

3 The Life Table and Single Decrement Processes

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The life table is one of the most important devices used in demography. In its classical form, it is a table that displays various pieces of information about the dying out of a birth cohort. One column of a classical life table is invariably “age.” The remaining columns tabulate age-related functions pertaining to mortality, such as the number of survivors to various ages, deaths in particular age intervals, age-specific death rates, probabilities of death in various age intervals, and so on. The life *table* is only one way of summarizing a cohort’s mortality experience; other ways, for example, are in graphical form or in the form of a mathematical function.

As an accounting device, the life table poses few conceptual difficulties. However, the profusion of columns and functions creates a cumbersome notational baggage. Probably the easiest way to elucidate the life table is to return to the concept of life-lines. These are normally displayed on a Lexis diagram. But if we imagine that a cohort is all born at the same instant of time, then the two dimensions of a Lexis diagram (age and time) can be collapsed into one. Figure 3.1 displays the life-lines of 10 individuals born on January 1, 1800. From these life-table corresponding to the 10 life-lines shown on figure 3.1.

The verbal description of life table columns is included on table 3.1, so there is no need to reiterate them in the text. The most frequently-used column of a life table is probably “expectation of life at age x ” or “life expectancy at age x ,” usually denoted e_x^o . It refers to

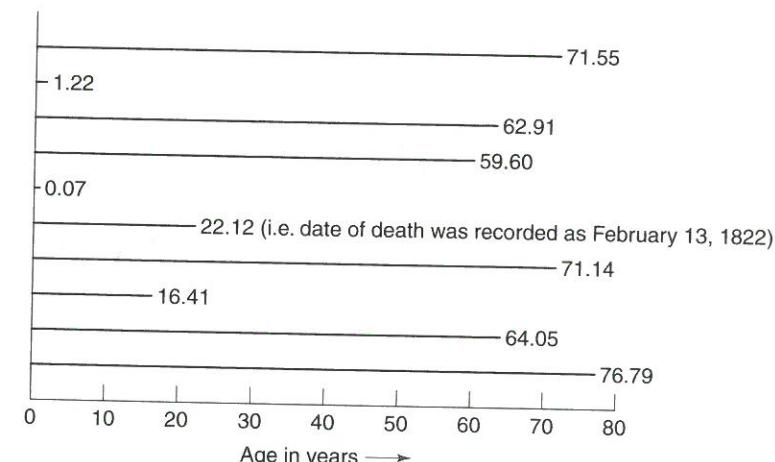


Figure 3.1 Age at death and life-lines of a hypothetical cohort of births (10 in all); date of birth: January 1, 1800

the average number of *additional* years that a survivor to age x will live beyond that age. It is calculated simply by dividing the total number of person-years lived by the cohort above exact age x by the number of survivors to that age.¹ Life expectancy at birth (e_0^o), the sum of all person-years lived by the cohort divided by the original number in the cohort, is also equal to the average age at death for the cohort, since life ends at the exact age when death occurs. The average age at death for someone who survives to age 50 is equal to $50 + e_{50}^o$, or 67.673 in table 3.1. Note that life expectancy at age 1 in this table exceeds that at age 0, a phenomenon that is not uncommon. Very high levels of infant mortality often mean that those who survive this hazardous year can actually look forward to more years of *additional* life than could newborns themselves.

The other column that needs an introduction is the n_{ax} column. This refers to the average number of person-years lived in the interval x to $x+n$ by those dying in the interval. It is found by dividing the total number of person-years lived in the interval x to $x+n$ by those dying in that interval by the total number dying in the interval. For example, in age interval 60–70, two people died, at ages 62.91 and 64.05. Thus, they lived $(2.91 + 4.05) = 6.96$ years in the interval. So $10n_{60} = 6.96/2 = 3.48$. The utility of this column is not obvious at this point but will become so in the next section.

It should be clear that some functions (l_x , T_x , e_x^o) refer to a single (exact) age, while other functions (n_{dx} , n_{px} , n_{qx} , n_{mx} , n_{ax}) refer to age intervals that begin with exact age x and extend for exactly n years. The length of these intervals need not be, and usually is not, constant within the same life table. Perhaps the most conventional format for a life table has a length of 1 year for the first age interval (i.e., the functions in the first row pertain either to exact age 0 or to the age interval 0 to 1); a length of 4 years for the second age interval (i.e., the functions in the second row pertain either to exact age one or to the age interval 1 to 5); and a length of 5 years thereafter (i.e., functions in the third row pertain either to exact age 5 or to age interval 5 to 10). Another convention is to use lower-case letters to refer to the number of deaths (n_{dx}) and deaths rates (n_{mx}) in a cohort whose experience is summarized in a life table, rather than using the nD_x and nM_x notation that pertains to equivalent functions in a population.

Table 3.1: Life table for hypothetical cohort of 10 births shown in figure 3.1

Exact age x	Number left alive at age x l_x	Number dying between ages x and $x+n$ $n d_x$	Probability of dying between ages x and $x+n$ $n q_x$	Probability of surviving from age x to age $x+n$ $n p_x$	Person-years lived between ages x and $x+n$ $n L_x$	Person-years lived above age x $T_x = \sum_{a=x}^{\infty} n L_a$	Expectation of life at age x $e_x^o = T_x / l_x$	Death rate in the cohort between ages x and $x+n$ $n m_x$	Average person-years lived in the interval by those dying in the interval $n q_x$
0	10	1	1/10	9/10	9 + .07 = 9.07	436.79 + 9.07 = 445.86	445.86 = 44.586	1 9.07	.07
1	9	1	1/9	8/9	8 · .4 + .22 = 32.22	404.57 + 32.22 = 436.79	436.79 = 48.532	1 32.22	.22
5	8	0	0	1	8 · 5 = 40	364.57 + 40 = 404.57	404.57 = 50.571	0	—
10	8	1	1/8	7/8	7 · 10 + 6.41 = 76.41	288.16 + 76.41 = 364.57	364.57 = 45.571	1 76.41	6.41
20	7	1	1/7	6/7	6 · 10 + 2.12 = 62.12	226.04 + 62.12 = 288.16	288.16 = 41.166	1 62.12	2.12

30	6	0	0	1	6 · 10 = 60	166.04 + 60 = 226.04	226.04 = 37.673	0	—
40	6	0	0	1	6 · 10 = 60	106.04 + 60 = 166.04	166.04 = 27.673	0	—
50	6	1	1/6	5/6	5 · 10 + 9.60 = 59.60	46.44 + 59.60 = 106.04	106.04 = 17.673	1 59.60	9.60
60	5	2	2/5	3/5	3 · 10 + 6.96 = 36.96	9.48 + 36.96 = 46.44	46.44 = 9.288	2 36.96	(2.91 + 4.05)/2 = 6.96/2 = 3.48
70	3	3	3/3	0	9.48	9.48	9.48 = 3.16	3 9.48	(1.55 + 1.14 + 6.79)/3 = 9.48/3 = 3.16
80	0	0	—	—	—	—	—	—	—

Because the columns of the life table are so closely related to one another, there are many arithmetic relations among the columns. For example:

$${}_n d_x = l_x - l_{x+n},$$

i.e., the number of deaths between age x and age $x + n$ is equal to the difference between the number of survivors to age x and the number of survivors to age $x + n$;

$${}_n d_x = l_x \cdot {}_n q_x,$$

i.e., the number of deaths between age x and age $x + n$ is equal to the number of survivors to age x times the probability of dying between age x and age $x + n$; and

$${}_n p_x = \frac{l_{x+n}}{l_x} = \frac{l_x - {}_n d_x}{l_x} = 1 - {}_n q_x,$$

i.e., the probability of surviving between age x and age $x + n$ is equal to one minus the probability of dying between those ages.

3.1 Period Life Tables

As illustrated in table 3.1, the construction of a life table for a cohort poses little difficulty. But because cohort data might be outdated, unavailable, or incomplete, actuaries and demographers have developed what is termed a "period" life table (sometimes also referred to as a "current" life table). This table presents exactly the same type of information as that contained in a cohort life table. But the information attempts to show what would happen to a cohort if it were subjected for all of its life to the mortality conditions of that period. Such a cohort is usually termed a "synthetic" or "hypothetical" cohort, as opposed to a "real" cohort consisting of actual births. Whereas the cohort life table (i.e., that pertaining to a real birth cohort) simply records information about what actually happened to that cohort, a period life table is a model of what would happen to a hypothetical cohort if a certain set of mortality conditions pertained throughout its life.

How should the period's "mortality conditions" be operationalized to produce a period life table? Almost always, the answer is "by the set of age-specific death rates for that period." These rates must then be transformed into other columns of the table. The key to this transformation is a conversion from the set of observed period age-specific death rates, ${}_n M_x$, to a set of age-specific probabilities of dying, ${}_n q_x$. This conversion is usually accomplished by referring to the relation between age-specific death rates and age-specific probabilities of dying in an actual cohort:

$${}_n m_x = \frac{{}_n d_x}{n L_x}$$

$$= \frac{\text{Number of deaths in the cohort between ages } x \text{ and } x + n}{\text{Number of person-years lived in the cohort between ages } x \text{ and } x + n}$$

$${}_n q_x = \frac{{}_n d_x}{l_x}$$

$$= \frac{\text{Number of deaths in the cohort between ages } x \text{ and } x + n}{\text{Number of survivors to age } x \text{ in the cohort}}$$

The formula for the conversion can be derived by replacing the l_x term in the formula for ${}_n q_x$ by an equivalent expression. Note that:

$$\begin{aligned} n L_x &= n \cdot l_{x+n} + n A_x, \\ \text{Number of person-} &\text{years lived by the} \\ \text{interval by members} &\text{of the cohort who} \\ \text{survive the interval} &\text{Number of person-years lived in the interval by members of the cohort who die in the interval} \end{aligned}$$

or

$$\begin{aligned} n L_x &= n \cdot l_{x+n} + n a_x \cdot {}_n d_x, \\ \text{Mean number} &\text{Number of} \\ \text{of person-years} &\text{members of the} \\ \text{lived in the} &\text{cohort dying in} \\ \text{interval by those} &\text{the interval} \\ \text{dying in the} & \end{aligned}$$

Rewriting this equation, we have:

$$\begin{aligned} n L_x &= n(l_x - {}_n d_x) + n a_x \cdot {}_n d_x \\ n \cdot l_x &= n L_x + n \cdot {}_n d_x - n a_x \cdot {}_n d_x \\ l_x &= \frac{1}{n} [n L_x + (n - n a_x) \cdot {}_n d_x] \end{aligned}$$

Now substituting this expression for l_x into the formula for ${}_n q_x$, we have:

$${}_n q_x = \frac{{}_n d_x}{l_x} = \frac{n \cdot {}_n d_x}{n L_x + (n - n a_x) \cdot {}_n d_x}$$

Finally, we divide both numerator and denominator of this last expression by $n L_x$, giving:

$${}_n q_x = \frac{n \cdot \frac{{}_n d_x}{n L_x}}{\frac{n L_x}{n L_x} + (n - n a_x) \frac{{}_n d_x}{n L_x}} = \frac{n \cdot {}_n m_x}{1 + (n - n a_x) {}_n m_x} \quad (3.1)$$

Equation (3.1), due to Greville (1943) and Chiang (1968), says that, for a cohort, the conversion from ${}_n m_x$ to ${}_n q_x$ depends on only one parameter: $n a_x$, the average number of person-years lived in the interval by those dying in the interval. No other information is required to perform this conversion, and any other information is redundant.

If persons dying in the interval do so, on average, half-way through the interval, then equation (3.1) becomes:

$${}_n q_x = \frac{n \cdot {}_n m_x}{1 + \frac{n}{2} {}_n m_x} = \frac{2n \cdot {}_n m_x}{2 + n \cdot {}_n m_x} \quad (3.2)$$

The $n a_x$ function is of little interest in a cohort life table because ${}_n q_x$ and ${}_n m_x$ can both, in principle, be directly observed. It gains its importance from its utility in making the ${}_n m_x \rightarrow {}_n q_x$

conversion for use in a period life table. In particular, if it is assumed that the hypothetical cohort in a period life table is to experience an observed set of period age-specific death rates, nM_x , then all that remains to complete the period life table is the adoption of a set of na_x values in order to make the $nM_x \rightarrow nq_x$ conversion. If we choose this common route, then we have assumed that the observed period age-specific death rates (nM_x) are to be reproduced in the hypothetical cohort passing through life in the period life table (nm_x). All that remains is to convert the nm_x 's to nq_x 's. Whether the strategy is implicit or explicit, techniques for period life table construction that start out with a set of nm_x s are focused upon the choice of a set of na_x values. We now mention several diverse strategies that are sometimes employed.

3.2 Strategies for Choosing a Set of na_x Values and/or for Making the $nm_x \rightarrow nq_x$ Conversion

3.2.1 Direct observation

If data on exact ages at death are available for a population (e.g. 60.19, 23.62, ...), then it is clearly possible to take all of the deaths during a period that fall within a particular n -year wide age interval and compute na_x directly. Note that this value would pertain to a population, rather than to a cohort. Such information is rarely available, and even if it were it is not always advisable to use it. The reason is that the na_x values observed in a population are influenced by that population's age distribution within the n -year wide age interval. Suppose, to take an extreme example, that a certain population had 100 times as many people aged 60 as those in the combined age-group 61–4. Then $5a_{60}$ would almost certainly lie between ages 60.00 and 61.00, regardless of mortality conditions. But it would not, in general, be sensible to suppose that those dying in a cohort passing from ages 60 to 65 would all die before age 61. For reasons discussed below, using observed na_x 's will usually reinforce biases already present in data subject to age-distributional anomalies.

3.2.2 Graduation of the nm_x function

The level and slope of the nm_x function itself provide strong clues about the ages of persons dying within an age interval. Given two populations with the same $5m_{60}$ values, the population in which mortality rises more rapidly with age during the interval will have a higher concentration of deaths at the upper part of that interval and, hence, a higher value of $5a_{60}$. While we cannot normally observe the slope of death rates *within* the 5-year age interval 60 to 65, we can observe the general slope of death rates based on, for example, $5m_{55}$, $5m_{60}$, and $5m_{65}$. In addition to being affected by the slope of the death rate function, the value of na_x is also affected by the level of mortality. Given a certain slope, the higher is mortality within a particular age interval, the more will deaths be concentrated at the beginning of that interval because fewer people will survive to be at risk of death near the end of the interval. This is the logic on which several systems of life table construction are based. Greville (1943) assumed that age-specific death rates were log-linearly related to age (a hypothesis first set forth in Gompertz' law of mortality, as we will see in section 9.1), and then showed how the $nm_x \rightarrow nq_x$ conversion could be made once the slope of that log-linear relation was ascertained.

Another approach consists of estimating na_x from information on the age distribution of deaths in the life table, assuming that this distribution, $d(a)$, follows a polynomial function of the second degree in the interval $x - n$ to $x + 2n$ (Keyfitz, 1966):

$$d(a) = A + Ba + Ca^2, \quad \text{for } x - n \leq a \leq x + 2n$$

Under this assumption, one can show that

$$na_x = \frac{-\frac{n}{24}nd_{x-n} + \frac{n}{2}nd_x + \frac{n}{24}nd_{x+n}}{nd_x}$$

Note that this equation produces an estimate of $na_x = n/2$ when deaths are symmetrically distributed in the three relevant age groups. This equation for na_x requires having estimates of nd_x , which is usually estimated from the $nM_x \rightarrow nq_x$ conversion itself and thus requires information on na_x . To solve this circularity problem, one must use iteration. It makes most sense to begin by taking $na_x = n/2$ in the $nM_x \rightarrow nq_x$ conversion to obtain a first set of nd_x estimates, and then using these nd_x to obtain a new set of na_x estimates with the above equation. This new set of na_x values can then be reused in the $nM_x \rightarrow nq_x$ conversion until stable estimates of na_x and nd_x are obtained. Two or three iterations are typically sufficient to produce stable estimates. Limitations of the method are that it does not permit the estimation of na_x in the first and last age groups and it requires that all age groups used in the estimation have the same width, n .

Keyfitz and Frauenthal (1975) have developed another approach to estimating nq_x which assumes that the age distribution and age-specific death rates are both linear between ages $(x - n)$ and $(x + 2n)$, conditions that may be mutually inconsistent. These assumptions produce the following estimation equation:

$$\frac{l_{x+n}}{l_x} = \exp \left[-n nM_x - \frac{n}{48 nN_x} (nN_{x-n} - nN_{x+n})(nM_{x+n} - nM_{x-n}) \right]$$

where nN_x = population aged x to $x + n$.

Keyfitz and Frauenthal's equation appears to produce satisfactory results in situations where the age distribution is rather smooth, but it does not necessarily give better estimates than other methods when the age distribution is erratic (Pressat, 1995).

3.2.3 Borrowing na_x values from another population

If there are reasons to believe that the level and shape of the nm_x curve is similar to that of another population for which na_x values have been accurately estimated, then a simple and reasonable expedient is to adopt that set of values. The borrowed values should correspond to the sex for which they are being used because na_x values vary significantly between the sexes. Keyfitz and Flieger (1968 and 1990) provide sets of na_x values for populations based on graduation techniques above age 10. Examples of several sets of these functions are shown in table 3.2. Note that at older ages the values of $5a_x$ tend to exceed 2.5 years, reflecting the rapid rise in mortality with age so that deaths are concentrated towards the upper end of the age range. At the very highest ages, the values of $5a_x$ start to decline as the increasingly high mortality levels leave fewer survivors available to die at the upper end of an age range.

A traditional method of life table construction due to Reed and Merrell (1939) amounts to borrowing na_x values from another population, although it is not usually recognized in this guise. Reed and Merrell used life tables for the US in which na_x had been estimated for actual cohorts, based upon very detailed US vital statistics. They compared the nm_x values to the nq_x values in the resulting life tables and fit a statistical relation between the two series. They then recommend inserting the values of nm_x into the resulting equation in order to derive nq_x . This operation is equivalent to reproducing (with an error term) the na_x values in the US life tables

Table 3.2: Average person-years lived between ages x and $x + n$ for persons dying in the interval ($n\alpha_x$)

e_0^o	Sweden, 1900		Sweden, 1985		United States, 1985		Guatemala, 1985	
	Males	Females	Males	Females	Males	Females	Males	Females
	51.528	54.257	73.789	79.830	71.266	78.422	60.582	64.415
Age x Average person-years lived for people dying in the interval x to $x + n$								
0	0.358	0.375	0.083	0.081	0.090	0.086	0.165	0.150
1	1.235	1.270	1.500	1.500	1.500	1.500	1.500	1.500
5	2.500	2.500	2.500	2.500	2.500	2.500	2.500	2.500
10	2.456	2.469	3.006	2.773	3.014	2.757	2.469	2.390
15	2.639	2.565	2.749	2.617	2.734	2.644	2.711	2.665
20	2.549	2.536	2.569	2.578	2.564	2.552	2.628	2.601
25	2.481	2.514	2.561	2.665	2.527	2.588	2.573	2.563
30	2.505	2.509	2.600	2.649	2.571	2.632	2.593	2.627
35	2.544	2.521	2.638	2.625	2.622	2.678	2.545	2.566
40	2.563	2.522	2.695	2.662	2.666	2.706	2.541	2.543
45	2.572	2.561	2.705	2.722	2.688	2.702	2.604	2.592
50	2.574	2.578	2.706	2.694	2.684	2.683	2.596	2.627
55	2.602	2.609	2.687	2.670	2.657	2.671	2.623	2.661
60	2.602	2.633	2.673	2.689	2.626	2.650	2.635	2.623
65	2.591	2.628	2.643	2.697	2.608	2.642	2.616	2.676
70	2.561	2.585	2.607	2.706	2.571	2.631	2.557	2.607
75	2.500	2.517	2.547	2.650	2.519	2.614	2.486	2.532
80	2.415	2.465	2.471	2.607	2.460	2.596	2.409	2.447
85+	3.488	3.888	4.607	5.897	5.455	6.969	4.611	4.836

Source: Keyfitz and Flieger, 1968: 491; and 1990: 310, 348 and 528.

on which their statistical relation was based. Since there is no special reason to believe in the widespread applicability of this US table, it seems better, in general, to borrow from a more suitable lender.

3.2.4 Using rules of thumb

There are two rules of thumb that are commonly implemented in choosing $n\alpha_x$. Except for infancy and possibly age 1, each of these works extremely well – leads to trivial error – when data are arrayed in one-year wide age intervals. One rule of thumb is that $n\alpha_x = n/2$: deaths are assumed to occur, on average, halfway through the interval. This assumption leads immediately to equation (3.2).

The other assumption is that the age-specific death rate is constant in the age interval x to $x + n$. In this case, as will be shown below,

$$npx = 1 - nq_x = e^{-n \cdot nm_x}$$

Here no conversion involving $n\alpha_x$ is required. Of course, a value of $n\alpha_x$ is implicit in this conversion formula; in particular, for this assumption,

$$n\alpha_x = n + \frac{1}{nm_x} - \frac{n}{1 - e^{-n \cdot nm_x}}$$

It can be shown that $n\alpha_x$ in this case is necessarily less than $n/2$. The reason is that, with a constant death rate in the interval, the number of deaths at any point in that interval will be proportional to the number of survivors, a number which declines throughout the interval. So there must be more deaths in the first half of the interval than in the second half.

The shape of the human mortality curve is sharply upward-sloping beyond age 30 or so. Therefore, the second rule of thumb tends not to be very attractive for this set of ages. It is often used, however, in nonmortality applications and has convenient aggregation properties.

Which of these four strategies should be used? The answer depends on data quality and on the demographic conditions generating the observations. Graduation is the most time-consuming alternative but perhaps the one in which most confidence can be invested. Adoption of a set of $n\alpha_x$ values from another, similar, population is probably a close second in terms of accuracy, and is exceedingly easy to apply. Direct computation is usually difficult and, in a population subject to age distributional disturbances, not advisable.

The strategy chosen should depend in part upon the sensitivity of results to error in choosing $n\alpha_x$. Here the results are reassuring. Examining the formula for the $nm_x \rightarrow nq_x$ conversion,

$$nq_x = \frac{n \cdot nm_x}{1 + (n - n\alpha_x)nm_x}$$

we see that $n\alpha_x$ is being multiplied by nm_x before it enters into the formula. With a death rate of 0.012, which is about that prevailing in the world at present, an error of as much as 0.2 years in $n\alpha_x$, which is relatively large error, would affect nq_x in the proportion of only $0.2(0.012) = .0024$, or about a quarter of 1 percent. Of course, if that error is repeated over and over again from age group to age group, it will cumulate in its effects. But even if every age has an $n\alpha_x$ that is in error by 0.2 in the same direction, life expectancy at birth will be in error by only about 0.2 years. We can agree with the World Health Organization (1977: 70) in its conclusion that “Although these various methods [of life table construction] are based upon very different assumptions, when applied to actual mortality rates they do not result in significant differences of importance to mortality analysis.”

3.3 The Very Young Ages

Life expectancy estimates are most sensitive to procedures used in the very young, high mortality ages. When estimation of nq_x for these ages can be made by assigning deaths to the appropriate birth cohorts, as described in chapter 2, it is usually best to do so. But when converting a death rate into a probability of dying, it is important to recognize that the value of $n\alpha_x$ is (empirically) a function of the level of mortality itself. Generally speaking, the lower the level of mortality, the more heavily will infant deaths be concentrated at the earliest stages of infancy; the influence of the prenatal and perinatal environment becomes increasingly dominant relative to the postnatal environment. Coale and Demeny (1983: 20) have reviewed this relation in many populations and have fit a line to the international and intertemporal data. In particular, they have fit the relation between values of $1\alpha_0$ and $4\alpha_1$ and the values of $1q_0$. We have adapted these relations to the typical circumstances encountered in life table construction. Results are shown in table 3.3. In the absence of other information, the formulas presented in this table can be recommended for use in deriving $n\alpha_x$ values below age 5.

Table 3.3: Values of $n a_x$ for use below age 5

	Males	Females
Value of ${}_1 a_0$		
If ${}_1 m_0 \geq .107$.330	.350
If ${}_1 m_0 < .107$	$.045 + 2.684 \cdot {}_1 m_0$	$.053 + 2.800 \cdot {}_1 m_0$
Value of ${}_4 a_1$		
If ${}_1 m_0 \geq .107$	1.352	1.361
If ${}_1 m_0 < .107$	$1.651 - 2.816 \cdot {}_1 m_0$	$1.522 - 1.518 \cdot {}_1 m_0$

Source: Adapted from Coale and Demeny (1983) West model life tables.

3.4 The Open-ended Age Interval

The formulas presented so far are incapable of dealing with the open-ended (or terminal) age interval. In this interval n is, in effect, infinity. A conventional way of dealing with this interval is to return to the formula for the death rate in a cohort. Since

$$n m_x = \frac{n d_x}{n L_x},$$

when $n = \infty$ we must have

$$\infty m_x = \frac{\infty d_x}{\infty L_x} \quad \text{or} \quad \infty L_x = \frac{\infty d_x}{\infty m_x}.$$

But the number of persons dying in the cohort above age x , whether the cohort is real or hypothetical, must equal the number of persons surviving to age x ($\infty d_x = l_x$), so:

$$\infty L_x = \frac{l_x}{\infty m_x}.$$

∞m_x is observed and l_x can be calculated on the basis of mortality at all ages below x . So the number of person years lived above x can be calculated and used to complete the life table. Of course, $\infty q_x = 1.00$ and $\infty p_x = 0.00$.

Procedures for dealing with the open-ended interval have become increasingly important as more people have survived to its beginning. The most commonly encountered open-ended interval begins with age 85, to which age nearly half of females in recent period life tables for developed countries will survive. Where data permit, the analyst should clearly adopt a high enough age for starting the open-ended interval that only a small fraction of the population survives to that age. In section 7.8, we will describe a more elaborate procedure for estimating person-years in the open-ended age interval.

3.5 Review of Steps for Period Life Table Construction

a. Calculate the set of age-specific death rates to be used ($n m_x$). The usual procedure is to assume, for each age-interval, that $n m_x = n M_x$. This equality means that we choose to reproduce, in the life table $n m_x$ values, the set of $n M_x$ values observed in a population during a particular period.

Box 3.1 Period Life Table Construction

A. Observed data:

$n N_x$ = mid-year population in age interval x to $x + n$

$n D_x$ = deaths between ages x and $x + n$ during the year

B. Steps for period life table construction:

1. $n m_x \approx n M_x = \frac{n D_x}{n N_x}$
2. $n a_x$:
3. $n q_x = \frac{n \cdot n m_x}{1 + (n - n a_x) \cdot n m_x}$
4. $n p_x = 1 - n q_x$
5. $l_0 = 100,000$
6. $l_{x+n} = l_x \cdot n p_x$
7. $n L_x = n \cdot l_{x+n} + n a_x \cdot n d_x$
(open-ended interval: $\infty L_x = \frac{l_x}{\infty m_x}$)
8. $T_x = \sum_{a=x}^{\infty} n L_a$
9. $e_x^o = \frac{T_x}{l_x}$

Example: Austria, males, 1992

Age x	$n N_x$	$n D_x$	$n m_x$	$n a_x$	$n q_x$	$n p_x$	l_x	$n d_x$	$n L_x$	T_x	e_x^o
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

Data source: United Nations, 1994.

b. Adopt a set of $n a_x$ values. For example,

- under 5, use Coale–Demeny equations shown in table 3.3;
- above 5, use values borrowed from another population (e.g. in Keyfitz and Flieger, 1990).

For actuarial application where a great deal of precision is required, graduation procedures will usually be preferred for estimating $n a_x$.

c. Compute $n q_x$ as:

$$n q_x = \frac{n \cdot n m_x}{1 + (n - n a_x) n m_x}$$

For the open-ended category, $\infty q_x = 1.00$

d. Compute $n p_x = 1 - n q_x$.

e. Choose a value of l_0 , the “radix” of the life table. This is the Latin term for root; its value will determine most of the remaining values of the life table. The choice of the radix is arbitrary. Values that have been used range from 1 to 1 million; 100,000 is perhaps the most conventional. l_x , $n d_x$, $n L_x$, and T_x columns will vary in exact proportion to the radix chosen. Thus the scale of a period life table is completely arbitrary and is totally unrelated to the size of the population whose mortality is being described in the table. Failing to grasp this point is a common source of confusion.

f. Calculate $l_{x+n} = l_x \cdot n p_x$, working sequentially from the youngest age to the oldest, e.g.,

$$l_1 = l_0 \cdot 1 p_0$$

$$l_5 = l_1 \cdot 4 p_1$$

$$l_{10} = l_5 \cdot 5 p_5$$

⋮

g. Derive $n d_x$ as $l_x - l_{x+n}$ (or as $l_x \cdot n q_x$).

h. Derive the person-years lived between ages x and $x + n$ as:

$$n L_x = n \cdot l_{x+n} + n a_x \cdot n d_x$$

This formula was used in deriving the $n m_x \rightarrow n q_x$ conversion. Once we have selected the $n a_x$ values for that conversion, we have used up our degrees of freedom in making the conversion from l_x to $n L_x$. This point is often overlooked. For the open ended interval that begins with age x^* , set

$$\infty L_{x^*} = \frac{l_{x^*}}{n m_{x^*}}$$

i. Derive

$$T_x = \sum_{a=x}^{\infty} n L_a$$

This is simply an instruction to add up the $n L_x$ column from age x to the final row of the life table, in order to derive person-years lived above age x . This operation starts at the bottom of the life table (i.e., the highest age) and proceeds to the top.

j. Derive life expectancy at age x as $e_x^o = T_x / l_x$. This formula for e_x^o divides the number of person-years that will be lived above age x by the number of persons who will live them.²

Box 3.1 shows an example of period life table construction using data from Austria.

A life table in which all age intervals are one year wide is often referred to as a “complete” life table, whereas tables containing larger age intervals, usually 5 years wide, are sometimes referred to as “abridged” life tables. Figures 3.2 and 3.3 show graphically some important columns of life tables. Figure 3.2 presents the $n m_x$ column for males and females in the US in 1992, and figure 3.3 shows the $n m_x$, l_x , and $n d_x$ columns from Swedish female life tables in 1895 and 1995. The age intervals in these life tables are one year wide ($n = 1$).

Table 3.4 presents estimates of life expectancy at birth in the major regions of the world for a recent period. These life expectancies are obtained by aggregating life expectancies at birth across individual countries. One way to aggregate life expectancies is by merging deaths

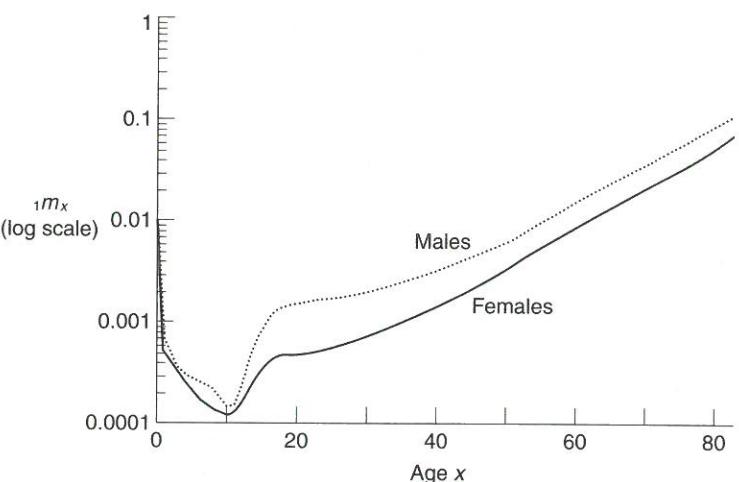


Figure 3.2 Age-specific death rates ($1m_x$) by age, US, 1992, males and females
Data source: National Center for Health Statistics, 1996.

and population at risk in the larger unit, and recalculating a life table in the conventional way described above using the aggregated age-specific mortality rates. It should be noted than when using the merging procedure, the resulting aggregate life expectancy could under rare circumstances be outside the range of life expectancies in the original populations being merged. A second way is to calculate a weighted average of country-level life expectancies. Because of the conventional interpretation given to life expectancy at birth, one appropriate set of weights to use might be the number of births in the respective regions. Relative population size is perhaps an equally attractive alternative.

The two procedures give similar results when the populations being merged are relatively homogeneous, but the difference can be substantial when aggregating populations that have diverse patterns and levels of mortality. Lutz and Scherbov (1992) recommend using the merging procedure rather than the averaging procedure because it may be more appropriate when dealing with populations open to migration and with changing mortality. The United Nations shifted from the averaging to the merging procedure in 1990, a shift that produced an increase of 2.5 years in their estimate of the global life expectancy at birth for the period 1980–5 (United Nations, 1989, 1991).

3.6 Interpreting the Life Table

A period life table summarizes the mortality experience of a population. Each parameter presented corresponds to a specific age or age interval, e.g. the probability of surviving or of dying between age x and $x + n$ ($n p_x$ and $n q_x$ respectively), the age-specific death rate between age x and $x + n$ ($n M_x$), or the life expectancy at age x (e_x^o). The verbal interpretation of each column was provided in table 3.1. Additional information can be gained by combining two or more ages. For example, the ratio l_y / l_x indicates the probability of surviving from age x to age y in the population, i.e., in a hypothetical cohort constructed from data on the population. Box 3.2 illustrates some of the most important interpretations that can be drawn from life table columns.

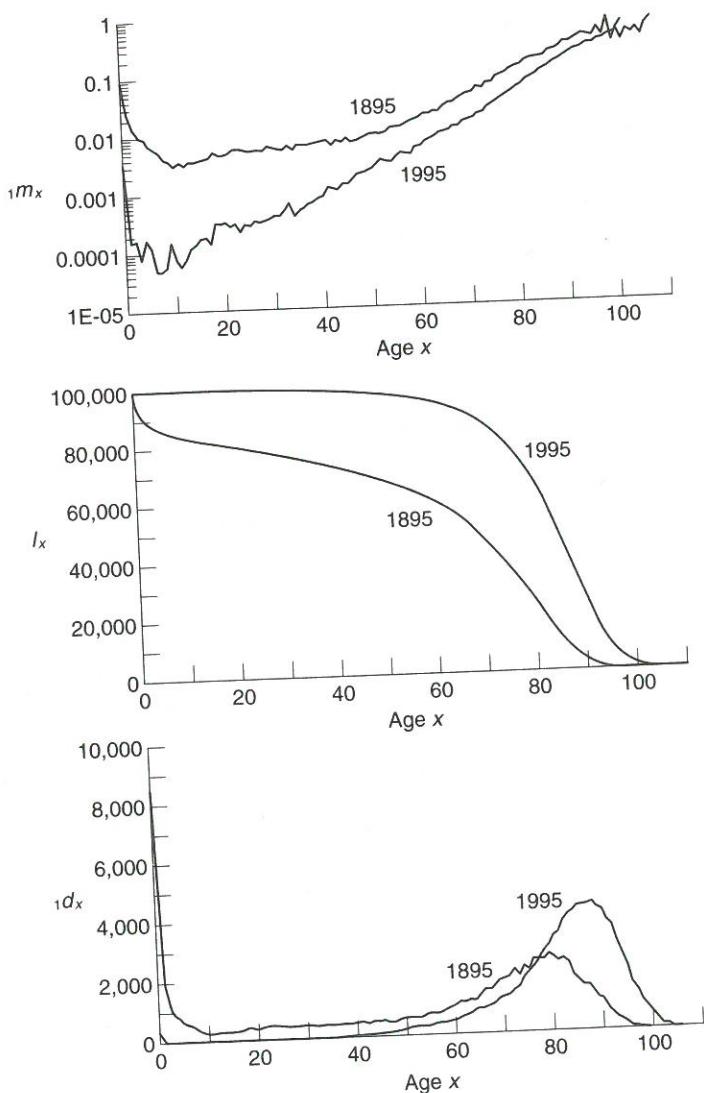


Figure 3.3 Age-specific death rates (${}_1m_x$), survivors (l_x), and deaths (${}_1d_x$) in Swedish female life tables, 1895 and 1995

Data source: Statistiska Centralbyrån and Berkeley Mortality Database.
<http://demog.berkeley.edu/wilmoth/mortality>

Assuming that the mortality experience of the population applies to an individual throughout his or her life, i.e., that at every age he or she is subjected to the mortality rates from which the life table is constructed, then the life table also illustrates the expected life experience of the individual. The most salient example is life expectancy. Life expectancy at age x is the average number of additional years to be lived by a member of the cohort who survives to age x . If we knew nothing else about an individual except the fact that he or she survived to age x , life

Table 3.4: Life expectancy at birth, by major areas, 1995–2000

Major area	Both sexes	Males	Females
Africa	51.4	50.0	52.8
Asia	66.3	64.8	67.9
Europe	73.3	69.2	77.4
Latin America and the Caribbean	69.2	66.1	72.6
Northern America	76.9	73.6	80.2
Oceania	73.8	71.4	76.3

Source: United Nations, 1999.

expectancy at age x would be our best guess about how long that individual would live. Hence, it is an expected value for a randomly-chosen individual.

A useful simplification has gained widespread currency and will be used later in this volume: the probability of surviving from birth to age x is designated $p(x)$ and the cumulative probability of dying between birth and age x is designated $q(x)$. So

$$p(x) = \frac{l_x}{l_0}$$

$$q(x) = 1 - p(x) = 1 - \frac{l_x}{l_0} = \frac{l_0 - l_x}{l_0} = \frac{x d_0}{l_0}$$

3.7 The Life Table Conceived as a Stationary Population

The stationary population is the first of two important population models that are described in this volume. The other model is that of a stable population, developed in chapter 7. In fact, the stationary population model is a special case of the more general stable population model. The concept of a stationary population is independent of the life table apparatus, but it is convenient to develop its features by reference to life table notation.

A stationary population results from the continued operation of three demographic conditions:

- 1) Age-specific death rates that are constant over time (but usually not constant over age);
- 2) A flow of births that is constant over time; the same number of newborns are added to the population per unit of time, whether the unit is a year, a month, or a day;
- 3) Net migration rates that are zero at all ages; in effect, the population is assumed to be closed to migration.³

The conversion of a life table into a stationary population model simply requires a little notational sleight-of-hand. If we assume that l_0 is the annual number of births in a population that meets the three conditions of a stationary population, then many of the other columns and elements of a life table take on a new meaning:

l_x is the number of persons who reach age x in any calendar year, $l_x = l_0 \cdot x p_0$;
 nL_x is the number of persons alive at any point in time between ages x and $x + n$;
 T_x is the number of persons alive at any point in time above age x , so that
 T_0 is the total size of the population;
 nd_x is annual number of deaths between ages x and $x + n$;
 e_0^o is the mean age at death for persons dying in any particular year.

Box 3.2 Interpreting the Life Table**1. The basic columns:**

- x = Exact age x
 l_x = Number of people left alive at age x
 $n d_x$ = Number of people dying between ages x and $x + n$
 $n q_x$ = Probability of dying between ages x and $x + n$
 $n p_x$ = Probability of surviving from age x to age $x + n$

- $n L_x$ = Person-years lived between ages x and $x + n$
 T_x = Person-years lived above age x
 e_x^0 = Expectation of life at age x
 $n m_x$ = Age-specific death rate between ages x and $x + n$
 $n a_x$ = Average person-years lived between ages x and $x + n$ for persons dying in the interval

2. Additional information:

- $(l_y)/l_x = y-x p_x$ = Probability of surviving from age x to age y
 $1 - (l_y)/l_x = y-x q_x$ = Probability of dying between ages x and y
 $l_x - l_y = y-x d_x$ = Number of people dying between ages x and y
 $T_x - T_y = y-x L_x$ = Number of person-years lived between ages x and y
 $(n d_x)/(l_0)$ = Probability that a newborn will die between ages x and $x + n$
 $(l_x - l_y)/l_0$ = Probability that a newborn will experience his death between ages x and y
 $(T_x - T_y)/l_0$ = Number of years that a newborn can expect to live between ages x and y

Example: Austria, males, 1992 (data shown in box 3.1)

Life expectancy at birth = 72.889 years

Life expectancy at age 50 = 26.422 years

(a male who has reached age 50 can expect to live 26.422 additional years)

Probability of surviving from birth to age 40 = $l_{40}/l_0 = 95,588/100,000 = .95588$

Probability that a person who survived to age 40 would die before age 60

 $= (l_{40} - l_{60})/l_{40} = 1 - l_{60}/l_{40} = 1 - 83,845/95,588 = .12286$

Number of years that a newborn male could expect to live in the age interval 25–50

 $= (T_{25} - T_{50})/l_0 = (4,821,324 - 2,429,176)/100,000 = 23.9$ years

Probability that a newborn will die between ages 70 and 75

 $5d_{70}/l_0 = 12,422/100,000 = .12422$

Probability that a newborn will die between ages 70 and 85

 $= (l_{70} - l_{85})/l_0 = (66,225 - 21,134)/100,000 = .45091$

The most difficult connection to understand is that involving $n L_x$. Table 3.5 demonstrates why the person-years lived between ages x and $x + n$ by a cohort of l_0 births, the function that we have previously designated $n L_x$, must also equal the number of persons alive between ages x and $x + n$ in a stationary population with l_0 annual births. In this table, we assume that a stationary population exists in which there are 365,000 annual births, a process that has extended indefinitely throughout the past. These births are evenly distributed over time so that there are 1,000 births per day. The probability of surviving from birth to various ages (expressed in days) is assumed to be as shown in the $x p_0$ column. With these assumptions, and no migration, the population size and age structure within the first year of life will be constant

Table 3.5: Life table and age structure of a stationary population

Age in days	Probability of surviving to age x	Population alive on:									
		Jan. 1	Jan. 2	Jan. 3	Jan. 4	Jan. 5	Jan. 6	Dec. 31		
0	1.000	1,000	1,000	1,000	1,000	1,000	1,000	1,000		
1	.970		970	970	970	970	970	970		
2	.950			950	950	950	950	950		
3	.946				946	946	946	946		
4	.942					942	942	942		
.				
364	0.900							900		

(hence the name, stationary population). This is readily seen by beginning with the cohort of 1,000 babies born on January 1 and following it forward as illustrated in the rest of the table.

It is clear that the number of persons at any particular age becomes constant over time because it is the product of a constant number of births and constant probabilities of survival. The number of people alive at any point in time (e.g., January 5) between exact ages 0 and 1 is:

$${}_1 N_0 = 1000 + 970 + 950 + 946 + 942 + \dots + 900$$

The number of person-years lived in the first year of life by an annual cohort of births will equal the number of daily cohorts, 365, times the person-years lived by each daily cohort. Each daily cohort lives $1000 \cdot (1/365)$ person-years on January 1, $970 \cdot (1/365)$ on January 2, and so on down to $900 \cdot (1/365)$ on December 31. So the total number of person-years lived in the first year of life by an annual cohort of births is:

$$\begin{aligned} {}_1 L_0 &= 365 \cdot [1000/365 + 970/365 + 950/365 + \dots + 900/365] \\ &= 1000 + 970 + 950 + \dots + 900. \end{aligned}$$

Thus, ${}_1 L_0 = {}_1 N_0$; the number of person-years lived by an annual cohort of births in an age interval will equal the number alive in that interval at any moment of time. Finally, note that both quantities will also equal the number of person-years lived in the age-time bloc jointly circumscribed by ages 0 and 1 and by a calendar year that extends from January 1 to December 31. Since there are ${}_1 N_0$ persons alive at any point in time between ages 0 and 1, there will be ${}_1 N_0 \cdot (1/365)$ person-years lived in that age interval on January 1, another ${}_1 N_0 \cdot (1/365)$ lived on January 2, and altogether $365 \cdot {}_1 N_0 \cdot (1/365) = {}_1 N_0$ over the course of the year.

Using life table notation to describe the functions of a stationary population, the birth rate is equal to the annual number of births divided by the total size of the population, or l_0/T_0 . Since life expectancy at birth is T_0/l_0 , it must be the case that, in a stationary population:

$$CBR = 1/e_0^0$$

The crude birth rate is the reciprocal of life expectancy at birth. Why this reciprocal relationship exists can perhaps be understood by imagining a population in which no one dies until age 60,

at which point everyone dies. Then life expectancy at birth would obviously be 60 years. If annual births are B , then the size of the population must be $60 \cdot B$ and the crude birth rate must be $B/(60 \cdot B) = 1/60$. Each birth lives 60 years; every 60 person-years lived in the population each year produces one birth.

Since a stationary population must be constant in size because the number of persons at each age is constant, then the crude death rate must equal the crude birth rate:

$$CDR = CBR = 1/e_0^o$$

Since the number of persons above age x must also be constant, then the number of persons arriving at age x each year, l_x , must equal the number of persons dying above age x that year. Therefore:

$$\infty M_x = \frac{l_x}{T_x} = \frac{1}{[T_x/l_x]} = \frac{1}{e_x^o}$$

So in a stationary population, the death rate of any open-ended population segment above age x must equal the reciprocal of the life expectancy at age x .

The proportion of the stationary population that is aged x to $x+1$ is:

$${}_1C_x^S = \frac{{}_1L_x}{T_0} = \frac{{}_1L_x}{l_0} \cdot \frac{l_0}{T_0} \simeq \frac{l_{x+0.5}}{l_0} \cdot CBR$$

In developing this final expression, we have assumed that ${}_1L_x$ is approximately equal to $l_{x+0.5}$, which would be exactly correct if the l_a function were linear in the interval between x and $x+1$.

Thus, the stationary population model provides explicit expressions that connect the major demographic parameters to one another: life expectancy, birth rates, death rates, and age structure. The explicitness of these relations is one reason why the stationary population has become an important demographic model. The model can be invoked in order to estimate one demographic parameter on the basis of another. For example, an archeologist who encounters a collection of skeletons and assigns ages to them (producing the equivalent of the ${}_nD_x$ function of a life table) can estimate the birth rate of the population that gave rise to the skeletons as $1/e_0^o$. Or a demographer who encounters the age distribution of the 1881 census of India (equivalent to the ${}_nL_x$ function of a stationary population) can estimate probabilities of survival from one age interval to the next (${}_5L_{x+5}/{}_5L_x$). In both cases, of course, the assumption of stationarity is required. The fact that, until the eighteenth century, the world population was growing very slowly means that, on average, the assumption of stationarity may not be too distortive in many applications. At least, the direction of bias would be hard to predict.

The fact that every human population has an underlying life table, whether or not it is accurately estimated, means that every population can form the basis of a model stationary population. This model is the population that would eventually emerge if age-specific mortality rates remained constant at values contained in the life table, if births were constant, and if there were no migration. What time span is implied by "eventually"? For full precision, it is equal to the human life span, the maximum age attained by any individual. For other purposes where less than complete precision is required, it could be a shorter period.

As noted earlier, the scale of the life table is set by l_0 , the arbitrarily-chosen radix whose value has a proportionate effect on l_x , ${}_nL_x$, T_x , and ${}_nD_x$. Because of this arbitrariness, the scale of the life table bears no necessary relationship to the size of the population that produced

Box 3.3 The Life Table Conceived as a Stationary Population

l_0	= Annual number of births and annual number of deaths
l_x	= Number of persons who reach age x in any calendar year
${}_nL_x$	= Number of persons alive at any point in time between ages x and $x+n$
T_x	= Number of persons alive at any point in time above age x
T_0	= Total size of the population
${}_nD_x$	= Annual number of deaths between ages x and $x+n$
e_0^o	= Mean age at death for persons dying in any particular year
Crude Birth Rate = Crude Death Rate =	$\frac{1}{e_0^o}$
Death Rate above age x =	$\frac{l_x}{T_x} = \frac{1}{e_x^o}$
Age Structure = ${}_nC_x^S$	$= \frac{{}_nL_x}{T_0} \simeq \frac{l_{x+n/2}}{l_0} \cdot n \cdot CBR$

Example: Austria, males, 1992 (data shown in box 3.1)

Number of annual births = $l_0 = 100,000$
Number of people reaching their 20th birthday in any calendar year = $l_{20} = 98,334$
Number of people alive between ages 30 and 35 = ${}_5L_{30} = 484,175$
Number of people above age 60 = $T_{60} = 1,544,893$
Total size of the population = $T_0 = 7,288,901$
Annual number of deaths between ages 50 and 55 = ${}_5D_{50} = 3,225$
Mean age at death = $e_0^o = 72.889$ years
$CBR = CDR = 1/e_0^o = 1/72.889 = .01372$
Death rate above age 60 = $1/e_{60}^o = 1/18.426 = .05427$
Proportion of people aged 25 to 30 = ${}_5L_{25}/T_0 = 487,127/7,288,901 = .0668$
or
${}_5C_{25}^S \simeq \frac{l_{27.5} + l_{30}}{l_0} \cdot 5 \cdot CBR \simeq \frac{\frac{l_{27.5}}{2} + \frac{l_{30}}{2}}{l_0} \cdot 5 \cdot CBR = \frac{\frac{97,704 + 97,151}{2}}{100,000} \cdot 5 \cdot .01372 = .0668$

it. Likewise, the scale of the model stationary population produced by any life table is also arbitrary and should not be confused with the size of the actual population to which it pertains.

Any population – any collection of individuals meeting some defined criteria for membership in the population – has a set of attrition rates that describe the process of leaving the population. These rates can be arrayed by duration of membership in the population. Hence, any collectivity has a life table that can be converted into a model stationary population. Without making direct reference to the stationary model, analysts often make use of stationary population relations in thinking about these collectivities. For example, a graduate program that matriculates 10 students per year and has a student body of 40 can be assumed to have a mean duration in graduate school of 4 years ($e_0^o = T_0/l_0$). If one million new cases of cancer are diagnosed each year and someone with newly-diagnosed cancer can be expected to live 8 years, then the population of persons with diagnosed cancer numbers 8 million ($T_0 = l_0 \cdot e_0^o$). If persons remain with a firm an average of 5 years, then the annual attrition rate is 0.20 ($CDR = 1/e_0^o$).

In order to be accurate, these inferences require that the population be stationary. In many instances, this is a reasonable approximation. In some instances, especially when mean duration in the population is long, they can be very misleading. The most important demographic example of serious error that can result from a casual invocation of stationary relations involves the relationship between the mean age at death in a population and life expectancy at birth in that population. In a stationary population, the mean age of people dying in any particular year is equal to life expectancy at birth in that population. The mean age at death in a cohort (life expectancy at birth in the cohort) results from combining age-specific death rates ($_n m_x$) with the distribution of years lived by the cohort ($_n L_x$). The mean age at death in the population results from combining those same death rates ($_n m_x$) with the age structure of the population ($_n N_x$). But we have already seen that, in a stationary population, $_n N_x = _n L_x$. So the mean age at death in the population must be the same as that in a cohort.

If the population is not stationary, however, the mean age of persons dying in a particular period can be very different from life expectancy at birth. The reason is that a particular set of age-specific death rates, $_n m_x$, are being applied to two age structures that can be very different from one another. The age structure in the life table is, as before, $_n L_x$. But in the absence of stationary conditions, there is no necessary connection between the $_n L_x$ column in the period life table (which is entirely a product of current age-specific death rates) and the $_n N_x$ column, representing the actual age structure of the population. For example, if the annual number of births has been growing over time instead of constant (as assumed in the stationary population model), then the actual age structure of the population will be younger than that implied by the stationary population model. Relative to births 30 years ago, for example, there will have been more births in the past year. So the ratio of persons under age 1 to persons aged 30 in the actual population will be higher than in the stationary population. So will the ratio of 30-year-olds to 60-year-olds.

Because annual births have been growing in most developing countries, this example represents the typical pattern of discrepancy between the age structure of actual populations and the age structure of the stationary population implied by current mortality. For example, males in Colombia in 1964 had a life expectancy at birth (based on vital statistics) of 58.2 years. But the mean age of males dying in Colombia in 1964 was only 26.1 years, less than half as large (Preston, Keyfitz and Schoen, 1972). The mean age of persons dying in 1964 would have been a horribly biased estimator of life expectancy at birth in that year. The reason for the discrepancy is simply that births in Colombia had been growing in the years prior to 1964, rather than constant as assumed in the stationary model.

The stationary model is applicable to the analyses of all populations. Consider the population of US graduate students. The mean duration of time in graduate school spent by persons receiving their Ph.D. in any particular year has been drifting steadily upwards, leading to calls for program reform. But the main reason for the drift is not that progress has been slowed for persons entering graduate school but that the number of entrants has been declining, lengthening the mean duration of persons in the graduate student population at any moment in time regardless of their attrition rates. Since the base populations became "older," the mean duration in graduate school of persons achieving the Ph.D. in any year grew higher.

In these examples, the stationary model helps us understand how common sense can go seriously awry. By understanding the stationary model, we can gain some novel insights; by recognizing when it does not apply, we can identify and avoid some serious errors.

3.8 Mortality as a Continuous Process

By its tabular nature the life table can display mortality functions only at particular ages or for discrete age intervals. But the risk of death surely acts continuously on cohorts; persons in no age interval, no matter how small, are exempt from the risk. Development of the mathematics of this continuous process illuminates some of what has already been discussed and sets the stage for some of what is to come.

Let us consider the dying out of a cohort using life table notation. Since the risk of death acts continuously on members of the cohort, the number left alive at age x , l_x , changes continuously and can be represented by a continuous function, denoted $l(x)$. Mortality also changes continuously rather than by discrete leaps. The number of deaths among members of the cohort between ages x and $x + n$ is:

$$_n d_x = l(x) - l(x + n)$$

and the death rate is, as before, $_n m_x = {}_n d_x / {}_n L_x$. We now let the age interval n identifying the death rate grow shorter and shorter. The key concept in the continuous development is the "force of mortality," denoted $\mu(x)$, and defined as:

$$\mu(x) = \lim_{n \rightarrow 0} \frac{{}_n d_x}{{}_n L_x} = \lim_{n \rightarrow 0} {}_n m_x$$

It is essential to recognize that, by dealing with a tiny interval of age instead of, say, an interval of $n = 1$, we are not altering the scale of ${}_n m_x$. For example:

$${}^1 m_{30} = \frac{{}^1 d_{30}}{{}^1 L_{30}} = \frac{\text{Deaths in a cohort between ages 30 and 31}}{\text{Person-years lived in the cohort between ages 30 and 31}}$$

and

$$0.5 m_{30} = \frac{0.5 d_{30}}{0.5 L_{30}} = \frac{\text{Deaths in a cohort between ages 30 and 30.5}}{\text{Person-years lived in the cohort between ages 30 and 30.5}}$$

By reducing the age interval (n) from one year to half a year, we have reduced both numerator and denominator by approximately one-half, thereby retaining the same approximate level of the ${}_n m_x$ function. The same result would obtain if we were to have made n equal to 0.25, to 0.10, or to a very tiny value. The force of mortality function retains the character of an annualized rate; it is a death rate per person-year of exposure⁴. Since ${}_n d_x = l(x) - l(x + n)$, and since ${}_n L_x = n \cdot l(x)$ for an interval n so small that person-years within the interval are negligibly reduced by death, we can write:

$$\mu(x) = \lim_{n \rightarrow 0} {}_n m_x = \lim_{n \rightarrow 0} \left[\frac{l(x) - l(x + n)}{n \cdot l(x)} \right] \quad (3.3)$$

By the definition of a derivative, the expression,

$$\lim_{n \rightarrow 0} \left[\frac{l(x) - l(x + n)}{n} \right]$$

is simply the derivative of the $l(x)$ function at x multiplied by (-1) (the derivative itself has $l(x+n) - l(x)$ in the numerator). When we divide the derivative of l_x by the value of l_x , we produce the derivative of the natural logarithm of $l(x)$. So:⁵

$$\mu(x) = \lim_{n \rightarrow 0} \left[\frac{l(x) - l(x+n)}{n \cdot l(x)} \right] = \frac{-d \ln(l(x))}{dx} \quad (3.4)$$

Let us now take the negative of (3.4) and integrate both sides between two exact ages y and z :

$$-\int_y^z \mu(x) dx = \ln l(z) - \ln l(y)$$

Now taking exponentials of both sides we have:

$$e^{-\int_y^z \mu(x) dx} = \frac{l(z)}{l(y)} \quad (3.5)$$

Or:

$$l(z) = l(y) e^{-\int_y^z \mu(x) dx} \quad (3.6)$$

Equation (3.6) is one of the most important equations in formal demography. It expresses the proportionate change in the size of a cohort between two ages completely in terms of the force of mortality function prevailing between those ages. It says that the proportionate change in cohort size between y and z is a simple function of the sum of the force of mortality function between those ages. The order in which the death rates occur is immaterial; all that matters is their sum. If the younger age is zero and the older is a , then:

$$l(a) = l(0) e^{-\int_0^a \mu(x) dx} \quad (3.7)$$

Note the similarity between equation (3.7) and equation (1.5):

$$N(T) = N(0) e^{\int_0^T r(t) dt}$$

The latter equation expresses the size of the total population at time T in terms of its size at time zero and the sum of intervening growth rates. Likewise, the size of a cohort at age a can be expressed in terms of its size at age zero and the sum of intervening death rates. The death rate at age x is simply acting as a (in this case, negative) growth rate at age x for the cohort. Because we choose to define death rates ($\mu(x)$) and $n m_x$ as positively valued functions, the negative sign must appear in equation (3.7) to make the analogy with growth rates complete.

All life table functions can be expressed in terms of $l(x)$ and $\mu(x)$. For instance, the number of person-years in the interval $[x, x+n]$ is:

$$n L_x = \int_x^{x+n} l(a) da$$

Since $n d_x = n L_x \cdot n m_x$, the number of deaths in a small interval da is $l(a)\mu(a)da$ and the continuous formula for $n d_x$ is:

$$n d_x = \int_x^{x+n} l(a)\mu(a) da$$

Note that, since the number of survivors to any age is equal to the number of deaths above that age, the following relationship must hold:

$$l(x) = \int_x^{\infty} l(a)\mu(a) da$$

Another internal relationship represents the equivalence of calculating person-years lived above a certain age as the sum over age of the number of survivors versus the sum over survivors of the time lived until death. As noted above, there are $l(a)\mu(a)da$ persons dying in the small interval $[a, a+da]$ and each one lives $(a-x)$ years beyond age x , so:

$$\int_x^{\infty} l(a) da = \int_x^{\infty} l(a)\mu(a)(a-x) da$$

Life expectancy can then be written in two equivalent forms, using the two relationships above:

$$e_x^o = \frac{\int_x^{\infty} l(a)\mu(a)(a-x) da}{\int_x^{\infty} l(a)\mu(a) da} = \frac{\int_x^{\infty} l(a) da}{l(x)}$$

The expression on the left corresponds to the definition of life expectancy in terms of ages at death whereas the expression on the right shows that it is also a sum of person-years lived.

Since $l(x)$ itself can be expressed in terms of $l(0)$ and $\mu(x)$ (equation 3.7), all life table functions can further be expressed in terms of $l(0)$ and $\mu(x)$ alone. Such expressions are provided for reference in appendix 3.1, at the end of this chapter.

3.9 Life Table Construction Revisited

From the above expressions for $n d_x$ and $n L_x$, we can derive the continuous expression for $n m_x$ as:

$$n m_x = \frac{\int_x^{x+n} l(a)\mu(a) da}{\int_x^{x+n} l(a) da} \quad (3.8)$$

The expression for $n m_x$ illuminates a feature of life table construction that we have heretofore suppressed. It shows that a cohort's death rate in the interval x to $x+n$ is a weighted average of the force of mortality function between ages x and $x+n$. The weights are supplied by the $l(a)$ function, the number of survivors in the cohort at age a , within the interval x to $x+n$. Now suppose that we are observing the age-specific death rate between ages x and $x+n$ in some population, rather than in a cohort. The population's age-specific death rate is denoted

nM_x . Given a certain underlying force of mortality function in that population, its death rate between ages x and $x + n$ will be:⁶

$$nM_x = \frac{\int_x^{x+n} N(a)\mu(a) da}{\int_x^{x+n} N(a) da} \quad (3.9)$$

where $N(a)da$ = number of persons in the interval of age a to $a + da$. A comparison of 3.8 and 3.9 shows that, even when a cohort and a population have exactly the same $\mu(a)$ function in the interval x to $x + n$, the value of nm_x for a cohort subject to that force of mortality function may not equal the value of nM_x for the population subject to that same function. The reason is that the $\mu(a)$ function is being weighted by $l(a)$ in the cohort and by $N(a)$ in the population. There are only two conditions in which we can be certain that $nm_x = nM_x$:

- 1) $\mu(a)$ is constant in the interval x to $x + n$: $\mu(a) = \mu^*$, for $x \leq a \leq x + n$. In this case, the constant value comes out of the integral sign in the numerators of (3.8) and (3.9) and: $nm_x = nM_x = \mu^*$.

Substituting this constant value into equation (3.5) gives:

$$np_x = \frac{l_{x+n}}{l_x} = e^{-nM_x \cdot n} \quad (3.10)$$

Equation (3.10) is, in effect, performing the $nm_x \rightarrow nq_x$ conversion (actually, it is an $nM_x \rightarrow nq_x$ conversion) when mortality is constant in the interval x to $x + n$. A formula for ascertaining the value of na_x in this case was presented in section 3.2.4. But the step involving na_x can be skipped and one can ascertain the value of nL_x directly from:

$$nL_x = \frac{n dx}{nm_x} = \frac{l_x - l_{x+n}}{nM_x}$$

- 2) The other case where nM_x will always equal nm_x (providing that the $\mu(a)$ function is the same for the cohort and population) occurs when $N(a)$ is proportional to $l(a)$ throughout the interval x to $x + n$. Substituting $N(a) = k \cdot l(a)$ into (3.9) gives the same expression as (3.8). This proportionality condition applies when the population's age distribution ($N(a)$) is *stationary* in the age interval x to $x + n$. It will be stationary, of course, when the preconditions described above for establishing a stationary population are met (or, possibly, by chance).

The most commonly observed departure from stationarity is that a population's age distribution is younger than that of the stationary population produced by the same $\mu(a)$ distribution. Most likely, it is younger because of a history of rising numbers of births or falling mortality, both of which are manifest in positive growth rates. In contrast to the first assumption, that $\mu(a)$ is constant between x and $x + n$, this assumption of stationarity does not automatically supply formulas for calculating all other life table functions, e.g., na_x and nL_x . One must use one of the procedures described in section 3.2 to complete the life table.

Because neither of these assumptions will apply in many cases, it should not be an automatic choice that the nm_x function chosen for a period life table simply be the set of nM_x values observed in the population. Anomalous features of the population's age distribution may render the nM_x function a poor estimator of nm_x , although within 5-year age intervals the distortions would rarely be large. One could, of course, simply argue that the period life table is *designed*

to reproduce the nM_x function, that nM_x is how we choose to operationalize period mortality conditions. But a more precise indication of those conditions is given by the $\mu(x)$ function. This function cannot be directly observed because it pertains to infinitesimal intervals of age. But its main features can be inferred from the nM_x function, particularly if the latter is adjusted for age-distributional disturbances.

Keyfitz (1966, 1968a) has been a principal exponent of adjusting nM_x before it is incorporated into the life table in the form of nm_x . In particular, his iterative life table system attempts to purge nM_x of the effects of population growth. When the population is growing, the age distribution of the population within an n -year wide interval will be younger than the age distribution of years lived by a cohort having the same $\mu(a)$ function. For age intervals in which the death rate rises with age (usually, those beyond age 30), nm_x will exceed nM_x because the latter is "biased" downwards by the population's youthful age distribution, just as the crude death rate is reduced by a young age distribution. Although Keyfitz's procedure is a useful advance on earlier ones, the difference that it makes for actual life table functions computed from data is, just as for other advances in life table construction, rather small. For this reason we shall not develop it in detail here. However, nonstationarity typically makes a larger difference in the highest, open-ended interval and we defer a discussion of how to deal with it to section 7.8. Table 3.6 shows the relationship between nm_x and nM_x and the growth rate of selected age groups in the US in 1985.

Let us now return briefly to the issue of using an na_x function that is directly observed in a population. We have seen that nM_x is, in general, biased downwards relative to nm_x in a growing population. Likewise, it is intuitively clear that na_x , the mean number of years lived in the interval for persons dying in the interval x to $x + n$, is also biased downwards in a growing population relative to the equivalent function in a cohort having the same force of mortality function. Suppose we convert nM_x into nq_x using the formula:

$$nq_x = \frac{n \cdot nM_x}{1 + (n - na_x) \cdot nM_x}.$$

nq_x will be biased downwards because nM_x is too low (the proportionate downward bias in the numerator is greater than that in the denominator). Now suppose that we choose a value of na_x that is directly observed for the same period (e.g., by getting detail on the exact ages at death for persons dying between ages 60 and 65 in 1996). Since na_x itself will be biased downwards, the denominator will be biased upwards by this choice. The bias in using the observed na_x values doesn't compensate for the bias in using nM_x , it exaggerates it.

The development of the relations in this section was deterministic. For what is often a more elegant development of some of these relations using probabilistic reasoning, see Mode (1985), Hoem (1972), or Chiang (1968, 1978).

Table 3.6: Comparison of nM_x and nm_x , US, females, 1985

Age	nM_x (1)	nm_x (2)	Ratio (2)/(1)	nr_x (growth rate of age group between 1/1/1985 and 1/1/1986)
15–19	0.000466	0.000466	1.0000	-0.001
70–5	0.025997	0.026048	1.0020	0.011
75–9	0.040951	0.041186	1.0057	0.024

Data source: Keyfitz and Flieger, 1990.

3.10 Decomposing a Difference in Life Expectancies

When analyzing changes in life expectancy at birth or studying differences in life expectancy between two populations, it is sometimes useful to estimate what mortality differences in a specific age group contribute to the total difference in life expectancy. The estimation method involves decomposition procedures that are not as straightforward as those developed in chapter 2. The main reason for complications is the interdependence among age groups in the determination of life expectancy. A change in the death rate between ages 20 and 25 has a direct effect on ${}_5L_{20}$, but it also has an indirect effect on all the ${}_nL_x$ above age 25 because of the change in the number of survivors at age 25. This latter change will have a bigger effect on life expectancy at birth when 25-year-olds have a longer life expectancy.

There are two main approaches in decomposing a difference in life expectancies, a continuous approach (Pollard, 1982) and a discrete approach (Arriaga, 1984). Although both procedures are formally identical (Pollard, 1988), Arriaga's formula is easier to apply to traditional life table data. The total effect, ${}_n\Delta_x$, of a difference in mortality rates between ages x and $x + n$ on the life expectancy at birth can be expressed as:

$${}_n\Delta_x = \frac{l_x^1}{l_0^1} \cdot \left(\frac{{}_nL_x^2}{l_x^2} - \frac{{}_nL_x^1}{l_x^1} \right) + \frac{T_{x+n}^2}{l_0^1} \cdot \left(\frac{l_x^1}{l_x^2} - \frac{l_{x+n}^1}{l_{x+n}^2} \right) \quad (3.11)$$

where l_x , ${}_nL_x$ and T_x are conventional functions of the life table and where superscripts 1 and 2 refer to time 1 and 2 or to population 1 and 2.

The first term in the right-hand side of equation (3.11),

$$\frac{l_x^1}{l_0^1} \cdot \left(\frac{{}_nL_x^2}{l_x^2} - \frac{{}_nL_x^1}{l_x^1} \right),$$

corresponds to the direct effect of a change in mortality rates between ages x and $x + n$, i.e., the effect that a change in the number of years lived between ages x and $x + n$ produces on the life expectancy at birth. The second term of the equation,

$$\frac{T_{x+n}^2}{l_0^1} \cdot \left(\frac{l_x^1}{l_x^2} - \frac{l_{x+n}^1}{l_{x+n}^2} \right),$$

corresponds to the sum of the indirect and interaction effects, i.e., the contribution resulting from the person-years to be added because additional survivors at age $x + n$ are exposed to new mortality conditions. For the open-ended age interval, there will be only a direct effect, and the following equation applies:

$${}_\infty\Delta_x = \frac{l_x^1}{l_0^1} \cdot \left(\frac{T_x^2}{l_x^2} - \frac{T_x^1}{l_x^1} \right) \quad (3.12)$$

It can be demonstrated that $e_0^o(2) - e_0^o(1) = \sum_0^\infty {}_n\Delta_x$.

Equations (3.11) and (3.12) pertain to the decomposition of differences of life expectancy at birth. The same equations can be used for decomposing a change in life expectancies at age a , replacing l_0 by l_a and estimating ${}_n\Delta_x$ for $x \geq a$. Box 3.4 shows an example of the method to decomposing change in e_0^o among American females between 1935 and 1995. In chapter 4, we will examine how we can further decompose differences in life expectancies by calculating the contribution of various causes of death.

Box 3.4 Age Decomposition of Differences in Life Expectancies at Birth

$l_x^1, {}_nL_x^1, T_x^1$ = Life table functions at time 1 (or in population 1)

$l_x^2, {}_nL_x^2, T_x^2$ = Life table functions at time 2 (or in population 2)

${}_n\Delta_x = \frac{l_x^1}{l_0^1} \cdot \left(\frac{{}_nL_x^2}{l_x^2} - \frac{{}_nL_x^1}{l_x^1} \right) + \frac{T_{x+n}^2}{l_0^1} \cdot \left(\frac{l_x^1}{l_x^2} - \frac{l_{x+n}^1}{l_{x+n}^2} \right)$ = contribution of mortality difference in age group x to $x + n$ to differences in life expectancy at birth

${}_\infty\Delta_x = \frac{l_x^1}{l_0^1} \cdot \left(\frac{T_x^2}{l_x^2} - \frac{T_x^1}{l_x^1} \right)$ = contribution of mortality difference in open-ended age group to differences in life expectancy at birth

$e_0^o(2) - e_0^o(1) = \sum_x {}_n\Delta_x$

Example: US, females, 1935–95

Age x	l_x^{1935}	${}_nL_x^{1935}$	T_x^{1935}	l_x^{1995}	${}_nL_x^{1995}$	T_x^{1995}	${}_n\Delta_x$	Percent
0	100,000	96,354	6,332,064	100,000	99,410	7,900,065	3.06	19.5%
1	95,458	377,877	6,235,709	99,321	396,947	7,800,655	1.11	7.1%
5	93,887	467,474	5,857,833	99,179	495,676	7,403,708	0.46	2.9%
10	93,174	464,534	5,390,358	99,096	495,275	6,908,032	0.32	2.0%
15	92,613	460,915	4,925,823	98,999	494,459	6,412,758	0.45	2.9%
20	91,681	455,193	4,464,909	98,772	493,254	5,918,299	0.64	4.1%
25	90,341	447,783	4,009,717	98,524	491,863	5,425,046	0.69	4.4%
30	88,746	439,466	3,561,935	98,206	489,996	4,933,183	0.65	4.1%
35	86,997	429,742	3,122,468	97,769	487,383	4,443,186	0.69	4.4%
40	84,847	418,269	2,692,726	97,152	483,743	3,955,802	0.67	4.3%
45	82,368	403,859	2,274,456	96,298	478,583	3,472,059	0.78	4.9%
50	79,012	384,356	1,870,596	95,048	470,679	2,993,477	0.84	5.4%
55	74,539	358,766	1,486,241	93,085	458,397	2,522,798	0.87	5.6%
60	68,688	324,494	1,127,475	90,071	439,689	2,064,401	0.95	6.1%
65	60,779	279,761	802,981	85,504	411,580	1,624,711	0.93	6.0%
70	50,757	223,797	523,220	78,775	372,191	1,213,130	0.96	6.1%
75	38,276	155,169	299,422	69,655	318,738	840,940	0.89	5.7%
80	23,930	89,054	144,253	57,275	248,061	522,201	0.48	3.1%
85+	12,281	55,200	55,200	41,424	274,139	274,139	0.26	1.7%
Sum							15.68	100.0%

Total difference: $e_0^o(1995) - e_0^o(1935) = 79.00 - 63.32 = 15.68$ years

Contribution of mortality change before age 1 = 3.06 years (19.5% of total difference)

Data source: Bell, F. C., A. H. Wade, and S. C. Goss, 1992. *Life Tables for the United States Social Security Area: 1900–2080*. Baltimore, Maryland, US Social Security Administration, Office of the Actuary, Actuarial Study No. 107.

3.11 Adaptation of the Life Table for Studying Other Single Decrement Processes

A single decrement process is one in which individuals have only one recognized mode of exit from a defined state. Mortality is one such process. Life tables can be used to study all single decrement processes. In each case, they describe quantitatively the process of attrition from a defined state arrayed by duration in that state. Individuals would always enter the state at duration zero and the cohort entering the state would typically be traced until the last

member had exited. In the case of the “classic” life table that we have developed, the defined state is “being alive” and the mode of exit is death. The functions of a classic life table are displayed by age because, in this case, age corresponds exactly to the duration of the state of being alive. Age is used in a life table only when it is a perfect surrogate for duration in the state.

Processes in which there are more than one recognized mode of exit are termed “multiple decrement processes.” Empirically, multiple decrement processes are far more common than single decrement processes. In fact, for a real cohort, mortality is the *only* single decrement process. For any state that we can define other than being alive (e.g., being single; living in one’s place of birth) one can leave the state by some form of status change (e.g., getting married, migrating to another place) as well as by death. This additional risk of status change exposes a person to multiple decrements. None of these additional risks is able to cancel out the risk of death; a real cohort is always subject to the risk of dying at the same time that it is subject to other risks.

Although the apparatus for studying single decrement processes may appear to be very specific to mortality, there are three circumstances that increase its applicability:

1) *The multiple sources of decrement can often be collapsed analytically into one*

Even mortality can be considered a multiple decrement process if the analyst chooses to recognize different causes of death. But for many purposes, including the calculation of life expectancy, this complication is often irrelevant. Likewise, the different modes of exit from marriage, from the labor force, or from any other state of interest can under some circumstances be ignored depending on the question asked. For example, we can calculate expected years to be spent in a firm by a new hire from data on entrances and exits without distinguishing among modes of exit.

2) *Life histories are often available for surviving members of a cohort*

It is very common in surveys to ask questions about events that have occurred in the past. These questions are addressed only to living members of a cohort. Although these persons were subject to the risk of mortality, we can be sure that none of them succumbed to the risk. For these persons, the force of mortality function was, in effect, zero at all prior ages. Therefore, their progress from one state to another need not be studied by multiple decrement processes but can be viewed as a single decrement process, assuming that there is only one remaining mode of leaving a state.

For example, let us define the state we are interested in as “never married.” Suppose that we take a survey of 50-year-old women and ask about their marital histories. These women could have left the state of being “never-married” only by getting married. Thus, getting married in their nuptiality table would be analogous to dying in the classic life table. The force of nuptiality function (the rate of first marriage for the never-married population aged x) replaces the force of mortality function. Other obvious translations of life table concepts and notation in this case are the following:

l_x = number of women who are never married at age x .

$n p_x$ = probability of staying unmarried in the age interval x to $x + n$ for a never-married woman aged x .

Box 3.5 Application of Life Table Construction to Analysis of Marital Histories

Example: Bangladesh, cohort of 655 women aged 45–9 in 1993–4, who all married before age 30. State of interest: “never married”

Age x	n	l_x	nd_x	nq_x	na_x	nL_x	T_x	e_x^o
0	5	655	0	0.00000	2.5	3275.0	9202.5	14.05
5	5	655	0	0.00000	2.5	3275.0	5927.5	9.05
10	2	655	119	0.18168	1.0	1191.0	2652.5	4.05
12	3	536	388	0.72388	1.5	1026.0	1461.5	2.73
15	3	148	106	0.71622	1.5	285.0	435.5	2.94
18	2	42	16	0.38095	1.0	68.0	150.5	3.58
20	2	26	13	0.50000	1.0	39.0	82.5	3.17
22	3	13	7	0.53846	1.5	28.5	43.5	3.35
25	5	6	6	1.00000	2.5	15.0	15.0	2.50
30								

Interpretation of the columns:

n = length of interval

l_x = number of women who are never married at age x

nd_x = first marriages between ages x and $x + n$

nq_x = probability of having a first marriage between ages x and $x + n$

na_x = average person-years lived in the never-married state between ages x and $x + n$ by women marrying in the interval (assumption: $na_x = n/2$)

nL_x = number of person-years lived in the never-married state between ages x and $x + n$

T_x = number of person-years lived in the never-married state above age x

e_x^o = expected number of years to be spent in the never-married state for a never-married person aged x . In this case, $e_0^o = 14.05$ can be interpreted as the mean age at marriage for those women.

Data source: Mitra, S. N., et al., 1994. *Bangladesh Demographic and Health Survey, 1993–1994*. Dhaka, Bangladesh, National Institute of Population Research and Training (NIPORT).

nL_x = person-years lived in the never-married state between ages x and $x + n$.

e_x^o = expected number of years to be spent in the never married state for a never married person aged x .⁷

The natural radix of this nuptiality table, l_0 , is simply the number of 50-year-old women who are reporting on their first-marriage histories. It is important to recognize that the experience described in the resulting nuptiality table (or marriage life table) pertains only to the surviving members of the cohort. This experience may not be representative of the full cohort that began life at age zero, or of the cohort members who survived to age 20. If the surviving members of the cohort had, age for age, higher or lower risks of marriage than the members who died, then the experience of the surviving members would clearly differ from that of the full cohort. The biases for many purposes are small and usually must be tolerated because the retrospective information from surviving members of the cohort is the only information available. Box 3.5 presents an example of a life table for first marriage constructed from a retrospective survey.

3) Single decrement processes can be modeled for cohorts subject to multiple decrements

Although a real cohort is always subject to mortality in addition to any other decrement that is operating, we can easily perform a thought experiment in which a hypothetical cohort is subject to only one form of decrement. Actuaries, biostatisticians, and demographers have developed techniques to carry out this experiment. These are used to produce what are sometimes called “associated single decrement life tables.” The term “associated” conveys that the single decrement table is associated with a multiple decrement process. The methods for constructing associated single decrement tables are developed in the next chapter.

Table 3.7 presents a few examples of the many processes that can be profitably studied by means of a life table. In general, a life table is valuable when the risk of leaving a state depends on the duration of time spent in the state. Without such duration dependence, there is little to be gained by arraying all functions by duration.

The life table apparatus, developed centuries ago, has acquired new salience because of recent statistical developments. These enable researchers to study simultaneously the duration dependence of some risk of attrition and the influence of identifiable characteristics, or covariates, on the level of that risk. These procedures, termed life tables with covariates or proportional hazards procedures, were introduced by Cox (1972) and have been elaborated by many others, including Kalbfleisch and Prentice (1980). A textbook on these procedures is Collett (1994).

Table 3.7: Examples of single decrement processes that can be studied by means of a life table^a

Process	State studied	State entered	State left when... when...	Vertical dimension of the table
Mortality	Being alive	Born	Die	Duration of life (age)
Nuptiality (first marriage)	Being unmarried	Born	Marry	Duration of single life (age)
Migration from place of birth	Living in place of birth	Born	Move to another place	Duration of residence (age)
Entering the labor force	Having never worked	Born	First enter labor force	Duration of life (age)
Becoming a mother	Having no births	Born	Have first birth	Duration of life (age)
Subsequent childbearing	Not having an additional birth	Have a birth	Have an additional birth	Duration since having a birth
Marital survival	Being in intact marriage	Marry	Marriage ends	Duration of marriage
Unemployment spells	Being unemployed	Become unemployed	Leave state of unemployment	Duration of unemployment
Incarceration	Being in jail	Enter jail	Leave jail	Duration of incarceration

^aAll of these processes can also be conceived as multiple decrement processes. Here we ignore other risks of leaving the state of interest.

Appendix 3.1: Life Table Relationships in Continuous Notation

$$l(x) = l(a)e^{-\int_a^x \mu(y) dy} \quad \text{for } x > a$$

$${}_n p_x = \frac{l(x+n)}{l(x)} = e^{-\int_x^{x+n} \mu(a) da}$$

$${}_n d_x = \int_x^{x+n} l(a) \mu(a) da = \int_x^{x+n} l(x) e^{-\int_x^a \mu(y) dy} \mu(a) da = l(x) \int_x^{x+n} e^{-\int_x^a \mu(y) dy} \mu(a) da$$

$${}_n q_x = \frac{{}_n d_x}{l(x)} = \int_x^{x+n} e^{-\int_x^a \mu(y) dy} \mu(a) da$$

$${}_n L_x = \int_x^{x+n} l(a) da = \int_x^{x+n} l(x) e^{-\int_x^a \mu(y) dy} da = l(x) \int_x^{x+n} e^{-\int_x^a \mu(y) dy} da$$

$${}_n m_x = \frac{{}_n d_x}{{}_n L_x} = \frac{\int_x^{x+n} l(a) \mu(a) da}{\int_x^{x+n} l(a) da} = \frac{\int_x^{x+n} e^{-\int_x^a \mu(y) dy} \mu(a) da}{\int_x^{x+n} e^{-\int_x^a \mu(y) dy} da}$$

$${}_n a_x = \frac{\int_x^{x+n} l(a) \mu(a)(a-x) da}{\int_x^{x+n} l(a) \mu(a) da} = \frac{\int_x^{x+n} e^{-\int_x^a \mu(y) dy} \mu(a)(a-x) da}{\int_x^{x+n} e^{-\int_x^a \mu(y) dy} \mu(a) da}$$

$$T_x = \int_x^\infty l(a) da = l(x) \int_x^\infty e^{-\int_x^a \mu(y) dy} da$$

$$\begin{aligned} e_x^o &= \frac{T_x}{l_x} = \frac{\int_x^\infty l(a) da}{l(x)} = \int_x^\infty e^{-\int_x^a \mu(y) dy} da \\ &= \frac{\int_x^\infty l(a) \mu(a)(a-x) da}{\int_x^\infty l(a) \mu(a) da} \end{aligned}$$

NOTES

1. In the first chapter, we demonstrated the equivalence of two methods for computing person-years, one summing time across individuals, one summing individuals across time (figure 1.1). A similar equivalence exists in computing person-years above age x , either as a sum across age-groups beginning with the age-interval x to $x+n$ or as a sum across individuals. The formula used in table 3.1 computes person-years lived above age x by adding person-years lived within each age-interval above age x . Alternatively, we could compute the person-years lived above age x for each member of the cohort and sum across individuals. For example at age 0, T_0 is also the sum of the age at death of all members of the cohort.

2. Since exposure is here measured in person-years, life expectancy is measured in years. If the time/age dimension of a life table were months, then ${}_nL_x$ would refer to person-months lived and life expectancy would be measured in months.
3. Actually, the stationary population model can be generalized to include non-zero rates of migration as long as age-specific rates of migration are constant over time. But we will not pursue this elaboration.
4. The argument here parallels the one for $r(t)$ in chapter 1. The annualized growth rate, continuously compounded, refers to an infinitesimal period but is still an annualized rate as long as time is measured in years.
5. Again, note the formal similarity between $\mu(x)$ in equation (3.4) and $r(t)$ in equation (1.3).
6. Actually, the expression for ${}_nM_x[0, T]$ is slightly more complicated because we can only measure that rate over a discrete period in which $N(a)$ and $\mu(a)$ do not usually remain constant. So what we are really observing is rather:

$${}_nM_x[0, T] = \frac{\int_0^T \int_x^{x+n} N(a, t)\mu(a, t) da dt}{\int_0^T \int_x^{x+n} N(a, t) da dt}$$

where $N(a, t)$ = number of persons aged a to $a + da$ at time t to $t + dt$, and
 $\mu(a, t)$ = death rate in the age interval a to $a + da$ at time t to $t + dt$.

We have simplified this expression by assuming that $N(a, t)$ and $\mu(a, t)$ do not vary over the time interval in which death rates are being measured.

7. In the case where information is available for the cohort of survivors only up to age 50, and if some women remain single at that age, e_x^0 must be truncated at that age. So it would be interpreted as the “expected number of years before age 50 to be spent in the never-married state for a never-married person aged x .”

4

Multiple Decrement Processes

- 4.1 Multiple Decrement Tables for a Real Cohort
- 4.2 Multiple Decrement Life Tables for Periods
- 4.3 Some Basic Mathematics of Multiple Decrement Processes
- 4.4 Associated Single Decrement Tables from Period Data
- 4.5 Cause-specific Decomposition of Differences in Life Expectancies
- 4.6 Associated Single Decrement Tables from Current Status Data
- 4.7 Stationary Populations with Multiple Sources of Decrement

In the previous chapter, we defined a single decrement process as one in which individuals have only one mode of exit from a defined state. A multiple decrement process is one in which individuals have more than one mode of exit. As we noted, multiple decrement processes are far more common in demography than are single decrement processes. These situations arise, for example, in fertility analysis when individuals are viewed as being exposed to the risk of pregnancy and to discontinuance of use of contraception; in migration, when individuals are exposed to the risk of moving to different places; in nuptiality, when married persons are exposed to the risks of divorce and widowhood; and in many other circumstances. And as we noted earlier, persons in a particular state in a real cohort are always exposed to the risk of death, in addition to whatever other risks they may have of leaving that state. Multiple decrement processes are sometimes referred to as situations of “competing risks.”

4.1 Multiple Decrement Tables for a Real Cohort

Conceptually, the construction of a multiple decrement table for a real cohort is no more challenging than the construction of a single decrement table. It is only necessary to add columns equivalent to other columns in a single decrement life table but which pertain exclusively to particular causes of decrement (i.e., to particular modes of exit from the table). The functions in these columns have a straightforward interpretation:

$$\begin{aligned} {}_n d_x^i &= \text{number of decrements from cause } i \text{ in the age interval } x \text{ to } x + n \\ {}_n q_x^i &= \text{probability of leaving the table from cause } i \text{ between ages } x \text{ and } x + n \text{ for} \\ &\quad \text{someone who reached age } x \\ &= {}_n d_x^i / l_x \end{aligned}$$

In both the ASDT and the parent life table the following relationship must hold:

$$\begin{aligned}\frac{nL_x}{l(x)} &= n \cdot {}_n p_x + {}_n a_x \cdot {}_n q_x \\ &= n - (n - {}_n a_x) \cdot {}_n q_x\end{aligned}$$

So equation (4.7) can be written as:

$$*_n a_x^i = n + R^i \frac{{}_n q_x}{*_n q_x^i} ({}_n a_x - n) \quad (4.8)$$

This equation can also be derived through a Taylor expansion.

Which of the general approaches to constructing an ASDT should be used in any particular application obviously depends upon the nature of the data and tenability of assumptions. Elandt-Johnson and Johnson (1980) have compared several of these approaches and concluded that results are not very sensitive to the procedure used, as should have been anticipated on the basis of the discussion in chapter 3. If the interval n is short, approach (b) is best since it is completely consistent and fully developed. If one is constructing cause-deleted tables in which relatively small causes of decrement are deleted, then approach (c) is best because the assumption of proportionality must be very good (the decrements that remain are a very high proportion of total decrements to which they are assumed proportional). In other situations, convenience may dictate the approach selected.

Box 4.2 presents an associated single decrement table for causes of deaths other than neoplasms. It is based upon the data for US females in 1991 that were presented in box 4.1. The table is constructed by Chiang's method (approach c), with the ${}^* a_x^{-i}$ values developed by graduation (equation 4.6) for $x = 10$ to 75, and using equation (4.8) for $x = 0, 1, 5$, and 80. For the last age group, we use here the assumption that ${}^* m_x^i = {}^n m_x^i$, in which case ${}^* a_{85}^{-i}$ is simply e_{85}^o / R^{-i} . In chapter 7, we will investigate how to obtain a better estimate of ${}^* a_{85}^{-i}$. The table shows that, in absence of neoplasms, life expectancy at birth would have been 82.46 years, a gain of 3.54 years relative to the life table with all causes present.

4.5 Cause-specific Decomposition of Differences in Life Expectancies

In section 3.10, we presented a method for estimating the contribution of age-specific mortality differences to differences between two life expectancies. This method can be easily extended to estimate the contribution of differences in cause-specific death rates by assuming that the distribution of deaths by cause is constant within each age group in each population. Under this assumption, the contribution of differences in all-cause mortality in a specific age group can be distributed proportionately to the difference in cause-specific mortality in the corresponding age group (Arriaga, 1989). The specific contribution of differences in mortality rates from cause i between ages x and $x + n$, ${}_n \Delta_x^i$, can be estimated with the following equation:

$$\begin{aligned}{}_n \Delta_x^i &= {}_n \Delta_x \cdot \frac{{}_n m_x^i(2) - {}_n m_x^i(1)}{{}_n m_x(2) - {}_n m_x(1)} \\ &= {}_n \Delta_x \cdot \frac{{}_n R_x^i(2) \cdot {}_n m_x(2) - {}_n R_x^i(1) \cdot {}_n m_x(1)}{{}_n m_x(2) - {}_n m_x(1)} \quad (4.9)\end{aligned}$$

Box 4.2 Associated Single Decrement Life Table for Causes of Death other than Neoplasms (via approach c)

$$R^{-i} = \frac{{}_n D_x - {}_n D_x^i}{{}_n D_x}$$

$l_x, {}_n p_x, {}_n a_x, e_x^o$ = functions in the master life table

$${}^* p_x^{-i} = [{}_n p_x]^{R^{-i}}$$

$${}^* l_x^{-i} = {}^* l_x^{-i} \cdot {}^* p_x^{-i}$$

${}^* a_x^{-i}$: calculated from equation (4.8) for $x = 0, 1, 5, 80$
from equation (4.6) for $x = 10$ to 75

$${}^* a_{85}^{-i} = {}^* e_{85}^{-i} = \frac{e_{85}^o}{R^{-i}}$$

Example: US, females, 1991; cause i = neoplasms

Age x	R^{-i}	l_x	${}_n p_x$	${}_n a_x$	e_x^o	${}^* p_x^{-i}$	${}^* l_x^{-i}$	${}^* a_x^{-i}$	${}^* e_x^{-i}$
0	0.99600	100,000	0.99217	0.152	78.92	0.99220	100,000	0.152	82.46
1	0.91322	99,217	0.99832	1.605	78.54	0.99846	99,220	1.605	82.10
5	0.83599	99,050	0.99908	2.275	74.67	0.99923	99,068	2.275	78.23
10	0.86205	98,959	0.99910	2.843	69.74	0.99922	98,992	2.875	73.29
15	0.91960	98,870	0.99764	2.657	64.80	0.99783	98,915	2.653	68.34
20	0.90562	98,637	0.99738	2.547	59.95	0.99763	98,700	2.548	63.48
25	0.86813	98,379	0.99686	2.550	55.10	0.99727	98,467	2.577	58.63
30	0.79593	98,070	0.99575	2.616	50.26	0.99661	98,198	2.585	53.78
35	0.70633	97,653	0.99416	2.677	45.46	0.99587	97,866	2.582	48.96
40	0.61668	97,083	0.99182	2.685	40.72	0.99495	97,462	2.637	44.15
45	0.56219	96,289	0.98670	2.681	36.03	0.99250	96,969	2.672	39.36
50	0.54014	95,008	0.97905	2.655	31.48	0.98863	96,242	2.695	34.64
55	0.54105	93,018	0.96629	2.647	27.10	0.98162	95,148	2.703	30.00
60	0.57492	89,882	0.94845	2.646	22.95	0.97003	93,399	2.695	25.51
65	0.61931	85,249	0.92331	2.631	19.05	0.95178	90,600	2.696	21.22
70	0.68006	78,711	0.88448	2.628	15.42	0.91991	86,231	2.686	17.16
75	0.74525	69,618	0.82573	2.618	12.09	0.86701	79,325	2.676	13.42
80	0.81683	57,486	0.72637	2.570	9.08	0.77017	68,776	2.637	10.07
85	0.89788	41,756	0.00000	6.539	6.54	0.00000	52,969	7.283	7.28

Probability of surviving to age 85 for all causes combined: 0.42

Probability of surviving to age 85 in the absence of neoplasms: 0.53

Life expectancy at birth for all cause combined: 78.92 years.

Life expectancy at birth in the absence of neoplasms: 82.46 years.

Data source: National Center for Health Statistics, 1996.

where

- $nR_x^i(j)$ = proportion of deaths from cause i in age group x to $x + n$ (nD_x^i/nD_x) in population j (or at time j), and
 $n\Delta_x$ = contribution of all-cause mortality differences in age group x to $x + n$ to differences in life expectancies, as expressed in equation (3.11)

It can be easily shown that

$$n\Delta_x = \sum_i n\Delta_x^i, \quad \text{and} \quad e_0^o(2) - e_0^o(1) = \sum_x n\Delta_x = \sum_x \sum_i n\Delta_x^i$$

The age- and cause-specific contribution to differences in life expectancies can thus be presented in a two-by-two table where the elementary contributions add up to the total difference in life expectancies. Box 4.3 presents an application of the age and cause decomposition method to analyzing the difference in male life expectancies at birth between China and India in 1990. It shows that about 68 percent of the 8.2 additional years of life expectancy at birth in China is attributable to lower rates of communicable diseases below age 5 in this country. However, the total difference in e_0^o is reduced by about one year due to lower rates of noncommunicable diseases in India in 1990.

4.6 Associated Single Decrement Tables from Current Status Data

We noted in chapter 3 that a restricted associated single decrement process can be directly observed when cohorts are asked about their event histories. Since the members of the cohort who respond in the survey have clearly had a force of mortality function of zero, we need not view them as subject to a multiple decrement process. Therefore, it is possible to proceed directly to the construction of an ASDT for the process under investigation. The only restriction on the kind of functions that can be displayed will result from limitations in the data. For example, a question might be asked on "what was your marital status five years ago," rather than the more complex set of questions needed to construct a complete marital history. From the 5-year question, it will be possible to estimate ${}_5p_x^M$, the probability that a person who was aged x five years earlier (i.e. who is aged $x + 5$ at the time of survey) will have remained single to the time of the survey. But no information will be available on ${}_5a_x^M$. It should be reiterated that tables constructed from such data will pertain only to the surviving members of the cohort who did not emigrate. Their force of decrement function may differ from that of the original members of the cohort.

Such applications require retrospective questions. John Hajnal (1953) was apparently the first to recognize that certain ASDT's could also be constructed from current status data. In particular, he proposed that an associated single decrement table for first marriages be constructed from data on the current marital status of the population, without any resort to retrospective questions. In our example, the proportion never-married at age x , which can be obtained by question on current status in a survey, is closely related to the l_x column of the birth cohort's ASDT. Under the assumption that there is no differential mortality or migration by first-marriage status, the l_x column of the cohort's ASDT (with a radix of one) will exactly equal the proportion single at age x .

To see this more formally, let us assume the population to be closed to migration. Then the force of decrement from all causes combined for the single population at age x will be:

$$\mu^s(x) = \mu^{Ds}(x) + \mu^M(x),$$

Box 4.3 Age and Cause Decomposition of Difference in Life Expectancies at Birth

$n m_x(1), n m_x(2)$ = all-cause mortality rate between ages x and $x + n$ at time 1 and time 2 (or in population 1 and 2)

$n R_x^i(1), n R_x^i(2)$ = proportion of deaths from cause i between ages x and $x + n$ at time 1 and time 2 (or in population 1 and 2)

$n\Delta_x$ = contribution of all-cause mortality differences in age group x to $x + n$ to differences in e_0^o (from equation 3.11)

$$n\Delta_x^i = n\Delta_x \cdot \frac{n R_x^i(2) \cdot n m_x(2) - n R_x^i(1) \cdot n m_x(1)}{n m_x(2) - n m_x(1)}$$

Example: India and China, males, 1990*

Age x	India				China				$n\Delta_x$	$n\Delta_x^1$	$n\Delta_x^2$	$n\Delta_x^3$
	$n m_x$	$n R_x^1$	$n R_x^2$	$n R_x^3$	$n m_x$	$n R_x^1$	$n R_x^2$	$n R_x^3$				
0	0.0267	0.882	0.073	0.046	0.0084	0.677	0.174	0.149	5.6	5.5	0.1	-0.0
5	0.0025	0.504	0.188	0.309	0.0009	0.174	0.337	0.488	0.8	0.6	0.1	0.2
15	0.0021	0.382	0.223	0.394	0.0015	0.068	0.380	0.552	0.3	0.4	-0.1	-0.0
30	0.0043	0.429	0.315	0.257	0.0028	0.101	0.573	0.326	0.6	0.6	-0.1	0.1
45	0.0139	0.304	0.592	0.104	0.0102	0.095	0.796	0.109	0.8	0.7	0.0	0.1
60	0.0388	0.248	0.722	0.030	0.0342	0.070	0.879	0.051	0.3	0.5	-0.1	-0.0
70	0.0929	0.247	0.728	0.025	0.1003	0.084	0.877	0.039	-0.3	0.7	-0.9	-0.1
Sum									8.2	9.0	-1.0	0.2

*In this example:

Cause 1 = Communicable diseases, maternal, perinatal and nutritional conditions;

Cause 2 = Noncommunicable diseases;

Cause 3 = Injuries.

$$\text{Total Difference} = e_0^o(\text{China}) - e_0^o(\text{India}) = 66.5 - 58.3 = 8.2 \text{ years} = \sum_{x=0}^{70} \sum_{i=1}^3 n\Delta_x^i$$

Data source: Murray, C. J. and A. D. Lopez, 1996. *The Global Burden of Disease: A Comprehensive Assessment of Mortality and Disability from Diseases, Injuries, and Risk Factors in 1990 and Projected to 2020*. Boston, Harvard University, School of Public Health.

where $\mu^{Ds}(x)$ is the force of mortality at age x for the single population and $\mu^M(x)$ is the force of first marriage (defined of course only for the never-married population). By relations developed above, the number of single persons in a cohort at age x , $S(x)$, will be found by cumulating the forces of decrement:

$$\begin{aligned} S(x) &= S(0) \cdot {}_x p_0 = S(0) \cdot e^{-\int_0^x \mu^s(a) da} \\ &= S(0) \cdot e^{-\int_0^x [\mu^{Ds}(a) + \mu^M(a)] da} \end{aligned}$$

where $S(0)$ is the number who were single in the cohort at birth.