

PREFACE

Perspective

Demography is the taproot of an interdisciplinary tree containing multiple branches whose demographic topics range from health, disease, marriage, and fertility to anthropology, population biology, paleontology, history, and education. Our book now adds a new branch to this tree—biodemography.

We have two major goals for this book. The first is to collate, merge, integrate, and synthesize the key literature from two epistemological domains concerned with demography. The first domain is the taproot itself; that is, mainstream human demography. This domain constitutes a field that straddles the social and formal sciences and serves as the primary pedagogical foundation for our book. The second domain is the emerging branch of demography that makes our book biodemography. That is the literature concerned with demographic concepts on or related to biology, including ecology and population biology of plants and animals, biogerontology, epidemiology, and biomedicine as well as the more applied areas such as wildlife biology, invasion biology, pest management, and conservation.

Our second goal is revealed in the book's subtitle, *Introduction to Concepts and Methods*, where our aim is to include the *conceptual* underpinnings for all demographic *methods*. Whereas the conceptual aspects serve as the basic ideas and then situate these ideas into demographic contexts, the methodological components provide a complementary operational framework. For example, life tables are useful for summarizing the actuarial properties of cohorts. But without a deeper appreciation of the underlying concepts of mortality, survival, risk, life-years, and life expectancy, life tables themselves are dry accounting tools at best and simple "cookbooks" at worst. Likewise, observing the ergodic dynamics of stable population theory using Leslie matrix population projections deepens an understanding of the formal mathematical properties that underlie these projections.

One goal we do not have for this book is to make any attempt to match, much less supersede, the scope or mathematical sophistication of any of the number of truly remarkable textbooks, reference books, handbooks, or book series in mainstream (human) demography. Rather, we strongly recommend that readers seek out these sources in order to both deepen and broaden their knowledge of demographic concepts and methods. A particularly deep source for demographic information is the awe-inspiring 140-chapter, four-volume series titled *Demography: Analysis and Synthesis—A Treatise in Population* edited by Graziella Caselli, Jacques Vallin, and Guillaume Wunsch (2006a). Other excellent sources of demographic concepts, models, methods, and techniques include two textbooks, one by Samuel Preston, Patrick Heuveline, and Michel Guillot titled *Demography: Measuring and Modeling Population Processes* (2001) and the other by Dudley Poston and Leon Bouvier titled *Population and Society: An Introduction to Demography* (2010). The book by Kenneth Wachter (2014) titled *Essential Demographic Methods* is an excellent source

for clear, succinct presentations of basic demographic concepts. Nathan Keyfitz's book *Applied Mathematical Demography*, the third edition of which was coauthored with Hal Caswell, is a treasure trove of demographic models and ideas (2010). Excellent edited books on demography include the 22-chapter book edited by Jacob Siegel and David Swanson titled *The Methods and Material of Demography* (2004) and the 28-chapter *Handbook of Population* edited by Dudley Poston and Michael Micklin (2005). The book by Frans Willekens titled *Multistate Analysis of Life Histories with R* (2014) is one of a number of excellent more specialized books in the Springer Series on Demographic Methods and Population Analysis, which is edited by Kenneth Land.

Organization of the Book

There are 11 chapters that we separate into two parts. The first part (chapters 1–7) consists of chapters covering more traditional (albeit biologically oriented) demographic content that is considered standard fare among mainstream demographers. Chapter 1 contains the demographic basics and foundational concepts, such as life course, rates, and Lexis diagrams. Chapter 2 contains life table concepts and methods, including construction of period, cohort, and abridged tables. Chapter 3 covers the basics of mortality, including its importance in demography, derivation of the force of mortality, mortality metrics, the main mortality models, demographic heterogeneity, and selection. Chapter 4 contains basic information on reproduction, ranging from age-specific and lifetime birth metrics to reproductive heterogeneity, parity progression, and fertility models. Chapters 5, 6, and 7 cover population concepts and methods. The first of these introduces stable population theory, including Lotka and Leslie models; the next introduces stage-based matrix models, including the Lefkovich model, and considers life table–stable theory congruency; and the last considers extensions of stable theory, such as two-sex and stochastic models.

In the second part (chapters 8–11) we move from the foundational concepts of demography to topics focused on areas that are either more specialized, more biologically relevant, more novel, or more idiosyncratic. This content includes chapter 8 on human demography, which summarizes various aspects of human demography as well as includes topics that are often not covered in books on general human demography, such as family demography and kinship. This is followed by chapters 9 and 10 on applied demography. Chapter 11 then contains descriptions of, and solutions to, demographic questions that we refer to as “demographic shorts.” These narratives include a wide range of demographic concepts that are novel, heuristic, inherently interesting, thought provoking, or too mathematically complex for other chapters, but they are nonetheless relevant to our larger goals.

We complete the book with four appendixes, including appendix I on data visualization for demographic data, appendix II on demographic storytelling, appendix III that presents ten visualization rules of thumb, and appendix IV on data management.

Editorial Strategies

The editorial challenges in producing this book involved technical, philosophical, and epistemological components concerning decisions on (1) which material to include from each of the two primary literature domains of biology and demography, (2) how best to collate, integrate, and synthesize this information, and (3) determining the best practices for illustrating concepts and methods. The purpose of this preface is to provide context and background for meeting these challenges.

Data selection

Because the richness of demographic concepts, methods, and models is best illustrated with the use of data, the paucity of high-quality databases for nonhuman species posed one of our greatest challenges. What is taken for granted by mainstream demographers, who have access to databases consisting of detailed demographic information on tens of thousands if not tens of millions of people, is only a fantasy for scientists studying the demography of nonhuman species. No databases exist in biology that are even remotely close to the quality and quantity of those available for human studies.

A related challenge is an outcome of the fact that most demographic models were inspired by, developed for, and applied to humans. Indeed, the contours of the life history of *Homo sapiens* have framed the demographic questions and shaped the mathematical models where the human life history consists of, for example, sexual mating (e.g., no hermaphroditism, self-fertilization, or sterile castes), continuous development (e.g., no dormant stages, metamorphosis, or strong seasonality), potentially 100 or more age classes (i.e., an extremely long potential life span), and mostly singleton births (i.e., not litters, clutches, broods, clones, or seed set). Application of these models, originally developed for humans, for use in biodemography requires that, to greater and lesser degrees, they be adapted to vastly different life histories across the Tree of Life, including for species from within and between different kingdoms, phyla, classes, families, and genera.

In light of the challenges of model applicability and data availability for biodemography, and given our overarching goals for this book, we devised a data use strategy in which we selected demographic information based on three purposes.

- (1) *Concept elucidation.* We believe that in order to understand the basics of biodemography, which involves life tables, mortality, reproduction, and stable population theory, we need to use databases consisting of detailed information on thousands, if not tens of thousands, of individuals that were both maintained and monitored under carefully controlled conditions. Although there are scores and perhaps hundreds of studies that meet most of these criteria, many studies lack the scale and raw data that are needed, such as age-specific births for each individual. We thus draw heavily on the fruit fly databases of coauthor Carey to elucidate the concepts and methods contained in the first five chapters.
- (2) *Human demography.* We felt that including human demography was important since it provides us with ways to broaden the reader's demographic

perspective as well as, and especially, add demographic depth and breadth. There are a number of concepts and models, such as multiple-decrement life tables, family demography models, and Lexis diagrams, that are regularly used in human demography but not in biodemographic contexts with nonhuman species.

- (3) *Applied biodemography*. Population biologists and applied ecologists have been developing and using models for well over a century, and many models and databases on nonhuman species are available in the literature that we could have used to parameterize the models presented. Whereas we illustrate many of the basic concepts using databases on either fruit flies or humans, we illustrate most of the applied content using other species, including birds, mammals, reptiles, and plants.

Tabulation and visualization

As strong believers in the power of visualization and illustration in teaching and learning, another editorial strategy we have used is to make liberal use of tables, graphs, and schematics to enhance conceptual and methodological clarity. Different content calls for different categories of each of these. For example, the different types of tables and figures we develop and use in our book include

- (1) *Heuristic models*. Small, simplified tables of hypothetical data used to illustrate a mathematical concept (similar to what statisticians refer to as *toy models*).
- (2) *Complete data*. Information for all age classes for species where the details contained in the patterns and quantities in all ages classes is important to illustrate the concept or method.
- (3) *Abridged data*. Usually, tables containing age-specific data for models and methods where it is less important to have complete age information.
- (4) *Summary information*. Tables typically containing information not age related.

Our visualization strategies include the abundant use of a wide variety of data graphs and schematics throughout the book, including appendixes for outlining and illustrating best practices in the visualization of demographic information. As Few (2013) notes, information flows to the viewer in the clearest and most efficient way when a chart is presented properly. Indeed, best practices in information design and typography matter because they help conserve the most valuable resource people have as writers and presenters—*reader and viewer attention* (Butterick 2015).

Concepts and models

As long-time instructors of a wide range of university subjects, including classes on evolution, aging, and demography, it is difficult for us to overstate the importance of using clear descriptions of the underlying concepts, including their mathematical foundation(s), and of using either hypothetical or real-world examples. The life table, for example, is essentially a tool for ordering actuarial information by age.

However, this tool can be transformed into an overarching concept when mortality is considered in actuarial and dynamic contexts, and into a mathematical model when various formulas are brought to bear on the data.

Epistemological

Unlike interdisciplinary fields such as biochemistry, historical economics, and mathematical statistics, which straddle two or more disciplines *within* larger scientific domains, the interdisciplinary field of biodemography bridges three scientific domains: the natural sciences (biology), the social sciences (demography), and the formal sciences (mathematical modeling). Whereas virtually all disciplines within the social sciences (demography) generate new knowledge primarily through observation, nearly all disciplines in the natural sciences (biology) generate new knowledge primarily through experimentation. Remarkably, integration of the formal sciences (i.e., mathematic/statistical modeling) into biology and especially into demography set the stage for the emergence of biodemography as a subfield of each of these parent disciplines. For example, the multistate models used widely in demography are virtually the same as the age/stage models used widely in ecology and population biology; the life-lived and -left concept discovered in formal demography is identical to the age structure and death rate identity discovered in biodemography; and the multiregional models used in demography are similar in concept to the metapopulation models used in population biology. Identifying these and many other interdisciplinary connections is important because the common mathematical models point to similar interdisciplinary concepts, which then lead toward interdisciplinary syntheses. Moreover, cross-references to similar mathematical models developed independently by scientists in different fields synergize science by making the scientists in the respective fields aware of the generality of the original models and thus of the underlying concepts themselves.

Human Demography in the Tree of Life Context

Human biology and the shaping of mainstream demography

For perspective on the challenges of using mainstream demographic concepts and tools in biological contexts, consider the entire corpus of formal demography, not only in the context of human demography but also in the context of the demography of species across the entire Tree of Life (Jones et al. 2013). As we discuss below, it becomes manifestly evident that classical demography is framed almost exclusively by *Homo sapiens*' life history traits, enabled by demographic databases on humans that are as large as they are detailed. Approaches are modeled using the birth, death, and migration processes that are specific to our species and that shape our populations. Our comparisons between the demographic characteristics of humans and the characteristics of species across the Tree of Life spectrum both highlight and underscore the conceptual constraints, methodological limitations, and empirical inadequacies for off-the-shelf application of demographic methods that were both informed by and created for use in human demography. The comparisons also provide insights into the species-specific demographic requirements for the

unmodified use of classical demographic tools such as the life table and stable theory, as well as the underlying motivation and need for biologists to develop new concepts and tools that are relevant to the great many species whose demography cannot be easily described and modeled using conventional tools.

Demographic characteristics

Humans exist as clearly defined individuals—single entities that are unequivocally, unambiguously, and unmistakably discrete. The existence of species as separate, identifiable individuals is an implicit requirement for virtually all types of the more conventional demographic analyses of cohorts and populations. However, clearly defined individuals do not exist for many species of plants (e.g., aspens) and animals (e.g., corals) whose populations consist of expanding clones. Different levels of individualism may also exist for nonhuman species. The best example here is that of social insects whose individualism can be considered at two levels—the individual as the single insect itself, the honeybee worker, and the individual as a superorganism representing the second tier of the hierarchy, the honeybee colony.

Whereas humans and most other species of animals can move, this is not the case for species of plants and for many species of animals, such as barnacles after they enter their sessile (anchored) stage. Humans are warm blooded so that the chronological age of each person essentially defines his or her stage in life. This is not the case for the vast majority of organisms because, with the exception of birds and mammals (homeotherms), members of all other groups of organisms cannot control their temperature (poikilotherms). This means that, to greater and lesser extents, their demographic traits are driven by temperature and other factors that affect their biological age. Humans do not hibernate, estivate, quiesce, diapause, or otherwise become dormant. This is not the case for a large number of species who often enter dormancy-related stages ranging from tardigrades, insects, and other arthropod species to bears, rodents, and small birds. Humans also do not undergo metamorphosis like species of holometabolous insects, amphibians, or even some plants. Unlike species that reproduce by cloning or self-fertilization, humans reproduce sexually. Humans pair-bond, breed throughout the season, produce singleton offspring, and create families that consist of offspring of overlapping ages, each of which is cared for by both parents for 15 to 20 years. Human family units may last 50 or more years. The model for human families is unique to *H. sapiens* even in broad outline much less in fine detail. Relative to preadult survival for the vast majority of nonhuman species, which produce hundreds and even tens of thousands of offspring, human survival is extremely high. Whereas humans can live more than a century and thus have over 100 age classes (years), the life spans of the vast majority of bird and mammal species are much shorter and therefore have many fewer age classes. This high survival and long life in humans has profoundly affected the demographic methods and models that have been developed for use in mainstream, formal demography.

Databases

Demographic databases on humans often contain precise records on the sex, age, marital and family status, and medical/health conditions for individuals as well as on their manners, causes, and ages of death. The size of these databases, and the

individual-level details they contain, enable demographers to estimate a wide variety of demographic rates for humans (e.g., reproduction; death; marriage; divorce) with great accuracy and precision for all but the most extreme ages. The databases on human demography stand in glaring contrast to the databases for all other species, those for model species (worms, flies, rodents) notwithstanding. No database exists on nonhuman species that is even remotely similar to databases for human demography with respect to numbers, cradle-to-grave details, and historical duration.

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