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Modal age at death: lifespan indicator in the era of longevity extension

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Abstract

This paper examines and demonstrates the importance of the adult modal age at death (M) in longevity research. Unlike life expectancy at birth (e_0) and median age at death, M is determined solely by old-age mortality as far as mortality follows a bathtub curve. It represents the location of old-age death heap in the age distribution of deaths, and captures mortality shifts more accurately than conditional life expectancies such as e_{65}. Although M may not be directly determined from erratic mortality data, a recently developed method for deriving M from the P-spline-smoothed mortality curve based on penalised Poisson likelihood is highly effective in estimating M. Patterns of trends and differentials in M can be noticeably different from those in other lifespan measures, as indicated in some examples. In addition, major mathematical models of adult mortality such as the Gompertz, logistic and Weibull models can be reformulated using M, which plays a critical role as the mortality level parameter in those models.

1 Introduction

Mankind has witnessed a substantial increase in the length of human life during the last two centuries. In economically developed countries that currently have relatively low levels of mortality, life expectancy at birth for both sexes rose from around 30 to 45 years in the mid-19th century to about 80 years in recent periods (Meslé and Vallin 2011). The longevity expansion resulted in a considerable growth of

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the elderly population and also led to increasing concern about inequalities in the lifespan (length of life) among populations and subpopulations.

Monitoring and analysis of these longevity trends and differentials need to be based on proper and effective summarisation of statistical data on human lifespan. There are two types of measures of mortality and survival. Some measures are expressed as proportion, estimated probability, hazard (force), or rate of death. Others, called lifespan indicators in this paper, are expressed in terms of the length of survival time. Three major types of overall lifespan indicators are the mean, median and mode of the length-of-life distribution: life expectancy, median age at death and modal age at death. The life expectancy at birth (e_0) has been widely used, but increasing attention has recently been given to the modal age at death.

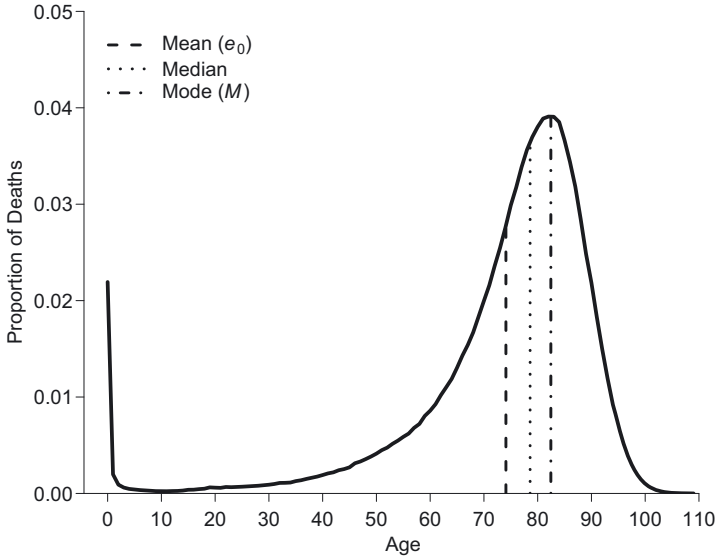
Typically, the age distribution of deaths in human life tables is bimodal, with the first local mode at the left end (age 0) and the second local mode at an old age (Figure 1). In this paper, the older mode (the modal age at death among adults) is denoted by M. The number of deaths at the younger mode is greater than that at the older mode in high-mortality regimes, but that at the older mode is greater in low-mortality regimes. In economically developed countries, the older mode has been higher than the mode at age 0 in most years during the last half century. In France, for instance, the number of life table deaths at the older mode surpassed that at age 0 in 1953 for females and in 1960 for males. Thus in this paper, M will be indicated simply as the modal age at death except in analyses of long-term trends.

Whereas both life expectancy at birth and median age at death are affected by mortality among infants, children and young-age and middle-age adults, M is solely determined by old-age mortality, as far as the mortality risk follows a bathtub curve (see Appendix A for a more detailed discussion). This feature gives a special significance to M because the lifespan extension during the recent few decades is mainly due to the reduction in old-age mortality (e.g. Wilmoth et al. 2000; Vallin and Meslé 2001; Meslé and Vallin 2006). Furthermore, the feature may make M suitable to be called a *longevity* measure: although developing a rigorous definition of 'longevity' is beyond the scope of this paper, the concept seems to have been used not for simply indicating a duration of lifetime but for emphasising old-age survival to very high ages.

Other widely-used measures of old-age survival are life expectancies at some selected early old ages such as 50 and 65. The life expectancy conditional on survival to the selected old age is independent of mortality at young ages. However, as shown later, changes in those conditional life expectancies tend to underestimate age shifts of old-age mortality.

It is useful to characterise M in the context of the common pattern of age distribution of deaths in human populations, which is illustrated in Figure 1 for French women in 1960–1964. As originally indicated by Lexis (1878), the common pattern may be described as a sequence of three phases: (1) a steep fall in early childhood, from the relatively high frequency of deaths among new-born babies; (2) a low and fairly flat curve in late childhood through middle age; and (3) a large, left-skewed heap of deaths in old age. Usually the shift from the first to the second

Figure 1:
Age distribution of life table deaths for French females, 1960–1964



Source: Human Mortality Database (2012).

phase can be located around the typical age of puberty, but transition from the second to the third phase appears more gradual. An improvement of old-age survival moves the heap to higher ages. Thus, the location of the old-age death heap on the age dimension may be considered as indicative of the level of longevity in the population. M, which is the location of the peak of the heap, is a summary measure representative of the location of old-age death heap.[1]

2 Modal age at death in longevity research

The use of M in longevity research is not a totally new approach. It has been advocated by some researchers in such fields as demography, actuarial sciences, statistics and biology in the past two centuries. According to Quetelet (1835, 1848, 1871), the mode is not an arithmetic mean but a typical value alongside a normal

[1] Although Figure 1 shows an example of death distributions in period life tables, those in cohort life tables follow the three-phase sequence as well. However, the old-age death heap tends to be steeper for synthetic than actual cohorts in modern human populations, because when the level of mortality is declining, mortality tends to increase with age faster in period than cohort life tables (Horiuchi and Wilmoth 1998).

curve which clearly accounts for the central value of the frequency distribution, representing the most common individual observation, limited by minimum and maximum values following the laws of nature.

Following the publication of Quetelet's work (1835) on the 'average man' (*l'homme moyen*), Lexis (1878) also stated that M represents the most central and natural characteristic of human longevity and that deaths occurring at and above M should be regarded as 'normal' deaths following the right-hand side of a normal distribution. Lexis theorised the idea of normal life duration, characteristic of a natural and ageing lifetime. He divided the distribution of deaths in three parts: (1) a J-curve right after birth corresponding to infant deaths; (2) the normal deaths around the late modal age at death which obey the law of accidental errors reflecting the natural lifetime; and (3) a transitional region between (1) and (2), where adult premature deaths partly overlap with the normal deaths.

Following the work of Lexis, a number of researchers studied the age distribution of deaths to better describe the shape of the human longevity and discuss its limits (Elderton 1903; Gumbel 1937; Greenwood and Irwin 1939; Clarke 1950; Benjamin 1959, 1963, 1964, 1982a, 1982b, 1988). However, M was not perceived as a key indicator of lifespan until the work of Kannisto (2000, 2001), who clarified that M is not invariant over time but depends on the conditions of mortality of each period. This work triggered various studies on changes in longevity in various settings (Cheung et al. 2005, 2008, 2009; Cheung and Robine 2007; Gurven and Kaplan 2007; Canudas-Romo 2008, 2010; Thatcher et al. 2010; Ouellette and Bourbeau 2011; Brown et al. 2012). Horiuchi (2003) used M for interspecies lifespan comparison because a consistent definition of infant mortality for different species is impossible.

Acsádi and Nemeskéri (1970) considered the mean, median and mode of age distribution of deaths in life tables as three major types of lifespan indicators: (1) the average length of life attained by individuals; (2) the probable length of life attained by half the individuals; and (3) the so-called normal age at death for most people, disregarding those who died as children. These three central tendency measures well reflect their orientation to different aspects of mortality (Cheung and Robine 2007; Canudas-Romo 2010). Although the adult modal age at death has been used earlier in order to characterise the natural and normal lifespan (Elderton 1903; Gumbel 1937; Greenwood and Irwin 1939; Clarke 1950; Le Bras 1976), life expectancy at birth (e_0) was considered the best index of the lifespan (Dublin 1923). The substantial decline in mortality at young ages during the first half of the 20th century was reflected in the steep increase in e_0. Currently, however, the extension of length of human life in low-mortality countries is primarily due to improvements in old-age survival. In these circumstances, the modal age at death is a useful lifespan indicator as it is solely determined by old-age mortality (Appendix A) and is free from any arbitrary selection of an age range for 'old ages' (Kannisto 2001).

In the existing literature on M, however, at least two questions seem to remain unanswered. The first one is empirically oriented. Could patterns of trends and differentials in M be noticeably different from those in widely-used lifespan measures such as e_0 and e_{65}? If so, M may be able to shed light on some aspects of mortality

trends and differentials that are not necessarily captured well by e_0 or e_{65}. Although trends in M and e_0 (and also the median age at death in some case) were compared for some countries (Kannisto 2001; Cheung and Robine 2007; Cheung et al. 2009; Canudas-Romo 2010; Office of National Statistics 2012), the comparisons did not include the life expectancy at an early old age (e.g. e_{65}), which is a widely-used indicator of old-age survival. Furthermore, to our knowledge, no systematic comparison in mortality differentials has been made among major lifespan indicators.

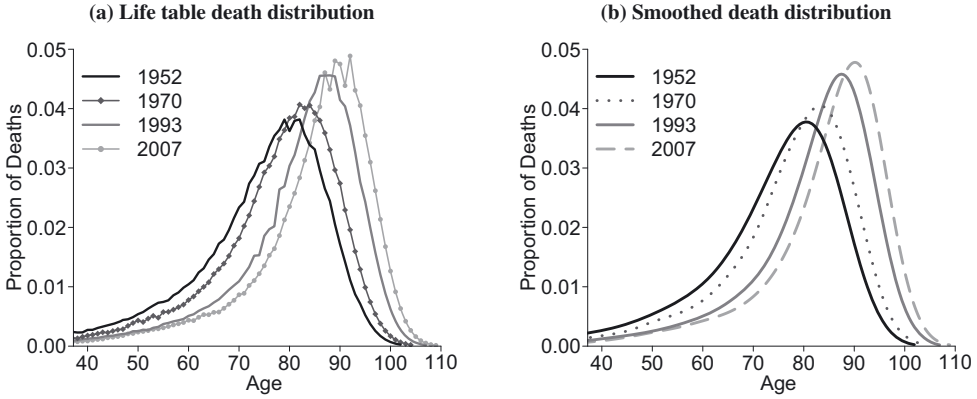
The second question is theoretically oriented. It is widely known that some mathematical equations, such as the Gompertz, logistic and Weibull models, fit empirical age variations of adult mortality quite well and are used broadly in mortality research, population projection and simulation studies. Could these models be reformulated using M as their key parameter? It should be noted that those models are used not only for parametric summarisation of adult mortality data but also to construct mathematically formulated theories on ageing and mortality. Classical examples include Strehler and Mildvan (1960) for the Gompertz model, Le Bras (1976) for the logistic model, and Rosenberg et al. (1973) for the Weibull model. Thus, if M plays critical roles in those models, the mathematical relationships may suggest a potential theoretical significance of M in ageing research. Although expressions for M in the Gompertz and logistic models were previously shown (Pollard 1991, 1998a, 1998b; Pollard and Valkovics 1992; Robine et al. 2006; Canudas-Romo 2008), it is not fully clear whether those models can be entirely reformulated using M, and if so, what roles M plays in the reformulated equations.

This paper will investigate the empirical and theoretical significance of M as a summary measure of longevity, with focus on these two questions. In the next section, we will describe the method for estimating M that is adopted in this paper and recommendable to prospective users of this measure. Then we will compare empirical patterns of trends and differentials in M, e_0 and e_{65}, and explore mathematical roles of M in some widely-used models of adult mortality. Since comprehensive international comparison is not a purpose of this paper, we will mainly use French civilian data from the Human Mortality Database (2012) to illustrate widely-observed patterns. (The time series do not include those in military services for 1914–1920 and 1940–1945.) Although M is important in studies of both period and cohort mortality, we will use period mortality data only, because the typical patterns of age variations in mortality and death are common in both period and cohort data.

3 Methods for estimating the modal age at death

Although a simple visual inspection of the age distribution of life table deaths is often sufficient to roughly locate the modal age area, determining M with greater precision is more challenging given the typical flatness and irregular pattern of deaths in this area. Indeed, multiple local modes of the death distribution are likely to be found at different adult ages, due to erratic data and flatness of the curve in the highest frequency region (Kannisto 2001). Figure 2(a) shows that this flat-topped and

Figure 2:
Age distribution of life table deaths and corresponding age-at-death distribution derived from the P-spline-smoothed mortality curve based on penalised Poisson likelihood, French females, selected years



Source: Human Mortality Database (2012).

irregular pattern around the modal age does not only characterise earlier time-periods and that it is found even in relatively large populations such as French females. The most intuitive approach for estimating *M* then would be to smooth the age distribution of life table deaths in the modal age area using a statistical model. A perfectly smooth curve around the modal age would indeed make it very easy to determine the precise age at which the peak of the heap of deaths occurs. Already in 1902, Pearson warned against choosing modal values based on a casual inspection of the adult age-at-death distribution and recommended instead interpolating a curve through the top of ordinates (Pearson 1902). Several parametric models, namely, quadratic, normal (Lexis), Gompertz, logistic and Siler models, have been used for directly or indirectly smoothing the distribution in the highest frequency region of adult deaths and thereby estimating *M* (Kannisto 2000, 2001; Cheung 2003; Horiuchi 2003; Cheung and Robine 2007; Gurven and Kaplan 2007; Canudas-Romo 2008, 2010; Cheung et al. 2008, 2009; Thatcher et al. 2010; Brown et al. 2012). However, these conventional parametric statistical modelling techniques have some limitations. They rest on *a priori* assumptions about the shape of the age distribution of deaths or the shape of the mortality curve. Moreover, most of these techniques also rest on *a priori* assumptions about the proper restricted age domain over which the models should be applied. Both assumptions could influence results and diminish the accuracy of estimated values of *M*.

Recently, Ouellette and Bourbeau (2011) proposed a flexible nonparametric smoothing method based on P-splines for estimating *M*, which relaxes these assumptions. Instead of smoothing the age distribution of life table deaths, this

P-spline approach for Poisson death counts uses data on observed deaths and person-years lived to obtain a smoothed age pattern of mortality (i.e. mortality curve) from which the corresponding smoothed age-at-death distribution can then be derived (Figure 2(b)). Everywhere in this paper, unless otherwise specified, M was estimated using this method. It is indeed our preferred method for estimating M because in addition to being free from any assumptions about the shape of the death distribution, it does not require users to select a proper restricted age domain because the smoothing procedure can be systematically applied from age 10 and onwards.[2] It is advisable, nonetheless, not to extend the smoothing up to the very last high ages, where deaths are scarce and person-years lived are small. At these latter ages, the P-spline-smoothed mortality curve may show unrealistic behaviour due to significant random fluctuations. This would have hardly any effect on the estimation of M though, since the modal age is a measure of the location of the heap of deaths and is thus insensitive to such extreme values. Still, we provide a simple rule of thumb that prevents undesirable patterns in the right-hand tail of the smoothed mortality curve: for each 1-year interval in the age range for smoothing, the observed number of deaths should be greater than ten. More specifically, the age range for smoothing should span ages 10 to j, where j is the highest age for which $D_i > 10$ for all $i \leq j$.[3] In cases where this rule of thumb fails to prevent unrealistic smoothed mortality behaviour at the highest ages, the threshold of ten observed deaths could be increased.

Note that to estimate M, it is preferable to obtain the smoothed age-at-death distribution directly from the P-spline-smoothed mortality curve than to smooth the age distribution of life table deaths derived from observed age-specific death rates. Indeed, the former case skips the process of constructing a period life table, which rests on a number of assumptions and often involves estimation procedures and adjustments (Preston et al. 2001, Chapter 3). It thus offers a more straightforward framework that remains closer to the observed data.

When compared to competing methods that have been used to estimate the modal age at death, the method of deriving M from the P-spline-smoothed mortality curve based on Poisson likelihood has, notably, an important advantage for empirical studies: it limits artificial fluctuations in estimated values of M (Ouellette and Bourbeau 2011). For example, the post-1950 upward linear trend in M for French females (Figure 3(a)), which is based on the Poisson P-spline smoothing method, is much steadier than if Kannisto's (2001) well-known quadratic estimation procedure had been used instead (root-mean-square error (RMSE) of 0.31 for the former and of 0.74 for the latter).

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[2] Mortality in infancy and early childhood presents unique features (in particular, a very steep downward slope between ages 0 and 1) which this P-spline method cannot cope well with, but this is not of interest for estimating M by any means.

[3] For instance, among French males in 2004, the number of observed deaths at ages 104 through 109 was 38, 13, 4, 7, 0 and 0 (Human Mortality Database 2012). In this case, the last four 1-year age groups (i.e. ages 106 through 109) would be excluded from smoothing.

A more detailed overview of the P-spline smoothing method for estimating M as well as an implementation guide written for the statistical programming environment R (R Core Team 2012) is provided in Appendix B. Conveniently, the MortalitySmooth package (Camarda 2012, 2013) in R features a function called 'Mort1Dsmooth' that performs smoothing of Poisson death counts with P-splines over a given range of ages or calendar years.[4] This function can therefore be used to obtain smoothed forces of mortality from observed death counts and person-years lived. The subsequent steps leading to M estimates are not contained in the current version of the MortalitySmooth package. However, we have included an R routine that covers these steps in Appendix B.

4 Trends and differentials in modal age at death

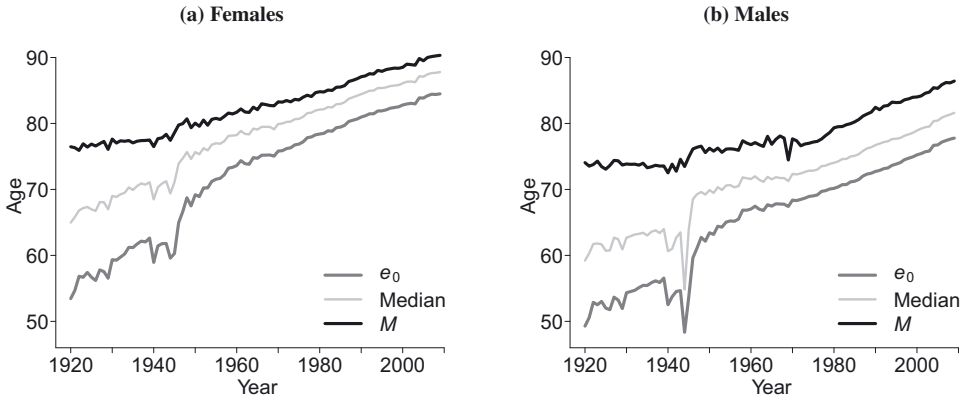
4.1 Differential trends in M, life expectancy at birth and median age at death

Because the age distribution of deaths is typically bimodal and that of adult deaths is highly skewed to the left, M is considerably older than e_0, and the median age is placed between them (Figure 1). In high-mortality regimes in which e_0 was around 40 years or lower, M was higher than e_0 by about 30 years or more (Cheung et al. 2008, Figure 7). In high-income countries during the past few decades, values of the three indicators are closer, but with the differences still noticeable: typically, M is higher than e_0 by about 5 years, and the median age is near the mid-point between M and e_0.

The change in the differences among the lifespan measures is a result of their differential trends, which are shown for French females and males in Figure 3. Similar patterns have previously been shown for some other countries and regions such as England and Wales, Finland, France, Japan (only since 1950), Sweden and Switzerland (Kannisto 2001; Cheung and Robine 2007; Cheung et al. 2009; Canudas-Romo 2010; Office of National Statistics 2012). High-income countries witnessed a substantial rise in e_0 and median in the last quarter of the 19th and the first half of the 20th century, due to the reduction in mortality among infants, children and young-age and middle-age adults. The rise has continued in the second half of the 20th century and recent years, though not as fast as in the earlier phase. On the contrary, the trajectory of M was almost flat or went only slightly upward in most of

[4] The package also includes a 'Mort2Dsmooth' function, for those interested in smoothing mortality data over ages and years simultaneously. This generalisation is particularly useful when dealing with small populations, for instance. The ability of the two-dimensional approach to borrow information from both neighbouring years and ages makes large random fluctuations less likely to distort the smoothed outcome (Camarda 2012). For an analysis of geographical disparities in M using this generalised approach, see Ouellette et al. (2012).

Figure 3:
The life expectancy at birth (e_0), median age at death and adult modal age at death (M) for civilian females and males in France, 1920–2009



Source: Human Mortality Database (2012).

the first half of the 20th century, until M started to increase during the second or third quarter of the century and the upward trend continued. During the last few decades, the three upward trajectories, all quite linear, appear nearly parallel, suggesting that the gain in e_0 was primarily attributable to the improvement in old-age mortality. It should be noted, however, that this is a description of the typical pattern, and there are some variations in the timing of acceleration/deceleration and concavity/convexity of slope among high-income countries, some of which also show sudden falls reflecting effects of wars and other disastrous events.

It should also be noted that when the latest figure of life expectancy is announced, many people may take it as the 'typical' (i.e. most frequent) length of life. For example, life expectancy at birth for French females is currently around 85 years. They tend to miss the fact that the typical age at death has actually been over 90 years in the period life tables since 2006.

4.2 Comparison of trends in M and conditional life expectancies e_{55}, e_{65} and e_{75}

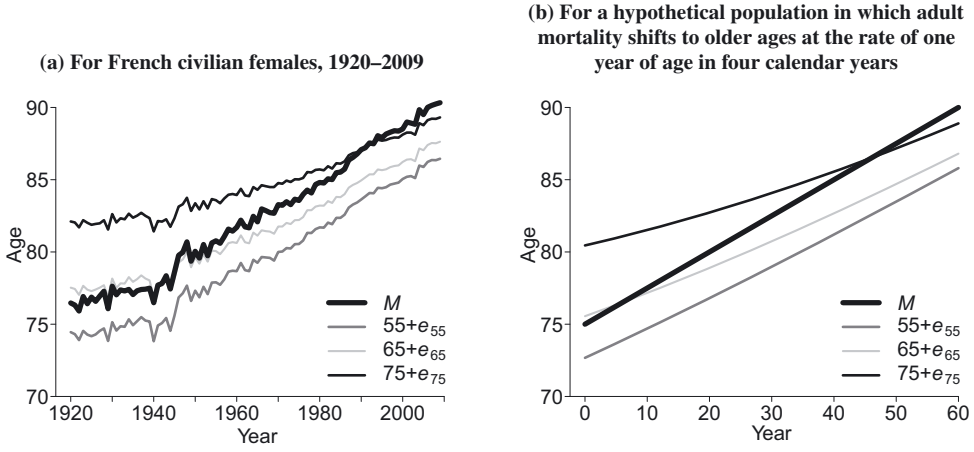
Conditional life expectancy, defined as the expectation of life conditional on survival to a certain age (i.e. e_x for $x > 0$), is widely used as a summary measure of old-age mortality. If an old age such as 65 is adopted as x, then e_x is not affected by mortality at young and middle ages, and determined by mortality at old ages only. Thus, it may seem reasonable to expect similar trends for M and conditional life expectancies such as e_{65}.

However, data from high-income countries that experienced significant declines in old-age mortality actually exhibit noticeably different trends between M and various e_x's. Figure 4(a) compares changes in e_{55}, e_{65} and e_{75} with those in M for French females from 1920 to 2009. M increased more steeply than the conditional life expectancies. In addition, life expectancy at older ages tended to increase more slowly.

In order to understand these different trends, we did a simple simulation of 'old-age mortality shift': a mortality curve, which had the same shape as the three-parameter logistic curve fitted to Swedish female data for 1973–1977 (Horiuchi and Coale 1990), was assumed to shift to older ages at the rate of 1 year of age in four calendar years, i.e. the force of mortality at age x and time t (in years) was given by $\mu(x,t) = \mu(x + 0.25, t + 1)$. Figure 4(b) shows the result of this simulation. M increased from age 75 to 90 in 60 calendar years, exactly capturing the pace of old-age mortality shift. Increases in e_{55}, e_{65} and e_{75} were noticeably slower. Patterns seen in Figures 4(a) and 4(b) appear fairly comparable, suggesting that differential trends in Figure 4(a) are not just a peculiarity of demographic history in France but reflect some general characteristics of M and conditional life expectancies.

It can be shown that in general, if the mortality curve makes a parallel shift to older ages, M increases exactly at the same pace as the shift of the mortality curve, but conditional life expectancies increase more slowly. (See Appendix C for the

Figure 4:
The adult modal age at death (M) and *total* life expectancies at age 55, 65 and 75 ($55 + e_{55}, 65 + e_{65}, 75 + e_{75}$)



Note: To make M, e_{55}, e_{65} and e_{75} comparable in the same graph, *total* life expectancies at age x are shown (i.e. x is added to e_x).
Source: Human Mortality Database (2012).

mathematical proof.) Thus, mortality shifts may not be accurately reflected in trends of conditional life expectancies at old ages.[5]

It should also be noted that changes in conditional life expectancies are highly age-dependent. As seen in the differential steepness of the three life expectancy curves in Figures 4(a) and 4(b), the size of change in the conditional life expectancy varies with the starting age such as 55, 65 and 75. There is no such dependency on the selected age range for the modal age at death, as the modal age above 55, that above 65 and that above 75 are all identical in any high-income country during any recent period.

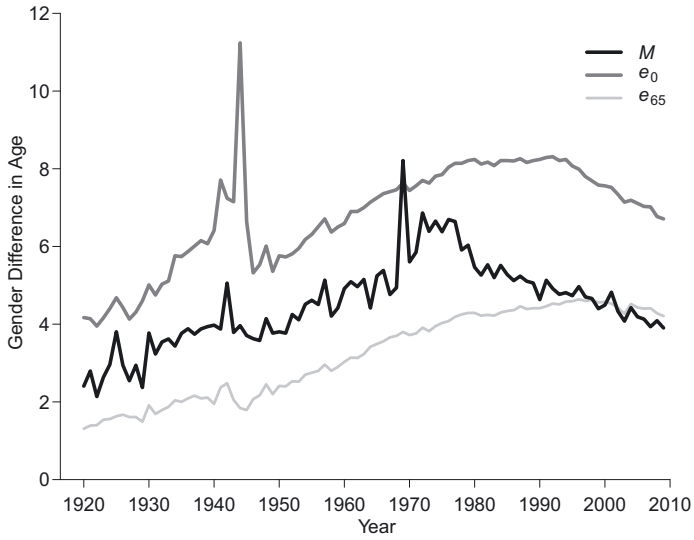
4.3 Gender longevity differentials in terms of M, e_0 and e_{65}

We now turn to issues in measurement of longevity differentials among populations and subpopulations, using gender differences (present subsection) and international differences (subsection 4.4) as examples. Differentials in terms of M, e_0 and e_{65} (selected as a widely-used conditional life expectancy) are compared. Because the analysis in 4.1 suggests that the median age at death is likely to fall between M and e_0, the median is not included in this comparison in order to avoid excessive complexities in figures.

Figure 5 shows gender differences (female minus male) in the three length-of-life measures for France from 1920 to 2009. For most of the period, the difference in e_0 is the largest, followed by that in M and then that in e_{65}. The greater differences in e_0 than in M were expected, because gender differentials in e_0 reflect mortality at all ages, whereas gender differences in M are determined by old-age mortality only. The smaller differences in e_{65} than in M were expected as well, because e_{65} seems less sensitive than M to horizontal differences on a mortality plot graph, as described in 4.2 and Appendix C. Male and female mortality curves can be compared on both the vertical and horizontal dimensions in a mortality plot graph: although the female mortality curve may be considered as being below the male mortality curve (i.e. for a given age, mortality for females is lower than mortality for males), the female mortality curve may also be deemed as being at the right of the male curve (i.e. for a given mortality level, females reach it at an older age than males).

[5] Results of the simulation (Figure 4(b)) and mathematical reasoning (Appendix C) should be viewed with caution as they are over-simplified models. Although trends of old-age mortality in some countries during certain periods were approximated as parallel shifts of mortality curves to older ages (Kannisto 1996; Bongaarts 2005; Cheung and Robine 2007; Canudas-Romo 2008), mortality curves do not necessarily make parallel shifts. In many populations, age shifts of higher mortality levels tend to be slower, and usually the time trajectory of M tends to be close to age shift of $\mu(x) = 0.12$. This trend is called compression of *old-age* mortality, which should be distinguished from the *overall* rectangularisation of the survival curve due to a reduction of young-age mortality. The old-age mortality compression was observed in a number of high-income countries during the last several decades (Kannisto 2000, 2001; Cheung et al. 2005, 2008, 2009; Thatcher et al. 2010).

Figure 5:
Gender difference (female minus male) in the adult modal age at death (M), life expectancy at birth (e_0) and life expectancy at age 65 (e_{65}) for France's civilian population, 1920–2009



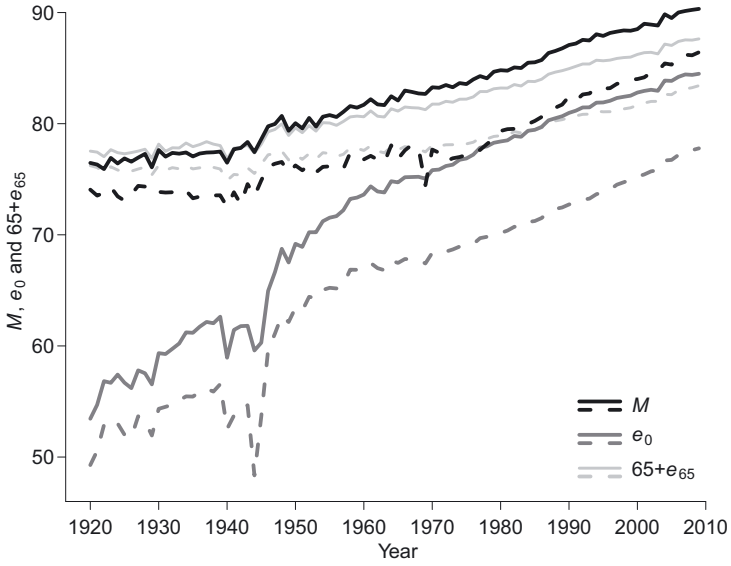
Source: Human Mortality Database (2012).

The three measures of gender longevity difference differ not only in levels (in years) but also in trends. The gender difference in e_0 continued to increase from 1920 to 1992 in France, and decreased thereafter. Such downturns were observed recently for many other high-income countries (Glei and Horiuchi 2007). Downturns can be seen for the gender differences in M and e_{65}, but the downturn was earlier (in the early 1970s) and more pronounced for M than for e_0, and the downturn for e_{65} was fairly recent (around 2000) and modest. As seen in Figure 6, the narrowing of the gender gap during the last few decades was more evident for M than for e_0 and e_{65}. Figure 7 shows that the old-age death heaps for females and that for males moved closer between 1972 and 2009. It seems that the narrowing distance between the two heaps was reflected more clearly in M than in e_0 and e_{65}, both of which might have been affected more by changes and differences in other aspects of male and female death distribution curves.

4.4 International longevity differentials in terms of M, e_0 and e_{65}

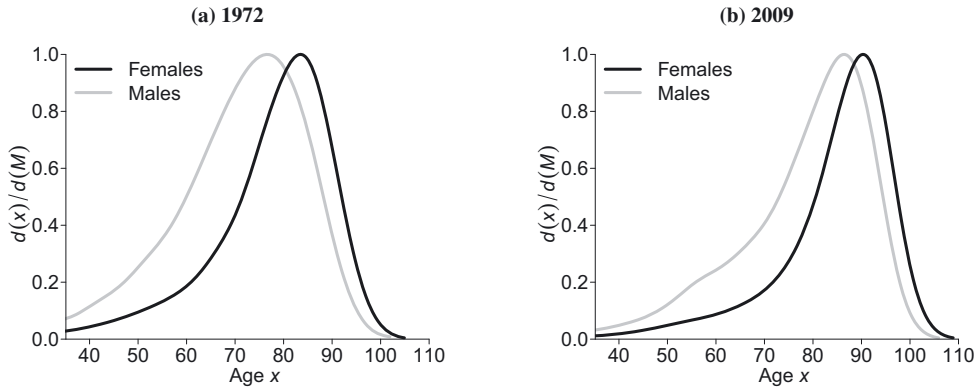
Figure 8(a) presents trends in the three lifespan measures for French and Japanese females from 1950 to 2009. At the beginning of the period, the Japanese lagged

Figure 6:
The adult modal age at death (M), life expectancy at birth (e_0) and total life expectancy at age 65 ($65 + e_{65}$) for civilian females (solid line) and males (dashed line) in France, 1920–2009



Source: Human Mortality Database (2012).

Figure 7:
Height-adjusted age distribution curves of adult deaths for females and males in France, 1972 and 2009

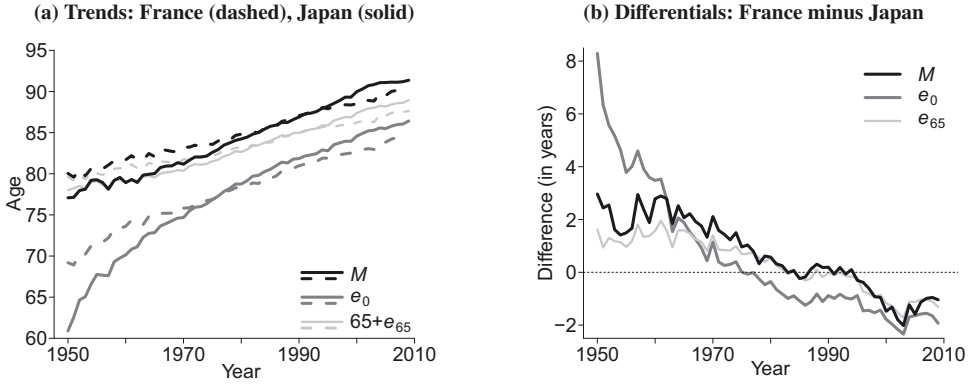


Note: The age-at-death distribution curves for period life tables were directly derived from the P-spline-smoothed mortality curves based on penalised Poisson likelihood.
Source: Human Mortality Database (2012).

behind the French in all three measures, but by the end of the period, the hierarchy was reversed. However, the timing of the French-Japanese reversals in M, e_0 and e_{65} differed. As shown in Figure 8(b), the reversal in e_0 occurred around 1975 and preceded that of M and e_{65}. Thus, during the 1975–1985 period, Japan had higher values of e_0, but France still had higher values of M and e_{65}. This situation is likely due to a 'crossover' from lower death rates at younger ages to higher death rates at older ages for Japan compared to France in this period. Figure 9 illustrates indeed how the mortality curves for Japan and for France changed between 1950 and 2009 (calendar years 1950, 1980 and 2009 were selected for purposes of illustration) and it confirms the occurrence and timing of this young-old mortality crossover. Prior to the crossover (before 1975), death rates at all ages were higher in Japan than in France, and thus Japan had lower values of M, e_0 and e_{65}. Then, while the young-old mortality crossover was taking place (from 1975 to 1985, as illustrated by the 1980 mortality curves in Figure 9), death rates at ages under 60 in Japan fell below those of France, which resulted in Japan recording higher values of e_0 (due to this measure's sensitivity to mortality at all ages, including infant, child and young-age adult mortality). Given that M and e_{65} are determined by mortality at old ages only, both measures remained higher in France until 1985. Finally, when death rates at almost all ages in Japan became lower than in France (after 1985), Japan recorded higher values of M, e_0 and e_{65}.

It should be noted that the concept of mortality crossover is not unfamiliar to demographers—the best-documented example being the mortality crossover at older ages between black and white populations in the US (Coale and Kisker 1986;

Figure 8:
International trends and differentials in adult modal age at death (M), life expectancy at birth (e_0) and total life expectancy at age 65 (65 + e_{65}), French and Japanese females, 1950 to 2009



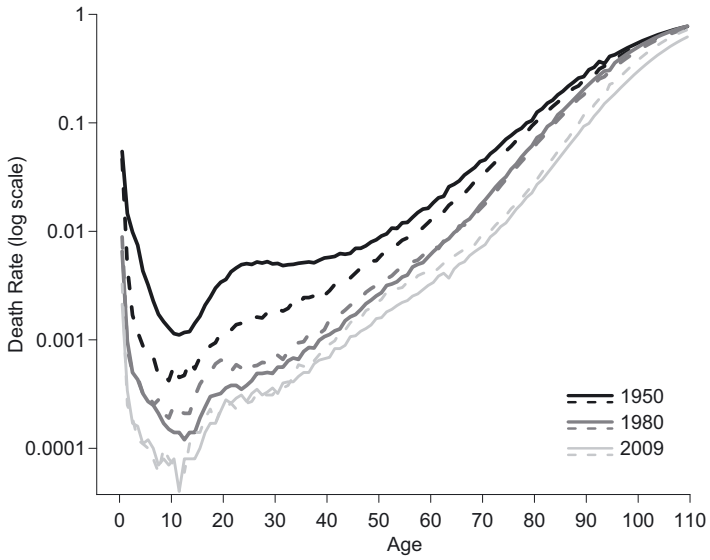
Source: Human Mortality Database (2012).

Kestenbaum 1992; Preston et al. 1996; Johnson 2000). However, when comparing two countries such as France and Japan, mortality crossovers are seldom examined. The above example demonstrates that these crossovers can actually produce reversals of e_0 and M trends, such that e_0 is higher in one country while M is higher in the other country.

5 Modal age at death in mortality models

It is known that observed age variations in adult mortality exhibit high degrees of mathematical regularity, and some mathematical equations fit those empirical variations very well. Those equations include the Gompertz, logistic and Weibull models, as well as their Makeham variants. In this section we show that the Gompertz, logistic and Weibull models can be reformulated using M as the parameter representing the overall level of adult mortality, and their Makeham variants can also be reformulated in similar manners. To our knowledge, this special advantage has not been found for the life expectancy or median age at death.

Figure 9:
Age-specific death rates, French (dashed line) and Japanese (solid line) females, 1950, 1980 and 2009



Note: Age-specific death rates in this figure were directly taken from life tables available in the Human Mortality Database (2012). It should be noted that at older ages, such death rates are smoothed based on the Kannisto model of old-age mortality (Thatcher et al. 1998; see also Wilmoth et al. 2007 for more details).
Source: Human Mortality Database (2012).

Conventionally, the force of mortality (or the instantaneous death rate) at age x in the Gompertz, logistic and Weibull models are expressed as follows:

$$\text{Gompertz:} \qquad \mu(x) = ae^{bx} \tag{1}$$

$$\text{Logistic:} \qquad \mu(x) = \frac{ae^{bx}}{1 + (a/g)e^{bx}} \tag{2}$$

$$\text{Weibull:} \qquad \mu(x) = ax^{b}. \tag{3}$$

Although these models have different mathematical characteristics, they are based on comparable conceptual schemes. Each model has two basic parameters a and b, with a summarising the overall level of adult mortality and b indicating the pace of age-related mortality increase, although different age trajectories such as exponential, logistic and polynomial increases are assumed. The logistic model has a third parameter, g, which is the upper bound of logistic growth. Parameters a, b and g are all assumed positive.

These models can also be expressed using M:

$$\text{Gompertz:} \qquad \mu(x) = be^{b(x-M)} \tag{4}$$

$$\text{Logistic:} \qquad \mu(x) = \frac{be^{b(x-M)}}{1 + (b/g)e^{b(x-M)}} \tag{5}$$

$$\text{Weibull:} \qquad \mu(x) = \frac{b}{M}\left(\frac{x}{M}\right)^{b}. \tag{6}$$

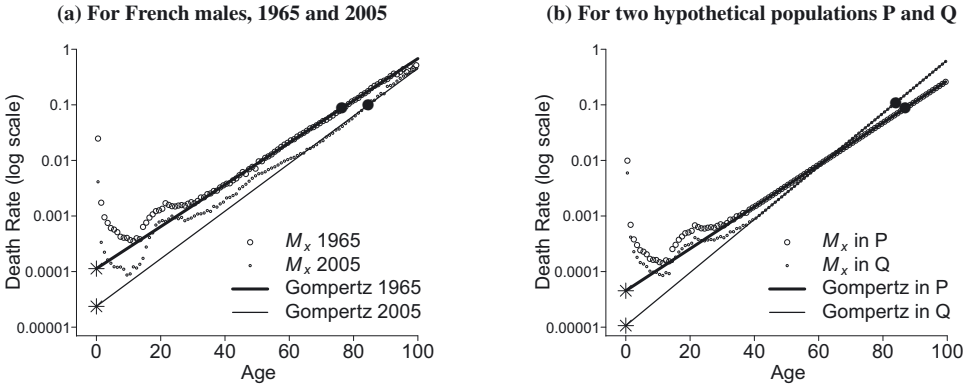
Derivations of Equations 4, 5 and 6 from their conventional forms are given in Appendix D. In addition, M and M-related measures such as $\mu(M), l(M)$ (i.e. the life table survival function) and $d(M)$ (i.e. the density function for the age-at-death distribution) in the Gompertz, logistic and Weibull models can be mathematically expressed, as shown in Appendix E.

In each of the three models, the mortality level parameter a was replaced by M. Although Equations 4, 5 and 6 may appear slightly more complicated than Equations 1, 2 and 3, M is more clearly interpretable than a. This is illustrated in Figure 10(a) in which the Gompertz model was fitted to death rates for ages 60 to 90 for French males in 1965 and 2005. Estimated values of a are 1.13×10^{-4} for 1965 and 2.4×10^{-5} for 2005 (indicated as asterisks), and estimated values of M (derived from the Gompertz parameter values) are 76.4 for 1965 and 84.5 for 2005 (indicated as filled circles).[6]

In the Gompertz model, a is the force of mortality at exact age 0 extrapolated from adult ages. Thus a is a highly hypothetical quantity and the interpretation of a is not

[6] Values of M estimated by Poisson P-splines are 76.8 for 1965 and 85.3 for 2005. The logarithmic mortality curve at old ages for 2005 does not appear very straight but looks slightly convex at younger old ages (centring around 70) and concave at older old ages (centring around 90). The 0.8 year difference between the two M estimates for 2005 may be due to this departure from the exponential curve.

Figure 10:
Age-specific death rates (M_x) and corresponding Gompertz models



Note: The Y-coordinates of asterisks indicate values of parameter a in equation 1, and X-coordinates of filled circles indicate M values estimated using the Gompertz model (equation E.1).
Source: Human Mortality Database (2012).

as straightforward as that of M. Actual central death rates for age 0 were 0.024779 in 1965 and 0.004129 in 2005, considerably higher than the estimated values of a. In addition, estimated values of a are extremely small and it is difficult to have an intuitive understanding of those values. On the contrary, the meaning of M values is intuitively clear.

Furthermore, when mortality schedules of two populations are compared, a paradoxical result about a could be obtained. Although a is generally considered to be a parameter indicating the overall level of mortality, it is possible for a population with higher adult death rates to have a lower value of a than the other population, if b is substantially different between the two schedules. Figure 10(b) shows mortality schedules of two hypothetical populations: although population Q has higher mortality at old ages and lower M than population P, the value of a for population Q is smaller than for population P. In contrast, a lower value of M almost always indicates higher mortality rates at old ages.

The above argument is applicable to the logistic and Weibull models as well. In the conventional form of each of those three models, the mortality level parameter a is obtained by extrapolating the age pattern of adult mortality to some 'reference age' such as 0 and 1: $\mu(0) = a$ in the Gompertz model (Equation 1), $\mu(0) = a/\{1 + (a/g)\} \approx a$ in the logistic model (Equation 2) and $\mu(1) = a$ in the Weibull model (Equation 3). The large gap between adult ages and the reference age could produce paradoxical results.

For each model, its Makeham variant could be set up by assuming that adult mortality is the sum of premature mortality, which is assumed to be constant over age and denoted by c below, and senescent mortality, which is represented by the

original model (Equations 4, 5 and 6):

$$\text{Gompertz–Makeham:} \qquad \mu(x) = c + be^{b(x-M_s)} \tag{7}$$

$$\text{Logistic–Makeham:} \qquad \mu(x) = c + \frac{be^{b(x-M_s)}}{1 + (b/g)e^{b(x-M_s)}} \tag{8}$$

$$\text{Weibull–Makeham:} \qquad \mu(x) = c + \frac{b}{M_s}\left(\frac{x}{M_s}\right)^b. \tag{9}$$

These Makeham variants use the modal age at death from senescent mortality (M_s), which is nearly equal to (though slightly higher than) the modal age at death from total mortality (M). For example, according to the logistic–Makeham model fitted to mortality data for Swedish women aged 55–95 in 1973–1977 (Horiuchi and Coale 1990), $M = 84.3$ and $M_s = 84.6$. This proximity is attributable to the fact that at old ages the estimated level of senescent mortality is considerably higher than that of premature mortality. It is estimated from the fitted model that 98 per cent of $\mu(M)$ is due to senescent mortality, and only 2 per cent to premature mortality.

In summary, this section has shown that the Gompertz, logistic and Weibull models and their Makeham variants can be reformulated using M. Algebraically, the M versions tend to be slightly more complicated than the original versions. However, the replacement of the original mortality level parameter by M makes those models more clearly and straightforwardly interpretable. We could not find such a special property for the life expectancy or median age at death. Thus, in addition to the empirical evidence discussed in the preceding section, this special mathematical feature may add to M's importance as a major indicator of old-age survival.

6 Conclusion

As discussed in this paper, M is a lifespan indicator that is solely determined by old-age mortality as far as mortality follows a bathtub curve. In the context of common pattern of age distribution of deaths, M is considered to represent the location of the old-age death heap.

When mortality data are erratic, for instance because of a small number of deaths or some data quality problem, it may be difficult to determine M. However, based on recent progress in the nonparametric regression methodology, a method has been developed for deriving M from the P-spline-smoothed mortality curve based on penalised Poisson likelihood, and it is highly effective in estimating M.

With selected examples in which M was estimated using this nonparametric method, we have shown that patterns of trends and differentials in M and those in other major lifespan indicators including the life expectancy at birth and conditional life expectancies such as e_{65} could be noticeably different, reflecting the characteristic of M as an indicator representing the location of the old-age death heap. In addition, M plays key roles in widely-used mortality models such as the Gompertz, logistic

and Weibull models as well as their Makeham variants, and M helps to formulate those models in more clearly interpretable ways, which seems to suggest the potential theoretical importance of M in ageing research.

As a summary measure of lifespan that reflects mortality rates at all ages, life expectancy at birth should remain a major demographic indicator. However, at a time when the length of human life is extending mainly due to a reduction in old-age mortality, it is also useful to have an additional lifespan indicator that places special focus on old-age survival. We recommend M to be included in the standard set of demographic indicators and widely used in longevity research.

Acknowledgments

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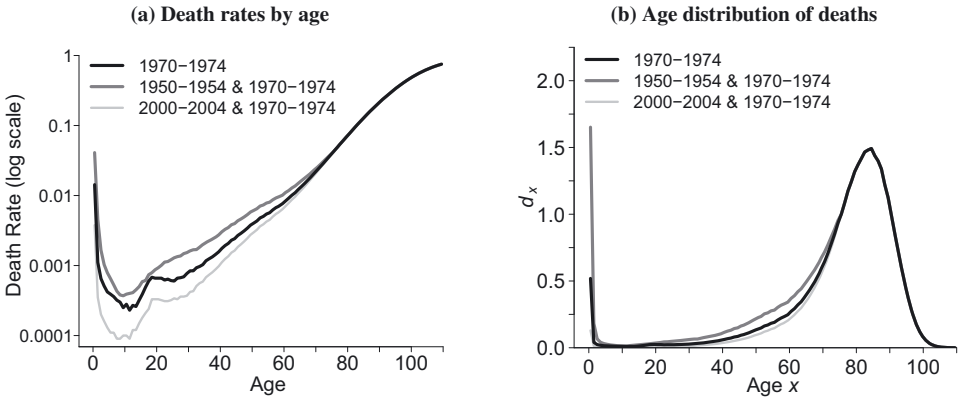
Appendix A: Determination of M by old-age mortality

This appendix shows that if mortality follows a bathtub curve, M is determined solely by old-age mortality. We will first present an artificial example and then develop a line of mathematical reasoning. The argument will be descriptive and not in the form of rigorous proof, partly because of the difficulty expressing the notion of 'determination of M by old-age mortality' as a mathematical equation or inequality and partly because the argument depends on descriptions of ranges and extents of numerical variations (e.g. very small values) rather than exact mathematical relationships.

We compare three different life tables that have the same age-specific death rates for ages 75 and over but different rates for under age 75. The first life table is the 1970–1974 life table for French females. The second life table was constructed by combining the 1950–1954 and 1970–1974 life tables for French females as follows: for ages 35 and below, the same age-specific death rates as those in the 1950–1954 life table; for ages 75 and above, the same age-specific death rates as those in the 1970–1974 life table; and between ages 35 and 75, the death rate changes gradually with age from the 1950–1954 level to the 1970–1974 level. The third life table was constructed by combining the 2000–2004 and 1970–1974 life tables in the same way. e_0 in the three life tables is 76.2, 71.6 and 78.5, respectively.

The left panel of Figure A.1 displays the three age trajectories of death rates and the right panel shows age distributions of deaths in the three life tables. In order to

Figure A.1:
Age patterns of mortality (left) and age distribution of deaths (right) in actual and hypothetical life tables for French females



Note: For comparison of the death distributions in old age, they are scaled in an unusual manner: d_{75} (the number of deaths between exact ages 75 and 76) is set to be 1.0 in all of the three life tables.
Source: Human Mortality Database (2012).

make the comparison easier, d_{75} (the number of deaths between exact ages 75 and 76) is set to unity in all of the three life tables. Although death distributions under age 75 are different, death distributions for ages 75 and over are identical, and the age interval with the highest number of deaths (the discrete M) is $[84, 85)$ for the three life tables. Thus, in this example, M is determined by mortality for ages 75 and over, regardless of mortality under age 75.

Now we show that in general, M is determined solely by old-age mortality if overall mortality follows a bathtub curve. We use life table functions $l(x)$, $d(x)$ and $\mu(x)$ with their regular definitions in the continuous life table model, as well as the life table ageing rate (LAR), which is defined as $k(x) = [1/\mu(x)] \cdot [d\mu(x)/dx] = d \ln \mu(x)/dx$ for any $x \geq 0$, i.e. the age-specific rate of age-related relative increase in mortality (Horiuchi and Coale 1990; Horiuchi and Wilmoth 1997). In this appendix, $l(x)$, $d(x)$, $\mu(x)$ and $k(x)$ are assumed to be differentiable.

The bathtub curve of human mortality can be split by two boundary ages, x_1 and x_2, into three phases: under age x_1 (childhood), from x_1 to x_2 (adolescence and early adult age), and x_2 and above (late adult age). Empirically, x_1 is around the age of puberty and x_2 is in middle age, somewhere between 30 and 50. These three phases approximately correspond to the three phases of $d(x)$ curve described in the introduction section. The three phases can be distinguished from each other in terms of $k(x)$: $k(x) < 0$ in the first phase, $|k(x)| < \lambda_1$ in the second phase, and $\lambda_1 \leq k(x) \leq \lambda_2$ and $|dk(x)/dx| < \lambda_3$ in the third phase. λ_1, λ_2 and λ_3 are parameters that characterise the variability of bathtub curves for human populations.

In the first phase, the logarithmic mortality curve is downward, i.e. $k(x) < 0$ for any x in $[0, x_1)$. In the neighbourhood of x_1, $\mu(x)$ is very low and $k(x)$ approaches zero. In the second phase, the mortality curve remains fairly flat. This may be expressed as $|k(x)| < \lambda_1$ in $[x_1, x_2)$: λ_1 is the threshold value that separates steep slopes ($|k(x)| \geq \lambda_1$) and not-steep slopes ($|k(x)| < \lambda_1$). The limited variation in $k(x)$ keeps $\mu(x)$ low through the second phase. In the last part of this phase, $k(x)$ gradually increases and approaches λ_1. In the third phase (late adult age), the force of mortality increases steeply (i.e. $k(x) \geq \lambda_1$) in a stable manner. The stability of slope can be described as limited variations of $k(x)$ in a relatively narrow range ($\lambda_1 \leq k(x) \leq \lambda_2$ at any x) and small change in $k(x)$ ($|dk(x)/dx| < \lambda_3$ at any x). In previous studies (e.g. Horiuchi and Coale 1990; Horiuchi 1997; Horiuchi and Wilmoth 1998), it appears that most smoothed values of $k(x)$ in adult age fall in the range between 0.05 and 0.15, if the time unit is year, and $|dk(x)/dx|$ remains under 0.004. Thus $\lambda_1 = 0.05$, $\lambda_2 = 0.15$ and $\lambda_3 = 0.004$ may be possible choices for modern human populations.[7]

Let M be the age of the maximum death density above age x_1:

$$M = \{x \mid \max[d(x)] \text{ for } x \geq x_1\}. \tag{A.1}$$

This may be considered a generalisation of the definition by Canudas-Romo (2010). By differentiating $d(x) = l(x)\mu(x)$ with respect to x, we get

$$\frac{dd(x)}{dx} = d(x)\left[k(x) - \mu(x)\right]. \tag{A.2}$$

Thus, if the $d(x)$ function has a local maximum or minimum at age y, then

$$\mu(y) = k(y). \tag{A.3}$$

This is obtained by setting $x = y$, and making use of the fact that the derivative of $d(x)$ at y is zero. Thus, if $d(M)$ occurs at one of the local maximums in the age range, the force of mortality, $\mu(x)$, and the life table ageing rate, $k(x)$, are identical at M, i.e.

$$\mu(M) = k(M). \tag{A.4}$$

This was initially found in the specific context of the Gompertz model (Pollard 1991, 1998a and 1998b; Pollard and Valkovics 1992), in which $k(x)$ is assumed constant over age, and then extended to the more general form (Robine et al. 2006; Canudas-Romo 2008).

The assumed properties of $k(x)$ in the third phase imply that the age-at-death distribution in late adult age is unimodal and M is determined by old-age mortality.

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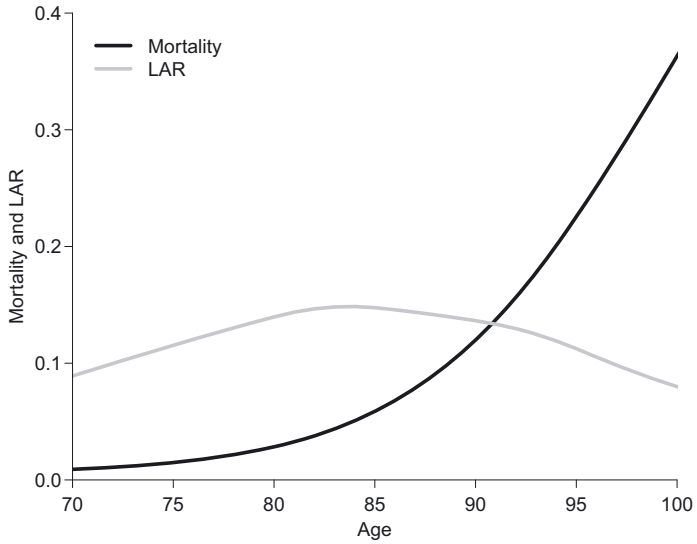
[7] This condition allows a deceleration of relative mortality increase at old ages ($dk(x)/dx < 0$) but does not allow a near-flattening of the mortality curve at extremely old ages, which was observed for ages 100 to 106 in a pooled population of male centenarians (Kannisto 1996). For our purposes, this problem does not matter because $d(x)$ is very small at extremely old ages.

Figure A.2:
Mortality and life table ageing rate (LAR) by age for French females, 2009



Note: The mortality curve was obtained by P-spline smoothing based on penalised Poisson likelihood, and the life table ageing rate curve was directly derived from the mortality curve.
Source: Human Mortality Database (2012).

This is illustrated in Figure A.2, which shows trajectories of the $\mu(x)$ and $k(x)$ in old age for French females in 2009. The two curves cross only once in the figure, indicating that there is only one local maximum value of $d(x)$ within the age range. For the $d(x)$ function to have two or more local maximums and minimums, the two curves need to cross with each other multiple times.

Since $\mu(x)$ remains low in the second phase, $\mu(x_2)$ is considerably lower than 0.05. Thus initially in the third phase, the $\mu(x)$ curve remains below the $k(x)$ curve. Because $\mu(x)$ increases steeply at the exponential rate of 0.05 per year or higher but $k(x)$ stays in the range between 0.05 and 0.15, the two curves eventually cross with each other, causing $d(x)$ to reach a local peak. Let the age of this local peak be denoted by y. This age is the only local mode in the third phase: once the two curves cross with each other, they will not cross again, because $\mu(x)$ continues to rise steeply and $k(x)$ remains stable (i.e. $d\mu(x)/dx > dk(x)/dx$ for any $x \geq y$), thereby enlarging the gap between them. Thus, the death distribution in late adult age is unimodal.

Because $\mu(y) = k(y)$, $\mu(y)$ must be between 0.05 and 0.15. Thus, the location of y, which is around age 90 in Figure A.2, is determined by the age trajectory of $\mu(x)$ in the range of 0.05 to 0.15, which is a very high level. Given that $\mu(x)$ continuously increases with age in the third phase, it can be stated that this $\mu(x)$ range is in old

age, if we consider 'old age' as adult age of high mortality. Therefore, the location of y is determined by the age trajectory of mortality in old age.

Finally, $y = M$ if $d(y)$ is greater than any $d(x)$ in the second phase. This seems intuitively clear, but can also be based on the fact that because both $|k|$ and μ are very small in the second phase and because k is greater than μ under age y in the third phase, we have $\int_x^y k(t)\,dt > \int_x^y \mu(t)\,dt$. This inequality leads to $l(y)/l(x) > \mu(x)/\mu(y)$ and then $d(y) > d(x)$ for any x in $[x_1, x_2)$.

Appendix B: Poisson P-spline smoothing method for estimating M: Overview and implementation in R

B.1 Overview of the method

Let D_i and E_i denote the observed death count and person-years lived in the age interval $[i, i+1)$. Assuming that the force of mortality (i.e. mortality curve) is a piecewise constant function, or to be more specific, that the force of mortality is constant within each 1-year age interval such as $\mu(x) = \mu_i$ for any x in $[i, i+1)$, then the various D_i can be seen as realisations of a Poisson distribution with mean $E_i \cdot \mu_i$.

Thus, in order to estimate μ_i, a Poisson regression model is used such that

$$\ln(\mathrm{E}(D)) = \ln(E \cdot \mu) = \ln(E) + \ln(\mu), \tag{B.1}$$

where D, E and μ respectively correspond to observed death, person-years lived and force of mortality vectors (each one including all the age-specific information). The unknown parameters of this regression model are estimated with a flexible nonparametric approach based on P-splines, which combines the concepts of B-splines and penalised likelihood (Eilers and Marx 1996). The main outcome of this is a fitted (i.e. smoothed) log force of mortality, which is described as a linear combination of B-splines whose coefficients have been penalised. For a brief introduction to P-splines and more details regarding their use in the specific context of mortality analysis, please refer to Ouellette and Bourbeau (2011, Appendix). Thus, smoothed forces of mortality resulting from the estimation procedure correspond to:

$$\hat{\mu}(x) = \exp(B(x)\hat{\alpha}), \tag{B.2}$$

where B is the B-spline basis matrix and $\hat{\alpha}$ is the vector of estimated penalised coefficients for each B-spline included in B.

Given the usual correspondence between the force of mortality, survival and density functions, the smoothed density function describing the age-at-death distribution is expressed as:

$$\hat{d}(x) = \hat{\mu}(x) \cdot \hat{l}(x) = \hat{\mu}(x) \exp\left(-\int_0^x \hat{\mu}(u)\,du\right) \tag{B.3}$$

and can be computed using standard numerical integration techniques. Finally, the estimated modal age at death is given by $\hat{M} = \max_x \hat{d}(x)$.

B.2 An R routine for computing M estimates from P-spline-smoothed mortality curves

Suppose that the "Mort1Dsmooth" function of the MortalitySmooth package in R (Camarda 2013) is used to smooth death counts with Poisson P-splines over a given range of ages as described above. This can be done with the following commands:

R > library("MortalitySmooth")
R > fit <- "Mort1Dsmooth"(x = age, y = D, offset = log(E))

where *age* is a vector with the age values for smoothing (e.g. 10, 11, . . . , 109), and the vectors *D* and *E* include the observed death counts and person-years lived in each age interval. The output of the "Mort1Dsmooth" function is a *fit* object that contains information about the fitting of the Poisson regression model and about the original data.

The "predict.Mort1Dsmooth" function can be used to obtain predictions of the smoothed mortality curve over very narrow age intervals (i.e. narrower than the original 1-year intervals), in order to come closer to the concept of force of mortality (or instantaneous death rate). For instance, if each 1-year interval is subdivided into 1,000 equal parts, then:

R > delta <- 0.001
R > age.narrow <- seq(from = min(age), to = max(age), by = delta)
R > log.mu.hat <- predict(object = fit, newdata = age.narrow)
R > mu.hat <- exp(log.mu.hat)

To compute the smoothed survival function corresponding to the P-spline-smoothed mortality curve, *mu.hat*, the latter must be integrated over age (Equation B.3). This integral can be evaluated using numerical approximation techniques. As long as the age intervals are very narrow (e.g. 0.001 as above) and the integrand is a smooth function, basic numerical integration methods can be used, such as the left Riemann sum:

R > l.hat <- exp(-cumsum(mu.hat ∗ delta))

The corresponding smoothed density function, which describes the age-at-death distribution, is then readily obtained (Equation B.3):

R > d.hat <- mu.hat ∗ l.hat

Finally, the estimated value of M is given by the age at which the peak of the heap of deaths occurs in the smoothed density function:

R > M.hat <- age.narrow[which.max(d.hat)]

Appendix C: Changes in the conditional life expectancy at old age in the context of mortality shift

Suppose that the mortality schedule above age y at time t_0 shifts to higher ages by u years in the period between t_0 and t:

$$\mu(x+u,t) = \mu(x,t_0) \quad \text{for any } x \geq y. \tag{C.1}$$

Note that in this case,

$$e_{x+u}(t) = e_x(t_0) \quad \text{for any } x \geq y \tag{C.2}$$

and M also increases by u, i.e.

$$M(t) = M(t_0) + u. \tag{C.3}$$

However, the increase in e_y is smaller:

$$\begin{aligned} e_y(t) &= \frac{T_y(t)}{l_y(t)} \\ &= \frac{{}_uL_y(t) + T_{y+u}(t)}{l_y(t)} \\ &= \frac{{}_uL_y(t)}{l_y(t)} + \frac{l_{y+u}(t)}{l_y(t)} e_{y+u}(t) \\ &= \frac{{}_uL_y(t)}{l_y(t)} + \frac{l_{y+u}(t)}{l_y(t)} e_y(t_0) \\ &< u + e_y(t_0). \end{aligned} \tag{C.4}$$

The inequality holds because ${}_uL_y(t)/l_y(t)$ (the mean number of years lived between ages y and $y+u$) must be lower than u and $l_{y+u}(t)/l_y(t)$ (the proportion of those who are alive at age y who survive to $y+u$) must be lower than one, unless mortality in the age range is null. Thus, the increase in e_y between t_0 and t is less than u.

Equation C.1 also implies that if mortality increases with age, then for any pair of ages y and x ($y < x$),

$$\frac{{}_uL_y(t)}{l_y(t)} > \frac{{}_uL_x(t)}{l_x(t)} \quad \text{and} \quad \frac{l_{y+u}(t)}{l_y(t)} > \frac{l_{x+u}(t)}{l_x(t)} \tag{C.5}$$

so that

$$e_y(t) - e_y(t_0) > e_x(t) - e_x(t_0). \tag{C.6}$$

□

Appendix D: Derivation of M versions of the Gompertz, logistic and Weibull models

In this appendix, the M versions of the Gompertz, logistic and Weibull models (Equations 4, 5 and 6) are derived from the corresponding conventional forms (Equations 1, 2 and 3, respectively). All of the derivations are based on a fundamental relation, Equation A.4 in Appendix A: $\mu(M) = k(M)$.

The life table ageing rate (LAR) for each model is as follows (Horiuchi and Coale 1990):

$$\text{Gompertz:} \qquad k(x) = b \tag{D.1}$$

$$\text{Logistic:} \qquad k(x) = \frac{b}{1 + (a/g)e^{bx}} \tag{D.2}$$

$$\text{Weibull:} \qquad k(x) = b/x. \tag{D.3}$$

For the Gompertz model, by setting $x = M$ in Equations 1 and D.1 and substituting them into Equation A.4, we get $a = be^{-bM}$. Substitution of this into Equation 1 leads to Equation 4. A similar derivation works for the logistic model: by setting $x = M$ in Equations 2 and D.2 and substituting them into Equation A.4, we obtain $a = be^{-bM}$ again, which is substituted into Equation 2, resulting in Equation 5. For the Weibull model, by setting $x = M$ in Equations 3 and D.3 and substituting them into A.4, we have $a = bM^{-(b+1)}$. Substitution of this into Equation 3 leads to Equation 6.

Appendix E: *M*-related measures in mathematical mortality models

Characteristics of M in the Gompertz model were investigated by Pollard and his colleagues (Pollard 1991, 1998a and 1998b; Pollard and Valkovics 1992). The work was elaborated further and extended to the logistic and Weibull models (Robine et al. 2006; Canudas-Romo 2008). In this appendix, mathematical expressions of $M, \mu(M), l(M)$ and $d(M)$ for the Gompertz, logistic and Weibull models are shown in terms of their conventional parameters. Some of the expressions for the Gompertz and logistic models were previously reported by Pollard and colleagues and/or Canudas-Romo, but are included here for consistency and comprehensiveness.

In what follows, $l(0)$ is set to unity. The expressions for $l(M)$ and $d(M)$ should be taken with caution, because they are obtained assuming that the age trajectory of mortality throughout the entire lifespan follows the model, which actually fits mortality at adult ages only. Thus, if the model fits mortality above age 30, the analytical expressions for $l(M^*)$ and $d(M^*)$, where $M^* = M - 30$, should be close to observed values of $l(M)/l(30)$ and $d(M)/l(30)$.

E.1 Gompertz model

M, $\mu(M)$, $l(M)$ and $d(M)$ for the Gompertz model are given by:

$$M = \frac{\ln(b/a)}{b} \tag{E.1}$$

$$\mu(M) = b \tag{E.2}$$

$$l(M) = e^{-1+(a/b)} \approx e^{-1} \tag{E.3}$$

$$d(M) = be^{-1+(a/b)} \approx b/e. \tag{E.4}$$

The expression for M (Equation E.1) is implied by $a = be^{-bM}$, which was derived earlier in Appendix D. The expression for $\mu(M)$ (Equation E.2) comes from Equation 4 by setting $x = M$. Derivation of Equation E.3 starts with the basic definition of the survival function:

$$l(x) = \exp\Big(-\int_0^x \mu(y)\,dy\Big). \tag{E.5}$$

Substituting Equation 1 into E.5 and making use of $a = be^{-bM}$, we get

$$l(x) = \exp\Big(-\Big[\frac{a}{b}e^{by}\Big]_{y=0}^{y=x}\Big) = \exp\Big(\frac{a}{b} - e^{b(x-M)}\Big), \tag{E.6}$$

so that $l(M) = e^{-1+(a/b)}$, which is approximated by e^{-1} because usually $a \ll b$. The expression for $d(M)$ is obtained simply as a product of $l(M)$ and $\mu(M)$.

E.2 Logistic model

M, $\mu(M)$, $l(M)$ and $d(M)$ for the three-parameter logistic model are expressed as:

$$M = \frac{\ln(b/a)}{b} \tag{E.7}$$

$$\mu(M) = \frac{b}{1+(b/g)} \approx b \tag{E.8}$$

$$l(M) = \left\{\frac{1+(b/g)}{1+(a/g)}\right\}^{-(g/b)} \approx \{1+(b/g)\}^{-(g/b)} \approx e^{-1} \tag{E.9}$$

$$\begin{aligned} d(M) &= \frac{b}{\{1+(b/g)\}^{1+(g/b)}\{1+(a/g)\}^{-(g/b)}} \\ &\approx \frac{b}{\{1+(b/g)\}^{1+(g/b)}} \approx be^{-1}. \end{aligned} \tag{E.10}$$

Interestingly, the Gompertz and logistic models have similar expressions for M. As in the case of the Gompertz model, derivations of M and $\mu(M)$ are simple ($\mu(M)$ is

approximated by b because $b \ll g$). As for $l(M)$, by substituting Equation 2 into E.5 and using $a = be^{-bM}$, we have

$$\begin{aligned} l(x) &= \exp\left(-\left[\ln\left\{(g + ae^{by})^{(g/b)}\right\}\right]_{y=0}^{y=x}\right) \\ &= \left\{\frac{g + ae^{bx}}{g + a}\right\}^{-(g/b)} \\ &= \left\{\frac{1 + (b/g)e^{b(x-M)}}{1 + (a/g)}\right\}^{-(g/b)}. \end{aligned} \tag{E.11}$$

By setting $x = M$, we have $l(M) = [\{1 + (b/g)\}/\{1 + (a/g)\}]^{-(g/b)}$. Because a/g is very small, this is close to $1/\{1 + (b/g)\}^{(g/b)}$. The denominator of the ratio converges to e as b/g approaches zero. Because b/g is fairly small, $l(M)$ is expected to be close to e^{-1}. Equations E.8 and E.9 imply that $d(M)$ can be approximated by be^{-1}. As the logistic b is usually in the range of 0.10 to 0.14 in low-mortality countries (Thatcher et al. 2010), this suggests that the number of deaths in a one-year period around M should be 4 to 5% of all adult deaths.

E.3 Weibull model

Expressions for M, $\mu(M)$, $l(M)$ and $d(M)$ in the Weibull model are shown below:

$$M = (b/a)^{1/(b+1)} \tag{E.12}$$

$$\mu(M) = b/M \tag{E.13}$$

$$l(M) = e^{-b/(b+1)} \approx e^{-1} \tag{E.14}$$

$$d(M) = (b/M)e^{-b/(b+1)} \approx b/(eM). \tag{E.15}$$

Derivations of these equations are similar to those for the Gompertz and logistic models. As for $l(M)$, substitution of Equation 3 into E.5 and using $a = bM^{-(b+1)}$ results in

$$\begin{aligned} l(x) &= \exp\left(-\left[\frac{a}{b+1}y^{b+1}\right]_{y=0}^{y=x}\right) \\ &= \exp\left\{-\left(\frac{a}{b+1}\right)x^{b+1}\right\} \\ &= \exp\left\{-\left(\frac{b}{b+1}\right)\left(\frac{x}{M}\right)^{b+1}\right\}, \end{aligned} \tag{E.16}$$

so that $l(M) = e^{-b/(b+1)}$, which is slightly higher than e^{-1} because the value of b in the Weibull model is typically in the range of 6 to 10. It is interesting to note that $l(M)$ in each of the three models is close to (though slightly larger than) $e^{-1} \approx 0.368$, suggesting that although the overall level of adult mortality changes substantially

over time, $l(M)/l(30)$ is expected to be fairly constant, because usually mortality above age 30 is well approximated by those models. Again, $d(M)$ is directly obtained as $l(M) \times \mu(M)$.

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