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Methods Protocol for the Human Mortality Database

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Introduction to V6 of the Methods Protocol

This version of the Human Mortality Database Methods Protocol (Version 6) introduces two changes to the way mortality rates and life tables are constructed. First, a new method is implemented to calculate a_0, the mean age at death for children who died in their first year of life. This was motivated by the fact that, in low mortality populations, the Coale and Demeny formula used until now in the HMD tended to under-estimate a_0. Detailed rationale and the equations connecting a_0 with infant mortality are provided in the study by Andreev and Kingkade (2015). Implementation of this method is described in section 7.1 below.

Second, birth-by-month data have been collected and are now used to more accurately estimate population exposures. Until now, we used the classic approach which assumes that births are uniformly distributed throughout the calendar year. In the event of a sharp discontinuity in the monthly distribution of births within a calendar year, this assumption results in the incorrect estimation of population exposures and induces false cohort effects on mortality surfaces when these surfaces are based on Lexis squares. Within the HMD universe, the non uniform distribution of births has been most pronounced at the beginning and at the end of the first and second World Wars in many European countries. More details on the new method are provided in section 6 and Appendix E below.

[1] This document grew out of a series of discussions held in various locations beginning in June 2000. The five individuals listed as authors wrote the original version and/or have actively contributed to subsequent versions, including through the development of additional methods. Several others assisted with the creation of this document through their active participation in meetings and ongoing discussions via email. The authors are fully responsible for any errors or ambiguities. They thank Georg Heilmann for his assistance with some of the graphs.

Last Revised: January 26, 2021 (Version 6)

Table of Contents

List of Figures

List of Tables

1 Introduction

The Human Mortality Database (HMD) is a collaborative project sponsored by the University of California at Berkeley (United States) and the Max Planck Institute for Demographic Research (Rostock, Germany).[2] The purpose of the database is to provide researchers around the world with easy access to detailed and comparable national mortality data via the Internet.[3] The database contains original life tables for almost 40 countries or areas, as well as all raw data used in constructing those tables.[4]

[2] The contribution of UC Berkeley to this project is funded in part by a grant from the U.S. National Institute on Aging. A third team of researchers based at the City University of New York is also working directly on this project. In addition, the project depends on the cooperation of national statistical offices and academic researchers in many countries.

[3] The HMD is accessible through either of the following addresses: www.mortality.org and www.humanmortality.de.

[4] By design, populations in the HMD are restricted to those with data (both vital statistics and census information) that cover the entire population and that are very nearly complete. Thus, the HMD covers almost all of Europe, plus Australia, Canada, Japan, New Zealand, Chile, Israel, Hong Kong, Republic of Korea, Taiwan and the United States. Outside this group,very few countries possess the kind of data required for the HMD. Few other regions and countries are still being considered for inclusion. In an effort to improve access to mortality information for countries that do not meet the strict data requirements of the HMD, we have also assembled a large collection of life tables constructed by other organizations or individuals. This collection, known as the Human Lifetable Database (HLD),

The raw data generally consist of birth and death counts from vital statistics, plus population counts from periodic censuses and/or official population estimates. Both general documentation and the individual steps followed in computing mortality rates and life tables are described here. More detailed information–for example, sources of raw data, specific adjustments to raw data, and comments about data quality–are covered separately in the documentation for each population.

We begin by describing certain general principles that are used in constructing and presenting the database. Next, we provide an overview of the steps followed in converting raw data into mortality rates and life tables. The remaining sections (including the Appendices) contain detailed descriptions of all necessary calculations.

2 General principles

2.1 Notation and terminology for age and time

Both age and time can be either continuous or discrete variables. In discrete terms, a person *of age* x (or *aged* x) has an exact age within the interval $[x, x+1)$. This concept is also known as *age last birthday.* Similarly, an event that occurs *in calendar year* t (or more simply, *in year* t) occurs during the time interval $[t, t+1)$. It should always be possible to distinguish between discrete and continuous notions of age or time by usage and context. For example, *the population aged* x *at time* t refers to all persons in the age range $[x, x+1)$ at exact time t, or on January 1st of calendar year t. Likewise, *the exposure-to-risk at age* x *in year* t refers to the total person-years lived in the age interval $[x, x+1)$ during calendar year t.

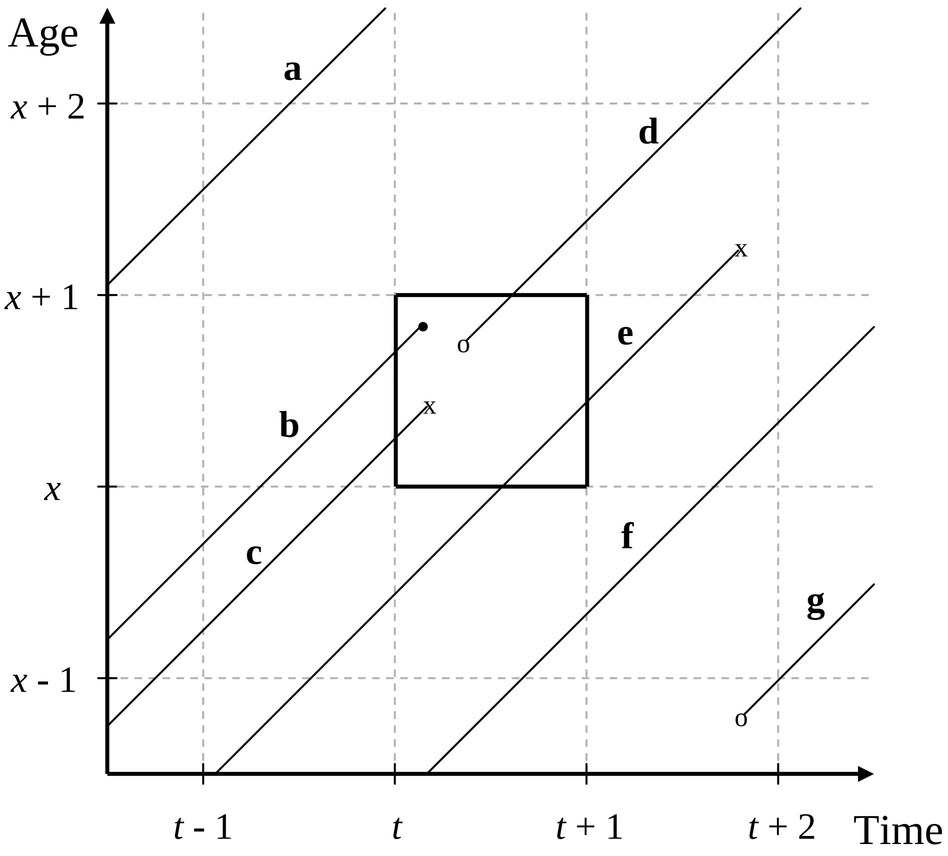
2.2 Lexis diagram

The Lexis diagram is a device for depicting the stock and flow of a population and the occurrence of demographic events over age and time. For our purposes, it is useful for describing both the format of the raw data and various computational procedures. Figure 1 shows a small section of a Lexis diagram that has been divided into 1×1 cells (i.e., one year of age by one year of time). Each 45° line represents an individual lifetime, which may end in death, denoted by **x** (lines **c** and **e**), or out-migration, denoted by a solid circle (line **b**). An individual may also migrate into the population, denoted by an open circle (lines **d** and **g**). Other life-lines may merely pass through the section of the Lexis diagram under consideration (lines **a** and f).

Suppose we want to estimate the death rate for the 1×1 cell that is highlighted in Figure 1 (i.e., for age x to $x+1$ and time t to $t+1$). If the exact coordinates of all life-lines are known, then the exposure-to-risk in person-years can be calculated precisely by adding up the length of each line segment within the cell (of course, the actual length of each segment must be divided by $\sqrt{2}$, since life-lines are 45° from the age or time axes). Following this procedure, the observed death rate for this cell would be 0.91, which is the number of deaths (in this case, one) divided by the person-years of exposure (about 1.1). This is the best estimate possible for the underlying death rate in that cell (i.e., the death rate that would be observed at that age in a very large population subject to the same historical conditions).

includes data for many countries not covered by the HMD. The HLD is available at www.lifetable.de.

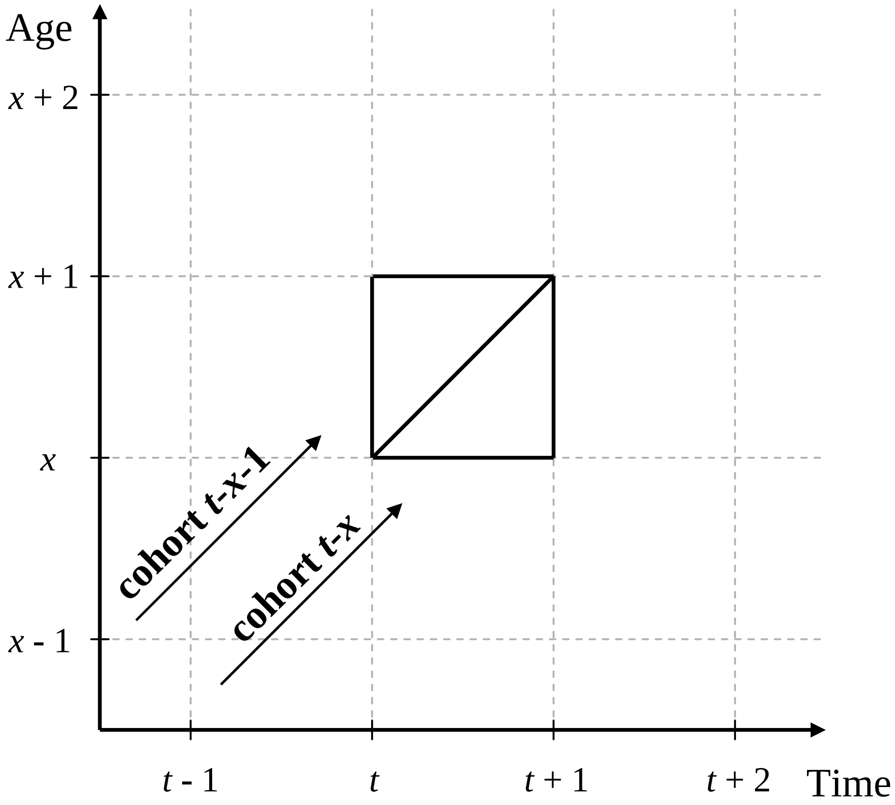
Figure 1: Example of a Lexis Diagram



However, exact life-lines are rarely known in studies of large national populations. Instead, we often have counts of deaths over intervals of age and time, and counts or estimates of the number of individuals of a given age who are alive at specific moments of time. Considering again the highlighted cell in Figure 1, the population count at age x is 2 at time t (lines **b** and **c**) and 1 at time $t+1$ (line **e**). Given only this information, our best estimate of the exposure-to-risk within the cell is merely the average of these two numbers (thus, 1.5 person-years). Using this method, the observed death rate would be $1/1.5 = 0.67$, which is lower than the more precise calculation given above because the actual exposure-to-risk has been overestimated. The estimation of death rates is inevitably less precise in the absence of information about individual life-lines, although estimates based on aggregate data using such a procedure are generally quite reliable for large populations.

Death counts are often available by age, year of death (i.e., period), and year of birth (i.e., cohort). Such counts can be represented by a Lexis triangle, ⊿ or ◸, as illustrated in Figure 2. Death counts at this level of detail are used in many important calculations in the HMD. One of the most important steps in computing the death rates and life tables for the HMD is to estimate death counts by Lexis triangle if these are not already available in the raw data.

Figure 2: Illustration of Lexis triangles



2.3 Standard configurations of age and time

For all data in this collection, age and time are arranged in 1-, 5-, and 10-year intervals. The configuration of a matrix of death rates (or some other quantity) is denoted by 1×1, 5×1, 5×10, etc. In this notation, the first number always refers to the age interval, and the second number refers to the time interval. For example, 1×10 denotes a configuration with single years of age and 10-year time intervals. In the HMD, death rates and life tables are generally presented in six standard configurations: 1×1, 1×5, 1×10, 5×1, 5×5, and 5×10. Furthermore, the database includes estimates of death counts by Lexis triangle and of population size (on January 1^{st}) by single years of age, making it possible for the sophisticated user to compute death rates and life tables in any configuration desired.

All ranges of age and time describe inclusive sets of one-year intervals. For example, the age group 10–14 extends from exact age 10 up to (but not including) exact age 15, and the time period designated by 1980–84 begins at the first moment of January 1, 1980, and ends at the last moment of December 31, 1984. In addition, the following conventions are used throughout the database for organizing information by age and time:

- 5-year time intervals begin with years ending in *0* or *5* and finish with years ending in *4* or *9*;

- 10-year time intervals begin with years ending in *0* and finish with years ending in *9*;
- incomplete 5- or 10-year time intervals are included in presentations of death rates or life tables if data are available for at least 2 years (at either the beginning or the end of the series);
- for raw data, data in one-year age groups are always provided up to the highest age available (followed by an open age interval only if more detailed data are not available);
- for all data on country pages, one-year age groups stop at age 109, with a final category for ages 110 and above;
- for 5-year age groups, the first year of life (age 0) is always separated from the rest of its age group (ages 1–4), and the last age category is for ages 110 and above. Thus, a 5×1 configuration contains data for single years of time with (typically) the following age intervals: 0, 1–4, 5–9, 10–14,. . . , 105–109, 110+.

It is important to note that data shown on country pages by single years of age up to 110+ have sometimes been approximated from aggregate data (e.g., five-year age groups, open age intervals) using the methods described here. Although there are some obvious advantages to maintaining a uniform format in the presentation of death rates and life tables, it is important not to interpret such approximated data literally. In all cases, the user must take responsibility for understanding the sources and limitations of all data provided here.

2.4 Female / male / total

In this database, life tables and all data used in their construction are available for women and men separately and together. In most cases, a single file contains columns labeled *Female*, *Male* and *Total* (note that this is alphabetical order). However, in the case of life tables, which already contain several columns of data for each group, data for these three groups are stored in separate files.

Raw data for women and men are always pooled prior to making *Total* calculations. In other words, death rates and other quantities are not merely the average of the separate values for females and males. For this reason, all *Total* values are affected by the relative size of the two sexes at a given age and time.

2.5 Periods and cohorts

Raw data are usually obtained in a period format (i.e., by the year of occurrence rather than by year of birth). Deaths are sometimes reported by age and year of birth, but the statistics are typically collected, published, and tabulated by year of occurrence. Although raw data are presented here in a period format only, death rates and life tables are provided in both formats if the observation period is sufficiently long to justify such a presentation. Death rates are given in a cohort format (i.e., by year of birth) if there are at least 30 consecutive calendar years of data for that cohort.

Cohort life tables are presented if there is at least one cohort observed from birth until extinction.[5] In that case, life tables are provided for all extinct cohorts and for some almost-extinct cohorts as well.[6]

2.6 Adjustments to raw data

Most raw data require various adjustments before being used as inputs to the calculations described here. The most common adjustment is to distribute persons of unknown age (in either death or census counts) across the age range in proportion to the number of observed individuals in each age group. Another common adjustment is to split aggregate data into finer age categories—in the case of death counts, from 5×1 to 1×1 data, and from 1×1 data to Lexis triangles[7].

2.7 Format of data files

Raw data for this database have been assembled from various sources. However, all raw data have been assembled into files conforming to a standardized format. There are different formats for births, deaths, census counts, and population estimates. The raw data files on the web page are always presented in one of these standardized formats. Output data—such as exposure estimates, death rates, and life tables—are also presented in standardized formats.

3 Steps for computing mortality rates and life tables

There are six steps involved in computing mortality rates and life tables for the core section of the HMD. Computational details are provided in later sections of this document, including the appendices. Here is just an overview of the process:

1. Births. Annual counts of live births by sex are collected for each population over the longest possible time period. At a minimum, a complete series of annual birth counts is needed for the time period over which mortality rates and period life tables are computed. These counts are used mainly for estimating the size (on January 1st of each year) of individual cohorts from birth until the time of their first census, and for other adjustments based on relative cohort size. When available, birth counts by month are recorded as well; these are used to account for non-uniformity in the temporal distribution of events when estimating exposure-to-risk (see section 6 and Appendix E).

2. Deaths. Death counts are collected at the finest level of detail available—ideally, cross-classified by age, period and cohort (Lexis triangles). Sometimes, however, death counts

[5] An extinct cohort is one whose members are assumed to have all died by the end of the observation period. A rule for identifying the most recent extinct cohort is given later in section 5.3.

[6] A simple decision rule is used to determine when it is acceptable to compute life tables for almost-extinct cohorts. In such cases, death rates for ages not yet observed are based on the average experience of previous cohorts. These procedures are described in section 7.2.2.

[7] These two common procedures are described in sections 4.1 and sections 4.2–4.4, respectively.

are available only for 1×1 Lexis squares or 5×1 Lexis rectangles. Before making subsequent calculations, deaths of unknown age are distributed proportionately across the age range, and aggregated deaths are split into finer age categories. Additional adjustments or *ad hoc* estimations may be necessary, depending on the characteristics of the raw data for a particular population. Any such adjustments are described in the population-specific documentation, and are summarized in Appendix F.

3. Population size. Below age 80, estimates of population size on January 1st of each year are either obtained from another source (most commonly, official estimates) or derived using intercensal survival methods. In most cases, all available census counts are collected for the time period over which mortality rates and life tables are computed. The maximum level of age detail is always retained in the raw data and used in subsequent calculations. When necessary, persons of unknown age are distributed proportionately into other age groups before making subsequent calculations. Above age 80, population estimates are derived by the method of extinct generations for all cohorts that are extinct (see section 5.3 for extinction rule), and by the survivor ratio method for non-extinct cohorts aged 90 or older at the end of the observation period. For non-extinct cohorts aged 80 to 89 at the end of the observation period, population estimates are obtained either from another source or by applying the method of intercensal survival.

4. Exposure-to-risk. Estimates of the population exposed to the risk of death during some age-time interval are based on annual (January 1st) population estimates, with small corrections that reflect the timing of deaths during the interval. Period exposure estimations are based on assumptions of uniformity in the distribution of events except when historical monthly birth data are available.

5. Death rates. For both periods and cohorts, death rates are simply the ratio of death counts and exposure-to-risk estimates in matched intervals of age and time.

6. Life tables. Period death rates are converted to probabilities of death by a standard method. Cohort probabilities of death are computed directly from raw data, but they are related to cohort death rates in a consistent way. These probabilities of death are used to construct life tables.

4 Common adjustments to raw data

In this section, we give formulas for four common adjustments to raw data: 1) redistributing deaths of unknown age, 2) splitting 1×1 death counts into Lexis triangles, 3) splitting 5×1 death counts into 1×1 data, and 4) splitting death counts in open age intervals into 1×1 data.[8]

[8] In recent years, some national statistical offices have begun reporting deaths by year of occurrence and by year of registration (these may differ if registration was delayed). In such cases, we tabulate deaths according to the year in which they occurred. If data are not available by Lexis triangle, we split them into triangles using the methods described in this document. If deaths that were registered late are available in the same format as other deaths, we first sum the two sets of data and then split them into triangles.

4.1 Distributing deaths of unknown age

The most common adjustment to raw data involves distributing observations (either deaths or census counts) where age is unknown into specific age categories. In general, such observations are distributed proportionally across the age range.

For example, suppose that death counts are available for individual triangles of the Lexis diagram but that age is unknown for some number of deaths. Formally, let

$$\begin{aligned}
D_L(x,t) &= \text{number of lower-triangle deaths recorded among those aged } [x,x+1) \text{ in year } t;\\
D_U(x,t) &= \text{number of upper-triangle deaths recorded among those age } [x,x+1) \text{ in year } t;\\
D_{\text{Unk}}(t) &= \text{number of deaths of unknown age in year } t;\\
D_{\text{Tot}}(t) &= \text{total number of deaths in year } t\\
&= \sum_x [D_L(x,t)+D_U(x,t)] + D_{\text{Unk}}(t) \qquad .
\end{aligned}$$

Then, the following pair of equations redistributes deaths of unknown age proportionally across upper and lower Lexis triangles over the full age range:

$$\begin{aligned}
D_L^*(x,t) &= D_L(x,t) + D_{\text{Unk}}(t)\cdot\frac{D_L(x,t)}{\sum_x [D_L(x,t)+D_U(x,t)]}\\
&= D_L(x,t)\cdot\left(\frac{D_{\text{Tot}}(t)}{D_{\text{Tot}}(t)-D_{\text{Unk}}(t)}\right)
\end{aligned} \tag{1}$$

and

$$\begin{aligned}
D_U^*(x,t) &= D_U(x,t) + D_{\text{Unk}}(t)\cdot\frac{D_U(x,t)}{\sum_x [D_L(x,t)+D_U(x,t)]}\\
&= D_U(x,t)\cdot\left(\frac{D_{\text{Tot}}(t)}{D_{\text{Tot}}(t)-D_{\text{Unk}}(t)}\right)
\end{aligned} \qquad , \tag{2}$$

for all ages x in year t.[9]

These calculations typically result in non-integer death "counts" for individual ages and Lexis triangles. In fact, such numbers are no longer true counts but rather estimated counts. However, since they are our best estimates of actual death counts, it is appropriate to use them in subsequent calculations. In all formulas given below, it is assumed that deaths of unknown age have been distributed proportionally, if needed, and the superscript, *, used in this section is suppressed for the sake of simplicity.

When raw death counts are available in a 1×1 or 5×1 format, deaths of unknown age (if any) are distributed across the existing age groups before splitting the raw counts into Lexis triangles, as described below. Note, however, that the final result of these calculations would not change if aggregate data were first split into finer age categories before redistributing deaths of unknown age. In other words, the ordering of these procedures does not matter.

Like death counts, census tabulations may contain persons of unknown age. If needed, a similar adjustment is made before proceeding with the calculations used for estimating population on January 1$^{\text{st}}$ as described in a later section.

[9] This adjustment reflects an assumption that the probability of age not being reported is independent of age itself.

4.2 Splitting 1x1 death counts into Lexis triangles

Death counts are often available only in 1×1 Lexis squares ⧄ and not in Lexis triangles ◸, ◿ .[10]Since many of our subsequent calculations are based on Lexis triangles, it is necessary to devise a method for splitting such 1×1 death data into triangles. In general, the proportion of deaths in lower and upper Lexis triangles varies with age, as shown by the regression model presented later in this section (see also Vallin (1973)). Nevertheless, an adequate procedure in many cases is simply to assign half of each 1×1 death count to the corresponding lower and upper triangles, since errors of overestimation for one triangle (in a lower-upper pair) are typically balanced by errors of underestimation for the other triangle in almost all subsequent calculations. This simple procedure was applied successfully to the analysis of mortality above age 80 in the Kannisto-Thatcher database (Andreev et al. 2003).

However, for a collection of mortality data in both period and cohort formats covering the entire age range, a more complicated procedure is needed for at least two reasons: (1) deaths in the first year of life are heavily concentrated in the lower triangle and should not be split in half, and (2) at any age, the distribution of deaths across the two triangles is affected by the relative size of the two cohorts, which may substantially fluctuate due to historical events such as abrupt falls and jumps in births due to the two world wars. Once the procedure for splitting 1×1 deaths is modified to take these matters into account, it is only a small step further toward a complete model that adjusts for several factors that are known to affect the distribution of deaths by Lexis triangle.

For these reasons, we have developed a regression equation for use in splitting 1×1 deaths into Lexis triangles. The equation is based on a multiple regression analysis of data for three countries, which is described more fully in Appendix A. The equation is expressed in terms of the proportion of deaths that occur in the lower triangle. In general, we denote this proportion as follows:

$$\pi_d(x,t) = \frac{D_L(x,t)}{D_L(x,t) + D_U(x,t)} \qquad . \tag{3}$$

When the values of $D_L(x,t)$ and $D_U(x,t)$ are not known, our task is to derive an estimated proportion in the lower triangle, denoted $\hat{\pi}_d(x,t)$. From this quantity, we compute estimates of lower- and upper-triangle deaths:

$$\hat{D}_L(x,t) = \hat{\pi}_d(x,t) \cdot D(x,t) \quad \text{and} \quad \hat{D}_U(x,t) = D(x,t) - \hat{D}_L(x,t) = [1 - \hat{\pi}_d(x,t)] \cdot D(x,t) \qquad ,$$

where $D(x,t)$ is the observed number of deaths in the 1×1 Lexis square.

[10] Sometimes death counts are available only by period-cohort parallelogram (i.e., holding calendar year and birth cohort constant, but covering more than one age year). Within each single year birth cohort, these deaths are simply split in half into the two respective Lexis triangles. Similarly, death counts may be available by age-cohort parallelogram (i.e., age and birth cohort are constant, but the parallelogram covers more than one calendar year), in which case we also split the deaths in half into Lexis triangles (for year t and year $t+1$).

The equation for estimating $\pi_d(x,t)$ differs by sex. For women, the equation is as follows:

$$\begin{aligned}\hat{\pi}_d(x,t) = 0.4710 &+ \hat{\alpha}_x^F + 0.7372 \cdot [\pi_b(x,t) - 0.5] \\ &+ 0.1025 \cdot I(t=1918) - 0.0237 \cdot I(t=1919) \\ &- 0.0112 \cdot \log \mathrm{IMR}(t) \\ &- 0.0688 \cdot \log \mathrm{IMR}(t) \cdot I(x=0) \\ &+ 0.0268 \cdot \log \mathrm{IMR}(t) \cdot I(x=1) \\ &+ 0.1526 \cdot [\log \mathrm{IMR}(t) - \log(0.01)] \cdot I(x=0) \cdot I(\mathrm{IMR}(t) < 0.01) \qquad . \end{aligned} \tag{4}$$

In this equation, *log* refers to the natural logarithm. The indicator function, $I()$, equals one if the logical statement within parentheses is true and zero if it is false. Dummy variables for years 1918 and 1919 are included to reflect the strong impact of the worldwide Spanish flu epidemic on the distribution of deaths within those two years. The estimated age effects, $\hat{\alpha}_x^F$, for the female version of the equation, are given in Table A.1 (in Appendix A) under the column for Model VI. Except for ages 0 and 1, the same age coefficient is used for more than one single-year age within a broader age group, and the coefficient for the age group 100–104 is used for all ages above 100 years. The birth proportion, $\pi_b(x,t)$, is defined formally as follows:[11]

$$\pi_b(x,t) = \frac{B(t-x)}{B(t-x) + B(t-x-1)}, \tag{5}$$

where $B(t)$ is the number of births (sexes combined) occurring in year t in the same population.[12] Wherever the available birth series is incomplete, we set $\pi_b(x,t) = 0.5$.

The infant mortality rate used for this analysis (both sexes combined) is found using a method proposed by Pressat (1972):

$$\mathrm{IMR}(t) = \frac{D(0,t)}{\frac{1}{3}B(t-1) + \frac{2}{3}B(t)} \qquad . \tag{6}$$

Note that the infant mortality rate can be computed in this manner before splitting 1×1 deaths into triangles. If $B(t)$ and $D(0,t)$ are known but $B(t-1)$ is unknown, then we set $B(t-1) = B(t)$ to calculate $\mathrm{IMR}(t)$. In general, the historical decline in infant mortality has been associated with a higher proportion of deaths in the lower triangle (relative to the upper triangle) across the age range, except at age 1. At age 0, the decline in infant mortality is associated with a rapidly increasing concentration of deaths within the lower triangle, until the IMR falls below one percent. Below that level, the historical trend reverses itself, and the proportion of infant deaths in the lower Lexis triangle tends to fall.

[11] The birth proportion provides information about the relative size of two successive birth cohorts, who both pass through the age interval $[x, x+1)$ during calendar year t. More precisely, it expresses the original size of the younger cohort (passing through the lower triangle of a 1×1 Lexis square) as a proportion of the total births for the two cohorts. Although this number measures the relative size of the two cohorts at birth, it can also serve as a useful indicator of their relative sizes at later ages.

[12] In the case of a country or area that has undergone territorial changes, it is important to adjust the birth series so that it refers always to the same population. See Appendix D for a general discussion of how we deal with changes in population coverage.

For men, the equation for estimating $\pi_d(x,t)$ is as follows:

$$\begin{aligned}\hat{\pi}_d(x,t) = 0.4838 &+ \hat{\alpha}_x^M + 0.6992 \cdot [\pi_b(x,t) - 0.5] \\ &+ 0.0728 \cdot I(t = 1918) - 0.0352 \cdot I(t = 1919) \\ &- 0.0088 \cdot \log \mathrm{IMR}(t) \\ &- 0.0745 \cdot \log \mathrm{IMR}(t) \cdot I(x = 0) \\ &+ 0.0259 \cdot \log \mathrm{IMR}(t) \cdot I(x = 1) \\ &+ 0.1673 \cdot [\log \mathrm{IMR}(t) - \log(0.01)] \cdot I(x = 0) \cdot I(\mathrm{IMR}(t) < 0.01) \quad . \end{aligned} \tag{7}$$

In this equation, $\pi_b(x,t)$ and $\mathrm{IMR}(t)$ are the same as in the female equation, since each is based on the total population. However, the age coefficients (as well as all other coefficients) are different and are given in Table A.2 (in Appendix A) under Model VI.

4.3 Splitting 5x1 death counts into 1×1 data

Death counts in a 5×1 configuration are split into 1×1 data using cubic splines fitted to the cumulative distribution of deaths within each calendar year. In principle, the same or a similar method could be applied to any configuration of death counts by age.[13] The method used here requires only that the raw data include death counts for the first year of life and for the first five years of life. Other than these two restrictions, it does not matter whether the raw data are strictly in five-year age groups (after age five) or in some other configuration. Also, there can be an open age interval above 90, 100, or some other age. The spline method is used to split death counts for all ages below the open age interval. Details of the computational methods are given in Appendix B.

4.4 Splitting death counts in open age intervals into Lexis triangles

In some cases the raw data provide no age detail on death counts above a certain age x. Instead, we know only the total number of deaths in this open age interval for some calendar year t, which we denote ${}_\infty D_x(t)$ In these situations we need a method for splitting ${}_\infty D_x(t)$ into finer age categories. One possibility would be to split death counts in the open age interval into 1×1 data and then to apply the method described earlier for splitting 1×1 death counts into Lexis triangles. However, the method for splitting the open age interval itself is inevitably arbitrary and imprecise, and it seems that little would be gained by such a 2-step procedure. Therefore, our method splits ${}_\infty D_x(t)$ immediately into Lexis triangles.

In order to distribute deaths in the open age interval, we fit the Kannisto model of old-age mortality (Thatcher et al., 1998) to death counts for ages $x^* - 20$ and above, where x^* is the lower boundary of the open age group (e.g., 80, 90, 100), thus treating death counts within a period as though they pertain to a closed cohort. We then use the fitted model to extrapolate death rates by Lexis triangle within the open age interval and use those rates to derive the number of survivors at each age. For details, see Appendix C.

[13] For some populations, we have death counts by period-cohort parallelograms covering five cohorts (e.g., deaths in year t for the $t-9$ to $t-5$ birth cohorts who will complete ages 5–9 in year t). In this case, we use the cubic spline method described here to split these deaths into single birth cohorts (see Appendix B for more details).

5 Population estimates (January 1st)

We describe four methods for deriving age-specific estimates of population size on January 1st of each year: 1) linear interpolation, 2) intercensal survival, 3) extinct cohorts, and 4) survivor ratios. For most of the age range, we use either linear interpolation of population estimates from other sources[14] or intercensal survival methods. At ages 80 and older, we use population estimates computed using the methods of extinct cohorts and survivor ratios (except for those cohorts who are younger than age 90 at the end of the observation period). We describe the four methods separately. In case of territorial changes (or other changes in population coverage) during the time period covered by HMD, adjustments to these methods are described in Appendix D.

5.1 Linear interpolation

In some cases, the available population estimates from other sources are for some date other than January 1st (e.g., mid-year estimates). When the period between one population estimate and the next (or a population estimate and a census count) is one year or less, we use linear interpolation to derive the January 1st population estimate.[15] When the period between population counts is greater than one year (e.g., census counts), we employ intercensal survival.

5.2 Intercensal survival methods

Intercensal survival methods provide a convenient and reliable means of estimating the population by age on January 1st every year during the intercensal period. There are two cases: (1) pre-existing cohorts (i.e., those already alive at the time of the first census), and (2) new cohorts (i.e., those born during the intercensal interval). We develop formulas for these two situations separately by first considering the simple case of a country that conducts censuses every five years on January 1st. We then propose a more general method that can be used for censuses occurring at any time of the year and for intercensal intervals of any length.

5.2.1 Specific example

Suppose that a country conducts censuses every five years, and suppose that each census occurs on January 1st. Therefore, population estimates by single years of age are available at five-year

[14] The main criteria for using population estimates from another source are that they are available and that they are believed to be reliable.

[15] We calculate the population as of January 1st of year t as a weighted average of the estimates in years t and $t-1$, where the weights are based on the proportion of the year between January 1st and the date of the available estimate. For example, if we have October 1st estimates, then the January 1st population (in a common year) at age x is calculated as:

$$P(x, 01.01.YYYY) = \frac{273}{365} \cdot P(x, 01.10.YYYY-1) + \frac{92}{365} \cdot P(x, 01.10.YYYY) \qquad .$$

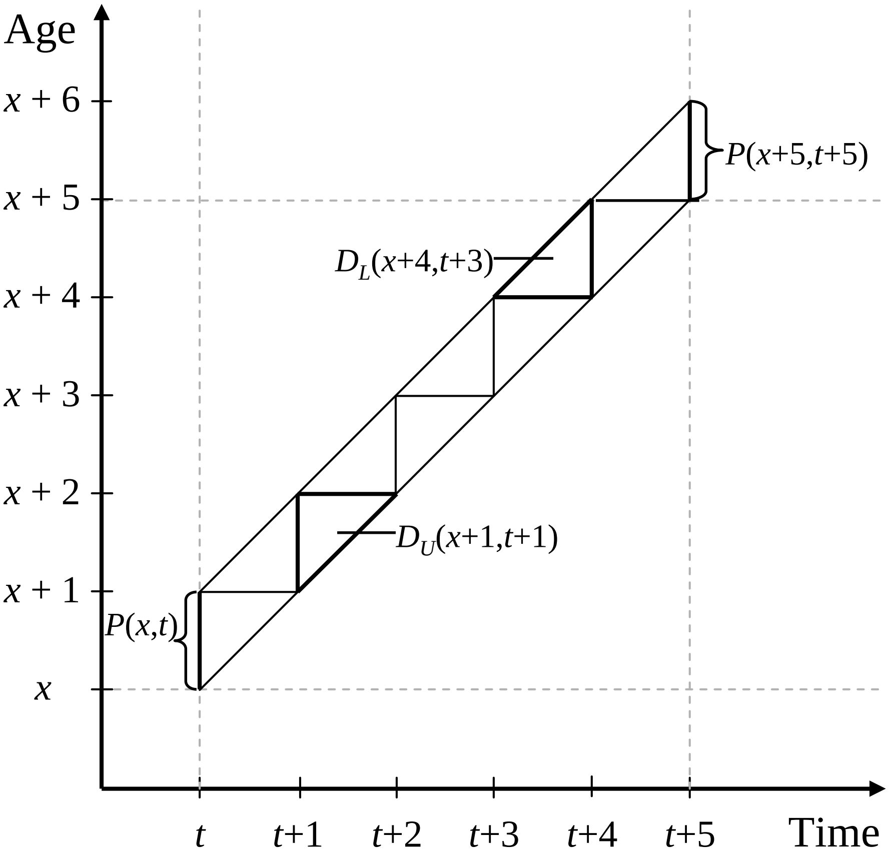
At the beginning or end of the data series, we cannot use linear interpolation because there are not two data points (e.g., the last population estimate in the series is for July 1st of year t). In these cases, we use *pre-censal* or *post-censal* estimation (see Section 5.2.3) to derive the January 1st estimate (i.e., by adding or subtracting deaths for each cohort).

intervals, but no comparable estimates are available for intervening years.

1. **Pre-existing cohorts**

   The Lexis diagram in Figure 3a depicts a cohort that is already alive at the time of the first census. The cohort aged x at time t is followed through time for 5 years. Suppose that all deaths in the population are recorded with a relatively high level of detail, such that for each year in the intercensal period, death counts are available by both age and year of birth. Thus, it is known with some precision how many life-lines ended by death in each of the small triangles shown in this figure.

   Figure 3a: Intercensal survival method: existing cohorts (example)



   The information represented by Figure 3a can be used to estimate the size of the cohort on January 1st of each intercensal year. The simplest procedure consists merely of subtracting death counts from the initial census count to obtain cohort population estimates on January 1st of each succeeding year. Unfortunately, the final step of such a computation usually yields an estimate of cohort size at time $t + 5$ that differs from the number given by the corresponding census. This inconsistency is caused by two factors: migration and error. Although both of these factors tend to be small relative to cohort size (at least for national populations), as a matter of principle they should not be ignored. The standard method consists of distributing implied migration/error uniformly over the parallelogram shown in Figure 3a. Then, estimates of cohort size for intercensal years are found by subtracting, from the initial census count, both the observed death counts and an estimate of net migration/error.

Formally, the procedure can be described as follows. Let $C_1(x)$ equal the census count for persons aged $[x, x+1)$ on January 1st of year t. Define $D^{\mathrm{v}}(x,t)$ as the death count in the vertical Lexis parallelogram, ▱:

$$D_i^{\mathrm{v}}(x,t) = D_U(x+i, t+i) + D_L(x+i+1, t+i) \qquad . \tag{8}$$

Assuming that there is no migration or error, note that

$$C_1(x) = \sum_{i=0}^{\infty} D_i^{\mathrm{v}}(x,t) \qquad . \tag{9}$$

This formula resembles one that is used for estimating population sizes at older ages (the extinct cohort method, see below).

Using census information about the size of a cohort at time t, we can *estimate* its size at the time of the next census, $t+5$, by the following formula:

$$\widehat{C}_2(x+5) = C_1(x) - \sum_{i=0}^{4} D_i^{\mathrm{v}}(x,t) \qquad . \tag{10}$$

However, if there is any migration into or out of this cohort during the intercensal period, or any error in the recording of census or death counts, this estimate will differ from the actual count at the time of the next census, $C_2(x+5)$. By definition, total migration/error is equal to the observed cohort size at the second census minus its estimated size, $\widehat{C}_2(x+5)$. We call this difference Δ_x:

$$\Delta_x = C_2(x+5) - \widehat{C}_2(x+5) \qquad . \tag{11}$$

Assuming that migration/error is distributed uniformly across the parallelogram shown in Figure 3a, the estimated population size on January 1st of each year is as follows:

$$P(x+n, t+n) = C_1(x) - \sum_{i=0}^{n-1} D_i^{\mathrm{v}}(x,t) + \frac{n}{5}\Delta_x \qquad , \tag{12}$$

for $n = 0, \ldots, 5$. By design, when $n = 0$ or 5 these population estimates match census counts exactly:

$$P(x,t) = C_1(x) \tag{13}$$

and

$$P(x+5, t+5) = C_2(x+5) \qquad . \tag{14}$$

2. **New cohorts**

The above formula applies only to cohorts already born at the time of the first census. For cohorts born between the two censuses, intercensal population estimates are obtained by subtracting the number of deaths occurring before the second census from the number of births for the cohort. For a cohort born in year $t+j$ within the intercensal interval, $[t, t+5)$, let

$$\begin{aligned} K &= \text{length of the interval } [t+j+1, t+5) \\ &= \text{age (at last birthday) of the cohort born in year } t+j \text{ at the time of the second census} \\ &= 4-j; \end{aligned}$$

and B_{t+j} is the birth count over the interval $[t+j, t+j+1)$.

An initial estimate of population size for the cohort born in year $t+j$ at the time of the second census is

$$\hat{C}_2(K) = B_{t+j} - D_L(0, t+j) - \sum_{i=0}^{k-1} D_i^{\text{v}}(0, t+j+1) \qquad , \tag{15}$$

and the difference between this estimate and the actual population count is

$$\Delta'_{t+j} = C_2(K) - \hat{C}_2(K) \qquad . \tag{16}$$

Thus, the estimated size of the cohort on January 1st of each year from birth until the second census is:

$$P(k, t+j+1+k) = B_{t+j} - D_L(0, t+j) + \frac{2k+1}{2K+1}\Delta'_{t+j} - \sum_{i=0}^{k-1} D_i^{\text{v}}(0, t+j+1) \qquad , \tag{17}$$

for $k = 0, \ldots, K$. As before, population estimates at time $t+5$ match the counts in the second census exactly: $P(K, t+5) = C_2(K)$.

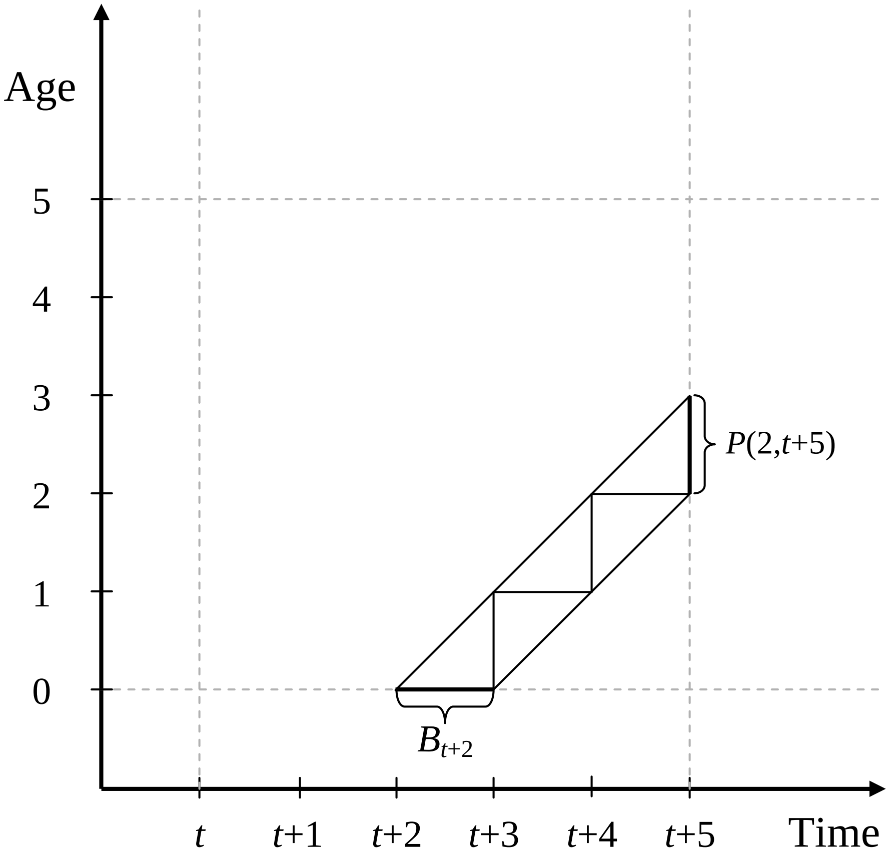
For example, consider the cohort born in year $t+2$. Thus, $j = 2$, and $K = 4 - j = 2$. In other words, the cohort born in year $t+2$ will be aged 2 at the time of the second census, as illustrated in Figure 3b. Population estimates for this cohort on January 1st of each year (until $t+5$) are as follows:

$$P(0, t+3) = B_{t+2} - D_L(0, t+2) + \frac{1}{5}\Delta'_{t+2} \qquad , \tag{18}$$

$$P(1, t+4) = B_{t+2} - D_L(0, t+2) - D^{\text{v}}(0, t+3)] + \frac{3}{5}\Delta'_{t+2} \qquad , \tag{19}$$

$$P(2, t+5) = B_{t+2} - D_L(0, t+2) + \Delta'_{t+2} - \sum_{i=0}^{1} D_i^{\text{v}}(0, t+3) \qquad . \tag{20}$$

Figure 3b: Intercensal survival method: new cohorts (example)



5.2.2 Generalizing the method

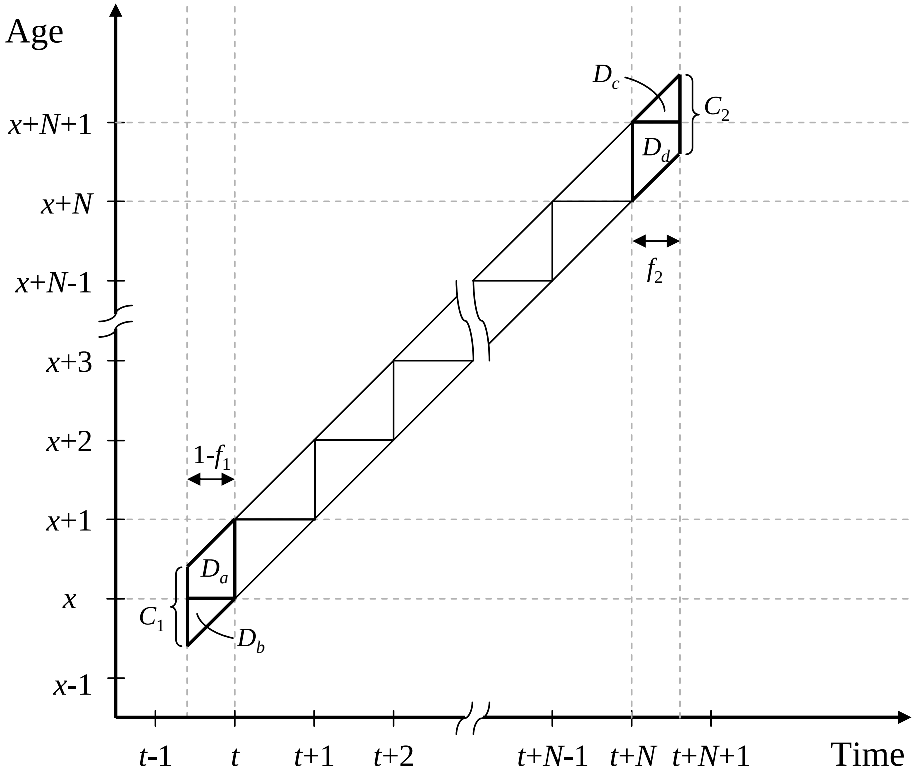
The arguments above make the explicit assumption that the two censuses bounding the intercensal period each occur on January 1st and are exactly five years apart. However, reality is typically more complicated. In this section, we generalize the method to allow for censuses that occur on any date of the year and for intercensal intervals of any length.

1. **Pre-existing cohorts**

   Figure 4a depicts an intercensal period bounded by two censuses that occur on arbitrary dates. Let t and $t+N$ be the times of the first and the last January 1st within the intercensal interval. Thus, N equals the number of complete calendar years between the two censuses. Let f_1 be the fraction of calendar year $t-1$ before the first census, and let f_2 be the fraction of calendar year $t+N$ before the second census. Thus, the two censuses occur at times $t_1 = t - 1 + f_1$ and $t_2 = t + N + f_2$, and the total length of the intercensal period is $N + 1 - f_1 + f_2$.

   The highlighted cohort in Figure 4a is of age x on January 1st of year t. This cohort was aged $x - 1$ or x at the time of the first census, and will be aged $x + N$ or $x + N + 1$ at the

Figure 4a: Intercensal survival method: pre-existing cohorts (in general)



time of the second census. If individuals are uniformly distributed across their respective age intervals at each census enumeration, the sizes of this cohort at the beginning and end of the intercensal interval are

$$C_1 = (1 - f_1) \cdot C_1(x-1) + f_1 \cdot C_1(x) \tag{21}$$

and

$$C_2 = (1 - f_2) \cdot C_2(x+N) + f_2 \cdot C_2(x+N+1) \qquad , \tag{22}$$

respectively. Although the assumption of a uniform distribution across age intervals is obviously incorrect, errors of exaggeration will tend to be balanced by those of understatement, yielding sufficiently accurate estimates in most cases.

Similarly, assuming a uniform distribution of deaths within Lexis triangles, deaths to this cohort in year $t-1$ after the first census enumeration will be composed of two components:

$$D_a = (1 - f_1^2) \cdot D_L(x, t-1) \tag{23}$$

and

$$D_b = (1 - f_1)^2 \cdot D_U(x-1, t-1) \qquad . \tag{24}$$

Likewise, under the same assumption, deaths to this cohort in year $t+N$ before the second census enumeration will be

$$D_c = f_2^2 \cdot D_L(x+N+1, t+N) \tag{25}$$

and

$$D_d = (2f_2 - f_2^2) \cdot D_U(x+N, t+N) \qquad . \tag{26}$$

Using these numbers along with death counts during complete calendar years of the intercensal interval, we estimate the size of the highlighted cohort at the time of the second census as follows:

$$\widehat{C}_2 = C_1 - (D_a + D_b) - (D_c + D_d) - \sum_{i=0}^{N-1} D_i^{\mathrm{v}}(x,t) \qquad . \tag{27}$$

The difference between the actual census count and this estimate, $\Delta_x = C_2 - \widehat{C}_2$, represents the total intercensal migration/error for this cohort. Finally, the size of the cohort on each January 1st of the intercensal interval is estimated as follows:

$$P(x+n, t+n) = C_1 - (D_a + D_b) + \frac{1 - f_1 + n}{N + 1 - f_1 + f_2}\Delta_x - \sum_{i=0}^{n-1} D_i^{\mathrm{v}}(x,t) \qquad , \tag{28}$$

for $n = 0, \ldots, N$.

2. **Infant cohort**

   The above formulas are applicable for cohorts that are aged 1 or more on the first January 1st of the intercensal interval. For the cohort aged 0 on this date (Figure 4b), and for new cohorts born during the intercensal interval (Figure 4c), different formulas are needed. For the infant cohort, the following modifications to the above formulas are necessary:

$$C_1 = (1 - f_1) \cdot B_{t-1} + f_1 \cdot C_1(0) \qquad , \tag{29}$$

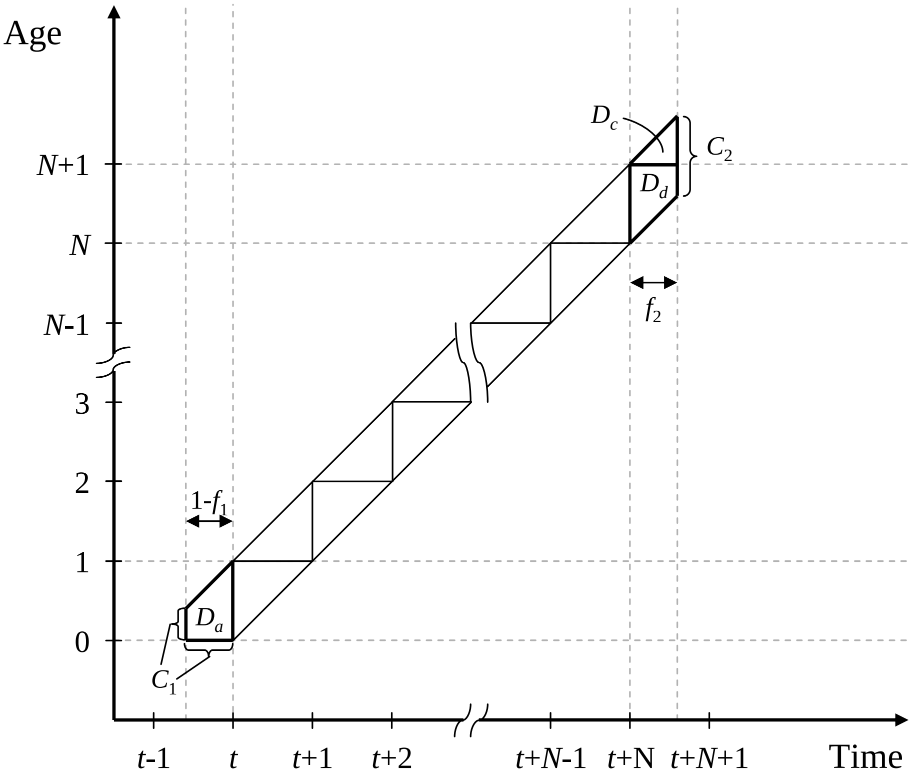
$$\hat{C}_2 = C_1 - D_a - (D_c + D_d) - \sum_{i=0}^{N-1} D_i^{v}(0,t) \qquad , \tag{30}$$

and

$$P(x+n, t+n) = C_1 + \frac{\frac{1}{2}\left(1 - f_1^2\right) + n}{N + \frac{1}{2}\left(1 - f_1^2\right) + f_2}\Delta_0 - D_a - \sum_{i=0}^{n-1} D_i^{\mathrm{v}}(x,t) \qquad , \tag{31}$$

for $n = 0, \ldots, N$, where $\Delta_0 = C_2 - \widehat{C}_2$. Note the following four differences between these formulas and those given earlier: (1) x disappears from the latter two equations since $x = 0$; (2) in the first formula, $C_1(x-1)$ is replaced by B_{t-1}, the number of births during the calendar year of the first census; (3) in the latter two formulas, D_b is absent as it is undefined; and (4) in the last term of the third equation, $1 - f_1$ is replaced by $\frac{1}{2}\left(1 - f_1^2\right)$ in both numerator and denominator. The formulas for D_a, D_c, D_a, and C_2 are unaltered.

Figure 4b: Intercensal survival method: infant cohorts (in general)



3. New cohorts

Lastly, we consider the case of a cohort born during complete calendar years of the intercensal interval. A cohort born in year $t + j$ will be aged $K = N - j - 1$ on the last January 1st before the second census. Defining f_2, D_c, and D_d as before, the following equations are used to estimate the size of new cohorts on January 1st of each year (from birth until just before the second census):

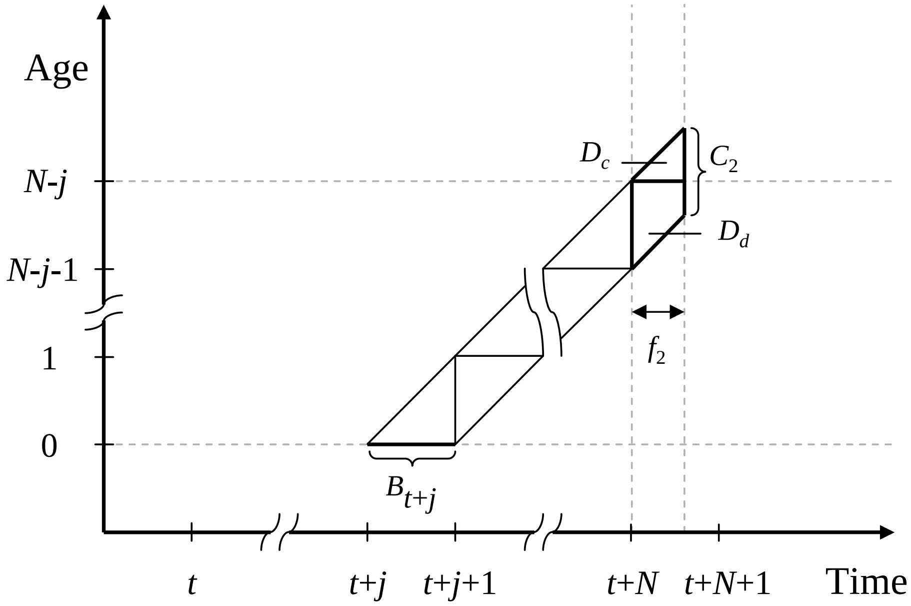
$$\widehat{C}_2 = B_{t+j} - D_L(0, t + j) - (D_c + D_d) - \sum_{i=0}^{K-1} D_i^{\mathrm{v}}(0, t + j) \qquad (32)$$

and

$$P(k,t+j+k+1) = B_{t+j} - D_L(0,t+j) + \frac{2k+1}{2K+1+2f_2}\Delta'_{t+j} - \sum_{i=0}^{k-1} D_i^{\text{V}}(0,t+j) \quad , \tag{33}$$

for $k = 0,\ldots,K$, where $\Delta'_{t+j} = C_2 - \widehat{C}_2$.

Figure 4c: Intercensal survival method: new cohorts (in general)



5.2.3 Pre- and postcensal survival method

For a short period before the first census or after the last census, population estimates can be derived simply by adding or subtracting deaths from population counts in a census (or, for new cohorts, from birth counts). The formulas are similar to those presented earlier, although they lack a correction for migration/error. Therefore, population estimates for recent years that are derived in this manner must be considered provisional. They will be replaced by final estimates once another census is available to close the intercensal interval. The purpose of such estimates is to allow mortality estimation during recent years or for a short period before an early census, when appropriate death counts are available during an open census interval.

Examples of pre- and postcensal survival estimation are shown in Figure 5. The size of the cohort born in year $t-x-1$ on January 1st of years $t-1$ and $t-2$ is estimated as follows:

$$P(x-1,t-1) = C_1 + D'_a + D'_b \tag{34}$$

and

$$P(x-2,t-2) = C_1 + D_a^{'} + D_b^{'} + D^{\mathrm{v}}(x-1,t-2) \qquad . \tag{35}$$

To estimate the size of the same cohort on January 1st of years $t+N+1$ and $t+N+2$, we have:

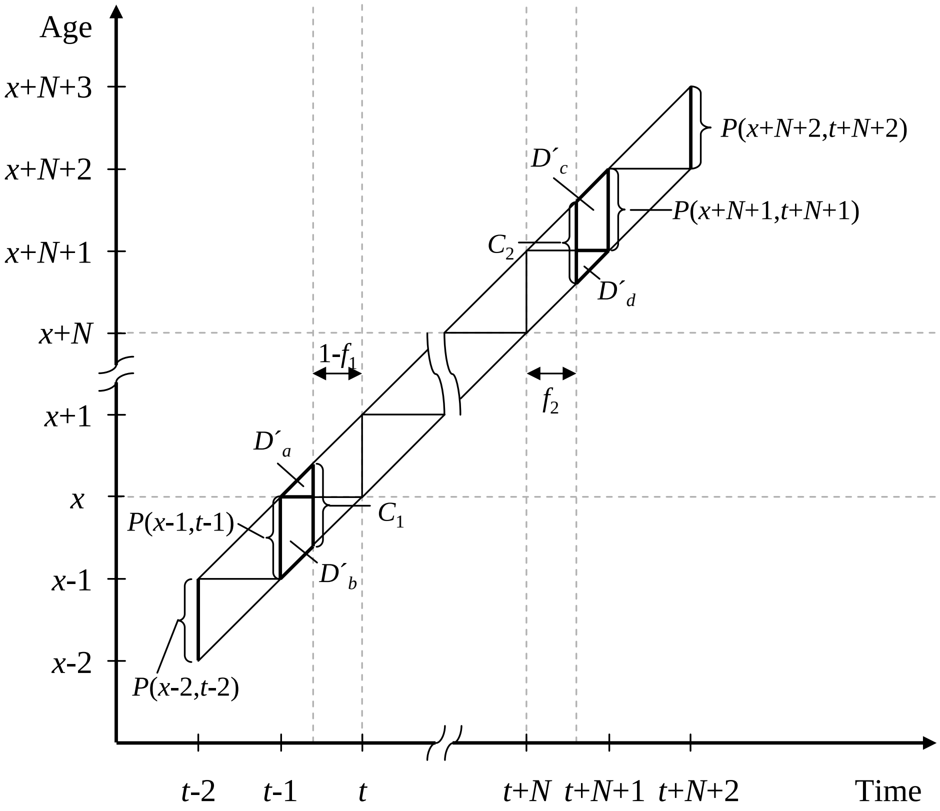
$$P(x+N+1,t+N+1) = C_2 - D_c^{'} - D_d^{'} \tag{36}$$

and

$$P(x+N+2,t+N+2) = C_2 - D_c^{'} - D_d^{'} - D^{\mathrm{v}}(x+N,t+N+1) \qquad . \tag{37}$$

In this notation, $D_a^{'}$, $D_b^{'}$, $D_c^{'}$, and $D_d^{'}$, are the complements of D_a, D_b, D_c, and D_d, respectively. That is, the sum of each pair of death counts equals the number of deaths in a Lexis triangle. For example, comparing Figures 4a and 5, we see that $D_a^{'} + D_a = D_L(x,t-1)$.

Figure 5: Pre- and post-censal survival method



5.2.4 Intercensal survival with census data in n-year age groups

The above discussion assumes that census data are available in single-year age groups. However, for many historical censuses the available counts refer to n-year age groups, where n is often 5. In these cases, we must first split the data into one-year age groups before computing population estimates using the method of intercensal survival. We employ a simple method for this purpose. We assume that a more recent census is available, which contains population counts by single years of age. Using the age distribution at the time of the later census, plus death counts in the intercensal interval, we estimate the age distribution of the earlier census by the method of reverse survival. However, these estimates may not sum to the total (or sub-totals) given in the earlier census. Therefore, we use only the estimated distribution of the population by age at the time of the earlier census, which is applied to the observed counts within n-year age intervals as a means of creating finer age categories. Thus, all counts contained in the earlier census are preserved in the process of making these calculations.

5.3 Extinct cohorts methods

The method of extinct generations can be used to obtain population estimates for cohorts with no surviving members at the end of the observation period. With this method, the population size for a cohort at age x is estimated by summing all future deaths for the cohort, which can be written as follows:

$$P(x,t) = \sum_{i=0}^{\infty} D_i^{\mathrm{v}}(x,t) \qquad . \tag{38}$$

This method assumes that there is no international migration after age x for the cohort in question, which is a reasonable assumption only for advanced ages. We use the method of extinct generations to estimate population sizes for ages 80 and above only, as illustrated in Figure 6.

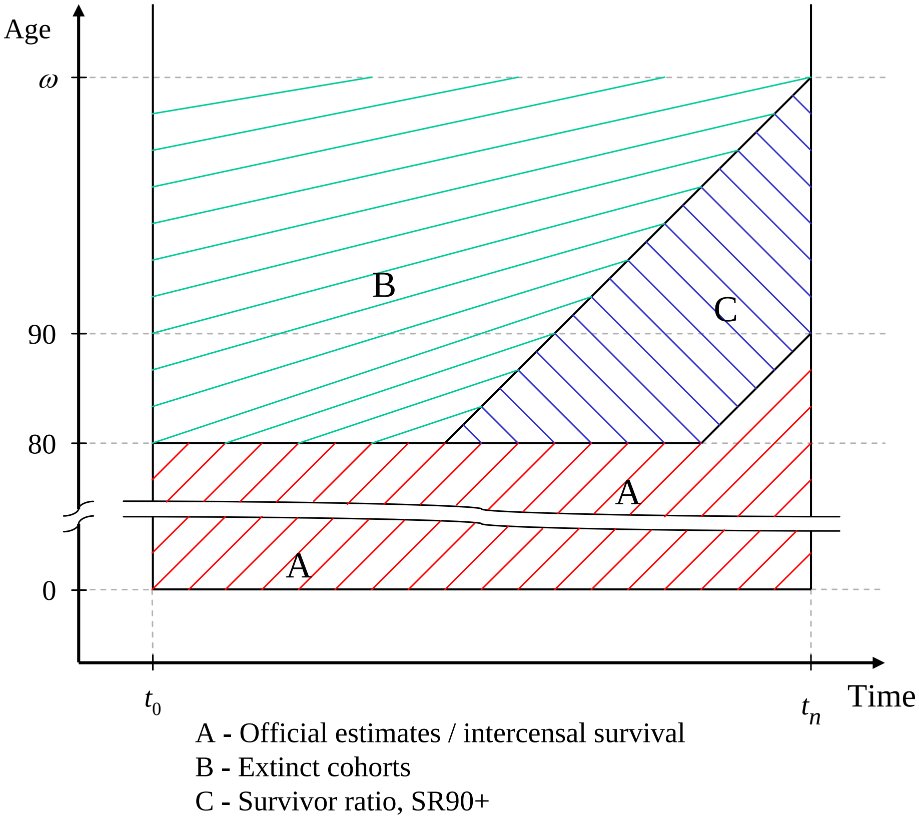
Prior to applying the method of extinct cohorts, it is necessary to determine which cohorts are extinct. For this purpose, we adopt a method proposed by Väinö Kannisto and used already in the Kannisto-Thatcher oldest-old mortality database (Andreev et al. 2003). We say that a cohort is extinct if it has attained age ω by end of the observation period (assumed to occur on January 1st of year t_n). Thus, we need to find ω or, equivalently, $\omega - 1$, the age of the oldest non-extinct cohort.

Consider a cohort aged x at the end of the observation period, where x is some very high age (like 120). We examine the most recent ℓ cohorts from a similar point in their life histories. Specifically, we consider the observed deaths for these cohorts from January 1st of the year when they were aged x until the end of the observation period (see illustration in Figure 7, where $l = 5$ and $x = \omega - 1$). For these cohorts over the specified intervals of age and time, we compute the average number of deaths:

$$\tilde{D}(x, t_n, l) = \frac{1}{l} \sum_{j=1}^{l} \sum_{i=0}^{j-1} D_i^{\mathrm{v}}(x, t_n - j) \qquad , \tag{39}$$

with $l = 5$. For very high ages, $\tilde{D}(x, t_n, l)$ will be close to zero. We define ω to be the lowest age x such that $\tilde{D}(x, t_n, l) \leq 0.5$. Equivalently, $\omega - 1$ is the highest age x for which $\tilde{D}(x, t_n, l) > 0.5$.

Figure 6: Methods used for population estimates


Age
ω
90
80
0
B
C
A
A
t_0
t_n
Time
A - Official estimates / intercensal survival
B - Extinct cohorts
C - Survivor ratio, SR90+

5.4 Survivor ratio

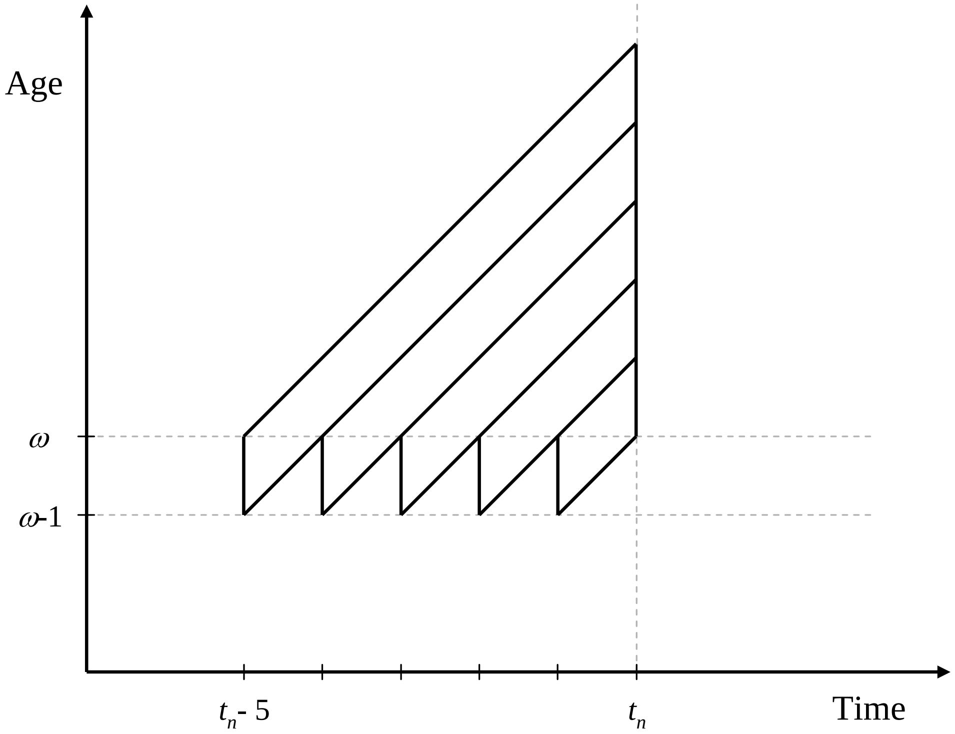
The survivor ratio method is used to estimate population sizes above age 80 for almost-extinct cohorts (see Figure 6). The method is applied to cohorts that are at least age 90 at the end of the observation period but not yet extinct (according to the rule given above).[16] Various versions of this method have been proposed and studied previously (see discussion in Andreev (1999)). We use the version that proved most reliable in an earlier comparative study (Thatcher et al. 1998).

Define a *survivor ratio* to be the ratio of survivors alive at age x on January 1st of year t to those in the same cohort who were alive k years earlier:

$$R = \frac{P(x,t)}{P(x-k,t-k)} \qquad . \tag{40}$$

[16] We make an exception for Sweden, Denmark, Norway, Finland, and Iceland, which have reliable January 1st population estimates by single year of age to the maximum age ω for the last year of observation. For these countries, we use the official population estimates for ages 90 and older on January 1st of year t_n and derive population estimates in earlier years (for each cohort) by adding observed death counts back to age 80 (like for the extinct cohort method).

Figure 7: Illustration of extinction rule (with $l = 5$ and $x = \omega - 1$)



Assuming that there is no migration in the cohort over the interval, this ratio can also be written:

$$R = \frac{P(x,t)}{P(x,t) + \dot{D}} \qquad , \tag{41}$$

where $\dot{D} = \sum_{i=1}^{k} \left[D^{\mathrm{v}}(x-i, t-i)\right]$, the total deaths in any of the parallelograms in Figure 8. Solving this equation for $P(x,t)$, we obtain:

$$P(x,t) = \frac{R}{1-R}\dot{D} \qquad . \tag{42}$$

The survivor ratio for the oldest non-extinct cohort (aged $\omega - 1$ at time t_n) is illustrated in Figure 8. This survivor ratio is unknown, since we do not know the size of the cohort, $P(\omega - 1, t_n)$, at the end of the observation period. However, comparable survivor ratios (i.e., with age $\omega - 1$ in the numerator) for all previous cohorts are available, since population size can be estimated using the method of extinct cohorts.

Suppose that a survivor ratio has approximately the same value for the cohort in question and for the previous m cohorts. That is, suppose that

$$R(x,t,k) = \frac{P(x,t)}{P(x-k,t-k)} \approx \frac{P(x,t-1)}{P(x-k,t-k-1)} \approx \cdots \approx \frac{P(x,t-m)}{P(x-k,t-k-m)} \qquad . \tag{43}$$

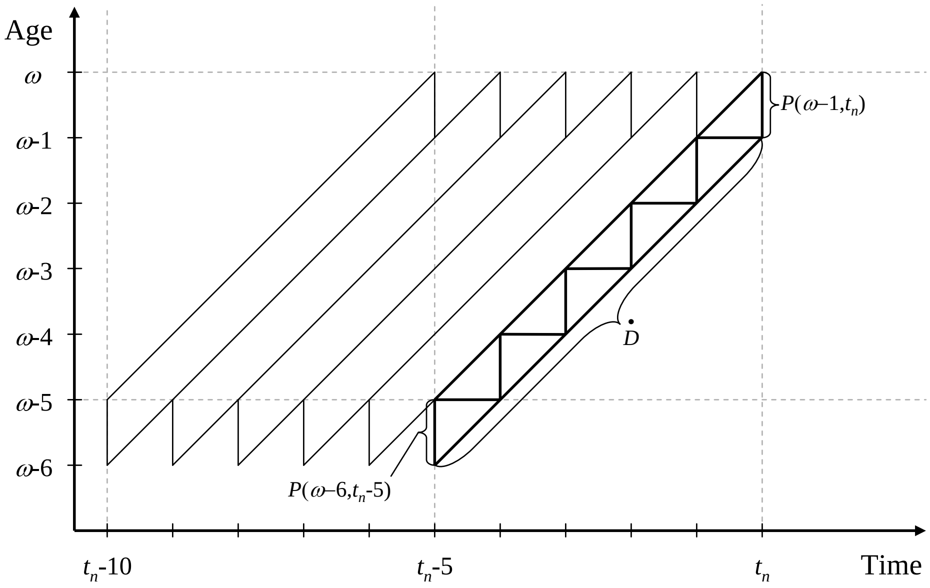
Then, we can estimate R by computing the pooled survivor ratio for the m previous cohorts:

$$R^*(x,t,k) = \frac{\sum_{i=1}^{m} P(x,t-i)}{\sum_{i=1}^{m} P(x-k,t-k-i)} \quad . \tag{44}$$

If both R^* and $\dot{D}$ are available for a given cohort, we can estimate $P(x,t)$ as follows:

$$\tilde{P}(x,t) = \frac{R^*}{1-R^*}\dot{D} \quad . \tag{45}$$

Figure 8: Survivor ratio method (at age $x = \omega - 1$, with $k = m = 5$)



In the simplest version of the survivor ratio method, this procedure is used to obtain $P(\omega-1, t_n)$, and then the size of this cohort in previous years is estimated by adding observed death counts back to age 80 (in a fashion similar to the extinct cohort method). It is then possible to apply the same method recursively to obtain $P(\omega-2, t_n)$, $P(\omega-3, t_n)$, etc., down to some lower age limit (e.g., 90 years). This method works well if its fundamental assumption is not violated, that is, if the survivor ratios for successive cohorts are nearly equal. A common occurrence, however, is that these survivor ratios increase over time as a result of mortality decline. Therefore, R^* tends to underestimate R, and $\tilde{P}$ tends to underestimate P.

These considerations motivate a modified version of the survivor ratio estimate:

$$\hat{P}(x,t) = c\tilde{P}(x,t) \tag{46}$$

$$= c\frac{R^*}{1-R^*}\dot{D} \quad , \tag{47}$$

where c is a constant that must be estimated. When mortality is declining/increasing/constant, c should be greater than/less than/equal to one. This leaves us with the problem of choosing the proper value of c.

Following Thatcher et al. (2002), we choose a value of c such that

$$\sum_{x=90}^{\omega-1} \widehat{P}(x,t_n) = P(90+,t_n) \qquad , \tag{48}$$

where $P(90+,t_n)$ is an official estimate of the population size in the open interval aged 90 and above at the end of the observation period. This version of the survival ratio method is known as SR(90+) and is used for the HMD (with $k = m = 5$) in all cases where $P(90+)$ is available and is believed to be reliable.[17] Otherwise, we use the simpler version of the survival ratio method (i.e., with $c = 1$).

6 Death rates

Death rates consist of death counts divided by the exposure-to-risk (person-years lived) from matching intervals of age and time. Period and cohort death rates are treated separately here, although they are derived from the same general assumptions.

6.1 ⧄ Period death rates

In the case of a one-year age group and a single calendar year (i.e., a 1×1 period death rate), the central death rate, $M(x,t)$, is estimated by the following formula:

$$M(x,t) = \frac{D(x,t)}{E(x,t)} \qquad , \tag{49}$$

where

$$D(x,t) = D_L(x,t) + D_U(x,t) \qquad ,$$

and $E(x,t)$ is the exposure-to-risk in the age interval $[x, x+1)$ during calendar year t, summarized by the Lexis square, ⧄. $D_L(x,t)$ and $D_U(x,t)$ refer to deaths in the lower triangle, ◿, and the upper triangle, ◸, respectively. The exposure-to-risk for ⧄ is always measured in terms of person-years and is computed by the following formula:

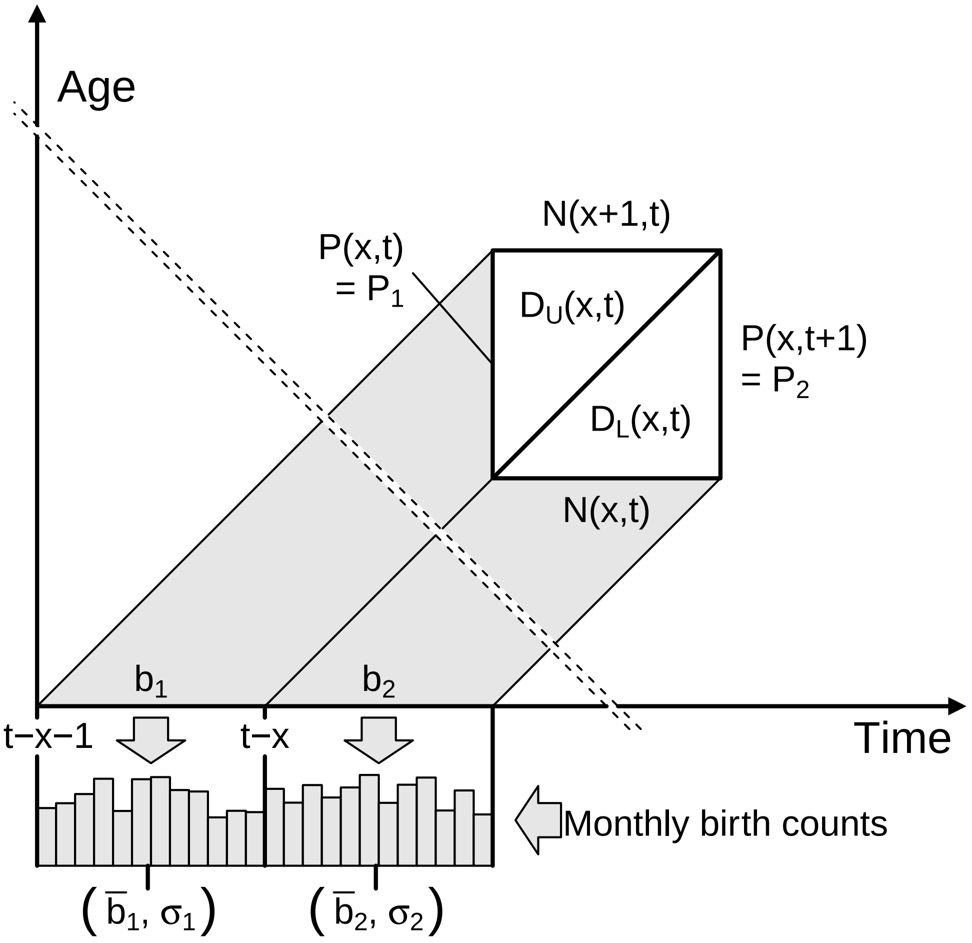
$$E(x,t) = E_L(x,t) + E_U(x,t) \qquad , \tag{50}$$

where

$$E_L(x,t) = s_1 P(x,t+1) + s_2 D_L(x,t) \qquad , \tag{51}$$

[17] For some populations, official population estimates are available only for age 85+. In such cases, we use SR(85+) and note this modification in the general comments (see country-specific documentation for details).

Figure 9: Data for period death rates and probabilities



and

$$E_U(x,t) = u_1 P(x,t) - u_2 D_U(x,t) \qquad . \tag{52}$$

The coefficients s_1, s_2, u_1 and u_2 are calculated using information about the distribution of birthdays within annual cohorts, which we approximate using data on birth counts by month for males and females combined:

$$s_1 = 1 - \bar{b}_2 \tag{53}$$

$$s_2 = \frac{1 - \bar{b}_2}{2} - \frac{\sigma_2^2}{2(1 - \bar{b}_2)} \tag{54}$$

$$u_1 = \bar{b}_1 \tag{55}$$

$$u_2 = \frac{\bar{b}_1}{2} - \frac{\sigma_1^2}{2\bar{b}_1} \qquad , \tag{56}$$

where $\bar{b}_1$ and $\bar{b}_2$ are the average times at birth for births that occurred in years $t - x - 1$ and $t - x$, respectively, expressed as a proportion of the year, and σ_1^2 and σ_2^2 are the corresponding variances of time at birth. This method assumes: (i) that the distribution of birthdays within a cohort remains constant over the life of the cohort (a sufficient condition is equal survival probabilities within the cohort) and (ii) that the density of deaths within a Lexis triangle is uniform along cohort lines and proportional to the distribution of birthdays for the cohort that passes through the triangle. For both $\bar{b}$ and σ^2, we assume births to be uniformly distributed within months. We therefore use exact month midpoints to calculate these two measures.

When information on births by calendar months is unavailable, we assume a uniform distribution of births within cohorts, which reduces the preceding formulas to the following simplified form:

$$E(x,t) = \frac{1}{2}\left[P(x,t) + P(x,t+1)\right] + \frac{1}{6}\left[D_L(x,t) - D_U(x,t)\right] \qquad . \tag{57}$$

Figure 9 illustrates data on births, deaths, and population that are used for computing these quantities. Appendix E provides a more extensive discussion and derivation of these formulas.

6.2 ▱ Cohort death rates

Cohort death rates are conceptually simpler and tend to be more robust to abrupt mid-year changes in birth distributions. A 1×1 cohort death rate is defined as:

$$M^c(x,t) = \frac{D^c(x,t)}{E^c(x,t)} \qquad , \tag{58}$$

where the superscript ^{c} indicates the age-cohort Lexis shape, ▱, seen in Figure 10. These quantities are estimated using death counts from the lower Lexis triangle in year t and the upper triangle in year $t + 1$, January 1st population counts in year $t + 1$, as well as information about the birth distribution in year $t - x$, when available. Except for age 0,[18] for cohorts we equate the observed rates, $M^c(x,t)$, with lifetable rates, m_x.

Death counts in ▱ are defined as:

$$D^c(x,t) = D_L(x,t) + D_U(x,t+1) \qquad . \tag{59}$$

Exposure estimates are calculated as follows:

[18] Age 0 calculations are described later in equation (84)

$$E^c(x,t) = P(x,t+1) + z_L D_L(x,t) - z_U D_U(x,t+1) \tag{60}$$

where z_L and z_U are calculated using information from the monthly birth distribution from the same cohort, and are held fixed over the life of the cohort:

$$\begin{aligned} z_L &= \frac{1-\bar{b}}{2} + \frac{\sigma^2}{2(1-\bar{b})} \\ z_U &= \frac{\bar{b}}{2} + \frac{\sigma^2}{2\bar{b}} \qquad , \end{aligned} \tag{61}$$

where $\bar{b}$ is the mean time of birth within the calendar year of birth, and σ is the corresponding standard deviation. Figure 10 helps to clarify how these quantities combine in the case of cohort exposures. In practice exposure calculations that assume uniformity vary little from those that use full information on a cohort's birth distribution. In the case of a uniform distribution of birthdays, exposure calculations simplify to

$$E^c(x,t) = P(x,t) + \frac{1}{3}\left[D_L(x,t-1) - D_U(x,t)\right] \qquad . \tag{62}$$

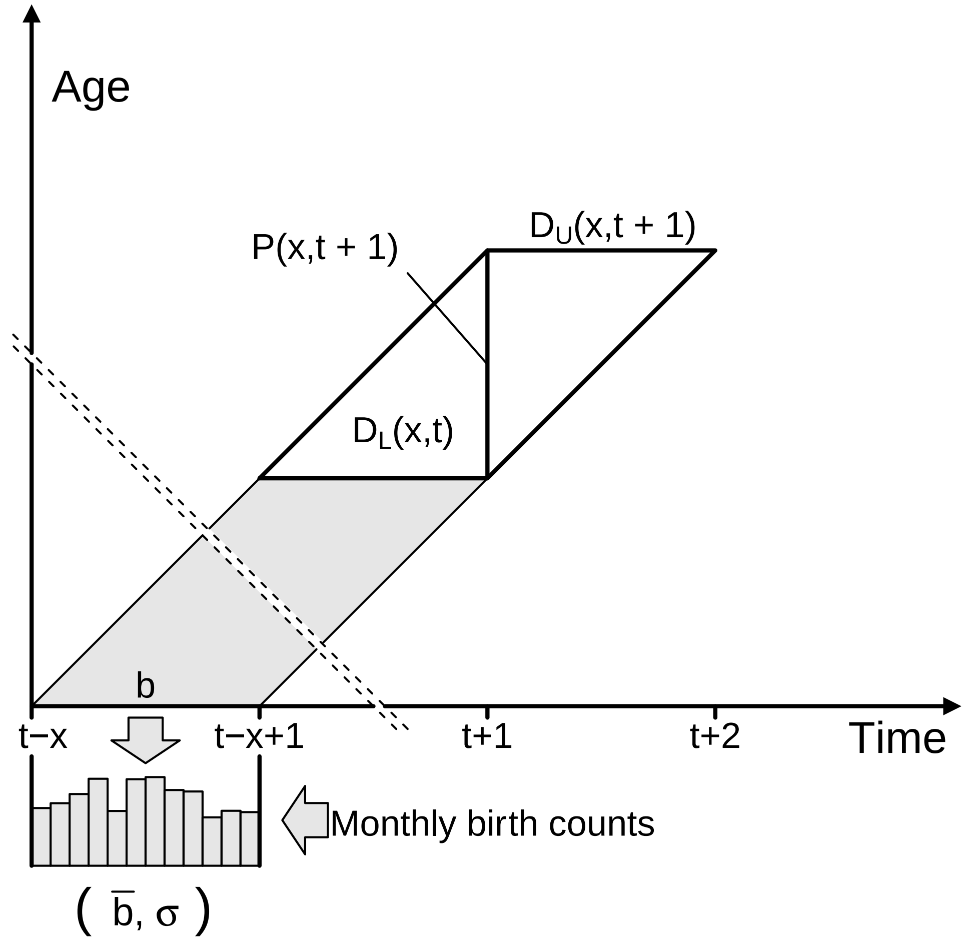
The exposure estimate at age 0 is an exception from the above. Since the cohort life table death rate m_0 is derived differently at age 0 than at other ages, we define

$$E^c(0,t) = \frac{D^c(0,t)}{m_0} \tag{63}$$

in order to ensure that $M^c(0,t) = m_0$.

Cohort exposure calculations refer to the age-cohort parallelogram, ▱, and there are no separate formulas for cohort exposures by Lexis triangles. See Appendix E for further discussion of these formulas.

Figure 10: Data for cohort death rates and probabilities



6.3 Death rates for multi-annual time intervals

For broader intervals of age and/or time (whether time is defined by periods or cohorts), death rates are always found by pooling deaths and exposures first and then dividing the former by the latter. Throughout the rest of this discussion, we will refer either to one-year or five-year death rates (i.e., M_x or ${}_5M_x$). For simplicity of notation, we will not specify a particular time interval, as the formulas for computing probabilities of death and/or life tables are the same for any interval of time. The difference between period or cohort rates should always be apparent from the context.

7 Life tables

Life table calculations do not depend on the organization of data over time. For any time interval, the same methods are used for computing life tables from a set of age-specific death rates. However, the methods used here are slightly different for period and cohort life tables. Period tables are computed by converting death rates to probabilities of death. Before this conversion, death rates at older ages are smoothed by fitting a logistic function. For cohort life tables, we compute probabilities of death directly from the data and perform no smoothing at older ages. As discussed in Appendix E, cohort probabilities of death computed in this manner are fully consistent with the cohort death rates described in the previous section.

For both periods and cohorts, we begin by computing *complete* life tables (i.e., single-year age groups) using our final estimates of death counts by Lexis triangle and population size (on January 1st) by single years of age. Then, the elements required to compute *abridged* tables (e.g., five-year age groups) are extracted from the complete tables. Deriving abridged tables from complete ones (rather than computing them directly from data in five-year age intervals) ensures that both sets of tables contain identical values for life expectancy and other quantities.

7.1 ⧄ Period life tables

A cohort life table depicts the life history of a specific group of individuals, whereas a period life table is supposed to represent the mortality conditions at a specific moment in time. Period life tables are said to be synthetic in that each age group of data comes from a different birth cohort.

Old-age mortality smoothing: Observed period death rates are only one result of a random process for which other outcomes are possible as well. At older ages where this inherent randomness is most noticeable, it is well justified to smooth the observed values in order to obtain an improved representation of the underlying mortality conditions. Thus, for period life tables by single years of age, we first smooth observed death rates at older ages by fitting a logistic function to observed death rates for ages 80 and above, separately for males and females.[19]

Suppose that we have deaths, D_x, and exposures, E_x, for ages $x = 80, 81, \ldots, 110+$ (for convenience, we choose $x = 110$ for the open category above age 110). We smooth observed death rates M_x by fitting the Kannisto model of old-age mortality (Thatcher et al. 1998), which is a logistic curve with an asymptote equal to one, to estimate the underlying hazards function, μ_x:

$$\mu_x(a,b) = \frac{ae^{b(x-80)}}{1 + ae^{b(x-80)}} \quad , \tag{64}$$

where we require $a \geq 0$ and $b \geq 0$. Assuming that $D_x \sim \text{Poisson}\left(E_x \mu_{x+0.5}(a,b)\right)$, we derive param-

[19] It is a common actuarial practice to fit a curve to death rates at older ages in the process of computing a life table. We use the logistic function because Thatcher et al. (1998) concluded that such a curve fits the mortality pattern at old ages at least as well as, and usually better than, any other mortality models. Fixing the value of the asymptote at one simplifies these calculations and avoids certain anomalies that may occur as a result of random fluctuations. In any event, estimates of this asymptote have been around one in most previous studies.

eter estimates $\hat{a}$ and $\hat{b}$ by maximizing the following log-likelihood function[20]:

$$\log L(a,b) = \sum_{x=80}^{110} \left[D_x \log \mu_{x+0.5}(a,b) - E_x \mu_{x+0.5}(a,b) \right] + \text{constant} \quad . \tag{65}$$

Substituting $\hat{a}$ and $\hat{b}$ into equation (64) yields smoothed death rates $\hat{M}_x$, where $\widehat{M_x} = \hat{\mu}_{x+{}^1/_2} = \mu_{x+{}^1/_2}(\hat{a}, \hat{b})$. In this model specification, $\hat{a}$ and $\hat{b}$ are constrained to be positive so that smoothed death rates cannot decline above age 80. For the rest of the calculations described here, fitted death rates replace observed death rates for all ages at or above Y, where Y is defined as the lowest age where there are at most 100 male deaths or 100 female deaths, but is constrained to $80 \leq Y \leq 95$.[21] Thus, complete period life tables for males and females are constructed based on the following vector of death rates: $M_0, M_1, \ldots, M_{Y-1}, \widehat{M}_Y, \ldots, \widehat{M}_{109}, {}_\infty\widehat{M}_{110}$.

Old-age mortality smoothing for the combined-sex lifetable: After obtaining smoothed death rates for males and females, we calculate the smoothed rates for the total population as a weighted average of those for males and females:

$$\hat{M}_x^T = w_x^F \hat{M}_x^F + (1 - w_x^F)\hat{M}_x^M \quad , \tag{66}$$

where superscripts T, F, and M represent total, female, and male, respectively, and w_x^F represents the weight for females aged x (these must still be determined).

For observed death rates, the analogous weights equals the observed age-specific proportion of female exposure:

$$\pi_x^F = \frac{E_x^F}{E_x^F + E_x^M} = \frac{E_x^F}{E_x^T} \quad . \tag{67}$$

In practice, the observed proportion of female exposure serves as the weight for ages less than Y as defined above. For ages Y and above, such weights could be calculated from observed exposures, but due to random fluctuations in such values at older ages, the resulting series of old-age death rates for the total population would not be as smooth as those for males and females. Consequently, we smooth π_x^F itself by fitting the following model by the method of weighted least squares:[22]

$$z = \text{logit}(\pi_x^F) = \log\left(\frac{\pi_x^F}{1-\pi_x^F}\right) = \beta_0 + \beta_1 x + \beta_2 x^2 \quad . \tag{68}$$

[20] Fitting the Kannisto model to data is often non-trivial, given that several data points in a given year may be zero or missing. In such low information settings, different optimizers can give different and conflicting results. The HMD implementation uses the `L-BFGS-B` method (Zhu et al. 1997) of the `optim` function in base `R` (R Development Core Team 2012), which in addition to the likelihood function requires an analytic gradient function and the specification of lower and upper bounds for the $\hat{a}$ and $\hat{b}$ parameters. We use 0 as the lower bound and 5 for the upper bound for both parameters. Both the likelihood and gradient functions are scaled down by a constant of 10^{-6}. Starting values for $\hat{a}$ and $\hat{b}$ come from a grid search. If this procedure fails for a given year of data, the `BFGS` method of `optim` is used (this exception only pertains to a small number of years in early Iceland).

[21] In other words, we use the fitted death rates for all ages at or above the greater of 80 or the lowest age where there are at most 100 male or 100 female deaths, and for all ages at or above age 95 regardless of the number of deaths. We begin using fitted death rates at the same age for both males and females.

[22] Note that when fitting the model in equation (68), we use exposure data from the same age-range used for fitting the logistic curve as a model of M_x at older ages.

We drop observations where E_x^F, E_x^M, or both equal 0 (in such cases, $\pi_x^F = 0$ or 1 and thus the logit is undefined), and for fitting equation (68), use weights equal to E_x^T.[23] The fitted values are obtained as follows:

$$\hat{z} = \hat{\beta}_0 + \hat{\beta}_1 x + \hat{\beta}_2 x^2 \quad \text{and} \quad w^F = \hat{\pi}_x^F = \frac{e^{\hat{z}}}{1+e^{\hat{z}}} \qquad . \tag{69}$$

Finally, the smoothed total death rates are calculated as:

$$\hat{M}_x^T = \begin{cases} \pi_x^F M_x^F + (1-\pi_x^F) M_x^M & \text{for } x < Y \\ \hat{\pi}_x^F \hat{M}_x^F + (1-\hat{\pi}_x^F) \hat{M}_x^M & \text{for } x \geq Y \end{cases} \qquad . \tag{70}$$

The basic lifetable calculations: We assume that death rates in the life table equal death rates observed in the population (at least for ages below Y). This assumption is technically correct only when the age structure of the actual population is identical to the age structure of a stationary (i.e., life table) population within each age interval (for more explanation, see Keyfitz (1985), or Preston et al. (2001)). In most situations, however, deviations from this assumption are likely to be small and unimportant for one-year age intervals. Next, we convert the life table death rates, m_x, into probabilities of death, q_x. Let a_x be the average number of years lived within the age interval $[x, x+1)$ for people dying at that age. We assume that $a_x = \frac{1}{2}$ for all single-year ages except age 0 (see below). We then compute q_x from m_x and a_x according to the following formula,

$$q_x = \frac{m_x}{1 + (1-a_x) \cdot m_x} \qquad , \tag{71}$$

for $x = 0, 1, 2, \ldots, 109$. For the open age interval, we set

$$_\infty a_{110} = \frac{1}{_\infty m_{110}} \tag{72}$$

$$_\infty q_{110} = 1 \qquad . \tag{73}$$

For infants, we use a revised version of the formulas for a_0 suggested by Andreev and Kingkade (2015), as outlined in the table 1. This method produces results similar to the classic Coale-Demeny formulas (Coale et al. 1983), but it accounts for more recent empirical regularities in the distribution of death in the first year of life, improving estimates for contemporary data. These formulas use cutpoints in m_0 to determine the values of the intercept a and slope b, where the final category is a simple constant value for a_0. These formulas are given separately for males and females.

[23] For fitting the model in equation (68), theoretically, the correct weights would be $\hat{\pi}_x^F(1-\hat{\pi}_x^F) \cdot E_x^T$, but the use of these would entail an iterative procedure because the weights depend on the fitted values themselves. Since there is relatively little variability in $\hat{\pi}_x^F(1-\hat{\pi}_x^F)$ compared to E_x^T over the observed range, using E_x^T as the weights should provide reasonable accuracy and is much more convenient.

Table 1: Andreev-Kingkade formulas for computing a_0 given m_0

m_0 range	formula: $a_0 = a + b \cdot m_0$
Males	
$[0, 0.02300)$	$0.14929 - 1.99545 \cdot m_0$
$[0.0230, 0.08307)$	$0.02832 + 3.26021 \cdot m_0$
$[0.08307, \infty)$	0.29915
Females	
$[0, 0.01724)$	$0.14903 - 2.05527 \cdot m_0$
$[0.01724, 0.06891)$	$0.04667 + 3.88089 \cdot m_0$
$[0.06891, \infty)$	0.31411

For a combined-sex life table, we compute a_0 as follows:

$$a_0^T = \frac{a_0^F D_0^F + a_0^M D_0^M}{D_0^F + D_0^M} \qquad , \tag{74}$$

where the superscripts F, M, and T denote values for the female, male, and total populations, respectively, and where D_0^i refers to all deaths at age zero (both lower and upper triangles) for population i.

To complete the life table calculation, let p_x be the probability of surviving from age x to $x+1$. Therefore,

$$p_x = 1 - q_x \qquad , \tag{75}$$

for all ages x. Let the radix of the life table, l_0, be $100,000$. Then, the number of survivors (out of 100,000) at ages $x > 0$ is

$$l_x = l_0 \cdot \prod_{i=0}^{x-1} p_i \qquad . \tag{76}$$

The distribution of deaths by age in the life-table population is

$$d_x = l_x \cdot q_x \tag{77}$$

for $x = 0, 1, \ldots, 109$. For the open age category, ${}_{\infty}d_{110} = l_{110}$.

The person-years lived by the life-table population in the age interval $[x, x+1)$ are

$$L_x = l_x - (1 - a_x) \cdot d_x \tag{78}$$

for $x = 0, 1, \ldots, 109$. For the open age category, ${}_{\infty}L_{110} = l_{110} \cdot a_{110}$. The person-years remaining for individuals of age x equals

$$T_x = \sum_{i=x}^{109} L_i + {}_{\infty}L_{110} \tag{79}$$

for $x = 0, 1, \ldots, 109$. For the open age category, ${}_{\infty}T_{110} = {}_{\infty}L_{110}$. Remaining life expectancy at age x is

$$\mathring{e}_x = \frac{T_x}{l_x}, \tag{80}$$

for $x = 0, 1, \ldots, 110$.

7.2 ▱ Cohort life tables

The methods used to compute m_x for cohorts were described in Section 6.2. In this case, the choice to equate m_x to M_x is more easily justified, since in the absense of migration, the actual population is the same as the life table population. Cohort death probabilities, q_x, are defined as:

$$q_x = \frac{D_L(x,t) + D_U(x,t+1)}{P(x,t+1) + D_L(x,t)} \qquad . \tag{81}$$

This formula remains the same for both uniform and non-uniform birth distributions. It is exact in the absence of migration, and it is a reasonable approximation in most situations, assuming that the direction and magnitude of migration are similar in both upper and lower triangles (see Pressat (1972)), and so it is used for the preparation of cohort lifetables with no further adjustment. The average time lived in the interval by those who die, a_x, is approximated as follows:

$$a_x = \frac{z_L D_L(x,t) + (1 - z_U) D_U(x,t+1)}{D_L(x,t) + D_U(x,t+1)} \qquad , \tag{82}$$

where z_L andy z_U and the means years lived in the interval by those dying in ◺ and ◸, respectively, per equation (60). In the case of uniformly distributed deaths within Lexis triangles, this formula becomes:

$$= \frac{\frac{1}{3} D_L(x,t) + \frac{2}{3} D_U(x,t+1)}{D_L(x,t) + D_U(x,t+1)} \qquad . \tag{83}$$

We assume $a_x = \frac{1}{2}$ if no deaths were observed in the interval. Both in the case of uniform and non-uniform birth distributions, the three quantities m_x, a_x and q_x relate to each other according to the identity given in equation (71). An advantage of the method used here is that cohort values of q_x, m_x, and a_x obey this classic formula even though the three quantities are derived independently from the original data. Once these three values are available, a complete cohort life table is calculated using the same formulas as in the case of period tables. The method for multi-year cohorts is similar, as described later.

As with period life tables, it is not appropriate to assume a uniform distribution of deaths over the age-cohort parallelogram or along cohort lifelines for age 0. We use a revised version of the Andreev-Kingkade method (Andreev and Kingkade (2015)), analogous to that presented earlier in table 1, to estimate the mean age at death, a_0, using q_0 instead of m_0, and then we solve equation (71) for m_0:

$$m_0 = \frac{q_0}{1 - (1 - a_0) \cdot q_0} \qquad . \tag{84}$$

Table 2 gives the q_0 cutpoints and corresponding linear coefficients used for a_0 approximation for infants in cohort lifetables.

Table 2: Andreev-Kingkade formulas for computing a_0 given q_0

	q_0 range	formula: $a_0 = a + b \cdot q_0$
Males		
	$[0, 0.0226)$	$0.1493 - 2.0367 \cdot q_0$
	$[0.0226, 0.0785)$	$0.0244 + 3.4994 \cdot q_0$
	$[0.0785, \infty)$	0.2991
Females		
	$[0, 0.0170)$	$0.1490 - 2.0867 \cdot q_0$
	$[0.0170, 0.0658)$	$0.0438 + 4.1075 \cdot q_0$
	$[0.0658, \infty)$	0.3141

For both-sex cohort life tables, a_0 is derived by taking the death-weighted average of the single-sex a_0 estimates, as per equation (74), and then m_0 is derived using equation (84).

Closing out cohort lifetables: If some members of a cohort are still alive at age 110, the above formulas are used for ages $x = 0, 1, \ldots, 109$ only. In this situation, for the open interval above age 110, we set

$$q_{110} = 1 \tag{85}$$

$$_{\infty}m_{110} = {}_{\infty}M_{110} = \frac{_{\infty}D_{110}}{_{\infty}E_{110}} \tag{86}$$

$$_{\infty}a_{110} = \frac{1}{_{\infty}m_{110}} \quad . \tag{87}$$

On the other hand, if the cohort dies out before age 110, the earlier definitions of q_x, m_x, and a_x are used up to and including the age of extinction (note that $q_x = 1$ in the final age group, which may be below 110) and all values are marked as *missing* at higher ages.

7.2.1 Multi-year cohorts

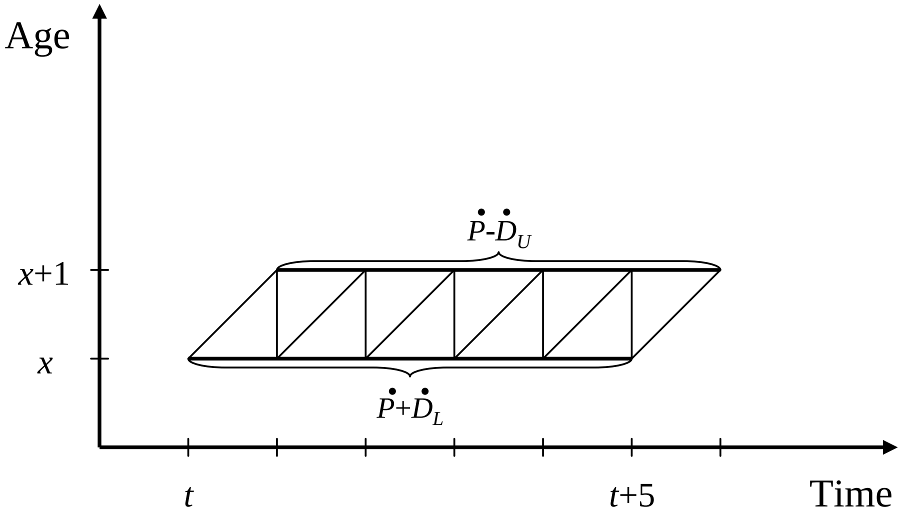
In the earlier section on death rates, we noted that death rates for multi-year intervals (either periods or cohorts) are found by pooling deaths and exposures first and then dividing the former by the latter. We now describe methods for computing cohort probabilities of death for time periods longer than one year using a similar principle (see Pressat (1972)).

Consider the example of an n-year birth cohort in the age interval from x to $x+1$. Let $\dot{P}$ denote the sum of the January 1$^{\text{st}}$ population estimates for the n individual birth cohorts when they are aged x. Likewise, let $\dot{D}_L$ and $\dot{D}_U$ denote the sums of lower and upper triangle deaths within the same age interval for the same group of cohorts (see Figure 11 for an illustration in the case where

$n = 5$). Therefore, the probability of death for this n-year cohort is

$$q_x = 1 - \frac{\dot{P} - \dot{D}_U}{\dot{P} + \dot{D}_L} = \frac{\dot{D}_L + \dot{D}_U}{\dot{P} + \dot{D}_L} \qquad . \tag{88}$$

Figure 11: Illustration of five-year cohort (assuming no migration)



Using this notation, the death rate for this n-year cohort is

$$m_x = M_x = \frac{\dot{D}_U + \dot{D}_L}{\dot{E}^c} \qquad , \tag{89}$$

where $\dot{E}^c$ is the sum of the cohort exposure parallelograms in the n-year cohort, according to the formulas described in equation (60).

The average time lived in the interval of those dying in the interval is:

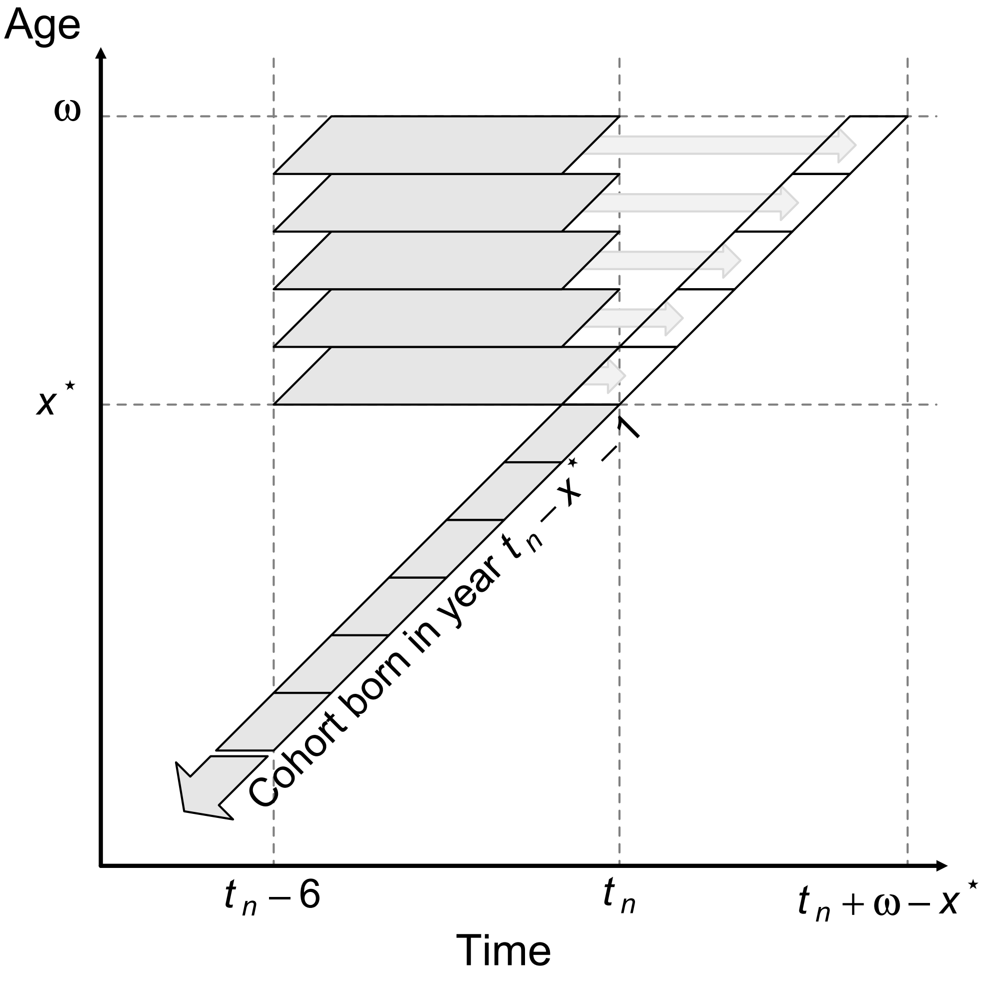
$$a_x = \frac{\sum_{i=0}^{n-1} \Big\{ z_L(x, t+i) D_L(x, t+i) + \Big[1 - z_U(x, t+i+1)\Big] D_U(x, t+i+1) \Big\}}{\dot{D}_L + \dot{D}_U} \qquad . \tag{90}$$

It is easy to confirm that the relationship between these three quantities obeys the classical formula exactly. As with single-year cohorts, however, we compute a_0 using the revised Andreev-Kingkade procedure described in the last section.

7.2.2 Almost-extinct cohorts

The above description assumes that all members of a cohort have died before we compute its life table. However, it is often desirable to compute life tables for cohorts that are almost extinct. Suppose that t_n denotes the last moment of the observation period and that the age of a cohort is x^* at time t_n. In order to compute a life table for this cohort, it is necessary to make some assumption about mortality at ages $x \geq x^*$. A simple solution is to assume that the cohort's deaths and exposures at these ages will equal the average of those quantities for the most recent five-year cohort for which such values are observed, as depicted schematically in Figure 12. Thus, the values of m_x, a_x, and q_x for an almost extinct cohort at ages $x \geq x^*$ are identical to those of a five-year cohort of comparable age observed just before time t_n.

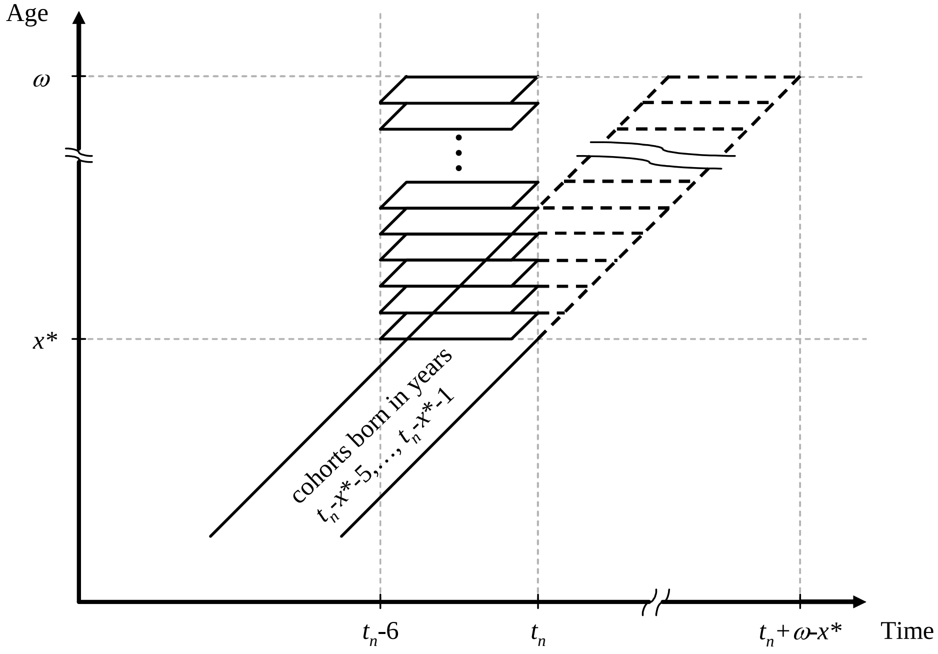
Figure 12: Life table calculations for almost-extinct cohorts



It is important to define some minimal value of x^* that is acceptable when making such calculations. For life tables that begin at age 0, we require that the total fictitious exposure (for ages $x \geq x^*$) be no more than one percent of the total lifetime exposure (in person-years lived) for the cohort. For life tables that begin at some age above 0, the fictitious exposure should be no more than one percent of the total exposure above the starting age. Figure 13 depicts life table calculations for five birth cohorts aged x^* to $x^* + 4$ at time t_n.

A small problem is that this method may produce $q_x = 1$ at some high age, even though there are some non-zero death and exposure counts at higher ages still. This is possible because the data at different ages refer to different groups of cohorts. In this situation, we have chosen to terminate the life table for an almost-extinct cohort at the lowest age where $q_x = 1$.

Figure 13: Life table calculations for almost-extinct cohorts aged x^* to $x^* + 4$ in year t_n



7.3 Abridged life tables

Abridged tables in the HMD are always extracted directly from complete single-age tables. This process can be described in just two steps. 1) Extract values of l_x, T_x, e_x for the abridged table directly from the complete table, and 2) compute the remaining values from these:

$$ {}_nL_x = T_x - T_{x+n} \tag{91}$$

$$ {}_nd_x = l_x - l_{x+n} \tag{92}$$

$$ {}_nq_x = \frac{{}_nd_x}{l_x} \tag{93}$$

$$ {}_na_x = \begin{cases} \frac{{}_nL_x - n \cdot l_{x+n}}{{}_nd_x} & \text{for } {}_nD_x > 0 \\ \frac{n}{2} & \text{for } {}_nD_x = 0 \end{cases} \quad , \tag{94}$$

where ${}_nD_x$ are death counts in the age interval $[x, x+n)$. For such calculations, $x = 0, 1, 5, 10, 15, \ldots, 110$. Of course, $n = 5$ except at both extremes of the age range. For the open interval, $n = \infty$ and $q_\infty = 1$. Therefore, where x^* is the lower age limit of the open age interval, we close out the abridged table using: ${}_{\infty}L_{x^*} = {}_{\infty}T_{x^*}$, ${}_{\infty}q_{x^*} = 1$, ${}_{\infty}d_{x^*} = l_{x^*}$, ${}_{\infty}m_{x^*} = \frac{l_{x^*}}{{}_{\infty}T_{x^*}} = \frac{1}{e_{x^*}}$ (i.e., the constant hazard in the open interval equals the reciprocal of remaining life expectancy at age x^*), and ${}_{\infty}a_{x^*} = e_{x^*}$.

Appendix A Linear model for splitting 1×1 death counts

Two equations are given in the main text for use in splitting death counts into Lexis triangles based on deaths counts in 1×1 Lexis squares (see equations 4 and 7). These equations were derived from a multiple regression analysis, as summarized in Table A-1. In this appendix, we give more detail about the regression analysis, but without repeating formulas already presented in the main text.

The regression analysis was performed separately for men and women. The dependent variable was the proportion of deaths occurring in the lower triangle out of the total in a 1×1 Lexis square, or $\pi_d(x,t)$ (see equation 3). The analysis included data for ages 0–104 from Sweden (1901–1999), Japan (1950–1998), and France (1907–1997). During these time periods, death counts in Lexis triangles are available across the age range in the raw data with only minor exceptions.[24] A series of regression models was fitted by weighted least squares.

The weight associated with each observed value of $\pi_d(x,t)$ was defined as follows:

$$w(x,t) = \frac{D(x,t)}{\sum_x D(x,t)} \quad . \tag{A.1}$$

Thus, the total weight for a given country in a given year was one. Alternatively, we might have used $w(x,t) = D(x,t)$, motivated by the knowledge that the variability of $\pi_d(x,t)$ is inversely related to $D(x,t)$. However, such a choice also has the effect of giving much more weight to the most populous country, Japan, which then dominates the analysis. The weights used here accord an equal importance to each country-year included in the analysis, while at the same time giving more weight within each country-year to observations derived from larger numbers of deaths.

The variables included in the models were chosen after an extensive exploratory analysis. Model I includes only age effects, which reflect the changing level of $\pi_d(x,t)$ across the age range and explain around 70 percent of the variability in the dependent variable. The proportion of births associated with the lower triangle, $\pi_b(x,t)$ (see footnote 12 and equation (5)), improves the fit further, as seen in Model II. The Spanish flu epidemic during the winter of 1918–1919 had the effect of increasing the proportions of lower-triangle deaths in 1918 (which includes more deaths from the second half of the calendar year) and of upper-triangle deaths in 1919 (for the opposite reason). Since this was a global epidemic, it seems reasonable to extrapolate the experience of Sweden and France (Japanese data begin later) onto the rest of the populations in the HMD.

For most age groups, the dependent variable, $\pi_d(x,t)$, has tended to increase over time, presumably in relation to changing levels and patterns of mortality. Partly as a matter of convenience, the infant mortality rate (IMR) was chosen to serve as a proxy variable for these sorts of temporal changes (Model IV). The IMR is convenient for this purpose because it can be estimated using only birth and infant death counts by calendar year. As explained in the main text, we used a simple method proposed by Pressat (1980) for computing the IMR. In this method, the denominator of the

[24] The available French data are not classified by Lexis triangle above age 100 for some years (1934–35, 1947, 1949, 1954, and 1956–67). In these cases, the data used as an input to the regression analysis had already been split into triangles by some method (in the data file provided by Jacques Vallin and France Meslé). Ideally, such data should have been excluded from this regression analysis. However, given the small number of observations involved and their small weight in the total analysis, their exclusion would have had only a minor effect on the estimated coefficients, and then only for the age group 100–104. On the other hand, the computer programming was simplified by leaving these observations in the analysis, and so they were included.

IMR is composed of two-thirds of the births from the current year plus one-third of the births from the previous year, since infant deaths in the current year are derived from both of these cohorts (although more were born in the current year than in the previous one).

The logarithmic transformation was used because it makes the relationship between the IMR and $\pi_d(x,t)$ more nearly linear across a broader range of observations. Even with this transformation, however, two other adjustments were needed to obtain a model that reflects well the patterns in the raw data. First, in Model VII (not shown here), we tested for possible interactions between $\log \text{IMR}$ and each age group. These interaction terms were statistically and practically significant for ages zero and one only (Model V). Second, at age zero the relationship between $\log \text{IMR}$ and $\pi_d(x,t)$ seems to turn around at very low values of the IMR. Therefore, we added an interaction term (for this age only) between $\log \text{IMR}$ and a dummy variable to indicate when the IMR is below 0.01 (Model VI). This cut-off level was chosen to maximize the R-squared statistic. For both males and females, R-squared obtained a maximum value (with four decimal points of precision) for a cut-off value in the range of 0.009 to 0.011, approximately. Therefore, the value of 0.01 was used for both sexes.

The color graphs on the following pages show actual values of $\pi_d(x,t)$ at ages 0 and 80 for the three countries, along with predictions from the model. For each age, two graphs are shown, depicting the changes in $\pi_d(x,t)$ as a function of both time and $\log \text{IMR}$. In the graphs organized by time, we also show the predicted trend in $\pi_d(x,t)$ for Sweden prior to the observation period, since the infant mortality rate was available back to 1751 and a birth series back to 1749. As illustrated by these graphs, the average value of $\pi_d(x,t)$ stabilizes at high values of IMR (due to the logarithmic transformation), so there should be no problem with applying this model to historical periods. In the backwards extrapolation for age 80, the lack of a birth series prior to 1749 is immediately apparent. For earlier cohorts, it was necessary to assume a constant cohort size, resulting in a loss of variability in predicted $\pi_d(x,t)$.

Figure A.1: Proportion of deaths in lower triangle by IMR, males age 0

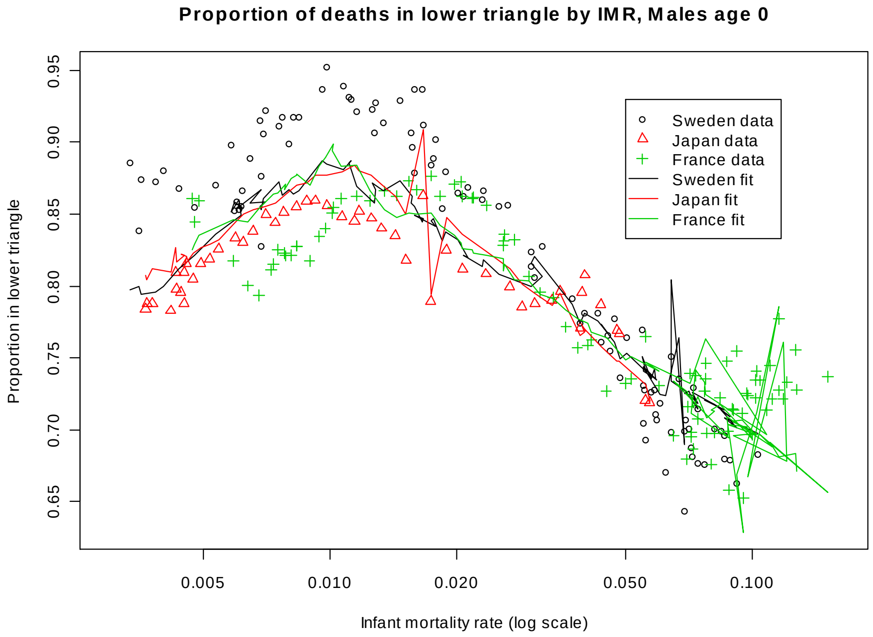


Figure A.2: Proportion of deaths in lower triangle, males age 0

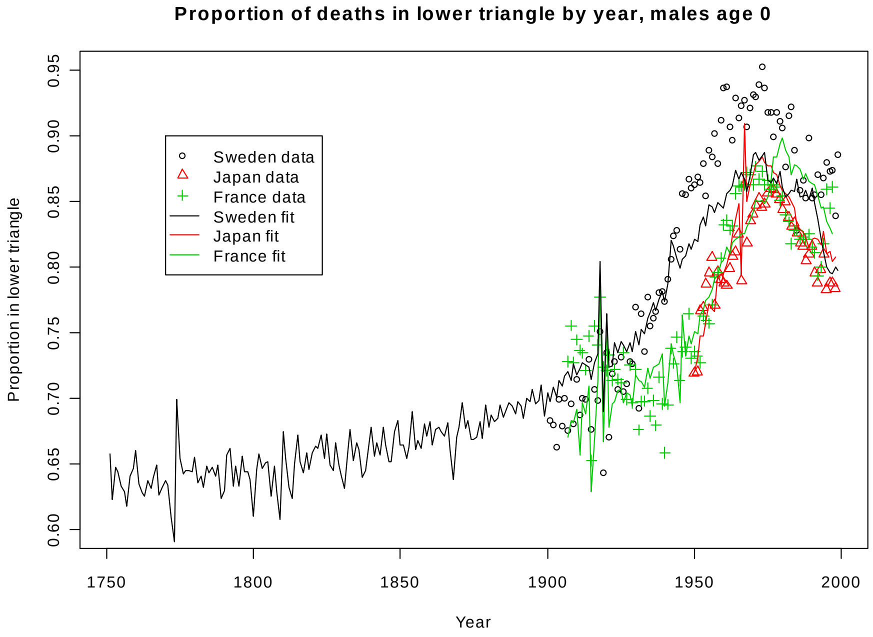


Figure A.3: Proportion of deaths in lower triangle by IMR, males age 80

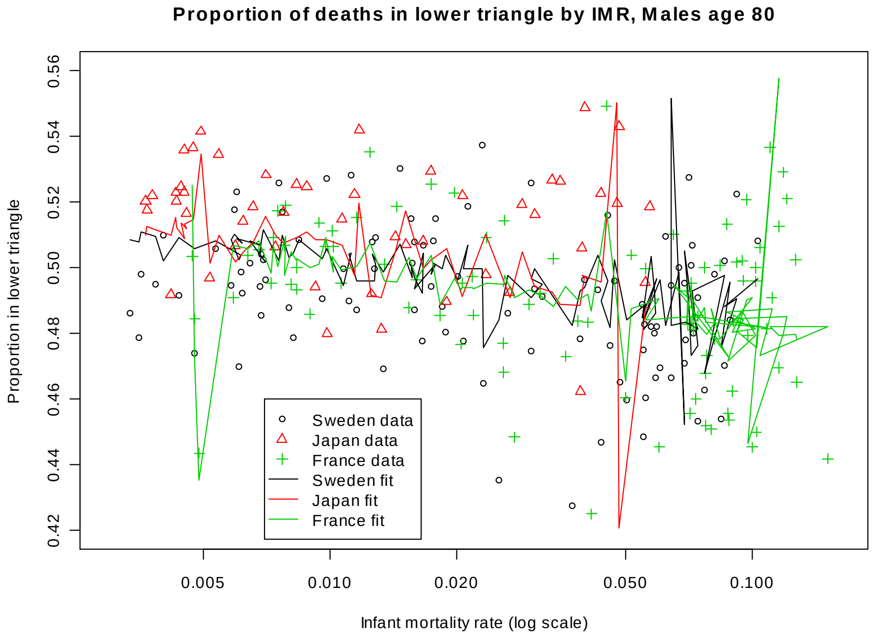


Figure A.4: Proportion of deaths in lower triangle, males age 80

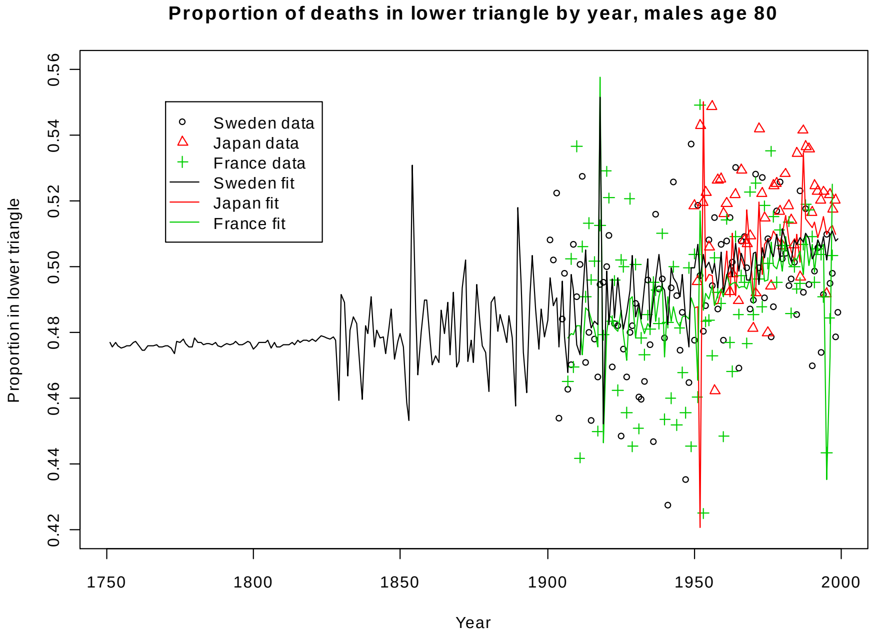


Table A.1: Linear models of the proportion of lower-triangle deaths [a]
Females ($n = 25{,}017$)[b]

	Null	**I**	**II**	**III**	**IV**	**V**	**VI**
Intercept	0.5104	0.5170	0.5172	0.5163	0.4712	0.4724	0.4710
Age Groups [c]							
0		0.2285	0.2295	0.2299	0.2368	0.0697	0.0392
1		0.0462	0.0480	0.0479	0.0570	0.1351	0.1365
2-4		-0.0003	0.0011	0.0006	0.0084	0.0116	0.0130
5-9		-0.0101	-0.0092	-0.0100	-0.0029	0.0004	0.0018
10-14		-0.0254	-0.0246	-0.0258	-0.0186	-0.0154	-0.0140
15-19		-0.0242	-0.0235	-0.0249	-0.0181	-0.0149	-0.0135
20-24		-0.0162	-0.0159	-0.0171	-0.0108	-0.0074	-0.0061
25-29		-0.0141	-0.0137	-0.0151	-0.0093	-0.0059	-0.0046
30-34		-0.0127	-0.0126	-0.0137	-0.0090	-0.0055	-0.0041
35-39		-0.0153	-0.0152	-0.0157	-0.0123	-0.0086	-0.0072
40-44		-0.0142	-0.0142	-0.0142	-0.0123	-0.0084	-0.0070
45-49		-0.0131	-0.0134	-0.0131	-0.0126	-0.0085	-0.0071
50-54		-0.0136	-0.0142	-0.0138	-0.0140	-0.0098	-0.0084
55-59		-0.0140	-0.0145	-0.0140	-0.0148	-0.0105	-0.0091
60-64		-0.0180	-0.0185	-0.0179	-0.0191	-0.0148	-0.0134
65-69		-0.0215	-0.0221	-0.0215	-0.0233	-0.0189	-0.0175
70-74		-0.0233	-0.0240	-0.0234	-0.0260	-0.0215	-0.0201
75-79		-0.0251	-0.0258	-0.0251	-0.0291	-0.0244	-0.0230
80-84		-0.0235	-0.0240	-0.0233	-0.0294	-0.0245	-0.0231
85-89		-0.0165	-0.0173	-0.0165	-0.0253	-0.0201	-0.0187
90-94		-0.0066	-0.0073	-0.0065	-0.0181	-0.0125	-0.0112
95-99		0.0055	0.0047	0.0055	-0.0086	-0.0027	-0.0014
100-104		0.0274	0.0267	0.0275	0.0114	0.0176	0.0190
Birth proportion – 0.5 [d]			0.7255	0.7220	0.7357	0.7377	0.7372
Year = 1918				0.0887	0.1019	0.1023	0.1025
Year = 1919				-0.0379	-0.0243	-0.0239	-0.0237
log *IMR*					-0.0127	-0.0111	-0.0112
(log *IMR*) × (Age = 0)						-0.0571	-0.0688
(log *IMR*) × (Age = 1)						0.0268	0.0268
(log *IMR* – log 0.01) × (Age = 0)							0.1526
R^2 [e]	0.0000	0.7113	0.7362	0.7558	0.7941	0.8170	0.8192

a. All models were fit by weighted least squares, with weights equal to the number of deaths in a 1×1 Lexis square divided by the total deaths for that country in that year. Thus, the total weight for each country-year combination is one (see main text of Appendix A for discussion).

b. All models were fit to data for ages 0-104 for Sweden (1901-1999), Japan (1950-1998), and France (1907-1997), after eliminating 78 observations with zero deaths in the 1x1 Lexis square.

c. Since coefficients for age groups are constrained to sum to zero, there is no omitted category.

d. The birth proportion equals the number of births in the younger cohort (born in t) divided by the total for the younger and older cohort (born in t-1). Data are centered about 0.5 (i.e., 0.5 is subtracted from the birth proportion for each observation).

e. R-squared here is the proportion of weighted variance (about the weighted mean) explained by the model.

Table A.2: Linear models of the proportion of lower-triangle deaths [a]
Males (n = 24,872)[b]

	Null	**I**	**II**	**III**	**IV**	**V**	**VI**
Intercept	0.5176	0.5226	0.5226	0.5223	0.4831	0.4853	0.4838
Age Groups [c]							
0		0.2294	0.2300	0.2304	0.2371	0.0555	0.0230
1		0.0370	0.0382	0.0385	0.0469	0.1234	0.1249
2-4		-0.0044	-0.0034	-0.0033	0.0035	0.0071	0.0086
5-9		-0.0088	-0.0080	-0.0080	-0.0021	0.0016	0.0031
10-14		-0.0200	-0.0193	-0.0194	-0.0139	-0.0101	-0.0086
15-19		-0.0274	-0.0269	-0.0274	-0.0230	-0.0190	-0.0175
20-24		-0.0056	-0.0057	-0.0069	-0.0019	0.0020	0.0035
25-29		-0.0014	-0.0006	-0.0019	0.0027	0.0066	0.0081
30-34		-0.0056	-0.0053	-0.0062	-0.0025	0.0016	0.0031
35-39		-0.0145	-0.0143	-0.0148	-0.0124	-0.0080	-0.0065
40-44		-0.0189	-0.0188	-0.0188	-0.0179	-0.0132	-0.0117
45-49		-0.0210	-0.0212	-0.0210	-0.0212	-0.0163	-0.0148
50-54		-0.0201	-0.0204	-0.0202	-0.0211	-0.0160	-0.0145
55-59		-0.0195	-0.0197	-0.0194	-0.0209	-0.0157	-0.0142
60-64		-0.0206	-0.0208	-0.0205	-0.0225	-0.0172	-0.0157
65-69		-0.0221	-0.0225	-0.0222	-0.0247	-0.0193	-0.0179
70-74		-0.0236	-0.0241	-0.0238	-0.0268	-0.0213	-0.0198
75-79		-0.0255	-0.0260	-0.0257	-0.0294	-0.0238	-0.0223
80-84		-0.0240	-0.0244	-0.0241	-0.0289	-0.0231	-0.0216
85-89		-0.0169	-0.0176	-0.0173	-0.0236	-0.0175	-0.0160
90-94		-0.0077	-0.0085	-0.0081	-0.0162	-0.0098	-0.0083
95-99		0.0063	0.0054	0.0057	-0.0043	0.0024	0.0039
100-104		0.0348	0.0339	0.0343	0.0229	0.0299	0.0313
Birth proportion − 0.5 [d]			0.6798	0.6778	0.6929	0.6992	0.6992
Year = 1918				0.0611	0.0725	0.0725	0.0728
Year = 1919				-0.0481	-0.0362	-0.0355	-0.0352
log IMR					-0.0108	-0.0088	-0.0088
(log IMR) × (Age = 0)						-0.0620	-0.0745
(log IMR) × (Age = 1)						0.0259	0.0259
(log IMR − log 0.01) × (Age = 0) × ($IMR < 0.01$)							0.1673
R^2 [e]	0.0000	0.6963	0.7163	0.7264	0.7492	0.7743	0.7768

See notes for Table A.1

Appendix B Computational methods for fitting cubic splines

B.1 Splitting nx1 data into 1x1 format

Aggregated death counts are split into a 1x1 format using cubic splines fitted to the cumulative distribution of deaths within each calendar year. Let $Y(x) = \sum_{u=0}^{x-1} D_u$ be the cumulative number of deaths up to age x, and assume that $Y(x)$ is known for a limited collection of ages always including $x = 1$ and $x = 5$. Following McNeil *et al.* (1977), we fit a cubic spline to $Y(x)$ in the form of the following equation:

$$Y(x) = \alpha_0 + \alpha_1 x + \alpha_2 x^2 + \alpha_3 x^3 + \beta_1 (x - k_1)^3 I(x > k_1) + \cdots + \beta_n (x - k_n)^3 I(x > k_n) \quad , \tag{B.1}$$

where $\alpha_0, \ldots, \alpha_3, \beta_1, \ldots, \beta_n$ are coefficients that must be estimated. The indicator function, $I(.)$, equals one if the logical statement within parentheses is true and zero if it is false. Along the x-axis, there are n "knots" denoted by k_i, $i = 1, \ldots, n$, and lower and upper boundaries denoted by a and b, respectively. In general, the knots are those values of x for which $Y(x)$ is known from the data, except for the lowest and highest such values.

We require that $k_1 = 1$, and k_n equals the lower limit of the open age interval. We always have $a = 0$ and $b = \omega$, where ω is set arbitrarily to the maximum of 105 or $k_n + 5$.[25] Thus, we know $n + 2$ values of $Y(x)$, for $x = 0, 1, \ldots, k_n$, and ω, but the above equation contains $n + 4$ unknown parameters. Therefore, two additional constraints are needed in order to compute the coefficients. Typical solutions usually involve constraining the slope of the function at the boundaries. At the upper boundary, for example, we constrain the slope to be zero. Thus, $Y'(\omega) = 0$. This choice is consistent with the usual tapering of the distribution of deaths at the oldest ages. However, a similar constraint at the lower boundary would not be appropriate, since deaths are highly concentrated at age 0. Instead, we constrain the slope of the function at age 1 to equal one half the increment (in cumulative deaths) between ages 1 and 5. Thus, $Y'(1) = \dfrac{Y(5) - Y(1)}{2}$. Since $Y'(1) \approx D(1)$, this formula is based on the observation that about half of all deaths between ages 1 and 5 tend to occur during the second year of life (at all levels of mortality). The first derivative of $Y(x)$ is as follows:

$$Y'(x) = \alpha_1 + 2\alpha_2 x + 3\alpha_3 x^2 + 3\beta_1 (x - k_1)^2 I(x > k_1) + \cdots + 3\beta_n (x - k_n)^2 I(x > k_n) \quad . \tag{B.2}$$

Fitting the cubic spline function consists of solving a system of $n + 4$ linear equations. These

[25] Note that this choice makes no difference, since we do not use the fitted spline curve to split death counts in the open age interval anyway.

equations can be written as follows:

$$\begin{pmatrix} 1 & 0 & 0 & 0 & 0 & 0 & \cdots & 0 & 0 \\ 1 & k_1 & k_1^2 & k_1^3 & 0 & 0 & \cdots & 0 & 0 \\ 1 & k_2 & k_2^2 & k_2^3 & (k_2-k_1)^3 & 0 & \cdots & 0 & 0 \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\ 1 & k_n & k_n^2 & k_n^3 & (k_n-k_1)^3 & (k_n-k_2)^3 & \cdots & (k_n-k_{n-1})^3 & 0 \\ 1 & \omega & \omega^2 & \omega^3 & (\omega-k_1)^3 & (\omega-k_2)^3 & \cdots & (\omega-k_{n-1})^3 & (\omega-k_n)^3 \\ 0 & 1 & 2 & 3 & 0 & 0 & \cdots & 0 & 0 \\ 0 & 1 & 2\omega & 3\omega^2 & 3(\omega-k_1)^2 & 3(\omega-k_2)^2 & \cdots & 3(\omega-k_{n-1})^2 & 3(\omega-k_n)^2 \end{pmatrix} \begin{pmatrix} \alpha_0 \\ \vdots \\ \alpha_3 \\ \beta_1 \\ \vdots \\ \beta_n \end{pmatrix} = \begin{pmatrix} 0 \\ Y(1) \\ \vdots \\ Y(k_n) \\ Y(\omega) \\ \left[Y(5)-Y(1)\right]/2 \\ 0 \end{pmatrix} \tag{B.3}$$

Writing this equation as $\mathbf{Ac} = \mathbf{d}$, the vector of coefficients can be found by computing $\mathbf{c} = \mathbf{A^{-1}d}$. Once the coefficients are computed by this method, the estimated equation is used to find fitted values, $\hat{Y}(x)$, for $x = 0, 1, 2, \ldots, k_n$. For all ages below the open age interval, deaths by single years of age are estimated by differencing:

$$\hat{D}_x = \hat{Y}(x+1) - \hat{Y}(x) \qquad , \tag{B.4}$$

for $x = 0, 1, 2, \ldots, k_{n-1}$.

The choice of constraints is very important. One drawback of the spline method is that the fitted curve may not be monotonically increasing over all ages. Since the curve depicts the cumulative deaths over age, a decreasing function between ages x and $x+1$ implies negative death counts at age x. We have tried to choose constraints that minimize the possibility of such an occurrence. Nevertheless, there seems to be no reliable solution at the oldest ages, and the spline function often starts to decline within the open age group. For this reason, we use a different method for splitting deaths from an open age interval into finer categories. Fortunately, the constraint applied to the slope at age 1 seems to work in all cases, yielding a curve that is always monotonically increasing at younger ages.

B.2 Splitting period-cohort data covering multiple cohorts

With minor modifications, the method described above can be used to split period-cohort data covering multiple cohorts (usually in the shape of a parallelogram) into data for single-year birth cohorts. For example, suppose we know the values of $Y(1), Y(4.5), Y(9.5), \ldots, Y(99.5)$, where by definition $Y(x+\frac{1}{2}) = \sum_{j=0}^{x-1}\left[D_L(j) + D_U(j)\right] + D_L(x)$ is the cumulative number of deaths up to and including the lower triangle of age x. Then, we can fit a cubic spline with knots at those values. Because $Y(4.5)$ is known instead of $Y(5)$, we use a modified constraint: $Y'(1) = \frac{Y(4.5)-Y(1)}{1.83}$.[26]

[26] This modification derives from assuming that the deaths between exact ages 2 and 5 are uniformly distributed. Following our earlier logic, these deaths comprise half of all deaths between ages 1 and 5. If they are uniformly distributed, losing the upper triangle at age 4 means we are missing $\frac{1}{2} \cdot \frac{1}{6} = \frac{1}{12}$ of all deaths between ages 1 and 5. Thus, we have: $Y^{'}(1) = \frac{Y(5)-Y(1)}{2} = \frac{\frac{12}{11}[Y(4.5)-Y(1)]}{2} = \frac{Y(4.5)-Y(1)}{1.83}$.

From the fitted values, $\hat{Y}(x+\frac{1}{2})$, we obtain estimates of deaths for single-year cohorts by computing first differences. Then, following our usual practice, the resulting period-cohort death counts are split 50/50 to obtain estimated death counts by Lexis triangle. These two steps can be summarized as follows:

$$\hat{D}_U(x) = \hat{D}_L(x+1) = \frac{1}{2}\left[\hat{Y}(x+\frac{3}{2}) - \hat{Y}(x+\frac{1}{2})\right] \qquad , \qquad \text{(B.5)}$$

for $x \geq 1$.

Finally, we derive $\hat{D}_L(1) = \hat{Y}(1.5) - D(0)$.

Appendix C Method for splitting deaths in an open age interval

Our method for splitting deaths in an open age interval treats deaths above age $x^* - 20$ as though they come from a stationary population (where x^* is the lower boundary of the open age interval). Accumulating deaths backwards from the open age interval within a given calendar year, we divide by all deaths at ages $x^* - 20$ and older to get the *observed* cumulative proportion of deaths in that range that lie above age x_i^*:

$$S(x^* - i) = \frac{{}_\infty D_{x^*-i}}{{}_\infty D_{x^*-20}} \qquad , \tag{C.1}$$

for $i = 0, 1, \ldots 20$, where ${}_\infty D_{x^*-i}$ is the number of deaths in the age interval from age $x^* - i$ and above (including the open age interval). This procedure yields a fictitious survival function (conditional on survival to age $x^* - 20$), corresponding to a kind of "synthetic extinct cohort" (i.e., an extinct cohort based on period death counts).

We fit the Kannisto model of old-age mortality (Thatcher et al., 1998) to this fictitious survival function. The Kannisto model has the following form:

$$\mu(x) = \frac{ae^{b(x-x_0)}}{1 + ae^{b(x-x_0)}} \qquad , \tag{C.2}$$

where $x_0 = x^* - 20$, and a and b are unknown parameters. The corresponding survival function is given by:

$$s(x) = \left(\frac{1 + a}{1 + ae^{b(x-x_0)}} \right)^{1/b} \qquad . \tag{C.3}$$

To summarize, we treat deaths within the calendar year as though they occurred in a stationary population with an age-specific pattern of mortality following the Kannisto model. Therefore, by assumption, the predicted proportion of deaths in the population above age x is:

$$\hat{S}(x) = \hat{s}(x), \quad \text{for } x = x_0, x_0 + 1, \ldots, \omega \qquad . \tag{C.4}$$

We fit the model in order to estimate parameters a and b.[27] Using equation (C0) and these estimates of $\hat{a}$ and $\hat{b}$, we predict:

$$d(x) = \hat{s}(x) - \hat{s}(x + 0.5), \quad \text{for } x = x^*, x^* + 0.5, x^* + 1, x^* + 1.5, \ldots, \omega \qquad . \tag{C.5}$$

Then, we apply these $d(x)$ to ${}_\infty D_{x^*}$ (and divide by the proportion surviving to age x^*) in order to derive the distribution of deaths by Lexis triangle within the open age interval beginning at age x^*:

$$\hat{D}_L(x) = {}_\infty D_{x^*} \cdot \frac{d(x)}{\hat{s}(x^*)} \quad \text{and} \quad \hat{D}_U(x) = {}_\infty D_{x^*} \cdot \frac{d(x + 0.5)}{\hat{s}(x^*)}, \quad \text{for } x = x^*, x^* + 1, \ldots .\omega \qquad . \tag{C.6}$$

If the estimated number of deaths in a given Lexis triangle is less than 0.25, we assume there are no deaths in that triangle or above. The estimated deaths at ages below that triangle (within

[27] To fit the model, we minimize the squared differences between the logarithms of observed and predicted cumulative proportions: $\sum_{i=0}^{19} [\ln S(x^* - i) - \ln \hat{S}(x^* - i)]^2$ stopping at $i = 19$ because $S(x^* - 20)$ and $\hat{S}(x^* - 20)$ equal 1.0 by definition.

the open age interval) are then adjusted proportionally (i.e., multiplied by a constant) so that their sum is equal to ${}_{\infty}D_{x^*}$. This entire procedure is applied separately to male and female death counts and then total death counts are obtained by summing.

C.1 Correction for Unusual Fluctuations in Deaths

In some cases, there may be an unusual fluctuation in death counts within the age range (from $x^* - 20$ to x^*) used to fit the Kannisto model. For example, a cohort in this age range may be particularly small relative to nearby cohorts because of some historical event (e.g., a war) and thus, experience fewer deaths. In such cases, we may want to exclude that outlier before fitting the model, or else we are likely to under-estimate the number of deaths at the start of the open age interval. In order to avoid this problem, we introduce a correction to the method described above. Prior to fitting the model, we first apply a procedure to identify any outliers, and if found, exclude the age range associated with the period of unusual fluctuations before fitting the model. In our experience, unusually small cohort sizes influence model fitting much more than unusually large cohorts, and so we only remove these. The procedure for identifying outliers proceeds as follows:

1. We calculate first differences in deaths $\Delta D(x)$:

$$\Delta D(x) = D(x+1) - D(x), \quad \text{for } x = x^* - 25, x^* - 24, \ldots, x^* - 2 \qquad . \tag{C.7}$$

   Figure C-1 shows an example where $\Delta D(80)$ has a large negative value (i.e., there was a large decrease in deaths between ages 80 and 81) and $\Delta D(84)$ has a large positive value (i.e., there was a large increase in deaths between ages 84 and 85).

2. We identify the trend in $\Delta D(x)$ by fitting a cubic smoothing spline that minimizes the following function:

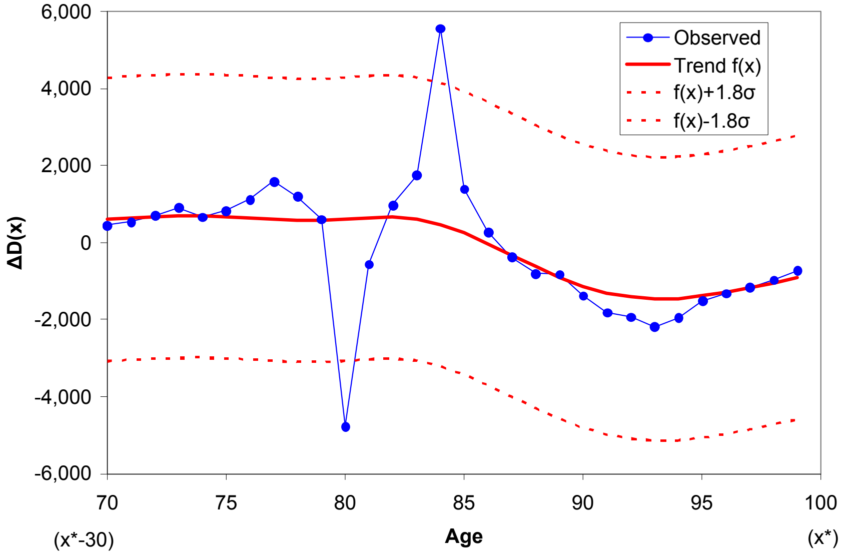
$$p \sum_{x=x^*-25}^{x^*-2} (\Delta D(x) - f(x))^2 + (1-p) \int_{x^*-25}^{x^*-2} \left[f''(x)\right]^2 \, dx \qquad , \tag{C.8}$$

   where p is the smoothing parameter and $f(x)$ is a standard cubic spline function (e.g., see McNeil et al., 1977 and equation B.1). As p tends toward 0, the result approaches the least-squares linear fit (i.e., a straight line), whereas for $p = 1$, the result is the natural cubic spline. As p varies from 0 to 1, the result moves from one extreme to the other. We use $p = 0.0005$ because it provides a suitable compromise between a trend that would identify too many fluctuations as outliers (e.g., linear fit) and one that requires the trend to pass through each of the observed data points (i.e., no outliers are identified). Figure C.1 shows the trend $f(x)$ plotted against observed values of $\Delta D(x)$.

3. We define $\Delta D(x)$ to be an outlier if:

$$|\Delta D(x) - f(x)| > 1.8\sigma \qquad , \tag{C.9}$$

Figure C.1: First differences in deaths, West German females, 1999



where σ represents the standard deviation of the difference between $\Delta D(x)$ and $f(x)$. Figure C.1 shows $f(x) \pm 1.8\sigma$. Any $\Delta D(x)$ that falls outside the range of plus or minus 1.8 standard deviations is defined as an outlier (e.g., $\Delta D(80)$ and $\Delta D(84)$ in this example).[28]

4. The age range associated with each period of unusual fluctuations will be identified by two outliers on $\Delta D(x)$: one at the age where the largest negative outlier fluctuation begins x_{min} and $\Delta D(x_{\text{min}}) < 0$, and one at the age where the largest positive outlier fluctuation ends x_{max} and $\Delta D(x_{\text{max}}) > 0$. We then substitute the interpolated values, based on a cubic smoothing spline similar to equation C.8), for all observations from ages x_{min} to x_{max} before fitting the model.[29] So, in this example, we substitute the *estimated* proportion of survivors for the *observed* proportion of survivors $S(80), S(81), \ldots, S(84)$ (see equation C.8) before fitting

[28] We designed this procedure using data for France, Sweden, and Czech Republic. Based on visual inspection of the data, we identified observations that appeared to be outliers. Then, we set the parameters ($p = 0.0005$ and $+1.8\sigma$) for the procedure such that we detected all "real" outliers (based on our subjective evaluation), but minimized the number of false positives. Nonetheless, in most cases, treating "false positives" as outliers did not change the mortality estimates, whereas excluding "real" outliers had a substantial effect on the estimates. The procedure has been tested for all HMD populations and yields satisfactory and consistent results.

[29] We only subistute the model values if the total age-span of the detected unusual fluctuation is less than 8 and if the total number of outlier deviations is less than 5.

the model, using $\tilde{D}(81), \tilde{D}(82), \ldots, \tilde{D}(85)$ instead of $D(81), D(82), \ldots, D(85)$, where $\tilde{D}(x)$ is derived by minimizing the following function:

$$\sum_{x=x^*-25}^{x^*-1} (D(x) - f(x))^2 + (1-p) \int_{x=x^*-25}^{x^*-1} \left[f''(x)\right]^2 \, dx. \tag{C.10}$$

C.2 Correction for Cohort Size

Another potential problem with the basic method for splitting the open age interval is that sometimes deaths for a particular cohort *within the open age interval* may be under- or over-estimated by the model as a result of variations in cohort size. For example, a cohort may be unusually small (e.g., those born in time of war) relative to other cohorts in that same period; if that cohort falls within the open age interval, then the model may over-estimate deaths for that cohort. To address this problem, we make a final correction for cohort size after splitting deaths in the open age interval as described above. This correction essentially redistributes deaths to take account of the size of each respective cohort relative to other nearby cohorts within the open age interval.

For each cohort born in year $t - x$, where x is the age at last-birthday on December 31st of year t for $x \geq x^*$, we perform the following steps:

1. We compare deaths for that cohort in the year in which they would attain age $x^* - 1$ relative to the average of deaths at the same age among nearby cohorts. For example, for $x = x^* + 3$ (the cohort represented by the period-cohort parallelogram in yellow in Figure C-2), we compute the ratio of deaths for that same cohort in year $t - 4$ (in the uppermost red parallelogram) to the average of deaths at the same age for the two previous cohorts and two later cohorts (shown in blue). If all five cohorts had the same number of deaths in the years they would attain age $x^* - 1$, then the resulting ratio would be 1.0.

2. We calculate similar ratios for ages $x^* - 5$ through $x^* - 2$ (as depicted in Figure C-2).

3. Then, we take the average of the ratios across these five age years ($x^* - 5$ to $x^* - 1$) as an estimate of the size of this cohort relative to nearby cohorts.

4. Next, we multiply the original estimate of deaths in the open age interval (derived using methods described in previous sections) by this adjustment ratio. Following the earlier example, the adjustment ratio based on the deaths shown in red in Figure C.2 is applied to the original estimates of $D_U(x^* + 2, t)$ and $D_L(x^* + 3, t)$ shown in yellow.

5. Finally, we make one last minor adjustment to ensure that the estimates add up to the original sum in the open age interval.

Of course, this procedure requires that the data are available to make these calculations. For the example shown in Figure C-2), we could not complete the calculations described above if the data series began in year $t - 4$. Therefore, given the estimate of $D_U(x - 1, t)$ where $x - 1 \geq x^*$, or $D_L(x, t)$ where $x \geq x^*$, we make no correction for cohort size if $t_{\min} \geq t - (x - x^*)$, where $t_{\min}$ is the first year of the data series. Furthermore, if the original raw death counts for the period used to make these calculations are not available by (at least) one-year age groups, we make no correction for cohort size.

Given that $t_{\text{min}} < t - (x - x^*)$, following the five steps listed above, we adjust the original estimates of $D_U(x-1,t)$ and $D_L(x,t)$ as follows in order to correct for fluctuations in cohort size:

$$\hat{D}_U(x-1,t) = r(x) \cdot D_U(x-1,t), \quad \text{for } x = x^*+1, x^*+2, \ldots, \omega \tag{C.11}$$

and

$$\hat{D}_L(x,t) = r(x) \cdot D_L(x,t), \quad \text{for } x = x^*, x^*+1, x^*+2, \ldots, \omega, \tag{C.12}$$

where

$$r(x) = \frac{1}{n}\sum_{j=1}^{n} r(x)_j, \tag{C.13}$$

$$n = \min(t - t_{\text{min}} - (x - x^*), 5), \tag{C.14}$$

$$r(x)_j = \frac{D_U[x^* - j - 1, t - j - (x - x^*)] + D_L[x^* - j, t - j - (x - x^*)]}{\sum_{i=x-m}^{x+1} \left(D_U[x^* - j - 1, t - j - (i - x^*)] + D_L[x^* - j, t - j - (i - x^*)]\right) / \left(l + m + 1\right)}, \tag{C.15}$$

where

$$l = \min(t - t_{min} - j - (x - x^*)), 2), \tag{C.16}$$

and

$$m = \min(x - x^*, 2). \tag{C.17}$$

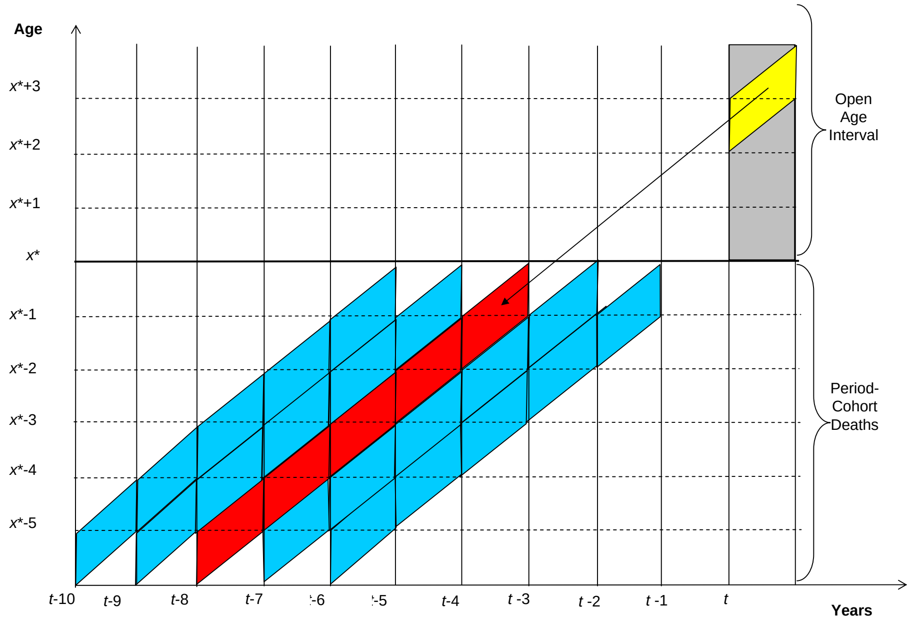
Then, we calculate the final estimates $\tilde{D}_U(x-1,t)$ and $\tilde{D}_L(x,t)$ using the following adjustment to ensure that they sum to the original death count in the open age interval:

$$\tilde{D}_U(x-1,t) = \hat{D}_U(x-1,t) \cdot \frac{{}_{\infty}D_{x^*}(t)}{\sum_{i=x^*}^{\omega} [\hat{D}_L(i,t) + \hat{D}_U(i,t)]} \tag{C.18}$$

and

$$\tilde{D}_L(x,t) = \hat{D}_L(x,t) \cdot \frac{{}_{\infty}D_{x^*}(t)}{\sum_{i=x^*}^{\omega} [\hat{D}_L(i,t) + \hat{D}_U(i,t)]} \tag{C.19}$$

Figure C.2: Example depicting the procedure to correct for cohort size



Appendix D Adjustments for changes in population coverage

Some of the countries included in the HMD have experienced changes in their territorial boundaries. These changes must be taken into account when computing death rates and life tables (unless the changes are very small in relation to population size). In general, death counts must always refer to the same territory as the exposure-to-risk when calculating death rates. Likewise, when using birth counts as a measure of relative cohort size (in splitting 1x1 death counts into Lexis triangles), the birth series must refer to the same territory. With these principles in mind, we make some special calculations for countries with changing territories during the time period covered by the HMD.

Before describing these calculations, let us consider the format of the relevant data. Although territorial changes may occur at any time during a calendar year, administrative data (i.e., birth and death counts) typically reflect such changes on January 1^{st}. Therefore, throughout this discussion we assume that the territorial change occurs on January 1^{st} and that birth and death counts within an individual calendar year always refer to an unchanging territory.

D.1 Birth counts used in splitting 1x1 deaths

As described earlier, we use a birth series as a measure of relative cohort size as part of our method for splitting 1x1 death data into triangles. Suppose that this birth series is based on a changing territory. Then, the size of two successive cohorts may appear to change merely as a result of past territorial changes. If we use such a series in our calculations, we will introduce "artificial cohort effects" into our estimated death counts. Therefore, we adjust the birth series so that it refers to the same territory.

Suppose that a territorial change occurs on January 1st of year t. Define

$$R_b(t) = \frac{B^+}{B^-} \tag{D.1}$$

to be the ratio of births in the new territory, B^+, to births in the old territory, B^-, either in year t or $t-1$ (see below). Therefore, in order to calculate $R_b(t)$ for the period covered by the birth series, we need birth data for the territory gained or lost during each territorial change. If territory was gained in year t, then we base the calculation on the number of births in year t. B^- is calculated as the total births minus the births in the territory added, while B^+ is simply the total births in year t. On the other hand, if territory was lost in year t, then we base the calculation on the number of births in year $t-1$. B^- is simply the total births (including the area lost) in year $t-1$, while B^+ is calculated as the total births in year $t-1$ minus the births for the territory lost.[30] Thus, in either case, the data for both the numerator and the denominator come from the same year (either t or $t-1$). For example, in 1954, the territory of Trieste was added to the Italian territory. Therefore, we calculate $R_b(1954)$ as the ratio of the births (in 1954) for the entire territory (including Trieste), B^+, to the births (in 1954) for the territory excluding Trieste, B^-, resulting in $R_b(1954) = 1.003$. If there was no territorial change in year t, then $R_b(t) = 1.0$ by default.

The formulas shown in equations 5 and 6 (p. 13) are then modified as follows:[31]

$$\pi_b(x,t) = \frac{B(t-x)}{B(t-x) + B(t-x-1) \cdot R_b(t-x)} \quad , \tag{D.2}$$

and

$$\text{IMR}(t) = \frac{D(0,t)}{\frac{1}{3}B(t-1) \cdot R_b(t) + \frac{2}{3}B(t)} \quad . \tag{D.3}$$

Note that if there is no territorial change in year $t-x$, then $R_b(t-x) = 1.0$ by default and thus, drops out of equation D.2 leaving it exactly as shown in equation 5. Similarly, if there is no territorial change in year t, then $R_b(t)$ drops out of equation D.3 and the result is identical to equation 6.

Ideally, we would like to have a birth series back to the earliest cohort for which we have death data ($\approx$ 100 years prior to the earliest calendar year of deaths). In that case, we need $R_b(t)$ factors back to the beginning of the birth series (if there were territorial changes). For example, suppose we have death data for 1900–2000 in country X and there was a territorial change in 1850. Individuals who died at age 50 in 1900 were born in either 1849 or 1850. In order to calculate the birth

[30] In some cases, the necessary birth data may not be available. In such cases, we simply use the population adjustment factor at age 0 (see p. 60): $R_b(t) = V(0,t)$.

[31] The birth ratio calculated in equation D.2 is used in order to split deaths in year t, based on data from the years in which the respective cohorts were born (i.e., years t-x and t-x-1). Yet, if a territorial change occurred between years t-x and year t, then the territory covered at the time of death, year t, is not the same as the territory covered at the time these cohorts were born. Equation D.2 implicitly assumes that the birth ratio for the two cohorts is the same for the territory covered in year t-x as in the territory covered in year t.

proportion, $\pi_b(50, 1900)$, shown in (D.2), we need $R_b(1850)$. Nonetheless, in many cases we will not have birth data prior to the earliest death data, in which case we set $\pi_b(x,t) = 0.5$ by default and assume $B(t-1) = B(t)$ in order to calculate IMR(t) (see p. 13).

D.2 Extinct cohort methods

When we estimate population sizes using extinct cohort methods, we apply a different form of adjustment for territorial changes. Suppose that we are estimating $P(x)$ by this method, and that some territorial change occurs at time t. Define

$$V(x,t) = \frac{P^+(x)}{P^-(x)} \tag{D.4}$$

to be the ratio of the population size at age x just after this change (i.e., on January 1st of year t) to the comparable value just before the change (i.e., on December 31st of year $t-1$).

For the country in question, we require population counts by age (and sex if available) for the territory that is gained or lost during the territorial change as well as for the entire country. Preferably, we use population estimates near the time of the territorial change, but sometimes we may only have data from a census at time t^* (close to the territorial change at time t). If a territory was added, then we must use data from the subsequent census, whereas if territory was lost, then we use data from the census prior to the territorial change.

In some cases, the available data may be aggregated into age groups, in which cases the $V(x,t)$ factor is calculated for the age group and then applied to each single year of age within that age group. In fact, such data may be preferable because random variations across age are smoothed. Therefore, even if data by single year of age are available, we may still calculate the $V(x,t)$ factors by five-year age groups. In any case, at very high ages (e.g., age 90 and older), the $V(x,t)$ factor is calculated using aggregate data even if data by single year of age are used at younger ages. Aggregating across an open age interval at very old ages is necessary because the population counts by single year of age can become very small at high ages, resulting in $V(x,t)$ factors that are very erratic (including even zero or undefined values). If data are not available by age, then we must use $V(t)$ calculated from the total population of all ages.

If there are no further territorial changes during the life of this cohort, then we estimate

$$P^+(x,t) = \sum_{0}^{\infty} D_i^{\mathrm{v}}(x,t) \tag{D.5}$$

and

$$P^-(x,t) = \frac{P^+(x,t)}{V(x,t)} \qquad , \tag{D.6}$$

where

$$D_i^{\mathrm{v}}(x,t) = D_U(x+i, t+i) + D_L(x+i+1, t+i) \qquad ,$$

as defined earlier in equation (8).

Now, suppose there is no territorial change at time t, but rather at time t_1, where $t_1 > t$. Define $N_1 = t_1 - t$ (i.e., the time until the territorial change). We estimate $P(x,t)$ as follows:

$$P(x,t) = \sum_{i=0}^{N_1-1} D_i^{\mathrm{v}}(x,t) + \frac{1}{V(x+N_1,t_1)} \sum_{i=N_1}^{\infty} D_i^{\mathrm{v}}(x,t) \qquad . \tag{D.7}$$

If there is also a territorial change at time t, then this formula gives the value for $P^+(x,t)$.

For cohorts who live through more than one territorial change (at older ages), the above formula requires a slight modification. For example, assume that s territorial changes occur at times $t_1, \ldots, t_s$, where $t_s > \cdots > t_1 > t$. Define $N_1 = t_1 - t, \ldots, N_s = t_s - t$. Then, we estimate $P(x,t)$ as follows:

$$\begin{aligned} P(x,t) = {} & \sum_{i=0}^{N_1-1} D_i^{\mathrm{v}}(x,t) + \frac{1}{V(x+N_1,t_1)} \sum_{i=N_1}^{N_2-1} D_i^{\mathrm{v}}(x,t) \\ & + \frac{1}{V(x+N_1,t_1)V(x+N_2,t_2)} \sum_{i=N_2}^{N_3-1} D_i^{\mathrm{v}}(x,t) + \cdots \\ & + \frac{1}{V(x+N_1,t_1)\cdots V(x+N_{s-1},t_{s-1})} \sum_{i=N_{s-1}}^{N_s-1} D_i^{\mathrm{v}}(x,t) \\ & + \frac{1}{V(x+N_1,t_1)\cdots V(x+N_s,t_s)} \sum_{i=N_s}^{\infty} D_i^{\mathrm{v}}(x,t) \qquad . \end{aligned} \tag{D.8}$$

D.3 Intercensal survival methods

When we estimate population sizes using intercensal survival methods, we apply a similar adjustment for territorial changes. Referring to Figures 4a-c, suppose that a change in the territorial coverage of vital statistics occurs on January 1st of year $t_1 = t + N_1$, where $N_1 \leq N$ and N equals the number of complete calendar years between the two censuses. Given $V(x,t)$, defined as above, the main formulas for existing cohorts (Figure 4a) would be modified as follows:

$$\begin{aligned} \hat{C}_2 = {} & \left[C_1 - (D_a - D_b) - \sum_{i=0}^{N_1-1} D_i^{\mathrm{v}}(x,t) \right] \cdot V(x+N_1,t_1) \\ & - (D_c - D_d) - \sum_{i=N_1}^{N-1} D_i^{\mathrm{v}}(x,t) \end{aligned} \tag{D.9}$$

and

$$P(x+n,t+n)=\begin{cases} C_1-(D_a-D_b)-\displaystyle\sum_{i=0}^{n-1}D_i^{\mathrm{v}}(x,t) & \\ \quad+\dfrac{1-f_1+n}{N+1-f_1+f_2}\cdot\dfrac{\Delta_x}{V(x+N_1,t_1)} & \text{for } 0\le n<N_1 \\ & \\ \left[C_1-(D_a-D_b)-\displaystyle\sum_{i=0}^{N_1-1}D_i^{\mathrm{v}}(x,t)\right]\cdot V(x+N_1,t_1) & \\ \quad+\dfrac{1-f_1+n}{N+1-f_1+f_2}\Delta_x-\displaystyle\sum_{i=N_1}^{n-1}D_i^{\mathrm{v}}(x,t) \qquad . & \text{for } N_1\le n<N \end{cases} \tag{D.10}$$

Note that equation (D.10) provides two different estimates of $P(x+N_1,t_1)$, corresponding to the territory covered by the statistical system just before and after January 1^{st} of year $t_1=t+N_1$. Thus, $P^-(x+N_1,t_1)$ comes from the top part of the formula and $P^+(x+N_1,t_1)$ from the bottom part, and it is easy to confirm that $P^+(x+N_1,t_1)=P^-(x+N_1,t_1)\cdot V(x+N_1,t_1)$.

Similarly, for the infant cohort (Figure 4b), the modified formulas are as follows:

$$\begin{aligned}\hat{C}_2=&\left[C_1-D_a-\sum_{i=0}^{N_1-1}D_i^{\mathrm{v}}(0,t)\right]\cdot V(N_1,t_1)\\ &-(D_c+D_d)-\sum_{i=N_1}^{N-1}D_i^{\mathrm{v}}(0,t)\end{aligned} \tag{D.11}$$

and

$$P(n,t+n)=\begin{cases} C_1-D_a-\displaystyle\sum_{i=0}^{n-1}D_i^{\mathrm{v}}(0,t) & \\ \quad+\dfrac{\frac{1}{2}(1-f_1^2)+n}{N+\frac{1}{2}(1-f_1^2))+f_2}\cdot\dfrac{\Delta_0}{V(N_1,t_1)} & \text{for } 0\le n<N_1 \\ & \\ \left[C_1-D_a-\displaystyle\sum_{i=0}^{N_1-1}D_i^{\mathrm{v}}(0,t)\right]\cdot V(N_1,t_1) & \\ \quad+\dfrac{\frac{1}{2}(1-f_1^2)+n}{N+\frac{1}{2}(1-f_1^2)+f_2}\Delta_0-\displaystyle\sum_{i=N_1}^{n-1}D_i^{\mathrm{v}}(0,t) \qquad . & \text{for } N_1\le n<N \end{cases} \tag{D.12}$$

Finally, we consider the case of new cohorts born during the intercensal period. For those born after the territorial change (i.e., in calendar year $t+N_1$ or later), the standard formulas can be used. For those born before the territorial change, however, modified formulas are needed. Consider the cohort born in year $t+j$ where $0 \leq j < N_1$. As before, define $K = N - j - 1$ (the age of the cohort on January 1st before the second census). Also define $K_1 = N_1 - j - 1$ (the age of the cohort on January 1st of year $t + N_1$). Then, the modified formulas are as follows:

$$\begin{aligned}\hat{C}_2 = &\left[B_{t+j} - D_L(0, t+j) - \sum_{i=0}^{K_1-1} D_i^{\text{v}}(0, t+j+1)\right] \cdot V(K_1, t_1) \\ &- (D_c + D_d) - \sum_{i=K_1}^{K-1} D_i^{\text{v}}(0, t+j+1)\end{aligned} \quad , \tag{D.13}$$

and

$$P(k, t{+}j{+}k{+}1) = \begin{cases} \begin{aligned} &B_{t+j} - D_L(0, t+j) - \sum_{0}^{k-1} D_i^{\text{v}}(0, t+j+1) \\ &\quad + \frac{2k+1}{2K+1+2f_2} \cdot \frac{\Delta'_{t+j}}{V(K_1, t_1)} \end{aligned} & \text{for } 0 \leq k < K_1 \\ \\ \begin{aligned} &\left[B_{t+j} - D_L(0, t+j) - \sum_{i=0}^{K_1-1} D_i^{\text{v}}(0, t+j+1)\right] \cdot V(K_1, t_1) \\ &+ \frac{2k+1}{2K+1+2f_2} \Delta'_{t+j} - \sum_{i=K_1}^{k+1} D_i^{\text{v}}(0, t+j+1) \quad . \end{aligned} & \text{for } K_1 \leq k < K \end{cases} . \tag{D.14}$$

Sometimes more than one territorial change occurs during an intercensal interval. In this situation, the formulas are only slightly more complicated. Suppose that s territorial changes occur at times $t_1 = t + N_1$, $\ldots$, $t_s = t + N_s$. The formulas above are for the case where $s = 1$. If $s = 2$, the formulas for existing cohorts would be as follows:

$$\begin{aligned}\hat{C}_2 = &\left[C_1 - (D_a + D_b) - \sum_{i=0}^{N_1-1} D_i^{\text{v}}(x, t)\right] \cdot V(x + N_1, t_1) \cdot V(x + N_2, t_2) \\ &- \sum_{i=N_1}^{N_2-1} D_i^{\text{v}}(x, t) V(x + N_2, t_2) - \sum_{i=N_2}^{N-1} D_i^{\text{v}}(x, t) - (D_c + D_d)\end{aligned} \tag{D.15}$$

and

$$P(x{+}n,t{+}n)=\begin{cases} C_1-(D_a+D_b)-\displaystyle\sum_{i=0}^{n-1}D_i^{\mathrm{v}}(x,t) & \\ \quad+\dfrac{1-f_1+n}{N+1-f_1+f_2}\cdot\dfrac{\Delta_x}{V(x+N,t_1)\cdot V(x+N_2,t_2)} & \text{for } 0\le n<N_1 \\[2ex] \left[C_1-(D_a+D_b)-\displaystyle\sum_{i=0}^{N_1-1}D_i^{\mathrm{v}}(x,t)\right]\cdot V(x+N_1,t_1) & \\ \quad+\dfrac{1-f_1+n}{N+1-f_1+f_2}\dfrac{\Delta_x}{V(x+N_2,t_2)}-\displaystyle\sum_{i=N_1}^{n-1}D_i^{\mathrm{v}}(x,t) & \text{for } N_1\le n<N_2 \\[2ex] \left[C_1-(D_a+D_b)-\displaystyle\sum_{i=0}^{N_1-1}D_i^{\mathrm{v}}(x,t)\right]\cdot V(x+N_1,t_1)\cdot V(x+N_2,t_2) & \\ \quad-\displaystyle\sum_{i=N_1}^{N_2-1}D_i^{\mathrm{v}}(x,t)V(x+N_2,t_2)+\dfrac{1-f_1+n}{N+1-f_1+f_2}\Delta_x-\displaystyle\sum_{i=N_2}^{n-1}D_i^{\mathrm{v}}(x,t)\quad . & \text{for } N_2\le n<N \end{cases} \tag{D.16}$$

These formulas can be adapted as well to cases where $s > 2$. Formulas for the infant cohort and new cohorts receive similar modifications to adjust for territorial changes.

D.4 Linear interpolation

When we use linear interpolation to calculate population size on January 1st (for example, when we have reliable population estimates referring to July 1st of each adjacent year), it is important to ensure that both populations refer to the same territory. When a territorial change occurs on January 1st of year *t,* we multiply the population estimate for the given date in year $t-1$ by $V(x,t)$ before performing linear interpolation. In this way, the population in year t-1 is adjusted to reflect the same territory as on January 1st of year t.

D.5 Period death rates around the time of a territorial change

In the event of a territorial change, the formula for the exposure-to-risk (shown in equation(50)), which is used to calculate the period death rate, requires a minor modification. Suppose there is a territorial change on January 1st of year $t+1$. The exposure-to-risk in the age interval $[x, x+1)$ during calendar year t is then calculated as follows:

$$E_x = s_1P^-(x,t+1) + s_2D_L(x,t) + u_1P(x,t) - u_2D_U(x,t) \qquad . \tag{D.17}$$

With an assumption of uniformity (of both birthdays and deaths), this becomes:

$$E_x = \big[P(x,t) + P^-(x,t+1)\big] + \frac{1}{6}\left[D_L(x,t) - D_U(x,t)\right] \qquad , \tag{D.18}$$

where $P^{-}(x, t+1)$ is the population at age x just before the territorial change.

D.6 Cohort mortality estimates around the time of a territorial change

Territorial changes present a special problem for cohort life table calculations. Fortunately, the solution is fairly simple. Let D_L and D_U be the cohort death counts at some age just before and after a territorial change (assumed to occur on January 1^{st}). Also, let P^{-} and P^{+} be population estimates (at the same age) just before and after this change. Define $D_U^{*} = \frac{P^{-}}{P^{+}} D_U$, which represents the upper-triangle deaths that would have occurred in the original territory. D_U^{*} substitutes into the equation (60) as follows:

$$M^{c}(x,t) = \frac{D_L(x,t) + D_U^{*}(x,t+1)}{P^{-}(x,t+1) + z_L D_L(x,t) - z_U D_U^{*}(x,t+1)} \quad . \tag{D.19}$$

This raw death rate is then taken as the life table rate, m_x. a_x is calculated as:

$$a_x = \frac{z_L D_L(x,t) + (1 - z_U) D_U^{*}(x,t+1)}{D_L(x,t) + D_U^{*}(x,t+1)} \quad . \tag{D.20}$$

Assuming a uniform distribution of deaths within Lexis triangles, it follows that

$$M^{c}(x,t) = \frac{D_L(x,t) + D_U^{*}(x,t+1)}{P^{-}(x,t+1) + \frac{1}{3}\left(D_L(x,t) - D_U^{*}(x,t+1)\right)} \tag{D.21}$$

and

$$a_x = \frac{\frac{1}{3} D_L(x,t) + \frac{2}{3} D_U^{*}(x,t)}{D_L(x,t) + D_U^{*}(x,t+1)} \quad . \tag{D.22}$$

In both cases, $q_x = \frac{D_L(x,t) + D_U^{*}(x,t+1)}{P^{-}(x,t+1) + D_L(x,t)}$.

These three quantities are mutually consistent, like other cohort quantities. Equivalent values are obtained if instead we define $D_L^{*}(x, t-1) = \frac{P^{+}(x,t)}{P^{-}(x,t)} D_L(x, t-1)$, which represents the lower-triangle deaths that would have occurred in the new territory, and compute using $P^{+}(x,t)$ instead of $P^{-}(x,t)$.

D.7 Other changes in population coverage

Sometimes there may be changes in the coverage of demographic data that are not due to territorial changes, but can be treated as such in order to make the appropriate adjustments to the formulas. For example, in some countries the vital statistics collection system changed from covering the *de facto* population to covering the *de jure* population at some time t. In order to account for this change in the birth and death count data, we treat it as a territorial change and calculate $V(x,t)$ factors based on the *de jure* population and the *de facto* population at the time of the change in population coverage. We then use $V(x,t)$ as an estimate of $R_b(t)$.

Appendix E Computing death rates and probabilities of death

The purpose of this appendix is to describe and justify the methods used for computing death rates and probabilities of death in the HMD. We consider the case where death counts are available by Lexis triangles and population estimates are available by single years of age for individual calendar years (see Figures 9 and 10 of the main text; also, see Appendices A and B for the methods used to split 1×1 or 5×1 data, if needed). We begin by exploring the implications of assuming uniform distributions of births and deaths, and show in that simple case how period death rates and probabilities of death are derived. We then generalize the method for situations where we have information about the distribution of births by month. Finally, we derive the main formulas for cohort death rates and probabilities of death.

E.1 Uniform distributions of births and deaths

In the absence of contrary evidence we assume that births are distributed uniformly within a calendar year. Also assuming equal survival probabilities to age x within the birth cohort, a uniform distribution of births in year $t-x$ implies a uniform distribution of birthdays at age x in year t. With such assumptions, it follows that the average contribution to $E_L(x,t)$ by the $N(x,t)$ persons celebrating their birthday at age x in year t would be one half, if none dies before the end of the year. Likewise, the average contribution to $E_U(x,t)$ by the $N(x+1,t)$ persons who survive to celebrate their birthday at age $x+1$ in that year would also be one half.

We also often assume that deaths are distributed uniformly within individual Lexis triangles. The main results following from this assumption are summarized in Table E.1. For example, with assumptions of uniformity, deaths in the age interval $[x,x+1)$ occur, on average, at age $x+\frac{1}{3}$ if they occur in ⊿ and at age $x+\frac{2}{3}$ in ◸ . Deaths in either triangle contribute, on average, $\frac{1}{3}$ of a person-year of exposure within the triangle where the death occurred. At the same time, all deaths result in, on average, an equivalent amount of lost exposure within their respective triangles (relative to what the individual would have contributed if s/he had exited the triangle as a survivor).

These relationships are not necessarily intuitive and must be derived using calculus. The uniformity assumption implies that the probability density of deaths is 2 over the triangle (because the total area is 1/2). The values in Table E.1 are then found by integrating over age and time. For

Table E.1: Implications of assuming uniform distributions of deaths within Lexis triangles (at age x)

	Lower triangle ⊿	Upper triangle ◸
Average age at death	$x+\frac{1}{3}$	$x+\frac{2}{3}$
Average contribution (per death) to exposure within triangle	$\frac{1}{3}$	$\frac{1}{3}$
Average lost exposure (per death) within triangle	$\frac{1}{3}$	$\frac{1}{3}$

example, the average age at death in a lower triangle, ⊿, is found by solving the following double integral:

$$\int_0^1 \int_0^t 2(x+s)\, \mathrm{d}s\, \mathrm{d}t = x + \frac{1}{3} \qquad . \tag{E.1}$$

Similarly, the average lost exposure for a death in the upper triangle, ◸, is:

$$\int_0^1 \int_t^1 2(1-s)\, \mathrm{d}s\, \mathrm{d}t = \frac{1}{3} \qquad . \tag{E.2}$$

Thus, assuming uniform distributions for both births and deaths, and equal survival probabilities within annual birth cohorts, the exposure to risk within the lower and upper triangles is as follows:

$$E_L = \frac{1}{2}N_x - \frac{1}{3}D_L = \frac{1}{2}(P_2 + D_L) - \frac{1}{3}D_L = \frac{1}{2}P_2 + \frac{1}{6}D_L \tag{E.3}$$

and

$$E_U = \frac{1}{2}N_{x+1} + \frac{1}{3}D_U = \frac{1}{2}(P_1 - D_U) + \frac{1}{3}D_U = \frac{1}{2}P_1 - \frac{1}{6}D_U \quad ,$$

where P_1 and P_2 are the population estimates for January 1 and December 31, respectively.

E.2 ⧄ Period death rates and probabilities

As depicted in Figure 9 (main text), period death rates and probabilities of death are measured over the 1×1 Lexis square, ⧄, that lies between exact ages x and $x+1$ during some calendar year. Therefore, these quantities reflect the blended experience of two birth cohorts. As explained in the main text, we begin by computing the period death rate within ⧄, which we then convert to a probability of death by assuming $a_x = 0.5$ and using equation (71). Although this is a standard method, it lacks the desirable property enjoyed by our method for computing cohort quantities, since it is not reversible: if we begin by computing the probability of death directly from data and converting it to a death rate, we obtain a slightly different result. We adopt the method used here because it includes an explicit calculation of the exposure-to-risk, which is needed for statistical modeling, and because the link between death rates and probabilities of death is well defined.[32]

Our method for converting death rates into probabilities of death has already been described in the main text. Furthermore, it is a familiar technique (Preston et al. 2001) and requires no particular justification here. Therefore, our only task in this section is to justify our method of computing the exposure-to-risk that forms the denominator of the period death rate. As before, we assume that there is no migration within ⧄ and deal with the case of a closed population (the error introduced by this assumption is usually negligible).

[32] It is common in the French demographic tradition to compute probabilities of dying directly from data, using the method of *partial quotients* (Pressat 1972). In this tradition, death rates are also computed directly from data, based on an explicit calculation of the exposure-to-risk. The main difference, relative to the method used here, is that death rates and probabilities of death are not linked by an explicit formula. In practice, however, there is very little difference between empirical results obtained using the two methods.

E.2.1 Period death rates and probabilities under uniformity

To compute the exposure-to-risk in a 1×1 Lexis square, ⧄, we are often required to make an additional assumption. Consider the $N(x,t)$ individuals who attain exact age x and the $N(x+1,t)$ individuals who attain exact age $x+1$ in calendar year t (see Figure 9).

Suppose, in each case, that the birthdays of these individuals (at age x and $x+1$) are distributed uniformly within the calendar year t. Then, neglecting deaths, the $N(x,t)$ individuals who attain age x in year t will contribute, on average, $1/2$ of a person-year to exposure within the lower triangle, ◺. Likewise, the $N(x+1,t)$ individuals who attain exact age $x+1$ in year t have already contributed, on average, $1/2$ of a person-year to exposure within the upper triangle, ◸. Thus, the major component of the exposure-to-risk in this case would be $\overline{N} = 1/2\,[N(x,t) + N(x+1,t)]$. If the two distributions of birthdays (at age x and $x+1$) are not uniform within the calendar year but are nevertheless similar to each other, then the correct multiplier would differ only slightly from $1/2$. This type of mild non-uniformity can be safely ignored in computing the exposure-to-risk. However, larger departures from this uniformity assumption can be more problematic.

In addition, the $D_L = D_L(x,t)$ deaths in ◺ result in an average lost exposure of $1/3$ of a person-year, which must be subtracted from $\overline{N}$. On the other hand, the $D_U = D_U(x,t)$ deaths in ◸ contributed an average of $1/3$ person-years each, which must be added to the total for the interval. Therefore, assuming uniform distributions of births and deaths, the person-years of exposure in this interval can be estimated as

$$E = \overline{N} - \frac{1}{3}\,(D_L - D_U) \qquad . \tag{E.4}$$

Notice that $N(x,t)$ is equivalent to the P_2 population aged x at the beginning of calendar year $t+1$ plus the D_L deaths in ◺, and that $N(x+1,t)$ is equivalent to the P_1 population aged x at the beginning of calendar year t minus the D_U deaths in ◸. Therefore, we can substitute $\frac{1}{2}\,[P_2 + D_L + P_1 - D_U]$ for $\bar{N}$ in equation (E.4). After simplifying, we get

$$E = \frac{1}{2}\,[P_1 + P_2] + \frac{1}{6}\,(D_L - D_U) \qquad \text{(Equation (57))},$$

and thus the period death rate is

$$M_x = \frac{D_x}{E_x} = \frac{D_L + D_U}{\frac{1}{2}\,[P_1 + P_2] + \frac{1}{6}\,(D_L - D_U)} \qquad .$$

E.2.2 Period death rates and probabilities under non-uniform distributions of birthdays and deaths

The assumption of uniformity within Lexis triangles is violated most severely in situations where there are rapid changes in the size of successive cohorts, owing to fluctuations in the birth series many years before. The worst situation is when a sharp discontinuity in births occurs in the middle of one calendar year, creating a cohort that is *heavy* at one end and *light* at the other such as the cohorts born at the start and end of the First and Second World Wars in some countries. Where data for birth counts are available by time intervals of less than a year, our exposure estimations account for the distribution of individuals within birth cohorts. Specifically, we collect data for birth counts by month of birth, which are used to calculate the coefficients s_1, s_2, u_1 and u_2, defined on page 30 in section 6.1.

Let b be a time at birth within a cohort, i.e., $0 \leq b \leq 1$, and let $f(b)$ be the corresponding probability density function. Our formulas require two measures of the cohort birth distribution, the mean, $\bar{b}$, and variance, σ^2. Since period exposures combine the experience of two cohorts, we differentiate using subscripts, $\bar{b}_1$ and σ_1^2 for the upper triangle, ◸, and $\bar{b}_2$ and σ_2^2 for the lower triangle, ◿, (See Figure 9 for an overview). Assume (i) equal survival probabilities within cohorts, (ii) that deaths are distributed uniformly over each lifeline within a Lexis triangle, and (iii) a closed population. From (i) and (iii) it follows that $f_1(b)$ and $f_2(b)$ also describe the distribution of birthdays over $N(x+1,t)$ and $N(x,t)$, respectively, in any year t over the life of the cohort.

As mentioned, we estimate the birth distribution using information on births by calendar months. Births are then assumed to be uniformly distributed within each month. Suppose there are discrete intervals defined by $0 = b_0 < b_1 < \cdots < b_n = 1$. The b_i are taken as the month endpoints, expressed as a proportion of the year, e.g., $b_1 = \frac{31}{365}$, and so forth. In general, the fraction of births in the i^{th} sub-interval is as follows:

$$f_i = \int_{b_{i-1}}^{b_i} f(b)\,\mathrm{d}b \quad \text{for } i = 1, 2, \ldots, n \qquad . \tag{E.5}$$

Clearly, $1 = \sum_{i=1}^{n} f_i$. The empirical density function, $f(b)$, is defined as:

$$f(b) = \frac{f_i}{b_i - b_{i-1}} \quad , \tag{E.6}$$

for $b_{i-1} < b \leq b_i$. For monthly data, f_1 is simply the fraction of births in January. Using the empirical $f(b)$:

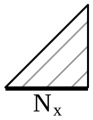
$$\begin{aligned} \bar{b} &= \int_0^1 b f(b)\,\mathrm{d}b \\ &= \sum_{i=1}^{n} f_i \left(\frac{b_{i-1} + b_i}{2} \right) \qquad . \end{aligned} \tag{E.7}$$

Similarly, we obtain an estimate of σ^2 as follows:

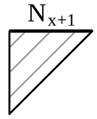
$$\begin{aligned} \sigma^2 &= \int_0^1 (b - \bar{b})^2 f(b)\,\mathrm{d}b \\ &= \sum_{i=1}^{n} f_i \cdot \left(\frac{b_{i-1}^2 + b_{i-1} b_i + b_i^2}{3} \right) - \left(\sum_{i=1}^{n} f_i \frac{b_{i-1} + b_i}{2} \right)^2 \qquad . \end{aligned} \tag{E.8}$$

Let us first establish that the average years lived in ◿ (by the cohort born in year $t - x$) would equal $1 - \bar{b}_2$, if there were no deaths. This is shown by solving the following integral:

$$\begin{aligned} s_1 &= \int_0^1 (1 - b)\, f_2(b)\,\mathrm{d}b \\ &= 1 - \bar{b}_2 \qquad . \end{aligned} \tag{E.9}$$



Likewise, the average years lived in ◸ (by the cohort born in year $t-x-1$) is equal to $\bar{b}_1$, among those that survive to age $x+1$ in year t:



$$\begin{aligned} u_1 &= \int_0^1 b\, f_1(b)\, \mathrm{d}b \\ &= \bar{b}_1 \qquad . \end{aligned} \tag{E.10}$$

Define z_L and z_U as the average years lived in ◿ and ◸, respectively by individuals that die in those triangles.[33] Assume that deaths in ◿ are distributed as follows:

$$f_L(a,b) = C_L \cdot f_2(b-a) \qquad , 0 \le a \le b < 1 \qquad , \tag{E.11}$$

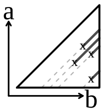
where C_L is some constant chosen so that $f_L(a,b)$ integrates to 1. Thus, we assume that the density of deaths within ◿ is constant along cohort lifelines yet proportional to the density of birthdays at age x. Integrating the density function over the triangle and equating to 1, we obtain:

$$C_L = \frac{1}{1-\bar{b}_2} \qquad ,$$

and thus

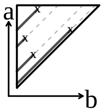
$$f_L(a,b) = \frac{f_2(b-a)}{1-\bar{b}_2} \qquad .$$

For a death at (a,b) within ◿, $1-b$ years of exposure are lost. The average amount of lost exposure per death in the triangle, z_L, is derived by solving the following integral:



$$\begin{aligned} z_L &= \int_0^1 \int_0^b (1-b) f_L(a,b)\, \mathrm{d}a\, \mathrm{d}b \\ &= \frac{1-\bar{b}_2}{2} + \frac{\sigma_2^2}{2(1-\bar{b}_2)} \qquad . \end{aligned} \tag{E.12}$$

Similarly for ◸, with the same assumptions, the distribution of deaths within ◸, $f_U(a,b)$, has the following form:



$$f_U(a,b) = \frac{f_1(b-a)}{\bar{b}_1} \qquad . \tag{E.13}$$

We derive z_U, the average years of exposure contributed to ◸ by those that die in the triangle, by solving the following integral:

[33] As we still assume deaths uniformly distributed over cohort lifelines within the triangle (but not between lifelines), this quantity is also equal to the average years *lost* by those dying in the triangle. In the case of full uniformity (of both births and deaths), z_L and z_U are both equal to $\frac{1}{3}$. These two quantities are also used in cohort exposure calculations, albeit calculated using birth distribution information from the same cohort (see equation (60)).

$$\begin{aligned} z_U &= \int_0^1 \int_0^b b f_U(a,b)\, \mathrm{d}a\, \mathrm{d}b \\ &= \frac{\bar{b}_1}{2} + \frac{\sigma_1^2}{2\bar{b}_1} \qquad . \end{aligned} \tag{E.14}$$

Then, the estimated exposure (in person-years lived) in the lower triangle is as follows:

$$\begin{aligned} E_L &= (1-\bar{b}_2)N(x) - z_L D_L \\ &= (1-\bar{b}_2)(P_2 + D_L) - \left(\frac{1-\bar{b}_2}{2} + \frac{\sigma_2^2}{2(1-\bar{b}_2)} \right) D_L \\ &= (1-\bar{b}_2)P_2 + \left(\frac{1-\bar{b}_2}{2} - \frac{\sigma_2^2}{2(1-\bar{b}_2)} \right) D_L \\ &= s_1 P_2 + s_2 D_L \qquad , \end{aligned} \tag{E.15}$$

and exposure in the upper triangle is:

$$\begin{aligned} E_U &= \bar{b}_1 N(x+1) + z_U D_U \\ &= \bar{b}_1(P_1 - D_U) + \left(\frac{\bar{b}_1}{2} + \frac{\sigma_1^2}{2\bar{b}_1} \right) D_U \\ &= \bar{b}_1 P_1 - \left(\frac{\bar{b}_1}{2} - \frac{\sigma_1^2}{2\bar{b}_1} \right) D_U \\ &= u_1 P_1 - u_2 D_U \qquad . \end{aligned} \tag{E.16}$$

These two equations justify the definitions of s_1, s_2, u_1 and u_2 given in equations (53) to (56). Thus, the total period exposure for ⧄ equals:

$$E(x,t) = E_L + E_U = s_1 P_1 + s_2 D_L + u_1 P_2 - u_2 D_U \qquad . \tag{E.17}$$

Table E.2: Implications of assuming non-uniform distributions of deaths within Lexis triangles (at age x)

	Lower triangle ⊿	Upper triangle ◸
Average age at death	$x + z_L$	$x + 1 - z_U$
Average contribution (per death) to exposure within triangle	z_L	z_U
Average lost exposure (per death) within triangle	z_L	z_U

E.2.3 Special case of uniform distributions of birthdays and deaths

Period exposure formulas in the case of a uniform distribution of birthdays and deaths are a specific case of the more flexible method presented here. If births and birthdays occur uniformly over the year for a birth cohort, then $\bar{b} = 1/2$ and $\sigma^2 = 1/12$. Thus, it is easy to confirm that $s_1 = u_1 = \frac{1}{2}$ and $u_2 = s_2 = \frac{1}{6}$. Following these formulas, the calculation of period exposures under the assumption of uniformity (i.e., when birth counts by month are unavailable) can be expressed as:

$$E(x,t) = \frac{P_1 + P_2}{2} + \frac{1}{6}(D_L - D_U) \qquad \text{(Equation (57))}.$$

The fact that equation (E.18) is a special case of equation (E.17) allows the use of a consistent method for period exposure calculations, with a convenient simplified form when information on the age distribution within cohorts is not available.

E.3 ▱ Cohort death rates and probabilities

Death rates and probabilities of dying are simpler conceptually for cohorts than for periods. As depicted in Figure 10 (main text), cohort rates and probabilities are measured over the age-cohort parallelogram, ▱, which follows the lives of individuals who turn age x in one calendar year until their next birthday, at age $x + 1$, in the following calendar year.

We assume that there is no migration and deal with the case of a closed population. This is usually a weak assumption because the effects of migration on calculated rates and probabilities are negligible as long as migratory flows have the same direction and a similar magnitude over the interval. The distribution of deaths within triangles is assumed to be proportional to the distribution of birthdays within the cohort: across cohort lines within Lexis triangles deaths are assumed to be distributed uniformly. Note that no assumptions are required on the distribution of population counts.

We first present cohort exposure formulas and then show how rates and probabilities follow. Recall the two quantities, z_L and z_U, given in equations (E.12) and (E.14). Here these are defined similarly, but with reference to the same cohort. Cohort exposures, E^c_x, are calculated as:

$$\begin{aligned} E^c_x &= P + z_L D_L - z_U D_U \\ &= P + \left(\frac{1-\bar{b}}{2} + \frac{\sigma^2}{2(1-\bar{b})}\right) D_L - \left(\frac{\bar{b}}{2} + \frac{\sigma^2}{2\bar{b}}\right) D_U \qquad . \end{aligned} \tag{E.18}$$

Assuming uniform distributions of birthdays and deaths, the cohort exposure calculation simplifies to the following:

$$E^c(x,t) = P(x,t) + \frac{1}{3}\left[D_L(x,t-1) - D_U(x,t)\right] \qquad \text{(Equation (62))}.$$

This formula is justified as follows: Consider the P individuals alive at the boundary between the two calendar years. If there were no deaths in ◸, these P individuals would contribute a total of P person-years of exposure over the complete age interval. However, as shown above, the D_U

deaths in ◸ result in an average lost exposure of z_U person-years, which must be subtracted from P, and the D_L deaths in ◿ contribute an average of z_L person-years, which must be added to the total for ▱ exposure.

Death rates follow by dividing the number of deaths by the total exposure to risk:

$$M_x = m_x = \frac{D_L + D_U}{E^c} \qquad .$$

As reflected in this equation, for cohorts there is no difference, either conceptually or empirically, between the population death rate, M_x, and the life-table death rate, m_x, assuming zero migration.

The probability of surviving from age x to age $x+1$, p_x, is:

$$p_x = \frac{N(x+1, t+1)}{N(x,t)} = \frac{P}{P + D_L} \cdot \frac{P - D_U}{P} = \frac{P - D_U}{P + D_L} \qquad ,$$

where $P = P(x, t+1)$, $D_L = D_L(x,t)$, and $D_U = D_U(x, t+1)$, as illustrated in Figure 10. Thus, the probability of surviving from age x to age $x+1$ is a product of the fraction surviving from age x to the end of the calendar year and the fraction surviving from the beginning of the next calendar year to age $x+1$. This probability is the same with or without the assumptions of uniform births or deaths. It follows immediately that

$$q_x = 1 - p_x = \frac{D_L + D_U}{P + D_L}$$

is the cohort probability of dying in the age interval $[x, x+1)$.

Let a_x be the average number of years lived between ages x and $x+1$ by individuals who die within this interval. Under the assumption that deaths are distributed uniformly within Lexis triangles, the average age at death is $x + 1/3$ in the lower triangle and $x + 2/3$ in the upper one (see Table E-1). It follows that

$$a_x = \frac{\frac{1}{3} D_L + \frac{2}{3} D_U}{D_L + D_U} \qquad .$$

Once again allowing for non-uniformity of births and birthdays, we obtain:

$$a_x = \frac{z_L D_L + (1 - z_U) D_U}{D_L + D_U} \qquad .$$

where the formulas for z_L and z_U are identical to those given earlier (equations (E.12) and (E.14)), except that both are derived using monthly birth counts for the same cohort. Recall that, in classical life table notation, death rates, probabilities of dying, and average years lived in the age interval are related by the following formula:

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

It is easy to confirm that the cohort formulas for these three quantities, when derived (as above) under either set of assumptions, satisfy this equation. Thus, the three quantities are mutually consistent, even though they have been derived independently from birth and death counts and population estimates. For cohorts, this relationship is exact, and there is no need to give preference to either rates or probabilities in the calculation of cohort life tables.

Appendix F Special methods used for selected populations

For the sake of comparability, we aim to follow the general principles described in this document for all populations included in the HMD. However, exact uniformity of methods is not always possible, because data at the required level of detail are not available in all situations. Therefore, in a few special cases, we have developed special methods to accommodate the realities of the available data. As of the current version of this document (dated May 31, 2007), the populations listed below have been treated with special methods. For the most up-to-date version of this table, go to the *Special Methods* link (http://www.mortality.org/Public/Docs/SpecialMethods.pdf) on the HMD website.

Population	**Special method**	**For more details:**
Belarus	The original death counts for all years were aggregated for ages 99+. Population estimates for almost extinct cohorts were derived using the survival ratio method at ages 85+ years.	See the "Data Quality Issues" section of the country-specific documentation
Belgium	Counts of live births (1895–1923, 1919) and infant deaths (1886–1955, 1958–1960) were corrected to include false stillbirths. Special methods were implemented to accommodate missing deaths for 1914-18.	See Appendices 2 and 3 of the country-specific documentation
Bulgaria	Population estimates were constructed for 1989–1992 by treating official estimates for 1988 as a "pseudo-census" and then applying the intercensal survival method.	See the "Data Quality Issues" section of the country-specific documentation
Canada	Death counts were adjusted for missing information (e.g., sex, age, year of birth) and errors in the year of birth. In some cases, the original death counts were aggregated by Lexis triangle into the 1×1 format because of apparent data quality problems.	See the "Death Count Data, Specific Details" section of the country-specific documentation
Finland	Imputation of Lexis triangles for deaths in 1999–2009, when the year of occurrence was not provided (only year of registration, age, sex, and year of birth)	See Appendix 2 in the country-specific documentation
France	Counts of live births and infant deaths (1899–1974) were corrected to include false stillbirths. During the World Wars, estimates (deaths, population) were used to include the military population.	See the country-specific documentation

Population	Special method	For more details:
Germany	We used a special method to derive the inter-censal population estimates for the period 1990–2011.	See Appendix 2 of the country-specific documentation
Germany, East and West	We used a special method to derive the inter-censal population estimates for the period 1987–2011.	See Appendix 2 of the country-specific documentation
Hong Kong	There were a few deaths of unknown sex for selected ages across the period covered by the HMD (1986–2017). Within a given year and age subgroup, deaths of unknown sex were redistributed proportionately based on the observed sex distribution of deaths where sex was known.	See NoteCode #1 in HKG-note.pdf.
Israel	The official annual population estimates for 1985–1995 and 1996–2007 were adjusted using a special method. Unlike the standard HMD method for producing inter-censal population estimates, this method takes into account the distribution of net-migration across years and cohorts within the inter-censal period.	See Appendix 2 of the country-specific documentation
Italy	The age distribution for death counts was estimated for years 1893-94. Census counts were adjusted for the years 1871, 1921, and 1951 to cover the same territory as the death counts. During the two World Wars, estimates of deaths and population were used to include the military population.	See the country-specific documentation (in particular Appendix 2)
Lithuania	The survival ratio method was used for ages 85+ rather than 90+ to derive population estimates for almost extinct cohorts. The original death counts were aggregated for ages 99+.	See the "Population Count Data, Specific Details" and "Data Quality Issues" sections of the country-specific documentation
New Zealand	The Māori and Non-Māori population counts were adjusted for 1991–1995 to follow the older definition of ethnicity. Due to the fact that deaths in 1995 are classified by a mixture of the previous and current definitions of ethnicity, a special adjustment factor was introduced for Māori and Non-Māori deaths. Census counts were adjusted for 1960 & 1970 to cover the *de jure* ("usual resident") population.	See Appendix 2 of the country-specific documentation

Population	**Special method**	**For more details:**
Norway	The sex distribution for births was estimated for the years 1846–1915.	See the country-specific documentation
Portugal	The survival ratio method was used for ages 85+ rather than 90+ to derive population estimates for almost extinct cohorts.	See the "Population Count Data, Specific Details" section of the country-specific documentation
Russia	Prior to calculation of HMD estimates, i) the original death counts for 1959–1989 were aggregated for ages 99+, and ii) official population estimates in recent years were aggregated for ages 80+. Population estimates for almost extinct cohorts were derived using the survival ratio method for ages 80+ rather than 90+.	See Appendix 2 of the country-specific documentation
Scotland	A special method was used to split population estimates by 5-year age groups during WWI.	See the country-specific documentation
Spain	Counts of live births and infant deaths (1930–1974) were corrected to include false stillbirths. The census counts were adjusted for the years 1940, 1950, and 1960 to cover the *de facto* population and the same territory as death counts.	See the country-specific documentation
Sweden	Death counts were adjusted for the years 1863, 1865, 1868, and 1870 to match a secondary, more reliable (but less detailed) data source.	See the "Data Sources" section of the country-specific documentation
Switzerland	Death counts were adjusted for females for the year 1878.	See the "Death Count Data, Deaths at 99+" section of the country-specific documentation
Ukraine	Due to data quality issues at older ages in official statistics, population estimates in recent years were aggregated for ages 80+. Population estimates for almost extinct cohorts were derived using the survival ratio method for ages 80+ rather than for ages 90+. In addition, prior to calculation of HMD estimates, the original death counts for 1959–1989 in ages higher than 99 were aggregated to an open interval of 99+.	See the "Data Quality Issues, Age Heaping in Deaths" section of the country-specific documentation

Population	**Special method**	**For more details:**
United Kingdom	During the two World Wars, for England & Wales and for Scotland, estimates (deaths, population) were used to include the military population. For the civilian population, a special method was used to split population estimates by 5 year age groups during WWI and WWII.	See the country specific documentation
United States	The original mortality data are tabulated in a mix of Lexis triangles, single-years of age and five-year age groups to protect confidentiality for all years 1959-2013. Population estimates have been adjusted to exclude the Armed Forces overseas (1940–1969) and the population of Alaska and Hawaii (1950–1958). Births were adjusted for 1959 to include Hawaii. The extinct cohort method was used for ages 75+ (rather than 80+) during 1933–39 because official population estimates extend only to age 75+.	See the country-specific documentation

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