CHAPTER 22

Mathematical Demography

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INTRODUCTION

Mathematical demography is a specialization in demography concerned with the articulation, analysis, and empirical application of theoretical models or representations of populations and demographic processes via the use of mathematics, including mathematical statistics. It has its roots in actuarial science, biology, mathematics, and statistics, fields with which it retains strong ties today (see, e.g., Jordan 1975; Keyfitz 1977a, 1977b; Lotka 1924[1956]; Smith and Keyfitz 1977).

The topics that can be covered in a survey of mathematical demography are numerous and diverse. Therefore, any survey of the field in the confines of a chapter in this *Handbook* must be selective. After some introductory materials on the theory of models and the nature of demographic phenomena and data, this chapter reviews the essential concepts and mathematics of the two basic classic population models that constitute the core of mathematical demography, namely, the life table/stationary population model and the stable population model. Recent contributions that extend these models are also reviewed in various ways. The third major topic reviewed is model schedules or age-specific rates of demographic events such as births and deaths, summary demographic indices, such as the total fertility rate and life expectancy, and recent developments in tempo adjustment formulas based thereon. Space limitations do not permit a detailed exposition of recent contributions to mathematical demography that generalize and extend the classic life table/stationary and stable population theories. After laying out the basics of these models, however, many recent contributions are cited, and the ways in which they build upon the classic models are described.

Models in Science and in Demography

This chapter first reviews some elements of the modern theory of models (Casti 1992a, 1992b; Land 1971, 2001). This theory defines formal models in generic terms and shows the universality of the uses of formal modeling systems across the sciences. The objective is to position the models studied in mathematical demography within this general framework.

Following Casti (1992b), a general definition of *models* is that they are tools by which individuals order and organize experiences and observations.

An implication of this definition is that many of the verbal characterizations of population phenomena that are used in demography are indeed models. They have stimulated research over the years and will continue to do so. As an example, Notestein's (1945) verbally stated *demographic transition model* stimulated demographers to focus attention on trends in birth and death rates and their relationship to economic development and improvements in health and longevity.

If models are tools for ordering experiences, what are "formal models"? *Formal models* encapsulate some slice of experiences and observations within the relationships constituting a formal system such as formal logic, mathematics, or statistics (cf., Casti 1992a). A *formal demographic model* thus is a way of representing aspects of demographic phenomena using a formal apparatus that provides a means for exploring the properties of the demographic phenomena mirrored in the model. Demographers construct formal models to assist in bringing a more clearly articulated order to their experiences and observations, as well as to make more precise predictions about certain aspects of the populations. Since most of the remaining discussion pertains to formal demographic models, the adjective "formal" will no longer be used with "models."

Some notation is useful. Consider a particular subset D of demographic phenomena and suppose that D can exist in a set of distinct *abstract states* $\Omega = \{\omega_1, \omega_2, \ldots\}$. The set Ω defines the *state space* of D. Whether or not a demographer can determine the state of D in a particular moment of study depends on the experiences, observations, or measurements (*observables*) at the demographer's disposal. As a simple example, suppose D is a human population in which two sexes are distinguished. Then a reasonable set of abstract states that distinguishes a two-sex population might be

$$\Omega = \{\omega_1 = \text{male}, \omega_2 = \text{female}\}.$$

Next, consider the concept of an observable. An *observable* of D is a rule f associating a real number to each ω in the state space Ω, i.e., an observable is a measuring instrument. More formally, an observable is a map $f\colon \Omega \to R$, where R denotes the set of real numbers. Using the example of a two-sex population and the usual "dummy variable" coding rule, one could define

$$f(\omega_1) = 0 \text{ and } f(\omega_2) = 1$$

as observables.

Generally, a full accounting of the complexities of population phenomena would require an infinite number of observables $f_\alpha\colon \Omega \to R$, where the subscript α ranges over a possibly uncountable index set. Thus, a complete accounting of demographic and related population phenomena D would be described by a large set Ω and the possibly *infinite set of observables* $F = \{f_\alpha\}$. But it is usually not necessary in demography to deal with such a large set of observables in order to build useful demographic models.

In brief, in building demographic models, demographers throw away most of the possible observables that could affect demographic phenomena and focus attention on *a proper subset A* of *F*, which may or may not capture the full complexity and nuances of demographic phenomena.

A *demographic model* D^* may now be characterized as an abstract state–space Ω together with a finite set of observables $f_i\colon \Omega \to R$, $i = 1, 2, \ldots, n$. Symbolically,

$$D^* = \{\Omega, f_1, f_2, \ldots, f_n\}.$$

But there is more to the notion of a demographic model than just the list of observables by which it is characterized. The essential "systemness" of D^* is contained in relationships that link the observables. These relationships are termed the *equations of state* for D^*. Formally, the equations of state can be written as

$$\Phi_i(f_1, f_2, \ldots, f_n) = 0, \quad i = 1, 2, \ldots, m,$$

where the Φ_i (.) are mathematical relationships expressing the dependency relations among the observables. This can be more compactly written as

$$\Phi(f) = 0. \tag{1}$$

There are two forms in which the equations of state that define demographic models are used. The first is to state relationships among observables that produce a *descriptive model* or *definition* of a demographic index or rate. Many demographic models, from population life tables used to estimate the years of life expected to be lived in a population to a formula for calculating the total fertility rate, are used in this descriptive or definitional sense. A second way in which the equations of state are used in demography is to state causal relationships among observables that produce an *explanatory model* in which variations across time or demographic space in certain observables are explained by variations in other observables.

To represent explanatory demographic models, Eq. (1) must be further developed. Suppose that the last m observables $f_{n-m+1}, \ldots, f_m$, called *endogenous* (i.e., determined within the system under consideration), are functions of the remaining observables $f_1, f_2, \ldots, f_{n-m}$, which are *exogenous* (i.e., determined outside the system under consideration). In other words, suppose that m functional relations are defined, with some finite number r of numerical parameters, β_1, $\beta_2, \ldots,$ β_r, for determining values of the endogenous observables as a function of the exogenous observables. Here the notation

$$\beta \equiv (\beta_1, \beta_2, \ldots, \beta_r)$$

will denote the vector of parameters and the notation

$$x \equiv (f_1, f_2, \ldots, f_{n-m})$$

and

$$y \equiv (f_{n-m+1}, f_{n-m+2}, \ldots, f_n)$$

will denote vectors of the exogenous and endogenous observables, henceforth *variables*, respectively. The equations of state become

$$y = \Phi_\beta\ (x). \tag{2}$$

This last expression, perhaps formulated with stochastic/random components, is in a form that encompasses many explanatory demographic models.

As an example of the application of these formal notations to the definition of a common demographic index, consider the mathematical model that underlies the definition of a common measure of fertility used in demography, the total fertility rate (TFR), a period fertility rate used more often than any other. The TFR is defined as the average number of births a woman would have if she were to live through her reproductive years (usually ages 15 to 49) and bear children at each age at the rates observed in a particular year or period. The actual childbearing of cohorts of women is given by the completed or cohort fertility rate (CFR), which measures the average number of births 50-year-old women had during their reproductive years.

Formally, let $f_p(t, a)$ denote the age-specific fertility rates for women aged a at time t, and let $f_c(t, a)$ represent the age-specific fertility rates at age a for cohorts of women born at time t. Then the equation of state (1) for the *period total fertility rate* for time t is

$$\mathrm{TFR}(t) = \int f_p(t, a)da \tag{3}$$

and the equation for the *cohort fertility rate* for the cohort born at time T is

$$\mathrm{CFR}(t) = \int f_c(t, a)da. \tag{4}$$

In applications, the integrals are replaced by finite summations and the sums are taken over the reproductive ages.

One question has been avoided to this point: What differentiates models from theories? These terms sometimes are distinguished and sometimes are used interchangeably. Usually, scientific theories are regarded as more general than scientific models. A *theory* is a *family of related models*, and a *model* is a formal manifestation of a particular theory (cf., Casti 1992b). In the presentation later of the life table/stationary population model, this distinction will be illustrated.

What Good are Models?

Consider next some uses of models in demography. What good are they? One list of the benefits of models was presented by the mathematical demographer Nathan Keyfitz over three decades ago (Keyfitz 1971a). Keyfitz noted that the development of demography had been greatly influenced by the demand for the prediction of future population; this stimulated the development of demographic models such as the life table and stable population models. He then identified the following benefits of models: Models focus research by identifying theoretical and practical issues. Models help in assembling and explaining data. Models permit the design of experiments, simulations, and other research studies out of which causal knowledge can be obtained. Models systematize comparative study across space and time. Models reveal formal analogies between problems that on their surface are quite different. And models help in the making of predictions. To the list provided by Keyfitz, the following benefits of models can be added: Models provide a “lens” through which patterns can be detected in demographic data that otherwise cannot be perceived. Models help to improve demographic measurement. And, in particular, models provide a locus for defining, developing, and interpreting summary measures of demographic events and phenomena.

The Nature of Demographic Phenomena and Data

In their discussion of the evolution of demography into a cumulative and integrated science, Morgan and Lynch (2001) identified four factors intrinsic or internal to the discipline that have facilitated this evolution. They are summarized here because they may be viewed as the basis on which the extraordinary development and application of mathematical models in demography has proceeded.

The first is the fact that *demographic phenomena are relatively easily measured.* Births and deaths, the core events studied by demography, are biologically based and thus are anchored in an unmistakable and universal reality. While the meaning of these events is socially constructed by the individuals involved and the cultures in which they participate, their actual occurrence is universally recognized. The same may be said for sex and age (or other dimensions of time), which are key variables in the study of human populations. That is, their social significance may vary, but the fact that there are objective sexes in a population or age (or duration since some event) is unchallenged. (See chapter 1, "Age and Sex," in this *Handbook* for more discussion.) Morgan and Lynch (2001) note that another topic studied by demographers, migration, may be less well developed due to the greater difficulty in defining migration. (See chapter 11, "Internal Migration," in this *Handbook*.)

A second key feature is that *demographic phenomena are inherently quantifiable.* This is due to the fact that births and deaths are categorical (in fact, they are dichotomous) and thus easily counted. Intermediate instances of birth and death are few and rare. The consequence is that repeated measurement and intersubjective agreement among observers would likely be high. This is not to say that demographic measurement is easy for a large population—only that it is relatively straightforward.

Third, the *presence of accounting identities* has facilitated the successful development of demography as a science. Traditional demography focuses on the description of the composition of human populations by age, sex, and other characteristics and the study of change therein (dynamics). The basic methods of demography are centered on the well-known *population accounting or balancing equation*:

$$P_t \equiv P_{t-1} + B_{t-1,\,t} - D_{t-1,\,t} + NM_{t-1,\,t}. \tag{5}$$

where P_t denotes the size of a population at accounting time (e.g., year) t, and $B_{t-1,\,t}$, $D_{t-1,\,t}$, and $NM_{t-1,t}$ denote, respectively, the flows into or out of the population from time $t-1$ to t by births, deaths, and net migration. Land and Schneider (1987) note that this identity is an instance of the general law of conservation of mass in physics. It also is an example of the equations of state (1), a functional relationship linking the observables of a demographic model of a population. Using identity (5), demographers can perform quality checks on their data and engage in indirect estimation when only fragments of data are available.

The fourth factor is the presence of *structural features or relationships among key concepts*. Not only can births and deaths be unambiguously identified and counted in human populations, and not only can the counts be related to each other via the basic demographic accounting equation (5), they also can be used to define populations at risk of one event or another and the corresponding dynamics or rates of occurrence of the events. These, in turn, can be used to build life table/stationary population models, stable population models, and related models to describe and/or explain the corresponding population processes. This chapter now turns to an exposition of some of the basics of these models.

LIFE TABLE/STATIONARY POPULATION THEORY AND EXTENDED MODELS

Classic Single-Decrement Population Life Table Theory/Models

Classic single-decrement population life table theory is a simple descriptive mathematical theory that demographers use to represent the age-specific mortality patterns to which a population is subject and to summarize those patterns in the form of estimates of years of life expected to be lived on average in a population. It also is the simplest mathematical theory of the age structure of a population, called a stationary population, subjected to certain patterns of fertility and mortality. The following detailed statement of the basic concepts and mathematics of this theory builds on expositions by Jordan (1975), Keyfitz (1977b), Preston, Heuveline, and Guillot (2001), and Schoen (1988). The theory consists of an interrelated set of mathematical functions that apply to entire families of functions. Thus, in keeping with the distinction between mathematical theories and mathematical models made earlier, the life table/stationary population theory is first presented. For purposes of empirical estimation of a life table for a particular population, the mathematical functions of the theory must be given specific algebraic expressions, as will be described later. These specific algebraic expressions transform life table theory into specific life table models that then can be estimated by corresponding methods. In the exposition that follows, however, the terms *theory* and *models* will not always be distinguished. Instead, conventional terminology will be adopted and the term model will be used in most places.

THE SURVIVAL FUNCTION. The normal mortality pattern observed among human lives, illustrated graphically in Figure 22.1, is familiar to demographers. The elimination

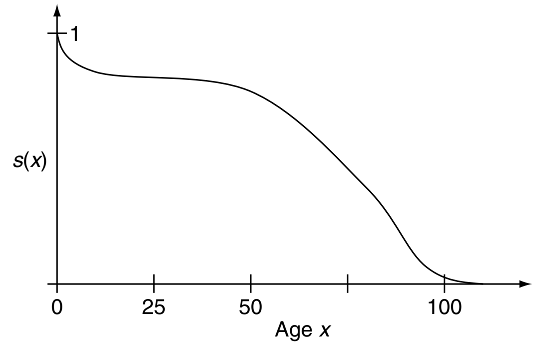

FIGURE 22.1. Graphic representation of the human survival function.

of lives by death is rapid in infancy, slows down during childhood, then increases throughout adolescence and middle life, accelerating as the end of the life span is approached. The life table is a mathematical model for expressing these facts. One approach to developing the life table model is via the survival function.

Definition: The probability that a new life, aged 0, will survive to attain age x will be regarded as a function of x and referred to as the *survival function, $s(x)$.*

Properties of $s(x)$: On the basis of general knowledge of the normal mortality pattern described above, the following three properties may be postulated for $s(x)$:

1. $s(x)$ is *a decreasing function* as x increases, since the probability of surviving to age x is greater than the probability of surviving to age $x + t$, $t > 0$;
2. Since the focus here is on normal patterns of human mortality, it is convenient and reasonable to assume that $s(x)$ is *a continuous function of x.*
3. At $x = 0$, $s(x) = 1$ and at the upper end of the life span, denoted ω (omega), $s(x) = 0$.[1]

THE LIFE TABLE. The main device for exhibiting mortality data in demography is the *life table* or the *mortality table*. The l_x and d_x functions of the life table have the following definitions:

$$\begin{aligned} l_x &= l(0) \cdot s(x) \qquad (6) \\ &= l_0 \cdot s(x), \text{ where } l(0) = l_0 \text{ is a positive constant,} \\ d_x &= l_x - l_{x+1}. \qquad (7) \end{aligned}$$

The value of l_0 is called the *radix* of the table, usually taken to be some large round number like $10^5 = 100{,}000$; d_x is the *annual decrement* of the table.

The interpretation of l_x as a "number living" or "number surviving" and of d_x as a "number dying" is a convenient aid in visualizing many of the relations that follow. But it should be remembered that neither l_x nor d_x has any absolute meaning; the sizes of both depend on the value of the radix chosen to construct the table. Note also that l_x, from property (2), is a continuous function of x, although tabulated values appear in life tables only for integral values of x.

The approach taken here to the definition of the life table is *classic* in the sense that it does not derive the survival function from the definition of a stochastic process governing the sample paths (life histories) of the individual members of a birth cohort. Rather, it begins by postulating properties of the survival function and supposes that the probabilities applying to the birth cohort group-as-a-whole will be exactly applicable to each individual in the cohort, so that one only needs to compute the expected values of the various life table functions. In this sense, it often is called a *deterministic model*. Generally, this deterministic approach to the concepts and functional relationships that define life table theory applies when the population base on which mortality events are defined and recorded is sufficiently large so that there are few irregularities in

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[1] The designation of a terminal age ω is merely a convenient simplifying device. No empirical fact supports the assumption that a life can survive for n years but not for n years and one second. Thus, it would be more realistic to say that the values of $s(x)$ are negligible for $x \geq \omega$. However, the more precise condition $s(\omega) = 0$ is retained because of its convenience in the subsequent mathematical analysis.

the data due to random or stochastic fluctuations. How large is "sufficiently large?" Opinions on this topic vary, but most demographers are comfortable with application of the deterministic model of the life table to the full human age range from birth to the end of life to a population base of at least 10,000 person-years of exposure per year, or an average of about 10,000 persons observed per year. For populations or longitudinal panels of individuals followed over time that are smaller, most demographers would recommend the use of a statistically based survival model approach to the definition and estimation of a life table model, as described later.

It is evident that the intensity of mortality varies at each *moment* of age, and it is important to have some way of measuring this *instantaneous* variation. The *slope* of the empirical *s(x)* described above is related to the number of deaths at that point [since $l_x = l_0 \cdot s(x)$, the *s(x)* graph may be thought of as an l_x curve with a change in the vertical scale], for the steeper the curve the greater the number of deaths. Since the slope is measured by the derivative, it is natural to turn next to the derivative of l_x.

THE FORCE OF MORTALITY. The mortality index just described is known as the *force of mortality/hazard function* and is denoted by the symbol μ_{x}. Its definition is

$$\mu_x = -\frac{Dl_x}{l_x} = -\frac{1}{l_x}\frac{d}{dx}l_x = -\frac{d}{dx}\ln l_x. \tag{8}$$

Properties of μ_x:

1. μ_x is a measure of mortality at the precise moment of attaining age x.
2. μ_x expresses this mortality in the form of an annual rate; this is because the derivative of l_x is

$$Dl_x = \lim_{h\to 0}\frac{l_{x+h} - l_x}{h},$$

so μ_x from (8), may be written

$$\mu_x = \lim_{h\to 0}\frac{l_x - l_{x+h}}{h \cdot l_x} = \lim_{h\to 0}\frac{{}_hq_x}{h}, \tag{9}$$

where q_x denotes the (conditional) probability that (x) will die within 1 year. The expression ${}_hq_x/h$ may be regarded as an annual rate of mortality based on the mortality during the age interval x to $x + h$.

3. The value of μ_x normally exceeds 1 at both ends of the life-span[2].

Empirical Force Function: Corresponding to the typical empirical bathtub-shaped survival curve, the empirical force of mortality typically looks like that shown in Figure 22.2.

Derivation of Life Table Functions from μ_x: From a mathematical point of view, μ_x is the most basic life table function in the sense that once given its values (functional

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[2] Consider the first 24 hours of life, for example, the value of ${}_{1/365}q_0$ may exceed 1/365 so that the ratio ${}_hq_0/h$ exceeds 1. Since there are no survivors at age ω, we may write ${}_{\omega-x}q_x = 1$, which is true for all x. But if x is an age such that $\omega - x$ is less than 1, it follows that $\frac{{}_{\omega-x}q_x}{\omega-x} > 1$, and hence values of μ_x exceeding 1 will occur in the year of age $\omega - 1$ to ω.

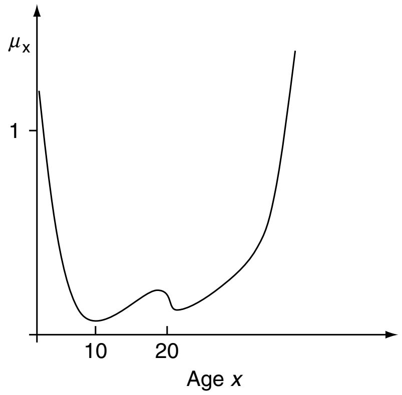

FIGURE 22.2. Graphic representation of the human force of mortality function.

form), all other life table values may be derived. The values of the force of mortality itself are independent of the life table radix, which implies that there is only one instantaneous rate of mortality. To demonstrate these derivations, recall that

$$\mu_x = -D \ln l_x.$$

Replace x by y and integrate both sides between the limits 0 and x:

$$\begin{aligned}\int_0^x \mu_y dy &= -\int_0^x D \ln l_y dy\\ &= -\ln l_y|_0^x = -\ln \frac{l_x}{l_0},\end{aligned}$$

so that the survival function can be written:

$$l_x = l_0 e^{-\int_0^x \mu_y dy}. \tag{10}$$

There is a similar expression for the (conditional) probability that (x) will survive to age $x+n$

$${}_n p_x = \frac{l_{x+n}}{l_x} = \frac{l_0 e^{-\int_0^{x+n} \mu_y dy}}{l_0 e^{-\int_0^x \mu_y dy}} = e^{-\int_x^{x+n} \mu_y dy}. \tag{11}$$

The probability ${}_n q_x$ may then be expressed as

$${}_n q_x = 1 - e^{-\int_0^n \mu_{x+1} dt}. \tag{12}$$

Alternatively, noting that

$$l_y \mu_y = -D l_y,$$

integrating between the limits of x and $x+n$ yields

$$\begin{aligned}\int_x^{x+n} l_y \mu_y dy &= -\int_x^{x+n} D l_y dy\\ &= -l_y|_x^{x+n} = l_x - l_{x+n} = {}_n d_x\end{aligned} \tag{13}$$

which defines the *annual decrement* when $n = 1$. Letting $y = x + t$, $0 \leq t \leq n$, and integrating from 0 to n, this last expression becomes

$$ {}_nd_x = l_x - l_{x+n} = \int_0^n l_{x+t}\mu_{x+t}dt. \tag{14}$$

Dividing by l_x gives the following expression for ${}_nq_x$:

$$\begin{aligned} {}_nq_x &= \frac{{}_nd_x}{l_x} = \frac{l_x - l_{x+n}}{l_x} \\ &= \frac{1}{l_x}\int_0^n l_{x+t}\mu_{x+t}dt = \int_0^n {}_tp_x\mu_{x+t}dt. \end{aligned} \tag{15}$$

The relationship between the central death rate and the force of mortality can be seen by writing out the integral expressions for the numerator and denominator

$$m_x = \frac{\int_0^1 l_{x+t} \cdot \mu_{x+t}dt}{\int_0^1 l_{x+t}dt} \tag{16}$$

From this, it is apparent that m_x is the weighted mean value of the force of mortality over the year of age x to $x + 1$ where the weights are the number of lives attaining each age $x + t$ in the interval. Depending on the specific functional form of the force function, $\mu_{x+1/2}$ is a more or less appropriate estimate for this average value.

The Person-Years Function: Two life table functions then can be defined:

$$ {}_nL_x = \int_x^{x+n} l_y dy = \int_0^n l_{x+t}dt \tag{17}$$

and

$$\begin{aligned} T_x &= \int_x^{\infty} l_y dy = \int_0^{\alpha} l_{x+t}dt \\ &= \sum_{y=x}^{\alpha} L_y = \sum_{t=0}^{\alpha} L_{x+t} \end{aligned} \tag{18}$$

where if $n = 1$

$$ {}_1L_x = L_x.$$

As a consequence of the definitions, note that

$$\frac{dL_x}{dx} = l_{x+1} - l_x = -d_x$$

and

$$\frac{dT_x}{dx} = -l_x.$$

Considering that l_x represents the mortality experience of a birth cohort as it ages, the integral ${}_nL_x$ is the *person-years* lived by that cohort between ages x and $x + n$. Similarly, T_x represents the *total person-years* in prospect for the group numbering l_x who have attained age x on the radix l_0. Note that the upper bounds in the two integrals defining T_x could be replaced by ω and $\omega - x$, respectively, if an upper bound on the life table has been set beyond which no one survives.

The Life Expectation Function: The *complete expectation of life at age x* is defined as:

$$e_x = \frac{T_x}{l_x} = \frac{1}{l_x}\int_0^\infty l_{x+t}dt = \int_0^\infty {}_tp_x dt \tag{19}$$

The life expectation function may be interpreted as representing the *expected average future lifetime* remaining at age x.

THE STATIONARY POPULATION. There are two ways of viewing the functions of the life table. The first, as just reviewed, is to view the table as tracking the survival of a birth cohort. This is the *cohort life table* view. An alternative perspective leads to a view of the life table as *a model of the age structure of a population* subject to certain conditions. In particular, following Jordan (1975), suppose that a population produces l_0 annual births, l_0 being the radix of a given life table, and suppose that these births are uniformly distributed over each calendar year. Let the deaths among the population occur in accordance with the given life table, and let there be no migration into or out of the population. Then, after the birth and death process has continued for a period of years at least equal to the terminal age of the life table, the total population and its age distribution remain constant (stationary).

To see the validity of this proposition, consider first the consequences of the assumption that the l_0 annual births are uniformly distributed over each calendar year. Clearly, this means that there will be l_0 births uniformly distributed over any year of time, and that in any fraction of a year h, however small, there will be $h\ l_0$ births. It follows that there will be l_x lives attaining age x in any year and $h\ l_0$ lives attaining age x in any time interval h, as survivors of the births which occurred in the corresponding periods of time x years ago.

Consider next the incidence of deaths. Each of the $h\,l_y$ lives attaining age x in any interval h is subject to the force of mortality μ_y, and hence the differential expression $h\,l_y\ \mu_y dy$ represents the number of lives dying at exact age y in that interval. Then the number dying between ages x and $x+1$ in any interval h will be given by $\int_x^{x+1} hl_y\mu_y dy = hd_x$. Two consequences are: (1) letting h equal 1, the number dying between ages x and $x+1$ in any year of time will be d_x; (2) since the number dying between ages x and $x+1$ in any fraction of a year h is proportional to h, it is clear that the deaths between ages x and $x+1$, and hence all deaths, occurring in any period of time are uniformly distributed over that period.

It may now be seen that such a population is indeed stationary. For the total of the deaths at all ages in any interval h is $\int_0^\omega hl_y\mu_y dy = hl_0$, which is the same as the number of births occurring in the interval. Since the interval h is an arbitrarily small period of time, it may be concluded that each life which leaves the population by death is simultaneously replaced by a new birth.

Furthermore, the distribution of the total population by ages is stationary. Consider the lives which are aged x last birthday at any time. These are the lives which have attained integral age x but not age $x+1$. In any interval h, the number of lives which leave this group by attaining age $x+1$ is hl_{x+1}, and the number which leave the group by death is hd_x, making a total decrement of $hl_{x+1} + hd_x = hl_{x+1} + h(l_x - l_{x+1}) = hl_x$. Thus, the total decrement is exactly equal to the number entering the group during the interval by attaining age x. In other words, when a life leaves this age group, either by death or by attaining age $x + 1$, its place is simultaneously taken by a life entering from the next lower age group. Under these circumstances, the number living at a given age last birthday is always constant.

Now $\frac{1}{r} l_{x+m/r}$ represents the number of lives attaining exact age $x + m/r$ in any interval of time $1/r$ and therefore approximates the number of lives between exact ages $x + m/r$ and $x + (m + 1)/r$ at any moment of time. Hence the number of lives between exact ages x and $x + 1$ at any moment of time is

$$\lim_{r \to \infty} \sum_{m=0}^{r-1} \frac{1}{r} l_{x+\frac{m}{r}} = \int_0^1 l_{x+t} dt = L_x.$$

Thus, L_x is the constant number of lives between exact ages x and $x + 1$ at any moment of time. Similarly, T_x is the number of lives aged x and over at any moment of time.

SUMMARY OF PROPERTIES OF THE STATIONARY POPULATION. This conception of the life table may be compared with the cohort-survivorship group interpretation. In particular, the following interpretations and relationships characterize the stationary population:

1. l_x represents the number of lives attaining age x in any year of time;
2. d_x represents the number of deaths between ages x and $x + 1$ in any year of time;
3. l_0 = number of births per year = $\sum_{x5} d_x$ = total deaths per year;
4. ${}_nL_x$ = number of persons living in the population between ages x and $x + n$ at any moment in time;
5. T_x = number of lives aged x and over at any moment in time;
6. T_0 = total size of the population;
7. ${}_nL_x/T_0$ = proportion of the population ages x to $x + n$ at any moment in time;
8. T_x/T_0 = proportion of the population aged x or older at any moment in time;
9. $L_0/T_0 = 1/e_0$ = birth rate = death rate
10. ${}_nm_x$ = ratio of the number of deaths between ages x and $x + n$ in any year of time to the number living between those ages at any moment in time.

Although the stationary population model is admittedly artificial, the theory is applicable when the stationary conditions are approximately realized. In addition, more realistic mathematical models of human populations, such as the stable and piecewise-stable population models described below, are generalizations of the stationary population model.

Estimation of Complete and Abridged Population Life Tables

It is difficult to find a mathematical expression, involving a small number of parameters, which will fit the force of mortality function for human populations closely over its entire range (see, however, the section below on model schedules). For this reason, traditional methods of estimation of population life tables have been dominated by three considerations.

First, the data available to demographers to use in the estimation of population life tables are limited and aggregated. Demographers typically do not have access to complete life history information giving details on birth dates, death dates, and populations exposed to risk at every point in some historical period. Rather, the usually available data consist of age-specific estimates of populations exposed to risk from censuses and age-specific enumerations of deaths from a vital statistics register. As explained in the next section, these are used to construct occurrence/exposure death rates from which demographers estimate life tables. Indeed, as noted by Preston and colleagues (2001), all of the various model specifications and estimation methods for constructing population life tables that have been developed can be viewed as devices for transforming occurrence/exposure data on death rates into age-specific probabilities of dying (i.e., the q_x's), from which the other life table functions can be calculated.

Second, there is no simple, universally accepted family of parametric mortality force functions (or survival functions) that can be used to estimate the life table over the entire age range of human life. Thus, one cannot simply conjoin the death rates with a parametric force function in say, a least squares curve-fitting procedure and obtain an accurate fit to the death rates throughout the age range.

Third, the preeminent interest of demographers in population life table estimation is the accurate estimation of the expectation of life function. For this, demographers place a high premium on the preservation of local irregularities in the death rates, provided they are based on population-level data and considered to be accurate.

DATA AVAILABLE FOR THE ESTIMATION OF POPULATION LIFE TABLES. Given complete, continuous-time observations on all births and deaths for all persons in a population exposed to the risk of mortality, it is possible to produce direct estimates of the life table survival function, l_x, and/or the central mortality rates, m_x (see Elandt-Johnson and Johonson 1980). However, the aggregate, population-level data available to demographers usually fall far short of this ideal situation. The more typical circumstance is that vital statistics and census agencies provide data for the computation of occurrence/exposure rates for a sequence of age intervals $[x_0, x_0 + n), \ldots, [x_i, x_i + n), \ldots, [x_i, x_\omega)$. By *occurrence/exposure rates* is meant rates of the form

$$ {}_nM_x = \frac{{}_nD_x}{{}_nK_x} \tag{20} $$

where ${}_nD_x$ denotes the number of deaths occurring (enumerated) to members of the population who are aged x to $x + n$ at last birthday during the period of observation, and ${}_nK_x$ denotes the average number of persons living in the population during the observation period and thus exposed to the risk of mortality. In this definition, n typically is 1 or 5 years, except for the first and last age intervals, where it may be shorter or longer respectively. In *period data*, rates of the form of Eq. (20) are computed for each age interval from, say, calendar-year deaths in the numerator and an estimate of the midyear population size (the average population exposed to the risk of mortality during the year) in the denominator. In *cohort data*, rates of the form of Eq. (20) are computed each year or each five years from estimates of the numerator and denominator as an initial one-year or five-year birth cohort ages through time.

ESTIMATION OF COMPLETE (UNABRIDGED) LIFE TABLES. A *complete* or *unabridged life table* is a table in which single-years-of-age define the estimation-age-intervals, i.e., the age intervals over which the table is estimated, except for an open-ended interval at the upper end of the table that may begin at age 85 or 95 or 100, depending on the availability of accurate data at the oldest ages.

Complete life tables usually are estimated for national populations, for example the United States population, by using census counts of the population in decennial census years and averages of death enumerations for three years surrounding the census year, e.g., 1979 to 1981, 1989 to 1991, 1999 to 2001. In the calculation of such tables, major empirical questions usually pertain to the accuracy of the age information in the census enumeration. Such information is subject to problems of age heaping, digit preference, and other inconsistencies. (See chapter 1 in this *Handbook* for more discussion.) Consequently, much of the methodology involved in the construction of these life tables involves methods of data adjustment to remove obvious inconsistencies. After adjustment, the death and population enumerations are usually combined into the conventional five-year age groups (5 to 9, 10 to 14, 15 to 19,..., 80 to 84) for the nonextreme ages. After grouping, the death and census enumerations typically are interpolated back to single years of age by one of a variety of osculatory interpolation methods (see Keyfitz 1977b; Keyfitz and Flieger 1971).

The product of this sequence of (1) data adjustment, (2) grouping into five-year age groups, and (3) interpolation is a series of single-year-of-age death counts and a corresponding series of single-year-of-age population estimates that are "smoother" than the observed series. These, in turn, will produce mortality rates that are smoother than those calculated from observed deaths and population counts. The ultimate justification is the assumption in the life table model that the survival curve is continuous.

Based on these considerations, assume in this section that the available data constitute a smooth series of deaths by single years of age at last birthday:

$$D_0, D_1, D_2, \ldots, D_x, \ldots, D_{84}$$

and a smoothed series of single age population estimates:

$$K_0, K_1, K_2, \ldots, K_x, \ldots, K_{84}$$

from which we obtain a corresponding smoothed series of occurrence/exposure death rates:

$$M_0, M_1, M_2, \ldots, M_x, \ldots, M_{84}.$$

With these data, there are two well-known life table models/methods for converting the occurrence/exposure rates to life table mortality probabilities. Each could be described as a "local" method of life table estimation, since each approximates the mortality force function (equivalently, the survival function) by functions that are continuous within age intervals but piecewise discontinuous between age intervals. This produces a life table that is faithful to the "local behavior" of the death rates and that yields an accurate estimate of the expectation of life function.

Method 1: Piecewise-Constant Force of Mortality (Equivalently, Piecewise-Exponential Survival Function) Model. At the level of the force of mortality function, this model begins by assuming that μ_{x+t} is constant within single ages:

$$\mu_{x+t} = \mu_x \quad (0 \leq t < 1) \tag{21}$$

This amounts to approximating the force function by a function that is constant within single ages but that differs between ages—called a *piecewise-constant force function*—as shown in Figure 22.3.

An immediate consequence of this assumption is that the definition of the life-table central mortality rate (16) simplifies to

$$m_x = \frac{\int_0^1 l_{x+t} \cdot \mu_x dt}{\int_0^1 l_{x+t} dt} = \frac{\mu_x \int_0^1 l_{x+t} dt}{\int_0^1 l_{x+t} dt} = \mu_x \tag{22}$$

Following the *general estimation algorithm format* of Schoen (1975), Schoen and Land (1979), and Land and Schoen (1982), the results may be summarized as the following estimation algorithm:

Data-Model Orientation Equation:

$$M_x = m_x = \mu_x \tag{23}$$

Flow Equation:

$$l_{x+1} = l_x e^{-M_x}. \tag{24}$$

Person-Years Equation:

$$L_x = [l_x - l_{x+1}]/M_x = [l_x - l_{x+1}]M_x^{-1} \tag{25}$$

Note that all of the columns of a complete life table can be calculated from these three equations.

Method 2: Piecewise-Hyperbolic Force Function (Equivalently, Piecwise-Linear Survival Function) Model. In one of the first attempts to describe algebraically the mortality experience of human lives, the 18th-century mathematician Abraham de Moivre (1725) proposed that the survivorship curve (l_x) of a life table could be represented by a single straight line. His hypothesis, that from an arbitrary number of births equal numbers would die each year until the entire cohort had expired, is of course unrealistic for any extended segment of the human age range. Nonetheless, a spin-off is in wide use today, that is, the assumption that between any two ages which are one unit apart, deaths tend to occur uniformly.

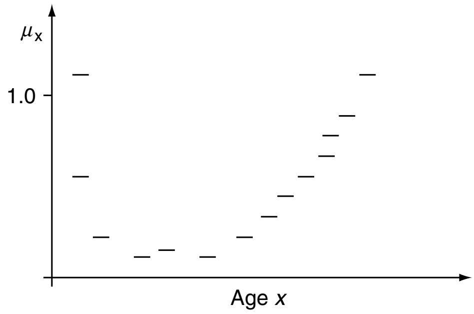

FIGURE 22.3. Piecewise-constant force of mortality.

A mathematical statement of the "uniform distribution of deaths" hypothesis is that the survival function decreases linearly with time (t) into an interval:

$$l_{x+t} = l_x + bt, \quad (0 \le t < 1) \tag{26}$$

with $b < 0$ (since l_{x+t} is a decreasing function). Because Eq. (26) is equivalent (after rearranging) to

$$l_{x+t} - l_x = bt, \tag{27}$$

it can in fact be seen that $b = -d_x = -(l_x - l_{x+1})$ by setting $t = 1$. Thus, Eq. (27) can be rewritten as

$$l_{x+t} = l_x - t \cdot d_x, \quad (0 \le t < 1) \tag{28}$$

and, since it is not required that the annual decrement be equal across single ages x, it follows that this is a *piecewise-linear survival function* specification. To derive the underlying mortality force function to which this survival curve applies, the definitional equation (8) given earlier may be applied:

$$\begin{aligned} \mu_{x+t} &= \frac{-1}{l_{x+t}} \frac{d}{dt} l_{x+t} = \frac{-1}{l_x - t \cdot d_x} \frac{d}{dt}[l_x - t \cdot d_x] \\ &= \frac{-1}{l_x - t \cdot d_x}[0 - 1 \cdot d_x] = \frac{d_x}{l_x - t \cdot d_x}, \quad (0 \le t < 1) \end{aligned} \tag{29}$$

Algebraically, this function is of the form $a/(b + ct)$, for a, b, and c constants, i.e., this life table model specifies a *piecewise-hyperbolic force of mortality function*.

Again, this model leads to the following estimation algorithm:

Data-Model Orientation Equation:

$$M_x = m_x \tag{30}$$

Flow Equation:

$$l_{x+1} = p_x l_x = \left[\frac{1 - \frac{1}{2}M_x}{1 + \frac{1}{2}M_x}\right] l_x \tag{31}$$

Person-Years Equation:

$$L_x = \frac{1}{2}(l_x + l_{x+1}). \tag{32}$$

INITIATING AND TERMINATING THE COMPLETE LIFE TABLE. A final topic is how to initiate the life table at the early ages and terminate it at the last ages. When occurrence/exposure rates are available and accurate for ages 0 to 5 (i.e., M_0, M_1, M_2, M_3, M_4), one converts these to life-table survival and/or death probabilities via Eqs. (23), (24) or (30), (31). However, the force of mortality usually is considered to be changing so rapidly in these early years of life as to require more elaborate procedures, especially for q_0 (equivalently p_0).

For this reason, and because standard occurrence/exposure mortality rates for age 0 mix deaths and/or population estimates for two calendar years of birthdays, a variety of *separation factors* have been developed to produce accurate estimates of q_0 from which to initiate the life table; see Keyfitz (1977b), Shryock and Siegel (1975), and Preston et al. (2001) for details.

For the oldest ages in the open-ended interval, the usual orientation equation is applied:

$$_{\infty}M_x =_{\infty} m_x. \tag{33}$$

This avoids the necessity of defining the oldest age to which a person can live. Inaccuracies in age reports for older people discourage further refinement. Furthermore, death registrations contain different error structures (in the numerator of $_{\infty}M_x$) from those in census counts (in the denominator of $_{\infty}M_x$).

Combining Eq. (33) with the definition $m_x = (l_x - l_{\infty})/_{\infty}L_x$ and the fact that $l_{\infty} = 0$, it follows that $_{\infty}M_x = l_x/_{\infty}L_x$, and thus

$$_{\infty}L_x = \frac{l_x}{_{\infty}M_x}, \tag{34}$$

where x is the start of the terminal age. With $l_{\infty} = 0$, we obtain $_{\infty}q_x = 1$. Also, the expectation of life at age x becomes

$$e_x = \frac{_{\infty}L_x}{l_x} = \frac{1}{_{\infty}M_x}, \tag{35}$$

so that the expectation of life is the reciprocal of the terminal death rate.

THE ESTIMATION OF ABRIDGED POPULATION LIFE TABLES. For most demographic research purposes, it is not necessary to calculate a complete life table. Rather, an *abridged life table*, that is, a life table defined on estimation age intervals larger than 1 year, say 5 or 10 years, provides sufficient accuracy for most purposes and is less cumbersome. Assume that the available data are in the form of a sequence of occurrence/exposure rates

$$_{1}M_0,\ _{4}M_1,\ _{n}M_5, \cdots,_{n}M_x, \cdots,\ _{\infty}M_{85}$$

where n is 5 or 10 years. Note that the only single age treated separately is age 0; then ages 1 to 4 are grouped; then the 5 or 10 age groupings; and finally the open-ended last age interval.

To estimate an abridged population life table, one could apply either of the piecewise exponential or linear survival function models/methods described above for complete tables. However, whereas both of these piecewise methods are accurate for the estimation of complete tables, they lose accuracy when applied to the estimation of abridged tables. Therefore, demographers have developed several additional methods for the estimation of abridged tables. These methods may be viewed as "adjustments" or "corrections" to the basic piecewise-exponential and piecewise-linear survival function models for the construction of complete life tables.[3] Several of these adjusted methods are now described.

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[3] The assumption of the data-model orientation equation in the estimation algorithms for complete life tables (e.g., Eq. [30]) is referred to as a *sectional stationarity assumption.* For abridged life table estimation, this assumption may be relaxed to a *sectional stability assumption.* For more details, see Keyfitz (1968, 1970).

Three adjustment methods may be viewed as modifications of the piecewise-exponential life table model. This is due to the fact that the empirical tenability of the basic assumption of the exponential model (that the force of mortality is constant within age intervals) is less adequate as the estimation age intervals of the life table increase beyond single ages. Thus, each of these three methods modifies this assumption. The modification then produces correction factors for the flow and person-years equations of the piecewise-exponential algorithm stated earlier (Keyfitz and Frauenthal 1975; Greville 1943; and Reed and Merrell 1939). In fact, the Keyfitz-Frauenthal method can be viewed as a generalization of the Greville method, which in turn is a generalization of the Reed-Merrell method. Since the correction factor introduced by the Keyfitz-Frauenthal method allows for the most variability from age interval to age interval, it also is the most computationally intensive and, of the three methods, generally provides the most accurate abridged table estimates.

Two additional abridged life table estimation methods can be viewed as modifications of the piecewise-linear survival function model. The description of these methods requires one to define the concept of the *average number of years lived in the interval x to $x+n$ by those dying in the interval, denoted* $_na_x$. This concept was introduced by Chiang (1960, 1968, 1972) in a reformulation of the classic linear survival function model. It is an application of the expectation of life function to the age interval x to $x+n$ and thus has the definition

$$_na_x = \frac{\int_0^n t l_{x+t}\mu_{x+t}dt}{\int_0^n l_{x+t}\mu_{x+t}dt}. \tag{36}$$

Note that the piecewise-linear l_x (uniform distribution of deaths) specification leads to

$$_na_x = \frac{_nL_x - n\cdot l_{x+n}}{_nd_x} = \frac{\frac{n}{2}(l_x + l_{x+n}) - n\cdot l_{x+n}}{l_x - l_{x+n}} = \frac{n}{2}, \tag{37a}$$

i.e., under the linear survival function specification the average number of years lived in the x to $x+n$ interval by those who die in the interval is $n/2$. But, in general, Eq. (37a) does not hold. Indeed, there is a general formula for transforming the central mortality rates, $_\mathrm{n}m_x$, of the life table to the age-specific probabilities of dying, $_\mathrm{n}q_x$ that uses Chiang's $_\mathrm{n}a_x$ (see Preston et al. 2001):

$$_nq_x = \frac{n\cdot_n m_x}{1+(n-_n a_x)_n m_x} \tag{37b}$$

For the piecewise-linear l_x model, with $_na_x = n/2$, Eq. (37b) implies:

$$_nq_x = \frac{n\cdot_n m_x}{1+\frac{n}{2}\,_nm_x} = \frac{2n\cdot_n m_x}{2+n\cdot_n m_x}, \tag{37c}$$

which is equivalent to:

$$_np_x = \frac{1-\frac{n}{2}\,_nm_x}{1+\frac{n}{2}\,_nm_x}. \tag{37d}$$

Using the data-model orientation equations of the piecewise-linear l_x model (Eq. (30), one then can use either Eq. (37b) or Eq. (37c) to transform the observed $_nM_x$ into estimates of the survival function.

Again, however, these equations hold only for the piecewise-linear l_x model, and, in general, if one wants to use Eq. (36) in the construction of an abridged life table, one must either (1) borrow estimates of $_na_x$ from another population that one assumes is applicable (see, e.g., Elandt-Johnson and Johnson 1980; Preston et al. 2001) or (2) estimate the $_na_x$ empirically. Each of these methods has limitations. For instance, when estimates of $_na_x$ are borrowed from another population, e.g., by using $_na_x$'s from an unabridged life table that is calculated for data surrounding decennial census years (when age-specific population estimates are most accurate) together with data on observed $_nM_x$'s and Eq. (37b) to calculate an abridged life table for an intercensal year, the implicit assumption is that there has been no change in the survival curve in the intervening years. This may be more accurate than the direct application of the piecewise-linear l_x model via Eqs. (37c) or (37d). But it nonetheless is an approximation. As noted, an alternative approach is to estimate the $_na_x$ empirically. Two methods that have been proposed for this purpose are the piecewise-quadratic survival function method of Schoen (1978) and Land and Schoen (1982) and the iterative method of Keyfitz (1968, 1970) that is based on the model specification that l_{x+t} is a cubic function over the interval x to $x + n$.

INITIATING THE ABRIDGED TABLE. An innovation in abridged life table estimation introduced by Keyfitz (1970) is a short-cut method for treating the youngest ages in the life table. This consists of assuming, for each of the three age intervals 0, 1 to 4, 5 to 9, a value for $_na_x$. For age 0, Keyfitz estimated the empirical regression

$$a_0 = 0.07 + 1.7M_0 \tag{38}$$

from data on a number of countries in which day, month, and year of birth were available. For ages 1 to 4, he found that $_4a_1$ may be set equal to 1.5 years without much loss in accuracy; for ages 5 to 9, $_5a_5$ can be set to 2.5 years. Under the (sectional stationarity) data-model orientation equations specified earlier, this yields two equations in each of the first three age intervals

$$l_{x+n} = l_x -_n M_x \cdot_n L_x \tag{39}$$

$$_nL_x = (l_x - l_{x+n})_n a_x + nl_{x+n} \tag{40}$$

which can be solved simultaneously for the unknown $_nL_x$ and l_{x+n}. Coale and Demeny (1983) have conducted similar empirical studies across many populations; an adaptation of their findings is given by Preston and associates (2001).

Example: Abridged Life Tables for U.S. Males, 1994. Table 22.1 displays abridged period life tables for U.S. males in 1994 based on the *Vital Statistics of the United States 1994* released by the National Center for Health Statistics (NCHS). Panel A is constructed under the piecewise-linear survival function model using the methods for the 0 to 1 and 85+ age intervals described above. Panel B is constructed under the Schoen-Land Piecewise-Quadratic Survival Function Model using the same procedures for the first and last age intervals.

For Panel A, the columns are the following:

$_nm_x$: $_n M_x = \frac{_nD_x}{_nK_x}$, where $_nD_x$ and $_nK_x$ were obtained from the life table of the *Vital Statistics of the United States*, and $_nM_x =_n m_x$ (Orientation Equation);

TABLE 22.1. Abridged Life Tables for United States Males, 1994

Panel A Piecewise-Linear Survival Function Model: U.S. Males, 1994

Age x	${}_nm_x$	${}_na_x$	${}_nq_x$	${}_np_x$	l_x	${}_nd_x$	${}_nL_x$	T_x	e_x
0	0.008857	0.085057	0.008786	0.991214	100,000	879	99,196	7,232,035	72.320347
1	0.000467	1.500000	0.001867	0.998133	99,121	185	396,023	7,132,839	71.960615
5	0.000229	2.500000	0.001142	0.998858	98,936	113	494,400	6,736,815	68.092357
10	0.000308	2.500000	0.001538	0.998462	98,823	152	493,737	6,242,416	63.167363
15	0.001262	2.500000	0.006292	0.993708	98,671	621	491,805	5,748,678	58.260800
20	0.001645	2.500000	0.008189	0.991811	98,051	803	488,246	5,256,873	53.613845
25	0.001781	2.500000	0.008864	0.991136	97,248	862	484,084	4,768,627	49.035870
30	0.002361	2.500000	0.011733	0.988267	96,386	1,131	479,101	4,284,544	44.452075
35	0.002956	2.500000	0.014671	0.985329	95,255	1,397	472,780	3,805,442	39.950159
40	0.003790	2.500000	0.018772	0.981228	93,857	1,762	464,882	3,332,662	35.507775
45	0.004911	2.500000	0.024258	0.975742	92,095	2,234	454,892	2,867,781	31.139248
50	0.007354	2.500000	0.036105	0.963895	89,861	3,244	441,196	2,412,889	26.851247
55	0.011202	2.500000	0.054483	0.945517	86,617	4,719	421,287	1,971,693	22.763376
60	0.018080	2.500000	0.086491	0.913509	81,898	7,083	391,780	1,550,407	18.931010
65	0.027170	2.500000	0.127208	0.872792	74,814	9,517	350,279	1,158,627	15.486701
70	0.040832	2.500000	0.185250	0.814750	65,297	12,096	296,246	808,348	12.379492
75	0.061032	2.500000	0.264762	0.735238	53,201	14,086	230,791	512,102	9.625796
80	0.098104	2.500000	0.393908	0.606092	39,115	15,408	157,057	281,311	7.191826
85+	0.190799	5.241114	1.000000	0.000000	23,708	23,708	124,254	124,254	5.241114

Panel B Piecewise-Quadratic Survival Function Model: U.S. Males, 1994

Age x	${}_nm_x$	${}_na_x$	${}_nq_x$	${}_np_x$	l_x	${}_nd_x$	${}_nL_x$	T_x	e_x
0	0.008857	0.085057	0.008786	0.991214	100,000	879	99,196	7,224,020	72.240196
1	0.000467	1.500000	0.001866	0.998134	99,121	185	396,023	7,124,823	71.879753
5	0.000229	2.500000	0.001142	0.998858	98,936	113	494,400	6,728,800	68.011345
10	0.000308	3.493513	0.001538	0.998462	98,823	152	493,888	6,234,401	63.086259
15	0.001262	2.669589	0.006293	0.993707	98,671	621	491,910	5,740,513	58.178069
20	0.001645	2.546252	0.008190	0.991810	98,050	803	488,282	5,248,602	53.529591
25	0.001781	2.605065	0.008866	0.991134	97,247	862	484,173	4,760,320	48.950572
30	0.002361	2.598266	0.011736	0.988264	96,385	1,131	479,210	4,276,148	44.365152
35	0.002956	2.601436	0.014675	0.985325	95,254	1,398	472,918	3,796,938	39.861153
40	0.003790	2.605368	0.018779	0.981221	93,856	1,763	465,060	3,324,021	35.416101
45	0.004911	2.664741	0.024277	0.975723	92,094	2,236	455,247	2,858,960	31.044057
50	0.007354	2.675823	0.036151	0.963849	89,858	3,248	441,739	2,403,713	26.750173
55	0.011202	2.692393	0.054598	0.945402	86,609	4,729	422,135	1,961,974	22.653119
60	0.018080	2.643413	0.086706	0.913294	81,881	7,100	392,673	1,539,839	18.805870
65	0.027170	2.614451	0.127580	0.872420	74,781	9,541	351,146	1,147,166	15.340300
70	0.040832	2.577242	0.185782	0.814218	65,241	12,121	296,838	796,019	12.201282
75	0.061032	2.555457	0.265542	0.734458	53,120	14,106	231,119	499,181	9.397217
80	0.098104	3.249195	0.329092	0.670908	39,014	12,839	130,876	268,062	6.870844
85+	0.190799	5.241114	1.000000	0.000000	26,175	26,175	137,187	137,187	5.241114

U = 0.002112
V = 0.161284
W = 0.003270
X = 0.029572
Y = 0.341311
Z = 0.037550

Data source: U.S. Vital Statistics, 1994.

Note: See Chart 1 of Schoen (1978) for details of the calculation of survival function, *lx*, using the weights U to Z.

${}_na_x$: for age 0, $a_0 = 0.07 + 1.7M_0$, (Eq. (38));

for ages 1–4, ${}_4a_1 = 1.5$;

for ages 5–9, ${}_5a_5 = 2.5$;

for ages 10–84, ${}_5a_x = \frac{n}{2} = \frac{5}{2} = 2.5$, (Eq.(37));

for ages 85 and above, ${}_\infty a_{85} = e_{85}$;

l_x: for ages 0, 1 to 4, and 5 to 9, the simultaneous equations (39) and (40) are solved, i.e., $l_{x+n} = l_x -{}_nM_x \cdot {}_nL_x$, where

$${}_nL_x = \frac{n \cdot l_x}{1 + (n -{}_na_x)_nM_x};$$

for instance, if age = 0,

$${}_1L_0 = \frac{1 \cdot l_0}{1 + (1 - a_0)_1M_0} = \frac{100000}{1 + (1 - .085).009} = 99{,}196;$$

$$l_1 = l_0 -{}_1M_0 \cdot {}_1 L_0 = 100000 - .009^*99196 = 99{,}121;$$

similar procedures apply for l_5, ${}_4L_1$, and ${}_5L_5$, with q_0 computed by application of Eq. (37b) and $p_0 = 1–q_0$;

for other age categories, the Piecewise-Linear Flow Equation gives:

$l_{x+n} ={}_np_x \cdot l_x = [\frac{1-\frac{n}{2}{}_nM_x}{1+\frac{n}{2}{}_nM_x}]l_x$;

${}_nL_x$: for the first three age categories, see calculations shown above;

for ages 10 to 84, use the Piecewise-Linear Person-Year Equation:

${}_nL_x = \frac{n}{2}(l_x + l_{x+n})$;

for ages 85+, use Eq. (34): ${}_\infty L_x = \frac{l_x}{{}_\infty M_x}$;

${}_nd_x$: ${}_n d_x = l_x - l_{x+n}$;

${}_np_x$: for ages under 85, ${}_np_x = \frac{1-\frac{n}{2}{}_nM_x}{1+\frac{n}{2}{}_nM_x}$, (Flow Equation);

for ages 85 + , ${}_\infty p_{85} = 0$;

${}_nq_x$: for ages under 85, ${}_nq_x = 1 -{}_np_x$;

for ages 85+ , ${}_\infty q_{85} = 1$;

${}_nT_x$: $T_x = \sum_{t=0}^{\infty} L_{x+1}$;

e_x^0: for ages under 85, $e_x = \frac{T_x}{l_x}$;

for ages 85 + , $e_x = \frac{{}_\infty L_x}{l_x} = \frac{1}{{}_\infty M_x}$.

In Panel B the assumption of the piecewise-linear survival function model is modified by the piecewise-quadratic survival function: $l_{x+t} = l_x + bt + ct^2$ (Land and Schoen 1982: 301–309). Several columns are calculated differently as follows:

${}_na_x$: the same with Panel A for the first three and the last age categories;

for ages 10 to 84,

$$ {}_na_x = \frac{n^2}{240}\left[\frac{l_x({}_nM_{x+n} + 38{}_nM_x +_n M_{x-n}) + l_{x+n}(14{}_nM_{x+n} + 72{}_nM_x - 6{}_nM_{x-n})}{l_x - l_{x+n}}\right] $$

l_x and ${}_nL_x$: the above expression for ${}_na_x$ yields corresponding expressions for flow and person-years equations that are given in Chart 1 of Schoen (1978)[4].

${}_nq_x$: for age under 85, ${}_nq_x = \frac{{}_nd_x}{l_x}$;

for age 85 + , ${}_\infty q_{85} = 1$;

${}_np_x$: for age under 85, ${}_np_x = 1 -_n q_x$;

for age 85 + , ${}_{85} = 0$.

Substantively, it can be seen that the assumption of the piecewise-linear l_x model that deaths within an age interval occur, on average, halfway through the interval results in an underestimation of the a_x for many age intervals. This, in turn, translates into slightly underestimated q_x's throughout much of the age range from childhood to the end of life (see Eqs. (37a–d))—which leads to a slightly larger e_0 estimated from the piecewise-linear survival function model in Panel A than from the piecewise-quadratic survival function model in Panel B. For these data, however, both models yield quite accurate estimates of e_0.

Multiple-Decrement Life Tables

The life table models just described may be extended and generalized in various ways. This section describes three extensions and generalizations to processes by which an individual can exit the life table in two or more ways, to processes that allow for entrances or increments into living states as well as exits or decrements from those states, and to situations in which only sample-level data are available with which to estimate the life table, rather than population-level data, and for which we therefore need to make a more careful use of statistical methods of estimation and inference. The exposition here is limited to a general sketch of the basic ideas of these additional life table models.

A first extension is to *multiple-decrement life* tables, which incorporate the simultaneous operation of several causes of decrement or exit to a particular body of lives. For example, one may be concerned with an insurance coverage in which disability and mortality are distinct causes of claim and the interacting effects of exposure to both causes of decrement must be analyzed. Or one may wish to study a mortality experience in terms of its component causes of death, such as cancer, heart disease, or accidents, treating each cause of death as a separate decrement.

To model such multiple-decrement processes, the state-space of the single-decrement life table model must be elaborated to incorporate the multiple modes of exit from the key defined state of the life table, being alive at age x. This is shown in Figure 22.4. Panel (a) of Figure 22.4 illustrates the state-space of the single-decrement life table, which consists of two states, namely, being alive at age x and being dead. To connect these two states, Panel (a) has a single arrow directed from the alive state to the dead state, which represents the operation of the age-specific force of mortality or decrement

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[4] Schoen (1978) has demonstrated empirically that an abridged life table estimated according to the quadratic survival function is more accurate than those estimated by several other abridged table methods, including the Keyfitz-Frauenthal method.

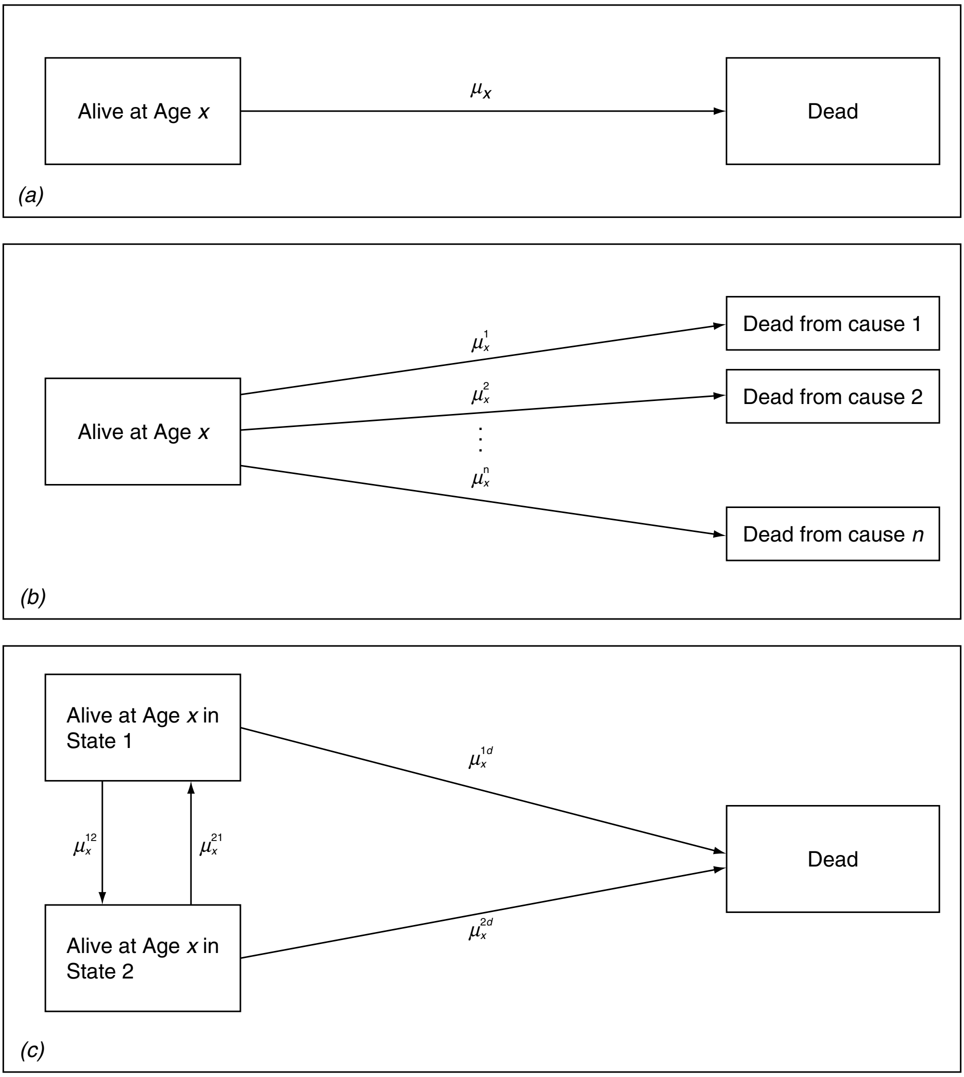

FIGURE 22.4. State space of the multiple decrement life table models.

of the life table at each age x. Because the force of mortality varies with age, the underlying mathematical model of this single-decrement process is that of a *time (age)-inhomogeneous stochastic process* (Land and Schoen 1982:278). This model specifies a simple, single-element state-space, consisting simply of being alive at age x, for those individuals in the life table model who have not yet exited or died. The only other state of this model is what is termed an absorbing state (because no returns to the living state are possible), which consists of having exited the table to the dead state.

By comparison, Panel (b) of Figure 22.4 shows a graphic representation of the state-space and forces of mortality for a multiple-decrement life table that has n possible forms of exit from the table. It can be seen that the major changes in the graphic representation of the life table model from Panel (a) to Panel (b) are that the absorbing or dead state now has been refined or disaggregated into *n* subcategories, and the single force of decrement of Panel (a) now is correspondingly disaggregated to allow for an instantaneous risk of decrement from the alive state to each of the absorbing or cause-specific death states. Detailed expositions of the mathematics of population multiple-decrement life tables and corresponding methods of estimation from occurrence/exposure rates can be found in Preston, Keyfitz, and Schoen (1972); Jordan (1975); Elandt-Johnson and Johnson (1980); Schoen (1988); and Preston et al. (2001).

Multistate Life Table and Projection Models

Panel (c) of Figure 22.4 is a graphic representation of a second generalization of the single-decrement life table, namely, to a *multistate* or *increment-decrement life table*. Rather than decomposing the dead or exit state of the life table into multiple causes or types of exit, the multistate life table disaggregates the single alive-at-age-*x* of the life table into multiple possible states that may be occupied by individuals alive. The multistate life table represented in Panel (c) of Figure 22.4 is for a simple two-living-state table. The two living states could take the form, for example, of two regions between which migration is possible in a biregional migration table, or the states of currently married or currently divorced in a nuptiality table, or the states of being in or out of the labor force in a labor force participation table, or the states of active or disabled in an active/disabled table. And, of course, the state-space could be refined to incorporate more than two living states at each age *x*. It can be seen that the major changes in the graphic representation of the life table model from Panel (a) to Panel (c) are the following: The alive at age *x* state now has been refined or disaggregated into two subcategories, and the single force of decrement from the alive state of Panel (a) now is correspondingly disaggregated to allow for an instantaneous risk of decrement from each alive state to the other alive state at each age *x*, with decrements to the receiving state referred to as increments to that state. At the same time, individuals alive in either state of the table are subjected at each age *x* to the risk of exit from the table to the dead state. A key property of multistate life tables is that, within the time period of the age intervals that define the table, they permit individuals alive in the table to exit or decrement from the state they occupied at the beginning of the age interval to another state and then to increment or return back to the original state. For life table models of demographic processes in which individuals may make multiple transitions within age intervals such as from nonmarried to married and back to nonmarried again, this is an indispensable property.

The multistate life table model has roots in mathematics, biostatistics, and actuarial science that date back to Du Pasquier (1912), Fix and Neyman (1951), and Sverdrup (1965). But its development and extensive empirical application by demographers mainly began in the 1970s. The generalization of the single-decrement population life table was initiated in the 1970s for applications to population-level (i.e., census and vital statistics) data on multiregional migration (Rogers 1975) and nuptiality on marriage and divorce (Schoen 1975; Schoen and Land 1979).

Hoem and Fong (1976) introduced an application to working life tables that used large-sample survey data rather than population-level data. Even for large-sample surveys, however, sample sizes for the estimation of age-specific transition probabilities may become small. The result is more age-to-age variability in the estimated transition probabilities. Accordingly, Hoem and Fong introduced a method of smoothing the age-specific estimates of transition probabilities by moving averages across the age intervals. Moving average and related methods of graduation or smoothing estimates of transition probabilities across age intervals subsequently has been used extensively for the estimation of labor force participation life tables by Schoen and Woodrow (1980), voting in U.S. presidential elections by Land, Hough, and McMillen (1986), and tables of school life by Land and Hough (1989).

A particularly active area of methodological development and empirical application of multistate life tables has been the estimation of years of active/disability-free/health life as contrasted to inactivity/disability/unhealthy years among the elderly population. The initial definition of active life expectancy in terms of a lack of limitations in activities of daily living was given by Katz and colleagues (1983). The standard life table method for estimating active life expectancy used by these authors is a *prevalence-rate-based life table* method of decomposing the ${}_nL_x$ column of a population life table into years lived in an active state and years lived in an inactive or disabled state, a method presented by Sullivan (1971; for a recent exposition, see Molla, Wagener, and Madans 2001). Due to its minimal data requirements (the existence of a population life table appropriate for the particular population for which estimates are desired and a set of age-specific prevalence rates or proportions of persons identified as either in the active or inactive states), the Sullivan method has been widely applied and remains useful today (see Crimmins, Saito, and Ingegneri 1997; Cambois, Robine, and Hayward 2001).

However, Rogers, Rogers, and Branch (1989) noted that one critical assumption of prevalence-rate-based life table methods is that transitions can only occur in one direction among the living statuses, specifically, from the active to the inactive state in active life expectancy tables. Using data on age-specific transition rates among the active and inactive statuses from longitudinal panel surveys of the elderly, they applied multistate life table methods to the estimation of active life expectancy. Subsequent research (Crimmins, Saito, and Hayward 1993) indicates that the Sullivan method for estimating active life expectancy generally yields estimates that do not differ greatly from those obtained by multistate models. Nonetheless, when data on transitions among living states are available, the methodological and empirical research accumulated over the past two decades suggests that multistate life table models should be applied.

Research by Zeng, Gu, and Land (2004) demonstrates that the disabled life expectancies based on conventional multistate life table methods are significantly underestimated due to an assumption of no functional status changes between the ages of individuals in a longitudinal panel at the date of the last wave in which they were interviewed and their subsequent death. Zeng and colleagues (2004) present a new method to correct the bias and apply it to 1998 and 2000 longitudinal survey data of about 9,000 oldest old Chinese aged 80 to 105. The results show that estimates of active life expectancy can be improved if data on the disability status of the elderly in the month or so prior to death are available. These data permit a more accurate estimation of individuals' functional status in the time period between a last wave of panel interviews and death. Zeng and associates (2004) also applied and extended methods developed by Molla and associates (2001) (based on Chiang 1960 and Keyfitz 1977b) to estimate standard errors of status-based active life expectancy (i.e., active life expectancy for persons with different functional status at initial age).

Benefiting from methodological advances in multidimensional demography (Rogers 1975; Willekens et al. 1982; Land and Rogers 1982; Schoen 1988), Bongaarts (1987) developed a multistate nuclear-family-status life table model. Zeng extended Bongaarts's nuclear-family-status life table model into a general multistate family household simulation macro model that includes both nuclear and three-generation family households (Zeng 1986, 1988, 1991). The multistate life table macro models developed by Bongaarts and Zeng are female-dominant one-sex models and assume that input rates are constant.

Based on Bongaarts' and Zeng's one-sex life table models, Zeng, Vaupel, and Wang (1997, 1998) developed a two-sex multistate dynamic macro projection model known as "ProFamy" that permits demographic schedules to change over time and uses as inputs only conventional data that are available from ordinary surveys, vital statistics, and censuses. Zeng, Land, Wang, and Gu (2005) extended the ProFamy model by adding cohabitation and race dimensions to all computation and estimation procedures. In addition to statuses defined by the number of coresiding children and parents and parity, the extended ProFamy family household projection model includes seven marital/union statuses: (1) never-married and not cohabiting, (2) married, (3) widowed and not cohabiting, (4) divorced and not cohabiting, (5) never married and cohabiting, (6) widowed and cohabiting, and (7) divorced and cohabiting. The ProFamy model has been used to generate U.S. household projections by race (Zeng et al. 2005), household automobile consumption forecasts in Austria (Prskawetz, Jiang, and O'Neill 2002); German households and living arrangement projections (Hullen 2000, 2003), and family household projections in smaller areas (e.g., Hullen 2001; Heigl 2001; Jiang and Kuijsten 1999a, 1999b; Yang and Zeng 2000).

The classic headship-rate method for projections of households is not linked to demographic rates, projects a few household types without size, and does not deal with household members other than heads. By comparison, the multistate ProFamy new method uses demographic rates as input and projects more detailed household types, sizes, and living arrangements for all members of the population. Projections using ProFamy and observed U.S. demographic rates in the 1990s show that the discrepancies between the projections and 2000 census observations are reasonably small, thus validating the new method.

Hazard Regression Models and Survival Curves from Longitudinal Studies

This section extends and generalizes the classic single-decrement population life table model by taking its basic survival process ideas and applying statistical methods of parameter estimation and hypothesis testing to them. While there are prior roots in the use of life table models for the estimation of survival curves following medical treatment in biostatistics (Berkson and Gage 1952) and in the application of panel regression models in sociology (Coleman 1964), the major paper that initiated this extension of life table/survival model ideas is the classic article on the intersection of regression models with life table concepts by Cox (1972). This article presented the use of regression models to control for multiple covariates simultaneously in the estimation of life tables and introduced the *proportional hazards regression model* and the partial likelihood method for its estimation from sample data. These developments are so associated with Cox's article that proportional hazards regression models are now known as *Cox regression models*.

Cox's paper has generated a voluminous literature on survival models and methods in biostatistics and related disciplines over the past three decades, as shown in the works of Allison (1995), Hosmer and Lemeshow (1999), Ibrahim, Chen, and Sinha (2001), Kalbfleisch and Prentice (2002), Klein and Moeschberger (1997), Lawless (2003), Therneau and Grambsch (2000), and Yamaguchi (1991). In addition to providing a procedure for bringing statistical methods of inference to bear on the use of sample data to estimate the life table model, a key feature of these models is that they provide a means to transform the life table as a primarily descriptive model, as in equation (1) above, and into an explanatory model, as in equation (2), in which heterogeneity in variations among individuals in survival times are explained, at least in part, in terms of certain exogenous variables or regression covariates. Regarding terminology, when a regression model for survival data is applied to a nonrepeatable process, such as time of survival to death, it is termed a *hazard regression model*; when the regression model is applied to a process that allows for multiple occurrences like entries into, and exits from, the labor force over the adult life course, it is termed an *event history model*. The event history terminology was introduced by Tuma, Hannan, and Groeneveld (1979). A recent account of event history models and statistical methods of estimation and inference is given in Singer and Willet (2003).

The proportional hazard regression model approach, and, more generally, the statistical approach to the estimation of single-decrement life tables from sample data, was introduced to demographers by Menken et al. (1981) and Trussell and Hammerslough (1983). Extensions to multistate hazard regression models and multistate life tables and associated empirical applications by demographers followed. Hoem and Funck-Jensen (1982) laid out the probability theoretical foundations of multistate life tables and indicated how regression models could be used to account for population heterogeneity in this context. Hayward and Grady (1990) applied regression models to longitudinal sample data on processes of work and retirement among a cohort of older men to estimate a multistate hazard/life table model. Land, Guralnik, and Blazer (1994) combined panel regression models to estimate hazards and expected transition probabilities to use in a multistate estimation of disability processes and active life expectancy among the elderly.

A related approach using longitudinal panel data and hazard regression models for the estimation of multistate life tables builds on the random walk model of human mortality and aging of Woodbury and Manton (1983) and the generalized latent-class model known as the grades-of-membership (GoM) model (Woodbury and Clive 1974; Manton, Stallard, and Singer 1994; Manton, Woodbury, and Tolley 1994). Applications of this combined random walk/GoM model to longitudinal panel data for the estimation of the interaction of mortality and disability dynamics and of active life expectancy have been made by Manton, Stallard, and Corder (1997) and Manton and Land (2000).

STABLE POPULATION THEORY AND ITS EXTENSIONS

Classic Stable Population Theory

Deterministic models of population growth exist in two forms: (1) those that use a continuous time variable and a continuous age scale (Lotka 1907; Sharpe and Lotka 1911) and (2) those using a discrete time variable and a discrete age scale (Bernadelli 1941; Lewis 1941; and Leslie 1945; Sykes 1969). Both have advantages. The discrete formulation is closer to demographic practice in population projections. But the continuous formulation is closer to continuous life table/stationary population theory. Thus, the classic single-sex stable continuous-time population theory is now presented.

Recall that the continuous-time formulation of the stationary population model requires that the number of births equal the number of deaths over any finite time interval. When it is not required that births equal deaths, but instead that each is assumed to occur according to rates that are forever fixed, the more interesting continuous-time model of a stable population is obtained, due to the work of Lotka (1907) and Sharpe and Lotka (1911). In this model, the births of a current generation are associated with those of the preceding generation to define several important constants that describe the ultimate growth and composition of such a population.

THE RENEWAL EQUATION AND STABLE GROWTH. The continuous single-sex model of population dynamics is expressed as an integral equation. To obtain $B(t)$, the number of female births at time t, women aged x to $x + dx$ at time t "at risk" of childbirth are the survivors of those born x years ago. Denote the number of females born x years ago by $B(t - x)$ and the life table survival probability (for surviving from birth to age x) by $p(x)$. Then this quantity is $B(t - x)p(x)dx$, where $x \leq t$. At time t, these women give birth to

$$B(t - x)p(x)m(x)dx \tag{41}$$

female children per year, where $m(x)\ dx$ is the annual rate of female childbearing among women aged x to $x + dx$.

Integrating Eq. (41) over all ages x and adding $G(t)$ to include births to women already alive at an initial time point (time zero) yields the *Lotka integral equation*:

$$B(t) = G(t) + \int_0^t B(t - x)p(x)m(x)dx, \tag{42}$$

where (Keyfitz 1977b):

$$\begin{aligned} G(t) &= \int_{\alpha - t}^{\beta - t} K(x + t)m(x + t)dx \\ &= \int_{\alpha - t}^{\beta - t} k(x)\frac{p(x + t)}{p(x)}m(x + t)dx, \end{aligned} \tag{43}$$

α and β being, respectively, the lower and upper bounds of the childbearing ages, and $k(x)dx$ denoting the number of women aged x to $x + dx$ at time zero. For $t \geq \beta$, $G(t)$ is zero; hence Eq. (42) reduces to

$$B(t) = \int_0^t B(t - x)p(x)m(x)dx, \text{ for } t \geq \beta. \tag{44}$$

Because Eqs. (42) and (43) show how a population of individuals born $t - x$ years ago gives rise to a new cohort of individuals at time t, this often is called *Lotka's renewal equation*.

On replacing $B(t)$ and $B(t - x)$ by Qe^{rt} and $Qe^{r(t-x)}$, respectively, and noting that $m(x)$ is nonzero only in the childbearing ages $\alpha \leq x \leq \beta$, the *characteristic equation* is obtained:

$$\Psi(r) = \int_{\alpha}^{\beta} e^{-rx} p(x) m(x) dx = \int_{\alpha}^{\beta} e^{-rx} \Phi(x) dx = 1, \tag{45}$$

where the product *p(x) m(x)*, denoted by $\mathbf{\Phi}(x)$, is called the *net maternity function.* To solve the integral equation in (45), the value of r for which $\Psi(r)$ is unity needs to be determined.

The terms inside the integral in Eq. (43) are always nonnegative, and e^{-rx} is a decreasing function of r, which guarantees the existence of a real root, i.e., a quantity that is a real number and for which $\Psi(r) = 1$. Differentiating $\Psi(r)$ with respect to r, the first derivative is always negative for all real values of r. Hence $\Psi(r)$ is a monotonically decreasing function. Thus, the curve of $\Psi(r)$ can cross the horizontal line of unity height only once, i.e., these can be only on real root of Eq. (45), as illustrated in Figure 22.5.

In addition to the real root, the characteristic equation (45) can be satisfied by complex values of r. These complex roots occur in complex conjugate pairs. To see this, suppose the complex number $u + iv$ is a root, where $i = \sqrt{-1}$. Euler's theorem indicates that the exponential of a complex number can be written

$$e^{rx} = e^{ux+ivx} = e^{ux}[\cos(vx) + isun(vx)],$$

and hence (45) is

$$\Psi(r) = \int_{\alpha}^{\beta} e^{-ux}[\cos(vx) - i\sin(vx)]\Phi(x)dx = 1. \tag{46}$$

Since there is no imaginary portion of the right-hand side, that on the left must vanish, i.e.

$$\int_{\alpha}^{\beta} e^{-ux} \sin(vx) dx = 0. \tag{47}$$

Thus, since the sin function is a symmetric function for which $\sin(vx) = \sin(-vx)$, it follows that $u - iv$ must also be a root of (45). It can be demonstrated that the real root r must be larger than the value of u in any complex root $u \pm iv$, that is, $r_1 > u$ (Lotka 1998).

For any r_k that is a root of (45),

$$B(t) = Q_k e^{r_k t}, \tag{48}$$

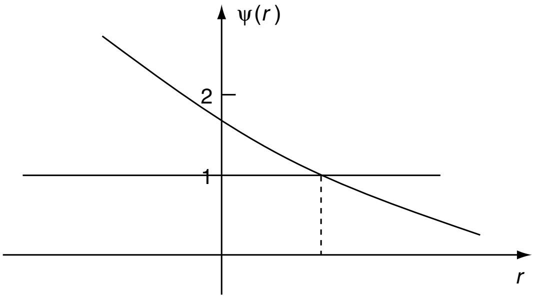

FIGURE 22.5. Graphic representation of the solution of the renewal equation for its real root.

is a solution, and, assuming the roots are distinct, they may be summed to give the general solution

$$\begin{aligned} B(t) &= \sum_{k=1}^{\infty} Q_k e^{r_k t} \\ &= Q_1 e^{r_1 t} + \sum_{k=2}^{\infty} Q_k e^{u_k t}[\cos(v_k t) + i \sin(v_k t)]. \end{aligned} \tag{49}$$

Since each complex root is accompanied by its complex conjugate, which is multiplied by the conjugate coefficient, the imaginary terms in the series on the right of Eq. (49) will cancel out, and a real trigonometric series remains. This is necessary for the solution to make sense, because the representation of counts of a real population of births could hardly include imaginary terms.

Consider next the problem of evaluating the Q_k to fit a given initial condition defined by $G(t)$. One begins by taking Laplace transforms of both sides of Eq. (46), often denoting $p(x)m(x)$ by $\Phi(x)$ the net maternity function:

$$B^*(r) = G^*(r) + B^*(r)\Phi^*(r), \tag{50}$$

where

$$B^*(r) = \int_0^{\infty} e^{-rt} B(t)dt,$$

$$G^*(r) = \int_0^{\infty} e^{-rt} G(t)dt,$$

and

$$\Phi^*(r) = \int_0^{\infty} e^{-rt} \Phi(t)dt.$$

It follows that (50) may be reexpressed as

$$B^*(r) = \frac{G^*(r)}{1 - \Phi^*(r)}. \tag{51}$$

When the integrals defining the Laplace transforms on the right-hand side of Eq. (51) exist (i.e., equal some definite finite real number), then their inverse transforms also exist, and $B(t)$, the inverse of $B^*(r)$ on the left-hand side of Eq. (51), is the solution to the integral equation Eq. (42). Feller (1941) showed that this solution is unique on the condition that $B^*(r)$ can be expressed in partial fractions

$$B^*(r) = \frac{G^*(r)}{1 - \Phi^*(r)} = \frac{Q_1}{r - r_1} + \frac{Q_2}{r - r_2} + \ldots + \frac{Q_k}{r - r_k} + \ldots \tag{52}$$

and that $\sum Q_k$ converges absolutely, the r_k being the roots (finite or infinite in number) of $\Phi^*(r) = 1$, which is identical with the characteristic equation $\Psi(r) = 1$ of Eq. (45). Inverting the terms of the expansion of Eq. (52) results in Eq. (49) once again. To determine the coefficients of the partial fractions in Eq. (52), one takes the derivatives:

$$Q_k = \lim_{r \to r_k} \frac{(r - r_k)G^*(r)}{1 - \Phi^*(r)} = \frac{G^*(r)}{-d\Phi^*(r)/dr}\Big|_{r=r_k},$$

which yields the following solution for the constants

$$Q_k = \frac{\int_0^\beta e^{-r_k t} G(t)dt}{\int_0^\beta x e^{-r_k x} p(x)m(x)dx}. \tag{53}$$

For the maximal root, this relationship may be expressed more meaningfully as

$$Q = \frac{V}{A}, \tag{54}$$

where

$$V = \int_0^\beta e^{-rt} G(t)dt \tag{55}$$

is called the called the *total reproductive value* of a (single-sex) population and

$$A = \frac{\int_\alpha^\beta x e^{-rx} p(x)m(x)dx}{\int_\alpha^\beta e^{-rx} p(x)m(x)dx} = \int_\alpha^\beta x e^{-rx} p(x)m(x)dx \tag{56}$$

is the *mean age of childbearing in the stable population.*

This completes the specification of the components of solution (57) for $B(t)$. For sufficiently large values of t, all terms beyond the first become negligibly small relative to the first, because $r_1 > u_k$ for all $k > 1$. Hence, ultimately

$$B(t) \cong Q e^{r_i t}. \tag{57}$$

Thus, after a sufficiently long period of time the "waves" corresponding to the complex terms of Eq. (49)—if any—will "wear off," and the birth trajectory will be purely exponential, as in Figure 22.6.

In brief, the birth trajectory in the continuous-time stable population model is an exponentially damped sinusoidal curve in which the sinusoidal waves, caused by "echoes" of past fluctuations in births that have left their imprint on the age structure of the initial ($t = 0$) population, gradually decline to insignificance and the exponential

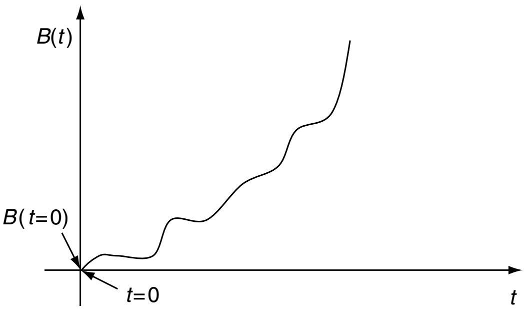

FIGURE 22.6. Illustration of the wearing off of population waves.

growth (at rate r) becomes dominant. This is the ultimate *stable growth* birth trajectory implied by the stable population model. Its defining parameter, r, is called the *intrinsic rate of growth* of the stable population, i.e., it is the rate at which the population ultimately will grow after the sinusoidal waves of its initial age structure wear off. This tendency for the effect of the initial age structure of a population to wear off after a sufficiently long period of time is the basis for the well-known *ergodic theorems* of stable population theory (Arthur 1982; Cohen 1979; Keyfitz 1977b; Lopez 1961; McFarland 1969; Sykes 1969; Parlett 1970).

NUMERICAL SOLUTION OF THE CHARACTERISTIC EQUATION. The solution of the characteristic equation developed in the preceding section is theoretical. To apply it in practice, the integral

$$\int_0^5 e^{-r(x+t)} p(x+t)m(x+t)dt,\ x = \alpha, \ldots, \beta - 5$$

usually is evaluated as the product of $e^{-r(x+2.5)}$, $L(x)/l(0)$, and $F(x)$, where $F(x)$ is the observed birthrate among women aged x to $x+4$ at last birthday. Thus, $\Psi(r)$ is approximated by

$$\sum_{x=\alpha}^{\beta-5} e^{-r(x+2.5)} \frac{L(x)}{l(0)} F(x), \tag{58}$$

with the summation taken over childbearing ages x, which are multiples of 5. Consequently, assuming that the childbearing ages lie between $\alpha = 10$ and $\beta = 50$, Eq. (45) may be solved numerically by determining that value of r for which

$$e^{-12.5r} \frac{L(10)}{l(0)} F(10) + e^{-17.5r} \frac{L(15)}{l(0)} F(15) + \ldots + e^{-47.5r} \frac{L(45)}{l(0)} F(45) = 1. \tag{59}$$

Several iterative methods have been proposed to find the r that satisfies (59). Of these, the method of *functional iteration* described by Keyfitz (1977b) is one of the most efficient. To apply that method, one begins by multiplying both sides of Eq. (59) by $e^{-27.5r}$ and chooses an arbitrary initial value for r, with which the resulting expression on the left-hand side of the equation is evaluated. Taking 1/27.5 of the natural logarithm of this quantity, an improved approximation of r may be obtained with which the same expression is evaluated; this continues until two consecutive approximations differ by less than a small prescribed amount.

To illustrate, applying the method of functional iteration to the 1995 life table for U.S. females and the fertility data in Table 22.2, results in $r = -0.00846$. The same computations carried out with comparable 1968 data by Keyfitz (1977b) yield an r of 0.005715, indicating a considerable decline in fertility, since mortality experienced a decline during the two decades [$e_0^0 = 74.0$ in 1968; $e_0^0 = 78.9$ in 1995]. Given a numerical approximation of r, one may apply the following expression to evaluate the *mean age of childbearing* in the stable population model:

$$A = \sum (x+2.5) e^{-r(x+2.5)} \frac{L(x)}{l(0)} F(x) \tag{60}$$

TABLE 22.2. Stable Population Parameters and Indices for United States Females, 1995

Age	Stationary population L(x)	Birth rate F(x)	Net maternity function Φ (x)	Moments of net maternity function	
				First	Second
10	495,268	0.00059	0.00291	0.03634	0.45425
15	494,466	0.02163	0.10697	1.87205	32.76090
20	493,251	0.04394	0.21674	4.87673	109.72646
25	491,839	0.04515	0.22208	6.10709	167.94502
30	489,978	0.03350	0.16414	5.33461	173.37496
35	487,380	0.01410	0.06873	2.57736	96.65110
40	483,739	0.00273	0.01320	0.56114	23.84831
45	478,577	0.00013	0.00062	0.02950	1.40143
Total		0.16178	0.79540	21.39483	606.16245

Reproduction rates		
Net reproduction rate	*NRR/R* (0)	= 0.79540
Gross reproduction rate	*GRR*	= 0.80888
Stationary population		
Mean age of childbearing	μ	= 26.90
Variance of age of childbearing	σ^2	= 38.48
Stable population		
Intrinsic rate of growth	r	= −0.00846
Intrinsic birth rate	b	= 0.00870
Intrinsic death rate	d	= 0.01715
Mean age of childbearing	A	= 27.32
Mean age	a	= 46.50
Mean length of generation	T	= 27.06

Comparison of age composition

	1995	stable
0–14	0.2076	0.1380
15–64	0.6447	0.5890
65+	0.1476	0.2729
	1.0000	1.0000

Data source: U.S. Census Bureau and Vital Statistics.

Table 22.2 reports numerical values of r and A for 1995 together with several other quantities defined in the next two subsections.[5]

THE NET MATERNITY FUNCTION. Net maternity functions of various countries at different points in time show a regularity that demographers have tried to capture by means of curve fitting. Lotka proposed a normal probability function, and Keyfitz (1977b) compared the fits of the normal curve with those provided by alternative probability functions (see also Hoem et al. 1981). Such a view of the net maternity function leads naturally to an examination of its moments:

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[5] For exemplary applications of life tables/stationary population and stable population models to the comparative study of the population dynamics of many national populations with a focus on population growth and aging, see Keyfitz and Flieger (1990).

$$R(n) = \int_{\alpha}^{\beta} x^n \Phi(x)dx,\ n = 0,\ 1,\ 2, \ldots .$$

The first three moments are of principal interest because they define the following demographic parameters:
Net Reproduction Rate:

$$\begin{aligned} NRR = R(0) &= \int_{\alpha}^{\beta} x^0 p(x)m(x) = \int_{\alpha}^{\beta} x^0 \Phi(x)dx \\ &= \int_{\alpha}^{\beta} e^{-0 \cdot x} \Phi(x)dx = \Psi(0); \end{aligned} \tag{61}$$

Mean Age of Childbearing in the Stationary Population:

$$\begin{aligned} \mu &= \frac{\int_{\alpha}^{\beta} xp(x)m(x)dx}{\int_{\alpha}^{\beta} p(x)m(x)dx} \\ &= \frac{\int_{\alpha}^{\beta} x\Phi(x)dx}{\int_{\alpha}^{\beta} \Phi(x)dx} = \frac{R(1)}{R(0)}; \end{aligned} \tag{62}$$

Variance of Age at Childbearing in the Stationary Population:

$$\begin{aligned} \sigma^2 &= \frac{\int_{\alpha}^{\beta} (x-\mu)^2 p(x)m(x)dx}{\int_{\alpha}^{\beta} p(x)m(x)dx} \\ &= \frac{\int_{\alpha}^{\beta} (x-\mu)^2 \Phi(x)dx}{\int_{\alpha}^{\beta} \Phi(x)dx} \\ &= \frac{R(2)}{R(0)} - \mu^2 \end{aligned} \tag{63}$$

The net reproduction rate gives the number of (female) children expected to be born to a (female) baby now born if the current schedule of fertility and mortality is maintained. A related measure, which does not consider the effects of mortality, is the *gross reproduction rate*:

$$GRR = \int_{\alpha}^{\beta} m(x)dx. \tag{64}$$

Example: As another example, Table 22.2 presents the net maternity function for United States females in 1996. Observe that the related parameters may be computed as follows:

$$NRR = R(0) = \sum_{x=10}^{45} \frac{L(x)}{l(0)} F(x) = 0.7954;$$

$$GRR = 5 \sum_{x=10}^{45} F(x) = 0.8089$$

$$\mu = \frac{\sum_{x=10}^{45}(x+2.5)L(x)F(x)}{\sum_{x=10}^{45}L(x)F(x)} = \frac{21.3948}{0.7954} = 26.90;$$

$$\sigma^2 = \frac{606.1625}{0.7954} - (26.90)^2 = 38.48$$

Lotka showed how these three parameters may be used to obtain a numerical approximation of r, the intrinsic rate of growth using an iterative solution. This is referred to as the *method of normal fit* by Keyfitz and Flieger (1971). Its application to the data in Table 22.2 yields the same r of -0.00846.

RELATIONS UNDER STABILITY. The age composition of a population that is undisturbed by migration is determined by the regime of fertility and mortality to which it has been subjected (Keyfitz 1969). If this regime has remained unchanged for a sufficiently long time period, the initial age composition of the population is "forgotten" in that its influence on the current age composition disappears entirely. Such a *stable population* is characterized by (1) a proportionally fixed age composition and (2) increases at a constant intrinsic rate of growth r.

Let $c(x, t)$ denote the proportional age composition of a female population at time r. The number at age x at time t, denoted $k(x, t)$, are survivors of $B(t-x)$ births x years ago, i.e.,

$$k(x,t) = B(t-x)p(x).$$

Integrating this quantity over all ages of life, the total female population is obtained. Thus, the proportion of this population which is at age x at time t is of density

$$c(x,t) = \frac{k(x,t)}{\int_0^{\omega} k(x,t)dx} = \frac{B(t-x)p(x)}{\int_0^{\omega} B(t-x)p(x)dx}. \tag{65}$$

If $c(x, t)dx$ is the proportion of females aged x to $x+dx$ at time t, the *crude death rate* at time t of this population is

$$d(t) = \int_0^{\omega} c(x,t)\mu(x)dx; \tag{66}$$

and the *crude birth rate* at time t is

$$b(t) = \int_{\alpha}^{\beta} c(x,t)m(x)dx; \tag{67}$$

which also may be found by setting $x = 0$ in the numerator of Eq. (64):

$$b(t) = c(0,t) = \frac{B(t)}{\int_0^{\omega} B(t-x)p(x)dx}. \tag{68}$$

Definitions (65) through (68) apply to any population, stable or not. However, in a stable population, they yield simplified analytic expressions. To see this, recall that at stability $B(t) = Qe^{rt}$. Substituting this into Eqs. (65) and (68) results in a stable population with the proportional age composition

$$c(x,t) = \frac{Qe^{r(t-x)}p(x)}{\int_0^\omega Qe^{r(t-x)}p(x)dx} = \frac{e^{-rx}p(x)}{\int_0^\omega e^{-rx}p(x)dx} = c(x), \tag{69}$$

and birthrate

$$b(t) = \frac{Qe^{rt}}{\int_0^\omega Qe^{r(t-x)}p(x)dx} = \frac{1}{\int_0^\omega e^{-rx}p(x)dx} = b, \tag{70}$$

from which is obtained

$$c(x) = be^{-rx}p(x). \tag{71}$$

Since under stability t has disappeared from the expressions for $c(x, t)$ and $b(t)$, these quantities are independent of time and may be denoted simply as $c(x)$ and b, respectively. Usually, $c(x)$ is called the *stable age composition* and b the *intrinsic birth rate*. The *intrinsic death rate*, d, may be found by subtracting the intrinsic rate of growth from the intrinsic birth rate:

$$d = b - r. \tag{72}$$

Since the net reproduction rate $R(0)$ is a measure of the level of intergenerational increase, it is concluded that

$$e^{rT} = R(0), \tag{73}$$

where T is the *mean length of a generation*. Taking natural logarithms of both sides and simplifying results in

$$T = \frac{1}{r}\ln R(0). \tag{74}$$

The *mean age of the stable population* is

$$a = \frac{\int_0^n xe^{-rx}p(x)dx}{\int_0^\omega xe^{-rx}p(x)dx} = \int_0^\omega xc(x)dx. \tag{75}$$

To illustrate, consider the numerical application of these concepts to the data of Table 22.2. When $r = -0.00846$

$$\begin{aligned} b &= \frac{1}{\sum_{x=0}^{85} e^{-r(x+2.5)}L(x)/l(0)} = 0.0087, \\ d &= b - r = 0.0172, \\ T &= \frac{1}{r}\ln(0.7954) = 27.06, \\ a &= \frac{\sum_{x=0}^{85}(x+2.5)e^{-r(x+2.5)}L(x)}{\sum_{x=0}^{85} e^{-r(x+2.5)}L(x)} = 46.50, \end{aligned}$$

To obtain the proportions of the stable population that are in various age groups, one defines

$$C(x) = \int_x^{x+5} c(a)da = b \int_x^{x+5} e^{-ra} p(a)da, \tag{76}$$

and evaluates it numerically for each 5-year age group as

$$\begin{aligned} C(x) &= be^{-r(x+2.5)} \frac{L(x)}{l(0)} \\ &= \frac{e^{-r(x+2.5)} L(x)}{\sum_{x=0}^{85} e^{-r(x+2.5)} L(x)}. \end{aligned}$$

After grouping into three age intervals, these proportions are given at the bottom of Table 22.2 in comparison with the age structure of the 1995 population. The stable-equivalent population exhibits an older and smoother[6] age distribution than that of the stationary population.

Nonstable Population and Variable-r Extensions of Stable Population Theory

The classic stable population model described above is a generalization of the stationary population model, which permits age-specific growth rates to be nonzero. The assumption of constancy of age-specific growth rates under stable population theory can be further relaxed to accommodate growth rates that vary with age. This generalizes to the nonstable population model, which is applicable to any population. Since the demographic relations in this general model are associated with varying growth rates by age, they are termed as variable-r relations (Preston et al. 2001). The most important development of the nonstable population model and variable-r method for demographic estimation dates back to the 1980s. Preston and Coale (1982) derived various extensions of the relations connecting major demographic parameters in stationary and stable populations to more general conditions. Much of their work is based on the following relation first shown by Bennett and Horiuchi (1981):

$$k(x,t) = B(t) e^{-\int_0^x r(a,t)da} p(x,t) \tag{77}$$

where $k(x, t)$ is the number of persons age x at time t; $B(t)$ is the number of births at time t; $p(x, t)$ is the life table survival probability from age 0 to age x at time t and $p(x,t) = e^{-\int_0^x \mu(a,t)da}$ with $\mu(x,t)$ being the force of mortality function at time t. Preston and Coale expanded this equation to include migration by adding the term, $e(x, t)$, or the net out-migration function, to $r(x, t)$. Thus, the formulation has been generalized from a closed population to an open population. For the convenience of exposition, t is dropped for the following equations, and all functions pertain to the time t.

The establishment of Equation (77) immediately leads to the following relations, which bear a remarkable resemblance to three fundamental formulas that characterize a stable population. Substituting Eq. (77) in Eq. (68), the *crude birth rate* of the population becomes

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[6] The smoothness is observed for five-year age grouping from 0 to 85+.

$$b = \frac{B}{\int_0^{\omega} k(x)dx} = \frac{B}{\int_0^{\infty} Be^{-\int_0^x r(a)da}p(x)dx} = \frac{1}{\int_0^{\infty} e^{-\int_0^x r(a)da}p(x)dx}. \tag{78}$$

In a similar fashion, Eq. (77) and (78) may be substituted in Eq. (69) to obtain the *age composition* of the population:

$$c(x) = \frac{k(x)}{\int_0^{\infty} k(x)dx} = \frac{Be^{-\int_0^x r(a)da}}{\int_0^{\infty} Be^{-\int_0^x r(a)da}p(x)dx} = be^{-\int_0^x r(a)da}p(x) \tag{79}$$

Substituting Eq. (79) into Eq. (67) yields the *characteristic equation* for any population:

$$1 = \int_{\alpha}^{\beta} e^{-\int_0^x r(a)da}p(x)m(x)dx \tag{80}$$

It is easy to demonstrate the connection of this formulation with that in the stable population model. If all age-specific growth rates are constant, that is, $r(a) = r$ at all a, then $e^{-\int_0^x r(a)da} = e^{-rx}$. Eqs. (78) and (79) then become precisely the corresponding functions in the stable population expressed in Eqs. (70) and (71), and Eq. (80) becomes the characteristic equation expressed in Eq. (45) for the stable population model. Table 22.3 shows a brief comparison of these major demographic relations for the stationary population, the stable population, and any nonstable population. As noted before, the variable r or $r(x)$ function is the age-specific growth rate plus the age-specific rate of out-migration, wherever applicable.

The basic relations shown above give rise to other variable-r relations that go beyond the analogs of the classic stable population relations (Preston and Coale 1982; Preston et al. 2001). They connect all major demographic functions to one another through the set of age-specific growth rates that are readily observable and can be utilized as a growth correction which allows all of the relationships of a stationary population to be reestablished. Therefore, variable-r extensions of the basic classic stable population relations find many useful applications in demographic estimation. Space limitations allow only a brief discussion of several such applications in studies of birth rates and fertility, mortality, multiple decrements, and estimation using discrete demographic data. More detailed expositions are available in Preston and Coale (1982) and Preston et al. (2001).

First, the birth rate can be estimated straightforwardly using Eq. (78) and given intercensal growth rates and a life table prevailing for the corresponding time period.

TABLE 22.3. Demographic Relations in Stationary, Stable, and Any Population

	Stationary population	Stable population	Any population
Crude birth rate	$b = \frac{1}{\int_0^{\infty} p(x)dx}$	$b = \frac{1}{\int_0^{\infty} p(x)e^{-rx}dx}$	$b = \frac{1}{\int_0^{\infty} p(x)e^{-\int_0^x r(a)da}dx}$
Proportionate age distribution	$c(x) = bp(x)$	$c(x) = be^{-rx}p(x)$	$c(x) = be^{-\int_0^x r(a)da}p(x)$
Characteristic equation	$1 = \int_{\alpha}^{\beta} p(x)m(x)dx$	$1 = \int_{\alpha}^{\beta} e^{-rx}p(x)m(x)dx$	$1 = \int_{\alpha}^{\beta} e^{-\int_0^x r(a)da}p(x)m(x)dx$

This offers an advantage of estimating the birth rate based on imperfect demographic data because it does not require a reported age distribution and therefore minimizes the bias introduced by a highly distorted age distribution at young ages in some populations (Preston and Coale 1982). Preston and Coale (1982) also observed that the period net reproduction rate can be estimated directly from the set of $r(x)$'s and the proportionate distribution of mothers' age at childbirth, $v(x) = B(x)/B$:

$$NRR = \int_{\alpha}^{\beta} p(x)m(x)dx = \int_{\alpha}^{\beta} v(x)e^{\int_0^x r(a)da} dx \tag{81}$$

Illustrative applications of this method to 1976 Swedish data (Preston and Coale 1982) and 1995 to 2000 Japanese data (Preston et al. 2001) show results that are nearly identical with those produced by the traditional method when single-age intervals are used or the person-years function used in the traditional method is the same as that computed by the intercensal survivorship ratios. Note that it is assumed that the population is closed to migration and the age-specific rates of net emigration have been added to growth rates before Eq. (81) is applied.

Intercensal mortality conditions for a closed population also can be inferred using Eq. (77) from two census age distributions. Preston and Bennett (1983) show that such estimates produce good results for high-quality census data. By multiplying both sides of Eq. (77) by the death rate at age x, $\mu(x)$ and integrating over the entire age range, Preston et al. (2001) connect the number of deaths with the number of births in any population:

$$B = \int_{0}^{\infty} D(x)e^{\int_0^x r(a)da} dx, \tag{82}$$

where the number of deaths, $D(x)$, is growth-corrected by the variable r function. This expands to yet another expression where the population at any age y is written as a function of the number of decrements above age y:

$$N(y) = \int_{y}^{\infty} D(x)e^{\int_x^y r(a)da} dx \tag{83}$$

Bennett and Horiuchi (1981) show the utility of this system of equations in checking the completeness of death registration in some populations. If the census count at age y implied by the number of deaths above age y and age-specific growth rates is too low, this suggests either that deaths above age y are underregistered or that the population count is inflated, the latter of which is less likely. Preston and associates (1996) further demonstrate, in their estimation of African-American mortality rates at older ages, that the incompleteness of death records does not disturb the reconstruction of life table functions using variable-r relations. The key insight here is that the observed number of deaths by age can be applied with a growth correction using the variable-r method and then used to infer the age distribution of deaths in the life table. And the remaining columns of the life table follow. This approach, which uses only the set of age-specific growth rates, is also useful if deaths are based on a sample of the population or if population data are subject to large distortions due to persistent age misreporting. An example is Merli's (1998) estimation of intersensal mortality in Vietnam from 1979 to 1989.

Another application of variable-r relations arises from the generalization of Eq. (77) to multiple-decrement situations by introducing the rate of decrement from cause i, $\mu^i(x)$, to adjust the growth rate $r(x)$ (Preston and Coale 1982). After some simple transformations using $\mu^i(x)$, two basic elements of a multiple-decrement life table are obtained: the observed number of decrements from cause i, $D^i(x)$ and the probability of a newborn succumbing to cause i, l_0^i/l_0, which are linked through the following equation:

$$\frac{l_0^i}{l_0} = \frac{\int_0^\infty D^i(x) e^{\int_0^x r(a)da} dx}{B}, \tag{84}$$

where the probability of succumbing to cause i can be calculated from $D^i(x)$ with variable-r correction, which is divided by the number of births. The advantage of this correction is displayed in an application to the estimation of the "case-fatality ratio" in epidemiology (Preston 1987a). If the actual population is stationary (that is, $r(x) = 0$), the case-fatality ratio is simply estimated as the ratio of annual deaths from the cause of interest to annual diagnoses. In a growing population (that is, when $r(x) > 0$ at all x); however, this ratio will underestimate the true case-fatality ratio, which is directly inferred from Eq. (84). Therefore, the estimation procedure using the growth correction displaces the one without (see Preston et al. 2001: 180). Other applications have been made to make estimates of marital survival (Preston and Coale 1982; Preston et al. 2001).

The above demographic relations have been presented mainly in continuous form and must be adapted to discrete time intervals for empirical applications because demographic data normally come in age intervals with lengths of multiples of 5 or 10. Preston and associates (2001) show that the geometric mean of population counts at both ends of the interval and the mean growth rate over the interval provide good approximations when the growth rate function is relatively regular during the period. A second approximation using five-year age intervals, introduced by Preston (1987a), equals the midpoint of an interval with the sum of counts in the five-year interval divided by five. Applications of this method have mainly occurred in single decrement survival processes and include the estimation of intercensal survival of a population (Preston and Bennett 1983; United Nations 1983), survival (Preston 1987a), and marital survival from multiple decrements (Preston 1987b). Using an intercensal approach, Preston and Strong (1986) also investigate survival from a single decrement in a multiple-decrement process.

Applications of variable-r methods also extend to the use of modeling age patterns of mortality and the iterative intracohort interpolation procedure for estimating intercensal age distributions as a refinement of the basic variable-r procedure (Coale 1984); see Preston et al. (2001) for details on these developments.

Population Momentum and Family Household Momentum

Extensions and applications of the stable population model/theory not only pertain to age composition and age-specific growth rates but also involve the effect of changes in these on changes in population size. Characterizing and modeling the momentum of population growth is another valuable application of the stable population model. *Population momentum* generally refers to the phenomenon by which an existing population age structure that is a legacy of past fertility and mortality conditions future population growth. Keyfitz (1971b) first articulated this notion by applying stable population theory to study relations between population size and age composition. He showed that even if the fertility rates of a growing stable population were immediately reduced to replacement level (i.e., $NRR = 1.0$) and maintained thereafter until the new equilibrium of a stationary population of fixed size and age composition is attained, the population would continue to grow, often by sizable amounts if it was a population with a young age structure. And any such population has a built-in growth potential in its age structure.

Note that Preston and Coale's (1982) derivation of the variable-r method shows how age-specific growth rates are linked to population momentum through the net reproduction rate. Eq. (81) indicates that if the $NRR = 1.0$, it is necessary that the mean of $e^{\int_0^x r(a)da}$ weighted by $\nu(x)$ (mothers' ages at childbirths) be 1.0 for $a \in [\alpha,\beta]$, which is achieved when the sum of $r(x)$ over the childbearing interval is 0.0. That is, the imposition of the replacement-level fertility results in the sum of age-specific growth rates approximating zero on average throughout the childbearing years.

Since its introduction by Keyfitz (1971b), population momentum has evolved into an influential demographic concept that bears critical policy implications for controlling population growth in many parts of the world that are undergoing the demographic transition from high to low rates of birth and death. Several structural efforts have been made to refine his original formulation. Keyfitz (1985) himself developed a basis for a more general expression by finding the exact form of the annual number of births in the eventual stationary population. Following this path, Preston and Guillot (1997) gave the formula for the momentum factor by relating the age structure of the eventual population with that of the initial population. Links between population momentum and aging have also been specified. Kim and Schoen (1997) articulate how population momentum coincides with population aging. Meanwhile, the age above which all of the population growth occurs has been identified to be near the middle of the reproductive life span (Kim, Schoem, and Sarma 1991; Kim and Schoen 1993; Preston 1986). Empirically, analyses show the value of the population momentum factor for the major regions of the world (Preston and Guillot 1997), and that momentum may account for most of the future growth in the world's population (Bongaarts and Bulatao 1999; National Research Council 2000).

The assumptions on which Keyfitz's (1971b) formulation of the momentum factor is based are hypothetical and therefore have limited usage in actual population projections. Some of the assumptions are modified by recent improvements (a complete exposition is given by Schoen and Jonsson 2003). In Keyfitz's framework, replacement-level fertility is achieved by a sudden decrease in fertility of the initial population to the replacement level. As he acknowledges, few populations experience instantaneous declines in fertility. Instead, the achievement of replacement-level reproduction takes place gradually and often over a number of years or decades. Keyfitz also requires that the fall in fertility be proportional at all ages by the factor $1/NRR$ with the scalar multiple (NRR) pertaining to the before-decline value. This ignores changes in the age pattern of fertility associated with changes in fertility levels. In addition, he does not raise the possibility that fertility transition can also be nonlinear. Historical time patterns of fertility changes show examples of both linear and exponential declines for a number of countries (United Nations 2000).

Attempts to generalize Keyfitz's initial contribution have proven fruitful in accommodating a gradual transition to replacement-level fertility. Schoen and Kim (1998) model momentum by imposing a gradual instead of a sudden decline in growth rates of births. There are also techniques to approximate long-term birth trajectories under declining fertility. A general way for determining the birth trajectory produced by a flexible pattern of decline in vital rates is provided by Li and Tuljapurkar (1999, 2000). Goldstein (2002) generalizes the expressions given by Keyfitz (1971b) and Frauenthal (1975) to a simpler result that focuses on the initial level of fertility and the speed of the decline. Goldstein and Stecklov (2002) used the Li-Tuljapurkar relationship to replace traditional population projections and got high correspondence between the two. These analytical extensions produce approximations that perform well under relatively short durations of population momentum (for up to 40 to 50 years), but tend to increasingly deviate from "true" (projected) trends in both hypothetical and actual populations as the duration of fertility decline lengthens (Schoen and Jonsson 2003). Furthermore, they cannot be applied to more general transition regimes that result in constant (stable) but nonzero growth.

In an effort to directly model changing vital rates and the gradual decline in fertility, Schoen and Kim (1994) and Kim and Schoen (1996) developed an analytical framework of a "quadratic hyperstable" (QH) model, wherein a population is generated by monotonic transitions (either increasing or decreasing) of the set of age-specific birth rates and grows by a quadratic exponential function. An age composition that changes over time is also specified. This dynamic model generalizes the stable population model by allowing fertility rates to change over time, accommodates stable-to-stable fertility transitions, and provides significantly more precise estimates of momentum of any length.

Schoen and Jonsson (2003) further extend the quadratic hyperstable population model to a new form which associates exponentially changing fertility to the resultant exponential quadratic birth sequence. Since the new QH model can be used to analyze long-term effects of monotonic transitions between any two sets of constant vital rates, it is a significant generalization of the stable population model. The Schoen-Jonsson QH model is a special case of the QH model, with new procedures to capture monotonic transitions between any levels of fertility. Schoen and Jonsson begin by specifying the QH model in a discrete form using a sequence of Leslie projection matrices that are generated by monotonically increasing/decreasing net maternity functions. This gives the birth trajectory whose structure resembles that of the Coale-Trussell Model Fertility Schedules (Coale and Trussell 1974). The advantage of this approach is that it offers a flexible pattern of change that not only applies to the proportional distribution of births by age of the mother required by early models, but also allows fertility to change monotonically in a specified fashion. They derive an exponentiated quadratic birth trajectory of the QH population in closed form.

Schoen and Jonsson apply the QH model to solve for the momentum associated with gradual transitions in fertility to replacement level. They consider both the transition to stationarity and any stable-stable transition. They first use the equation of an exponentiated quadratic birth trajectory to determine the cumulative change in the size and structure of the QH population over the period of fertility decline. Then they hold fertility constant at replacement level to find the ultimate stationary population. By doing so, they find two factors that determine the relative size of the eventual birth cohort. The first factor is essentially the same factor presented in different ways in previous works by Li and Tuljapurhar (1999), Goldstein (2002), and Schoen and Kim (1998), that is, a continuation of the initial stable growth for half the period of decline. The second is an offsetting factor previously overlooked. It takes into account the changing age composition of the population experiencing the declining fertility rate that is no longer stable. Therefore, it is a factor that reflects the interaction between the changing age composition, age pattern of fertility, and the level of fertility. Considering this factor reduces the growth in the number of births. Using the same approach, they model the transition from an initial stable population to another stable population and provide explicit expressions to bridge between any two stable rates.

Schoen and Jonsson apply the theoretical model to populations with high fertility (Singapore 1957) and moderate fertility (Mexico 1983). They compare the effects of both linear declines and exponential declines in *NRR* on population momentum using the Li-Tuljapurhar (1999) method, the Goldstein (2002) models, and the new QH model. The results indicate that both the Li-Tuljapurhar and Goldstein approximations lose accuracy for declines longer than 50 or so years, and they tend to overestimate the growth because they do not reflect the offsetting growth factor mentioned above. The QH model, on the other hand, proves successful for estimating momentum values over any length of the transition regardless of the beginning fertility level because it reinforces the role of the interaction between the two factors in moderating the growth.

Keyfitz's original concept of population momentum has also led to the discovery of a new type of momentum—the momentum of family/household types. Using data from national surveys and vital statistics, census micro files, and the "ProFamy" multistate household family projection method (discussed above), Zeng and associates (2005) prepared projections of U.S. elderly (ages 65 and over) households from 2000 to 2050. Medium projections, smaller and larger family scenarios with corresponding combinations of assumptions of marriage/union formation and dissolution, fertility, mortality, and international migration were performed to analyze future trends of U.S. households and their possible higher and lower bounds, as well as the enormous racial differentials.

Under a constant scenario with everything (marriage union formation and dissolution, fertility, mortality, migration, and so forth) after 2000 assumed to remain the same as in 2000, they found that the proportional distributions of household types/size and living arrangements of the elderly change considerably until 2020 or so and remain more or less stable afterward (except the percent of the oldest-old (ages 85 and over) living alone continues to increase substantially after 2020). Why would distributions of households and elderly living arrangements change considerably from 2000 to 2020 while the demographic parameters remain constant in the same period? The answer of Zeng and associates (2004) is that *family/household momentum* plays an important role.

The cohorts who were younger in 2000 experienced and will experience stabilized (or constant) higher rates of marriage/union disruption and lower marriage/union formation than the cohorts who were older in 2000 and had already completed most of their family life course. The profiles of households and elderly living arrangements in 2000 represent the mixed cumulative life course experiences of younger and older cohorts in the past few decades. Although the marriage/union formation and dissolution rates are assumed to remain constant during the period of 2000 to 2050, the distributions of households and elderly living arrangements would change considerably because the older cohorts, who had more traditional family patterns, will be replaced by the younger cohorts with modern family patterns. Family household momentum is similar to the population momentum concept of Keyfitz (1971b), in which population size could continue to increase after the fertility is equal to or even below the replacement level. The ProFamy method/program and the family household projections provide empirical evidence for the first time to numerically illustrate the concept of family household momentum.

MODEL SCHEDULES, SUMMARY INDICES, AND QUANTUM/TEMPO ADJUSTMENTS

Modeling Demographic Schedules

In almost all models of mathematical demography such as the single-decrement, multiple-decrement, multiple increment-decrement life tables, multistate population and family household simulation and projection models, and the stable population model and its extensions, age-sex-specific demographic rates are needed. The age-sex-specific demographic rates, ordered across the full age range from birth to death, are termed *demographic schedules*. The classic examples of demographic schedules are age-sex-specific mortality rates, age-specific fertility rates, age-sex-specific marriage and divorce rates, and age-sex-specific migration rates.

The most commonly used demographic schedules of age-specific rates of fertility and marriage are defined as the number of events occurring in an age interval divided by the total number of persons of the same age. Without transformation, however, these age-specific rates often cannot be used for computing status transitions for constructing life tables and family household simulations and projections, because their denominators do not distinguish the at-risk and not-at-risk populations for experiencing the events; they may be biased in measuring the period quantum and changes in period tempo (to be discussed below). Thus, more sophisticated age-specific occurrence/exposure rates, which are defined as the number of events occurred in the age interval divided by the person-years lived at risk of experiencing the event within the age interval, are required (see Eq. (22) for the case of mortality).

For many years, statisticians and demographers tried to establish analytical formulas for describing the patterns of human mortality, fertility, marriage, divorce, and migration. Examples of such efforts in modeling mortality schedules are the Gompertz, Logistic, Weibull, Heligman & Pollard, Quadratic, and Kannisto models (Thatcher, Kannisto, Vaupel 1998; Zeng and Vaupel 2003). Rogers (1986) proposes parametric models to describe the demographic schedules of migration, mortality, and nuptiality. Coale and McNeil (1972) develop a double-exponential first-marriage model, including age-specific model standard schedules of frequency distribution of first marriage and three parameters: the proportion eventually ever married, the lowest age at first marriage, and the average age at first marriage. Coale and Trussell (1974) propose a fertility double-exponential model, including model standard schedules of age-specific natural fertility and age-specific deviation from natural fertility due to birth control and parameters of total natural fertility level and level of birth control; a statistical version of the Coale-Trussell model was developed by Brostrom (1985), Trussell (1985), and Xie and Pimentel (1992).

As an illustrative example in modeling demographic schedules, this section summarizes the relational Gompertz fertility model originally proposed by Brass (1968, 1974, 1975, 1978; see also Booth 1984; Paget and Timaeus 1994) and its extension by Zeng et al.

(2000). Define H(x) as the cumulated fertility rate up to exact age x. Define the total fertility rate (TFR) as in Eq. (3), that is, as the sum of age-specific fertility rates over all ages. The model then assumes that H(x)/TFR follows the Gompertz distribution:

$$\mathrm{H(x)/TFR} = \exp(\mathrm{A}\exp(\mathrm{Bx})) \tag{85}$$

where A and B are constants. Using the complementary log-log transformation

$$\begin{aligned} -\ln(-\ln(\mathrm{H(x)/TFR})) &= -\ln(-A) - B\,\mathrm{x} \\ \mathrm{Y(H(x)/TFR)} &= -\ln(-A) - B\,\mathrm{x} \end{aligned} \tag{86}$$

where Y stands for the complementary log-log transformation of H(x)/TFR.

Observed data from various populations show that the linear relationship expressed in equation (86) yields a reasonably good fit, except at extreme ages (Pollard and Volkovics 1992). To improve the fit, Brass introduces the standard fertility schedule and derives the following Relational Gompertz Fertility Model, which substantially improves the empirical fittings, including those at extreme ages, as compared to the original Gompertz fertility model expressed in Eq. (86):

$$\mathrm{Y(H(x)/TFR)} = \alpha + \beta\ \mathrm{Y_s(H_s(x)/TFR_s)} \tag{87}$$

where H_s (x) is the cumulated fertility rate up to exact age x in the standard fertility schedule and TFR_s is the total fertility rate of the standard schedule. A_s and B_s are constants.

Equation (87) establishes that the Y transformation of an observed schedule is a linear function of the Y transformation of the Standard Schedule, and the two parameters α and β can be estimated using Ordinary Least Squares (OLS) regression or other estimation procedures. The TFR summary index can be estimated directly or indirectly from the empirical fertility data. Its standard schedule can be easily established by using the observed rates in the population under study or, if the data are poor in the population under study, by using rates from another demographically similar population.

Studies by Brass and others produce clear statistical meanings for the parameters α and β. The α parameter determines the age location (i.e., early or late) of the fertility distribution, and the β parameter determines the spread or degree of concentration of the distribution. More specifically, the smaller the α, the later the process, and when α is equal to 0, the age location of the schedule is identical to the standard. The smaller the β, the more dispersed the curve of the schedule, and when β is equal to one, the spread or the degree of the concentration of the schedule is identical to the standard (United Nations 1983). Despite their clear statistical meanings, however, it is remarkably difficult to estimate or project α and β directly for purposes of projecting or simulating demographic rates for the future years for four main reasons. First, there are no observed values of α and β from demographic data resources (such as vital statistics, surveys, or censuses) for past years that can be used as a basis for future trend extrapolation. Second, estimates of α and β are not compatible across time and regions (Zeng et al. 2000). Third, it is difficult to connect changes in the values of α and β with the quantity of changes in timing and concentration of the demographic process. For example, if one tells policy makers or the public that α will decrease by 0.2 and β will decrease by 0.1 in the fertility schedule in 10 years, few understand the demographic meaning of the terms. Fourth, linking α and β with socioeconomic and human behavior variables, such as changes in women's education and labor force participation, for future trends extrapolation is even more implausible. In sum, α and β are demographically unmeasurable, uninterpretable, incompatible across time and regions, and unpredictable. It is, therefore, important to find a way to link α and β with variables that are demographically measurable, interpretable, and predictable. The simple method proposed and tested by Zeng and associates (2000) is intended to solve this problem. This research is what Rogers (1986: 60) anticipated in his statement "[a]lthough the model schedule parameters are not always demographically interpretable, future research is likely to link them to variables that are."

Define M as the median age, i.e., the exact age at which 50% of the events have occurred, and N and O as first and third quartiles, i.e., the exact age at which 25% and 75% of the events have occurred, respectively. Define M_S, N_S, and O_S as the median age, the first, and the third quartiles of the standard schedule. Zeng and associates (2000) then propose the following estimator to link the parameter β with the interquartile range:

$$\beta = (O_S - N_S)/(O - N), \tag{88}$$

where $(O_S - N_S)$ is the interquartile range of the standard schedule that is known and may be denoted as I_S. Let $(O - N)$, the interquartile range of the schedule to be estimated or projected, be denoted by I. Now only the value of I needs to be estimated, rather than both the O and N values. Then an analytical formula for estimating β can be expressed as follows:

$$\beta = I_S/I \tag{89}$$

After β is estimated, the estimation of α is straightforward. Following equation (87), and setting x equal to the median age (M) of the schedule to be estimated or projected: $Y(H(M)/TFR) = \alpha + \beta Y_S(H_S(M)/TFR_S)$. $Y(H(M)/TFR)$ is equal to $\ln(-\ln(0.5))$. $Y_S(H_S(M)/TFR_S)$ can be obtained from the standard schedule by linear interpolation if M is not an integer. Thus, α can be quickly estimated. Once α and β are estimated, H(x) and f(x) can be computed based on equation (87) for H(x) and using $f(x) = H(x + 1) - H(x)$. The single-year age-specific rates f(x) can thus be derived using the above proposed method based on the three parameters of total rate, median age, interquartile range, and a standard schedule. The three parameters are all demographically interpretable, measurable, and predictable, and the standard schedule can be easily established based on the proper data. The method has been successfully tested on 180 reliable observed demographic schedules in various countries and periods and to nearly 10,000 simulated schedules with various combinations of possible values (including the extremes) of α and β (Zeng et al. 2000).

The method that uses median age and interquartile range instead of α and β as input proposed by Zeng and associates (2000) relaxes the traditional unrealistic assumption in population projections that the curve of the fertility schedule moves to the right or left in a parallel way. Instead, using this method, one assumes that the demographic events would be delayed or advanced, while the curve becomes more spread or more concentrated or, more specifically, that young people delay the events more than older persons, or vice versa. It is also useful for formulating assumptions about future demographic trends for purposes of policy analysis and planning. It can be used to indirectly estimate demographic schedules when the detailed age-specific data are not currently available, which is useful for developing countries and subregion studies in developed countries.

Model Standard Schedules and Summary Demographic Indices

Despite their remarkable success, model demographic schedules as discussed above have not been fully satisfactory, especially for applications in many developing countries where the empirical data needed to estimate the model parameters are not readily available. Since the 1950s, population studies for developing countries have progressed rapidly, and demographers have realized that it is extremely important to establish reasonable models of mortality for such efforts because many developing countries do not have reliable life tables. Given the fact that analytical formulas cannot describe well the different age patterns of human mortality, demographers have tried to find a set of model standard schedules of life tables to represent various mortality patterns and levels. The result is model life tables. Empirically based model life tables are identical to ordinary real life tables in every way, except that they relate to no particular single place or time. Since the 1950s, at least nine different sets of empirical model life tables have been published. The two most widely used families of model life tables are discussed here.

The initial version of the Coale and Demeny (1966) regional model life tables was derived from a set of 192 life tables by sex recorded for human populations that were chosen from an original set of 326 life tables from Europe (206), Latin America (33), Asia (32), Oceania (22), North America (18), and Africa (15). Coale-Demeny regional model life tables are of four "families of regions" called "North," "South," "East," and "West." The North model table is based on nine life tables from Norway, Sweden, and Iceland. It is characterized by relatively low infant and old age mortality but high adult mortality caused by an unusually high incidence of tuberculosis. The South model table is derived from 23 Mediterranean life tables from Portugal, Spain, Sicily, and southern Italy. It has high mortality under age 5, particularly among infants, low adult mortality, and high mortality over age 65. The East model table was generated from 31 primarily Central European life tables from Austria, Germany, Bavaria, Prussia, north Italy, Poland, and Czechoslovakia. It has high infant and high old-age mortality, relative to childhood and adult rates. The West model table is regarded as describing an "average" mortality pattern and is by far the most frequently used. Coale and Demeny (1966; 1983) recommend its use when no reliable information on the age pattern of mortality is available. The West models are based on a diverse array of about 130 life tables which were considered to be accurate but which did not fit into any of the other three groups. They include life tables from the Netherlands, Finland, France, England and Wales, Japan, Ireland, Israel, Australia, Canada, and South Africa. In 1985, a second version of the model life tables was published by Coale and Demeny (1985). The upper boundary of the life tables in the second version was raised to age 100 instead of age 80 in the 1966 version.

In 1982, the United Nations published a set of model life tables based entirely on empirical life tables from developing countries. As many accurate life tables were collected from developing countries as possible. After careful data quality evaluation, 36 male and 36 female life tables from 10 Latin American countries, 11 Asian countries and 1 African country were selected. These life tables were then divided into five groups: "Latin American," "Chilean," "South Asian," "Far Eastern," and "General." The "General" pattern was produced as an average of all the original empirical model life tables. The different patterns have roughly the following characteristics:

1. Latin American: relatively high infant, child, and adult mortality and relatively low old-age mortality

2. Chilean: extremely high infant mortality
3. South Asian: high mortality under 15 and over 55, but relatively low mortality at adult ages
4. Far Eastern: very high mortality at old ages
5. General: average mortality pattern

As discussed above, almost all of the internationally published fertility and nuptiality models (e.g., Coale and McNeil 1972; Coale and Trussell 1974; Brass 1968; Zeng et al. 2000) aim to model age-specific rates of fertility and marriage, which are defined as the number of events occurring in an age interval divided by the total number of persons of the same age. These age-specific rates, however, cannot be used for computing status transitions for constructing multistate life tables and family household projections or simulation because their denominators do not distinguish between the at-risk and not-at-risk populations experiencing the events. Furthermore, similar to the situation in many developing countries a couple of decades ago, when reliable life tables were not available, the age-sex-specific occurrence/exposures rates of marriage/union formation and dissolution and age-parity-marital/union-status-s occurrence/exposures rates of fertility, which are needed for family household projections or simulations, are not readily available for many developing countries and some developed countries. These occurrence/exposure rates at the national level can be estimated from national surveys which collected fertility and marriage histories data but are usually not available for local or small areas. Therefore, there is an imperative need to establish model standard schedules of the age-sex-specific occurrence/exposure rates of marriage/union formation and dissolution and age-parity-specific occurrence/exposure rates of marital and nonmarital fertility. The basic ideas and approach for establishing such model standard schedules of marriage/union formation and dissolution and fertility may be similar to those used for creating the model life tables, but intensive innovative investigations are called for in future studies.

Model standard schedules of marriage/union formation and dissolution, fertility, and mortality model life tables have three practically useful properties. First, they can serve as a standard for smoothing the observed age-specific demographic rates with poor quality. Second, they can be used to perform indirect estimation in case the directly observed rates are not complete. Third, they can be used to project future age-sex-specific demographic rates for population and family household projections or simulations.

Age-sex-specific demographic schedules are useful in analysis and modeling, but they should be accompanied by summary indices, because the numerous age-sex-specific numbers cannot concisely represent the *quantum* or *level* and *tempo* or *timing* (of the rates by age) of demographic processes. Thus, *summary demographic indices* are necessary in demographic studies. Furthermore, as Keyfitz (1972) points out, demographic projections based on trend extrapolation of each age-sex-specific rate can result in an excessive concession to flexibility and readily produce erratic results. Accordingly, demographers focus on forecasts of the summary indices in population and family household projections or simulations. Demographers define and estimate various summary indices depending on the purpose of their studies and data availability. Two of the most commonly used summary indices are the period life expectancy and the period Total Fertility Rate.

It has been noted earlier that the period life expectancy (mathematically defined in Eq. [20]) is the average life span of a hypothetical cohort subjected to the observed period age-specific death rates. Similarly, demographers interpret the conventional period TFR(t) (i.e., the observed period total fertility rate in year t, mathematically defined in Eq. [3]) as the total number of births an average member of a hypothetical female cohort would have during her reproductive life if the hypothetical cohort *exactly* (with no changes in quantum, tempo, and shape of the schedule) experienced the observed period age-specific fertility rates. This interpretation is equivalent to imagining that the observed period age-specific fertility rates are *constantly* extended a sufficient number of years into the future (e.g., 35 years), so that a hypothetical cohort would have gone through the whole reproductive life span (e.g., ages 15 to 50). The observed period TFR(t) is the total number of births an average member of the hypothetical cohort would have during her whole reproductive life. A topic of recent interest among mathematical demographers has been the development of formulas for adjustment of standard period life expectancy and period TFR(t) for changes in quantum and tempo.

Quantum/Tempo Adjustment Formulas

THE BONGAARTS-FEENEY QUANTUM ADJUSTMENT FORMULA. It is well known in demography that the observed period TFR(t) is biased if cohort tempo is changing (Ryder 1956, 1959, 1964, 1980, 1983; Keilman 1994; Keilman and Van Imhoff 1995). The demographic literature on fertility measures includes many criticisms of and alternatives to the period TFR(t), but there has been no agreement on its replacement. An important recent development was initiated by Bongaarts and Feeney (1998), who derive a simple and effective *quantum adjustment formula*[7]:

$$\mathrm{TFR}^*(t) = \mathrm{TFR}(t)/(1 - r(t)) \tag{90}$$

where $\mathrm{TFR}^*(t)$ is the adjusted period order-specific total fertility rate that reduces bias caused by changes in the timing of fertility, TFR(t) is the observed period order-specific total fertility rate in year t, and $r(t)$ denotes the observed annual changes in order-specific period mean age at childbearing in year t.[8] To simplify the notation, subscripts for the order of births are suppressed, but it should be kept in mind that all of the derivations and discussion refer to order-specific fertility.[9] Similar to the conventional interpretation of the classic period TFR(t), as stated above, Bongaarts and Feeney (1998: 287–289) assume, in deriving their quantum adjustment formula, that the observed period age-parity-specific fertility rates are extended a sufficient number of years into the future (e.g., 35 years), with changing period tempo, but assuming a constant quantum and an invariant shape of the schedule.

One important question, however, needs to be addressed: Does the Bongaarts-Feeney (abbreviated as B-F hereafter) formula work when its underlying assumption of

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[7] Bongaarts and Feeney (1998: 287) refer to their formula as a "tempo adjustment formula." A more complete description is that it is a formula for adjusting the quantum for tempo effects. While this phrasing may seem trivial, it is an important distinction in view of the tempo adjustment formula presented later in this Section.

[8] The annual change $r(t)$ is defined as the difference of the mean age at experiencing the event between two successive years. The unit of $r(t)$ is "years old/per year."

[9] If one does not distinguish the orders of births, errors in the estimates may likely occur. For example, when people reduce their fertility they do so primarily by reducing childbearing at higher birth orders. As a result, the mean age at childbearing for all births without order specification declines even when the timing of individual births does not change (Bongaarts and Feeney 1998; Bongaarts 1999).

an invariant shape of the fertility schedule and its implied equal changes in timing of births across reproductive ages do not hold, as is likely the case in the real world? Bongaarts and Feeney (1998) present a successful test of their adjustment method by comparing the completed fertility of true cohorts born from 1904 to 1941 in the United States with the weighted averages of the adjusted period $TFR^{*}(t)$ over the years during which the true cohorts were in the childbearing ages. But they do not perform a sensitivity analysis directly targeting the underlying assumption about the invariant shape of the schedule and its implied assumption about equal changes in timing of births at all reproductive ages. Consequently, there are questions raised about the sensitivity of the B-F formula to the likely violation of its assumption (Kim and Schoen 2000; Van Imhoff and Keilman 2000; Kohler and Philipov 2001). If the B-F method is very sensitive to the likely violation of its underlying assumption, it should not be used unless an appropriate correction is made.

Zeng and Land (2001) present a sensitivity analysis of the B-F method, based on fertility data in the U.S. from 1918 to 1990 and in Taiwan from 1978 to 1993, and the Brass Relational Gompertz fertility model and its extension (as discussed earlier). Zeng and Land (2002) conclude that the adjusted $TFR^{*}(t)$ using the B-F formula, which assumes an invariant shape of the fertility schedule, usually does not differ significantly from an adjusted $TFR^{*}(t)$ that allows systematic changes (with constant rate) in the shape of the fertility schedule. This finding is consistent with an analysis by Kohler and Philipov (2001) in which they show that the biases in the B-F formula are quite small if a constant rate of increase in the variance of the fertility schedule prevails over time. This finding implies that the B-F method is usually not sensitive to its underlying assumption on invariant shape of the fertility schedules and equal changes in timing across ages. That is, it is generally robust for producing reasonable estimates of the adjusted period $TFR^{*}(t)$ that reduce distortion caused by tempo changes, except in abnormal conditions. The B-F method may be sensitive to substantial nonsystematic changes (i.e., large and time-varying changes in the tempo and shape of the schedule). Another important point is that the adjusted $TFR^{*}(t)$ using the B-F method neither represents actual cohort experiences in the past nor forecasts any future trend. Rather, as compared to the conventional TFR(t), it merely provides an improved reading of the period fertility measure that reduces the tempo distortion, and it is a hypothetical cohort measure, similar to the period life table measures in a general sense.

The word “improved” is used above to indicate that the adjusted $TFR^{*}(t)$ using the B-F method is relatively more reasonable than the conventional TFR(t) in measuring the period fertility level because it reduces the tempo distortion. But the observed period TFR(t), whose denominator is the age-specific total number of women in the population, also does not distinguish those who are at risk and those who are not at risk of giving birth of the particular order (van Imhoff and Keilman 2000). This is one of the reasons why the observed period TFR is distorted by changes in the timing of fertility and needs to be adjusted. However, the adjusted $TFR^{*}(t)$ using the B-F method still is not entirely free of distortion; it is not only based on certain simplifying assumptions, but also on the restricted data of period fertility rates whose denominator does not distinguish the at-risk and not-at-risk populations. For example, if a substantial number of women postponed their first (or second) births a few years ago and now give birth in the current year, the observed total fertility rate of first (or second) births would not be low (say, 0.8). However, if other women delay births substantially and this resulted in a large annual increase in mean age at childbearing of first (or second) birth (say, 0.3

year), the adjusted TFR of first (or second) births using the B-F method in this case could be unreasonably high (say, 1.14). The fact that the adjusted U.S. TFR of second births by the B-F method in the year 1944 exceeded one (Zeng and Land 2001) might be a concrete example of such cases.

Zeng and Land (2001) recommend the application of the B-F method to adjust the observed parity-specific period TFR when the timing of fertility is changing under normal conditions. However, the application of the B-F method under abnormal conditions is problematic. In particular, when observed annual changes in the timing of fertility exceed 0.25, and the annual changes in the interquartile range exceed 0.1 and have large fluctuations, one must be cautious in applying the B-F method, since the adjustments may be incorrect. Zeng and Land (2001) also recommend presentation of both observed period TFR and the adjusted TFR using the B-F method. The observed TFR reveals the implications of fertility for population growth (or decline), and the adjusted TFR reflects a better reading of the period fertility level, reducing the distortion caused by changes in tempo.

THE ZENG-LAND TEMPO ADJUSTMENT FORMULA. Zeng and Land (2002) show that, under conditions of changing tempo, not only are observed period total fertility rates biased, but also observed changes in the period tempo of fertility are biased. Zeng and Land (2002) derive a *tempo adjustment formula* as follows for adjusting the bias in observed changes in the period tempo of fertility, based on the same assumptions as those imposed in the B-F method:

$$r^*(t) = r(t)/(1 - r(t)). \tag{91}$$

where $r(t)$ are *observed changes* in the period tempo, and the $r^*(t)$ are *adjusted changes* in the tempo in year t, reducing the bias caused by changes in the timing of childbearing.

Eq. (91) implies that, similar to the fact that the observed period quantum is distorted by changing tempo, observed changes in period tempo are distorted also.[10] The relative error rate of the observed annual changes in period tempo can be computed as:

$$\text{Relative bias} = [r(t) - r^*(t)]/r^*(t) = -r(t). \tag{92}$$

The relative bias of the observed annual change in period tempo as an estimate of the actual change in tempo is of the same magnitude as the annual change itself with an opposite sign. For example, if the observed annual change in the period tempo of fertility is 0.1 years, it underestimates the actual value of the annual increase by 10% (the actual value is 0.111). If the observed annual change in period tempo of fertility is −0.09 years, it overestimates the actual value of the annual decrease by 9% (the actual value is −0.0826). As compared to the conventionally observed TFR(t) and r(t), both the B-F adjusted quantum ($TFR^*(t)$) and Zeng-Land adjusted changes in tempo ($r^*(t)$) do better; they adjust the bias in the observed quantum and changes in tempo due to changes in fertility timing.

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[10] Even under conditions similar to scenario 4 of Bongaarts and Feeney (1998), which assumes that TFR(t) changes over time, Eqs. (91) and (92) still are valid.

AN EXTENSION OF RYDER'S TRANSLATIONAL EQUATION. In the process of deriving the tempo adjustment formula, Zeng and Land (2002) also derive an alternative quantum adjustment formula using $r^*(t)$ as input:

$$\mathrm{TFR}^*(t) = \mathrm{TFR}(t)(1 + r^*(t)) \tag{93}$$

Zeng and Land (2002) show analytically that the relationship between the adjusted $\mathrm{TFR}^*(t)$ and the observed period $\mathrm{TFR}(t)$, using $r^*(t)$ and $r(t)$ as the input respectively and the B-F formula, can be easily generalized to real cohorts (instead of only hypothetical cohorts), provided the assumptions of constant quantum, constant changes in tempo and invariant shape of the schedule hold for all real cohorts concerned. In this generalized case, the mathematical proof of Eqs. (90), (91), (92), and (93), as well as the general relationship expressed in these four equations, still hold, but the symbolic terms need to be changed as:

$$\mathrm{CFR} = \mathrm{TFR}(1 + r_c) \tag{94}$$

where CFR is the constant cohort complete fertility rate, TFR is the constant period total fertility rate, and r_c is the constant changes in cohort tempo, which are defined as the difference of the mean age at childbearing between two successive cohorts. Eq. (94) may be referred to as a *period-cohort quantum equation.*

$$\mathrm{CFR} = \mathrm{TFR}/(1 - r_p) \tag{95}$$

where r_p denotes the constant annual changes in period tempo, defined as the difference of the mean age at childbearing between two successive years.

Based on Eqs. (94) and (95), a relationship between r_c and r_p can be derived:

$$r_c = r_p/(1 - r_p) \tag{96}$$

Eq. (96) may be referred to as a *period-cohort tempo equation.*

The period-cohort quantum Eq. (94) and Eq. (95) can be regarded as alternatives to Ryder's *basic translation equation*. Using the notation defined in this chapter, Ryder's basic translation equation (Ryder 1956, 1964) can be expressed as: $\mathrm{CFR} = \mathrm{TFR}/(1 - r_c)$, which differs from the period-cohort quantum equations expressed in Eqs. (94) and (95). The discrepancy between Ryder's basic translation equation and the period-cohort quantum Eqs. (94) and (95) is due to different assumptions. Ryder assumes that fertility rates at each age change according to its own polynomial, ignored all moments of order higher than 1, and then approximated the age-specific polynomial as a straight line (Ryder 1964). Zeng and Land assume that all cohorts postpone or advance the births by an equal amount as compared with the immediate preceding cohort and that the shape of the cohort age-specific schedules is assumed to be invariant, but the curve shifts to the right or left when the timing changes. As tested by Zeng and Land (2001), the assumptions of the invariant shape of the fertility schedule and equal changes in cohort tempo usually are not sensitive to the estimates except in abnormal conditions.

The numerical difference between using Ryder's basic translation equation and the period-cohort quantum Eqs. (94) and (95) is rather small if r_c is small. However, the period-cohort quantum equations, as expressed in Eqs. (94) and (95), have led to a derivation of the period-cohort tempo Eq. (96). This is an extension of the Ryder's basic translation equation and expands demographic knowledge to an analytical expression of the relationship between period and cohort changes in tempo. Furthermore, the period-cohort quantum and period-cohort tempo equations are based on simpler and more reasonable assumptions and are derived in a much easier way, as compared to Ryder's basic translation equation.

The Zeng-Land extension not only expands knowledge of relationships among formulas in mathematical demography but is also useful in modeling the quantum-tempo of periods and cohorts for population and family household projection or simulation. For example, the period-cohort and quantum-tempo relationships expressed in Eqs. (94), (95), and (96) may be used in component population projections, which begin with estimates of an initial age distribution and projections of age-specific fertility, mortality and migration rates. Following trend extrapolation or expert opinion approaches, one may first project (or assume) the future cohort TFR and changes in mean age at childbearing. Using Eqs. (94), (95), and (96), one can then estimate the future period TFR and changes in the period mean age at childbearing to formulate the needed period projection matrices. Such estimates or projections of period TFR and period age at childbearing based on understandings of the cohort trends and taking into account the important effects of changes in cohort tempo on the period quantum and period tempo certainly make more sense than just solely extrapolating the distorted period rates.

Finally, the analytical formulas concerning the quantum/tempo adjustments and relationships discussed in this chapter may be extended to other nonrepeatable demographic events, such as first marriage, order-specific divorce, and leaving the parental home. The relationships of period, cohort (or hypothetical cohort) quantum, and tempo changes analyzed here and other related studies may also turn out to be useful in examining quite different topics, such as the effect of delayed retirement in a public pension system on the system's finance.

CONCLUSION

This chapter illustrates how mathematics is used by demographers to develop theories and models of populations and has surveyed much of the literature of this specialty. Specifically, this chapter reviews some of the essential concepts and mathematics of the two basic classic population models that constitute the core of mathematical demography—the life table/stationary population model and the stable population model. Despite the fact that these core models have been quite thoroughly studied for decades, both continue to be subjects of active research in mathematical demography. Extensions of the classic single-decrement life table model to multistate and stochastic representations continue to be areas of methodological research and empirical application. In the case of stable population theory, the topics of population momentum and related generalizations of the classic model are foci of continued research interest. The third major topic reviewed is model schedules or age-specific rates of demographic events such as births and deaths, summary demographic indices, such as the total fertility rate and life expectancy, and recent developments in tempo adjustment formulas based thereon. The implications of quantum/tempo adjustment formulas for population models and summary demographic indices also are subjects of current debate and research interest.

Even in a long chapter, however, there are many topics of importance in mathematical demography that cannot be included. A few of these are the following. First, two-sex models: all of the models reviewed here are one-sex models. Especially for the study of marriage and divorce (or more generally, union formation and dissolution) processes, fertility, and long-range population projections, it is important to take into account the interaction of the sexes; Schoen (1988) includes a review of the essential concepts and models for interacting populations. Another topic not reviewed that is receiving increasing attention is the cross-disciplinary integration of biological and demographic models (Yashin and Iachine 1997). The incorporation of genetic data into demographic surveys (Finch, Vaupel, and Kinsella 2001) and its use in the study of the biodemography of aging and longevity (Wachter and Finch 1997) will stimulate this cross-disciplinary fertilization and evolution of the models of demography.

In brief, mathematical demography is indispensable to the development of formal representations of the structure of populations and population processes. It will continue to evolve and generate new contributions, generalizations, and extensions.

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