TABLE 2

Estimates of Longevity for Fossil Hominids

Hominid Species	Life Span (years)	Incremental Change
Australopithicus afarensus	46.6	
Homo habilis	55.0	8.4
H. erectus	62.0	7.0
H. sapiens (pre-historical)	72.9	10.9
H. sapiens (contemporary)	122.0	49.1

Note: Estimates based on hominoid body size range from 42–44 years for *Australopithecus* to 50 years for *Homo erectus*. Incorporation of brain mass increased estimates for *Homo habilis* from 43 years to 52–56 years and for *Homo erectus* from 50 years to 60–63 years.

SOURCE: Carey and Judge (2001).

See also: *Aging and Longevity, Biology of; Evolutionary Demography.*

BIBLIOGRAPHY

Carey, James R., and D. S. Judge. 2001. "Life Span Extension in Humans Is Self-Reinforcing: A General Theory of Longevity." *Population and Development Review* 27: 411–436.

Goldwasser, L. 2001. "The Biodemography of Life Span: Resources, Allocation, and Metabolism." *Trends in Ecology and Evolution* 16: 536–538.

Judge, D. S., and J. R. Carey. 2000. "Post-reproductive Life Predicted by Primate Patterns." *Journal of Gerontology: Biological Sciences* 55A: B201–B209.

Wilmoth, J. R., L. J. Deegan, H. Lundstrom, and S. Horiuchi. 2000. "Increase of Maximum Life-Span in Sweden, 1861–1999." *Science* 289: 2366–2368.

JAMES R. CAREY

LIFE TABLES

The life table is a device that describes a cohort's or a population's mortality experience. The life table, sometimes called table of mortality (*table de mortalité* in French, and similarly labeled in most languages other than English) is one of the oldest and probably the single most valuable tool in demography. It has many applications that range well beyond mortality analysis. It is called a table, because in its classical presentation it is made of a number of numerical columns representing various indicators of mortality, but the information it contains can be also conveyed in graphical form.

The concept of a life table comes from a cohort perspective. If one could follow a birth cohort of 100,000 individuals through time in a closed population (a population without in- and outmigration), the number of survivors at various ages would correspond to the "number left alive at age x," in the life table its l_x column. The difference between survivors at two consecutive ages, x and $x+n$, would correspond to the number of deaths between x and $x+n$, in the life table denoted by $_nd_x$. The ratio of $_nd_x$ to l_x produces another column of the life table, the probability of dying between age x and $x+n$, denoted by $_nq_x$. Thus, data on cohort survival can be readily converted into a life table.

In its classical form, the life table includes the following columns:

x = exact age

l_x = number still alive at age x

$_nd_x$ = number dying between ages x and $x+n$ = $l_x - l_{x+n}$

$_nq_x$ = probability of dying between ages x and $x+n$, conditional on survival to age x = $_nd_x / l_x$

$_np_x$ = probability of surviving from age x to age $x+n$, conditional on survival to age x = l_{x+n} / l_x

$_na_x$ = average number of person-years lived in the interval between age x and $x+n$ by those dying in the interval

$_nL_x$ = number of person-years lived between ages x and $x+n$ = $nl_x + _na_x \cdot _nd_x$

$_nm_x$ = death rate between ages x and $x+n$ = $_nd_x / _nL_x$

T_x = person-years lived above age x (sum of $_nL_x$ for ages x and higher)

$\mathring{e}_x$ = expectation of life at age x = T_x / l_x

Traditionally, a life table where $n = 1$ is called an "unabridged" or a "single-year" life table, and the left subscript can be omitted. A common alterna-

tive is to use 5-year age groups starting with age 5, and to present information for the age group 0–4 (that is, below exact age 5) in two groups: age 0 (i.e., less than age 1) and ages 1–4. In this case, the life table is called "abridged." It formerly was common practice to end a life table with an open-ended age interval starting at age 85. With the large proportions of survivors to age 85 in many low-mortality populations, though, the preferred practice is to present more detailed information above age 85, carrying it up to age 100 and concluding with an open-ended interval above that age. Because of the distinctive mortality differences between the sexes, life tables are commonly also presented separately for males and for females.

Although the life table is in principle a cohort concept, it is not commonly used in this fashion. The reason for this is both practical and substantive. Exhaustive cohort mortality data are rarely available, because that would require systematic death registration for a period spanning 100 years or more. In other words, it would be necessary to wait for a cohort to be extinct or near extinct to be able to construct a full cohort life table and obtain an accurate estimate of its life expectancy at birth. Accuracy would be compromised if the population was not closed—that is, if it were depleted not only by death but also outmigration—and if death registration included deaths of immigrants. A further and more substantive drawback of cohort life tables is that they refer to a period stretching over a century, during which mortality conditions are likely to have changed. For descriptive and policy purposes, typically less heterogenous and more timely information is necessary.

The limitations of cohort life tables have led demographers to design period life tables, based on the concept of "synthetic" cohorts. A synthetic cohort is a hypothetical cohort of persons subject through their life to the age-specific mortality rates of one specific period. This contrasts with a real cohort where each age-specific rate pertains to a different year. The theoretical construct of synthetic cohorts allows one to construct period life tables and compute life-cycle indexes (such as the life expectancy at birth) on the basis of observations relating to, and hence reflecting the mortality conditions for, a well-defined and relatively short time period. In practice, the period chosen is most often a single calendar year, or a two-year period bracketing a census count, or a quinquennium.

Life Table Construction

The construction of a period life table is not as straightforward as for a cohort, because many of the life table functions, including survivors at various ages, are not directly observable. One related life table function that can be estimated from actual data is $_nM_x$, the set of age-specific death rates in the population. This is commonly calculated as $_nD_x / _nN_x$, where $_nD_x$ is the number of deaths between age x and $x+n$ observed in a population during a specific period, and $_nN_x$ is the population aged x to $x+n$ at the middle of that period. The basic step in constructing a period life table is to estimate death probabilities, $_nq_x$, for the synthetic cohort, from $_nM_x$, the age-specific death rates observed in a population for a particular period.

Strictly speaking, $_nM_x$ is not exactly equivalent to $_nm_x$, the mortality rate observed in the corresponding synthetic cohort. This is because in a cohort (real or synthetic), $_nm_x$ results from $_nd_x$ and $_nL_x$, both of which are entirely produced by mortality conditions. That is, in a cohort, the number of survivors at various ages (and thus the corresponding person-years lived) is fully a product of underlying mortality conditions. Similarly, the number of deaths in the age-interval is also the product of mortality conditions applied to the number of survivors. Thus $_nm_x$ is an unbiased mortality measure. By contrast, $_nM_x$ is the product of specific mortality conditions applied to the population in the corresponding age-group, $_nN_x$. Unlike $_nL_x$, $_nN_x$ is not entirely produced by the mortality conditions to which the synthetic cohort is subject. It is also affected by the age distribution of the actual population within that age group, which is itself the product of past fluctuations in the number of births, past variations in mortality, and past migration. Thus $_nM_x$ and $_nm_x$ can differ. For most purposes, however, the difference is not large enough to produce significant differences in life table indexes such as life expectancy at birth. In life table construction, it is common to assume that $_nM_x = _nm_x$; there are, however, more involved methods of construction that do not require this simplifying assumption.

The second operation in constructing a period life table involves converting the set of $_nm_x$ to $_nq_x$. This is done by using the following exact equation, derived from the equation for $_nL_x$ specified earlier:

$$_nq_x = \frac{n \, _nm_x}{1 + (n - _na_x) \, _nm_x}.$$

This equation relates an age-specific mortality rate in a cohort (real or synthetic) to the corresponding probability of dying in the age interval x to $x+n$. After this operation, one can readily calculate the number of survivors at various ages in the synthetic cohort and the remaining columns of the life table.

This equation shows, however, that $_nm_x$ is not the only input for the $_nm_x$ to $_nq_x$ conversion. The conversion also involves $_na_x$, the average number of person-years lived between x and $x+n$ by persons dying during the age interval. These values are usually not readily available in a population. When dealing with an unabridged life table, it is not consequential to make the assumption that life table deaths occur on average at the middle of the single-year interval ($_1a_x = 0.5$).

When dealing with five-year age groups, there are a number of methods for estimating $_na_x$ in a population. One method involves graduation techniques that yield reliable results but that are not easy to implement. Another strategy consists of borrowing $_na_x$ from another population with comparable mortality levels and patterns and for which $_na_x$ values have been accurately estimated. The assumption that $_na_x = n/2$ is also used sometimes in abridged life tables. For the first two age groups (for ages 0 and 1–4), however, this assumption is seriously inadequate because mortality risks decrease rapidly within this age range, and thus deaths are more concentrated toward the beginning of the age interval rather than equally distributed. At these ages, it is possible to use estimation equations based on empirical populations at various mortality levels. These equations permit the estimation of $_1a_0$ and $_4a_1$ from the recorded level of $_1m_0$. Similar adjustments may be necessary in very old age groups, in which the reverse phenomenon occurs: deaths are more concentrated toward the upper end of the age interval.

With $_nN_x$, $_nD_x$, and $_na_x$ in hand, all life table columns can be derived. It is also necessary to choose an arbitrary value for l_0, called the *radix* of the life table, to which the columns l_x, $_nd_x$, $_nL_x$, and T_x are proportional. It is common to choose 100,000 as the value for l_0. At the other end of the life table, for an open-ended age interval starting at age x^*, it is usually assumed that $_\infty L_{x^*} = l_{x^*} / _\infty M_{x^*}$.

An abridged period life table for the female population of Austria in 1992 is presented in Table 1. In its first two columns, this table also shows the empirical data—population numbers by age, derived from census statistics and numbers of deaths by age, derived from vital statistics—from which the life table was calculated.

The functions of the life table describe the level and age-pattern of mortality of a population. The $_nq_x$ and $_nm_x$ columns are two related ways of showing how the risk of mortality varies by age, conditional on survival to age x. The $_nd_x$ column, if divided by l_0, can be viewed as the probability for a newborn to die in a particular age group. The l_x column, divided again by l_0, corresponds to the probability of surviving from birth to age x. More generally, l_y / l_x (with $y > x$) corresponds to the probability of surviving from age x to age y, conditional on survival to age x, and $1 - l_y / l_x$ is the probability that a person who survived to age x will die between age x and y. Furthermore, $(l_x - l_y) / l_0$ is the probability that a newborn will die between ages x and y, and $(T_x - T_y) / l_0$ is the number of years that a newborn can expect to live between ages x and y. Figure 1 shows l_x, $_1q_x$, and $_1d_x$ functions for the female population of Sweden. These data, presented for four different years during the twentieth century, illustrate how the age-pattern of life table functions varies as a country experiences mortality decline.

Perhaps the most widely-reported life table measure is $\mathring{e}_0$, the life expectancy at birth. In a period life table, it corresponds to the average number of years that a newborn cohort would live if subjected through the life course to the age-specific mortality rates of the particular period to which the life table pertains. By extension, this number can be said to represent the length of life an average individual can expect at birth under the given mortality conditions. In a life table pertaining to an actual cohort that is now extinct, $\mathring{e}_0$ corresponds to the observed mean age at death for that particular cohort. Life expectancy, as was indicated above, is also calculated for ages other than zero. For age x, $\mathring{e}_x$ can be interpreted as the number of years that an individual can expect to live above age x, conditional on survival to age x.

Life Table Applications

The life table has many applications beyond the measurement of mortality. One of these applications
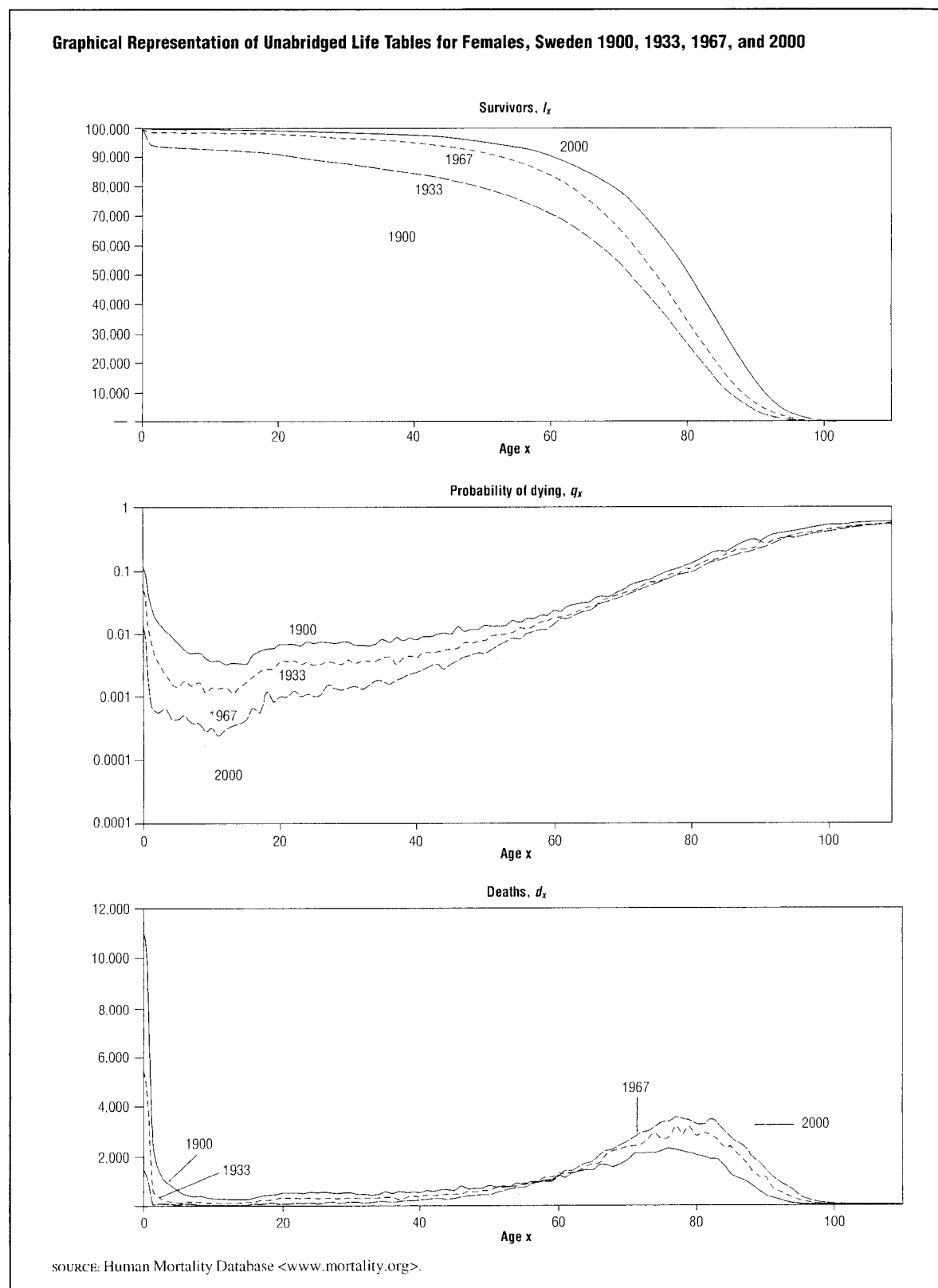
TABLE 1

Abridged Life Table, Austria 1992, Females

Exact age x	Mid-year population in age interval x to $x+n$ $_nN_x$	Deaths between ages x and $x+n$ during the year $_nD_x$	Death rate between ages x and $x+n$ $_nm_x$	Average person-years lived in the interval by those dying in the interval $_na_x$	Probability of dying between ages x and $x+n$ $_nq_x$	Probability of surviving from age x to $x+n$ $_np_x$	Number surviving at age x l_x	Number dying between ages x and $x+n$ $_nd_x$	Person-years lived between ages x and $x+n$ $_nL_x$	Person-years lived above age x T_x	Expectation of life at age x $\overset{\circ}{e}_x$
0	47,925	419	0.008743	0.068	0.008672	0.991328	100,000	867	99,192	7,288,901	72.889
1	189,127	70	0.000370	1.626	0.001479	0.998521	99,133	147	396,183	7,189,709	72.526
5	234,793	36	0.000153	2.500	0.000766	0.999234	98,986	76	494,741	6,793,526	68.631
10	238,790	46	0.000193	3.143	0.000963	0.999037	98,910	95	494,375	6,298,785	63.682
15	254,996	249	0.000976	2.724	0.004872	0.995128	98,815	481	492,980	5,804,410	58.740
20	326,831	420	0.001285	2.520	0.006405	0.993595	98,334	630	490,106	5,311,431	54.014
25	355,086	403	0.001135	2.481	0.005659	0.994341	97,704	553	487,127	4,821,324	49.346
30	324,222	441	0.001360	2.601	0.006779	0.993221	97,151	659	484,175	4,334,198	44.613
35	269,963	508	0.001882	2.701	0.009368	0.990632	96,492	904	480,384	3,850,023	39.900
40	261,971	769	0.002935	2.663	0.014577	0.985423	95,588	1,393	474,686	3,369,639	35.252
45	238,011	1,154	0.004849	2.698	0.023975	0.976025	94,195	2,258	465,777	2,894,953	30.734
50	261,612	1,866	0.007133	2.676	0.035082	0.964918	91,937	3,225	452,188	2,429,176	26.422
55	181,385	2,043	0.011263	2.645	0.054861	0.945139	88,711	4,867	432,096	1,976,988	22.286
60	187,962	3,496	0.018600	2.624	0.089062	0.910938	83,845	7,467	401,480	1,544,893	18.426
65	153,832	4,366	0.028382	2.619	0.132925	0.867075	76,377	10,152	357,713	1,143,412	14.971
70	105,169	4,337	0.041238	2.593	0.187573	0.812427	66,225	12,422	301,224	785,699	11.864
75	73,694	5,279	0.071634	2.518	0.304102	0.695898	53,803	16,362	228,404	484,475	9.005
80	57,512	6,460	0.112324	2.423	0.435548	0.564452	37,441	16,307	145,182	256,070	6.839
85	32,248	6,146	0.190585	5.247	1.000000	0.000000	21,134	21,134	110,889	110,889	5.247

SOURCE: United Nations (1994).

FIGURE 1

Graphical Representation of Unabridged Life Tables for Females, Sweden 1900, 1933, 1967, and 2000

Survivors, l_x

Probability of dying, q_x

Deaths, d_x

SOURCE: Human Mortality Database <www.mortality.org>.

concerns the relationship between the mortality level of a population and its age structure. In particular, a life table can be conceived as a stationary population, which is a population closed to migration, where the annual number of births (B) and mortality conditions (embodied in the life table) are constant over time. If these conditions apply, the population will have an age distribution, $_nN_x$, that is proportional by a factor B/l_0 to the $_nL_x$ column of the life table, and a total population size, $P = B\, \mathring{e}_0$. The annual number of deaths in this population will equal the annual number of births, and the crude death and birth rates will have the value of $1/\mathring{e}_0$. In this population all demographic parameters, including total population size, are constant over time. The growth rate of this population is zero—hence the designation "stationary."

It follows that if a population can be assumed to be stationary, population parameters can be directly translated into life table parameters. For example, in a stationary population, $\mathring{e}_0 = P\,/\,B$, and $_nL_x = {_nN_x} \cdot l_0\,/\,B$. Also, in a stationary population, the observed distribution of deaths, $_nD_x$, is proportional to the distribution of deaths in the life table, $_nd_x$. Thus, the observed mean age at death equals $\mathring{e}_0$, which is not the case in non-stationary populations. These equalities are useful for estimating mortality or other single-decrement processes in any population or sub-population that can be assumed to be stationary.

The life table can also be used to project a population in the future. If a particular life table can be assumed to represent mortality conditions of a specific population between time t and $t+5$, and if there is no migration between t and $t+5$, the population aged x to $x+5$ at time t, $_5N_x(t)$ can be projected to time $t+5$ using the $_5L_x$ column of the life table and the following equation:

$$_5N_{x+5}\,(t+5) = {_5N_x}(t)\,\frac{_5L_{x+5}}{_5L_x}$$

This equation rests on the assumption that the population is stationary between age x and $x+5$, an assumption that is not very problematic for this purpose. The births that occurred between t and $t+5$ can also be projected to time $t+5$ to calculate the population under age 5 at time $t+5$ using the following equation:

$$_5N_0\,(t+5) = B[t,\,t+5]\,\frac{_5L_0}{5\,l_0}$$

Naturally, an important component of population projections involves making assumptions about the future course of mortality and the construction of corresponding life tables. The above equations describe the mechanical use of life tables for projection purposes, once life tables for future time periods have been estimated.

Mortality Models

Comparison of life tables in various populations has led demographers to observe regularities of age-patterns of mortality. In particular, across populations and time periods, age-specific mortality risks tend to follow a U-shape curve, with higher mortality risks at younger and older ages, with the lowest risks in the neighborhood of age 10 (see Figure 1). Another observation is that mortality rates are highly intercorrelated within a population. When mortality rates are higher at particular ages, they also tend to be higher at other ages. Although with a given level of mortality—as indexed, for example, by the value of the expectation of life at birth—somewhat different age-specific mortality rates may be associated in different populations, this variability is within relatively narrow bounds.

These observations have led demographers to search for parsimonious representations of mortality patterns, or mortality "models." The purpose of mortality models is the representation of complex age/level variations in life table columns with a small number of parameters. Mortality models can permit the estimation of mortality indicators in settings where the data ideally required for life table construction (an accurate census count of the population and accurate death registration for years fairly close to the time of the census, or corresponding statistics derived from an accurate population register) are absent. In such situations it may be still possible to estimate a limited number of population parameters, which, along with a model, can be useful for estimating a full life table.

Mathematical mortality models are the oldest parsimonious representations of mortality patterns. The purpose of such models is to present a functional form relating mortality risks to age, with a small number of parameters adjusting for varying levels and patterns across populations. Mathematical mor-

tality models have not been very successful because the shape of the mortality curve is too complex to be easily summarized in a functional form. An important contribution of mathematical representations of mortality, however, is the Gompertz "law" of mortality, according to which the logarithm of the death rate is a linear function of age. The Gompertz equation is frequently used to represent or estimate mortality rates past middle adult ages, although it tends to overestimate mortality rates at older ages.

The most widely-used mortality models are model life tables. In their classical form, model life tables are a set of life tables indexed along two dimensions, *family* and *level*. A family is a group of model life tables with similar age patterns of mortality, often based on the experience of populations that are geographically close. Within a family, tables are indexed by level, from low to high life expectancy at birth. These model life tables are estimated by grouping high-quality empirical life tables with similar age patterns of mortality, and by observing how age-specific mortality rates typically vary as the overall mortality level changes. Regression equations are then used to construct model life tables for various families and mortality levels.

The most commonly used sets of model life tables were developed by A. J. Coale and P. Demeny and by the United Nations. Coale and Demeny model life tables are mostly based on the experience of European populations during the first half of the twentieth century, whereas United Nations tables are based on the experience of developing countries during the second half the twentieth century.

Model life tables are convenient to use, because within a family, a unique life table can be selected on the basis of only one life table indicator. The use of model life tables thus can flexibly accommodate various data configurations of the populations under study. However, the choice of the family of life tables appropriate for application to actual populations is not always straightforward, and the full range of age variations in actual mortality experience may not be fully represented in the currently available model life tables.

Another category of mortality models is the relational model, to which the *logit* model developed by William Brass belongs. Brass (1971) observed that any two life tables can be related to each other in a linear way after performing a "logit" transformation of $q(x)$, the probability of dying before age x. The logit system is thus a system in which a "standard" life table can be adjusted for varying levels and age-patterns of mortality across populations after solving for the two linear parameters relating empirical life table values to the standard. The Brass logit system is often used to smooth an empirical life table or to complete a life table with missing values.

Multiple-Decrements

Although life tables were originally developed to study mortality, the same logic can be used to study many other processes. The only requirement is that the process must be a single-decrement process, which means that there is only one mode of exiting a defined state of interest with no possible return to that state. When studying mortality, the state of interest is being alive, and the only way to leave that state, with no return permitted, is through death. The same logic can be applied, for example, to first marriages, in which case the state of interest is being never married and the event of interest is first marriage. Other single-decrement processes include first migration from place of birth, marital survival, or entry to the labor force.

In reality, single-decrement processes are rare. For a real cohort, mortality is in fact the only true single-decrement process. Other states such as "being never married" can be left not only by marriage, but also by death. Mortality always operates in addition to other processes, and thus multiple-decrement processes are far more common than single-decrement processes. Nonetheless, single-decrement life table logic can be applied to multiple decrements if the different sources of exits can be merged into one combined source of decrement, or if sources of decrements other than the one of interest can be ignored because they are very infrequent during the age-range under study. Also, if information is available only for individuals who did not experience other sources of decrement, the process of interest can be studied as a single-decrement process. For example, data on first marriages reported by individuals aged 85 can be used to reconstruct a life table in the single state where first marriage is the only source of decrement. Such strategy will provide an unbiased single-decrement life table if survivors had the same risks of experiencing a first marriage as those who did not survive (independence of probabilities).

In a multiple-decrement environment, it is sometimes useful to present information on the var-

ious modes of exits. Such analysis is commonly performed in a multiple-decrement life table, which is a life table where several sources of decrement affect the number of people still alive, and where each source of decrement is specified in various columns. For example, in a cause-specific life table, there are as many $_n d_x^i$ columns as there are causes of death i. The sum of $_n d_x^i$ in an age group is equal to $_n d_x$, the number of deaths from all causes in the corresponding single-decrement life table.

There are also methods that permit construction of a single-decrement life table in the absence of, or net of, other sources of decrement. Such life tables are sometimes called "associated single-decrement life tables" or "cause-deleted life tables." This approach involves information on a population subject to various sources of decrement, but it models the process of interest by reconstructing a hypothetical cohort where that process would be the only possible source of attrition. For example, if various causes of death are taken to be different modes of exiting the cohort, an associated single-decrement life table would permit estimation of the survival of a cohort in the absence of a particular cause (or group of causes).

Life table analysis is a powerful tool that has regained interest in the social sciences with recent developments in statistical techniques. If data on cohort survival is available at the individual level and includes covariates, it is possible to use a set of techniques termed "survival analysis" or "event-history analysis." The main purpose of these techniques is to estimate the influence of individual-level characteristics on the age-specific risk of attrition, the so-called "hazard rate." Because of their roots in classical life-table analysis, some of these procedures have been termed "life tables with covariates."

As noted earlier, the underlying assumption of single- and multiple-decrement life tables is that once the event of interest is experienced, individuals can never return to their original state. In reality, there are many processes where individuals can experience reverse flows. For example, if the state of interest is being "currently married," there are return flows as individuals who experience divorce or widowhood remarry and become "currently married" again.

Such processes can be analyzed through increment-decrement life tables, sometimes called multistate life tables. In an increment-decrement life table, there are as many l_x columns as there are states (excluding "being dead"), and these l_x columns can increase or decrease depending on the observed rates of transition from one state to the other. Among other uses, increment-decrement life tables allow estimation of the expected number of years in a particular state. For example, they can permit the estimation of the number of years that a newborn can expect to live in the "currently married" state, which could not be done using classical, single-decrement life tables.

Historical Note

The concept of life tables was first created in 1662 by John Graunt (1620–1674) in his *Natural and political observations made upon the bills of mortality* (1662). Further developments were made by the Huygens brothers and Gottfried Leibniz (1646–1716). The first systematic construction of a life table is credited to the astronomer Edmund Halley (1656–1742) in 1693. During the seventeenth century, life table construction was significantly improved due to the work of Willem Kersseboom (1691–1771), Nicolaas Struyck (1686–1769), and Antoine Deparcieux (1703–1768). However, these scientists lacked the two necessary data sources for the construction of a period life table—deaths and population by age. Therefore, early life tables were accurate only if the population under study was a closed cohort or a stationary population, and thus they had limited applicability. Taking advantage of the exhaustive Swedish data, Pehr Wargentin (1717–1783) constructed the first scientifically correct period life table in 1766.

Before the seventeenth century, death was believed to be either a magical or sacred phenomenon that could not and should not be quantified. The invention of life tables was thus an important scientific breakthrough, not only because of the technical aspects of life table construction, but also because of the concept of mortality as a measurable phenomenon following observable regularities.

See also: *Actuarial Analysis; Brass, William; Demography, History of; Event-History Analysis; Farr, William; Gompertz, Benjamin; Graunt, John; Mortality, Age Patterns of; Multistate Demography; Renewal Theory and Stable Population Model; Stochastic Population Theory.*

BIBLIOGRAPHY

Brass, William. 1971. "On the Scale of Mortality." In *Biological Aspects of Demography*, ed. W. Brass. London: Taylor and Francis Ltd.

Coale, Ansley J., and Paul Demeny. 1983. *Regional Model Life Tables and Stable Populations*. New York: Academic Press. (First edition 1965, Princeton: Princeton University Press.)

Dupâquier, Jacques. 1996. *L'invention de la table de mortalité: de Graunt à Wargentin: 1662–1766*. Paris: P.U.F.

Keyfitz, Nathan. 1985. *Applied Mathematical Demography*, 2nd edition. New York: Wiley.

Keyfitz, Nathan, and Wilhelm Flieger. 1990. *World Population Growth and Aging: Demographic Trends in the Late Twentieth Century*. Chicago and London: University of Chicago Press.

Pressat, Roland. 1972. *Demographic Analysis: Methods, Results, Applications*. Chicago: Aldine-Atherton.

Preston, Samuel H., Patrick Heuveline, and Michel Guillot. 2001. *Demography: Measuring and Modeling Population Processes*. London: Blackwell Publishers.

Schoen, Robert. 1988. *Modeling Multigroup Populations*. New York: Plenum Press.

United Nations. 1982. *Model Life Tables for Developing Countries*. New York: United Nations Population Studies, no. 77.

MICHEL GUILLOT

LIMITS TO GROWTH

For demographers, limits to growth is an old subject, at least as it relates to population growth, harking back to political economist T. R. Malthus (1766–1834) or even earlier writers. Since the 1972 publication of the Club of Rome study *Limits to Growth* the term has come to refer to both population and economic growth—that is, growth in population and growth in per capita resource use, the product of which gives the growth rate of total resource use. This total resource use is a flow from nature's sources (mines, wells, forests, fisheries, grasslands), through the transformations of production and consumption within the economy, and back as wastes to nature's sinks (atmosphere, oceans, a neighbor's back yard). Just as an animal lives from its metabolic flow, beginning with food from the environment, and ending with the return of wastes to its environment, so the economy lives from its metabolic flow, or "throughput." The throughput, like the metabolic flow, is entropic and irreversible. That is not to say that most waste materials are not recycled by biogeochemical processes powered by the sun. It is only to point out that such recycling is external to the animal or economy—whose life therefore depends on these natural services provided by its environment.

Two Kinds of Dissipative Structures

In physical terms human bodies are dissipative structures, which is to say that their natural tendency is to decay, die, and fall apart. The same is true for artifacts that we accumulate as wealth. A car, a house, or a shirt is a dissipative structure that requires a throughput to be maintained and replaced. A population of inanimate objects (e.g., shirts) inevitably wears out and depreciates over time, requiring new production to make up for the loss, as well as maintenance expenditures (replacing buttons) to slow down the rate of depreciation to a minimum. For demographers it is easy to think in terms of two populations of dissipative structures, one consisting of human bodies, the other of artifacts—basically extensions of human bodies. Each population, if it is to remain in a steady state, has both short-term maintenance requirements and long term reproduction requirements, each supplied by the entropic throughput from and back to nature. If these two steady-state populations are so large that the throughput necessary to maintain them requires inputs from nature's sources and outputs to nature's sinks at rates beyond nature's replenishing and absorptive capacities, then the throughput flow becomes ecologically unsustainable, and so do the two populations.

Definition of Limits to Growth

The limits to growth, in twenty-first century usage, refers to the limits of the ecosystem to absorb wastes and replenish raw materials in order to sustain the economy (the two populations of dissipative structures). The economy is a subsystem of the larger ecosystem, and the latter is finite, non-growing, and,