distribution, and the multivariate imputations generated by the algorithm show reasonable distributional properties. Further, empirical studies have shown that this method produces results comparable to those for the EM algorithm and the exact methods of Bayesian posterior simulation (Heeringa et al., 2002).

MI inference requires that the imputation process be independently repeated multiple times, $m = 1, \dots, M$. In theory, MI inference is most efficient at recovering statistical information from incomplete cases when $M = \infty$. Obviously, analysts' tolerance for MI would have faded away quickly if each analysis required an infinite number of independently imputed data sets. Fortunately, research has shown that virtually all of the efficiency gains possible in an MI analysis can be achieved using as few as $M = 5$ to $M = 20$ independent repetitions of the imputation process (e.g., Rubin, 1986).

Although there are no exact criteria to establish that an MCMC or SR imputation algorithm has converged to a stable joint posterior distribution, graphical methods such as *trace plots* and *autocorrelation plots* can be used to monitor the progress of the algorithm (Van Buuren, 2011). As the number of iterations progresses, trace plots should show the successive iterations' posterior estimates of means and variances converging to a stable distribution. Autocorrelation plots should show that the autocorrelation of sequential draws declines, ultimately varying randomly about zero. SAS PROC MI provides users with the option to output these diagnostic charts for MCMC and FCS imputations (Berglund and Heeringa, 2014).

The example exercise presented in Section 12.6 will demonstrate the application of the Stata mi impute chained SR command to a multivariate missing data problem.

12.4.4 Estimation and Inference for Multiply Imputed Data

Once the item missing data have been multiply imputed under a suitable imputation model and the $m = 1, \dots, M$ completed replicate data sets have been stored in an appropriate data format, the next step in a complete MI analysis is to compute MI estimates of the population parameters and the variances of the MI estimates. The MI estimates and standard errors can then be used to construct CIs for the population quantities of interest to the survey analyst.

Many of the major software systems now include a pair of programs for conducting MI analysis: one program to perform the MIs of item missing data, and a second to perform MI estimation and inference based on the multiple files that are produced by the imputation procedure. Examples of such pairs of programs/commands include Stata's `mi impute` and `mi estimate`, PROC MI and PROC MIANALYZE in SAS, and %IMPUTE and %DESCRIBE/%REGRESS in IVEware.

Although the MI software mentioned above supports coordinated processing of both the imputation and estimation/inference phases of an MI analysis, provided that some care is taken in choosing the imputation model, the imputation and estimation phases can be performed separately by different persons (i.e., imputation by data producers, analysis by data users) or by using separate programs (e.g., conducting imputations in IVEware, and then estimation and inference in PROC MIANALYZE).

12.4.4.1 Estimators for Population Parameters and Associated Variance Estimators

MI estimates of population parameters (denoted here by θ) are computed using a simple averaging of the parameter estimates obtained by performing design-based analyses of the $m = 1, \dots, M$ completed data sets output from an MI algorithm:

$$\bar{\theta} = \frac{1}{M} \sum_{l=1}^M \hat{\theta}_l, \quad (12.1)$$

where:

$\hat{\theta}_l$ = estimate of θ from the completed data set $l = 1, \dots, M$.

The corresponding MI variance for the estimate $\bar{\theta}$ is estimated as a function of the average of the estimated sampling variances for each repetition estimate and a between-imputation variance component that captures the imputation variability over the M repetitions of the imputation process:

$$var(\bar{\theta}) = \bar{U} + \left(\frac{M+1}{M} \right) \cdot B, \quad (12.2)$$

where:

$$\bar{U} = \text{within-imputation variance} = (1/M) \sum_{l=1}^M U_l = (1/M) \sum_{l=1}^M \text{var}(\hat{\theta}_l).$$

$$B = \text{between-imputation variance} = (1/(M-1)) \sum_{l=1}^M (\hat{\theta}_l - \bar{\theta})^2.$$

In applications involving complex sample survey data, the estimated sampling variance of each repetition estimate, $\text{var}(\hat{\theta}_l)$, is computed using an appropriate Taylor Series Linearization (TSL) or replication variance estimator.

12.4.4.2 Model Evaluation and Inference

Based on the estimates of the within and between components of the MI variance estimator, the *fraction of missing information* is computed as

$$\hat{\gamma}_{mi} = \left[\frac{((M+1)/M) \cdot B}{((M+1)/M) \cdot B + \bar{U}} \right] = \left[\frac{((M+1)/M) \cdot B}{T} \right]. \quad (12.3)$$

If missing data for a single variable y were imputed based only on the distribution of the observed values of that same variable, the fraction of missing information would equal the missing data rate for y . However, more generally, when the model for imputing y conditions on observed values of other related variables (denoted here by x_1 and x_2), for example, $\hat{y}_{i,mis} = \hat{B}_0 + \hat{B}_1 \cdot x_{1i} + \hat{B}_2 \cdot x_{2i}$, the imputation borrows strength from the multivariate relationships and the fraction of information lost will often be reduced: $0 < \hat{\gamma}_{mi} <$ Missing rate for y (see Nishimura et al., 2016 for a discussion of exceptions). We note that the fraction of missing information is specific to an *estimate* of interest.

CIs for descriptive population parameters or single parameters in superpopulation regression models are constructed from the MI estimate, its standard error, and a critical value from the Student t distribution (Rubin and Schenker, 1986):

$$\text{CI}_{(1-\alpha)}(\theta) = \bar{\theta} \pm t_{\tilde{v}_{mi}, 1-\alpha/2} \cdot se(\bar{\theta}), \quad (12.4)$$

where:

\tilde{v}_{mi} = the degrees of freedom for the MI variance estimate (Theory Box 12.2).

The unique feature of the MI CI for population parameters is the degrees of freedom determination for the Student t distribution. Current software uses the “small sample” method of Barnard and Rubin (1999) to determine the degrees of freedom, v , for constructing the CI. Theory Box 12.2 provides a brief description of this degrees of freedom calculation. The MI CIs are routinely reported for individual descriptive parameters or regression model parameters by the MI analysis programs in Stata (`mi estimate`) and SAS

(PROC MIANALYZE). Simulation studies have demonstrated that for large sample sizes, this MI CI provides true coverage of the population value that is very close to the nominal $100(1 - \alpha)\%$ coverage level.

THEORY BOX 12.2 DEGREES OF FREEDOM FOR MI INFERENCES FROM COMPLEX SAMPLE SURVEY DATA

In general, large sample MI CIs for population values are based on a Student t distribution with the following degrees of freedom:

$$v_{mi} = (M - 1)\hat{\gamma}^2, \quad (12.5)$$

where:

$\hat{\gamma}$ = the estimated fraction of missing information (12.3).

Barnard and Rubin (1999) point out that this large sample approximation may not be suitable for “small” samples. Even in small simple random samples, this formula can lead to an estimate of degrees of freedom that exceeds the number of complete observations ($df \sim n - 1$). For most complex sample designs, application of this large sample formula results in values of v_m that greatly exceed the nominal design-based degrees of freedom (#clusters – #strata). Barnard and Rubin propose the following adjustment to establish the degrees of freedom for small samples or designs with limited degrees of freedom:

$$\tilde{v}_{mi} = \left(\frac{1}{v_{mi}} + \frac{1}{\hat{v}_{obs}} \right)^{-1}, \quad (12.6)$$

where:

v_{mi} = the large sample MI degrees of freedom;

\hat{v}_{obs} = the degrees of freedom for the complete data,

$$= \left(\frac{v_{com} + 1}{v_{com} + 3} \right) \cdot v_{com} \cdot (1 - \hat{\gamma}_{mi}),$$

v_{com} = the degrees of freedom for the complete case analysis;

$\hat{\gamma}_{mi}$ = the estimated fraction of missing information.

In the analysis of a small simple random sample, the degrees of freedom for the Student t reference distribution would be $v_{com} = n - 1$. The complete data degrees of freedom for an analysis of a complex sample survey data set would be the now familiar $v_{com} = v_{des} \approx \#clusters - \#strata$.

[Chapter 3](#) discussed the approximate nature of the current rules for determining design-based degrees of freedom for complex sample survey data. The same or greater level of approximation must hold in any MI inferences from complex sample survey data. Additional research in this area is certainly needed. The Barnard and Rubin approximation to the effective degrees of freedom is now incorporated in MI estimation software such as Stata `mi estimate` and SAS PROC MIANALYZE.

Li et al. (1991) have developed an MI *F*-test statistic that serves the function of a Wald statistic to test multiparameter hypotheses. In Stata, this multiparameter *F*-test is invoked using the `mi test` postestimation command.

12.5 Fractional Imputation

12.5.1 Background

We have seen in Section 12.4 that the Bayesian approach to analysis with item missing data is embodied in the now highly developed literature on theory, methods, and algorithms for MI. FI is now developing as a “frequentist” or design-based alternative to Bayesian MI for handling item missing data in complex sample survey data sets. The basic concept of fractionally imputing missing values using multiple “donors” or draws and apportioning the full survey weight across the resulting multiple records for a case was first mentioned by Kalton and Kish (1984). Over the next four decades, theoretical development of FI was extended in further work by Fay (1996), Kim and Fuller (2004), Durant and Skinner (2006), Kim (2011), and Kim and Yang (2014). However, like many good ideas in statistics, applications of FI in actual survey analyses were delayed by a lack of software in major statistical analysis systems. This was rectified in 2015 when the SAS system incorporated an FI hot deck imputation option into its SURVEYIMPUTE procedure.

The underlying theory and methods of the FI technique have now been developed for the case in which an explicit parametric imputation model (e.g., normal, multinomial) is assumed Kim (2011) as well as approaches in which the predictive distribution for the missing items is implicit in the hot deck imputation method (Kim and Fuller, 2004; Kim and Yang, 2014). The example application in Section 12.6 will focus on the nonparametric FI hot deck method.

The following sections will highlight key features of the FI approach to imputation model choice, the FI process, and how fractionally imputed data sets can be analyzed with standard design-based weighting and variance estimation methods.

12.5.2 Creating the FIs

FI is a “frequentist” and “design-based approach” to analyzing item missing data in complex sample surveys. FI creates FIs using an EM algorithm and an iterative I, W, P process (additional details on these three steps are provided below). Like the Bayesian MI methods, FI utilizes an imputation model for the data to obtain imputed values for y_{mis} and an iterative algorithm that results in a multiple records for the i -th case, $\mathbf{y}_{i(j)} = \{y_{mis,i(j)}, y_{obs,i}\}, j = 1, \dots, M(i)$. Note here that the number of fractionally imputed records for each case is not necessarily equal to a constant M , but can vary across cases and certainly does when an FI hot deck algorithm is used to create the imputations.

I Step: FI performs the I (Imputation) step only once, drawing $M(i)$ imputed values for each missing value for the i -th case from a “proposal” or initializing distribution $h(y_{mis}|y_{obs})$ that assigns positive probability to each possible outcome for $y_{mis}|y_{obs}$. In hot deck FI (Kim and Fuller, 2004), imputations for $y_{mis,i}$ are obtained by drawing $j = 1, \dots, M(i)$ donor values from imputation cells defined by the cross-classification of observed variables $y_{obs,i}$ for that case. *Fully efficient FI hot deck imputation* (FEFI; SAS, 2015) creates an imputed record for each possible outcome for $y_{mis}|y_{obs}$ that is present in the full set of donor records.

W Step: Once the initial set of $M(i)$ distinct values for $y_{mis}|y_{obs}$ has been chosen from the proposal distribution, $h(y_{mis}|y_{obs})$, or obtained from hot deck donors, an initial value of the *fractional weight* is calculated for each of the $M(i)$ imputed values:

$$w_{ij}^{*(t)} = \frac{f(y_{obs,i}, y_{mis,i(j)}; \hat{\theta}^{(t)})}{h(y_{mis,i(j)} | y_{obs,i})}, \quad (12.7)$$

where:

$w_{ij}^{*(t)}$ = the fractional weight for imputed value $j = 1, \dots, M_i$ at iteration t .

$f(y_{obs,i}, y_{mis,i(j)}; \hat{\theta}^{(t)})$ = the complete data likelihood for observation i evaluated for $y_{obs,i}$, $y_{mis,i(j)}$, and current iteration parameter estimate, $\hat{\theta}^{(t)}$.

Together, the I step and the W step form the Expectation step in the EM algorithm.

P Step: The P step of the FI algorithm is the Maximization step. Given the updated values of w_{ij}^* , these fractional weights are used to update the weighted estimates of θ . For an explicit model $f(y|\theta)$, such as a normal or multinomial distribution, the updated estimates of θ for iteration t can be obtained by solving the weighted score equations corresponding to $f(y|\theta)$:

$$\sum_{i=1}^n w_i \sum_{j=1}^{M_i} w_{i(j)}^{*(t)} S(\hat{\theta}^{(t)}, y_{obs,i}, y_{mis,i(j)}) = 0. \quad (12.8)$$

If all variables in \mathbf{y} are categorical and the imputation model is implicit in hot deck draws from donor records, the joint probabilities for the vector

of response values for the categorical variables that comprise the y can be estimated as

$$\pi^{(t)}(\mathbf{y}) = \frac{\sum_{i=1}^n w_i \sum_{j \in D_i} w_{ij}^{*(t)} \cdot I\{(y_{obs,i}, y_{mis,i(j)}) = \mathbf{y}\}}{\sum_{i=1}^n w_i}, \quad (12.9)$$

where:

D_i is the set of all possible $y_{mis,i(j)}$ given $y_{obs,i}$.

Once the P step of the iterative algorithm is complete, the EM algorithm cycles back to the W step where the updated estimates of the distributional parameters (e.g., $\pi^{(t)}(\mathbf{y}), \hat{\theta}^{(t)}$) are used to produce updated fractional weights, $w_{ij}^{*(t+1)}$. These updated weights are then used in a new P step to update the parameters, that is, $\pi^{(t+1)}(\mathbf{y})$ and $\theta^{(t+1)}$. The iterative cycle of W and P steps continues until specified convergence criteria are met for the fractional weight values, $w_{ij}^{*(final)}$.

To summarize, FI uses an EM algorithm to solve for $j = 1, \dots, M(i)$ fractional weight factors, w_{ij}^* , that can be applied to the final survey weight for a case i , w_i . These weighting factors are used to create compound *imputation weights*, $w_{ij}^* \cdot w_i$, to be used in standard design-based analysis of the resulting $n^* = \sum_{i=1}^n M_i$ fractionally imputed records. Under the EM algorithm, the values of w_{ij}^* are refined subject to the following constraints:

- (i) $w_{ij}^* > 0$;
- (ii) $\sum_{j=1}^{M_i} w_{ij}^* = 1.0$; and
- (iii.a) $\sum_{i=1}^n w_i \sum_{j=1}^{M_i} w_{ij}^* S(\hat{\theta}, y_{obs,i}, y_{mis,i(j)}^*) = 0$,

where $\sum_{i=1}^n w_i \sum_{j=1}^{M_i} w_{ij}^* S(\hat{\theta}, y_{obs,i}, y_{mis,i(j)}^*) = 0$ is the weighted score equation used to solve for the pseudo maximum likelihood estimate of the parameters of $f(y|\theta)$, or alternatively:

$$(iii.b) \pi(\mathbf{y}) = \frac{\sum_{i=1}^n w_i \sum_{j \in D_i} w_{ij}^* \cdot I\{(y_{obs,i}, y_{mis,i(j)}) = \mathbf{y}\}}{\sum_{i=1}^n w_i},$$

when the FI is nonparametric, as in hot deck FI.

The consistency property of design-based estimates from FIs of continuous variables assumes that the number of FIs for each case, M_i , is large, but Kim (2011) recommends $M = 10$ as a practical choice. The number of FIs for categorical variables is limited by the discrete number of categories for $y_{mis}|y_{obs}$. When FIs for categorical variables utilize a hot deck method, fully efficient fractional imputations (FEFI) are obtained by creating one fractionally imputed record for each possible value of y_{mis} (from the available donors) in the hot deck imputation cells.

12.5.3 Estimation and Inference with Fractionally Imputed Data

Survey data are collected from finite populations. As noted above, the FI method has been developed within the general design-based framework for finite population estimation and inference. Following Kim (2011), in this finite population context, a survey analyst may be interested in estimating a finite population parameter, say \mathbf{B} , that is a function of a vector of variables $\mathbf{y} = \{y_1, \dots, y_p\}$. As discussed in [Chapter 7](#), we may assume that the finite population \mathbf{y} are a realized set of values from a superpopulation model, $f(\mathbf{y}|\theta)$. In the complete population of elements, the analyst's statistic of interest is the unique solution to a population estimating equation of the form:

$$\sum_{i=1}^N U(\beta; \mathbf{y}_i) = 0. \quad (12.10)$$

For example, if β is the slope parameter in the simple linear regression of y_1 on y_2 , the estimating function $U(\beta, \mathbf{y})$ can be written as is:

$$U(\beta, \mathbf{y}) = \sum_{i=1}^N [(y_{1i} - \bar{y}_1) \cdot (y_{2i} - \bar{y}_2) - \beta \cdot (y_{2i} - \bar{y}_2)^2] = 0. \quad (12.11)$$

Given a probability sample of n of the N population elements, a consistent estimator of β is obtained (assuming no missing data) by solving the weighted estimating equation:

$$\sum_{i=1}^n w_i \cdot U(\beta; y_{obs,i}) = 0, \quad (12.12)$$

where:

w_i = the full response survey weight for case $i = 1, \dots, n$.

When y is not fully observed, this weighted estimating equation can be extended using the fractionally weighted imputations for y_{mis} :

$$\sum_{i=1}^n w_i \sum_{j=1}^{M_i} w_{ij}^* \cdot U(\beta; y_{obs,i}, y_{mis,i(j)}) = 0, \quad (12.13)$$

where:

$y_{mis,i(j)}$ = the j th imputed value of y_{mis} .

w_{ij}^* = the fractional weight for j th imputed value of y_{mis} for case $i = 1, \dots, n$.

Under FI, estimates of the population parameter β are solved by a weighted averaging over the imputed values for y_{mis} .

In short, if the missing data have been fractionally imputed, there is no need for special combining rules such as those employed in MI estimation and inference. Using the composite imputation weights formed as the product of the final survey weight, w_i , and the fractional weight variable, w_{ij}^* , standard survey analysis software such as the Stata svy commands can be used for estimation. Using only the fractionally imputed records and the imputation weight for each case, standard TSL, Jackknife Repeated Replication (JRR), Balanced Repeated Replication (BRR), or bootstrap methods for variance estimation can be applied. CI formation and Wald tests of hypotheses also follow the standard approaches described for complex sample survey data described in [Chapters 5 through 11](#).

12.5.4 FI Software

The FEFI hot deck method of imputation has now been implemented in SAS PROC SURVEYIMPUTE. PROC SURVEYIMPUTE can be used to generate an output data set with imputation weights for each fractionally imputed record. The analyst may request that PROC SURVEYIMPUTE utilize the user-specified stratum and cluster codes to generate replicated imputation weights for subsequent use in JRR or BRR variance estimation. Section 12.6 will illustrate an application of the SAS PROC SURVEYIMPUTE FEFI option to the 2011–2012 NHANES data.

At the time of the writing of this second edition, an R package to perform FI is currently being developed (personal communication with Professor Jae Kim). The companion web site for this book will report on these and other new developments as they occur and provide appropriate links to any open-source documentation and user guides that are available.

12.6 Application of MI and FI Methods to the NHANES 2011–2012 Data

The imputation analysis examples presented in this section focus on 2011–2012 NHANES measures of DBP for the U.S. adults. The example will focus on MI and FEFI treatment of the item missing data for 2011–2012 NHANES adult respondents who agreed to participate in the MEC phase of the study. Recall that, in this analysis, the nonresponse adjustment factor included in the NHANES MEC survey weight, WTMEC2YR, serves as compensation for the 4.3% of NHANES interview respondents who did not consent to participate in the MEC, but that this phase nonresponse adjustment does not address problems with item missing data in the MEC phase.

12.6.1 Problem Definition

Table 12.2 provides an overview of item missing data rates for a selected set of items from the 2011–2012 NHANES data. Although actual missing data rates can vary substantially across surveys, the missing data rates displayed in this table show a typical pattern. Missing data on key demographic variables such as age, gender, and race are generally extremely low (typically <1% of interviewed cases). Significantly higher rates of missing data occur for variables that measure personal or family income, assets, benefit amounts, or other such financial variables. The poverty index variable (INDFMPIR) is a constructed measure derived from survey measures of household income and family characteristics and holds an 8.7% missing data rate in the 2011–2012 NHANES. Among 2011–2012 NHANES MEC participants, missing data rates for the physical measures are 1.6% for BMI (BMXBMI) and 8.9% for DBP (BPXDI1_1).

TABLE 12.2

Item Missing Data Rates for Selected 2011–2012 NHANES Variables ($n = 5,615$)

Variable	Variable Name	<i>n</i>	% Missing
Age	AGEC	5,615	0.0
Gender	RIAGENDR	5,615	0.0
Marital status	MARCAT	5,315	5.3
Race/ethnicity	RIDRETH1	5,615	0.0
Body mass index	BMXBMI	5,525	1.6
Poverty index	INDFMPIR	5,128	8.7
DBP	BPXDI1	5,112	8.9

The aim of this example is to impute the missing values for these seven MEC variables and perform two analyses of the imputed data. The first analysis will be to estimate the population proportion of the U.S. adults with diastolic hypertension, which we conservatively define as measured DBP ≥ 90 mmHg. The second analysis will involve estimating a simple logistic regression model of the probability of diastolic hypertension as a function of adults' age, gender, and race/ethnicity. Four approaches to the treatment of the item missing data will be compared: (1) analysis of complete cases; (2) MI of missing data using the Stata `mi impute chained` command (no design variables in the imputation model); (3) MI in which the imputation model includes fixed effects of the strata and sampled clusters (Section 12.4.1); and (4) fully efficient hot deck fractional imputation (FEFI) as implemented in SAS PROC SURVEYIMPUTE. Conditional on each treatment of missing data, the analyses will utilize the available survey weights in estimation and incorporate design stratification and cluster sampling in the estimation of standard errors for single analyses.

12.6.2 Imputation Models for the NHANES DBP Example

The first step in the analysis of DBP is to select the variables that will be included in the imputation model. For the MI analyses, the imputation model includes the following mixture of continuous and categorical variables:

Imputation model variables: MI method

BPXDI1_1: Diastolic blood pressure

MARCAT: Marital Status

RIAGENDR: Gender

RIDRETH1: Race/Ethnicity Category

AGEC, AGECSQ: Linear and quadratic terms for age (years)

BMXBMI: Body mass index (kg/m^2)

INDFMPIR: Poverty Index (continuous scale with values in the range 1–5)

Optional design variables:

WTMEC2YR: NHANES MEC survey weight variable

DESCODE: Categorical variable formed by combining unique values of the NHANES primary stage stratum and cluster codes (Section 12.4.2.1).

Note that the imputation model includes three variables (MARCAT, BMXBMI, and INDFMPIR) that will not be incorporated in the final analysis model. Also, recall that the 2011–2012 NHANES MEC data have no missing values for the age, gender, and race/ethnicity variables (Table 12.2). Therefore, only DBP, marital status, BMI, and the poverty index variables require imputations. The linear and quadratic terms for age and the gender and

race/ethnicity predictors are used by the `mi impute chained` command in Stata to build the regression models that are used to impute missing values for BPXDI1_1, MARCAT, BMXBMI, and INDFMPIR, but their observed distribution will not be altered across the $M = 5$ MIs.

The imputation model for the FI approach utilizes the same variable set, but to facilitate the hot deck imputation, the four continuous variables were converted to the following grouped categorical variables prior to imputation:

`AGE4CAT` (1 = 18–24; 2 = 25–44; 3 = 45–64; 4 = 65+)
`POVCAT` (1 = 0.00–0.99; 2 = 1.00–1.99; 3 = 2.00–2.99; 4 = 3.00–3.99; 5 = 4.00–4.99; 6 = 5.00)
`BMICAT` (1 = <18.5; 2 = 18.5–24.9; 3 = 25.0–29.9; 4 = 30+)
`DBPCAT` (1 = <80.0; 2 = 80.0–89.9; 3 = 90+).

Before actually imputing the missing data, the `misstable patterns` command is used to display the generalized pattern of missing data in the imputation model variable set:

```
misstable patterns bpxdi1_1 bmxbmi indfmpir ///
marcat riagendr ridreth1 agec agecsq weight descode ///
if age18p==1
```

Percent	Pattern*			
	1	2	3	4
79%	1	1	1	1
7	1	1	1	0
7	1	1	0	1
4	1	0	1	1
1	1	1	0	0
<1	0	1	1	1
<1	1	0	0	1
<1	1	0	1	0
<1	0	1	1	0
<1	0	1	0	1
<1	1	0	0	0
<1	0	0	1	1
<1	0	1	0	0
<1	0	0	1	0
100%				

*Variables: (1) bmxbmi, (2) marcat, (3) indfmpir, (4) bpxdi1_1

The misstable patterns output identifies 14 patterns of missingness across the four variables that have missing values (completely observed variables are not displayed).

The data set includes complete observation of all variables for 79% of cases, with an additional 7% of the cases missing only the DBP measure, 7% missing only the poverty index, and a residual 7% displaying a generalized pattern of missingness on one or more variables.

12.6.3 Imputation of the Item Missing Data

12.6.3.1 Multiple Imputation

After examining the rates and patterns of item missing data for the variables included in the imputation model, the next step is to multiply impute the item missing data for BPXDI1_1, MARCAT, BMXBMI, and INDFMPIR. We illustrate the MI step here using one general purpose program for imputation of item missing data: the Stata mi impute chained command (imputation by CEs). This command is capable of multiply imputing generalized patterns of missing data for a multivariate vector of survey variables. Using the following commands, the missing data are independently imputed $M = 5$ times using the CEs (i.e., SR) technique, and five completed data sets with the observed and imputed values are created.

```
* set output data set to "full long" style
mi set flong

mi register imputed marcat bmxbmi indfmpir bpxdi1_1

mi register regular riagendr ridreth1 agec descode wtmec2yr

mi impute chained ///
(mlogit) marcat ///
(regress) bmxbmi ///
(regress, include(i.descode wtmec2yr)) bpxdi1_1 ///
(regress) indfmpir = i.riagendr i.ridreth1 agec agecsq, ///
add(5) rseed(2016) replace
```

Before the imputation is performed, the `mi set flong` command specifies that the output file should be in the `flong` format, with the original input record for each case plus M additional records for each case representing the $m = 1, \dots, M$ imputation replicates for the case. The current data set will be expanded to contain $n \times (M + 1)$ records. On this file the generated system variable, `_mi_m`, will be set to 0 for the original record and values of `_mi_m = 1, 2, \dots, M` for the imputation replicate records. The `mi register` command that follows identifies the fully observed variables that should be included in the imputation model. This syntax includes the survey

weight variable (WTMEC2YR) and the composite design stratum and cluster variable (DESCODE) in the predictive model for the DBP variable. As noted above, the MI was also run excluding these two “design variables” from the DBP prediction model.

Immediately following the `mi impute chained` command is the list of variables that will be included in the imputation process. Recall that only the variables BPXDI1_1, MARCAT, BMXBMI, and INDFMPIR have missing data. Preceding each variable, the form of the regression model to be used by the CEs algorithm to predict the conditional distribution of the missing values is listed in parentheses, for example, (`mlogit`) for the nominal categorical variable MARCAT. Variables for age, gender, and race are included (after the equal sign) to be used as predictors in each of the regression models that `mi impute chained` will use to predict (impute) missing values of the other four variables. We note that the addition of the `include()` option when specifying the form of the regression model for DBP (`regress`) will only include the design variables in the imputation model for DBP, and not the other three variables. Using the “`i.`” syntax, gender, race, and `decode` are represented as categorical variables with a reference category parameterization.

The initial output from the `mi impute chained` command is displayed below. The first portion of this output is a summary identifying the exact form of each regression model and the independent variables used in the imputation models for each variable. The second part of the output table summarizes the distribution of cases by the counts of missing values. As noted above, Stata `mi impute chained` provides the user with the option to control the exact set of predictors for the regression model that will be used to impute missing data for individual variables.

```

Conditional models:
bmxbmi: regress bmxbmi i.marcat indfmpir bpxdil_1 i.riagendr i.ridrethl agec
agecsq
marcat: mlogit marcat bmxbmi indfmpir bpxdil_1 i.riagendr
i.ridrethl agec agecsq
indfmpir: regress indfmpir bmxbmi i.marcat bpxdil_1 i.riagendr
i.ridrethl agec agecsq
bpXdil_1: regress bpxdil_1 bmxbmi i.marcat indfmpir i.decode
wtmec2yr i.riagendr i.ridrethl agec agecsq

Performing chained iterations ...

Multivariate imputation                               Imputations =      5
Chained equations                                     added =          5
Imputed: m=1 through m=5                            updated =         0

Initialization: monotone                           Iterations =      50
                                                               burn-in =       10

marcat: multinomial logistic regression
bmxbmi: linear regression
bpXdil_1: linear regression
indfmpir: linear regression

```

Variable	Observations per m				Total
	Complete	Incomplete	Imputed		
marcat	5315	300	300		5615
bmxbmi	5525	90	90		5615
bpxdil_1	5112	503	503		5615
indfmpir	5128	487	487		5615

(complete + incomplete = total; imputed is the minimum across m of the number of filled-in observations.)

We strongly recommend that users visually examine and compare the key statistics for the original and imputed versions of variables included in the MI run. To display selected results from the data set that is created by the `mi_impute chained` command, the following Stata descriptive command can be used:

```
svy: mean bmxbmi indfmpir bpxdil_1 [pweight=wtmec2yr], ///
over(_mi_m)
```

Table 12.3 displays the weighted estimates of means for BMI, poverty index, and DBP from each of the $M = 5$ imputation replicates as well as the estimated mean based only on analysis of observed values for each variable.

TABLE 12.3
Weighted Estimates of Means for Selected Variables before and after Multiple Imputation in Stata (among Adults Who Completed the NHANES Interview and MEC Surveys)

Variable	Statistic	Estimates before Imputation		Multiple Imputation Repetition Estimates ^a ($n = 5615$)				
		n_{obs}	Value	$m = 1$	$m = 2$	$m = 3$	$m = 4$	$m = 5$
BMI	Mean	5,525	28.6	28.65	28.62	28.62	28.64	28.64
Poverty index	Mean	5,128	2.9	2.83	2.84	2.84	2.83	2.83
Diastolic BP	Mean	5,112	71.6	71.57	71.58	71.64	71.61	71.62

^a Estimates from imputation model with design variables and weight included.

12.6.3.2 FEFI: Hot Deck Method

As noted in Section 12.5, FEFI by the hot deck method is now accessible to analysts through the user-friendly SAS PROC SURVEYIMPUTE command (Kim and Fuller, 2013). The following command syntax initiates an FI of the missing data in our small 2011–2012 NHANES data extract:

```
proc surveyimpute data=c12 method=FEFI varmethod=Jackknife;
  id seqn ;
  class age4cat povcat riagendr marcat ridreth1 bmicat dbpcat ;
  var age4cat povcat riagendr marcat ridreth1 bmicat dbpcat ;
```

```

impjoint povcat bmicat ;
strata sdmvstra ;
cluster sdmvpsu ;
weight wtmecc2yr ;
output out=nhanesFEFI outjkcoefs=nhanesJKCOEFS;
run;

```

The FEFI method is selected on the command statement using the `method=FEFI` option. To obtain the vector of replicated imputation weights suitable for design-based variance estimation using the delete-one JRR methods (Chapter 3), the `varmethod=Jackknife` option is also specified on the command line. The `class` statement identifies the categorical variables that will be used to form hot deck cells to identify the set of potential donor values for each FI. The `var` statement lists the variables for which any missing values will be imputed by the FEFI hot deck method. The `impjoint` statement in the command sequence specifies combinations of variables (here poverty index and BMI category) that must be jointly imputed, thereby preserving the joint distribution of these two variables based on the observed data. Univariate hot deck imputation will be performed for all single variables that are not specified as an `impjoint` group. The standard design variables are specified in the `strata`, `cluster`, and `weight` statements. PROC SURVEYIMPUTE requires the `weight` variable for construction of the imputation weights for fractionally imputed cases, and the `stratum` and `cluster` variables are required for the construction of the JRR replicate imputation weights. The `output` statement specifies the output file that will contain the expanded data file with the fractionally imputed cases, as well as the output file name for the JRR replicate weights that are produced when `varmethod=Jackknife` is specified.

The following output illustrates the header information included in the PROC SURVEYIMPUTE results file. Additional output (not shown) summarizes: the pattern of missing data across the imputation model variables (similar to the Stata `misstable` output); the distribution (proportions) of the observed variable categories for each of the 14 missing data patterns; and an iteration/convergence history for the EM algorithm used to derive the final fractional weights for each case.

The SURVEYIMPUTE Procedure		
Imputation Information		
Data Set	WORK.C12	
Weight Variable	wtmecc2yr	Full sample 2 year MEC exam weight
Stratum Variable	sdmvstra	Masked variance pseudo-stratum
Cluster Variable	sdmvpsu	Masked variance pseudo-PSU
Imputation Method	FEFI	
Number of Observations Read	5615	
Number of Observations Used	5615	

Sum of Weights Read	2.32E8
Sum of Weights Used	2.32E8
Class Level Information	
Class	Levels
age4cat	4
povcat	6
riagendr	2
marcat	3
ridreth1	5
bmicat	4
dbpcat	3
Design Summary	
Number of Strata	14
Number of Clusters	31

To explore the contents of the FEFI output file for the 2011–2012 NHANES data set, SAS PROC SURVEYFREQ is used to display the weighted and unweighted distributions of the imputed variables (shown here for DBPCAT, the original trinomial categorization of the continuous DBP measures):

```
proc surveyfreq data=imputed varmethod=jackknife ;
weight impwt ;
repweights imprepwgt_: / jkcoefs=nhanesjkcoefs ;
tables dbpcat
run ;
```

Here are the results:

dbpcat	Frequency	Weighted Frequency	Std Err of Wgt Freq	Percent	Std Err of Percent
<80	7908	176933527	9936029	76.2636	1.2399
80-89.9	2431	40958305	3682808	17.6542	0.9141
90+	1625	14110707	2236180	6.0821	0.7971
Total	11964	232002539	14006079	100.000	

Following the FEFI of the missing items, the original data set of $n = 5,615$ cases is expanded to a total of 11,964 records, each with a new imputation weight. Based on the fractionally imputed data, the estimated proportion of the U.S. adult population with measured DBP ≥ 90 mmHg is 0.061, with a design-based estimate of the standard error equal to 0.008.

12.6.4 Estimation and Inference

12.6.4.1 Multiple Imputation

Once the MIs are complete, the data are ready for analysis. In this example, two MI analyses of the imputed data are performed. The first analysis computes the MI estimate and 95% CI for the proportion of the U.S. adults who have DBP ≥ 90 mmHg. The second analysis uses MI methods to fit a logistic regression model of the probability of high DBP (HIGH_DIASTOLIC) as a simple additive function of RIAGENDR (gender), RIDRETH1 (race/ethnicity), AGEC, and AGECSQ (linear and quadratic terms for age in years).

Each analysis uses the $M = 5$ multiply imputed data sets and applies the general procedures for MI estimation and inference outlined in Section 12.4. In Stata, including the `mi` prefix with the `estimate` modifier invokes an MI analysis for the MI data sets produced by the `mi impute chained` command, or independently developed MI data sets that include the correct variable coding (i.e., `_mi_m`) for the M repetitions.

MI Analysis 1: Estimation of the proportion of the U.S. adults with DBP ≥ 90 mmHg—The Stata commands required to generate the MI estimate of the proportion of the U.S. adults with high DBP are as follows:

```
mi svyset sdmvpsu [pweight=wtmec2yr], strata(sdmvstra)
gen high_diastolic = 0
replace high_diastolic = 1 if bpxdi1_1 >= 90

mi estimate: svy: tab high_diastolic
```

The active Stata data set for this analysis is the output file generated by the Stata `mi impute chained` MI run. The initial command is the now-familiar `svyset` command in which the stratum, cluster, and survey weight variables for the 2011–2012 NHANES are specified. The second and third command lines use the imputed data for the continuous DBP measures to derive the binary indicator of high DBP for all cases in the new data set, including cases with imputed values of DBP. The fourth command in the sequence includes the `mi estimate` modifier that informs Stata that the active data set includes MIs and that MI computations for estimates, standard errors, degrees of freedom, and 95% CIs are desired. Following the `mi estimate` modifier is the standard Stata `svy: tab` command for design-based estimation of the proportion and its standard error. Table 12.4 provides the MI estimate of the proportion of the U.S. adults with DBP ≥ 90 mmHg, its standard error, and a 95% CI for the population proportion. For comparison purposes, the table also reports the same statistics for a standard complete case analysis.

Following expression (12.1) above, the final MI estimate of the proportion with high DBP is $p = 0.061$ (0.008) for imputations that incorporated the design variables and $p = 0.060$ (0.007) when the design variables are excluded from the imputation model.

TABLE 12.4

Estimates of the Proportion of the U.S. Adults with DBP ≥ 90 . Comparison of Complete Case and Imputation Analyses

Analysis Type	<i>n</i>	<i>p</i>	<i>se(p)</i>	95% CI (<i>p</i>)	<i>df</i>
Complete case	5,112	0.061	0.008	(0.046–0.080)	17
MI no design	5,615	0.060	0.007	(0.045–0.076)	15.10
MI model design	5,615	0.061	0.008	(0.044–0.078)	15.18
FEFI hot deck ^a	5,615	0.061	0.008	(0.045–0.077)	31

Source: 2011–2012 NHANES.

^a Imputed data set includes $n = 11,964$ records with fractional weights.

Following Barnard and Rubin (1999), the approximate degrees of freedom (12.6) for the Student *t* distribution used to construct the CI for the MI estimate of the population proportion with high DBP are 15.2, which is slightly less than the 17 degrees of freedom assumed for a design-based analysis of the 2011–2012 NHANES complex sample survey data.

MI Analysis 2: Estimation of the logistic regression model for high DBP—The next step in the example exercise is to extend the analysis to a logistic regression model in which the probability of high DBP is modeled as a function of the selected covariates. The Stata command required to fit the logistic regression model to the multiply imputed data sets is:

```
mi estimate: svy: logistic high_diastolic i.ridreth1 ///
i.riagendr agec agecsq
```

The standard Stata svy: logistic command is preceded by the mi estimate: modifier to invoke the MI analysis of the $M = 5$ multiply imputed data sets. Table 12.5 (further below) provides the MI estimates of the regression parameters and standard errors along with the *p*-values for the *t*-tests of the null hypothesis $H_0: B_j = 0$ for each parameter indexed by j .

Finally, to illustrate the MI multi-parameter test of Li et al. (1991), consider a joint test of the null hypothesis that the effects of gender and race/ethnicity on high DBP levels are not significantly different from zero. To perform this test following the MI logistic regression analysis, the Stata mi test command is used:

```
mi test 2.riagendr 2.ridreth1 3.ridreth1 ///
4.ridreth1 5.ridreth1
```

The Stata output generated by this test command is shown below.

```
note: assuming equal fractions of missing information

( 1) 2.riagendr = 0
( 2) 2.ridreth1 = 0
```

(3) 3.ridreth1 = 0			
(4) 4.ridreth1 = 0			
(5) 5.ridreth1 = 0			
F(5, 14.9) =	13.13	Prob > F =	0.0001

TABLE 12.5

Estimated Logistic Regression Models for Diastolic Hypertension (DBP ≥ 90) of U.S. Adults (Comparison of Complete Case and Imputation Analyses)

Predictor ^a	Category	Complete Case Analysis			Multiple Imputation: Ignore Design		
		(n = 5,112)			(n = 5,615)		
		\hat{B}_j	se(\hat{B}_j)	p-value	\hat{B}_j	se(\hat{B}_j)	p-value
Intercept	Constant	-2.250	0.199	<0.001	-2.252	0.217	<0.001
Race/ethnicity	Other Hisp.	-0.726	0.245	0.009	-0.634	0.272	0.045
	White	0.131	0.225	0.567	0.164	0.226	0.480
	Black	0.658	0.246	0.016	0.641	0.246	0.020
	Other	0.050	0.245	0.841	0.032	0.258	0.901
Gender	Female	-0.545	0.208	0.017	-0.554	0.203	0.018
Age (centered)	Continuous	0.008	0.007	0.241	0.009	0.007	0.207
Age (centered) squared	Continuous	-0.002	0.0003	<0.001	-0.002	0.0003	<0.001
Multiple Imputation: Include Design							
Predictor ^a	Category	(n = 5,615)			FE Fractional Imputation		
		(n = 5,615)			(n = 5,615)		
		\hat{B}_j	se(\hat{B}_j)	p-value	\hat{B}_j	se(\hat{B}_j)	p-value
Intercept	Constant	-2.259	0.201	<0.001	-2.283	0.183	<0.001
Race/ethnicity	Other Hisp.	-0.614	0.263	0.039	-0.620	0.210	0.006
	White	0.163	0.228	0.485	0.118	0.209	0.576
	Black	0.642	0.240	0.017	0.600	0.230	0.014
	Other	0.080	0.245	0.751	0.042	0.223	0.853
Gender	Female	-0.530	0.198	0.018	-0.499	0.188	0.012
Age (centered)	Continuous	0.009	0.007	0.222	0.008	0.006	0.245
Age (centered) squared	Continuous	-0.002	0.0003	<0.001	-0.001	0.0002	<0.001

Source: 2011–2012 NHANES.

Note: MI degrees of freedom are determined separately for each estimate.

^a Reference categories are Mexican (race/ethnicity) and Male (gender).

Based on the test results, the hypothesis of no effect of gender and race/ethnicity on DBP is rejected.

12.6.4.2 FI Estimation and Inference

FI Analysis 1: Estimation of the proportion of the U.S. adults with DBP $\geq 90 \text{ mmHg}$ —After FEFI of the missing data, the following SAS syntax is used to generate estimates of the population proportion of the U.S. adults with high DBP:

```
data imputed ;
  set nhanesfefi ;
  if dbpcat=3 then high_dbp=1 ; else high_dbp=0 ;
run ;

proc surveyfreq data=imputed varmethod=jackknife ;
  weight impwt ;
  repweights imprepwt_ : / jkcoefs=nhanesjkcoefs ;
  tables high_dbp ;
  format high_dbp yn;
run ;
```

A SAS data step is used to collapse the three-category DBPCAT variable into a new binary indicator (HIGH_DBP) for DBP $\geq 90 \text{ mmHg}$. The PROC SURVEYFREQ command is then run to generate weighted estimates and design-based standard errors for the proportion of interest. Note the use of the varmethod=jackknife option and “repweights” statement, which directs PROC SURVEYFREQ to use the delete-one JRR method for variance estimation. The jkcoefs=nhanesjkcoefs option on the repweights statement identifies the SAS data file that contains the imputation replicate weights previously output by PROC SURVEYIMPUTE. The estimated proportion of adults with high DBP and the standard error are displayed in [Table 12.4](#).

FI Analysis 2: Estimation of the logistic regression model for high DBP—Following the FEFI of the missing values, the logistic regression model for the probability of high DBP is estimated using SAS PROC SURVEYLOGISTIC:

```
proc surveylogistic data=imputed varmethod=Jackknife;
  class riagendr (ref='1') ridreth1 (ref='1') / param=ref;
  model high_dbp (event='1') = ridreth1 riagendr agec
    agecsq;
  weight ImpWt;
  repweights ImpRepWt_ : / jkcoefs=nhanesJKCOEFS;
  testeth_gender: test ridreth12, ridreth13, ridreth14,
    ridreth15, riagendr2 ;
run;
```

The parameter estimates and standard errors for the fitted model are presented in the lower right panel of [Table 12.5](#). Using standard SAS “test” syntax for specifying a Wald test of a multiparameter null hypothesis produces the following result:

Linear Hypotheses Testing Results					
Label	F Value	Num DF	Den DF	Pr > F	
testeth_gender	11.48	5	31	<.0001	

Comparing these test results to those obtained from the special MI test of the same hypothesis (see above), the values of the F statistic and the denominator degrees of freedom for the reference distribution differ; however, both tests conclusively reject the null hypothesis that race/ethnicity and gender are not significant predictors of high DBP in U.S. adults.

We note that with appropriate conversion of the PROC SURVEYIMPUTE output data sets to Stata format, the fractionally imputed data could also be analyzed using the Stata commands `svy: tab` and `svy: logistic`.

12.6.5 Comparison of Example Results from Complete Case Analysis, MI, and FEFI

[Tables 12.4](#) and [12.5](#) provide a comparative summary of the results for the two example analyses under complete case analysis (listwise deletion), MI and FEFI approaches to the missing data problem. Looking first at [Table 12.4](#), to three decimal places, a comparison of estimates and CIs for the proportion of adults with high DBP shows only very minor differences. The 95% CIs based on the MI- and FI-imputed data sets are slightly narrower than those for the complete case analysis, but practically speaking, the implications for inference concerning the population proportion, P , are negligible.

Turning to [Table 12.5](#), the upper left panel of [Table 12.5](#) provides estimates of the logistic model parameters (log odds) and standard errors for a complete case analysis in which there is listwise deletion of cases with missing values on the dependent variable or one or more predictors.

Comparable estimates based on the two MI approaches and the FEFI are provided in the remaining three panels. On first observation of the comparative results in [Table 12.5](#), the estimated coefficients in the fitted regression models are not identical—an expected outcome given that the imputation procedures have permitted 503 additional cases with at least one original missing value to enter the analysis. Furthermore, the MI and FI methods differ in their approach to weighting the imputed data and combining the imputed data to produce final estimates. A comparison of the standard errors for the estimated model coefficients for the complete case analysis and

the two MI analyses shows no consistent pattern; however, we do observe that FEFI method standard errors are generally smaller than those for the complete case or MI approaches.

In this particular analysis example, the differences in results for the MI and FI treatments of the missing data are not large enough to lead an analyst to reverse their decision concerning the statistical significance of the individual predictors in the model. Readers should bear in mind that the results of these comparative analyses do not necessarily transfer to other missing data problems with different variables, rates of missing data, or strength of associations among variables in the imputation models.

EXERCISES

12.1 These exercises consider data from the 2011–2012 NHANES. The objective of this set of exercises is to perform a typical imputation and analysis session. The logical steps include examination of missing data, imputation of missing data values using an MI software procedure of choice, and analysis of the imputed data sets using a companion software procedure of choice capable of handling multiply imputed data sets.

Begin by downloading the subset of data from the 2011–2012 NHANES: `c12_exercises_nhanes.dta` or `c12_exercises_nhanes.sas7bdat` (available from the book web site). Note that this data set is limited to adults 18+ years of age and those that completed the NHANES medical examination ($n = 5,615$).

The variables used in the imputation and analysis are: gender (RIAGENDR), BMI (BMXBMI), race/ethnicity (RIDRETH1), age (AGE), total cholesterol (LBXTC), and systolic blood pressure (BPXSY1). The data set also contains the NHANES complex design variables and survey weight (SDMVSTRA, SDMVPSU, WTMEC2YR).

- a. Examine simple descriptive statistics for these variables (means, proportions, ranges, and counts of missing values), keeping in mind that the full n is 5,615. Use a software procedure of your choice for this step.
- b. Pay close attention to the types of the variables with missing data (continuous, ordinal, binary, or nominal) and the amount of missing data, that is, what percent are missing on each variable.
- c. Prepare a table similar to [Table 12.2](#) to outline the missing data problem.

12.2 Using your software of choice and the data from 12.1, examine the missing data patterns that exist in the file.

- a. How many unique missing data patterns exist?
- b. Which variables have some missing data?
- c. Which variables have full data?

- 12.3 Prepare a combined Stratum and PSU variable as demonstrated previously in this chapter, and call this variable STRATA_PSU. This variable should have 31 unique values and should be treated as a categorical variable in your imputation. Prepare and execute syntax to impute the missing values using the software of your choosing. Use the SR/FCS/CE approach for MI. Keep in mind what type of model should be used for the imputation, depending on the type of variable to be imputed. For example, linear regression for continuous variables, ordinal or cumulative logit regression for ordered variables, binary logistic regression for binary variables, and so forth. Use $M = 10$ to prepare 10 imputed data sets during this step, and be sure to use a seed value so that your results can be replicated at a later time.
- a. Provide output from the imputation process and make sure it verifies that 10 imputations were performed and lists the types of imputation models used for the imputed variables.
 - b. What is the name of the variable that identifies the imputation number 1–10? Note that this will depend on the software procedure that you are using.
 - c. How many observations does this “concatenated” file contain? If you changed the number of imputations, how would that impact the number of observations in this file?
 - d. Why do we include the STRATA_PSU and WTMEC2YR variables in the imputation?
- 12.4 Perform an appropriate design-based descriptive analysis of total cholesterol (LBXTC) within each imputed data set (1–10) contained in the concatenated imputed data set. For example, if the imputed variable is continuous, estimate means within each imputed data set using the correct survey weight (WTMEC2YR) and design variables (SDMVSTRA, SDMVPSU), and estimate appropriate standard errors for the estimated means using TSL or a replication technique. Create a table showing the estimated means and proportions (and estimated standard errors) for LBXTC from each imputed data set.
- a. Why do the means change over the 10 data sets? Is this expected?
 - b. Why is this analysis not yet complete and what else should be accounted for in the analysis of imputed data sets?
- 12.5 Next, perform an MI analysis to estimate mean LBXTC and compute a variance estimate for the estimated mean that incorporates the design-based standard errors from the analysis of each imputed data set in addition to the between-imputation variance in the estimates. (Use a command designed to analyze multiply imputed data sets and incorporate the complex sample design features in addition to the variability introduced by imputing the missing values multiple

times. In Stata Version 14+ this command would be `mi estimate`, in SAS it would be PROC MIANALYZE, and in IVEware it would be %DESCRIBE.)

- a. What is the overall estimated mean for systolic blood pressure for all imputed data sets combined?
- b. What is the standard error of the estimated mean, and what has been accounted for in the standard error when using the `mi estimate` modifier with the `svy: mean` command (in Stata) or a similar command in another software package?
- c. Obtain the within- and between-imputation variance components by either calculating these statistics manually or requesting them from the software package of choice (Section 12.6.1).

12.6 Finally, fit a linear regression model with total cholesterol as the dependent variable and age, gender, race, and BMI as predictors. Fit the model first using a standard design-based analysis of complete cases only, and then perform an MI analysis using the software of your choice.

- a. Prepare a table comparing estimated regression parameters and standard errors under the two analysis approaches (complete cases only and MI).
- b. Have the MIs of the item missing values and subsequent MI analysis changed any of your conclusions about the significance of the predictor variables?



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13

Advanced Topics in the Analysis of Survey Data

13.1 Introduction

Chapters 5 through 10 of this book have presented design-based approaches to the most common statistical analyses of complex sample survey data. Models certainly played an important role in defining these analyses, but in each case, the estimation and inferences for population parameters were based on the final survey weights (incorporating unequal probabilities of selection into the sample, nonresponse adjustments and calibration adjustments) and the large sample properties associated with the expected sampling distribution of estimates under repeated sampling from the chosen probability sample design. As described in Section 2.2, the “tried and true” design-based techniques for the analysis of complex sample survey data are appealing because they require minimal assumptions, produce consistent estimates of the target population parameters, and provide robust measures of the sampling variability of the estimates.

Most survey practitioners accept these design-based methods as the method of choice for simple descriptive estimation of population characteristics. Moving to more analytical treatments of survey data such as multiple linear and logistic regression, there has been some controversy over time about the best analytic approaches (Section 3.4 and Theory Box 7.3); however, as a practical choice, most survey analysts today will follow a design-based approach to estimating regression models.

As survey analysis problems move away from the safety of simple descriptive analysis objectives and large sample sizes, the role of explicit statistical models becomes more critical, and today, the cutting edge developments in survey data analysis are focused on *model-driven* approaches to the analysis of survey data. Some common applications in which statistical models must play a role include:

- Survey data with multiple levels (e.g., classrooms within schools), where the relationships among variables measured at different levels of the data hierarchy and the variability among sampled units at

a given level are each substantively important (and accommodated by multilevel or hierarchical linear models [HLMs])

- Longitudinal or repeated measures models (see [Chapter 11](#) for details)
- Latent variable models such as structural equation models (SEMs) and
- Small area estimation

This final chapter will provide a brief overview of important recent developments in several of these areas and describe areas of active and future research. Section 13.2 summarizes current work by survey statisticians who are looking more generally at the role Bayesian models and methods can play in the analysis of survey data sets. Over the past two decades, applications of *generalized linear mixed models* (GLMMs) to multilevel modeling of hierarchical data (e.g., schools, classrooms, students) have grown to be increasingly important. As was discussed in [Chapter 11](#), these models, along with *generalized estimating equation* (GEE) models, are important in the analysis of longitudinal survey data and other survey data sets containing repeated measurements over time from the sampled units. In Section 13.3, we consider multilevel models for *cross-sectional* complex sample survey data with multiple levels of substantive interest. Section 13.4 provides a summary of recent work on the application of latent variable models, such as SEMs, to complex sample survey data, and presents examples of fitting SEMs to complex sample survey data using state-of-the-art software procedures. A brief review of the recent developments in the applications of survey data to *small area estimation* problems is provided in Section 13.4. Finally, nonparametric methods have always been important statistical tools for data analysts, and recently there has been increased interest in theoretical developments and applied research on the application of nonparametric analyses to complex sample survey data. Section 13.5 reviews this recent work on nonparametric methods.

13.2 Bayesian Analysis of Complex Sample Survey Data

We briefly introduce Bayesian approaches to the analysis of survey data in this section. We assume that readers have some prior knowledge of Bayesian analysis methods, and introduce terminology that might seem foreign to some readers without rigorous definitions. We recommend Gelman et al. (2013) for readers who are interested in learning more about Bayesian data analysis techniques.

Many leading survey statisticians see a model-based approach as providing a necessary principled framework for addressing problems in survey inference:

Bayesian methods provide a unified framework for addressing all of the problems of survey inference, including inferences for descriptive or analytical estimands, small or large sample sizes, inference under planned ignorable sample selection methods such as probability sampling, and problems where modeling assumptions play a more central role such as missing data or measurement error.

**R.J.A. Little in Chambers and Skinner
2003**

Briefly, *Bayesian inference* is focused on the *posterior distribution* of some parameter of interest θ (e.g., a population mean), denoted by $p(\theta|y)$, under an assumed model for the observed data y , denoted by $f(y|\theta)$, and a posited *prior distribution* for the parameter θ , denoted by $p(\theta)$. A Bayesian analysis of complex sample survey data involves analyzing the data to obtain a posterior distribution of parameters defining a model of interest, and then using the model to determine a *posterior predictive distribution* for the unobserved elements of the population. Once a posterior predictive distribution is available, predictions on survey variables for elements not included in the sample can be computed, and inferences can be made to the total population.

Complex sample design effects, which recall arise (primarily) from stratification, cluster sampling, and weighting due to differential inclusion probabilities/nonresponse adjustment/calibration adjustment, can be directly modeled or not, depending on the degree to which they are *informative* about the variables of interest in the analysis. Compared to a strictly design-based approach to inference, this is a distinguishing feature of more model-driven approaches. Design-based methods always incorporate weights and design variables such as strata and clusters in the analysis, which ensures robust variance estimation but sometimes leads to losses in efficiency (i.e., larger standard errors). Bayesian methods for survey data analysis do not rely on large sample asymptotic theory; but in exchange, they are heavily model-driven and require many assumptions, especially concerning choices of prior distributions and distributions for the observed data. In addition to the unifying theoretical framework cited in the opening quote in this section, Little (2003) identifies several features that should make the Bayesian approach appealing to survey analysts:

- Standard design-based inference (confidence intervals [CI], test statistics) can be derived in the Bayesian framework using reasonable assumptions concerning the distribution of the data and the prior distribution for the parameter of interest.

- Survey applications typically assume noninformative priors; however, information gleaned from repeated and past surveys could be used to develop informed priors—for example, information on the tails of the distribution that generates outlier values in a single survey.
- When sample sizes are large and diffuse priors apply, Bayesian estimates and posterior probability intervals are similar to design-based estimates and CIs.

As noted above, a Bayesian approach to inference from survey data can, if necessary, directly incorporate the features of the complex sample design in estimation and inference. *Ignorable sampling mechanisms* are important when making inferences based on Bayesian methods. If the sampling mechanism (e.g., stratification variables, measures of size in probability proportionate to size (PPS) sampling, cluster definitions) and the parameter of interest (e.g., mean household net worth) are *a priori* independent, and the sampling indicator (or the probability of inclusion in the sample) is independent of the variable of interest, then the sampling design is *noninformative*. If the sampling indicator depends only on the observed values of survey variables of interest, then the sampling mechanism is *ignorable*. In other words, as long as the unobserved data are not associated with the probability of inclusion in the sample, the design can be labeled as ignorable. Ignorable sampling mechanisms are closely related to the missing at random (MAR) concept ([Chapters 11](#) and [12](#)).

Ignorable mechanisms are important because inferences about the parameter of interest can be made without explicitly modeling the sampling mechanism. So how does one make a complex design “ignorable” when using a Bayesian inference approach to an analysis? Incorporating stratification and cluster sampling is relatively straightforward in Bayesian models, and is quite similar to how design effects are handled in multilevel modeling approaches. Effects of sampling strata are generally treated as fixed (or parameters to be estimated), and effects of sampling clusters are treated as random. Introducing these effects in Bayesian models makes the complex design ignorable. However, there are many modeling issues that arise: there could be a loss of degrees of freedom if there are many strata; one could decide to only include “significant” stratum effects; one could choose to use covariates on which the strata were based rather than indicators for the strata themselves; and one has to posit a distribution for the random cluster effects, including an assumption of whether the random effects are independent of the residual errors. None of these issues are truly unique to Bayesian approaches, and they are all shared with more model-based multilevel modeling approaches (Section 11.2.3.1).

Bayesian analysis methods are mathematically and computationally intensive, and often require simulations to determine posterior distributions. A popular choice for estimating a posterior distribution is the *Gibbs*

sampling technique (see Gelman et al., 2013, for an overview). The hardest aspect of performing Bayesian analyses of complex sample survey data is properly accounting for unequal probabilities of selection via sampling weights (Gelman, 2007). This is currently an active area of research. Current suggestion for maintaining the ignorability assumption when selection probabilities are unequal is to allow model parameters to vary as a function of selection probabilities (i.e., include interactions of predictors with selection probabilities in models), or stratify by selection probabilities (Holt and Smith, 1979). Zheng and Little (2005) proposed an estimation method based on penalized splines for estimating totals from PPS sampling designs, where selection probabilities are known for all population members, and show promising properties of their method compared to more standard model-based approaches.

Si et al. (2015) recently presented a novel approach that employs Bayesian methodology to make robust finite population inferences about means or proportions of interest in the scenario when only final survey weights (and no stratum or cluster codes) are provided for the respondents in a public-use survey data set (e.g., the Monitoring the Future Study; see Miech et al., 2016). This model-based approach simultaneously predicts the distribution of the weights among *non-sampled* cases in the population of interest and the values of the survey variable of interest for these cases (as a function of the weights), enabling simulations of the full population means or proportions based on posterior distributions for these descriptive parameters (given the sampled cases and their data). These authors demonstrated the advantages of this approach relative to classical design-based methods (e.g., Chapter 5) in terms of the efficiency of descriptive finite population estimates, for both full populations and subpopulations. The authors implemented this approach in the popular Stan software for Bayesian analysis, and we have provided annotated example code implementing this approach on the book's web site.

Little (2015) outlined an inferential paradigm for finite population inference that he refers to as "Calibrated Bayes." This approach involves using Bayesian methods for finite population inference that explicitly incorporate complex sampling features into the models, and making sure that the resulting estimates have good repeated-sampling (or "frequentist") properties. Even more recently, Zhou et al. (2016a,b) have developed Finite Population Bayesian Bootstrap (FPBB) inference approaches for complex samples in the context of imputation of item-missing data. These authors propose to "uncomplex" complex sample survey data by first using Bayesian methods to simulate data for a *population* of interest based on the data set in hand (accounting for weighting, cluster sampling, etc.), and then applying straightforward methods for simple random samples (SRS) to impute missing values and analyze the simulated population data. These authors provide R code for implementing their approach in Zhou et al. (2016b). Their FPBB method is also now available as an option in the latest release of IVEware (Raghunathan et al., 2016; Chapter 12).

Because fully weighted estimators reduce bias at the cost of increasing sampling variance, a compromise is often required, and various *weight trimming* approaches (Potter, 1990), or methods of reducing extreme weights without introducing severe bias (i.e., keeping the mean squared error relatively small), have been developed for the Bayesian analysis framework. Holt and Smith (1979) proposed a Bayesian approach to estimating means where the means of strata defined by sampling weights (or inverses of probabilities of selection) were treated as random variables (or random effects), and showed that this approach had the effect of “smoothing” the sampling weights (as opposed to weight trimming). Elliott and Little (2000) built on this approach for estimation of means, showing improved performance of a weight smoothing model based on a nonparametric spline function for the underlying means of the strata based on the sampling weights. Elliott (2007) expanded this “weight smoothing” method to linear and generalized linear models (GLM).

There are presently a variety of statistical software options enabling Bayesian analysis of complex sample survey data using the approaches outlined above (which can each be applied in a general Bayesian inference framework). The BUGS software (Bayesian Inference Using Gibbs Sampling)* is currently a popular tool for Bayesian data analysis and is capable of fitting some of the models discussed in this section using a multilevel modeling approach (see Gelman and Hill, 2006, for nicely worked examples). Recent years have seen the continued development of the Stan software (<http://mc-stan.org>), which can be used to analyze complex sample survey data using Bayesian methods (see http://rpubs.com/corey_sparks/157901 for a worked example). Software implementing the “weight smoothing” approaches discussed above is also freely available.[†] We will continue to provide links and updates on any developments in terms of statistical software for Bayesian analysis of complex sample survey data on the book web site.

13.3 GLMMs in Survey Data Analysis

13.3.1 Overview of GLMMs

GLMMs comprise a broad class of regression-type models that include a number of specific analytic forms, such as *HLMs* or *multilevel models*, models for *repeated measures* on individuals, or *growth curve models* of longitudinal change in individual attributes (Chapter 11). We use the adjective “generalized” to acknowledge that linear mixed modeling techniques are now available for continuous, nominal, ordinal, and count-type data. GLMMs

* <http://www.mrc-bsu.cam.ac.uk/bugs/>

† <http://www.sph.umich.edu/~mrelliot/trim/trim.htm>

are *subject-specific models* that analyze the influence of both *fixed effects* and *random effects* on individual attributes. The label “subject-specific” refers to the fact that GLMMs are modeling the relationships of specific covariates with a dependent variable of interest *for a given higher-level unit*, by explicitly controlling for the random effects of randomly sampled individuals (higher-level units in a longitudinal study) or clusters of observations (higher-level units in a cross-sectional study). This is in contrast to the *marginal modeling* or *population averaged* approach that is employed by the GEE technique. This modeling technique is an alternative for the analysis of repeated measures or other dependent sets of observations on population units that does *not* explicitly incorporate random subject effects, and adjusts standard errors for the clustering present in the observations in a manner similar to Taylor Series Linearization (TSL) (using robust *sandwich estimates* of standard errors).

Following Fitzmaurice et al. (2004), a general expression for the GLMM is:

$$g\{E(Y_{it} | b_i)\} = \eta_{it} = \mathbf{X}_{it}\boldsymbol{\beta} + \mathbf{Z}_{it}\mathbf{b}_i, \quad (13.1)$$

where:

$g(\cdot)$ = a known link function, often identity (Normal) but also log (Poisson) or logistic ([Chapters 8 and 9](#)).

\mathbf{X}_{it} = row vector of $j = 1, \dots, p$ covariates for subject i , at observation $t = 1, \dots, T$.

$\boldsymbol{\beta}$ = vector of $j = 1, \dots, p$ fixed effects regression parameters.

\mathbf{Z}_{it} = row vector of $k = 1, \dots, q$ covariates for subject i , at observation $t = 1, \dots, T$.

\mathbf{b}_i = vector of $k = 1, \dots, q$ random effects.

From this general expression, more specific expressions for individual models may be derived. For example, a simple *random intercept model* for change in a continuous random variable, y , over times $t = 1, \dots, T$, can be written as follows:

$$\begin{aligned} y_{it} &= \mathbf{X}_{it}\boldsymbol{\beta} + b_i + e_{it} \\ &= (\beta_0 + b_i) + \beta_1 x_{it,1} + \dots + \beta_p x_{it,p} + e_{it}, \end{aligned} \quad (13.2)$$

where:

$b_i \sim N(0, \tau^2)$ = random effect for individual i .

$e_{it} \sim N(0, \sigma^2)$ = random error term.

$cov(b_i, e_{it}) = 0$.

The notation in the general expression (13.2) suggests a GLMM for modeling multiple dependent observations on a single individual, such as longitudinal measures in a panel survey (Fitzmaurice et al., 2009; see also [Chapter 11](#)). However, by using slightly different subscripts, we can show that the GLMM also represents a model where the dependency is not among repeated

observations on a single individual but among units that are clustered in a hierarchical data set. Consider for example a survey such as the National Assessment of Educational Progress (NAEP), where measures on individual students are nested within randomly sampled schools. The random intercept model can be rewritten to model fixed effects on individual student test performance, $y_{i(s)}$, while accounting for the random effects of the school clusters:

$$\begin{aligned} y_{i(s)} &= \mathbf{X}_{i(s)}^T \boldsymbol{\beta} + b_s + e_{i(s)} \\ &= (\beta_0 + b_s) + \beta_1 x_{i(s),1} + \cdots + \beta_p x_{i(s),p} + e_{i(s)}, \end{aligned} \quad (13.3)$$

where:

$b_s \sim N(0, \tau^2)$ = random effect for school s .

$e_{i(s)} \sim N(0, \sigma^2)$ = random error term.

$\text{cov}(b_s, e_{i(s)}) = 0$.

The literature generally refers to models such as 13.3 that incorporate dependence among observations due to hierarchical clustering of the ultimate observational units as *HLMs* or *multilevel models* (Raudenbush and Bryk, 2002; Goldstein, 2003). Because the dependence among observations results from hierarchical levels of clustering, HLMs are often described by decomposing the fixed and random components for the overall GLMM into models for the individual levels. For example, consider the simple model (13.3) for test scores where clusters of students are nested within schools. The Level 1 model is the model of the student test outcome, controlling for the effects (which may be school-specific) of covariates for that student. Note that the Level 1 model below allows the intercept and the effects of the student-level covariates to be unique to the sampled schools:

Level 1:

$$y_{i(s)} = \beta_{0(s)} + \beta_{1(s)} x_{i(s),1} + \cdots + \beta_{p(s)} x_{i(s),p} + e_{i(s)}. \quad (13.4)$$

Level 2 of the multilevel specification defines equations for each of the random school-specific coefficients in the Level 1 model. In the case of Equation 13.3, only the intercept randomly varies across sampled schools. For example, suppose that the school-specific intercept is defined by the fixed overall intercept, β_0 , and the random school effect, b_s , while the effects of the covariates are fixed across schools (i.e., defined by fixed effect parameters only):

Level 2:

$$\beta_{0(s)} = \beta_0 + b_s$$

$$\beta_{1(s)} = \beta_1$$

...

$$\beta_{p(s)} = \beta_p.$$

$$(13.5)$$

A complete treatment of GLMMs is beyond the scope of this intermediate-level book on applied survey data analysis. There are many texts that describe the theory and applications of GLMMs in detail, including (in no particular order) Diggle et al. (2002), Gelman and Hill (2006), Fitzmaurice et al. (2004), Verbeke and Molenberghs (2000), Molenberghs and Verbeke (2005), West et al. (2014), Raudenbush and Bryk (2002), and Goldstein (2003). Our objective here is to acquaint the reader with GLMMs, introduce several key issues in the application of these models to complex sample survey data, and describe current research findings that address these issues. Throughout the following discussion, we will focus on cross-sectional data arising from a stratified multistage sample design. We will refer to individual survey respondents as Level 1 units, and the sampled clusters within which the survey respondents are nested as Level 2 units. Readers interested in multilevel models for longitudinal survey data should refer to [Chapter 11](#).

13.3.2 GLMMs and Complex Sample Survey Data

As was mentioned above, GLMMs are specifically designed to address nonindependence or “dependency” of observations. In HLMs, the dependency arises because observational units are hierarchically clustered, such as students within classrooms and classrooms with schools. In repeated measures or longitudinal models, the dependency arises because observations are clustered within individuals—for example, daily diaries of food intake for National Health and Nutrition Examination Survey (NHANES) respondents, or longitudinal measures of household assets for Health and Retirement Study (HRS) panel respondents ([Chapter 11](#)).

This problem of lack of independence for observations should sound familiar. The design-based survey data analysis techniques that have been the core subject of this book are constructed to address the intraclass correlation among observations in sampled clusters. It is natural to draw the analogy between these two estimation problems. Take, for example, two parallel sets of data. The first data set records scores on a test administered to students who are clustered within classrooms, schools, and school districts. The second data set includes test scores for the same standardized test administered to a probability sample of students in their homes, where households were selected within area segments and primary sampling units (PSUs) of a multistage national sample design. In both cases, there is a hierarchical ordering of units—districts, schools, classes, and students in the first case, and PSUs, area segments, households, and students in the second case.

If the survey analyst was only interested in inferences concerning national student performance on the standardized test, robust inferences could be obtained using standard design-based estimates of population parameters (such as the mean test performance) and their standard errors (see, e.g., [Chapter 5](#)). School districts would define the ultimate clusters in the first data set, and PSUs would form the ultimate clusters of the second. However,

the survey analyst using the first data set may have broader analytic goals. Specifically, he/she may be interested in estimating the proportion of variance in test scores that is attributable to the student, the class, the school, and the district. The analyst working with the second data set may not be especially interested in the *components of variance* associated with PSUs, secondary sampling units (SSUs) within PSUs, households, and individuals. The first analyst will likely pursue a *model-based analysis*, specifying an HLM form of the GLMM. Following this approach to the analysis of complex sample survey data, the first analyst would specify the best possible probability model for the data set in hand, which includes the specification of an appropriate random effects structure to reflect the multistage cluster sampling and estimate the variance components of interest. The variance of the estimated parameters in this case would be estimated with respect to the specified model, and if the weights and stratum codes were associated with the dependent variable of interest, these would also need to be accounted for in the model specification. The second analyst will be satisfied with a standard *design-based analysis*, in which weighted estimates of the parameters of interest are computed, and TSL or replication estimates of the overall variance of the sampling distribution (computed with respect to the sample design) are used to develop CIs and test statistics. Interested readers can refer to Hansen et al. (1983) for more discussion of the differences between model-based and design-based approaches.

Consider another problem in which a cluster sample of individuals is asked whether they have experienced any hay fever symptoms in the past week. The dependent variable for each individual is an indicator of whether they experienced hay fever symptoms ($y_{ij} = 1$) or did not ($y_{ij} = 0$), where i indexes individuals and j indexes ultimate clusters. The independent variables in the analysis might include age, gender, and an indicator of a previous allergy diagnosis. To estimate the relationship of hay fever symptoms with age, the survey analyst could choose among three approaches that all use variants of logistic regression modeling:

1. A cluster-specific model-based analysis using a GLMM, in which the $\text{logit}[P(y_{ij} = 1)]$ is modeled as a function of *fixed effects* that include the constant effects of age, gender, and previous allergy diagnosis, and *random effects* of the randomly sampled ultimate clusters (enabling estimation of between-cluster variance).
2. A marginal model-based analysis using a GEE model, in which the logit model relating symptoms to the covariates is estimated using GEE methods and the covariance matrix for the model coefficients is separately estimated using the robust Huber–White *sandwich estimator* (Diggle et al., 2002).
3. A marginal design-based analysis using a program/command/procedure such as Stata's `svy: logit` command, with a single

record for each individual, multiple individuals (rows) per ultimate cluster, and the ultimate clusters identified as the “clusters” for variance estimation purposes (see, e.g., [Chapter 8](#)).

The GLMM analysis is a cluster-specific analysis, explicitly controlling for the random cluster effects, and would yield estimates of the fixed effects (or regression parameters) associated with the covariates *in addition to* estimates of the variance of the random cluster effects. The GEE and svy: logit approaches are population-averaged (or marginal) modeling techniques and would provide comparable estimates of robust standard errors for the estimated logistic regression coefficients for the covariates. The GEE and design-based population-averaged approaches would *not* separately estimate the variance of the random cluster effects or their contributions to the total sampling variability. This is the key distinction between these alternative approaches to analyzing clustered or longitudinal data: GLMMs enable analysts to make inferences about between-subject (or between-cluster) variance, based on the variances of the subject-specific (or cluster-specific) random effects explicitly included in the models, while GEE and design-based modeling approaches are only concerned with overall estimates of parameters and their total sampling variance.

It is increasingly common to see survey samples designed to be optimal for analysis under a GLMM-type model. For example, a multistage national probability sample of school districts, schools, classrooms, and students could be consistent with a GLMM model that would enable the education researcher to study the influence of each level in this hierarchy on student outcomes. To achieve data collection efficiency, the sampling statistician designing the sample of individuals for the hay fever study could select a primary stage sample of the U.S. counties and then a sample of individuals within each primary stage county. The result would be a two-level data set with individuals nested within the sampled counties.

However, even when care is taken to design a probability sample to support multilevel or longitudinal analysis using GLMM-type models, there are several theoretical and practical issues to be addressed when fitting these models to complex sample survey data:

1. *Stratification*: If the stratification used in the sample selection (regions, urban/rural classification, population size, etc.) is *informative*, that is, associated with the survey variables of interest (which is typically the case in practice), the stratum identifiers, or at a minimum the major variables used to form the strata, will need to be included as fixed effects in the model.
2. *Cluster sampling*: In the general sample design context, clustering of population elements serves to reduce the costs of data collection. The increase in sampling variance attributable to the intraclass correlation

of characteristics within the cluster groupings is considered a “nuisance,” inflating standard errors of estimates to no particular analytical benefit. In the context of a specific analysis involving a hierarchical linear (or multilevel) model, the clustering of observations is necessary in order to obtain stable estimates of the effects and variance components at each level of the hierarchy. Ideally, the sample design clusters may be integrated into the natural hierarchy of the GLMM and the cluster effects on outcomes can be directly modeled using additional levels of random effects—say nesting students within classrooms, classrooms within schools, and schools within county PSUs.

3. *Weighting:* Conceptually, one of the more difficult problems in the application of GLMMs to complex sample survey data is how to handle the survey weights. Theoretically, if the weights were *non-informative*, they could be safely omitted from the model estimation. If the sample design and associated weights are *informative* for the analysis, fixed effects of the variables used to build the weights or appropriate functional forms of the weight values themselves could be included in the model (DuMouchel and Duncan, 1983; Little, 1991; Korn and Graubard, 1999, Section 4.5; Fuller, 2009, [Chapter 6](#)). But there are other complications with weighting in GLMMs, as we discussed in [Chapter 11](#). Attrition adjustments that are often included in longitudinal survey weights can yield different weight values for each measurement time point. Clusters in a multistage sample design may not enter the sample with equal probability. Even in a national equal probability multistage sample of students, the most efficient samples require that counties and school units are selected with PPS. Conditional on a given stage of sampling, the observed units would enter with varying probability.

In this section, we focus on approaches for fitting GLMMs to cross-sectional complex sample survey data that use the weights associated with different randomly sampled units to define the (pseudo) likelihood function for the observed data. These approaches are identical to the approaches outlined in [Chapter 11](#) for weighted multilevel modeling, with the difference being that Level 1 units are generally survey respondents (rather than different time points), and the Level 2 units are generally ultimate clusters (rather than individuals in a longitudinal survey):

- Survey weights for the Level 1 respondents need to reflect probabilities of selection *conditional* on the higher-level ultimate cluster to which the respondent belongs being selected into the sample (including possible adjustments for nonresponse).
- The (adjusted) conditional weights for Level 1 respondents need to be appropriately scaled within Level 2 ultimate clusters, with the “normalizing” approach (which ensures that the sum of the scaled

weights within a given ultimate cluster is equal to the sample size for that cluster) generally serving as a good multipurpose approach for estimation (Pfeffermann et al., 1998; Rabe-Hesketh and Skrondal, 2006; Carle, 2009).

- Survey weights for the sampled Level 2 ultimate clusters, reflecting the probabilities of selection for the clusters, need to be accounted for in the (pseudo) likelihood function as well (much like the “baseline” weights for sampled individuals at Level 2 in [Chapter 11](#)); see Pfeffermann et al. (1998) or Rabe-Hesketh and Skrondal (2006) for the technical details underlying this requirement.

We use the weights associated with different levels of the data hierarchy to compute unbiased estimates of both the fixed effects and the variance components in a given GLMM. Ideally, such estimates will be unbiased with respect to both the sample design and the model being specified (Pfeffermann, 1993). A failure to use the weights associated with Level 2 ultimate clusters, for example, could lead to biased estimates of the variance components describing between-cluster variability in the larger population. This makes it essential for these weights to be included in a given survey data set if analysts of those data will be interested in fitting GLMMs. The use of the weights in estimation provides some protection against model misspecification, as discussed in [Chapter 7](#); estimates of the fixed effects and variance components in a given GLMM will still be unbiased with respect to the sample design if a model has been misspecified. Importantly, the weights associated with Level 1 respondents need to be conditional, as indicated above. A failure to use these conditional weights (e.g., if an analyst were to use the *overall* survey weights reflecting all stages of sample selection that are typically provided in public-use survey data sets) could lead to bias in the estimates of multilevel model parameters (Pfeffermann et al., 1998).

When using the weights associated with all randomly sampled units to define the pseudo-likelihood function used to estimate the parameters in a given GLMM, the variances of the maximum likelihood estimates can be computed using a variation of TSL developed by Binder (1981, 1983) for GLMs fitted to complex sample survey data ([Chapter 8](#)). This variance estimation approach can explicitly account for multistage stratified cluster sampling, and is sometimes referred to as a robust, sandwich-type approach to computing standard errors in the software that implements these approaches. Pfeffermann et al. (1998) and Rabe-Hesketh and Skrondal (2006) provide technical details regarding these variance estimation approaches.

13.3.3 Alternative Approaches to Fitting GLMMs to Survey Data: The PISA Example

We now consider an example of fitting a GLMM to cross-sectional survey data arising from a complex sample design. These data come from the 2000

Program for International Student Assessment (PISA), and were also analyzed by Rabe-Hesketh and Skrondal (2006) using the `gllamm` command that they developed for Stata (www.gllamm.org). The dependent variable of interest in this case (ISEI) is continuous, and measures the socioeconomic status (SES) of a given student. The predictor variable of interest in this case is COLLEGE (an indicator of whether the highest level of education for either parent is college). Also included in the data set (freely available online for Stata users) is an ID code for the sampled school (the PSU in the case of this sample design), the overall final student weight (not conditional!), or `W_FSTUWT`, and a final school weight (`WNRSCHBW`). The data can be loaded into Stata's working memory using the following command:

```
use http://www.stata-press.com/data/r13/pisa2000
```

We desire to fit the following GLMM to these data:

$$\begin{aligned} ISEI_{ij} &= \beta_0 + \beta_1 \text{COLLEGE}_{ij} + u_{0j} + u_{1j} \text{COLLEGE}_{ij} + e_{ij} \\ \begin{pmatrix} u_{0j} \\ u_{1j} \end{pmatrix} &\sim N\left(\begin{pmatrix} 0 \\ 0 \end{pmatrix}, \begin{pmatrix} \sigma_0^2 & 0 \\ 0 & \sigma_1^2 \end{pmatrix} \equiv D\right) \\ e_{ij} &\sim N(0, \sigma^2). \end{aligned}$$

We note that this model includes two random effects (u_{0j} and u_{1j}), allowing each school (denoted by j) to have a unique intercept and a unique relationship of COLLEGE with ISEI. The random effects are assumed to follow a bivariate normal distribution, with mean vector 0, unique variance components for each random effect, and zero covariance. The random errors are assumed to follow a normal distribution with constant variance. We desire to compute weighted estimates of the two fixed effects and the two variance components for the PISA target population. The intercept represents the expected ISEI for students who do not have any college-educated parents, the fixed effect for COLLEGE represents the change in the expected ISEI for students with college-educated parents, and the variance components describe variation among the schools in the intercepts and the college effects, respectively.

We first use the `mixed` command in Stata (appropriate for the approximately normal dependent variable) to fit a standard GLMM for comparison purposes, completely ignoring the weights:

```
mixed isei college || id_school: college, ///
covariance(independent) variance
```

We note in this syntax that the dependent variable (ISEI) is listed first, followed by the predictor variable. The two vertical bars indicate the first level of clustering, which is defined by the values of `ID_SCHOOL`. The inclusion of COLLEGE after a colon following the cluster identifier means that the effects

of this predictor are allowed to randomly vary across clusters (schools), and a random intercept will be included in the model by default. The covariance structure for the two random effects is independent (meaning that they have zero covariance), and estimates of variance components are desired in the output (instead of the default standard deviations). The estimates of the parameters in this model are included in [Table 13.1](#).

Next, we fit a model including a fixed effect of the final overall student weight, but not using the weights to estimate the parameters of interest:

```
mixed isei college w_fstuwt || id_school: college, ///
covariance(independent) variance
```

Estimates of the parameters in this model are included in [Table 13.1](#) as well.

We now fit the model of interest using the weights to define the pseudo-likelihood function (and thus computing weighted estimates of the parameters of interest). We first compute the conditional student weight by dividing the final student weight (accounting for all probabilities of selection) by the final school weight. We then fit the model of interest, specifying (1) the conditional student weights, via the [pweight = ...] option; (2) the final school weights, via the pweight() option after the cluster identifier; and (3) the weight scaling method, which in this case is "size" for the "normalizing" method. We also fitted the model using the "effective" weight scaling method ("Method 1" in Pfeffermann et al., 1998), and the results were virtually identical (as suggested by Carle, 2009).

```
gen conwt = w_fstuwt / wnrscbw

mixed isei college [pw = conwt] || id_school: college, ///
covariance(independent) variance pweight(wnrscbw) pwscale(size)
```

TABLE 13.1

Parameter Estimates (and Standard Errors) from the Different Multilevel Modelling Approaches for the PISA Data

Parameter	No Weights	Weights as a Covariate	Scaling Method 1: Effective	Scaling Method 2: Size
<i>Fixed Effects</i>				
Intercept	38.79 (0.62)	36.82 (1.14)	35.89 (0.91)	35.89 (0.91)
COLLEGE	12.65 (0.90)	12.60 (0.90)	14.28 (1.42)	14.28 (1.42)
WEIGHT		<0.01 (<0.01)		
<i>Variance Components</i>				
Var(Intercepts)	16.14 (5.45)	13.94 (5.22)	17.74 (6.43)	17.79 (6.43)
Var(College)	43.12 (10.85)	42.26 (10.58)	41.03 (13.74)	41.06 (13.73)
Var(Residuals)	219.33 (7.20)	219.92 (7.22)	214.96 (12.82)	214.92 (12.84)
Pseudo Log(L)	-8,611.88	-8,609.91	-1,439,307.8	-1,443,258.0

The results from fitting this model are also included in [Table 13.1](#). Examining the results from the different approaches, we can make the following conclusions:

- Parental college education has a strong positive effect on mean SES, regardless of the method used.
- The weighted estimates of the fixed effects are different from the unweighted estimates, especially so for the intercept (i.e., the mean for students with non-college-educated parents).
- Including the final student-level weight as a covariate changes interpretations of parameters, as the intercept now corresponds to the mean for someone with weight equal to zero (using weight deciles, for example, may be a more effective approach).
- The weighted estimates of the variance components also differ:
 - There is more evidence of variability across schools in the means for students with non-college-educated parents (i.e., the random intercepts) when computing weighted estimates.
 - There is less variability in college versus non-college gaps (i.e., the random coefficients) across the sampled schools.
- Different weight scaling methods do not result in different estimates or conclusions; in this case, one would use the “size” method (Method 2), as per Carle (2009).
- The robust, sandwich-type standard errors for the weighted estimates are generally larger, as expected, but this does not change the overall inferences.

We provide code for fitting the same model using other software (e.g., Mplus) on the book’s web site.

This worked example has illustrated the importance of examining the sensitivity of GLMM results to alternative estimation approaches. In this example, our inferences were generally quite similar whether the weights were used or not, suggesting that these weights were not especially informative about the parameters in this model. This will not always be the case for different surveys (e.g., West et al., 2015); for example, a recent series of simulation studies by Zheng and Yang (2016) in an *item response theory* (IRT) context demonstrates the importance of accounting for survey weights when using multilevel models for IRT investigations. Existing software makes it very straightforward to perform these kinds of analyses examining the sensitivity of estimated parameters in multilevel models to the use of survey weights for estimation.

In addition to assessing changes in parameter estimates due to the use of weights, assessment of changes in estimated standard errors when fully accounting for the complex sampling features is also important. In this

regard, Stapleton and Kang (2016) evaluate design effects for weighted parameter estimates in multilevel models fitted to educational survey data. These authors found that ignoring complex sampling features (i.e., stratification and cluster sampling) in variance estimation *above and beyond* the levels being modeled (e.g., fitting a weighted multilevel model with students nested within schools, but ignoring higher-level PSUs, such as school districts, or counties; see Rabe-Hesketh and Skrondal, 2006) generally has a minor impact on inferences, and that accounting for the fixed effects of stratum identifiers at Level 2 of a given multilevel model (for higher-level clustering units, such as schools) is a reasonable strategy for inferential purposes.

13.4 Fitting Structural Equation Models to Complex Sample Survey Data

Analysts of survey data, and particularly social scientists, are often interested in fitting SEMs to the data, exploring complicated direct and indirect relationships between variables and testing causal hypotheses in complex theoretical models. There are a number of complete texts devoted to structural equation modeling, latent variable modeling, and related methods (including *confirmatory factor analysis* [CFA] and *exploratory factor analysis* [EFA]). For a good practical introduction to these techniques, we recommend Kline (2015) or Schumacker and Lomax (2004). For more theoretical background on SEMs, readers can turn to the classic text from Bollen (1989).

Relatively recent statistical and technical developments have enabled analysts to fit SEMs to complex sample survey data sets using readily available statistical software, and to make inferences based on those models that correctly adjust for complex sampling features. Much of the pioneering work in this area has been done by the authors of the *Mplus statistical software* (<http://www.statmodel.com>). Some of the most fundamental work introducing methods for fitting SEMs to complex sample survey data can be found in an article by Muthén and Satorra (1995), who established a theoretical framework for fitting design-adjusted models and making inferences based on those models. These authors describe how the final survey weights should be used in estimation of SEMs, and outline methods for computing design-based standard errors for weighted estimates of SEM parameters that reflect complex sampling features. Stapleton (2006) provides a practical overview of these approaches, including the relevant theory and examples using the LISREL software. In this section, we will present illustrations of fitting SEMs to complex sample survey data using existing procedures in Mplus and Stata, and we will also discuss software procedures in other packages that can be used to fit these models.

The approach to computing weighted estimates of SEM parameters involves three broad steps. Generally speaking, when fitting SEMs, one tries to find

estimates of the SEM parameters that minimize the differences between the variances and covariances of observed variables *implied* by the specified SEM, and the actual sample variances and covariances of the observed variables. When fitting these models to complex sample survey data, the first step involves computing *weighted* estimates of the variances and covariances of the observed variables for use in estimation. Then, given a hypothesized SEM, one defines a weighted estimate of the population log-likelihood function for the observed data, where each individual respondent's contribution to the log-likelihood is weighted by their final survey weight (similar to the pseudo-likelihood approach outlined in [Chapters 8 and 9](#)). This population log-likelihood function will include the weighted estimates of the variances and covariances of the observed variables (essentially the “observed data” that is input to the estimation process); minimizing the log-likelihood essentially amounts to finding the parameter estimates that minimize the aforementioned difference between the model-implied and observed covariance matrices. The key difference is that the weights are accounted for when defining this log-likelihood function, given the specified model and the observed variables. See Stapleton (2006, p. 36) for additional details on this estimation process.

Given weighted estimates of the parameters defining a SEM (e.g., path coefficients, variances of error terms, covariances of latent variables, etc.), one then needs to compute estimates of standard errors for the weighted estimates that reflect the complex sampling features. Muthén and Satorra (1995) outlined procedures for variance estimation based on TSL, and demonstrated the superiority of their proposed approach over competing variance estimation approaches. A key message arising from this work was that variance estimates for weighted estimates of parameters in a given SEM can be *extremely biased* if the complex sampling features are not correctly accounted for (e.g., assuming that one is working with a simple random sample). Stapleton (2006) used simulation studies to reiterate the advantages of this pseudo-likelihood approach and subsequent nonparametric variance estimation for minimizing the bias in the parameters estimates and ensuring that variance estimates reflect complex sampling features.

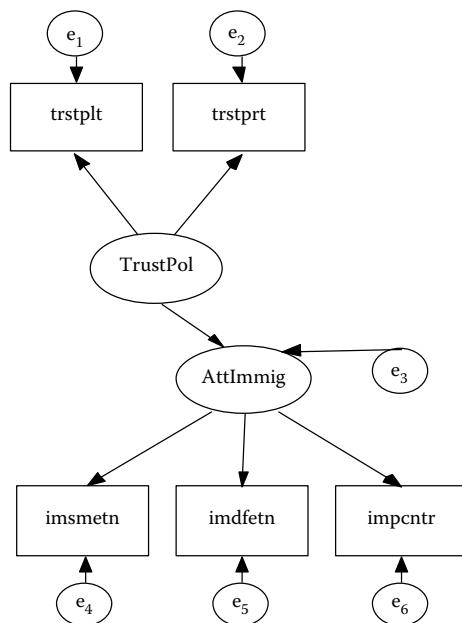
Fitting SEMs also involves the assessment of several different types of model information criteria and/or model fit statistics. The standard chi-square test statistic used to assess the overall differences between the model-implied variances and covariances and the direct weighted estimates of the variances and covariances needs to be adjusted in a manner similar to that described in [Chapter 6](#) for categorical data analysis. This adjustment involves division of the test statistic by the “average design effect” for the estimates involved in the analysis, following the Rao–Scott methodology introduced in [Chapter 6](#). Other commonly used measures of goodness of fit (GOF) for SEMs (e.g., root mean square error of approximation [RMSEA], comparative fit index [CFI]) can be easily adapted to fully account for complex sampling features, and we will demonstrate computation of these measures in the forthcoming illustrations.

In terms of available software implementing these approaches for fitting SEMs to complex sample survey data, we are aware of only six packages that make this possible at the time that this second edition is being written: Mplus, Latent GOLD, Stata (Version 14+), LISREL, the lavaan.survey package in R (Oberski, 2014), and the user-written add-on PROC LCA for the SAS software (for latent class analysis; see <https://methodology.psu.edu/downloads/proclcalta>). Interested readers can find multiple examples of using Mplus to fit these models in Chapter 9 of the Mplus documentation (Muthén and Muthén, 2015). As mentioned earlier, we will now consider some illustrations using both Mplus and Stata.

13.4.1 SEM Example: Analysis of ESS Data from Belgium

We now consider an example of fitting an SEM using a design-based approach. We analyze data collected from a probability sample of 1,703 adults as part of the European Social Survey (ESS) in Belgium, and we focus on a specific subset of all of the variables measured. Included in this data set (available on the book's web site) is a survey weight variable representing the inverse of an area-specific response rate (WEIGHT), along with a sampling cluster identifier for variance estimation purposes (PSU). Our overall research question concerns whether a latent construct representing a person's overall trust in politicians and political parties is predictive of a second latent construct representing a person's general attitude toward immigration. The latent trust in politicians/political parties construct is thought to be indicated by two observed variables in the ESS: trust in politicians (TRSTPLT, ranging from 0 to 10 with 88 representing missing data) and trust in political parties (TRSTPRT, ranging from 0 to 10 as well). The latent construct capturing a person's general attitude toward immigration is thought to be indicated by three observed variables in the ESS: IMSMETN (the country should allow few/many immigrants of the same race/ethnicity as the majority, where 1 = few and 4 = many, and 8 = missing), IMDFETN (" of different race/ethnicity "), and IMPCNTR (" from poorer countries outside Europe). The overall SEM of interest is displayed in Figure 13.1.

Before fitting this SEM, we first apply the method of Raykov et al. (2015) to compute a weighted estimate of Cronbach's *alpha coefficient* for each set of observed variables. This weighted estimate of the coefficient alpha captures the approximate composite reliability of the items indicating each construct that one would see if the whole target population had been measured (see the additional discussion about alpha following the illustration below). This method also enables computation of a 95% CI for the coefficient alpha for each set of observed variables. This approach is possible using the Mplus software, and we include the Mplus code below from Raykov et al. (2015) that can be used to compute these two weighted estimates of alpha, along with supplemental R code to form CIs for the two alpha coefficients given the weighted estimates of alpha and their (linearized) standard errors. First, we focus on estimation of Cronbach's alpha for the three observed immigration attitude variables:

**FIGURE 13.1**

Structural equation model fitted to the ESS Belgium data.

```

TITLE: WEIGHTED ESTIMATION OF IMMIGRATION ALPHA;
DATA:           FILE = M:\immig.dat;
VARIABLE:      NAMES = psu trstplt trstprt imsmetn imdfetn
               impcntr weight;
USEV = psu imsmetn imdfetn impcntr weight;
MISSING = ALL(8);
WEIGHT = weight;
CLUSTER = psu;
ANALYSIS:     TYPE = COMPLEX;
ESTIMATOR = MLR;
MODEL:
F1 BY imsmetn@1;
F2 BY imdfetn@1;
F3 BY impcntr@1;
imsmetn@0;
imdfetn@0;
impcntr@0;
F1-F3 (P1-P3);
F1 WITH F2-F3 (P12-P13);
F2 WITH F3 (P23);
MODEL CONSTRAINT:
NEW(ALPHA);
ALPHA = 1.5*2*(P12+P13+P23)/(P1+P2+P3+2*(P12+P13+P23));
OUTPUT:        CINTERVAL;
  
```

Running this code in Mplus produces the output shown below:

New/Additional Parameters				
ALPHA	0.880	0.010	91.631	0.000

The weighted estimate of alpha for the immigration variables is 0.880, with a linearized standard error of 0.010. We then use the R code below to form a 95% CI for this coefficient alpha:

```
ci.alpha_in_cds = function(alpha, se)
{
  l = log(alpha/(1-alpha)) # use logit
  # transformation first
  sel = se/(alpha*(1-alpha)) # get SE of logit of alpha
  ci_l_lo = l-1.96*sel # lower and upper endpoint
  # of 95%-CI
  ci_l_up = l+1.96*sel # for logit of alpha
  ci_lo = 1/(1+exp(-ci_l_lo)) # transform back both ends
  ci_up = 1/(1+exp(-ci_l_up)) # of a CI for
  # original alpha
  ci = c(ci_lo, ci_up) # print the resulting CI
  ci # of coefficient alpha to screen
}
```

Inputting the estimates from Mplus into this function produces the following output:

```
> ci.alpha_in_cds(0.880, 0.010)
[1] 0.8589776 0.8982597
```

We see clear evidence of high reliability of these three immigration attitude variables in the target ESS population: these are correlated, reliable indicators of attitudes toward immigration.

We repeat this process for the two trust in politics variables:

```
TITLE: WEIGHTED ESTIMATION OF TRUST ALPHA;
DATA:      FILE = M:\immig.dat;
VARIABLE:   NAMES = psu trstplt trstpprt imsmetn imdfetn
            impctrn weight;
            USEV = psu trstplt trstpprt weight;
            MISSING = ALL(88);
            WEIGHT = weight;
            CLUSTER = psu;
ANALYSIS:   TYPE = COMPLEX;
            ESTIMATOR = MLR;
```

MODEL:

```
F1 BY trstplt@1;
F2 BY trstprt@1;
trstplt@0;
trstprt@0;
F1-F2 (P1-P2);
F1 WITH F2 (P12);
```

MODEL CONSTRAINT:

```
NEW(ALPHA);
ALPHA = 1.5*2*(P12)/(P1+P2+2*(P12));
```

OUTPUT: CINTERVAL;

The weighted estimate of coefficient alpha for the two trust variables is 0.689, with a linearized standard error of 0.006. We then use the same R function to form a 95% CI for this alpha coefficient:

```
> ci.alpha_in_cds(0.689, 0.006)
[1] 0.6771198 0.7006364
```

While this analysis provides weaker evidence of high reliability for these two measures, we still see that the 95% CI covers 0.7, which would generally be considered an acceptable value of Cronbach's alpha when justifying that observed indicators are reliably indicating the same construct. We therefore have faith in the quality of the *measurement model* that defines the latent constructs being analyzed in the larger SEM (Figure 13.1).

Importantly, despite the popularity of alpha as a tool for scale construction and reliability assessment in the social sciences, the limitations of alpha as an approximate measure of the composite reliability of the items forming a hypothetical scale (or indicating a hypothetical construct) have been well established for decades. Referring to alpha as a composite measure of reliability is really only justified if: (1) the observed items are unidimensional (i.e., the items are not measuring different constructs); (2) the factor loadings for the latent construct of interest are uniformly high; and (3) the errors associated with the observed variables in the factor model are uncorrelated (Raykov, 1997). If these properties are not apparent when examining the coefficient alpha for a set of observed variables, more general composite measures of reliability should be presented. Raykov and Traynor (2015) outline a method similar to that described above using a combination of the Mplus and R software for estimating the composite reliability of a set of observed items following a design-based approach. We will consider whether the observed items have these essential properties when evaluating our larger overall SEM.

Next, we fit the full SEM using both Mplus and Stata, where our focus is on the path coefficient in the *structural model* that relates the latent trust construct to the latent immigration construct. First, we consider the following Mplus code:

```

TITLE:      ESS SEM Example, Complex Sampling Features
DATA:       FILE = M:\immig.dat;
VARIABLE:   NAMES = psu trstplt trstprt imsmetn imdfetn
            impcntr weight;
            USEV = psu trstplt trstprt imsmetn imdfetn impcntr
            weight;
            MISSING = trstplt (88) trstprt (88)
            imsmetn (8) imdfetn (8) impcntr (8);
WEIGHT = weight;
CLUSTER = psu;
ANALYSIS:  TYPE = COMPLEX;
MODEL:     F1 BY imsmetn imdfetn impcntr;
            F2 BY trstplt trstprt;
            F1 ON F2;
OUTPUT:    STANDARDIZED SAMPSTAT;

```

We note in the Mplus code how the complex sampling features (weight and cluster variables) are explicitly indicated, the analysis type is set to COMPLEX for the design-based approach, and the SEM defines two latent variables (F1, indicated by the three immigration attitude variables, and F2, indicated by the two trust variables), with F1 being regressed on F2 in the structural portion of the model. By default, Mplus uses *full information maximum likelihood (FIML) estimation*, drawing on all available information from each of the 1,703 sampled cases when estimating the model parameters (including those cases with some missing data). For more detail on FIML as an approach for analyzing data sets with missing values, we refer readers to Allison (2012). Executing this code in Mplus produces the selected output indicated below.

Chi-Square Test of Model Fit		
Value		1.103*
Degrees of Freedom		4
P-Value		0.8939
Scaling Correction Factor for MLR		1.419
RMSEA (Root Mean Square Error Of Approximation)		
Estimate		0.000
90 Percent C.I.		0.000 0.016
Probability RMSEA <= .05		1.000
CFI/TLI		
CFI		1.000
TLI		1.003

The various design-adjusted GOF measures (model chi-square, RMSEA, and CFI/Tucker-Lewis Index [TLI]) all suggest that the fit of this model is quite good, with the model chi-square being small and nonsignificant, the RMSEA value being less than 0.05, and the CFI and TLI values close to 1.0.

MODEL RESULTS					
		Estimate	S.E.	Est./S.E.	Two-Tailed P-Value
F1	BY				
	IMSMETN	1.000	0.000	999.000	999.000
	IMDFETN	1.316	0.054	24.559	0.000
	IMPCNTR	1.122	0.047	23.964	0.000
F2	BY				
	TRSTPLT	1.000	0.000	999.000	999.000
	TRSTPRT	1.007	0.063	15.916	0.000
F1	ON				
F2		-0.071	0.011	-6.407	0.000
Intercepts					
	TRSTPLT	3.868	0.068	56.653	0.000
	TRSTPRT	3.838	0.064	59.937	0.000
	IMSMETN	2.203	0.030	73.711	0.000
	IMDFETN	2.511	0.031	80.704	0.000
	IMPCNTR	2.504	0.028	88.621	0.000
Variances					
	F2	3.958	0.298	13.271	0.000
Residual Variances					
	TRSTPLT	0.765	0.252	3.034	0.002
	TRSTPRT	0.649	0.277	2.345	0.019
	IMSMETN	0.266	0.016	16.619	0.000
	IMDFETN	0.096	0.020	4.890	0.000
	IMPCNTR	0.223	0.022	10.337	0.000
	F1	0.363	0.038	9.506	0.000

Next, we consider the weighted estimates of the path coefficients in the model in Figure 13.1 and their linearized standard errors:

We note how Mplus scales the latent variables by default by setting the path coefficients from the latent variables to one of the observed variables equal to 1.0. We also note that the estimated path coefficient from regressing the latent immigration attitude variable (F1) on the latent trust variable (F2) is negative and strongly significant, suggesting that increased trust in politics

STANDARDIZED MODEL RESULTS					
STDYX Standardization					
		Estimate	S.E.	Est./S.E.	Two-Tailed P-Value
F1	BY				

	IMSMETN	0.768	0.022	35.544	0.000
	IMDFETN	0.934	0.014	67.751	0.000
	IMPCNTR	0.827	0.019	43.047	0.000
F2	BY				
	TRSTPLT	0.915	0.029	31.096	0.000
	TRSTPRT	0.928	0.032	29.398	0.000
F1	ON				
	F2	-0.228	0.032	-7.091	0.000

and politicians results in less favorable attitudes toward immigration. Mplus can also produce standardized versions of these weighted estimates:

We see that the items indicating each latent construct tend to be highly correlated with that construct, with the loadings being uniformly high and no evidence of multidimensionality in each case. This supports our use of coefficient alpha in describing the initial reliability. Examination of modification indices for this model (not shown) also suggests that allowing the errors associated with the observed variables to be correlated would not result in substantial reductions in the overall model chi-square, further supporting the use of coefficient alpha. We therefore have confidence in making inference about the negative relationship between trust in politics and politicians and attitudes toward immigration in the larger Belgian population based on this SEM.

Next, we consider the code for fitting this same SEM in Stata. We start by setting the complex sampling features using the `svyset` command, and then we fit the model using the `svy: sem` command (which is designed for multivariate normal observed variables):

```
svyset psu [pweight = weight]

svy: sem ///
(Trust -> trstplt trstpprt) ///
(Immig -> imsmetn imdfetn impcntr) ///
(Immig <- Trust) ///
if trstplt != 88 & trstpprt != 88 & ///
imsmetn != 8 & imdfetn != 8 & impcntr != 8
```

We note how the `svy: sem` command allows users to indicate the names of the latent variables in a given SEM (which are required to start with a capital letter), and then use arrows to indicate those observed variables that are indicating a given latent variable, or which latent variable is predicting another latent variable in the structural portion of the model.

The resulting weighted estimates of the path coefficients and their linearized standard errors (not shown) are quite similar to those produced by Mplus, with slight differences emerging because Stata is using listwise deletion to handle missing values (rather than FIML). This results in a slight reduction in the number of cases analyzed (1,676). An important difference

between the two packages at the time of this writing is that Stata does not yet compute design-adjusted GOF measures (e.g., RMSEA, CFI), unlike Mplus.

We include examples of code from other packages and procedures (e.g., the lavaan.survey package in R) that can be used to fit this model using a design-based approach on the book web site. Importantly, both Mplus and Stata (and selected other packages as well) can also fit generalized SEMs to observed variables that are not necessarily normal using design-based approaches (e.g., using the svy: gsem command in Stata). The brief illustration above is designed to demonstrate the ease with which analysts can fit SEMs to data collected from complex samples; we do not consider model diagnostics or model selection in great detail here, and instead refer readers to many other excellent texts on these aspects of fitting SEMs (e.g., Kline, 2015). The important point demonstrated here is that one should use software that correctly accounts for the complex sampling features when fitting these models if population inferences are the objective of a given SEM analysis.

Several additional technical papers on the topic of fitting SEMs to complex sample survey data are available at the Mplus web site: <http://www.statmodel.com/papers.shtml>. For readers interested in published examples of these types of applications using the Mplus software, we suggest Zajacova et al. (2009), Stapleton (2008), or Striegel-Moore et al. (2008).

13.5 Small Area Estimation and Complex Sample Survey Data

Chapters 4 and 5 introduced estimation and inference for subclasses of the survey population. Included under the general umbrella of subclass analysis is estimation for geographic domains of the survey population. Surveys such as the NCS-R, NHANES, and HRS generally support separate estimation and analysis for large geographic areas such as Census Regions or Divisions; however, the potential to directly estimate statistics for smaller geographic units such as individual states, counties, or municipalities is limited by poor precision due to the size and distribution of the multistage sample design. In cases such as the estimation of unemployment rates where direct state- or metropolitan-level estimates are important, major survey programs such as the U.S. Current Population Survey (CPS) expand the stratification, primary stage sample allocation, and overall sample size of the survey to enable stand-alone estimation for these critical geographic reporting units.

Over the past 50 years, a class of statistical techniques labeled *small area estimation methods* (Rao and Molina, 2015) has been developed to address the problem of estimating population characteristics for small areas. Most of these techniques blend survey data, ancillary population data, and a population model to estimate small area statistics. For larger domains, methods such as generalized regression (GREG) estimation or calibration methods

(DeVille and Särndal, 1992) simply use population data to adjust direct regression estimates computed from the survey data. Other techniques such as synthetic estimation or structure preserving estimation (SPREE) use survey data to model the structure of relationships in the survey population and then combine that structure with administrative or population data for the target small area to generate a small area estimate. Additional techniques such as composite estimation or the James–Stein method create an estimate that is a weighted function of a direct survey estimate for the small area and a model-based estimate or a direct estimate for a larger domain. Computation of the direct estimates or regression coefficients used to form small area estimates should generally incorporate survey weights (if applicable), which will ensure design consistency of the estimates, and the variances of small area estimates should reflect the sampling distributions of the (weighted) direct survey estimates, given any complex sampling features (You and Rao, 2002, 2003; Ghosh and Maiti, 2004; Pfeffermann and Sverchkov, 2007).

Recent advances in methodology for small area estimation have centered on the application of GLMMs of the form in Equation 13.1 (Jiang and Lahiri, 2006) and Bayesian methods (Section 13.2). In particular, Chen et al. (2014) discuss how to account for survey weights when using Bayesian hierarchical models for small area estimation, and provide empirical evidence of bias and variance reduction when using their approach. These authors also include a link demonstrating the use of R software for this type of small area estimation. Interested readers are encouraged to examine Rao and Molina (2015) for a comprehensive, state-of-the-art treatment of various area-level and unit-level GLMM models for small area estimation. The second edition of that text features many worked examples, including illustrations of small area estimation using software.

13.6 Nonparametric Methods for Complex Sample Survey Data

Another area that is (at present) wide open for additional research is the application of nonparametric statistical methods to the analysis of complex sample survey data. Breidt and Opsomer (2009) provide an excellent overview of recent developments in theory and methods, and we highlight some important recent work in this section.

In Chapter 11 of *Analysis of Survey Data*, Chambers et al. (2003) provide a detailed but largely theoretical discussion of possible methods for incorporating complex design features into nonparametric regression methods designed for exploratory data analysis (EDA), such as localized *smoothing models*. Their focus is on “scatterplot smoothing,” or modeling the functional relationship between some dependent variable y and some independent

variable x . The authors perform a series of simulations evaluating different methods for incorporating complex sample design features into smoothing methods, but results were not clear in terms of optimal methods or whether survey weights should be incorporated in the analyses. Further, only the case of stratification was considered, and the authors indicate that extensions of their theory for cluster sampling designs are needed. The authors conclude that their proposed design adjustments to standard smoothing methods can be beneficial when sampling schemes are *informative* (i.e., probability of selection is related to the survey variable of interest), and that there would be little loss of efficiency when using their suggested design adjustments if a sampling scheme was not informative.

Opsomer and Miller (2005) provide additional guidance on the amount of smoothing that should be done in nonparametric regression applications with survey data, and Whittaker and Scott (1999) discuss the Averaged Shifted Histogram (ASH) approach for estimating multivariate nonparametric regression models with complex sample survey data. Harms and Duchesne (2009) present an evaluation of design adjustments for the local linear regression estimator, and Bellhouse and Stafford (2001) discuss how to handle complex sampling features when performing local polynomial regression. Design-adjusted smoothing models can be fitted to complex sample survey data using the `svysmooth()` function in the R `survey` package (Lumley, 2010); see <http://r-survey.r-forge.r-project.org/survey/example-graphics.html> for an example.

In terms of *nonparametric density estimation*, which is used for comparing population subgroups in terms of distributions on continuous survey variables, estimating quantiles, and generating smooth estimates of density functions without relying on parametric models, Buskirk and Lohr (2005) examined the finite-sample and asymptotic properties of a modified kernel density estimator incorporating both survey weights and kernel weights. These authors presented regularity conditions under which the sample estimator of the density function is consistent and normal under various modes of inference used with sample survey data, and also presented methods for incorporating clustering when computing design-based confidence bands for a density function. The authors present applications of their design-adjusted density estimation methods to the National Crime Victimization Survey (NCVS) and NHANES, but unfortunately their methodology has yet to be programmed in any of the more general-purpose statistical software packages.

Our hope is that these promising methods, which to date have largely been evaluated using theoretical simulations and only a handful of applications, will continue to be studied and will be more widely available for analysts of survey data as statistical software for survey data analysis continues to develop. As with other methods discussed in this book, we aim to update readers with any software or methodological developments on the book web site.

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Appendix A: Software Overview

A1 Introduction

Today, most analysts can access procedures for survey data analysis either from within the major statistical software packages such as Stata, SAS/STAT (referred to as SAS from this point forward), SPSS, and SUDAAN (SAS-callable version) or via stand-alone and/or more specialized software such as SUDAAN (stand-alone version), Mplus, R, WesVar, and IVEware. In the overview and evaluation of software for survey data analysis presented in this appendix, we make a distinction between software packages with integrated survey procedures (e.g., Stata) and software that is more specifically tailored to complex sample survey data analysis (SUDAAN). The reason for this distinction is clear: programs that cannot perform a full range of data management, analysis, graphing, and other tasks require more work and setup costs for the research analyst in order to perform survey data analyses correctly. Although this penalty is often minor, research analysts generally prefer to work efficiently within a single, unified software system and minimize the amount of time and effort needed for data management and data set up prior to analysis.

For this reason as well as general availability, we focus on four major commercial software packages (Stata, SAS, SPSS, and SUDAAN) heavily used by a wide range of analysts working in varied fields. Although SUDAAN is primarily a data analysis package for complex sample survey data, the fact that it functions as both a stand-alone and SAS-callable tool essentially makes it a SAS-like product and therefore, by extension, is an add-on to the SAS suite of procedures and functionality. In addition to the four packages mentioned, we also present a brief summary of the survey data analysis capabilities in other software packages including IVEware, Mplus, R, and WesVar. We also include code samples for these software packages on our web site. For those readers interested in replicating the example analyses in Chapters 5 through 13 using SAS, SPSS, SUDAAN, IVEware, WesVar, R, and Mplus, please refer to the book web site: <http://www.isr.umich.edu/src/smp/asda/>.

This appendix presents an overview of modern software packages that correctly perform survey data analysis and evaluates the relative strengths and weaknesses of each. We consider key features such as overall ability to analyze survey data (including sample design structures accommodated), available variance estimation methods, range of analytic techniques offered,

hypothesis testing ability, and effectiveness in dealing with common issues such as subpopulation analysis and ease of graphical display of results (including diagnostics). Although cost of software is an obvious consideration for most users, the wide variability in pricing and purchasing options makes this type of financial comparison impractical. Given anticipated version changes and rapid software development, we plan to regularly update our web site examples as software developments emerge. Rather than recommend a particular tool as the “best” solution, our goal is to objectively evaluate and consider the pertinent features of the major software in use at this time.

A1.1 Historical Perspective

Prior to the late 1990s, most survey data analysts used specialized software tools for correct estimation of population parameters and variance estimation tasks. Some of the more popular tools in the 1990s were SUDAAN, IVEware, WesVar, and early Stata and PC SAS routines. Going back further in time, packages such as OSIRIS (PSALMS and REPERR; University of Michigan, 1982), Super CARP/PC CARP (Fuller et al., 1989), and other stand-alone programs were in use in the 1970s and 1980s ([Chapter 1](#)).

Only during the past two decades have a majority of major statistical software producers incorporated options to analyze complex sample survey data as part of their overall package. The early survey data analysis tools were generally developed for the individual needs of a group of researchers analyzing survey data and for their time were often very well designed. Indeed, each of the major software packages in use today owes a debt to the early software and work of the researchers who developed these tools and in turn promoted the use of correct analytic techniques for survey data analysis. However, most of these early packages required extra data management steps and data transfer from package to package, resulting in additional time demands on the analyst. With the advent of survey procedures included within major software packages, the survey analyst is now able to easily do the necessary work without the extra burden of switching between software packages—data management and survey analysis capabilities are integrated into a single software system.

A1.2 Software for Analysis of Complex Sample Survey Data

The software reviewed in detail in this appendix includes four commonly used data analysis tools: SAS/STAT (SAS® version 9.4 and SAS/STAT 14.1), Stata (version 14.1), SPSS Complex Samples (version 22), and SUDAAN (version 11.0.1). We limit our review to the PC platform, but many of these tools are also available on UNIX/LINUX/MAC platforms as well. As mentioned earlier, the additional software packages reviewed in less detail are WesVar (version 5.1), the R survey Package (version 3.31), Mplus (version 7.4), and IVEware (version 0.3). Please see the book web site for code examples for

TABLE A1

Ability of Software to Accommodate Various Complex Sample Designs

Sample Design	Stata	SAS	SUDAAN	SPSS	IVEware	WesVar	Mplus	R
With and without replacement	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Equal and unequal weighting	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Nonstratified and stratified	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Single and multistage	Yes	No	Yes	Yes	No	Yes	Yes	Yes

all of these software packages as well as links to external sites for software, documentation, and statistical assistance.

For a systematic approach to selection of a survey data analysis tool, consider the software and respective features outlined in [Tables A1](#) through [A4](#). For each software package, these tables present the types of complex sample design structures that can be specified, available variance estimation methods, ability to perform common analytic techniques such as those detailed in this book, and key options such as hypothesis testing, subpopulation analysis, and ability to impute and/or analyze multiply imputed data sets. Although these tables are not intended to provide readers with a complete list of every possible analytic technique, they include common procedures routinely used by survey data analysts. Subsequent sections provide detailed reviews of the features summarized in [Tables A1](#) through [A4](#) for

TABLE A2

Variance Estimation Capabilities and Additional Analysis Features of the Software Packages

	Stata	SAS	SUDAAN	SPSS	IVEware	WesVar	Mplus	R
<i>Variance Estimation Method^a</i>								
TSL (Taylor Series)	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes
JRR (delete one)	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes
JRR (replicate weights)	Yes	Yes	Yes	No	No	Yes	Yes	Yes
BRR	Yes	Yes	Yes	No	No	Yes	Yes	Yes
BRR (w/Fay's adjustment)	Yes	Yes	Yes	No	No	Yes	Yes	Yes
Bootstrap	Yes	No	No	No	No	No	Yes	Yes
Single cluster per stratum	Yes	Yes	Yes	Yes	No	Yes	Yes	Yes
<i>Features of Survey Analysis</i>								
Subpopulation analysis	Yes	Yes	Yes	Yes	Yes ^b	Yes	Yes	Yes
Finite population correction for SWOR designs	Yes	Yes	Yes	Yes	No	Yes	Yes	Yes

^a See [Chapter 3](#) for a discussion of each of these variance estimation methods.

^b Restricted to the conditional subclass analysis approach.

TABLE A3

Available Analytic Techniques in the Software Packages

Analytic Technique	Stata	SAS	SUDAAN	SPSS	IVEware	WesVar	Mplus	R
<i>Descriptive</i>								
Means	Yes	Yes	Yes	Yes	Yes	Yes	NA ^a	Yes
Totals	Yes	Yes	Yes	Yes	Yes	Yes	NA ^a	Yes
Ratios	Yes	Yes	Yes	Yes	Yes	Yes	NA ^a	Yes
Percentiles	No	Yes	Yes	No	No	Yes	NA ^a	Yes
Contingency tables	Yes	Yes	Yes	Yes	Yes	Yes	NA ^a	Yes
<i>Regression</i>								
Linear	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Binary logistic	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Ordinal logistic	Yes	Yes	Yes	Yes	Yes ^b	No	Yes	Yes
Multinomial logistic	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No
Poisson regression	Yes	No	Yes	No	Yes	No	Yes	Yes
Probit	Yes	Yes	No	Yes	Yes ^b	No	Yes	Yes
Cloglog	Yes	Yes	No	Yes	Yes ^b	No	No	Yes
<i>Survival Analysis</i>								
Cox proportional hazards model	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes
Kaplan–Meier estimation	No	No	Yes	Yes	No	No	Yes	Yes
<i>Missing Data</i>								
Multiple imputation of missing data	Yes	Yes	Yes	Yes ^c	Yes	Yes ^d	Yes	Yes
Analysis of multiply imputed data sets	Yes	Yes	Yes	Yes ^c	Yes	Yes ^d	Yes	Yes

^a Not applicable; this product is designed as a modeling tool.^b Can be done using the SASMOD feature of IVEware.^c Limited to a subset of survey commands to analyze completed data sets.^d Limited to table analysis only; not available for regression.

each software package, and available features will continue to be updated on the web site for the book as new developments occur.

A2 Overview of Stata® Version 14.1

Stata (www.stata.com) is an outstanding software tool for the survey data analyst. This package offers the ability to handle numerous sample design structures, a full range of variance estimation methods, extensive survey commands, the ability to perform correct subpopulation analyses for every

TABLE A4

Hypothesis-Testing Capabilities in the Software Packages

	Stata	SAS	SUDAAN	SPSS	IVEware	WesVar	Mplus	R
<i>Means, Totals, and Ratios</i>								
Confidence limits and <i>t</i> test ^a	Yes	Yes	Yes	Yes	Yes	Yes	NA	Yes
<i>Contingency Tables</i>								
Rao-Scott adjusted <i>F</i> ^b	Yes	Yes	Yes	Yes	No	Yes	NA	Yes
Wald and Pearson chi-square ^b	Yes	Yes	Yes	Yes	No	Yes	NA	Yes
Wald and Rao-Scott likelihood ratio ^b	Yes	Yes	Yes	Yes	No	No	NA	Yes
<i>Regression</i>								
<i>Linear</i>								
Linear contrasts ^c	Yes	Yes	Yes	Yes	No	Yes	Yes	Yes
Wald <i>F</i> and adjusted <i>F</i> ^d	Yes	Yes	Yes	Yes	No	Yes	No	Yes
Wald chi-square and adjusted chi-square ^d	Yes	Yes	Yes	Yes	No	No	Yes	No
<i>Logistic and GLM (Binary, Ordinal, Multinomial, Poisson, Cloglog, Probit)</i>								
Linear contrasts ^c	Yes	Yes	Yes	Yes	No	Yes	Yes	Yes
Wald <i>F</i> and adjusted <i>F</i> ^d	Yes	Yes	Yes	Yes	No	Yes	No	No
Wald chi-square and adjusted chi-square ^d	Yes	Yes	Yes	Yes	No	No	Yes	Yes
Archer and Lemeshow GOF ^e	Yes	No	No	No	No	No	No	No
Fagerland and Hosmer GOF (multinomial logistic regression) ^e	Yes	No	No	No	No	No	No	No
Test of parallel lines assumption (ordinal logistic regression) ^e	Yes ^f	Yes ^g	No	Yes ^f	No	No	No	No
<i>Survival Analysis</i>								
<i>Cox PH Model</i>								
Linear contrasts ^c	Yes	Yes	Yes	Yes	No	No	Yes	Yes
Wald <i>F</i> and Wald chi-square ^d	Yes	Yes	Yes	Yes	No	No	Yes	Yes
<i>Survival Curves</i>								
Corrected standard errors for estimates	No	No	Yes	Yes	No	No	Yes	Yes

^a Test of means significantly different from 0 and test of difference between means (Sections 5.6 and 5.6.1).

^b Tests for independence of rows and columns in contingency table analysis or differences in population proportions (Sections 6.4.3 and 6.4.4).

^c Test of individual parameter = 0, test of linear contrasts between parameters in regression models, and,

^d Test of multiple parameters in the model (overall or partial tests; Section 7.3.4.1 and similar sections of [Chapters 8 through 10](#)).

^e Test significance for goodness of fit (adjusted for complex sample design) for overall model (Section 8.5.2).

^f Tests assumption of proportional odds or “equal slopes” in ordinal logistic regression (adjusted for complex sample design) (Section 9.3.6).

^g Test can be performed using data step coding; see SAS PROC SURVEYPHREG documentation/examples.

command, and many theoretically advanced options for significance testing (e.g., second-order design corrections for chi-square statistics; see [Chapter 6](#), and goodness-of-fit tests; see [Chapters 8](#) and [9](#)). Another valuable feature is the ability to create and analyze multiply imputed data sets; see [Chapter 12](#).

A key feature in Stata is the convenient method of declaring the “survey” or complex design variables one time prior to analysis. This approach allows the analyst to specify the complex design variables and probability (or survey) weights through use of the `svyset` command, and once they are declared, these variables will be in effect for the entire survey data analysis session or until changed. The `svyset` command allows users to specify different forms of survey weights, such as probability or replicate weights. In addition, there are lesser-used options to declare variables for finite population corrections (FPCs) and explicit poststratification adjustments within the `svyset` command syntax.

In practice, analysts may encounter public-release data sets that employ a sampling error calculation model ([Chapter 4](#)) where each stratum includes only a single cluster for sampling error computations, as opposed to more traditional sampling error calculation models specifying two or more sampling error clusters per stratum. Most survey data analysis software is designed to recognize multiple sampling error clusters in each stratum for variance estimation, and the “singleton” or “lonely” sampling error cluster can interfere with variance estimation procedures. Fortunately, this problem can be addressed in Stata through use of the `singleunit` option in the `svyset` command. This feature allows the Stata user to declare that the sampling error calculation model for the survey data set includes only one sampling error cluster in at least one of the sampling error strata, and offers four options for how variance estimation should proceed in this situation: `singleunit(missing)`, `singleunit(certainty)`, `singleunit(scaled)`, and `singleunit(centered)`. The `singleunit(missing)` option is the default option and simply causes the program to stop execution without reporting standard errors; `singleunit(certainty)` informs Stata to include the “singleton” primary sampling unit (PSU) with certainty (i.e., the PSU does not contribute to variance estimation), `singleunit(scaled)` uses the average sampling variance among all strata with multiple units for the single-unit stratum, and `singleunit(centered)` uses deviations from the grand mean across PSUs to calculate the variance contribution from a stratum with a single PSU. See [Chapter 4](#) and the Stata help function for `svyset` for more details on this topic.

Variance estimation methods available for each of Stata’s survey data analysis procedures include the Taylor Series Linearization method, Jackknife Repeated Replication (JRR), Balanced Repeated Replication (BRR) with an option for Fay’s adjustment, Successive Differences using Replicate weights (SDR), and Bootstrap using bootstrap weights. The ability to use these varied approaches is a distinct advantage in situations that may call for a replicated variance estimation approach, such as JRR, rather than a Linearization

method. There are numerous reasons for a replication approach. For example, one situation that often arises with public-use data files is the availability of “replicate weights” instead of the more typical primary-stage stratum and cluster code variables in addition to a final survey weight variable. This is generally due to confidentiality concerns and the desire to publish “masked” variables for public use that represent the design structure without jeopardizing confidentiality. Stata users can specify replicate weights for JRR or BRR variance estimation within the `svyset` command. See [Chapter 3](#) for more details on variance estimation methods and the use of replicate weights.

The range of Stata survey commands is extensive. Every analytic command includes design-based significance testing options if statistically appropriate. An additional advantage of the Stata software is the consistency of syntax between the specialized survey commands and standard commands, thus allowing a Stata user new to survey data analysis a nearly immediate knowledge of the syntax required to execute the survey commands. At the simplest level, a Stata user merely needs to add the `svy:` modifier in front of a standard analysis command to invoke design-based estimation, provided that the relevant design variables have been identified using the `svyset` command.

All of Stata’s survey procedures provide users with the correct approach to the analysis of subpopulations via the `subpop()` option. An unconditional subpopulation analysis, invoked via use of the `subpop()` option, ensures that (1) the full complex design structure is recognized during the process of variance estimation, and (2) the subpopulation sample size is treated as a random variable. See Section 4.5 for more details.

Given the array of Stata survey procedures and the manner in which the commands are organized (one for each separate type of analysis instead of a single procedure/command that optionally does many things), it would be impractical to list all of the survey commands here. In terms of descriptive analyses ([Chapters 5](#) and [6](#)), users can estimate means, proportions, ratios, totals, and one-way frequency tables or two-way cross-tabulations. For linear regression modeling ([Chapter 7](#)), linear regression for continuous outcomes and a number of related techniques such as constrained linear regression and Tobit regression are available. For binary outcome variables, logistic and probit regression modeling procedures are available ([Chapter 8](#)), along with a number of convenient options such as skewed logistic regression and complementary log–log regression. For categorical outcomes, ordered logistic, probit regression, multinomial logistic, conditional logistic, and stereotype logistic regression can be performed ([Chapter 9](#)). In terms of count outcomes, Stata offers Poisson regression, negative binomial regression, and generalized negative binomial regression along with zero-inflated or zero-truncated options as appropriate for these models. Analysts working with time-to-event (or survival) survey data can also fit design-based Cox proportional hazards models or other parametric survival models ([Chapter 10](#)).

Each of these survey commands has additional analytic options available (many of which are detailed in the chapters of this book). In addition, a variety of postestimation commands are also available, such as those that compute design effects (DEFF/DEFT), misspecification effects (MEFF), subgroup contrasts, design-adjusted Wald tests for multiple regression parameters, goodness-of-fit tests for logistic regression, subpopulation sizes, and other useful statistics. For example, after fitting a linear regression model, residuals and model diagnostics are available postestimation, and examples of using these commands are presented in Chapter 7. Given that Stata code is presented throughout the text, we refrain from providing detailed examples of Stata commands here. Please see the book web site for sample programs and the Stata web site (www.stata.com) for full documentation.

In summary, Stata offers an extensive range of design-based survey analysis capabilities, all common variance estimation methods, simple specifications for subpopulation analysis, and numerous tools for design-adjusted hypothesis testing. In addition, Stata 11 and later versions include multiple imputation capabilities. The `mi` suite of commands enables both multiple imputation with a variety of methods and analysis of multiply imputed data sets while incorporating Stata `svy` commands. This combination is especially convenient for survey analysts faced with missing data. We demonstrate use of the `mi` commands in detail in Chapter 12.

A3 Overview of SAS Version 9.4

The current version of SAS (SAS version 9.4 and SAS/STAT version 14.1, www.sas.com) offers seven survey procedures including six survey analysis procedures and one sample selection procedure. There are numerous sampling/analytic techniques within each procedure rather than the one command per analytic technique approach implemented by Stata. This is essentially a difference in style and structure and does not necessarily represent a loss of capability overall. Although SAS does not offer as many survey procedures or analytic techniques when compared with Stata, it can perform most common complex sample survey analyses using either repeated replication or Taylor Series Linearization methods for variance estimation.

The seven procedures currently offered for sample selection and survey data analysis are PROC SURVEYSELECT, PROC SURVEYMEANS, PROC SURVEYFREQ, PROC SURVEYREG, PROC SURVEYLOGISTIC, PROC SURVEYPHREG, and PROC SURVEYIMPUTE. PROC SURVEYSELECT is primarily a sampling tool offering the ability to select probability samples from *sample frame* data bases. As this is not an analysis procedure, we do not focus on PROC SURVEYSELECT in this appendix. PROC SURVEYMEANS and PROC SURVEYFREQ offer descriptive analytic capabilities for means,

ratios, totals, quantiles, contingency tables, and other types of descriptive analyses. For regression analysis, the main procedures are PROC SURVEYREG (for linear regression), PROC SURVEYPHREG (for survival models), and PROC SURVEYLOGISTIC (binary, ordinal, and multinomial logistic regression). Each of the analysis procedures offers the option of JRR, BRR, or Taylor Series Linearization for variance estimation as well as a DOMAIN or implied DOMAIN statement for correct subpopulation analysis ([Chapter 4](#)). New in SAS v9.4 and SAS/STAT 14.1 is PROC SURVEYIMPUTE. This procedure has the ability to impute item missing data using the fully efficient fractional imputation (FEFI) hot-deck or a number of traditional hot-deck options. PROC SURVEYIMPUTE also includes options for generation of imputation-adjusted replicate weights and can output a completed data set with replicate imputation weights designed for subsequent analysis of a fractionally imputed data set. [Chapter 12](#) provides a worked example using the PROC SURVEYIMPUTE FEFI method. SAS software is also capable of multiply imputing and analyzing data sets through use of PROC MI (to impute missing data), survey procedures (estimation for imputed data sets), and PROC MIANALYZE (to combine MI analyses and produce final MI estimates and inferential statistics).

By default, the SAS survey analysis procedures provide a method to deal with a single PSU per stratum when performing variance estimation (Taylor Series), and will collapse strata with a single PSU for the variance estimation step. Alternatively, the analyst can opt not to collapse all single PSUs into one stratum for variance estimation via use of the “NOCOLLAPSE” option in PROC SURVEYREG only. In this situation, the stratum with the single PSU contributes a zero to the estimate of variance.

The SAS survey analysis procedures can analyze data arising from various types of complex samples using the sampling with replacement, “ultimate cluster” sampling error calculation model, and formulas described in [Chapter 3](#). The design is defined in each procedure using the STRATUM and CLUSTER statements. The survey weight variable is declared through use of the WEIGHT statement. For example, typical PROC SURVEymeans syntax is as follows:

```
proc surveymeans data=one;
stratum str;
cluster cluster;
weight weight;
var income;
run;
```

Several optional features for survey data analysts are in place. For example, replicate weights can be accommodated by declaring the replicate weights in the WEIGHT statement. The analyst could also specify the variance estimation method in the procedure statement through use of the varmethod=jackknife or varmethod=brr options (the default

variance estimation method for each analysis procedure is Taylor Series Linearization). The example syntax below illustrates typical use of SAS PROC SURVEYMEANS with a JRR variance estimation method and use of four replicate weights:

```
proc surveymeans varmethod=jackknife data=one;
  repweights rwgt1 rwgt2 rwgt3 rwgt4;
  var income;
  run;
```

Subpopulation analyses can be correctly performed in all SAS survey analysis procedures with the use of the domain statement or the “implied domain” statement (for PROC SURVEYFREQ). In the case of PROC SURVEYFREQ, use of the domain variable as the first variable in the TABLES statement functions as a DOMAIN statement. Multiply imputed data sets can be used with all SAS survey procedures with required output read into and analyzed by PROC MIANALYZE. Although PROC MIANALYZE is not considered a “survey” procedure, it is capable of analyzing output from each of the survey procedures outlined in this section. PROC MIANALYZE requires the design-based estimates of the standard errors and/or the variance–covariance matrix for proper analysis, and with this approach, the analyst can account for both the complex sample and the variability in estimates introduced by multiple imputation (Berglund and Heeringa, 2014). As an alternative to multiple imputation, PROC SURVEYIMPUTE offers a number of imputation methods such as FEFI and more traditional hot-deck methods along with built-in generation of imputation-adjusted replicate weights and output data sets for analysis of imputed data sets. See [Chapter 12](#) for more on imputation techniques for survey data and the SAS documentation for PROC SURVEYIMPUTE/PROC MI/PROC MIANALYZE for more SAS-related details.

A3.1 SAS SURVEY Procedures

The core analytic SAS procedures can be separated into descriptive procedures (PROC SURVEYMEANS and PROC SURVEYFREQ), regression procedures (PROC SURVEYREG, PROC SURVEYPHREG, and PROC SURVEYLOGISTIC), and an imputation procedure (PROC SURVEYIMPUTE). PROC SURVEYMEANS offers the ability to perform survey data analysis for means, means within subpopulations, percentiles, ratios, and totals, all taking into account the complex design variables and the survey weights. One common analytic technique is a significance test for a linear combination of means (e.g., a difference between means) including a correct standard error for the difference. As of SAS v9.4, this feature is not included directly in PROC SURVEYMEANS but can be approached either with an SAS Institute submacro (smsub.sas, support.sas.com) or with use of contrasts in PROC SURVEYREG (see the SAS documentation for PROC SURVEYREG

for details). We recommend use of PROC SURVEYREG with a CONTRAST statement due to the ease of extending the concept of linear contrasts to a regression model. The PROC SURVEYMEANS default output includes an estimated mean, design-based standard error, sample size (n), and design-based 95% confidence limits for the mean. When using the ratio option in the procedure, the defaults change to comply with the usual output for a ratio rather than a mean (see the book web site for examples). Here is basic PROC SURVEYMEANS syntax with statements specifying the strata, cluster, weight, and domain variables:

```
proc surveymeans data=one;
stratum str;
cluster cluster;
weight weight;
var income;
domain sex;
Run;
```

PROC SURVEYFREQ performs contingency table analyses including estimation of proportions and population totals with design-based standard errors. The CHISQ option on the TABLES statement requests bivariate tests of association through use of the Rao–Scott chi-square test and the likelihood ratio test (Rao and Scott, 1984), and the Wald chi-square test (Chapter 6). First-order corrections in Rao–Scott chi-square tests are the default but second-order tests are available as well using the CHISQ (secondorder) option on the TABLES statement. The default output from PROC SURVEYFREQ includes weighted and unweighted frequencies a standard error for the weighted frequency, and weighted estimates of percentages and their standard errors. Other output such as “DEFF” for design effects can be requested within the procedure.

The SURVEYFREQ procedure includes an implied domain feature rather than an explicit statement for subpopulation analyses, as illustrated in the example syntax below (where SEX defines the domain variable, EDUCAT defines the row variable of the contingency table, and MARCAT is the column variable):

```
proc surveyfreq data=one;
strata strata;
cluster cluster;
weight weight;
tables sex*educat*marcat;
run;
```

PROC SURVEYREG is the SAS tool for linear regression with survey data (Chapter 7). This procedure computes weighted estimates of the parameters in specified linear regression models, along with design-corrected standard errors and variance–covariance matrices computed using the user-specified variance estimation option (TSL is the default). Subpopulation analyses can

be defined via the DOMAIN statement. For hypothesis tests, the analyst can request linear contrasts and tests of model effects. Significance testing can be performed with the use of either the ESTIMATE or CONTRAST statement and custom hypothesis testing of linear combinations of regression parameters is available (see the book web site for examples). The procedure also includes design-based Wald F -tests for regression parameters, design effects, and confidence limits for parameter estimates, along with many other options. See [Chapter 7](#) for more details on variance estimation and significance testing for linear regression analysis of survey data. We include a simple example of PROC SURVEYREG code below:

```
proc surveyreg data=one;
strata strata;
cluster cluster;
weight weight;
model income=sex age educationyrs;
run;
```

The SAS survey analysis procedure for logistic regression is PROC SURVEYLOGISTIC, which performs logistic regression for discrete categorical outcomes, including binary, ordinal, and nominal dependent variables. This procedure utilizes the pseudo maximum likelihood method of parameter estimation (Binder, 1983) along with the usual variance estimation options, an optional DOMAIN statement, and significance testing options for survey data analysis. Multiparameter hypothesis tests are available through the use of the TEST and/or CONTRAST statements. Various extensions of logistic regression modeling are available through use of the “link” option on the model statement. The four types of links are cloglog, glogit, logit, and probit. Here is generic syntax for PROC SURVEYLOGISTIC with the default logit link (more examples are available on the book web site):

```
proc surveylogistic data=one;
strata strata;
cluster cluster;
weight weight;
model diabetes (event='1')=sex age educat;
run;
```

The SURVEYPHREG procedure performs survival analysis based on the Cox proportional hazards model for “time-to-event” data derived from a complex sample design. This procedure produces standard survival model output including hazards ratios, output data sets, and ODS GRAPHICS plots. Subpopulation analysis is specified using an optional DOMAIN statement. Multiparameter hypothesis tests are available through the use of the TEST and/or CONTRAST statements. See [Chapter 10](#) for statistical details

on fitting these models and relevant adjustments for complex sample survey data. Here is generic syntax for PROC SURVEYPHREG:

```
proc surveypreg data = depress;
strata strata;
cluster psu;
weight analysiswt;
model aged depressed*dep_indicator(0)=bodyweight smoke;
run;
```

The fully efficient fractional hot-deck imputation method along with four traditional hot-deck imputation methods is available in PROC SURVEYIMPUTE. The following generic syntax uses the FEFI method with the default JRR (JK) variance estimation method. An output data set called “survey_imputed” with output JK weights is ready for subsequent analysis:

```
proc surveyimpute data=one method=fefi varmethod=jk;
class Department Response;
var Department Response;
strata stratum;
cluster cluster;
weight analysiswgt;
output out=survey_imputed
outjkcoefs=DrugAbuseJKCOEFS;
run;
```

Given the range of the analysis capabilities available in the SURVEY procedures, SAS is an excellent choice as a survey data analysis tool, especially for analysts who are already familiar with the data management and standard analysis procedures of the SAS system.

A4 Overview of SUDAAN® 11.0.1

SUDAAN® (<http://www.rti.org/sudaan/>) is another excellent tool for the survey data analyst. The history of this package is long and impressive. It began as a single-procedure tool during the early 1970s and has since evolved into a key software tool capable of analyzing many types of correlated data sets. The software can be executed as either an SAS-callable or stand-alone product and offers a wide range of features and commands. One important benefit of the SUDAAN package is that the syntax very closely mirrors that of SAS and the experienced SAS user will find learning and invoking the program relatively easy. On the other hand, knowledge of SAS command syntax is not required to use the program to full effect as it is well organized

with excellent documentation containing thorough language and example manuals.

SUDAAN can handle single PSUs per stratum using the MISSUNIT option on the NEST statement. The SUDAAN MISSUNIT option informs the software to use deviations of values for the “single” sampling error clusters from overall means to compute the contributions of those single-PSU strata to variance estimates (see the SUDAAN documentation for more details).

The three commonly used methods for variance estimation are included: Taylor Series Linearization, JRR, and BRR. The list of SUDAAN analysis commands is lengthy, with descriptive (PROC DESCRIPT, PROC CROSSTAB, PROC RATIO, PROC VARGEN), regression (PROC REGRESS, PROC LOGIST/RLOGIST, PROC MULTILOG, AND PROC LOGLINK), survival analysis (PROC KAPMEIER, PROC SURVIVAL), and weight adjustment and imputation (PROC WTADJUST, PROC WTADJX, PROC IMPUTE) commands included. Each of the analysis commands listed includes hypothesis-testing tools appropriate for the corresponding analytic technique (see the SUDAAN language and example guides for complete details). SUDAAN can also impute missing data using PROC IMPUTE and optionally analyze multiply imputed data sets within any of its procedures.

One potential drawback of SUDAAN is the lack of data management tools, but then again, this tool is not promoted as a general-purpose statistical software package. In practice, it is often used for the analysis of survey data rather than data set construction, and given its ability to read in various types of external data sets and work seamlessly with SAS, this is not a major concern. Another common task is production of graphics based on survey analyses, and though SUDAAN does not contain a graphics capability, its SAS interface enables easy movement between SUDAAN and SAS statistical graphing procedures and SAS/ODS (Output Delivery System). The analyst needs only to save the SUDAAN output as an SAS-type file and can then use the output data set with the key SAS tools for graphing, reporting, or further data analysis. Alternatively, the analyst could save output in another format such as an ASCII file and use the file with other software as needed.

A4.1 SUDAAN Procedures

There are four descriptive procedures in SUDAAN. The DESCRIPT procedure is designed for estimation of means, totals, proportions, percentages, and quantiles ([Chapter 5](#)) with design-based standard errors estimated using the selected variance estimation method. The DESCRIPT procedure also includes the ability to perform linear contrasts of estimates for individual levels of categorical variables (e.g., testing the difference of means for two subpopulations). Strata and cluster codes that enable estimation of complex sample standard errors are declared in the NEST statement, and the optional DESIGN= specification on the procedure statement allows the analyst to specify the appropriate sample design. The example code below illustrates

SUDAAN syntax using the default of DESIGN=WR (With-Replacement selection of first-stage PSUs, or “ultimate clusters”; [Chapter 3](#)), with the use of FILETYPE=SAS for reading an SAS data set and the SUBPOPN statement for unconditional identification of a specific subpopulation for analysis. Subpopulation analysis is available on every SUDAAN procedure and provides correct subpopulation analyses similar to the Stata `subpop()` or the SAS DOMAIN statements.

```
proc descriptor data=one filetype=sas;
nest strata cluster;
weight weight;
var income;
subpopn sex=1;
run;
```

The RATIO procedure is designed to estimate weighted ratios of selected observed variables and includes options similar to those of the DESCRIPT procedure. The PROC RATIO syntax is very similar to the preceding DESCRIPT commands but requires the addition of the numerator and denominator variables defining the ratio of interest:

```
proc ratio data=one;
nest strata cluster;
weight weight;
numer depressedwoman;
denom depressed;
run;
```

The third descriptive procedure, PROC CROSSTAB, is used for estimation of frequency and contingency tables, percentages, odds ratios, and risk ratios, all with design-based estimates of variances and standard errors. The analyst can also obtain complex design-adjusted chi-square and Cochran–Mantel–Haenszel (CMH) tests ([Chapter 6](#)). SUDAAN also offers design-corrected CMH tests for trends, a convenient tool for analysts working with categorical variables.

Sample PROC CROSSTAB syntax presented below includes the usual design variable specification in the NEST statement, a SUBPOPN statement to restrict analysis to the subpopulation of women (SEX = 1) and a TABLES statement that defines the cross-tabulation of interest. This example also includes the TEST statement requesting a design-based chi-square test of association. The design-adjusted test statistics available for testing hypotheses about bivariate associations between categorical variables include: Wald F and adjusted Wald F , Wald chi-square and adjusted chi-square, and Satterthwaite (1946) tests.

```
proc crosstab data=one filetype=sas;
nest strata cluster;
```

```

weight weight;
class marcat;
subpopn sex=1;
tables depressed*marcat;
test chisq;
run;

```

The fourth descriptive procedure, PROC VARGEN, is new in SUDAAN Release 11. The VARGEN procedure adds the ability to calculate point estimates and standard errors for functions of estimated means, totals, ratios, percentages, and other statistics. For examples of PROC VARGEN features, see the SUDAAN Language and Examples guides (SUDAAN 11.0.1, Language Guide, RTI [2012]).

Sample VARGEN code below demonstrates basic usage of this command. After the XPER statistics are compiled (weighted estimates of population % who have ever drunk alcohol or ever smoked), a PARAMETER statement is used to compute the difference between the weighted estimates of percentages, EVERDRINK_PER and EVERSMOKE_PER. The CLASS statement is used to separate the output by males and females using the variable SEX, coded 1 if the individual is a male and 2 if female. The CLASS statement is required if the DIFFVAR statement is called. In this procedure, a DIFFVAR statement is used to generate contrasts between males and females for all statistics that are created from the XPER and PARAMETER statistics:

```

proc vargen data = one;
weight analysiswt;
nest stratum cluster;
class sex;
diffvar sex=(1 2) / name = "Male vs. Female";
xper everdrink_per : everdrink / value = 1 name =
"Percent Ever Drink";
xper eversmoke_per : eversmoke /value = 1 name =
"Percent That Have Ever Smoked";
parameter drink_smoke: everdrink_per - eversmoke_per
/ name="Percent Ever Drink minus Percent Ever Smoke";
run;

```

SUDAAN regression procedures include PROC REGRESS (used for linear regression), PROC LOGIST (RLOGIST for SAS-callable SUDAAN, to avoid confusion with SAS PROC LOGISTIC) for logistic regression with binary dependent variables, PROC MULTILOG for logistic regression with ordinal or nominal outcomes, and PROC LOGLINK for count outcomes. Each of the SUDAAN regression procedures uses generalized estimating equations (GEE) for efficient estimation of robust and complex design-corrected variances and standard errors. (Refer to the SUDAAN documentation for details on the implementation of the GEE estimation technique.) These procedures all include appropriate hypothesis testing capabilities.

Linear regression is implemented through PROC REGRESS. This procedure outputs the usual weighted estimates of regression parameters along with robust and complex design-corrected standard errors as well as a design-corrected variance-covariance matrix, model tests, and parameter tests via the TEST statement. Each SUDAAN modeling procedure includes the ability to estimate linear contrasts of regression parameters by using either the CONTRAST or EFFECTS statements as well as optional tests of groups of parameters via the TEST statement. The REGRESS procedure also includes various printed output options such as design effects as well as output data sets for further analysis. Although the SUDAAN SAS-callable version runs within the SAS program, it does not interface with the SAS Output Delivery System directly, but instead produces SAS-type output files. These files can then be used directly within SAS for subsequent analysis.

One typical use of SUDAAN output within SAS might be examination of regression diagnostics and associated graphics using SAS ODS GRAPHICS. Here is syntax for a typical SUDAAN PROC REGRESS example, with a TEST statement (design-adjusted Wald F-test) to test the null hypothesis that the regression parameters for both AGE and SEX are equal to 0, and an OUTPUT statement for producing an SAS data file including estimated parameters (beta) and their standard errors:

```
proc regress data=one;
nest strata cluster;
weight weight;
model income=age sex;
test waldf;
effects sex age / name="test effects of age and sex";
output beta sebeta / filename=outestimate filetype=SAS;
run;
```

Logistic regression analysis is performed using either PROC LOGISTIC or PROC RLOGIST (for SAS-callable SUDAAN). Sample design and weight variables are declared in the usual manner for SUDAAN. Test of contrasts or “chunk” parameter testing is included through use of the EFFECTS statement or the CONTRAST statement. The user should declare the categorical variables in their model using a CLASS statement prior to the MODEL statement. Beginning with SUDAAN Version 9, PROC LOGISTIC/RLOGIST offered the Hosmer–Lemeshow Goodness-of-Fit test (Hosmer et al., 2013). Here is example code for SAS-callable SUDAAN using the JRR variance estimation method, an EFFECTS statement for testing the parameters associated with the indicator variables AGE1, AGE2, and AGE3 against 0, and the HLTEST statement for the H–L Goodness-of-Fit test:

```
proc rlogist data=one method=jrr;
nest str secu;
weight weight;
```

```

class maritalcat;
model depressed=maritalcat female age1 age2 age3;
effects age1 age2 age3 / name="age dummy test";
print / htest=default;
run;

```

Ordinal and multinomial logistic regression is available in PROC MULTILOG. SUDAAN uses a cumulative logit modeling (proportional odds) approach for ordinal dependent variables, and a generalized logit modeling approach for nominal categorical outcomes. See [Chapter 9](#) for details and statistical background on these methods. The user must declare the method in the MODEL statement and the outcome as a categorical variable in the CLASS or SUBGROUP statement of the procedure. For example, the following SUDAAN code uses PROC MULTILOG with an ordinal outcome (self-rated health status, ranging from 1 to 5) and the same predictors as the previous logistic example, along with a test specification for Wald chi-square tests rather than the default Wald F-test:

```

proc multilog data=one;
nest str secu;
weight weight;
class maritalcat healthstatus;
model healthstatus=maritalcat female age1 age2 age3 /
cumlogit;
test waldchi;
effects age1 age2 age3 / name="age dummy test";
run;

```

For a nominal categorical outcome, the syntax would differ in that the categorical variable must be declared in the CLASS statement (e.g., marital status) and the use of "/GENLOGIT" is required on the model statement, indicating a generalized logit estimation method rather than the cumulative logit model for ordinal regression. Like all SUDAAN procedures, the MULTILOG procedure can read in multiply imputed data sets and account for the added variability introduced by imputation as well as the complex sample design.

For Poisson or count-type outcomes ([Chapter 9](#)), SUDAAN offers PROC LOGLINK, which, like PROC LOGIST and PROC MULTILOG uses GEE for estimation and includes relevant design-adjusted hypothesis tests. The dependent variable must be continuous and greater than or equal to 0 for count-type regression models and an offset or logarithm of the offset can also be specified for fitting rate models ([Chapter 9](#)). The predictor variables can be either continuous or categorical. Categorical variables are declared in the CLASS statement prior to modeling. The LOGLINK procedure offers a full range of tests and output options. It can also handle multiply imputed data sets and subpopulation analyses. The example syntax below illustrates

the use of PROC LOGLINK with a count outcome (the number of incidents of asthma per year), a TEST statement for a Wald F -test of the null hypothesis that the regression parameters are equal to 0, and use of the SUBPOPN statement for a subpopulation analysis of black females:

```
proc loglink data=one;
nest str secu;
weight weight;
subpopn female=1 & black=1;
class race;
model numincidents=age race;
test waldf;
run;
```

The SURVIVAL procedure in SUDAAN is used for survival (or time-to-event) analysis with discrete and continuous proportional hazards models that include censored data. This procedure can treat time as either continuous or discrete. For continuous time, SUDAAN uses the Cox proportional hazards model and for discrete time, the program uses a log-likelihood function able to handle ties for time to event ([Chapter 10](#)). Estimated hazard ratios and design-adjusted estimates of standard errors are produced along with optional hypothesis tests for regression parameters and linear contrasts specified by the analyst. The SURVIVAL procedure can also handle time-dependent covariates correctly. Any of the major variance estimation methods can be selected along with the full array of sample design types. One important note is that PROC SURVIVAL does not currently handle multiply imputed data sets. For goodness-of-fit evaluation, Martingale residuals (Therneau et al., 1990) and normalized Schoenfeld (Schoenfeld, 1982) and score residuals are available output options. Here is an example of typical syntax where the event of interest is onset of depression (MDE), the outcome is years until event or censoring (AGEMDE), and the predictors are all time-invariant and categorical (SEX, RACECAT, and EDUCATION).

```
proc survival data=one;
nest str secu;
weight weight;
event mde;
class sex racecat education;
model agemde=sex racecat education;
run;
```

For Kaplan–Meier estimation of survival curves, SUDAAN offers the KAPMEIER procedure ([Chapter 10](#)). The procedure will produce weighted estimates and design-based estimates of standard errors for survival functions ([Chapter 10](#)). SUDAAN's easy output of data facilitates graphical display of survival curves using software such as SAS, Stata, or R. Use of an

OUTPUT statement is required with PROC KAPMEIER and the TIME and EVENT statements are also mandatory. Optional features include unconditional restriction of estimation to a subpopulation via the SUBPOPN statement, alternative methods for variance estimation (JRR, BRR, or Taylor Series), and the STRHAZ statement for estimation of survival rates for subpopulations. Here is an example of SUDAAN syntax for PROC KAPMEIER. The code illustrates the use of the EVENT, TIME, CLASS, STRHAZ, and SUBPOPN statements along with the required OUTPUT statement:

```
proc kapmeier data=one design=wr;
nest str secu;
weight weight;
subpopn women=1;
event depression;
time onsetage;
class agegroup;
strhaz agegroup;
output / kapmeier=all filename="c:\km_all_out"
filetype=sas replace;
run;
```

Imputation of missing data and analysis of imputed datasets can be performed in SUDAAN. PROC IMPUTE is new in Release 11 and serves as a replacement for the former HOTDECK procedure (from Release 10). This procedure includes four methods of item missing data imputation: (1) weighted sequential hot-deck imputation discussed in Cox (1980) and Iannacchione (1982), (2) cell mean imputation (Korn and Graubard, 1999), (3) linear regression imputation, and (4) logistic regression imputation.

Generic syntax for IMPUTE below details use of a required PROC statement, a WEIGHT statement to declare the survey weight, an IMPBY statement to define the variables whose cross-classification defines the imputation classes, and an IMPVAR statement to list the variables that require imputation. As usual, many other optional statements and features are available:

```
PROC IMPUTE DATA=one;
WEIGHT wgtvar;
IMPBY variable(s);
IMPVAR variable(s) / [MULTIMP=integer];
RUN;
```

Most SUDAAN analysis procedures support analysis with multiply imputed data, with the exception of the VARGEN, SURVIVAL, and KAPMEIER commands.

In summary, SUDAAN is an excellent tool for survey data analysis. It accommodates a wide range of sample designs and offers a variety of variance estimation methods, numerous analytic tools, and frequent updates as new statistical theory and methods emerge. It is relatively easy to learn given

the similarity to SAS syntax, and produces output files that are ready to use in other more general packages for graphing and reporting or further analysis. See the book web site for the SUDAAN code that replicates the example analyses in Chapters 5 through 12.

A5 Overview of SPSS® V22

We next review IBM/SPSS Version 22 (www.spss.com) with a focus on the Complex Samples module. This module offers many survey data analysis tools as well as the full range of usual SPSS features to perform data management, analysis, and graphing tasks (via commands that are a part of the main SPSS package). An added feature of this software is that it offers a dual option of running the procedures with either a point-and-click approach (and optionally saving the generated syntax) or running the procedures directly via generation of command syntax by the analyst. The tutorials for each of the Complex Samples (CS) commands are excellent and provide a step-by-step path through the command options as well as interpretation and examples of model fit and other considerations that arise during the analysis process.

All survey data utility and analysis commands are contained in the Complex Samples section of the installation. SPSS V22 offers a number of complex samples routines including sampling plan (CSSample) and analysis plan (CSPlan) “wizards” for sample selection and data preparation prior to analysis, along with a number of “Complex Samples” analysis commands: frequencies (CSTABULATE), descriptives (CSDESCRIPTIVES), crosstabs (CSTABULATE), ratios (CSRATIOS), general linear models (CSGLM), logistic regression with binary or multinomial outcomes (CSLOGISTIC), ordinal regression (CSORDINAL), and Cox regression (CSCOX) for survival analysis.

The analysis plan wizard allows the analyst to specify a number of complex sample designs, such as With-Replacement selection of ultimate clusters (WR), equal-size clusters Without Replacement (WOR), and unequal-size clusters Without Replacement (WOR) along with the FPC ability. All analysis commands use the Taylor Series Linearization method for variance estimation and allow the use of a subpopulation indicator, the ability to perform appropriate design-based hypothesis tests, and additional options such as estimation of design effects and other optional statistics. Version 22 of SPSS does offer the option to use multiple imputation for missing data problems. However, it does not offer the ability to analyze multiply imputed data sets with Complex Samples procedures (standard SPSS procedures can be used with multiply imputed data sets). This limitation effectively means that SPSS can be used to impute missing data in survey data sets but another software tool would be required to correctly analyze these data sets.

A5.1 SPSS Complex Samples Commands

Two commands comprise sampling and analysis plan setup utilities: CSSAMPLE and CSPLAN. The CSSAMPLE procedure provides the ability to generate probability samples from existing sample frames (similar to PROC SURVEYSELECT in SAS), while the CSPLAN routine is designed to establish the complex sample “analysis plan” in preparation for analysis. The CSPLAN command asks the analyst to specify the survey weight and stratum and PSU (or cluster) variables required for sampling error calculations to the program. This command generates a “plan” file that is then saved for use with any of the SPSS CS analysis commands. Here is an example of a typical CSPLAN command, including the setup of the complex design features and identification of the survey weight and the stratum and cluster codes for sampling error calculations. The file generated by running this command (csplan1.csplan) can then be used throughout the analysis session and/or edited during the session if desired.

```
* Analysis Preparation Wizard.
CSPLAN ANALYSIS
  /PLAN FILE='C:\csplan1.csplan'
  /PLANVARS ANALYSISWEIGHT=NCSRWTLG
  /SRSESTIMATOR TYPE=WR
  /PRINT PLAN
  /DESIGN STRATA=SESTRAT CLUSTER=SECLUSTR
  /ESTIMATOR TYPE=WR.
```

There are four SPSS “CS” commands for descriptive analysis and four for various forms of regression analysis. In the descriptive group, CSFREQUENCIES and CSCROSSTABS are used for analysis of categorical data, CSDESCRIPTIVES for continuous variables, and CSRATIOS for ratios. CSTABULATE drives both CSFREQUENCIES and CSCROSSTABS for one and two-way table analysis and generates unweighted and weighted frequency counts, weighted estimates of proportions, linearized standard errors, confidence limits, design effects, and a Wald F-test of equal cell proportions. There are also options for subpopulation analysis and for handling missing data with either listwise or table-by-table deletion. The SPSS program menus list two options that use the CSTABULATE command: frequencies and crosstabs. Here is typical SPSS syntax for this command including options for estimated population cell size, linearized standard errors, confidence limits, design effects, and a test for cell homogeneity for a single categorical measure of obesity (OBESE6CA):

```
* COMPLEX SAMPLES FREQUENCIES.
CSTABULATE
  /PLAN FILE='C:\CSPLAN1.CSAPLAN'
  /TABLES VARIABLES=OBESE6CA
  /CELLS POPSIZE
```

```
/STATISTICS SE CIN(95) DEFF
/TEST HOMOGENEITY
/MISSING SCOPE=TABLE CLASSMISSING=EXCLUDE.
```

Note that the analysis command refers to the “plan” file generated earlier, describing the complex design features.

The CSDESCRIPTIVES command performs descriptive analyses of continuous variables and includes similar options to CSTABULATE except for the test of equal cell proportions. The following syntax example illustrates the use of a subpopulation indicator variable for women (SEXF) and requests the square root of the design effect (or DEFT) along with the standard output of standard errors, confidence limits, and a design effect. A *t*-test of the null hypothesis that the mean of AGE is equal to 0 is also requested:

```
* COMPLEX SAMPLES DESCRIPTIVES.
CSDESCRIPTIVES
  /PLAN FILE='C:\CSPLAN1.CSAPLAN'
  /SUMMARY VARIABLES=AGE
  /SUBPOP TABLE=SEXF DISPLAY=LAYERED
  /MEAN TTEST=.05
  /STATISTICS SE DEFF DEFFSQRT CIN(95)
  /MISSING SCOPE=ANALYSIS CLASSMISSING=EXCLUDE.
```

The CSCROSSTABS command is designed for the design-based analysis of two-way or *n*-way contingency tables. This code is actually using a variant of the CSTABULATE command for *n*-way contingency table analysis and includes options for weighted estimates of row and column percentages, linearized standard errors, DEFF, DEFT, confidence limits, and coefficient of variation (for design corrections; [Chapter 6](#)) along with a design-based test for independence of rows and columns. For 2 × 2 tables, the analyst can request odds ratio and risk ratio statistics. This example illustrates a 2 × 4 cross-tabulation of SEX by REGION along with many of the available table options:

```
* Complex Samples Crosstabs.
CSTABULATE
  /PLAN FILE='C:\csplan1.csaplan'
  /TABLES VARIABLES=SEX BY REGION
  /CELLS POPSIZE ROWPCT COLPCT
  /STATISTICS SE CV CIN(95) DEFF
  /TEST INDEPENDENCE
  /MISSING SCOPE=TABLE CLASSMISSING=EXCLUDE.
```

The CSRATIOS command utilizes the CSDESCRIPTIVES command and performs a ratio analysis ([Chapter 5](#)) by declaring the numerator and denominator variables for the ratio statistic. This example illustrates estimation of the ratio of taxable income (TAXINC) to all income (ALLINC) and requests

that SPSS output linearized standard errors and 95% confidence limits using the default missing data option of table-by-table exclusion:

```
* Complex Samples Ratios.
CSDESCRIPTIVES
  /PLAN FILE='c:\csplan1.csaplan'
  /RATIO NUMERATOR=TAXINC DENOMINATOR=ALLINC
  /STATISTICS SE CIN(95)
  /MISSING SCOPE=ANALYSIS CLASSMISSING=EXCLUDE.
```

The SPSS regression commands for complex sample survey data include CSGLM for continuous outcomes, CSLOGISTIC for binary or nominal outcomes, CSORDINAL for ordinal logistic regression, and CSCOXREG for survival analysis with the Cox Proportional Hazards model (Cox, 1972; [Chapter 10](#)). All of these commands include subpopulation analysis options, complex design-corrected standard errors, and hypothesis testing appropriate for the procedure used.

The CSGLM command performs regression analyses for continuous dependent variables and offers the usual features such as design-based standard errors for parameter estimates, design-based confidence limits for parameters, design effects and square roots of design effects, subpopulation analysis, and hypothesis testing. Specifically, the hypothesis tests include unadjusted and adjusted Wald F and chi-square tests for model parameters, and degrees of freedom specifications based on either the sample design or a fixed number of degrees of freedom. There is an optional estimated means technique for estimation of marginal effects for factors included in the model. This example shows syntax for a basic linear regression for household income (HHINC) with a number of options specified (confidence limits, design effects, and F -tests):

```
* COMPLEX SAMPLES GENERAL LINEAR MODEL.
CSGLM HHINC WITH AGE REGION
  /PLAN FILE='C:\CSPLAN1.CSAPLAN'
  /MODEL AGE REGION
  /INTERCEPT INCLUDE=YES SHOW=YES
  /STATISTICS PARAMETER SE CINTERVAL DEFF
  /PRINT SUMMARY VARIABLEINFO SAMPLEINFO
  /TEST TYPE=F PADJUST=LSD
  /MISSING CLASSMISSING=EXCLUDE
  /CRITERIA CILEVEL=95.
```

See the book web site for replication of example analyses presented in [Chapter 7](#) using the CSGLM procedure.

The CSLOGISTIC command is used to fit design-based logistic regression models to binary or multinomial outcomes. This command offers options and hypothesis testing specific to logistic regression modeling. The command also includes two options for assessing model fit: a classification approach

or calculation of Pseudo R-Square values (Cox and Snell, 1989). Analysts can request that estimates of odds ratios and confidence limits for the ORs be displayed, in addition to hypothesis tests including the Wald F and chi-square tests, both design-adjusted and unadjusted. The Pseudo R-Square statistics are based on calculations suggested by Cox and Snell (1989), Nagelkerke (1981), and McFadden (1974) but are not design-adjusted in this version of SPSS. Other available options include display of correlations and covariances among parameter estimates, subpopulation analysis, and design effects. The CSLOGISTIC command can also perform pairwise comparisons of predicted probabilities between levels of categorical predictor variables for fixed values of model covariates (see [Chapter 8](#) and the SPSS documentation for details). Here is example syntax to fit a logistic regression model to a dichotomous outcome (MDE), with common options of odds ratios, confidence limits, design effects, and specification of the reference category for the outcome variable (see the book web site for additional examples):

```
* COMPLEX SAMPLES LOGISTIC REGRESSION.  
CSLOGISTIC MDE (LOW) WITH SEXF BMI AGECENTERED  
/PLAN FILE='C:\CSPLAN1.CSAPLAN'  
/MODEL SEXF BMI AGECENTERED  
/INTERCEPT INCLUDE=YES SHOW=YES  
/STATISTICS PARAMETER EXP SE CINTERVAL DEFF  
/TEST TYPE=F PADJUST=LSD  
/MISSING CLASSMISSING=EXCLUDE  
/CRITERIA MXITER=100 MXSTEP=5 PCONVERGE=[1E-006  
RELATIVE] LCONVERGE=[0] CHKSEP=20 CILEVEL=95  
/PRINT SUMMARY VARIABLEINFO SAMPLEINFO.
```

The CSORDINAL command is designed for fitting ordinal logistic regression models. There are a number of link options within the CSORDINAL command, including logit, complementary log-log, and probit. The command includes options specific to this type of logistic regression analysis for ordinal outcomes, such as calculation of Pseudo R-Square statistics (not design-adjusted) (Cox and Snell, 1989) for model fit, a design-adjusted test for the proportional odds assumption ([Chapter 9](#)) as well as the usual options for any type of logistic regression (hypothesis tests and output options noted above). Here is an example of the syntax for the CSORDINAL command:

```
* COMPLEX SAMPLES ORDINAL REGRESSION.  
CSORDINAL ED4CAT (ASCENDING) WITH MDE BMI  
/PLAN FILE='C:\CSPLAN1.CSAPLAN'  
/LINK FUNCTION=LOGIT  
/MODEL MDE BMI  
/STATISTICS PARAMETER EXP SE CINTERVAL  
/NONPARALLEL TEST  
/TEST TYPE=F PADJUST=LSD  
/MISSING CLASSMISSING=EXCLUDE
```

```
/CRITERIA MXITER=100 MXSTEP=5 PCONVERGE=[1E-006
RELATIVE] LCONVERGE=[0] METHOD=NEWTON CHKSEP=20 CILEVEL=95
/PRINT SUMMARY VARIABLEINFO SAMPLEINFO.
```

For design-based survival analyses, SPSS includes the CSCOXREG command. This command models hazard rates using the Cox Proportional Hazards model for outcomes representing times to events, and can handle both time-varying and time-invariant covariates. One key difference between CSCOXREG and the other SPSS CS commands is that the structure of the data set is often organized with multiple and varying numbers of records per individual. (See the discussion of discrete time survival models, “person-time” data structures, and time-varying covariates in [Chapter 10](#).) The “person-time” data structure is used to reflect discrete observational times when events of interest such as year one of life to onset of an illness or censoring can be observed. The analyst can provide a multiple record file or a one record per individual file, or create the needed data set within the command directly. The CSCOXREG command includes subpopulation analysis, hypothesis testing, control over the degrees of freedom used for significance testing (either based on the sample design or a fixed value), and the ability to perform multiple comparisons of hazard rates for groups defined by categorical variables. Like all SPSS regression commands, predictors that are categorical are defined as “factors” and “covariates” are treated as continuous predictors. Other options include declaration of the “event” of interest, a variable representing time at which the event occurred (for noncensored cases), and a test of the proportional hazards assumption (see [Chapter 10](#) for details). Options for displaying estimated survival plots for models with and without covariates are also built into the command, which is a nice feature, and simple Kaplan–Meier curves can be displayed as well. Here is an example of the use of the CSCOXREG command for modeling time until onset of depression or time to censoring if no event occurred (AGEEVENT):

```
* COMPLEX SAMPLES COX REGRESSION.
CSCOXREG AGEVENT BY OBESE6CA WITH SEXF
  /PLAN FILE='C:\CSPLAN1.CSAPLAN'
  /VARIABLES STATUS=MDE(1)
  /MODEL OBESE6CA SEXF
  /PRINT SAMPLEINFO EVENTINFO
  /STATISTICS PARAMETER EXP SE CINTERVAL
  /TESTASSUMPTIONS PROPHAZARD=KM
  /PLOT SURVIVAL CI=NO
  /TEST TYPE=F PADJUST=LSD
  /CRITERIA MXITER=100 MXSTEP=5 PCONVERGE=[1E-006 RELATIVE]
  LCONVERGE=[0] TIES=EFRON CILEVEL=95
  /SURVIVALMETHOD BASELINE=EFRON CI=LOG
  /MISSING CLASSMISSING=EXCLUDE.
```

As previously mentioned, the CSCOXREG command can also produce Kaplan–Meier survival curves when used as a survival model without predictors. This approach will output a survival curve and baseline survival and cumulative hazards tables along with complex design-corrected standard errors, and offers numerous types of plots such as survival, failure, hazard, and log–log of the survival function. This code illustrates how to request a K–M survival curve from the CSCOXREG command.

```
* Complex Samples Cox Regression.  
CSCOXREG AGEEVENT  
  /PLAN FILE='c:\ncsr_p1wt.csaplan'  
  /VARIABLES STATUS=mde(1)  
  /PRINT SAMPLEINFO EVENTINFO BASELINE  
  /STATISTICS PARAMETER SE  
  /TESTASSUMPTIONS PROPHAZARD=KM  
  /PLOT SURVIVAL CI=YES  
  /TEST TYPE=F PADJUST=LSD  
  /CRITERIA MXITER=100 MXSTEP=5 PCONVERGE=[1E-006  
RELATIVE] LCONVERGE=[0] TIES=EFRON CILEVEL=95  
  /SURVIVALMETHOD BASELINE=EFRON CI=LOG  
  /MISSING CLASSMISSING=EXCLUDE.
```

A6 Overview of Additional Software

In this section, we present an abbreviated overview of four additional software tools for complex sample survey data analysis: WesVar (version 5.1), the R survey Package (version 3.31), IVEware (version 0.3), and Mplus (version 7.4). For each of these software packages, we provide general guidance on overall features and recommended usage but omit syntax examples. Please refer to the book web site for analysis examples and code samples.

A6.1 WesVar

WesVar Version 5.1 is an excellent software tool for survey data analysis and is produced by the Westat organization (www.westat.com/wesvar). WesVar is primarily a repeated replication tool for the analysis of survey data (in terms of variance estimation) and is available free of charge. It features a point-and-click interface, organizes projects in “workbooks” for shared use, and is quite flexible in terms of data types accepted. For example, the software is able to read in data sets from SPSS, SAS, Stata, SPlus/R, Excel/Access, ASCII, and relational database products. A key strength of WesVar is its ability to create replicate weights within the program as well as handle existing replicate and probability weights. It also offers a full range of repeated

replication methods for variance estimation, such as JRR for two-per-stratum or n -per-stratum cluster samples, BRR, and BRR with Fay's adjustment. Subpopulation analyses can be performed with the use of a subgroup variable statement in each procedure. The analytic procedures of WesVar include the usual descriptive analyses plus the optional estimation of percentiles adjusting for complex design features. In terms of procedures for regression analysis, WesVar can fit linear regression models to continuous outcomes and logistic regression models to dichotomous or unordered outcomes. All analytic techniques include design-adjusted hypothesis tests as well as the ability to use multiply imputed data sets. Westat provides excellent online documentation rich with examples for readers interested in using WesVar.

A6.2 IVEware (Imputation and Variance Estimation Software)

IVEware V0.3 is a free software tool produced and maintained by the University of Michigan Survey Methodology Program (www.iveware.org). IVEware runs either as a stand-alone tool or as an external software-callable tool. Though the software was originally based on SAS macros, Version 0.3 can now be executed from an XML-based editor by calling SAS, R, SPSS, Stata, or the stand-alone version of IVEware. In addition, the software can be run from within the SAS, R, SPSS, or Stata packages. Given the wide range of execution options, please see the IVEware V0.3 User's Guide and web site for examples (Raghunathan et al., 2016).

This software offers imputation and variance estimation for complex sample survey data analyses through the following macros: %IMPUTE, %DESCRIBE, and %REGRESS. In addition, the package offers %SASMOD, which allows the SAS user to perform complex sample survey data analyses for additional SAS procedures not included in the %DESCRIBE or %REGRESS modules (see the user documentation for a list of %SASMOD procedures available). Additional macros include %SYNTHESIZE, which produces synthesized and optionally imputed data sets which address data security concerns, %BBDESIGN, a macro that uses a weighted finite population Bayesian Bootstrap to expand data sets to create population data sets that reflect the complex sample design, and %COMBINE, used to combine multiple data sources for imputation and/or subsequent analysis.

The %DESCRIBE, %REGRESS, and %SASMOD modules are used for survey data analysis. All three analysis modules can utilize multiply imputed (%IMPUTE), synthesized (%SYNTHESIZE), weighted finite population Bayesian Bootstrap data sets (%BBDESIGN) or standard survey data sets, and analyze the survey data using appropriate design-based techniques for variance estimation. Please refer to the IVEware User's Guide for details on correct combining rules for data sets from %SYNTHESIZE and %BBDESIGN. The %DESCRIBE module will perform various descriptive analyses such as estimation of means, contingency tables, and ratios with design-based variances estimated using the Taylor Series Linearization method. The %REGRESS

module provides the user with a variety of regression techniques, including linear, logistic (binary, multinomial, ordinal), Tobit, Poisson, and proportional hazards modeling for survival analysis. The %SASMOD command enables use of SAS procedures with the JRR variance estimation approach and permits design-based estimation for procedures not covered by the SAS SURVEY procedures. An advantage of IVEware is the ability to impute missing data using the flexible multivariate sequential regression technique of Raghunathan et al. (2001) and then analyze the multiply imputed data sets using the correct design-based variance estimation methods.

A6.3 Mplus

Mplus Version 7.4 (<http://www.statmodel.com/>) is a relatively new (initially developed during the late 1990s) and advanced analysis tool designed primarily for complex statistical modeling. Mplus includes complex design corrections for every analytic technique in the package, including advanced structural equation modeling (Chapter 13). These techniques are analytically advanced, including single and multilevel models, observed and latent variables, and approaches for cross-sectional and longitudinal data. Mplus offers the ability to handle multiply imputed data sets or files with missing data and can analyze a wide range of outcomes: continuous, categorical (binary, nominal, ordinal), count, censored, or various combinations of these variables.

A very useful feature of Mplus is the flexibility to approach survey data analysis in two ways. The first approach, termed the “design-based approach” in this book and elsewhere, uses variables that represent the stratification and clustering inherent to the sample design and subsequently adjusts variances taking these design features (and sample weighting) into account. The second approach incorporates design features directly within the multiple levels of the model framework (multilevel modeling) and accounts for stratification and clustering within the model specification.

Multiply imputed data sets can be used with all Mplus routines and sub-population options are also available. Though Mplus is a very useful and advanced addition to the set of software for survey data analysis, most analysts would perform data management and descriptive analyses in other software because Mplus does not offer a direct or simple way to accomplish these tasks.

A6.4 R survey Package

The R survey package (visit <http://www.r-project.org/>, where links to CRAN web sites can be used to download the specific package) is a free software tool that offers a full range of survey data analysis techniques. R and the R survey package (version 3.31 reviewed here) are excellent software tools that can analyze survey data using the Taylor Series Linearization

method, repeated replication techniques (JRR or BRR) or bootstrap techniques for design-based variance estimation. Another nice feature is that the survey package is frequently updated by the developer, Thomas Lumley (2016). It handles multistage cluster designs and unequally weighted sample designs, and offers estimation of descriptive statistics, linear and generalized linear models, and cox proportional hazards models for survival analysis. All descriptive analysis and modeling commands include appropriate hypothesis testing options. Also included are survey-adjusted graphics and options such as subpopulation analysis and special survey weighting adjustments that employ raking, calibration, and poststratification to external controls. Multiple imputation and analysis of multiply imputed data is available in the R `mi` tools suite of commands. For a guide to use of the package with complex sample survey data, see Lumley (2010). In summary, this is an excellent survey analysis tool provided that the analyst is familiar with the use of R procedures and R language concepts. However, it does not offer extensive point-and-click tools and would be somewhat of a challenge to learn for an inexperienced data analyst.

A7 Summary

This appendix has presented a brief overview of current software packages with the goal of providing practical guidance on basic capabilities and options for the survey data analyst. Each of the reviewed software packages has basic programs to analyze complex sample survey data and most include important features such as subpopulation analysis, hypothesis testing, ability to handle strata with single PSUs, multiple imputation analysis, and other key survey data analysis features. Although the software alternatives may differ in terms of program offerings for more specialized analyses or advanced modeling (e.g., Structural Equation Modeling in Mplus, Kaplan–Meier survival function estimation in SUDAAN and SPSS, Fractional Imputation in SAS), each of the packages (Stata, SAS, SPSS, SUDAAN, WesVar, IVEware, R, and Mplus) is capable of performing the near totality of analyses that survey practitioners will need to use on a day-to-day basis. The ultimate choice of software is a complex decision that will also involve data management considerations, existing familiarity with the software system, and other factors specific to the individual analyst. In the end though, given the common underlying theory and methods, basic features, and usability inherent in all of these software packages, it would be difficult to make a bad choice.

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