

## Life tables in Palaeodemography: a Methodological Note

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**ABSTRACT** Several errors in the early literature discussing life-table analysis of skeletal populations are potentially misleading to the researcher unacquainted with the mathematical methods of palaeodemography. Additional errors document the hazards of borrowing life-table methods and equations from other applications without fully realizing their context, interpretation, and the potential restrictions on their use. A simple generalization of the life-table equations explicitly to reveal their dependence on the *entry age* and *width* of the age intervals used will facilitate the correct computation of life tables and readily accommodate the use of unconventional or otherwise non-standard cohorts. A general procedure for computing a life table for a skeletal population is presented, and a numerical example is included to illustrate the method.

*Keywords:* Life table, palaeodemography, mortality, population structure, biostatistics.

Although the construction of a life table for a skeletal population follows a simple procedure, some confusion exists in the early literature as to the correct form for several of the life-table equations. In many cases these errors are inadvertent transcriptive or typographic mistakes, but in other instances they document the borrowing and misapplication of life-table methods from another context. The errors are in any case confusing to the uninitiated, and the formulae in which they occur will not yield correct results if applied as published. The purpose of this article consequently is threefold: (i) to document several errors and discuss their origins; (ii) to clarify two concepts in demography that facilitate the correct application of life-table equations, regardless of the specific age intervals chosen for the analysis; and (iii) to present a general procedure for computing a life table for a skeletal population, and provide a numerical illustration. It is appropriate to emphasize at the outset that the intended audience is not the experienced palaeodemographer, but rather the researcher less familiar with numerical methods of skeletal population analysis, whose specific interests nevertheless may be complemented by a general understanding of life-table construction.

There are two reasons why errors in published life tables are not more common. First, the

researcher familiar with the theory and methods of palaeodemography and of life-table construction has recognized the errors documented here and has simply ignored them. Second, and perhaps more commonly, many researchers in palaeodemography have not found it necessary to develop a life-table program from first principles, and so have never directly confronted the errors and ambiguities in the literature that might easily confound their efforts. A researcher with palaeodemographic interests is more likely to obtain an existing program for life-table construction with the results that (i) the analysis of mortality data may begin immediately, and (ii) the researcher is not encouraged to review the published equations for accuracy and validity.

A predictable objection to this article is that the errors discussed here are found in the early, formative literature dealing with life-table analysis in palaeoanthropology, and need not be unearthed and illuminated. The objection would be valid except for the fact that the errors appear in publications whose intent is in part to serve as primers and tutorials on the use of life tables for the study of populations. These publications are early, but nevertheless continue to serve as important references, which the newcomer to palaeodemography is likely to consult for the fundamental theory and methods of life-table

analysis. By documenting these errors, researchers working without the benefit of a life-table program, or who are designing a program, may be spared much needless frustration, and be further encouraged to consider life-table analysis as a useful tool for investigating the interaction between cultural processes and biological populations.

## Errors

The most frequent errors in the literature are found in the equation for approximating the stationary age structure  $L_x$  of a population. An article by Deevey<sup>1</sup> contains the following (incorrect) approximation for the age structure  $L_x$

$$L_x = \frac{l_x + l_{x+1}}{2} \quad (1)$$

If the apparent simplifications were made, the equation would state that age structure  $L_x$  is equal to survivorship  $l_x + 1/2$ . This is certainly a typographical error; the intended symbol  $l_{x+1}$  was printed incorrectly as  $l_x + 1$ , yet this incorrect equation also appears in a palaeodemographic study by Swedlund and Armelagos<sup>2</sup> who cite Deevey's article as a source for their methodology. A more recent publication by Swedlund and Armelagos<sup>3</sup> also contains an incorrect expression for approximating the age structure  $L_x$

$$L_x = \left( \frac{L_x + L_{x+1}}{2} \right)^n \quad (2)$$

Here 'L' has been used on the right-hand side of the equation where 'l' was intended, with the result that the population age structure at age  $x$  has been defined in terms of itself.

Additional errors are found in the published form of the integral for the exact age structure  $L_x$ . This type of error usually is less troublesome since population age structure generally is not computed directly from the integral form for  $L_x$ . Instead, the integral is replaced routinely by a piecewise continuous approximation before computing  $L_x$  values. A special form of the integral for  $L_x$  is presented correctly by Deevey,<sup>1</sup>

but in two publications by Swedlund and Armelagos<sup>2,3</sup> the integral is incorrect. In the earlier article, the differential element  $dx$  is absent from the integral. In the 1976 publication the differential element  $dx$  has been mis-stated as the quantity  $d_x$ , or the proportion of individuals in the population who die at age  $x$ . Moreover, in the same equation the limits of integration (from  $x$  to  $x + 1$ ) have vanished and the quotient  $(x + 1)/x$  has appeared as part of the integrand. The result is the following non-sequitur<sup>3</sup>

$$L_x = \int \frac{x+1}{x} l_x d_x \quad (3)$$

The age structure  $L_x$  now has become a function not only of survivorship  $l_x$  but also of age interval  $x$  and the proportion of deaths  $d_x$  in each cohort.

There also is an occasional tendency to blur the important distinction between a formal variable of integration and a true independent variable used to denote a quantity involved in the analysis. The inclination is to use the symbol 'x' as a 'universal variable' without regard for its intended meaning. This results in expressions such as<sup>1</sup>

$$\int_x^{x+1} l_x dx \quad (4)$$

when in fact the following is intended

$$\int_x^{x+1} l_t dt \quad (5)$$

There are important differences between the two, both as mathematical expressions and as descriptions of the underlying demographic processes.

In the process of adapting the life-table studies on natural populations of animals (e.g. Deevey<sup>1</sup>) to skeletal human populations (e.g. Swedlund and Armelagos<sup>2</sup>), the definition of the *entry age* into a cohort, or age interval, and the effect of *cohort width* on the computation of age structure  $L_x$ , became critical issues. (Strictly speaking, *cohort* refers to a group of people, whereas *age interval* denotes a set of chronological ages that are treated uniformly by some analysis. Unless the context requires it, the terms will be used here interchangeably.) The

## Life Tables in Palaeodemography

133

Table 1. Life table for Meinarti Cemetery, AD 1050-1150, Levels 9-7.<sup>2,3</sup>

Age	Cohort	$d'(x)$	$d(x)$	$l(x)$	$q(x)$	$L(x)$	$T(x)$	$e(x)$
0	0	10	3.92	100.0	0.039	98.04	2180.39	21.8
1	1	15	5.88	96.08	0.061	93.14	2082.35	21.7
2	2-6	44	17.25	90.20	0.191	407.84	1989.22	22.1
7	7-10	17	6.67	72.94	0.091	278.43	1581.37	21.7
11	11-15	8	3.14	66.27	0.047	323.53	1302.94	19.7
16	16-20	7	2.75	63.14	0.043	308.82	979.41	15.5
21	21-25	50	19.61	60.39	0.325	252.94	670.59	11.1
26	26-30	33	12.94	40.78	0.317	171.57	417.65	10.2
31	31-35	25	9.80	27.84	0.352	114.71	246.08	8.8
36	36-40	15	5.88	18.04	0.326	75.49	131.37	7.3
41	41-45	19	7.45	12.16	0.613	42.16	55.88	4.6
46	46-50	11	4.31	4.71	0.917	12.75	13.73	2.9
51	51+	1	0.39	0.39	1.000	0.98	0.98	2.5

concepts of entry age and cohort width are embedded in any life-table analysis, but the nature of skeletal population data requires that they receive explicit consideration. Very often neither published equations nor accompanying discussions distinguish the two adequately or emphasize their role in a general formulation of life-table equations.

The *entry age* is defined as the chronological age at which an age interval or cohort begins. By *cohort width* is meant the set of ages-at-death that are contained in the given age interval. In many published life tables the ages given are actually entry ages into cohorts of varying widths. Age '7', for example, in the life table for Meinarti cemetery<sup>4</sup> (adapted here as Table 1), is the entry age only for a cohort of width 4 years, that is, a cohort containing ages-at-death of 7, 8, 9 and 10. Similarly, the ages-at-death of 11, 12, 13, 14 and 15 form a cohort of width 5 years, labelled in the life table only as age '11'.

A clear distinction between entry age and cohort width is essential in understanding the integral form for population age structure  $L_x$ , and especially in formulating a numerical approximation for  $L_x$ . The point is illustrated effectively by reviewing the equation found in Deevey.<sup>1</sup> After correcting the typographical error, the equation reads:

$$L_x = \frac{l_x + l_{x+1}}{2} \quad (6)$$

The equation technically is correct only for cohorts of 1-year width. Deevey, discussing life tables for populations of animals, does in fact use

cohorts of 1-year width, and so the equation presented is valid in that context.

Problems develop when the equation that Deevey uses is applied to a population in which some or all of the cohorts have widths different from 1 year. This appears to be what happened in an early article by Swedlund and Armelagos.<sup>2</sup> The incorrect equation in Deevey<sup>1</sup> was duplicated and used to generate a life table for the skeletal population from Meinarti cemetery, a Nubian Christian burial site.<sup>5</sup> The authors recognized the typographical error but did not perceive the 1-year cohort width implicit in Deevey's formulation. Their 1969 article consequently contains life tables in which the age structure has been derived on the basis of a constant cohort width of 1 year. This is strictly correct only for the first two age intervals in their tables, as the remaining cohorts have widths of 4 and 5 years. Except for Tableau I, the tables in the 1969 publication contain incorrect values of  $L_x$ . The same tables, however, contain approximately correct values for the expectation of life  $e_x$ , a quantity that is derived from the  $L_x$  values. On the basis of the equations presented in the article, these values for  $e_x$  cannot be obtained; the errors and inconsistencies were recognized, however, and the tables reappear with corrected  $L_x$  values in subsequent publications.<sup>3,4</sup>

The width of an age interval also is critical in expressing the general integral form for population age structure. For example, when Deevey, Swedlund and Armelagos, and others present the following integral for  $L_x$

$$L_x = \int_x^{x+1} l_x dx \quad (7)$$

it must be realized (apart from the double role played here by the symbol 'x') that this integral is correct only for a cohort of entry age x and width of 1 year. The ambiguity largely is the fault of the notation employed. In equation (7) x is the entry age of the xth cohort, whereas x+1 is intended to represent the entry age of the immediately following cohort, and is not necessarily the value of x incremented by 1 year. In order to compute  $L_x$  for the age interval 10-14, for example, the integral must be evaluated from age 10 ('x', the entry age of the cohort, and the lower limit of integration) to age 15 ('x+1', the entry age of the following cohort, and the upper limit of integration). This is confusing at best, and technically accurate only when x is regarded strictly as a discrete variable that assumes only the values of the cohort entry ages (Keyfitz and Flicger<sup>6</sup> make a similar point). In the context of life tables for animal populations, cohorts characteristically all have widths of 1 year, and so the notation is of course appropriate.<sup>1,7,8</sup>

The ambiguity could be resolved by subscripting x to indicate that the entry age for a specific cohort is intended. The integral for  $L_x$  could then be stated as

$$L_{x_i} = \int_{x_i}^{x_i+1} l(t) dt \quad (8)$$

or, equivalently, by making a change of variable

$$L_{x_i} = \int_0^{n_i} l(x_i + t) dt \quad (9)$$

where  $x_i$  and  $n_i$  are the entry age and the width, respectively, of the  $i$ th cohort. The latter form of the integral for  $L_x$  is found in Keyfitz and Flicger,<sup>6</sup> and with a slight variation in Bennett.<sup>9</sup> The advantage offered by this notation is the ability precisely and unambiguously to specify the quantities involved in the equation. On the other hand, the use of doubly subscripted variables imparts an esoteric if not intimidating appearance to the otherwise uncomplicated procedure of

computing a life table. A functional compromise is to use a single subscript  $i$  to index the discrete age intervals directly (see, for example, Chiang<sup>10</sup>). The integral for age structure, or stationary age distribution  $L_i$ , would then take the form

$$L_i = \int_0^{n_i} l(x_i + t) dt \quad (10)$$

where it is understood that the subscript  $i$  refers to the  $i$ th age interval, whose entry age  $x_i$  and width  $n_i$  have been specified elsewhere. The trapezoid approximation to  $L_i$  then can be expressed as

$$L_i = \frac{n_i}{2} (l_i + l_{i+1}) \quad (11)$$

which, except for errors in notation, is the formula provided by Swedlund and Armelagos.<sup>3</sup> This notational scheme suffers no loss of information, and the use of the single subscript directly to index the age intervals facilitates the development of a program for computing life tables.

The use of existing life-table methods and equations, without a full understanding of their context and interpretation, and possibly restricted applicability, can unwittingly lead to their inappropriate use with population data that have been summarized using a different set of entry ages and cohort widths. Even when life-table equations are presented correctly, the importance of cohort width may remain obscure. Hassan,<sup>11</sup> for example, briefly summarizes the life-table equations for cohort widths of 1 and 5 years, but does not discuss the general form the equations will take for an arbitrary cohort width of  $n$  years, nor are the general equations necessarily discernible from the specific. In palaeodemography, where the age resolution obtainable from skeletal data can vary dramatically, it is especially important that discussions of life-table construction clearly separate the quantities of entry age and cohort width, and explicitly reveal the dependence of the computed quantities on both. This allows the researcher working with skeletal material the option of using 'non-standard' cohort widths should the nature of the data require it.

### Generating a life table for a skeletal population

To integrate the salient points of the preceding discussion, and further clarify the concepts of entry age and cohort width, a brief demonstration of life-table construction for a skeletal population is provided. Many refinements are possible, and even desirable under certain conditions, but the method presented here is in common use.<sup>2,3</sup> Sufficient discussion of the underlying principles is provided so that a functional life-table program could; if necessary, be produced by algorithmically following the procedure described and using the equations provided. A numerical example, using a data set collected by the author<sup>12</sup> is provided to illustrate the method.

The construction of a life table generally begins with a data set consisting of age-at-death, and perhaps sex, for the members of a skeletal population. The first step in generating the life table is to tabulate the numbers of deaths occurring in a pre-defined series of age intervals. Because the use of age intervals is so fundamental to demographic work, their selection and treatment becomes important. The age interval is based on the concept of a *cohort*, or a group of individuals who are born into an age interval together and experience identical mortality rates throughout their lives. The cohort is an idealization, but it forms

a useful theoretical concept in demographic analysis.

A given age interval  $i$  is defined by two quantities, an entry age  $x_i$  and a width  $n_i$ . Specification of these two quantities depends considerably on the age resolution obtainable from analysis of the skeletal population. For human populations and for many animal populations, there is little advantage in working with cohorts of width less than 1 year, and skeletal analysis fails to provide such resolution. To increase the sample sizes in each age interval, individuals are commonly pooled into age intervals of 5-year widths, although the youngest age intervals often have widths of a single year. Typical age intervals for a skeletal population are 0 (less than 1 year), 1-4, 5-9, 10-14, . . . , 80-84 and 85+, with corresponding entry ages of 0, 1, 5, 10, . . . , 80 and 85 years and widths of 1, 4, 5, 5, . . . , 5 and 5 years. The width of the terminal cohort is variable, and may be adjusted to include the oldest individual in the population under study.<sup>13</sup> Table 2 is an example life table for a skeletal population consisting of 355 individuals. The cohorts and their corresponding entry ages and widths form the first three columns in the table. The width of the terminal cohort is given as 16 years, since the oldest individual in this population was aged 101 years at death.

With age intervals established for the population, and using the notational system

Table 2. Example life table based on 355 individuals.<sup>12</sup> (Forest Hill Cemetery, Kansas City, MO.)

Age	Cohort	$W$	$d'(x)$	$d(x)$	$l(x)$	$q(x)$	$L(x)$	$T(x)$	$e(x)$
0	0	1	7	1.97	100.00	0.020	99.01	6696.34	67.0
1	1- 4	4	5	1.41	98.03	0.014	389.30	6597.32	67.3
5	5- 9	5	4	1.13	96.62	0.012	480.28	6208.03	64.3
10	10-14	5	3	0.85	95.49	0.009	475.35	5727.75	60.0
15	15-19	5	2	0.56	94.65	0.006	471.83	5252.39	55.5
20	20-24	5	2	0.56	94.08	0.006	469.01	4780.56	50.8
25	25-29	5	3	2.25	93.52	0.024	461.97	4311.55	46.1
30	30-34	5	3	2.25	91.27	0.025	450.70	3849.58	42.2
35	35-39	5	3	2.25	89.01	0.025	439.44	3398.87	38.2
40	40-44	5	3	2.25	86.76	0.026	428.17	2959.44	34.1
45	45-49	5	10	2.82	84.51	0.033	415.49	2531.27	30.0
50	50-54	5	16	4.51	81.69	0.055	397.18	2115.77	25.9
55	55-59	5	16	4.51	77.18	0.058	374.65	1718.59	22.3
60	60-64	5	19	5.35	72.68	0.074	350.00	1343.94	18.5
65	65-69	5	43	12.11	67.32	0.180	306.34	993.94	14.8
70	70-74	5	38	10.70	55.21	0.194	249.30	687.61	12.5
75	75-79	5	56	15.77	44.51	0.354	183.10	438.31	9.8
80	80-84	5	40	11.27	28.73	0.392	115.49	255.21	8.9
85	85+	16	62	17.46	17.46	1.000	139.72	139.72	8.0

described above, the raw death counts in each age interval form the values of  $d'_i$ , listed in the fourth column of Table 2. Each entry in this column specifies the observed number of deaths in the age interval  $i$ . The twelfth cohort, for example, defined by the index value  $i = 12$ , entry age  $x_{12} = 50$ , and width  $n_{12} = 5$ , has  $d'_{12} = 16$  deaths.

The fifth column contains the proportion of individuals in the population dying in each age interval. This is determined using the formula

$$d_i = \frac{d'_i R}{N} \quad (12)$$

where  $N$  is the total number of individuals in the population. The quantity  $R$  is the *radix* of the table, an arbitrary base on which the table is constructed, and representing a standard number of births from which the cohort arises. If the radix is unity,  $d_i$  is interpreted as the probability that a given individual will die within age interval  $i$  (between ages  $x_i$  and  $x_i + n_i$ ). Unity is a useful radix, but 100, 1000 and 100 000 are also commonly used, in which case  $d_i$  is properly interpreted as the number of individuals dying between ages  $x_i$  and  $x_i + n_i$  out of  $R$  births. A radix of 100 has been used in Table 2. For cohort 12 ( $i = 12$ )

$$d_{12} = \left( \frac{16}{355} \right) 100 = 4.51 \quad (13)$$

Following the tabulation of  $d_i$ , the sixth column in Table 2 contains the values of survivorship  $l_i$ . Survivorship represents the number of individuals attaining (surviving to) exact age  $x_i$ , and is obtained by subtracting the deaths in the previous age interval from the survivorship of the same age interval

$$l_i = l_{i-1} - d_{i-1} \quad (14)$$

For computational purposes the equation is more useful in the following form

$$l_{i+1} = l_i - d_i \quad (15)$$

These survivorships are computed by setting the survivorship of the initial age interval ( $l_1$ ) equal

to the radix  $R$  of the life table. Subsequent  $l_i$  values are computed using equation (15). If a radix different from unity is used, the survivorship value represents a number of individuals rather than a simple proportion of the overall population. From Table 2 the age interval  $i = 12$  has

$$l_{12} = l_{11} - d_{11} = 84.51 - 2.82 = 81.69 \quad (16)$$

Age-specific mortality rates  $q_i$  form the seventh column of the table. The value of  $q_i$  specifies the mortality rate experienced by individuals in age interval  $i$ , and is equivalent to the probability that an individual reaching age  $x_i$  will die within age interval  $i$ , i.e. before reaching age  $x_i + n_i$ . The mortality rates are computed by taking the ratio of those dying during age interval  $i$  to those living at the beginning of the same age interval:

$$q_i = \frac{d_i}{l_i} \quad (17)$$

For cohort 12 in Table 2 this yields

$$q_{12} = \frac{d_{12}}{l_{12}} = \frac{4.51}{81.69} = 0.055 \quad (18)$$

The age structure, or stationary age distribution  $L_i$ , is the next quantity in the life table, determined by integrating the survivorship  $l_i$  over the width of the cohort. The result specifies the number of persons alive in a given age interval (between the chronological ages  $x_i$  and  $x_i + n_i$ ) in a population in which exactly  $R$  births occur each year. An equivalent interpretation of  $L_i$  is the total number of person-years lived between ages  $x_i$  and  $x_i + n_i$  out of  $R$  births.

For living populations, information regarding the intrinsic rate of growth of the population is often obtainable, permitting the survivorship function  $l_i$  used in the integration to be realistically specified. For skeletal populations, data on birth and death rates generally are not available, but a satisfactory assumption is that the population represented was a stationary one. (In a stationary population, birth rate and death rate are equal, net migration is zero, and the relative age distribution is constant.) The assumption is a

*Life Tables in Palaeodemography*

reasonable one, as no living population can sustain a non-zero growth rate for very long. For a stationary population the survivorship changes at a constant rate over any given age interval, and the integral for the stationary age distribution  $L_i$  takes the form

$$L_i = \int_0^{n_i} l(x_i + t) dt = \int_{x_i}^{x_{i+1}} l(t) dt \quad (19)$$

The integral can be approximated numerically using the trapezoid rule, resulting in

$$L_i = \frac{n_i}{2}(l_i + l_{i+1}) \quad (20)$$

Except for errors in notation, this is the formula found in Swedlund and Armelagos.<sup>3</sup> When the index  $i$  reaches the last cohort in the life table,  $l_{i+1}$  should be taken as zero when computing the terminal  $L_i$  value. For the twelfth cohort in Table 2

$$L_{12} = \frac{n_{12}}{2}(l_{12} + l_{13}) = \frac{5}{2}(81.69 + 77.18) = 397.18 \quad (21)$$

The ninth column in Table 2 is  $T_i$ , or the total number of person-years lived by the members of the cohort  $i$  beyond age  $x_i$ :

$$T_i = \int_0^{\infty} l(x_i + t) dt = \int_{x_i}^{\infty} l(t) dt \quad (22)$$

The  $T_i$  integral is similar to that for the stationary age distribution  $L_i$ , and this permits the integral for  $T_i$  to be approximated in terms of the  $L_i$

$$T_i = \sum_{k=i}^{\infty} L_k \quad (23)$$

where  $k$  is a dummy variable used to index the various age intervals. In other words,  $T_i$  is the sum of the  $L_i$  values from age interval  $i$  to infinity (or, practically, the last age interval in the life table). The  $T_i$  value for age interval  $i=12$  in Table 2, for example, is the sum of the  $L_i$  values

from age interval 12 to the final age interval in the table

$$T_{12} = (397.18 + 374.65 + 350.00 + \dots + 139.72) = 2115.77 \quad (24)$$

The tenth and final column in the life table is  $e_i$ , or the expectation of life for individuals reaching age interval  $i$ . This is equivalent to the average lifetime remaining to those individuals attaining age interval  $i$ . The expectation of life  $e_i$  is computed as the average value of the survivorship curve from age interval  $i$  to infinity

$$e_i = \frac{\int_0^{\infty} l(x_i + t) dt}{l_i} = \frac{\int_{x_i}^{\infty} l(t) dt}{l_i} \quad (25)$$

The integral in the latter equation is just  $T_i$ , however, which leads to the result

$$e_i = \frac{T_i}{l_i} \quad (26)$$

For cohort 12, dividing  $T_{12}$  by  $l_{12}$  yields the expectation of life at age  $x=50$

$$e_{12} = \frac{2115.77}{81.69} = 25.9 \quad (27)$$

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