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Mortality as a Function of Survival

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ABSTRACT Everyone has a *chronological age*. Because survivorship declines relentlessly in populations with age-specific death rates greater than zero, everyone also has a *survivorship age* ("s-age"), the age at which a proportion s of the population is still alive. S-ages can be estimated for both periods and cohorts. While trajectories of mortality over chronological ages differ (e.g., across populations, over time, by sex, or by any subpopulation), mortality trajectories over s-ages are similar, a sign that populations experience similar mortality dynamics at specific levels of survivorship. We show that this important demographic regularity holds for 23 sex-specific populations analyzed during a period comprising more than 100 years.

KEYWORDS Survivorship age • Risk of dying • Postponement of mortality • Aging

Introduction

Empirical research supports the view that human mortality is being postponed to later ages (Bongaarts and Feeney 2002; Canudas-Romo 2008; Kannisto 2000; Vaupel and Gowan 1986; Vaupel et al. 2021; Wilmoth and Horiuchi 1999). Popular sayings like "age 75 is the new 65" reflect the change in the relationship between mortality and the age variable (Burger et. al. 2012). Mortality postponement can be observed through changes in demographic indicators such as the mortality hazard $\mu(x)$, survival function $s(x)$, and density of deaths function $f(x)$, occurring at any given chronological age x. Each of these indicators describes a specific characteristic of the mortality regime in a population. They are interrelated, and one can be expressed in terms of the other one. However, it is not clear how the postponement of mortality to older ages affects the relationship between these demographic indices.

For example, the survivorship function $s(x,y)$ indicates the proportion of a population still alive at age x and at year y. According to the 1910 life table for Swedish females (Human Mortality Database 2021), the survival function was .90 at age 5 (i.e., $s(5,1910) = .90$). In 2019, the survival function was .90 at age 70 (i.e., $s(70,2019) = .90$). This simple comparison shows the magnitude of change in the relationship between survival and the age variable that has taken place over time. The question thus arises: was the risk of dying at age 5 in 1910 the same as the risk of dying at age 70 in 2019, given that 90% of the population was still alive at both ages? In terms

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of demographic functions:[1] given that $s(5,1910) = s(70,2019)$, might $\mu(5,1910)$ be similar to $\mu(70,2019)$? What about any other proportion of survivors and any other population? This is a bold conjecture that we investigate in this article.

The groundbreaking study of Zuo et al. (2018) shed light on this issue. By analyzing percentiles in the distribution of deaths after age 65, they showed that old-age deaths follow an advancing front, like a traveling wave. They demonstrated that (1) deaths occurring after the first quartile have been shifting toward older ages at a similar pace since 1950, and (2) the distance between age 65 and the first quartile has increased, whereas the distance between upper percentiles has remained constant over time. Findings from Zuo et al. (2018) provided new insights on the long-lasting debate about the compression or expansion of mortality at older ages (Bergeron-Boucher et al. 2015; Kannisto 2000; Myers and Manton 1984; Nusselder and Mackenbach 1996; Thatcher et al. 2010; Wilmoth and Horiuchi 1999). They showed that conclusions about compression or dispersion of deaths are heavily driven by reliance on chronological age. Wilmoth and Horiuchi (1999), Canudas-Romo (2008), and Beltrán-Sánchez and Subramanian (2019) alluded to this, whereas Zuo et al. (2018) provided compelling evidence of shifting patterns in the age distribution of deaths.

Notwithstanding the relevance of the Zuo et. al. (2018) findings, their choice to start their analysis at age 65 by truncating the distribution of deaths at that age is problematic. The selection of the onset age disregards the mortality dynamics at younger ages. Steady shifts in death percentiles start well before age 65 as there is evidence that major reductions in death rates have taken place at younger ages (e.g., Beltrán-Sánchez and Subramanian 2019; Bergeron-Boucher et al. 2015). Ages before and after 65 are both part of the same continuous process of aging. Therefore, truncating at chronological ages could distort the signal and trigger misleading dynamics of demographic indicators.

Modeling Mortality as a Function of Survivorship

The use of percentiles as an alternative dimension in the analysis of mortality is not new and can be traced back to Paccaud et al. (1998), Wilmoth and Horuchi (1999), Kannisto (2000), and Wilmoth (2005), among others. In particular, Wilmoth (2005) introduced formal expressions of summary demographic measures such as life expectancy based on percentiles of the distribution of deaths. More recently, Beltrán-Sánchez and Subramanian (2019) used percentiles to examine trends in period and cohort mortality in high-income countries. An interesting application of this perspective can be found in the articles by Medford et al. (2019) and Alvarez et al. (2021a), in which they analyzed survival trajectories and health profiles of Danish centenarians in terms of percentiles. They showed that the life spans of the longest-lived

[1] The fact that $s(5,1910) = s(70,2019) = .9$ can also be seen as the result of the cumulative force of mortality adding up to the same values for ages 0 to 5 in 1910 and ages 0 to 70 in 2019. This is due to $s(x,y) = e^{-\int_0^x \mu(a,y)\,da}$. However, this fact does not necessarily imply that $\mu(5,1910) = \mu(70,2019)$ are also identical since the shape of function $\mu(x,y)$ over the age variable x can be very different for these two points in time (i.e., years 1950 and 2019).

individuals have been lengthening across cohorts. Another relevant strand of research relates to the work done on formalizing mathematical relationships between demographic functions. In this regard, Finkelstein and Vaupel (2009) provided formulations to denote the survival function in terms of life expectancy, and Cohen (2010) showed that life expectancy is the death-weighted average of the reciprocal of the survival-specific force of mortality.

In this article, we develop a framework to study mortality in terms of survivorship ages (or s-ages) and examine sex-specific mortality dynamics in 23 populations from 1900 to 2018. We start our analysis at birth to capture the entire continuous process of human aging. An extensive literature has shown that when mortality trajectories over chronological ages are compared (e.g., across populations or subpopulations, over time, or by sex), the curves differ. Here, we show that when such mortality trajectories over s-ages are compared, they are much more similar. Our key contribution is demonstrating that the main change over time has been the relationship between chronological age and human survival, whereas the relationship between survival and the risk of dying has remained more regular.

Survivorship Ages

Survival is customarily seen as a function s of age x. The survivorship function $s(x)$ gives the proportion of a cohort still alive at age x. If the force of mortality, $\mu(x)$, is positive at all ages, then $s(x)$ is monotonically decreasing, and therefore a one-to-one function of x such that at every age x there is a unique value of s. Consequently, chronological age x can be seen as a function of survival s (Cohen 2010; Wilmoth 2005). In this case, $x(s)$ is the survivorship age or s-age such that $x(s) = s^{-1}(x)$ (i.e., the inverse of the survival function). Thus, $x(s)$ indicates the age at which proportion s of a person's birth cohort is still alive, where $x(1)$ is the s-age at which everyone is alive and $x(0)$ denotes the s-age at which there are no survivors left in the population. Note that, from this perspective, $x(s)$ is a function of s, whereas s denotes a scalar. Instead of taking chronological age as what varies over a lifetime, survival is what varies, and chronological age is a function of it.[2]

Function $s(x)$ is continuous and strictly decreasing over x. Therefore, the inverse function theorem (Leach 1961) gives the sufficient condition for $x(s)$ to be continuous and differentiable over s. This condition allows one to define the negative derivative of $x(s)$ with respect to s as

$$\psi(s) = -\frac{dx(s)}{ds}. \tag{1}$$

[2] This link could have been defined in terms of the cumulative distribution function, $F(x)$, and the results would have been identical because $s(x) = 1 - F(x)$. Indeed, the use of $F(x)$ leads to percentiles of the distribution of deaths used in Beltrán-Sánchez and Subramanian (2019), Wilmoth and Horiuchi (1999), and Zuo et al. (2018). In this study we chose to use $s(x)$ because it is more intuitive to think about changes in mortality as the population dies out (i.e., as s goes from 1 to 0). Cohen (2010) pioneered this idea by expressing life expectancy in terms of the hazard of s.

Function $\psi(s)$ is the density function of s (Gilchrist 2000; Unnikrishnan Nair and Sankaran 2009; Unnikrishnan Nair et al. 2013), and it measures the distance between s-ages, $x(s)$, as survivorship s falls from 1 to 0.

Provided that $x(s) = s^{-1}(x)$, the inverse function theorem guarantees that $\frac{ds(x)}{dx} = \left(\frac{dx(s)}{ds}\right)^{-1}$. Note that for any given survival function $s(x)$, the corresponding density function is given by $f(x) = -\frac{ds(x)}{dx}$. Hence,

$$f(x) = \left(\psi(s)\right)^{-1}. \tag{2}$$

Equation (2) indicates that if $x(s) = s^{-1}(x)$, the density functions $f(x)$ and $\psi(s)$ are also reciprocal.

By definition, the mortality hazard of x is $\mu(x) = \frac{f(x)}{s(x)}$. Thus, Eq. (2), and given that $s(x(s)) = s$, leads to

$$\mu(x) = \frac{f(x)}{s(x)} = \frac{1}{s\psi(s)} = \mu(s).$$

This indicates that the mortality hazard at survival level s can be expressed in terms of the density function $\psi(s)$ as

$$\mu(s) = (s\psi(s))^{-1}. \tag{3}$$

Function $\mu(s)$ has a meaningful demographic interpretation as it measures the risk of dying for the proportion s of the population that are still alive. This function is crucial in our study because it links mortality and survival without the influence of chronological ages.

It is important to highlight that $\mu(x)$ and $\mu(s)$ are both mortality hazards. The only difference between them is the domain where they operate. On one hand, hazard $\mu(x)$ is expressed in terms of chronological ages x. This means that the value of $\mu(x)$ changes as x increases from 0 to ω. On the other hand, hazard $\mu(s)$ is expressed in terms of survival level s, where s is a scalar. Thus, the value of $\mu(s)$ changes as s falls from 1 to 0.

Dynamics of the Risk of Dying in Terms of Survival

Assume that all the quantities defined in the previous section vary with respect to time y, such that $\psi(s,y)$ and $\mu(s,y)$ are, respectively, the density function and the mortality hazard of s at time y. Changes over time in $\mu(s,y)$ are captured by the rate of mortality improvement, denoted by $\rho(s,y)$:

$$\rho(s,y) = -\frac{\frac{\partial \mu(s,y)}{\partial y}}{\mu(s,y)} = -\frac{\partial \ln \mu(s,y)}{\partial y}. \tag{4}$$

In this sense, $\rho(s,y)$ measures how the risk of dying calculated at specific survival level s has changed over time.

Moreover, function $b(s,y)$ indicates how the risk of dying changes as survival s decreases:

$$b(s,y) = -\frac{\frac{\partial \mu(s,y)}{\partial s}}{\mu(s,y)} = -\frac{\partial ln \mu(s,y)}{\partial s}. \quad (5)$$

This function is analogous to the life table aging rate (Horiuchi and Coale 1990; Wilmoth and Horiuchi 1999), yet $b(s,y)$ measures the relative mortality change over s rather than changes over chronological age x. For example, $b(s,y) = .02$ means that mortality (at level of survival s) is rising at an exponential rate of 2% at year y.

Further Developments and Applications

The framework introduced in this section offers a novel view on mortality dynamics and allows the reexpression of well-known demographic measures in terms of s-ages. Some of these applications are illustrated in the online appendix. For example, we derive expressions for life expectancy[3] in terms of s-ages. In this case, life expectancy indicates the expected remaining lifetime of s survivors in a population. Similarly, other summary measures of longevity can also be conceived in terms of s-ages (e.g., life span variability indicators, or the entropy of $x(s)$).

Furthermore, functions $x(s,y)$, $\mu(s,y)$, $\psi(s,y)$, $\rho(s,y)$, and $b(s,y)$ can also be expressed in terms of parametric models. To illustrate this, we assume that mortality follows a Gompertz model and develop closed-form expressions of these functions (see online appendix). We explore different model specifications to show how our framework can be used to gain new insights about well-known mortality models. Along the same lines, our framework allows us to develop novel stochastic models to forecast mortality as a function of survival.

It is important to highlight that the derivations shown in the appendix are solely for illustration purposes, whereas the aim of this article is to examine the empirical relationship between mortality and survival using the framework developed in this section. In the remainder of the article, we assess this relationship with data for 23 sex-specific populations spanning the years 1900–2018.

Data

The framework introduced in the Survivorship Ages section is used to examine the relationship between mortality and survival using data by sex and calendar year covering the period 1900–2018 for 23 populations available in the Human Mortality Database (2021): Australia, Austria, Belgium, Canada, Czech Republic, Denmark, Finland, France, Germany, Great Britain, Hong Kong, Italy, Israel, Japan, Korea,

[3] Such expressions complement Wilmoth (2005) and Cohen's (2010) results.

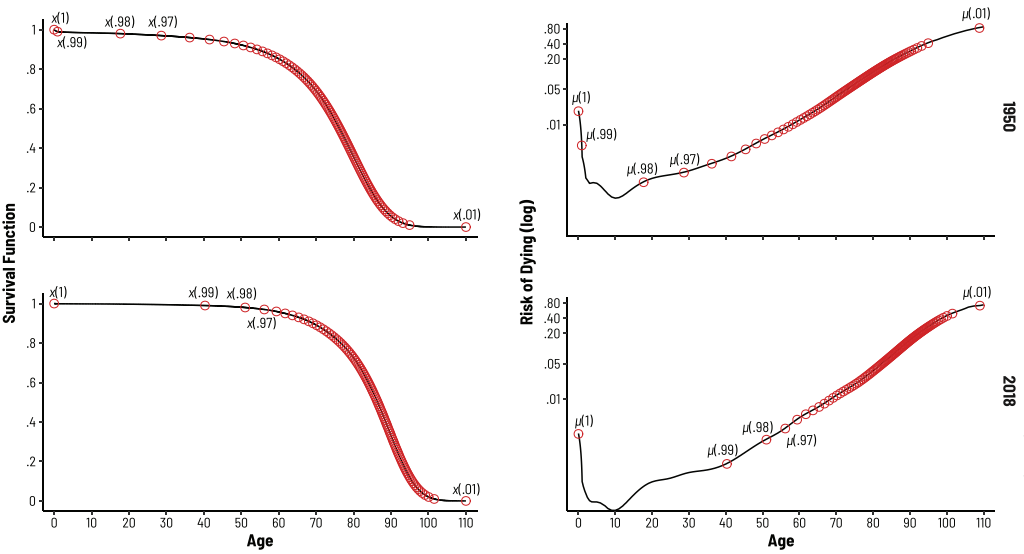

Fig. 1 Survival function and associated risk of dying for Swedish females, 1950 and 2018. Red circles indicate the location of s-ages.

Luxembourg, the Netherlands, New Zealand, Norway, Portugal, Sweden, Switzerland, and the United States.

Continuous mortality quantities are required to calculate s-ages. For this reason, raw death rates were smoothed over time and over age using two-dimensional P-splines (Camarda 2012). Given the nonparametric properties of such P-splines, we ensured that the smoothing procedure did not distort estimations of the risk of dying or any of the quantities analyzed here. Having continuous estimates of mortality over age and time permits calculation of s-ages and associated functions with serviceable precision. This standard smoothing procedure has been useful in previous mortality investigations (Colchero et al. 2016; Jones et al. 2014). Once continuous surfaces of mortality are computed, the calculation of $x(s)$ and associated functions is straightforward using the expressions developed earlier.

Two sensitivity analyses were performed to test whether the results were driven by the choice of the smoothing algorithm (see online appendix). In the first analysis, a generic spline model (de Boor 2001) was used to smooth death rates by age. In the second sensitivity analysis, any smoothing algorithm was applied to the data. Instead, a linear interpolation was used to calculate s-percentiles and associated functions. In both analyses, our results are almost identical to the ones produced with P-splines (Camarda 2012), indicating that our results are robust and do not hinge on the smoothing algorithm employed.

Results

Figure 1 illustrates the location of s-ages in the survival function and the corresponding force of mortality for Swedish females in 1950 and 2018. Function $x(s)$ indicates

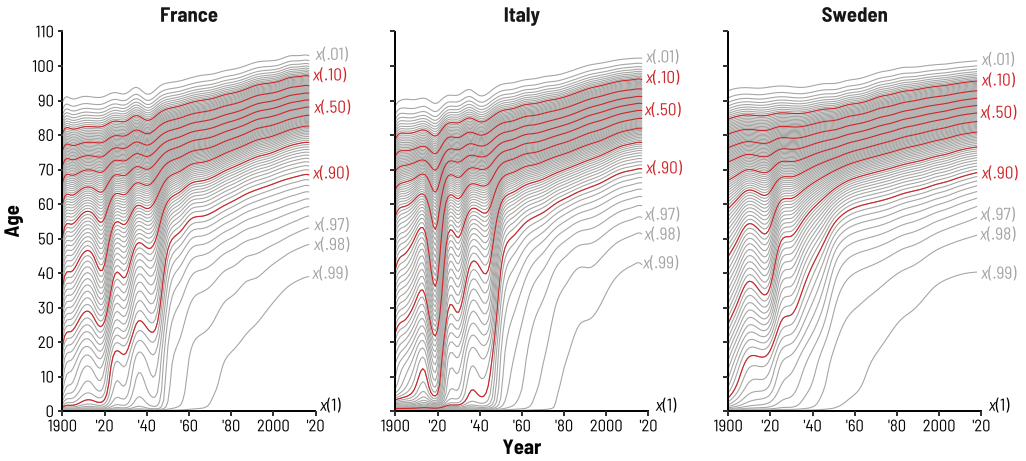

Fig. 2 Survivorship ages for females in France, Italy, and Sweden, 1900–2018. Red lines indicate deciles.

the age at which survivorship is s, and $\mu(s)$ is the force of mortality at that specific survival level. We start the calculation of s-ages at birth, so that $x(1)$ represents 100% of the population and it is always located at birth. We end the analysis at $x(.01)$ because noise when survivorship falls under $s = .01$ is high. It is not possible to estimate the location of $x(0)$ from aggregated data such that if there is a maximum life span ω, then $x(0) = \omega$; otherwise $x(0) = \infty$. The values of $x(s)$ and $\mu(s)$ are indicated in Figure 1 by the red circles.

Figure 1 shows that ages $x(s)$ are not equidistant. For example, $x(1)$ and $x(.99)$ were very close to each other in 1950. In 2018, there is almost 40 years between $x(1)$ and $x(.99)$. Similarly, $x(.99)$ and $x(.98)$ are located less than 15 years apart in 2018. Subsequent s-ages are closer to each other, indicating a greater concentration of deaths at those s-ages. Changes over time in the location of s-ages reflect changes over time in survivorship. The following sections describe changes over time in s-ages and how they trigger changes in the force of mortality.

The Steady Postponement of Survival

Figure 2 depicts trends in s-ages, $x(s)$, from 1900 to 2018 for females in France, Italy, and Sweden. These countries were chosen to illustrate the framework because they exhibit high-quality data dating back to 1900. Nonetheless, similar results hold across all 23 populations analyzed in this study (see online appendix for further details).

Figure 2 shows that major shifts in survival occurred in the top s-ages. At the beginning of the twentieth century, 90% of the population (i.e., $x(.90)$) survived to age 2 in France and Italy and to age 5 in Sweden. Thereafter, deaths unfolded into a much wider age interval. For example, in 2018, 90% of the population in each of these countries survived to age 70. Even more impressive is that, in 2018, 99% of the population (i.e., $x(.99)$) survived to age 35. Figure 2 also shows that major shifts of s-ages from $x(.99)$ to $x(.80)$ produced a relocation in all subsequent $x(s)$. For

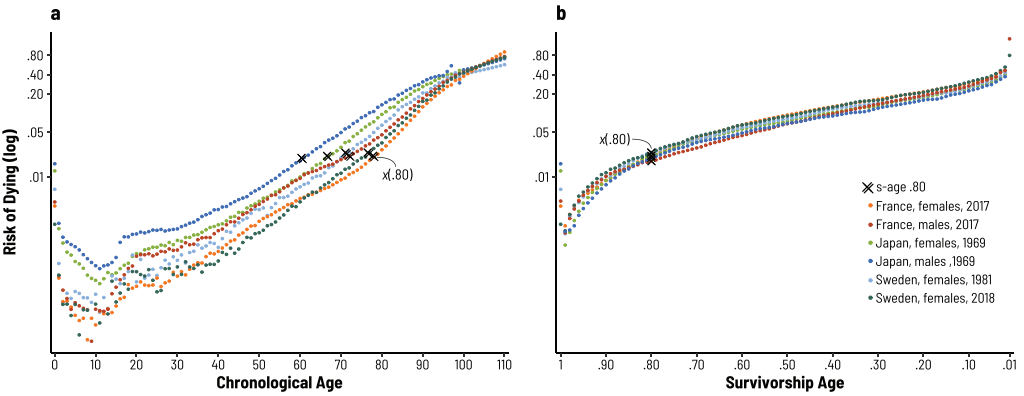

Fig. 3 Mortality trajectories for six different sex-specific populations during different years. Panel a shows the risk of dying over chronological ages. Panel b depicts the risk of dying over survivorship ages. Black crosses indicate the location of s-age $x(.80)$. Note that these figures were calculated from raw data without smoothing to show the differences and similarities between mortality trajectories.

example, in France, $x(.10)$ (i.e., the age where only 10% of the population is still alive) shifted from age 87.61 in 1950 to age 97.04 in 2018.

This figure also shows that distances between consecutive s-ages from $x(.90)$ to $x(.01)$ have remained approximately constant over time, and this is particularly observed after the 1950s. Wilmoth and Horiuchi (1999) provided some evidence of parallel shifts in the concentration of deaths, and Zuo et al. (2018) analyzed this issue in depth after age 65. In the present study, we show that steady shifts in the concentration of deaths also hold for survival probabilities. We show that those steady shifts already begin at the age where 90% of individuals are still alive (i.e., s-age $x(.90)$), which is located well before age 65.

Our results show that the Zuo et al. (2018) findings regarding an increasing distance between age 65 and the 25th percentile is the consequence of truncating the distribution of deaths at age 65. Sensitivity analyses in which calculation of s-ages starts at various chronological ages (e.g., $x(1)$ is set at, respectively, ages 35, 50, and 65; see online appendix) confirm that truncating at any chronological age distorts the distances between s-ages because they are compressed (Kannisto 2000; Thatcher et. al. 2010). Truncating at chronological ages triggers misleading results about demographic patterns of survival, the risk of dying, and associated functions of these indicators (i.e., life expectancy and life span inequality indicators).

The Constant Dynamics of the Risk of Dying

Panel a of Figure 3 shows the risk of dying over chronological age x for six different sex-specific populations during different years. Panel b also shows the risk of dying for the same populations, but in this case, the risk of dying is expressed in terms of s. As mentioned in the Survivorship Ages section, both hazards $\mu(x)$ and $\mu(s)$ are indicators of the risk of dying and the only difference between them is the domain of x and s. In this sense, Figure 3 clearly shows the important finding that when trajectories

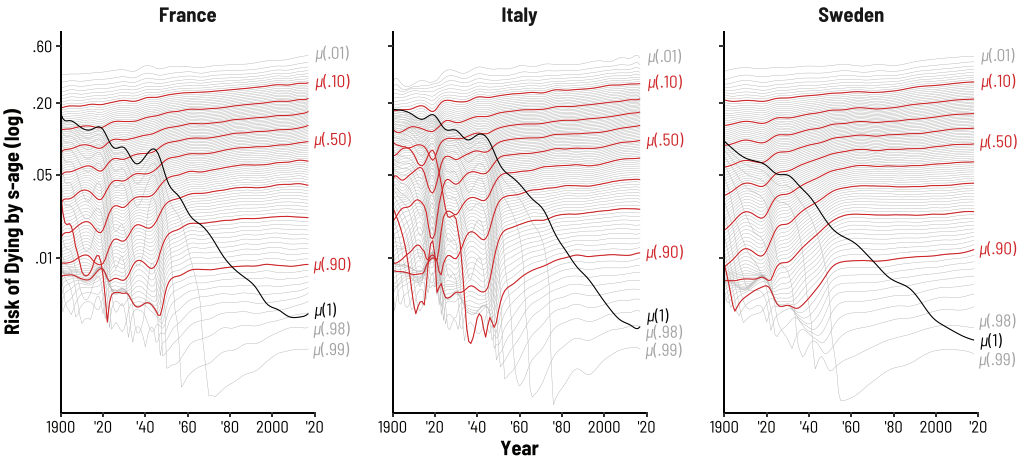

Fig. 4 Trends over time in risk of dying by s-age for females in France, Italy, and Sweden, 1900–2018. Red lines indicate deciles.

of mortality over age x are compared, the curves differ, but when such trajectories over s are compared, they are similar. We now examine this finding in detail.

Figure 4 depicts trajectories over time in the risk of dying in terms of survivorship over time, $\mu(s,y)$. Two key patterns are apparent. First, major shifts in s-ages reported in Figure 2 coincide with pronounced declines in $\mu(s,y)$ prior to the 1950s. In particular, $\mu(1,y)$ plummeted. Also note that $\mu(.99,y)$ declined substantially in the first half of the twentieth century but has since roughly stabilized (Ebeling 2018). Figure 4 shows that the relationship between the risk of dying and survival suffered distortions at the beginning of the survival curve (i.e., $s=1, .99, \ldots, .90$). Yet, after 1980, declines in $\mu(s,y)$ ceased, with the exception of the risk of dying at birth, $\mu(1,y)$, which continues trending downward.

Second, Figure 4 shows steady patterns in $\mu(s,y)$ for $s=.90, \ldots, .01$ since the 1950s. The risk of dying for survival levels between .90 and .50 has remained almost constant over time after this decade. For survival levels between .50 and .01, there have been small increases in $\rho(s,y)$. These patterns indicate a regular association between the risk of dying and survival. This is an important finding entailing that, over time, what has changed is the relationship between the age variable and survival (as shown in Figure 2), while the demographic relationship between survival and the risk of dying has remained stable for more than half a century.

Figure 5 depicts values of the rate of mortality improvement, $\rho(s,y)$. As expected from the results shown in Figures 2 and 4, fluctuations in $\rho(s,y)$ are noticeable prior to 1950. Such fluctuations can be attributed to deaths occurring during the two world wars and the Spanish flu epidemic (Johnson and Mueller 2002). Thereafter, $\rho(s,y)$ takes values close to zero at all survivorship s. At first glance this finding might seem surprising, given that previous research has shown mortality improvements at different chronological ages (Rau et al. 2008). However, it is important to highlight that $\rho(s,y)$ does not measure mortality improvement by chronological age. Instead, $\rho(s,y)$ is an indicator that captures changes over time in mortality at different levels of survival s. Thus, values of $\rho(s,y)$ close to zero after the 1950s imply that the

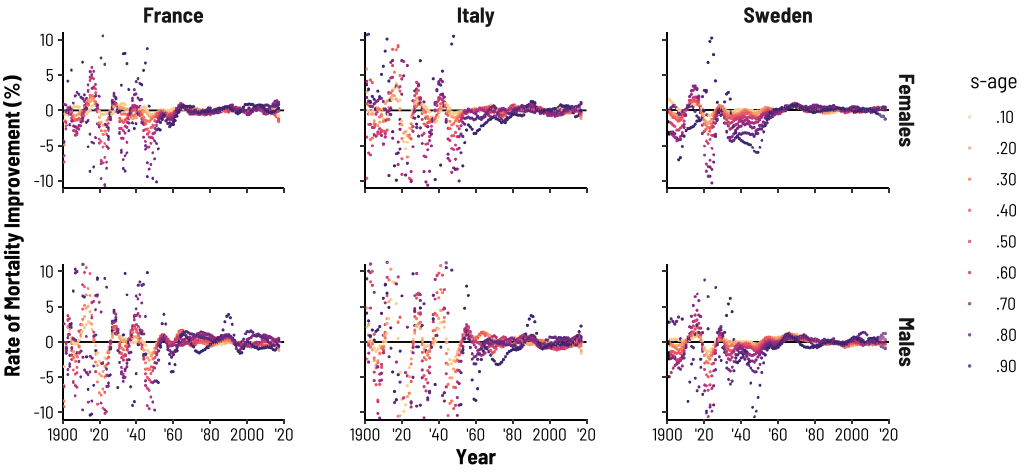

Fig. 5 Rates of mortality improvement by s-age for both sexes in France, Italy, and Sweden, 1900–2018

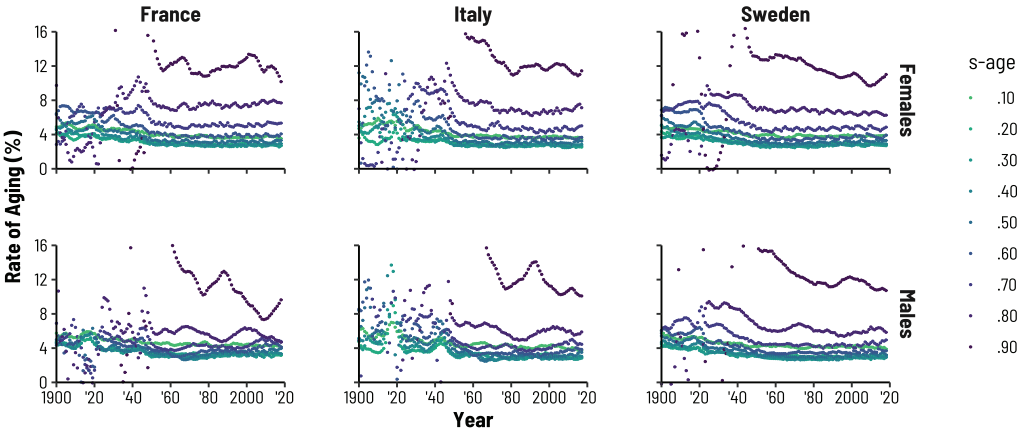

Fig. 6 Rate of change in the risk of dying with respect to change in survival s for both sexes in France, Italy, and Sweden, 1900–2018

relative change in mortality has remained more or less constant over time at any level of survivorship s below .90.

Finally, Figure 6 shows trends in the rate of aging, $b(s,y)$. This function takes different values depending on s. For example, $b(s,y)$ for Sweden in 2018 was about .08 and .04 for s equal to .9 and .3, respectively. This indicates that the risk of dying increases faster when survival is 90% than when survival is 30%. Over time, fluctuations in $b(s,y)$ are observed prior to the 1950s (similar to the results shown in previous figures). After this decade, $b(s,y)$ remains approximately constant over time, particularly for s below .70. For example, $b(.10,y)$ for French females took values of .038 in 1950, .038 in 1970, .036 in 1990, and .037 in 2018. The analysis of function $b(s,y)$ provides further evidence of the stable relationship between mortality and survival after the decade of the 1950s.

Discussion

Everyone has a chronological age x and, depending on the population they are in, a value of s. When trajectories of mortality over age x are compared (e.g., across populations, over time, or females vs. males), the curves differ. When mortality trajectories over s are compared, they are much more similar. This is an important demographic regularity that holds for all 23 populations analyzed here.

In this study we show that during the first half of the twentieth century, major shifts in survival occurred at ages where the first 30% of the population die. It is also around those s-ages where most of the changes in the shape of the trajectory of mortality were observed. However, for the remaining 70% of the population, the relationship between survival and the risk of dying has remained steady over time.

This steady relationship is clearer after the 1950s, when 90% of the population has experienced similar mortality patterns. These findings indicate that, over time, what has changed is the relationship between mortality and chronological ages, but the relationship between survival and the risk of dying has remained remarkably regular. In other words, after the 1950s, populations have experienced similar dynamics in the risk of dying at levels of survivorship below .90.

The relationship between survival and the risk of dying is regular but it is not immutable. In our results for France, Sweden, and Italy, we show that this steady relationship was altered during some periods before 1950. Such alterations are associated with the massive number of deaths that occurred during the two world wars and the Spanish flu pandemic. After such events ceased, the relationship between demographic indicators became regular again.

Chronological Ages and Survivorship Ages

In this article, we introduce the concept of survivorship age with the purpose of examining mortality as a function of survival. It is worth emphasizing the conceptual differences between s-ages and chronological ages as well as their demographic interpretation.

The chronological age of an individual is calculated as the time difference between two life events: birth and any given date. For example, the full life span is calculated between dates of birth and death. Therefore, the calculation of chronological ages requires information that is only related to that particular individual. Conversely, the calculation of s-ages entails additional information about the population in which the specific individual lives. This is because a person's s-age is calculated as the time difference from birth to the date at which a proportion s of the population was still alive.

At any specific date, every person has a unique chronological age, and because everyone lives in populations, every person also has a unique survivorship age. Chronological ages can be known exactly at any moment. However, survivorship ages can only be estimated using demographic data, which are usually gathered *a posteriori*. In other words, s-ages can only be calculated when demographic data become available. This is the main computational difference between these age indicators, but at the same time, this is what makes s-ages demographically meaningful.

Contrary to chronological ages, s-ages relate a person's life span to the dynamics of the population. All individuals will die in a specific population, and their mortality and survival chances do not exclusively depend on themselves, but also on the mortality and survival chances of their peers. This intrinsic relationship between an individual life span and its own population is embedded in the definition of survivorship ages.

A key contribution of this article is the introduction of a formal framework to study mortality in terms of survivorship ages. As mentioned earlier, survivorship ages relate the life span of individuals to the actual source of demographic change, that is, death and survival. Therefore, this perspective is specifically developed for demographic studies. Here, we show that the use of s-ages provides important insights about the dynamics of human mortality. Further research endeavors aimed at the development of mortality quantities and models (e.g., life span inequality indicators, stochastic models) in terms of s-ages will enrich the demographic toolkit and enhance our knowledge about further regularities in the mortality and survival of populations.

While we highlight the advantages of using survivorship ages in demographic studies, it is unlikely that they will replace chronological ages as the main time dimension. Chronological age has a long history of being used to quantify longevity (Thane 2020) and is widely used in social sciences as the main time variable with which to describe demographic events (Field and Syrrett 2020). Chronological ages are widely used as a time variable because of their simplicity and interpretability, and we acknowledge the advantages of using such ages in demographic research. Nonetheless, we also highlight their shortcomings. Specifically, our results raise awareness about how truncating to chronological ages might result in misleading conclusions about the dynamics of the risk of dying and related indicators. An example of this issue is the increasing distance between the 25th percentile and age 65, reported in Zuo et al. (2018), which we show is an artifact of starting the demographic analysis at age 65, such that the postponement of human mortality is not fully captured. Researchers should therefore be cautious when truncating at chronological ages and be aware that the substantial postponement of mortality might affect their results.

Limitations

The empirical calculation of s-ages and related measures developed in this article requires continuous mortality quantities. Consequently, the application of our framework entails (1) the use of a smoothing or interpolation algorithm and (2) high-quality mortality data. Regarding the first condition, we show in the online appendix that the choice of the smoothing algorithm (e.g., P-splines, interpolation techniques) does not have an impact on our results. However, the use of high-quality demographic data plays an important role in the precise calculation of s-ages. We foresee this requirement to represent a limitation in the application of our framework, as not all populations exhibit high-quality detailed data. This is the case for some Latin American populations (Alvarez et al. 2020), where data quality is poor and demographic estimations are unreliable. Furthermore, for some populations the life table data are only available in abridged age intervals (e.g., 5- or 10-year intervals). The use of grouped data might result in unreliable estimations of s-ages and related measures. A possible

approach to tackle this issue is to apply nonparametric models to ungroup binned data (Rizzi et al. 2015) before the calculation of s-ages.

In the online appendix we illustrate the potential of our framework by introducing closed formulas to compute s-ages and related measures under the assumption that mortality follows a Gompertz distribution. We chose this distribution for its simplicity and because it is a well-known referent in mortality modeling. While parametric formulas for $x(s)$, $\psi(s)$, and $\mu(s)$ are sound for this distribution, they might not fit well when tested with empirical data. It has been shown that the Gompertz distribution describes only a specific chronological age range. For example, it does not describe mortality patterns at young ages and does not capture the age hump (Remund et al. 2018). It has also been shown that $\mu(x)$ deviates from the Gompertzian pattern around ages 70–80 (Wilmoth and Horiuchi 1999) and converges toward a constant level at the extreme end of life (Alvarez et al. 2021b). Models that account for unobserved heterogeneity (Beard 1959; Vaupel et al. 1979) can be considered as an alternative to model mortality at old s-ages. Furthermore, the application of our framework to parametric distributions that cover the whole age range (e.g., Siler 1979; Thiele 1871) might provide a more thorough description of the trajectory of mortality over the whole s-age range.

Unsolved Demographic Questions

Our results shed light on the demographic mechanisms of senescence. We show that the relative rate of change in the force of mortality, $b(s,y)$, is approximately constant over time—in particular, after the 1950s and for levels of s below .7. This indicates that populations experience similar dynamics in the risk of dying at specific levels of survivorship. Why? What is the source of this regularity? This is a basic research question that remains unsolved. One possible explanation, which requires further analysis, is that a person's s-age appears to be a good measure of a person's health, more closely tied to the risk of death than chronological age.

As described by Zuo et al. (2018) and further analyzed here, there is an advancing front of survival. Theories of senescence (e.g., Baudisch and Vaupel 2012; Colchero et al. 2021, 2016; Le Bourg 2001; Omholt and Kirkwood 2021; Wachter et al. 2014) attempt to explain why the risk of death increases with age. Analyzing mortality as a function of survivorship might cast new theoretical light on how rapidly we age and why death rates are falling over time. Beyond this, s-age will almost certainly augment chronological age as a powerful concept in the demographic analysis of mortality. ■

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