

Modal Age at Death: Lifespan Indicator in the Era of Longevity Extension

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Abstract

This paper examines and demonstrates importance of the adult modal age at death (M) in longevity research. Unlike the life expectancy at birth (e_0) and median age at death, M is determined solely by old-age mortality as far as mortality follows the regular pattern. 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} . Due to these characteristics, patterns of trends and differentials in M can be noticeably different from those in other lifespan measures, as indicated in some examples. In addition, M plays central roles in major models of adult mortality such as the Gompertz, logistic and Weibull models. 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 penalized Poisson likelihood is highly effective in estimating M .

1 Introduction

The mankind 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, the life expectancy at birth for both sexes rose from around 30 to 45 years in the mid-nineteenth century to about 80 years in recent periods (Meslé and Vallin 2011). The longevity expansion resulted in a considerable growth of 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 summarization 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 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 zero) 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 zero in most years during the last half a 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.

[Figure 1 about here]

Whereas both the 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 the regular, smooth pattern of “bath-tub” shape (see Appendix 1 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 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 defining “longevity” is beyond the scope to this paper, the concept seems to have been used not for simply indicating a duration of lifetime but for emphasizing old-age survival for reaching 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 underestimate age shifts of old-age mortality, which are accurately reflected in changes in M .

It is useful to characterize 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 second phase can be located around the typical age of puberty, but the transition from the second to third phase appears 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.

In this paper, we will examine and discuss usefulness of M in longevity research, combining previous findings and new results. We will briefly review past studies on M , investigate empirical patterns of trends and differentials in M in comparison with those in the other lifespan measures such as e_0 and e_{65} , clarify roles of M in broadly used mathematical models of adult mortality, and present a recommended method for estimating. Since a comprehensive international comparison is not a major 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 (i.e., bath-tub pattern of mortality risk and three-phase pattern of death distribution) are common in both period and cohort data.

2 Modal age at death in longevity research

Use of M in longevity research is not a totally new approach. It has been advocated by some fellows in the past two centuries. According to Quételet (1835, 1848, 1871), the mode is not an arithmetic mean but a typical value alongside a normal 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 Quételet's work "*l'homme moyen*", Lexis (1878) also stated that M represents the most central and natural characteristic of the 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 theorized the idea of normal life duration, characteristic of a natural and aging 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 and the limits of the human longevity (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), clarifying 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; Robine et al. 2006; 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, as 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 characterize the natural and normal life span (Elderton 1903; Gumbel 1937; Greenwood and Irwin 1939; Clarke 1950; Le Bras 1976), life expectancy at birth (e_0) was considered as the best index of the life span (Dublin 1923). The substantial decline in mortality at young ages during the first half of the twentieth century was reflected in the steep increase in e_0 . However, currently, 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 (Horiuchi 2003) and is free from any arbitrary selection of age range for “old ages” (Kannisto 2001).

3 Trends and differentials in modal age at death

3.1 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 the life expectancy at birth (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 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 males and females in Figure 2. 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; Robine et al. 2006; 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 nineteenth century and the first half of the twentieth century, due to the reduction in mortality among infants, children, and young-age and middle-age adults. The rise continued in the second half of the twentieth century and recent years, though not as fast as in the earlier phase. On the contrary, the trajectory of M was almost flat or only slightly upward in the first half of the twentieth century, but M started to increase in 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.

[Figure 2 about here]

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, the 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.

3.2 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 e_x 's. Figure 3a 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.

[Figure 3 about here]

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 3b 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 3a and 3b appear fairly comparable, suggesting that differential trends in Figure 3a 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 at the same pace as the shift of mortality curve, but conditional life expectancies increase more slowly (Appendix 2). Although mortality curves do not make exact parallel shifts in actual populations, past trends of old-age mortality in high-income countries can be approximated well as shifts of mortality curves to older ages (Kannisto 1996; Bongaarts 2005; Cheung and Robine 2007; Canudas-Romo 2008). Thus, mortality shifts are more accurately reflected in M trends than in changes of conditional life expectancies at old ages.

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 3a and 3b, the size of change in the conditional life expectancy varies with the starting age such as 55, 65 and 75. Such dependency on the selected age range is lacking 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.

3.3 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 3.4) as examples. Differentials in terms of M , e_0 , and e_{65} (selected as a widely used conditional life expectancy) are compared.

[Figure 4 about here]

Figure 4 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 3.2 and Appendix 2. 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).

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 5, the narrowing of gender gap during the last few decades was more evident for M than for e_0 and e_{65} . Figure 6 shows that the old-age death heap for females and that for males became 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.

[Figure 5 and Figure 6 about here]

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

Figure 7a 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 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 7b, the reversal in e_0 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 appears to be 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 8 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 illustrative purposes) and it confirms the occurrence and timing of such 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 the lowest values of M , e_0 , and e_{65} . Then, while the young-old mortality crossover was taking place (from 1975 to 1985), 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, they 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 the lowest values of M , e_0 , and e_{65} .

[Figure 7 and Figure 8 about here]

When comparing male trends in the three length-of-life measures from 1950 onwards for France with those for Japan (Figure 9a), another interesting situation emerges: during the 2004-2009 period, France recorded greater values of M whereas Japan had higher values of both e_0 and e_{65} (Figure 9b). As shown in Figure 10, this seems to be linked to a mortality crossover between “younger-old” (around age 75) and “older-old” (around age 85) in the final five years of study (year 2009 was selected to represent those years). When contrasting the 1985 and 2009 mortality curves specifically for each country, the main difference is that mortality at ages 60-90 declined much more rapidly in France than in Japan. This eventually led to the above-mentioned crossover and to higher recorded values of M (but not e_0 nor e_{65}) for males in France than in Japan. The M - e_{65} reversal during the 2004-2009 period seems to be mainly due to the fact that M is a measure of the age at which the peak of deaths occurs in the age distribution of deaths (i.e., around age 85 for 2004-2009), making it particularly sensitive to mortality changes in the area of the death heap, whereas e_{65} does not have such distinctive characteristic.

[Figure 9 and Figure 10 about here]

It should be noted that the concept of mortality crossover is not unfamiliar to demographers - the best documented one being the mortality crossover at older ages between black and white populations in the U.S. (Coale and Kisker 1986; Kestenbaum 1992; Preston et al. 1996; Johnson 2000). However, when comparing two countries such as France and Japan, mortality crossovers are seldom examined. The two examples above demonstrate that such crossovers can actually produce M - e_0 reversals, even M - e_{65} reversals.

In sum, the examples given in this section show that trends and differentials in M could be noticeably different from those in other lifespan measures such as life expectancy at birth, conditional life expectancies, and median age at death. Obviously, differences between patterns of M and those of the other two overall lifespan measures (life expectancy at birth and median age at death) are due to the fact M is determined by old-age mortality only. Differences between M and conditional life expectancies such as e_{65} seem to be primarily attributable to the fact that M is specifically an indicator of location of the old-age death heap, capturing changes in the heap location in a population and differences in the heap location among populations, whereas conditional life expectancies lack this distinctive characteristic.

4 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, all of which can be re-formulated using M as the parameter representing the overall adult mortality level, and their Makeham variants can also be re-formulated in similar manners (Robine et al. 2006). To our knowledge, this special advantage has not been found for the life expectancy or median age at death.

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

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

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

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

Although these models have different mathematical characteristics, they are based on comparable conceptual schemes. Each model has two basic parameters a and b , a summarizing 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 :

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

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

Weibull:
$$\mu(x) = \frac{b}{M} \left(\frac{x}{M} \right)^b \quad (6)$$

Derivations of equations 4, 5 and 6 from their conventional forms are given in Appendix 3. 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 life table death density function) in the Gompertz, logistic, and Weibull models can be mathematically expressed, as shown in Appendix 4.

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 11a, 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).

[Figure 11 about here]

In the Gompertz model, a is the force of mortality at exact age zero extrapolated from adult ages. Thus a is a highly hypothetical quantity and the interpretation of a is not 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 11b 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 that 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 distance 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 constant over age and denoted by c below, and senescent mortality, which is represented by the original model (equations 4, 5 and 6):

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

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

Weibull-Makeham:
$$\mu(x) = c + \frac{b}{M_s} \left(\frac{x}{M_s} \right)^b \quad (9)$$

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 percent of $\mu(M)$ is due to senescent mortality, and only 2 percent is due to premature mortality.

Although all of the above-mentioned models are presented in terms of $\mu(x)$, the model by Lexis is formulated with respect to the life table death density function, $d(x)$. As described previously, a main feature of the Lexis model is the normal distribution of $d(x)$ above age M :

$$d(x) = l(M) \frac{2}{s\sqrt{2\pi}} \exp\left(-\frac{(x-M)^2}{2s^2}\right) \quad \text{for any } x \geq M, \quad (10)$$

where s is the standard deviation of the normal distribution. The Lexis model fits post- M death distributions in empirical life tables very well (Cheung and Robine 2007; Cheung et al. 2009). It can be shown (Robine et al. 2006) that relationships among s , $e(M)$ (i.e., life expectancy at M) and $\mu(M)$ in the Lexis model are numerically specified as

$$e(M) = \sqrt{2/\pi} \cdot s \approx 0.798s \quad (11)$$

and
$$\mu(M) = \sqrt{2/\pi} / s \approx 0.798/s. \quad (12)$$

5 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 12a shows that this flat-topped and irregular pattern around the modal age does not only characterize 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 modeling 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 of these could influence results and diminish the accuracy of estimated values of M .

[Figure 12 about here]

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 observed deaths counts and population exposures 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 12b). This method is our preferred one 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 10¹ and onwards. It is advisable, nonetheless, not to extend the smoothing up to the very last high ages, where deaths are scarce and population exposures are small. At these latter ages, the P-spline-smoothed mortality curve may show unrealistic behavior due to significant random fluctuations. This would have hardly any effect on estimated values of M though, since the modal age is a measure of the location of the heap of deaths. Still, we provide a simple rule of thumb that prevents undesirable pattern 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 $i \leq j$.² In cases where this rule of thumb fails to prevent realistic smoothed mortality behavior at the highest ages, the threshold of ten observed deaths could be increased.

In the remainder of this section, we first provide a more detailed overview of the P-spline smoothing method for estimating M . Then, we discuss how to use the method in the statistical programming environment R (R Core Team 2012).

Let D_i and E_i denote the observed death count and population exposure (i.e., exposure-to-risk) at age i . 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 realizations 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

¹ Infant and early childhood mortality presents unique features (in particular, a very steep downward slope between ages 0 and 1) which this P-spline method cannot cope well with, and that are not of interest for estimating M anyway.

² For instance, among French males in 2004, the number of observed deaths at ages 104 thru 109 was 38, 13, 4, 7, 0, and 0 (Human Mortality Database 2012). In this case, then the last four 1-year age groups (i.e., ages 106 thru 109) would be excluded from smoothing.

$$\ln(E(D)) = \ln(E \cdot \mu) = \ln(E) + \ln(\mu), \quad (13)$$

where D , E and μ respectively correspond to observed death, exposure, 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 penalized 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 penalized. 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:

$$\hat{\mu}(x) = \exp(B(x)\hat{\alpha}), \quad (14)$$

where B is the B-spline basis matrix and $\hat{\alpha}$ is the vector of estimated penalized 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:

$$\hat{d}(x) = \hat{\mu}(x) \cdot \hat{l}(x) = \hat{\mu}(x) \exp\left(-\int_0^x \hat{\mu}(u) du\right) \quad (15)$$

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

Note that to estimate M , it is preferable to obtain the smoothed death density function, \hat{d} , directly from the P-spline-smoothed mortality curve, $\hat{\mu}$, (see equation 15), 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.

Conveniently, the MortalitySmooth package (Camarda 2012a, 2012b) 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.³ This function can therefore be used to obtain smoothed forces of mortality, $\hat{\mu}$, from observed deaths counts and population exposures (see equation 14). The subsequent steps leading to M estimates are not implemented in the current version of MortalitySmooth. However, we have included an R routine that covers these steps at the end of this article (see Appendix 5).

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 the regular pattern. In the context of common pattern of age distribution of deaths, M is considered to represent the location of old-age death heap. Due to these unique characteristics of M , patterns of trends and differentials in M and those in other

³ The package also includes a Mort2Dsmooth function, for those interested in smoothing mortality data over ages and years simultaneously. This generalization is particularly useful when dealing with small populations, for instance. The ability of the two-dimensional approach to borrow information from both neighboring years and ages makes large random fluctuations less likely to distort the smoothed outcome (Camarda 2012b). For an analysis of geographical disparities in M using this generalized approach, see Ouellette et al. (2012).

major lifespan indicators including the life expectancy at birth, median age at death, and conditional life expectancies such as e_{65} could be noticeably different, as shown in the selected examples. 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 manners than their conventional formulations.

When mortality data are erratic due to, for instance, a small number of deaths or some data quality problem, it may possibly 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 penalized Poisson likelihood, and it is highly effective in estimating M .

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

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Appendix 1 Unimodality of adult death distribution

Consider the life table survival function $l(x)$ and death density function $d(x) = -dl(x)/dx$ such that $d(x) \geq 0$ for any age x in $[0, \omega]$ and $d(x) = 0$ for any $x > \omega$. Suppose $d(x)$ is differentiable on the open interval $(0, \omega)$. If the $d(x)$ function has a local maximum or minimum at age y , then

$$\mu(y) = k(y) \quad (\text{A.1})$$

where $\mu(x) = d(x)/l(x)$ and $k(x) = d \ln \mu(x)/dx$. This is obtained by differentiating $d(x) = l(x)\mu(x)$ with respect to x , setting $x = y$, and making use of the fact that the derivative of $d(x)$ at y is zero. Thus, the force of mortality, $\mu(x)$, and the life table aging rate, $k(x)$, are identical at M , i.e.,

$$\mu(M) = k(M) \quad (\text{A.2})$$

This equation indicates that as far as adult mortality increases with age monotonically, smoothly and gradually, there is only one mode in adult age. In this context, monotonicity means $d\mu(x)/dx > 0$ for any adult age, smoothness means differentiability, and a gradual change means lack of abrupt change in $k(x)$. This is illustrated in Figure A1, 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 multiple times.

[Figure A1 about here]

Variations in $k(x)$ are relatively small in human populations, as suggested by the Gompertz model, which assumes constancy of $k(x)$ over adult age. Empirically, most smoothed values of $k(x)$ in adult age fall in the range between 0.05 and 0.15 in modern human populations, if the time unit is year (e.g., Horiuchi and Coale 1990; Horiuchi 1997; Horiuchi and Wilmoth 1998).

The $\mu(x)$ and $k(x)$ curves do not cross in young adult age or middle age, where $\mu(x)$ is considerably lower than 0.05. As $\mu(x)$ increases steeply and $k(x)$ remains fairly stable, the two curves eventually cross with each other, making $d(x)$ reach a local maximum. The age at the crossing point is likely to be significantly old (around age 90 in the Figure A1), because the force of mortality must be in the range of 0.05 to 0.15, which is high (Thatcher et al. 2010). Thus equation A.2 suggests that essentially, M is determined solely by the trajectory of old-age mortality, because mortality at younger ages is far below the regular range of $k(x)$.

Once the two curves cross with each other, they are unlikely to cross again, as $\mu(x)$ continues to rise further and $k(x)$ remains stable, thereby enlarging the gap between them. Mathematically, it is possible for the two curves to cross with each other repeatedly, even if $\mu(x)$ continues to increase monotonically. Their crossovers can occur if $k(x)$ raises and falls very steeply within an extremely short period of time. However, a $\mu(x)$ pattern with such abrupt changes in $k(x)$ cannot be considered as a gradually increasing curve. (In erratic data, the discrete $k(x)$ may fluctuate considerably, possibly producing multiple crossovers between $\mu(x)$ and $k(x)$.)

Appendix 2 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 :

$$\mu(x+u, t) = \mu(x, t_0) \quad \text{for any } x \geq y. \quad (\text{A.3})$$

Note that in this case,

$$e_{x+u}(t) = e_x(t_0) \quad \text{for any } x \geq y \quad (\text{A.4})$$

and M also increases by u , i.e.,

$$M(t) = M(t_0) + u. \quad (\text{A.5})$$

However, the increase in e_y is smaller:

$$\begin{aligned} e_y(t) &= \frac{T_y(t)}{l_y(t)} \\ &= \frac{{}_uL_y(t) + T_{y+u}(t)}{l_y(t)} \\ &= \frac{{}_uL_y(t)}{l_y(t)} + \frac{l_{y+u}(t)}{l_y(t)} e_{y+u}(t) \\ &= \frac{{}_uL_y(t)}{l_y(t)} + \frac{l_{y+u}(t)}{l_y(t)} e_y(t_0) \\ &< u + e_y(t_0) \end{aligned} \quad (\text{A.6})$$

because $\frac{{}_uL_y(t)}{l_y(t)} < u$ and $\frac{l_{y+u}(t)}{l_y(t)} < 1$ unless mortality between y and $y+u$ is zero. Thus, the

increase in e_y between t_0 and t is less than u .

Equation A.3 also implies that if mortality increases with age, then for any pair of ages y and x ($y < x$),

$$\frac{{}_uL_y(t)}{l_y(t)} > \frac{{}_uL_x(t)}{l_x(t)} \quad \text{and} \quad \frac{l_{y+u}(t)}{l_y(t)} > \frac{l_{x+u}(t)}{l_x(t)} \quad (\text{A.7})$$

so that

$$e_y(t) - e_y(t_0) > e_x(t) - e_x(t_0). \quad (\text{A.8})$$

Appendix 3 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.2 in Appendix 1: $\mu(M) = k(M)$.

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

Gompertz:
$$k(x) = b \tag{A.9}$$

Logistic:
$$k(x) = \frac{b}{1 + (a/g) e^{bx}} \tag{A.10}$$

Weibull:
$$k(x) = b/x \tag{A.11}$$

For the Gompertz model, by setting $x=M$ in equations 1 and A.9 and substituting them into equation A.2, 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 A10 and substituting them into equation A.2, 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 A.11 and substituting them into A.2, we have $a = b M^{-(b+1)}$. Substitution of this into equation 3 leads to equation 6.

Appendix 4 *M*-related measures in mathematical mortality models

Characteristics of *M* in the Gompertz model were investigated by Pollard and his colleagues (Pollard 1991, 1998; Pollard and Valkovics 1992). The work was elaborated further and extended to the logistic model and Weibull model (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. $l(0)$ is set to be 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 $d(M)/l(30)$.

A.4.1 Gompertz model

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

$$M = \frac{\ln(b/a)}{b} \quad (\text{A.12})$$

$$\mu(M) = b \quad (\text{A.13})$$

$$l(M) = e^{-1+(a/b)} \approx e^{-1} \quad (\text{A.14})$$

$$d(M) = b e^{-1+(a/b)} \approx b/e \quad (\text{A.15})$$

The expression for M (equation A.12) is implied by $a = be^{-bM}$, which was derived earlier in Appendix 3. The expression for $\mu(M)$ (equation A.13) comes from equation 4 by setting $x=M$. Derivation of equation A.14 starts with the basic definition of survival function:

$$l(x) = \exp\left(-\int_0^x \mu(y)dy\right) \quad (\text{A.16})$$

Substituting equation 1 into A.16 and making use of $a = be^{-bM}$, we get

$$l(x) = \exp\left(-\left[\frac{a}{b}e^{by}\right]_{y=0}^{y=x}\right) = \exp\left(\frac{a}{b} - e^{b(x-M)}\right), \quad (\text{A.17})$$

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 $\mu(M)$.

A.4.2 Logistic model

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

$$M = \frac{\ln(b/a)}{b} \quad (\text{A.18})$$

$$\mu(M) = \frac{b}{1+(b/g)} \approx b \quad (\text{A.19})$$

$$l(M) = \left\{ \frac{1 + (b/g)}{1 + (a/g)} \right\}^{-(g/b)} \approx \{1 + (b/g)\}^{-(g/b)} \approx e^{-1} \quad (\text{A.20})$$

$$d(M) = \frac{b}{\{1 + (b/g)\}^{1+(g/b)} \{1 + (a/g)\}^{-(g/b)}} \approx \frac{b}{\{1 + (b/g)\}^{1+(g/b)}} \approx be^{-1}. \quad (\text{A.21})$$

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 A.16 and using $a = be^{-bM}$, we have

$$\begin{aligned} l(x) &= \exp\left(-\left[\ln\{(g + ae^{by})^{(g/b)}\}\right]_{y=0}^{y=x}\right) \\ &= \left\{ \frac{g + ae^{bx}}{g + a} \right\}^{-(g/b)} \\ &= \left\{ \frac{1 + (b/g)e^{b(x-M)}}{1 + (a/g)} \right\}^{-(g/b)}. \end{aligned} \quad (\text{A.22})$$

By setting $x=M$, we have $l(M) = \left[\frac{1 + (b/g)}{1 + (a/g)}\right]^{-(g/b)}$. 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 A.19 and A.20 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 one-year period around M should be 4 to 5% of all adult deaths.

A.4.3 Weibull model

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

$$M = (b/a)^{1/(b+1)} \quad (\text{A.23})$$

$$\mu(M) = b/M \quad (\text{A.24})$$

$$l(M) = e^{-b/(b+1)} \approx e^{-1} \quad (\text{A.25})$$

$$d(M) = (b/M)e^{-b/(b+1)} \approx b/(eM). \quad (\text{A.26})$$

Derivations of these equations are similar to those for the Gompertz and logistic models. As for $l(M)$, substitution of equation 3 into A.16 and using $a = bM^{-(b+1)}$ results in

$$l(x) = \exp\left(-\left[\frac{a}{b+1}y^{b+1}\right]_{y=0}^{y=x}\right) = \exp\left\{-\left(\frac{a}{b+1}\right)x^{b+1}\right\} = \exp\left\{-\left(\frac{b}{b+1}\right)\left(\frac{x}{M}\right)^{b+1}\right\}, \quad (\text{A.27})$$

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 over time substantially, $l(M)/l(30)$ 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 $l(M) \times \mu(M)$.

Appendix 5 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 2012a) is used to smooth death counts with Poisson P-splines over a given range of ages (see section 5 for an overview of the Poisson P-spline approach). 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 population exposures by age. 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 15). 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))
```

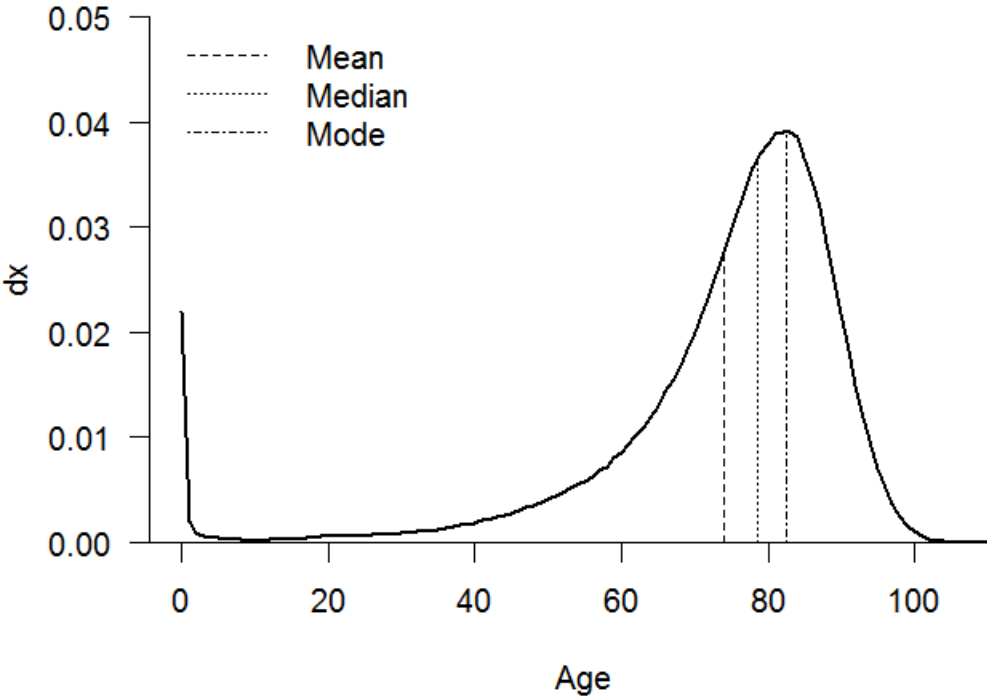
The corresponding smoothed density function, which describes the age-at-death distribution, is then readily obtained (equation 15):

```
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)]
```

Figure 1: Age distribution of deaths for French females, 1960-1964

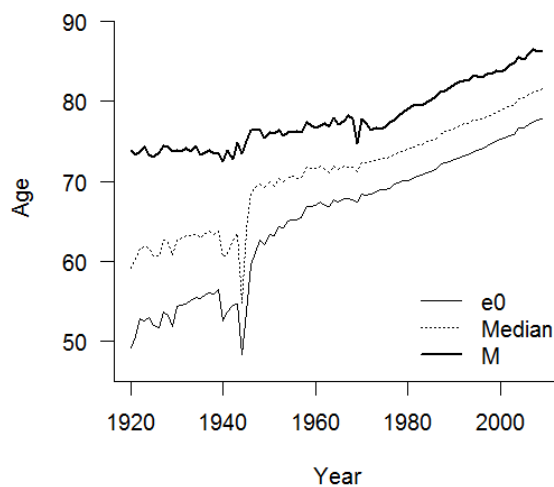
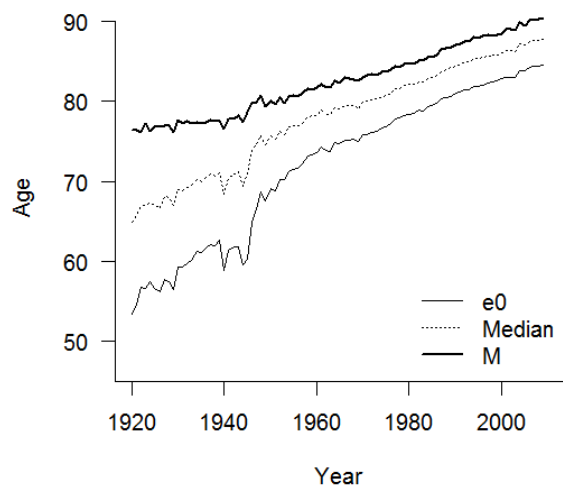


Source: Human Mortality Database (2012).

Figure 2: 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

(a) Females

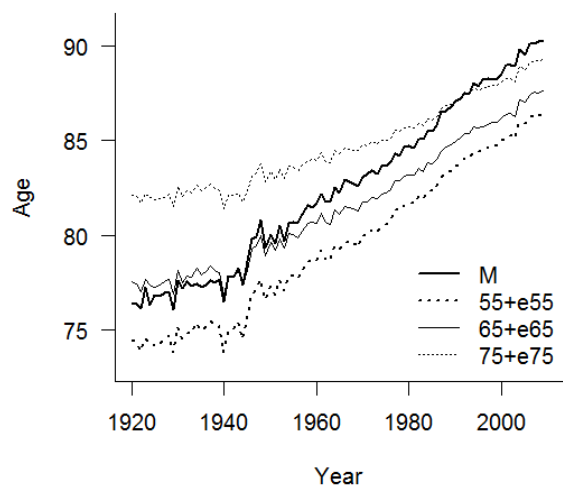
(b) Males



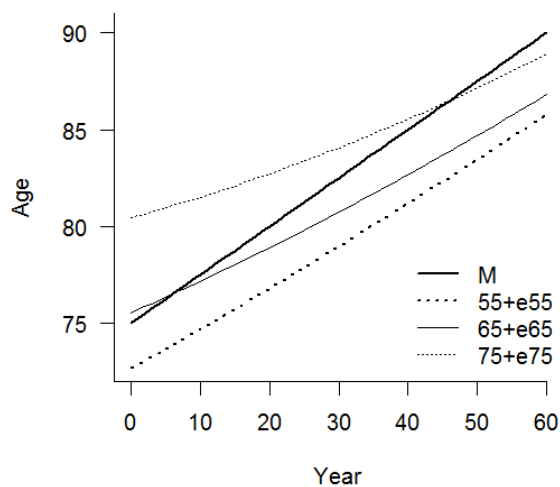
Source: Human Mortality Database (2012).

Figure 3: The adult modal age at death (M) and *total* life expectancies at age 55, 65 and 75 ($55+e_{55}$, $65+e_{65}$, $75+e_{75}$)

(a) For French civilian females, 1920-2009



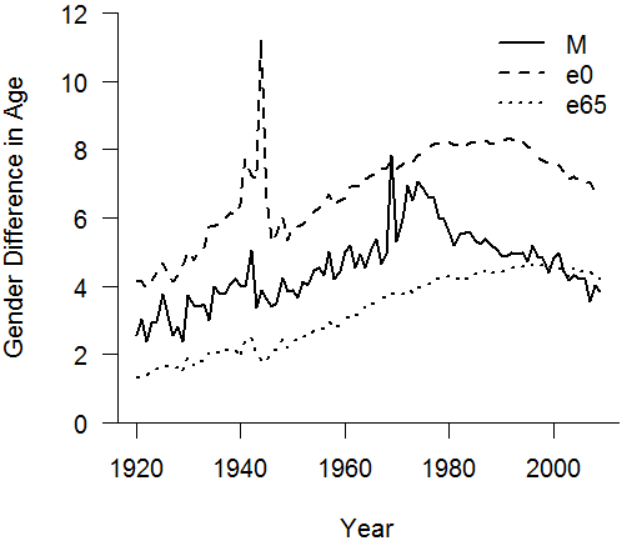
(b) For a hypothetical population in which adult mortality shifts to older ages at the rate of one year of age in four calendar years



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).

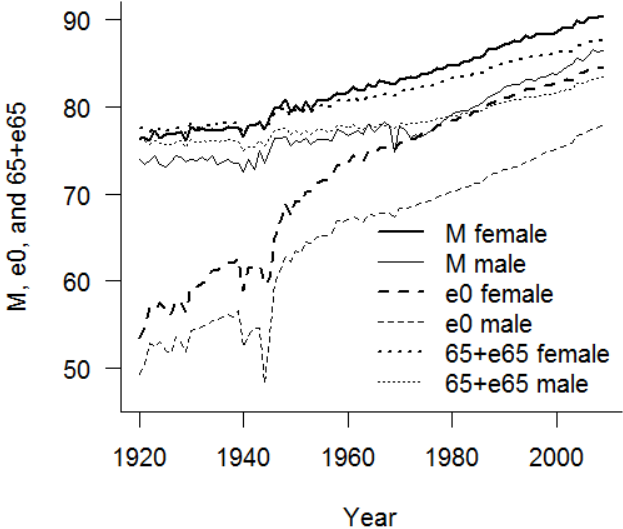
Source: Human Mortality Database (2012).

Figure 4: 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, 1920-2009



Source: Human Mortality Database (2012).

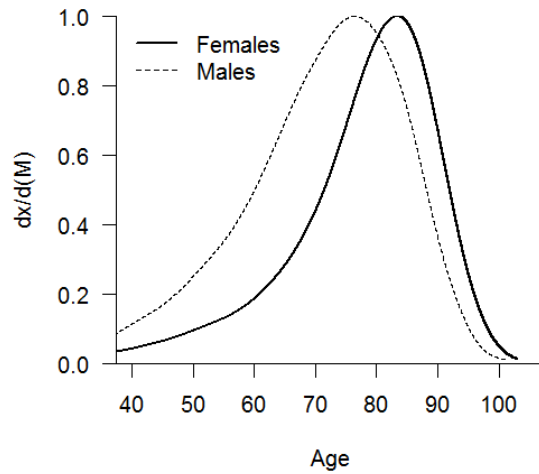
Figure 5: The adult modal age at death (M), life expectancy at birth (e_0), and total life expectancy at age 65 ($65+e_{65}$) for civilian females and males in France, 1920-2009



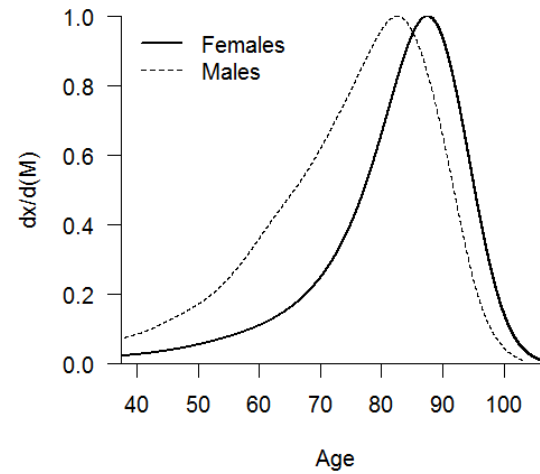
Source: Human Mortality Database (2012).

Figure 6: Height-adjusted age distribution curves of adult deaths for females and males in France, 1972 and 2009

(a) 1972



(b) 2009

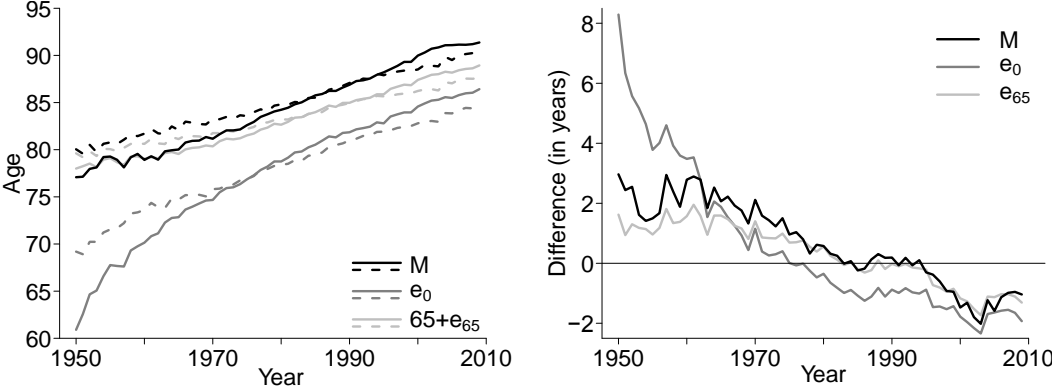


Note: The age-at-death distribution curves for period life tables were directly derived from the P-spline-smoothed mortality curves based on penalized Poisson likelihood.

Source: Human Mortality Database (2012).

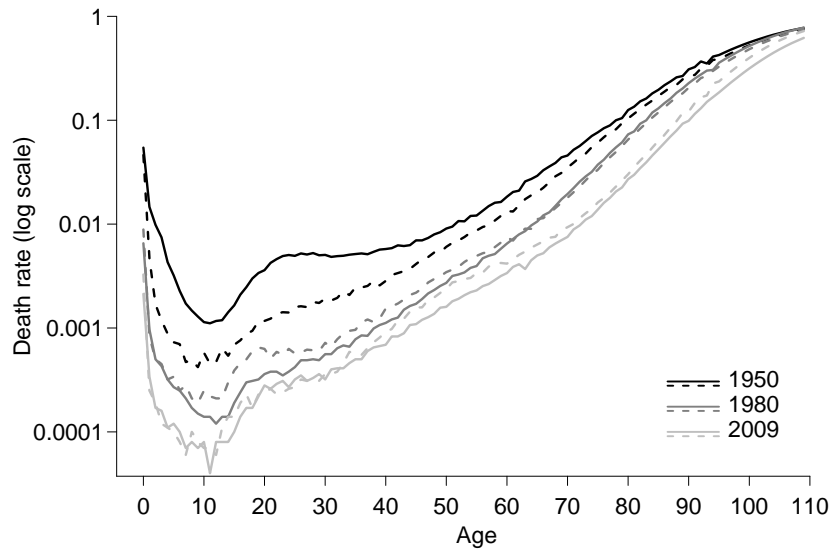
Figure 7: International trends and differentials in adult modal age at death (M), life expectancy at birth (e_0), and total life expectancy at age 65 ($65+e_{65}$), French and Japanese females, 1950 to 2009

(a) Trends: France (dashed), Japan (solid) (b) Differentials: France minus Japan



Source: Human Mortality Database (2012).

Figure 8: Age-specific death rates, French (dashed line) and Japanese (solid line) females, 1950, 1980, and 2009

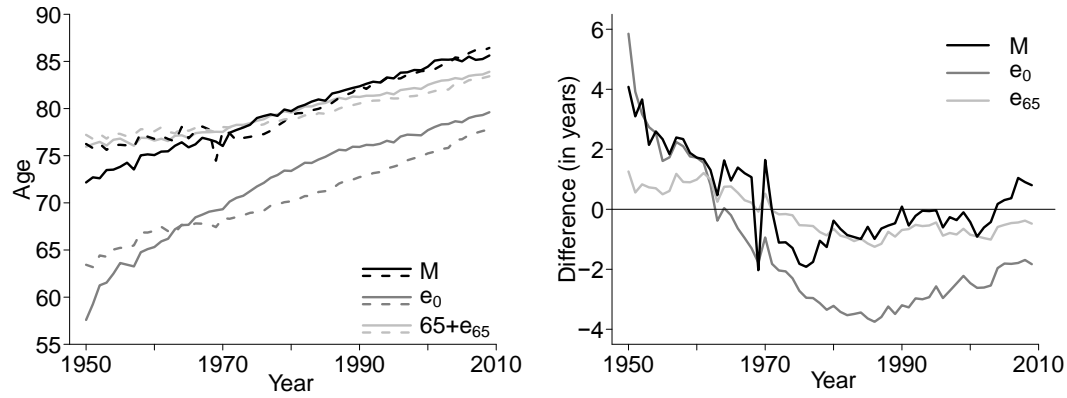


Note: Age-specific death rates in this figure were directly taken from life tables available in the Human Mortality Database (2012). It should be noted that at older ages, such death rates are smoothed based on the Kannisto model of old-age mortality (Thatcher et al. 1998; see also Wilmoth et al. (2007)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

Source: Human Mortality Database (2012).

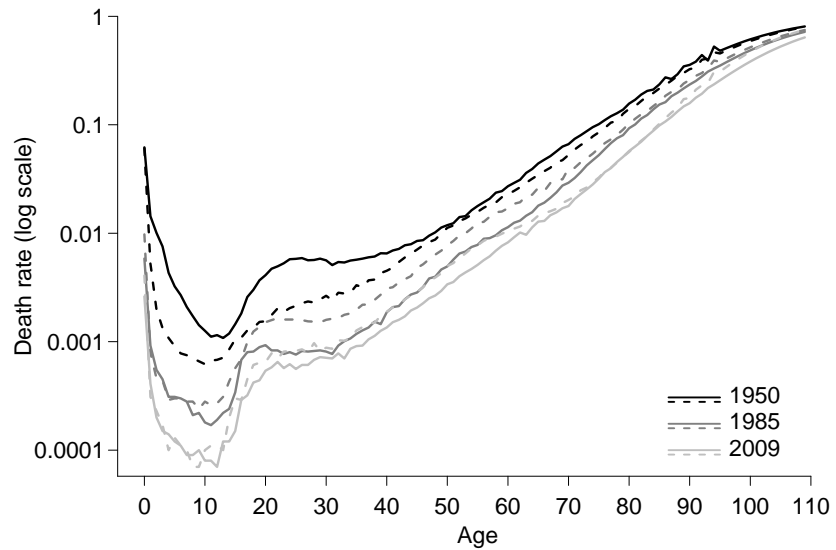
Figure 9: International trends and differentials in adult modal age at death (M), life expectancy at birth (e_0), and total life expectancy at age 65 ($65+e_{65}$), French and Japanese males, 1950 to 2009

(a) Trends: France (dashed), Japan (solid) (b) Differentials: France minus Japan



Source: Human Mortality Database (2012).

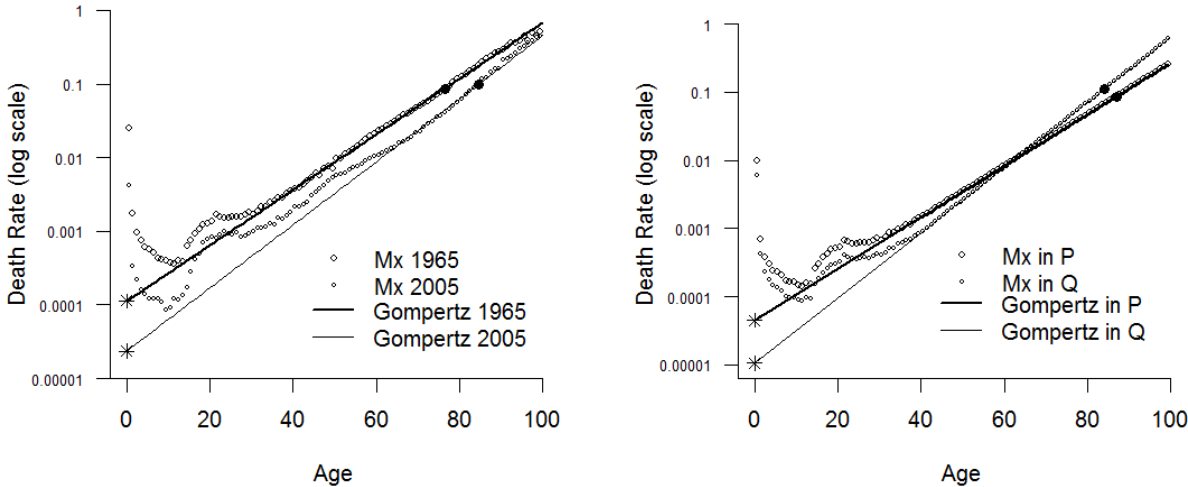
Figure 10: Age-specific death rates, French (dashed line) and Japanese (solid line) males, 1950, 1980, and 2009



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).

Figure 11: Age-specific death rates (M_x) and corresponding Gompertz models
(a) For French males, 1965 and 2005 **(b) For two hypothetical populations P and Q**

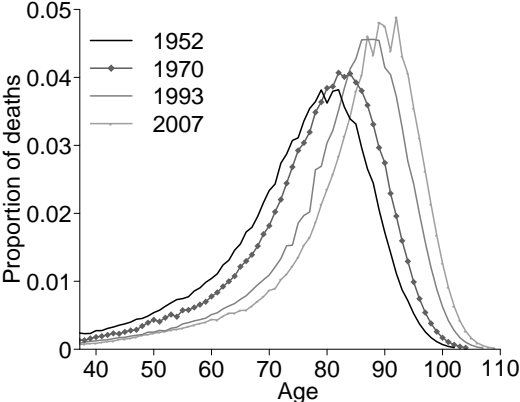


Note: The Y-coordinates of asterisks indicate values of parameter a in equation 1, and X-coordinates of filled circles indicate M values estimated using the Gompertz model (equation A.12).

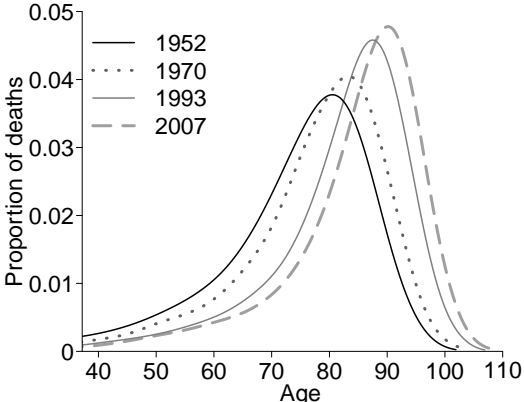
Source: Human Mortality Database (2012).

Figure 12: Age distribution of life table deaths and corresponding age-at-death distribution derived from the P-spline-smoothed mortality curve based on penalized Poisson likelihood, French females, selected years

(a) Life table death distribution

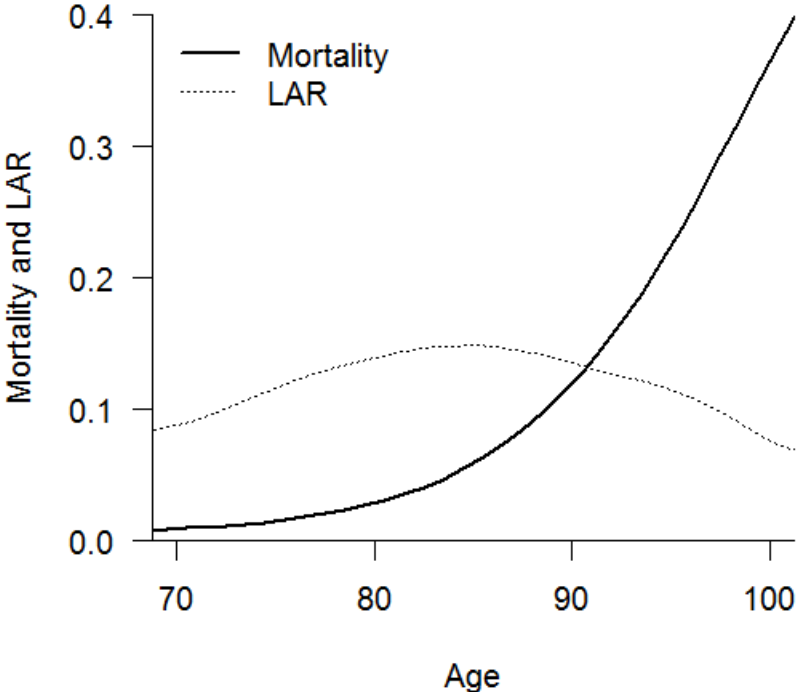


(b) Smoothed death distribution



Source: Human Mortality Database (2012).

Figure A1: Mortality and life table aging rate (LAR) by age for French females in 2009



Note: The mortality curve was obtained by P-spline smoothing based on penalized Poisson likelihood, and the life table aging rate curve was directly derived from the mortality curve.

Source: Human Mortality Database (2012).