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POPULATION AGING is a key feature of twenty-first-century demographic trends. Projections by the United Nations suggest that by 2100 in Europe, people aged 65 and over are expected to form about 30 percent of the population, and more than one person in eight will be aged 80 or older (United Nations Department of Economic and Social Affairs 2015). Given that mortality declines are expected to continue, responses to population aging have included advocating policies to stimulate both fertility and immigration.

Mortality improvement has sometimes been presented as the primary driver of long-term population aging since it is the driver of individuals' aging. However, since the determinants of population aging became a topic of study from the 1950s (e.g. Valaoras 1950; Coale 1956; United Nations 1956), primacy has usually been given to fertility decline. According to Coale, "one can say with every confidence of being correct that a lower course of fertility produces an older population than would a higher course, all other factors being the same; and with fair confidence that most mortality improvements in the past have produced a younger population than would have resulted from unchanged mortality" (Coale 1956, p. 114). While this conclusion remains the standard view, mortality improvement is now recognized as an increasingly important factor in population aging, especially in low-fertility societies where the majority of the world's population now live (United Nations Department of Economic and Social Affairs 2015). This is because mortality improvement at older ages has become substantial, especially from the middle of the twentieth century (Bongaarts and Bulatao 2000). The effect of migration on population aging is generally regarded as minor in most situations (United Nations Department of Economic and Social Affairs 1973; Goldstein 2009; Murphy 2016a).

The conclusion that fertility decline has been the most important factor in population aging in high-income countries is widely accepted. This is consistent with a stylized demographic transition model in which fertility and mortality are initially broadly constant over time with population growth close to zero and there is no change in age structure. Subsequent mortality improvement is initially concentrated at younger ages, both

because it was easier to reduce mortality at these ages and because a large fraction of these populations were young. Together with a tendency for fertility to increase around the start of fertility transition (Dyson and Murphy 1985), this tends to make population structures younger. In the next phase, this rejuvenation effect is more than offset by subsequent fertility decline, and populations start to age. At a later stage, mortality improvement occurs mainly at older ages and reinforces aging arising from fertility decline. Finally, in high-income countries when fertility has been relatively constant at low levels for an extended period of time and mortality improvement continues, mortality change comes to dominate population aging. The formal dynamics of how population structures evolve under changing fertility and mortality was further developed by Coale (1972) and Lee (1994) and by Chesnais (1990), who provided estimates of age-structure changes with a stylized demographic transition change model.

Empirical evidence for the dominant role of fertility is surprisingly thin, especially for quantifying the relative importance of fertility and mortality. Conclusions are still often based on static models such as those of Coale (1956), supplemented by a small number of studies of counterfactual population projections starting from earlier time points, typically comparing actual values with projections using constant fertility or mortality rates from the chosen baseline (e.g. Hermalin 1966). This approach was recently used by Bengtsson and Scott (2011) for Sweden, assuming constant fertility over the twentieth century. The authors concluded that "the primary cause of population aging in Sweden up to now was, as elsewhere, declining fertility" and that declining mortality became influential only in the last decades of the twentieth century (Bengtsson and Scott 2011, p. 259). Counterfactual population projections remain a key method for analyzing the determinants of aging (Lee and Zhou 2017).

Neither a simple demographic transition model nor long-term fixed fertility and mortality regimes that underpin stable population and population projection models are observed in practice. Conclusions are principally deductive: what happens when fertility and mortality vary in stable population models is demonstrated, and a similar response is expected in the real world. These approaches provide qualitative conclusions rather than quantifying the contribution of fertility and mortality to population aging.[1]

As a challenge to this orthodoxy, Preston, Himes, and Eggers (1989) analyzed factors associated with population aging in the United States and Sweden in the period 1980–1985. They concluded that mortality improvement was the main driver of population aging at this time. Their analysis was based on an innovative approach, referred to subsequently as the PHE model (initials referring to authors' names), that decomposes changes in population aging into births, mortality, and net migration. A similar conclusion on the importance of mortality for population aging was reached by Caselli and Vallin (1990) by comparing actual and projected population

trends in France and Italy over the period 1960–2040. Preston and Stokes (2012, p. 231), using the PHE model to investigate sources of population aging in the period 2005–10, concluded that "in more developed countries, the massive improvements in survivorship from one birth cohort to the next have been the most important source of aging." They attribute over four fifths (82 percent) of population aging in more developed countries (excluding Eastern Europe) to inter-cohort mortality change in this recent period.

These various results, based on different approaches, are not necessarily inconsistent with the standard model set out above, since they are confined to the most recent period. My focus here is on population aging as a long-term process across multiple countries. In what follows, I summarize the PHE method used to estimate the contribution of fertility, mortality, and migration to population aging in Europe and describe the data from the Human Mortality Database used to fit the PHE model; use mean population age as an index of population aging compared with alternative indicators and extend the PHE approach to include parental fertility as an explicit variable in the model; apply the PHE approach over an extended period beginning in 1850 to 11 European countries to provide estimates of the demographic determinants of population aging for over a century in Europe (excluding Eastern Europe); and discuss how this approach provides a clearer understanding of the drivers of population aging over the past 150 years and consider the implications of these findings for the future.

Methods, data, and models

The Preston, Himes, and Eggers (PHE) method

The approach developed in Preston, Himes, and Eggers (1989) is based on earlier work on age-specific growth rates (Horiuchi and Preston 1988) arising from development of the Preston–Coale synthesis model (Preston and Coale 1982). The decomposition allocates overall population changes over time into those due to fertility, mortality, and migration as follows:

$$P(a,t) = B(t-a)\, exp\left(\int_0^a \{-\mu(x,t-x) + m(x,t-x)\}\, dx\right) \qquad (1)$$

where for age a at time t: $P(a,t)$ is population, $\mu(a,t)$ is the force of mortality, $m(a,t)$ is the net migration rate, and $B(t)$ is the number of births.

PHE can be summarized by noting that the annual change in population numbers in a particular year at a given age is simply the difference at that age between numbers alive at the start and end of that year. The numbers alive are determined by the size of the birth cohort they are drawn from, with allowance for mortality and migration in the intervening period using equation (1).

Let $r(a,t)$ denote $(\partial P(a, t)/\partial t) / P(a, t)$, the proportional rate of growth of $P(a, t)$. This rate is found by taking the logarithm of both sides of equation (1) and differentiating with respect to time. I thereby obtain

$$r(a, t) = \frac{\partial B(t - a)}{\partial t}/B(t - a) - \int_0^a \frac{\partial \mu(x, t - x)}{\partial t}dx + \int_0^a \frac{\partial m(x, t - x)}{\partial t}dx$$

$$(2)$$

The first term on the right is the rate of growth of births at time $t - a$. The second and third terms are the rates of change in subsequent cohort survival and lifetime net migration. The average age of these changes at time t uniquely decomposes the change in population mean age to those due to births, survival probability, and net migration of adjacent cohorts in the period. Population aging occurs when the population distribution shifts toward older ages. This may be measured by the first derivative of mean population age in continuous formulation or as the annual change in discrete form. Although change in mean age of a population is not a commonly used indicator of population aging, median age is widely used (e.g. United Nations Department of Economic and Social Affairs 2015). I justify the use of mean age when considering alternative indicators of aging later.

Since my interest is in long-term changes, I sum the annual values to show the cumulative effect of fertility, mortality, and migration over extended time intervals. I present data looking backward in time from the latest available date to various start dates. This form of presentation does not give special status to a possibly arbitrary start date some years in the past.

I use the following notation for the cumulative effect of the birth cohort, mortality, and migration terms of equation (1): $\Delta MeanAge[t_1, t_2]$ is the change in overall mean age between years t_1 and t_2, and analogously for the other components. The decomposition of mean age can thus be written:

$$\Delta MeanAge[t_1, t_2] = \Delta Births[t_1, t_2] + \Delta Survival[t_1, t_2]$$

$$+ \Delta NetMigration[t_1, t_2] \qquad (3)$$

This formula may be extended if the terms in equation (1) are further decomposed multiplicatively. For example, births may be expressed as the product of total population size and crude birth rate. If so, one can replace $\Delta Births[t_1, t_2]$ by $\Delta Population[t_1, t_2] + \Delta CBR[t_1, t_2]$ in equation (3). This point is developed in more detail later. These data may be shown as values in 5-year intervals for comparison with results of Preston, Himes, and Eggers (1989) and Preston and Stokes (2012).

Period changes in population mean age are decomposed into changes in three components: births, cohort survival, and lifetime net migration.

The last two are functions of age-specific mortality and net migration rates. However, the PHE model does not include fertility explicitly. The first component in the PHE model is the number of births rather than fertility rates; the latter are used as the basis of stable population and population projection models that have been the main approaches to date for investigating the contribution of fertility and mortality to population aging. The *direct* effect of mortality improvement experienced by older cohorts at any age will lead to population aging, and improvement among younger cohorts has the opposite effect, *ceteris paribus*, in the immediate future. However, lives saved in the past at young ages will lead to more potential parents and possibly additional subsequent births; this *indirect* effect may offset population aging. Thus, for example, infant mortality levels 80 years ago will directly affect the current number of 80-year-olds, but those levels are also likely to affect the number of births to this group as parents when they were aged 20–40—about 40–60 years ago—and therefore indirectly to affect the size of later birth cohorts. The same point holds for migration since it is of the same form as mortality in equation (1) (Murphy 2016b).[2]

Depending on the age of an individual, only mortality and migration rates for periods up to about 100 years earlier *directly* influence population numbers according to equation (1). However, rates in this period as well as earlier ones will also have an *indirect* effect on the population distribution by affecting cohort size and therefore the number of potential parents and the cohort size of their offspring. Thus the current population distribution depends on rates stretching back for unlimited periods in the past. In practice, the effect of earlier rates becomes attenuated so that the current distribution is insensitive to rates more than a few generations earlier (Arthur 1982), although the converse is that more recent rates are highly influential and need to be included and analyzed appropriately. It is not possible, however, to separate the influence of the three components (births, survival, migration) through the indirect pathways without additional information or assumptions.

The calculation of mean population age in a given year depends on the numbers in each cohort alive at that time given by equation (1), which is determined by the birth cohort size *a* years earlier and rates in the previous *a* years up to a maximum of 110 years in our case. High proportions surviving to older ages mean that these people contribute substantially to the mean age of the population and therefore to trends in population aging. The number of survivors of cohorts born around 80 years earlier is influential, but the number of centenarians is small, so these cohorts contribute little to the estimates of mean ages.

A limitation of the PHE approach is that equation (1) requires detailed demographic rates for a century or so before the first change in mean age can be calculated. This is one reason why estimates to date are based on short-term comparisons, typically five years and only for recent periods,

although population aging is intrinsically determined by much longer time scales than are other demographic developments (Chesnais 1990).

On the other hand, the PHE approach is an accounting method that requires no assumptions.[3] It uniquely allocates changes in population aging to the three components. The PHE method is transitive, that is, the change in each of the components of equation (3) between times t_1 and t_2 is simply the value between times t_1 and an intermediate time t_3 plus the value between t_3 and t_2. Results do not depend on decisions about the period over which analysis is undertaken or the choice of baseline year, and it produces meaningful results over arbitrarily long time scales.

Human Mortality Database

The PHE approach requires detailed cohort mortality and net migration rates and annual numbers of births over an extended period. Data can be drawn from the Human Mortality Database (HMD), which includes estimates of mortality rates and population size by single year of age and sex for each calendar year, together with information on total annual numbers of births and deaths. These estimates are constructed using a uniform method applied to information from validated official statistics such as censuses, vital registration, and population estimates (Wilmoth et al. 2007; Human Mortality Database 2016). Since I am interested in long-term trends, I confine attention to countries with well over 100 years of continuous data: five Nordic countries, five from Western Europe, and one from Southern Europe (see Table 1). These countries account for just over half of the total population size of Northern, Western, and Southern Europe as defined by the United Nations. Most have data available from 1850, so I present most results from that year or from 1900, apart from Sweden which starts at 1751. I also construct an overall European value for the period 1850–2012 based on an average of available country values weighted by population size.

Cohort life tables from age zero to the age reached by the last available year (or age 110 if reached earlier) are available for some cohorts in HMD (Table 1). For other cohorts, I derived my own life tables. As cohort mortality rates are available for earlier cohorts, I constructed partial life tables for these cohorts from the age that the cohort reached at the start year up to age 110. Cohort mortality rates are also available for later cohorts up to around 1980, so I constructed cohort life tables to the age reached at the last available year for these cohorts. For those born after about 1980, only period mortality rates are available, so I calculated approximate cohort life tables for those born in year t using mortality rates for age 0 in year t, age 1 in year $t+1$ etc. up to the latest available year. Net migration, $m(a,t)$, is calculated using the balancing equation since population size and estimates of expected deaths to the cohort are available at age a and time t.

TABLE 1 Availability of data by first and last year and mean ages for 11 European countries

Country	Period data		Cohort rates		Cohort life tables		Mean age (years) at:	
	First	Last	First	Last	First	Last	First year	Last year
Denmark	1835	2011	1764	1981	1835	1920	27.7	40.5
England and Wales	1841	2013	1764	1983	1841	1922	26.0	40.2
Finland	1878	2012	1807	1982	1878	1921	26.8	41.8
France	1816	2013	1737	1983	1816	1922	28.9	40.9
Iceland	1838	2013	1767	1983	1838	1922	28.0	37.2
Italy	1872	2012	1794	1982	1872	1921	28.3	44.0
Netherlands	1850	2012	1777	1982	1850	1921	27.6	40.8
Norway	1846	2014	1770	1984	1846	1923	27.7	39.6
Scotland	1855	2013	1777	1983	1855	1922	26.5	41.3
Sweden	1751	2014	1676	1984	1751	1923	28.0	41.2
Switzerland	1876	2011	1805	1981	1876	1920	28.6	41.5

NOTE: First mean age is for 1850 or later first available year for each country; last mean age is for the last available year.
SOURCE: Author's analysis of Human Mortality Database.

I extend the model to include explicit consideration of fertility later. Because annual information on age-specific fertility is not available over the extended period for which mortality data are available, I estimate fertility rates as follows. The distribution of age-specific fertility rates $f(a)$, with $\sum_a f(a) = 1$, is assumed to be given by a beta distribution, $\beta(2.7, 2.7)$, scaled to be between ages 15 and 45, with a mean of 30 years and standard deviation of 6 years. This is a typical fertility pattern for populations over this period.

The actual number of births in year t, $B(t)$, is therefore given by:

$$B(t) = k(t) \Sigma_a P(a, t) f(a)$$

where, as before, $P(a,t)$ is the population aged a in year t. This provides an estimate of $k(t)$, the level of fertility in year t, as the expected number of children per adult with the given fertility distribution, and $k(t)f(a)$ as the age-specific fertility rates. From these values I derive estimates of TFR, GRR, NRR etc.

This indirect standardization method is similar to that of Calot and Sardón (2001), with the standard population being that of a typical fertile population. I use the schedule for populations with both sexes combined rather than just for women as in most applications, but this makes no difference to the substantive conclusions (Keilman, Tymicki, and Skirbekk 2014). For further details of the method see Murphy (2016a).

Results

Comparison of indexes of aging

Because change in population mean age is not a commonly used indicator of population aging, I need to establish that the choice of indicator does not lead to differences in interpretation of the contribution of fertility and mortality to population aging. I start by comparing it with two more widely used indicators of population aging—proportion of people aged 65 or over and median age—both of which are available for all countries from the United Nations Department of Economic and Social Affairs (2015).

These three indicators show almost identical trends in the 11 European countries chosen (see Figure 1: note that the averages and percentage series are shown with different numerical scales), so use of alternative indicators does not explain the different interpretations of the determinants of population aging. Mean age has more general advantages as a summary statistic: it is sensitive to the value of every observation; it gives more weight to observations at the extremes of the age distribution; and it is directly linked to the wider set of statistical indicators such as covariance with age that arise in the formulation of the PHE model (Chu 1997; Vaupel and Canudis Romo 2002).

FIGURE 1   Alternative indicators of population aging, European countries 1850–2014
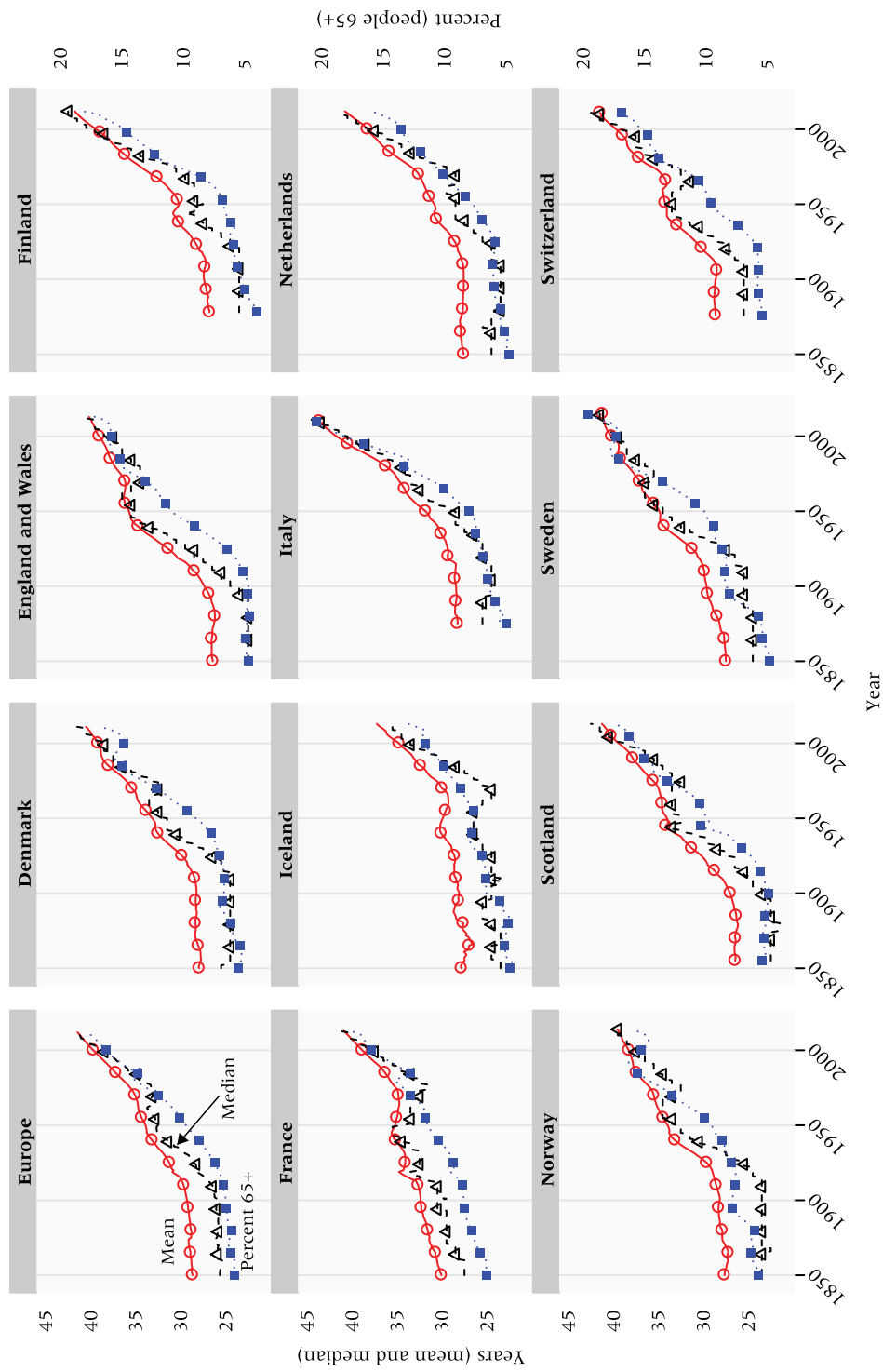
SOURCE: Author's analysis of Human Mortality Database.

TABLE 2 Summary of correlations between alternative indicators of population aging, overall European series 1850–present

	Mean	Median	Prop. 65+
(a) European series: correlation coefficients			
Mean	—	0.996	0.989
Median	0.957	—	0.977
Prop. 65+	0.908	0.784	—
(b) All countries: mean and (standard deviation)			
Mean	—	0.990 (0.008)	0.974 (0.015)
Median	0.927 (0.030)	—	0.946 (0.034)
Prop. 65+	0.720 (0.179)	0.553 (0.268)	—

NOTES: European series covers years 1850–2012. All countries includes unweighted averages of the 11 individual countries over periods of data availability shown in Table 1. Pearson correlation coefficients (shaded) and partial correlation coefficients after control for year.
SOURCE: Author's analysis of Human Mortality Database.

In the period from 1850, the overall mean age increased by about 13 years, from 28 to 41 years, and the proportions aged 65 and over by 12 percentage points, from 5 percent to 17 percent (Table 1). Often starting in the nineteenth century, population aging accelerated from the early twentieth century. A broadly similar pattern of aging is observed in all countries, with some variations. France exhibits a generally linear trend over time, while Italy shows sharp acceleration at the end of the period. The smallest increases are observed in Sweden, France, and Iceland, countries with very different demographic histories, suggesting that different factors are responsible for similar outcomes. Table 2 presents Pearson and partial correlation coefficients, with allowance for a linear time trend, between the three series for all countries from 1850 (or the first available year if later) to the last available year. Mean age is correlated at 0.99 with both median age and proportion aged 65 and over for the overall European series, slightly higher than the correlation between the median and proportion aged 65 and over. The average correlation coefficients of the mean with the other two variables for the 11 individual countries over the period are 0.99 and 0.97 respectively. The values are somewhat smaller for the partial correlation coefficients, but average values for mean age are below 0.9 only for the partial correlation with proportion aged 65 and over.

Sensitivity of estimates to start year

In order to apply equation (1) in a given year, estimates of birth cohort numbers, mortality, and migration for a century or so before that year are required. Accordingly, I would be able to make estimates only from about a century after the initial date of Table 1, long after the aging process had started in Europe. I therefore make the following assumptions between the mid-eighteenth and nineteenth centuries to extend estimates back to the mid-nineteenth century:

(i) Mortality was similar to that of the initial year for which data are available.

(ii) Net migration was close to zero before the initial year.

With these assumptions, births a years before the initial year, T, can be estimated, by reverse survival as

$$B(T - a) = P(a, T) / \exp\left(- \int_0^a \mu(x, T) \, dx\right).$$

The key question is whether the results obtained with these major assumptions are substantially different from values using full information for the whole period. I assess their validity in two ways. First, I consider whether they are reasonable given our knowledge of historical trends. Mortality showed more improvement in Sweden from the mid-eighteenth to the mid-nineteenth century than in England and Wales and France, but all of these changes were small compared to those in later periods (Human Mortality Database 2016; Wrigley and Schofield 1981; Vallin 1991; Lee 2003). Thus, the assumption that mortality was approximately constant appears reasonable.

International migration in Western Europe was less common between the mid-eighteenth and mid-nineteenth centuries than in later periods. Large-scale intercontinental migration started only from the second half of the nineteenth century when an estimated 55 million Europeans left for the Americas and Australasia between then and 1910 (Hatton and Williamson 1998; Baines 1995; Cohn 2011). However, these studies do not include intra-European migration, for which there is some information from national censuses and other sources before the mid-nineteenth century. Numbers of emigrants in six of the countries included here that are located around the North Sea—Denmark, England, Netherlands, Norway, Scotland and Sweden—are available (van Lottum 2007, Table 5.1). The overall proportions living abroad per 1,000 population, 5 in 1800 and 15 in 1850 compared with 54 in 1900, suggest that intra-European migration was also relatively uncommon and that levels were particularly small between the mid-eighteenth and mid-nineteenth centuries. In more recent periods, assumptions of both stability in mortality and negligible net migration are clearly less valid than before 1850.

The second approach to appraising assumptions (i) and (ii) is to compare results obtained with complete data and those with data left-censored at later periods. Sweden has full information available from 1751. Since mortality improved there more in the period 1750–1880 than in the other countries for which estimates exist—England and Wales (Wrigley and Schofield 1981) and France (Vallin 1991)—Sweden provides a stringent test. I compute the components of change in mean age between selected years and 2014 using equation (2) and compare results using complete data with those obtained if information was available only from 1850, 1900, and

**TABLE 3 Effect of censoring at 1850, 1900, and 1950 on aging decomposition results to 2014, Sweden**

	Initial year				
	1850	1900	1950	1900	1950
Overall change in mean age between initial year and 2014	13.72	11.59	6.35	11.59	6.35
Difference (in years) of complete and censored values between initial year and 2014 for:	Censor year 1850			Censor year 1900	
Birth cohort	1.70	0.28	0.00	2.46	1.13
Survival	−1.82	−0.28	−0.02	−1.34	−0.43
Net migration	0.12	0.01	0.02	−1.11	−0.69
Mean absolute difference of component values (in years)	1.21	0.19	0.01	1.64	0.75
Mean absolute difference as percent of overall change	8.8	1.6	0.2	14.1	11.8

SOURCE: Author's analysis of Human Mortality Database.

1950 (this last date being the same as that of Preston and Stokes (2012), who used information from the UN database available from that date augmented by occasional earlier estimates).

I present results in Figure 2 and Table 3. The observed overall mean age increased by 13.7 years, from 27.5 to 41.2 years, over the period 1850–2014 (solid line in Panel a). Errors due to using censored rather than complete estimates in equation (1) are the differences between the open and solid symbols for each of the three components. As one moves away from the start date, the differences between the complete and censored values become smaller since they must be identical from about 100 years ahead. Errors in the individual components between a particular year and 2014 depend on the degree of censoring of the data used. For example, the change in the overall mean age between 1900 and 2014 is 11.6 years, of which 2.5 years is attributed to the birth cohort term using complete data (the same complete values are presented in Figure 2, Panels a and b). The share attributed to the birth cohort component over this period using data with a censoring date of 1900 was 4.9 years (Panel b), or 2.5 years larger than the complete value, whereas the value between 1900 and 2014 with a censoring date of 1850 was only 0.3 years less (Panel a). The average absolute error across the three components for estimates between 1900 and 2014 using data censored at 1850 was only 0.2 years, or 1.6 percent of the total observed change between 1900 and 2014 (Table 3). After about 50 years ahead, the complete values and those with 1850 as the censoring year are essentially the same. I attribute this to the fact that international migration levels were

FIGURE 2   Effect of censoring at 1850, 1900, and 1950 on aging decomposition results, Sweden
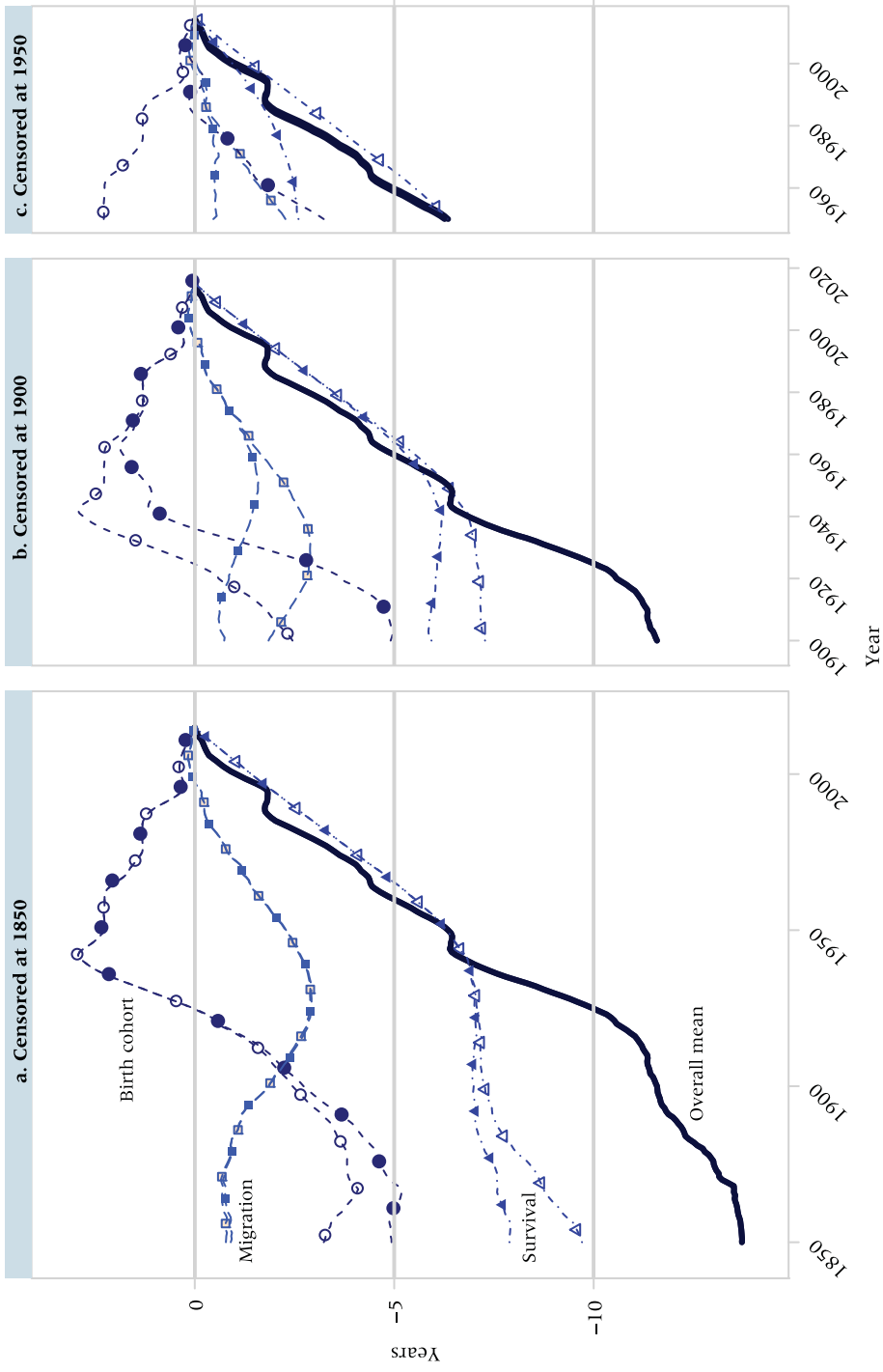
NOTE: Censored values, solid symbols; complete values, open symbols.
SOURCE: Author's analysis of Human Mortality Database.

much lower before the age of mass migration starting around 1850, with substantial out-migration mainly to the US especially in the last quarter of the nineteenth century, and to the limited improvements in mortality that occurred before the mid-nineteenth century. Discrepancies increase with a later censoring date and, unsurprisingly, are largest for the 1950 censor date estimates, since the assumptions of zero net migration and fixed mortality before 1950 for the previous 100 years are clearly inappropriate.

Both historical studies and calculations based on Swedish data suggest that the biases involved in making the constant-mortality and no-migration assumptions in the period before the first available year are likely to be relatively small for all countries from 1900. I conclude that acceptable estimates of the components of population aging can be produced throughout the twentieth century.[4]

Inclusion of the direct effect of fertility

Equation (1) does not include an explicit measure of fertility, usually identified as the prime driver of population aging over the entire period covered here. To separate out the fertility component, I decompose the birth cohort term into the product of a fertility measure (births per individual), which reflects current behavioral choices and constraints, and number of individuals at risk, which depends on earlier fertility, mortality, and migration.

There are alternative ways of specifying the fertility measure, and the choice is to some extent arbitrary. To assess the robustness of my approach, I present two sets of estimates using the crude birth rate (CBR) and a gross reproduction rate (GRR) measure based on the fertility estimation approach described earlier. The crude birth rate is not independent of the population age structure and is therefore not a "pure" fertility index with the direct "children per woman" interpretation of an index such as TFR or GRR, but it is simple, widely available, and forms one component of natural population growth.

In general, the birth cohort term $B(t)$ in equation (1) can be written as the product of a fertility measure $F(t)$ and the corresponding population at risk at time t, $R(t)$. ($R(t)$ is thus defined as $B(t)/F(t)$. If F is the CBR, the population at risk is the overall population size; for GRR, it is an appropriately weighted average of individuals in fertile age groups.) With this decomposition, the birth cohort term on the right hand side of equation (2) is replaced by two terms showing the separate effects of changes in fertility and in population at risk.

$$\frac{\partial B\,(t-a)}{\partial t}/B\,(t-a) \;=\; \frac{\partial F\,(t-a)}{\partial t}/F\,(t-a) + \frac{\partial R\,(t-a)}{\partial t}/R\,(t-a)$$

This decomposition treats mortality and migration (of the current population) symmetrically with fertility (of the parental generation), and also includes a population-at-risk term as a separate component. It therefore

FIGURE 3 Decomposition of overall birth cohort component into CBR and GRR fertility components
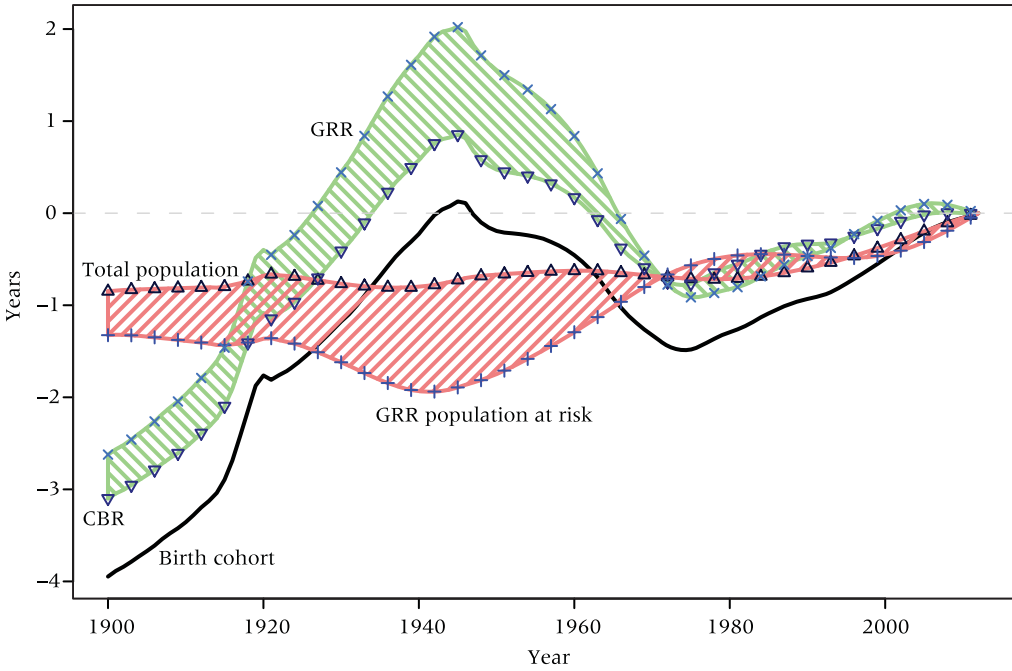
SOURCE: Author's analysis of Human Mortality Database.

addresses one major difference between the original PHE and stable or population projection approaches, namely that the former has no explicit fertility term. The formulation is closer to the standard cohort component model for which the sufficient statistics are baseline population size and structure, together with fertility, mortality, and net migration rates. This formulation is similar to that of Lee and Zhou (2017), who decompose births using TFR rather than GRR or CBR, although they do not fit these enhanced models.

While mortality and migration are uniquely specified in equation (1), alternative fertility measures may be used, so I consider how robust results are to different choices. Figure 3 shows the birth cohort component of overall population change decomposed into two sets of fertility and population-at-risk terms; Table 4 shows corresponding total and partial correlation coefficients and variances of these series from 1900. For the overall European series, the Pearson correlation coefficient is 0.99 between the birth cohort and CBR fertility series and 0.88 between birth cohort and GRR; the partial correlation coefficients are around 0.99. These results confirm that these series show similar underlying patterns.

The hatched areas of Figure 3 show the range of the contribution of the two fertility measures and corresponding population-at-risk terms to population aging and therefore indicate the sensitivity of results to these

TABLE 4 Summary of correlations between alternative decompositions of birth cohort component of change in mean age, overall European series 1900–2012

	(a) Correlation coefficients					(b) Variance over period 1900–2012
	Birth cohort	CBR	GRR	Total population	GRR pop. at risk	
Birth cohort	—	0.986	0.876	0.522	0.118	1.21
CBR	0.989	—	0.924	0.373	−0.006	1.02
GRR	0.996	0.991	—	0.152	−0.374	1.39
Total population	−0.005	−0.151	−0.048	—	0.691	0.04
GRR pop. at risk	−0.950	−0.961	−0.975	0.152	—	0.33

NOTE: Pearson correlation coefficients (shaded) and partial correlation coefficients after control for year.
SOURCE: Author's analysis of Human Mortality Database.

alternative choices (individual country values are available on request). The GRR population-at-risk term is more variable than the CBR term since it is based on a population averaged over a smaller age band than the total population. The fertility rate series gives the direct effect of fertility, and the population-at-risk series include the indirect effect of all other components. The variability of the latter component is much smaller than the former (Table 4b) and therefore the birth cohort series is much more similar to the fertility series than to the population-at-risk series. The two fertility series provide similar substantive results concerning the relative contribution of the direct effect of fertility, mortality, and migration to population aging across these countries. I conclude that the separation of the birth cohort term into these two components is robust to alternative fertility specifications.

Components of population aging in Europe 1850–present: Final results

Having established that data availability from about 1850 is unlikely to affect results from 1900 and that robust estimates of the direct fertility component exist, I now present the final results. While generalized statements about the determinants of population aging exist, the likelihood that their effects are not constant across time and space has been advanced on both theoretical and empirical grounds (Hermalin 1966). However, conclusions from the published PHE studies to date relate to estimates based on short five-year windows concentrated in periods around the end of the twentieth century and so may not be typical of longer periods.

I start by discussing changes in the components of population mean age averaged across the 11 European countries weighted by population size, covering the majority of people living in Europe (excluding Eastern Europe). Although data are available only from 1850, this is not a major limitation since changes in population aging appear to have been small before that date and immediately thereafter. For example, the proportion aged 60 and over in England was 8 or 9 percent in the period 1541–1800 and about 6.6 percent in 1841, a value slightly lower than in earlier periods (Wrigley and Schofield 1981, Table A.3.1), and there was very limited population aging in the reminder of the nineteenth century (Figure 1). The overall population mean age increased by only 0.6 years in the period 1850–1900, but by 2.0 years in the following 25 years based on countries with available data as the effect of fertility decline began to exert itself (Coale and Watkins 1986). I therefore discuss results only from 1900 (based on all available data) since earlier values are small and are based on an assumption of earlier constant fertility and mortality, so that changes tend to be attributed to the birth cohort component.

Population mean age rose monotonically by 12.4 years between 1900 and 2012, with an increasing trend apart from a deceleration in 1950–75, before rising even more rapidly in the period 1975–2012 (Table 5). I present analyses based on dividing the birth cohort term in equation (1) into CBR and total population components rather than the GRR measures, but results are similar in both cases. The fertility, mortality, and net migration components exhibit different trends. Mortality improvement had little effect on population aging in the first part of the period. In fact, in the nineteenth century it made population average ages slightly younger rather than older, as Coale and others noted. In later periods, mortality improvement was monotonically associated with population aging, a process that accelerated steadily over the twentieth century, especially from about mid-century (Table 5). Over the whole period since 1900, mortality improvement accounted for 66.2 percent of the increase in mean age, the great majority occurring in the second half of the century.

Although the late nineteenth century was the age of mass emigration from Europe, and the late twentieth century might be characterized as the age of mass immigration, the overall long-term direct effect of migration on population structure to date is minimal.[5] However, migration had some role in reducing aging in the early twentieth century in both Sweden and France, but the reasons were different. In Sweden, older cohorts were "hollowed out" by earlier emigration, whereas contemporary inflows of younger people in France led to a shift toward younger average ages. In general, migration had little effect on population aging, neither accelerating nor retarding it over the period. However, its direct effect will accelerate population aging in the twenty-first century if net migration does not continue the increasing trend of recent periods.

The role of birth cohort size, in contrast, is larger and more complex. Changes in this series are more similar to those in the fertility rates than in the population-at-risk series, so the following comments relate to both fertility and birth cohort series. In the period up to 1945, fertility was by far the most important factor in population aging. However, the sharp increase in births in many European countries for several decades following 1945 meant that fertility trends tended to make populations younger rather than older, although this trend was not sufficient to completely offset the increasing influence of mortality improvement. In the three decades following 1945, fertility/birth cohort effects substantially retarded population aging in Europe, before the pattern reversed in recent decades and for the first time fertility and mortality act strongly together to reinforce population aging.

While the terms in equation (1) relate directly to specific components of population change over time, the population at risk underlying equation (3) is ill-defined. It combines earlier fertility, mortality, and migration experiences in a way that does not permit these components to be

TABLE 5 Change in components of overall population aging by time period, overall European series, 1900–2012

| Component	1900–1924		1925–1949		1950–1974		1975–2012		1900–2012	
	Years	Percent	Years	Percent	Years	Percent	Years	Percent	Years	Percent
Total	2.09	100.0	2.75	100.0	1.67	100.0	5.94	100.0	12.45	100.0
Survival	0.29	13.8	0.95	34.5	2.33	139.2	4.68	78.8	8.25	66.2
Net migration	−0.56	−26.8	0.41	14.9	0.63	37.7	−0.22	−3.7	0.26	2.1
Birth cohort	2.36	113.0	1.39	50.6	−1.29	−76.9	1.48	24.9	3.95	31.7
of which:										
CBR	*2.21*	*105.8*	*1.36*	*49.4*	*−1.24*	*−74.2*	*0.77*	*12.9*	*3.10*	*24.9*
Total population	*0.15*	*7.1*	*0.03*	*1.2*	*−0.05*	*−2.7*	*0.71*	*12.0*	*0.85*	*6.8*

SOURCE: Author's analysis of Human Mortality Database.

separately identified. The population-at-risk term can be taken to represent the unattributed component of population aging and may be interpreted as the residual after the direct effect of the other components has been estimated. The effect has been small over the whole period, accounting for 0.8 years out of a total change of just over 12 years, a magnitude similar to that for net migration.

Increases in population aging in the period up to 1950 were driven largely by fertility decline (Table 5). From the middle of the twentieth century, direct mortality effects start to dominate, with birth cohort effects becoming negligible since annual births were relatively constant as compared with earlier periods. These findings are consistent with the conventional depiction of trends in population aging as set out in the introduction, although the key role of the postwar baby boom driven by fertility increase has received less attention. The sharp reduction in population aging due to birth cohort effects in the postwar period is inconsistent with the simplified demographic transition model. The reason is that the postwar baby boom led to larger numbers of births in this period, and infants have the largest influence on attenuating population aging since they are the maximum possible distance below the mean age. It is clear from Table 5 that the baby boom was primarily due to increased fertility over the period rather than to larger populations at risk. While the main discussion about different patterns of population aging between high-income and middle- or low-income countries has been concerned with the different pace of aging, the baby boom represents an additional factor, which will continue to play a key role in population aging for decades to come. Most discussion about the relative effect of fertility and mortality on population aging has compared monotonic fertility and mortality decline. However, a rise followed by a sharp fall in fertility will lead initially to a deceleration in population aging, followed by an increase as these large cohorts move into age groups above the population mean age (although this effect may be offset by the additional offspring that they may contribute to younger generations). The full effects will become apparent over long time-scales, a fact that demonstrates the importance of the choice of period analyzed.

The question remains of how far these trends reflect a common pattern across these European countries or a range of distinct patterns. Much analysis has been based on a framework of progression toward a regime of low fertility and mortality, albeit occurring with different lags (Coale and Watkins 1986). However, the heterogeneity of experience must be recognized, especially in relation to trends in population aging (Figure 4). The reason fertility has been emphasized as a determinant of population aging is that it alters age-specific population growth and therefore the relative number of young to old people. Changes in population growth rates might be expected to have a strong effect on population aging. Growth has varied substantially and there is a general tendency for countries that have grown

FIGURE 4 **Final decomposition of population aging, Europe, 1900–2014**
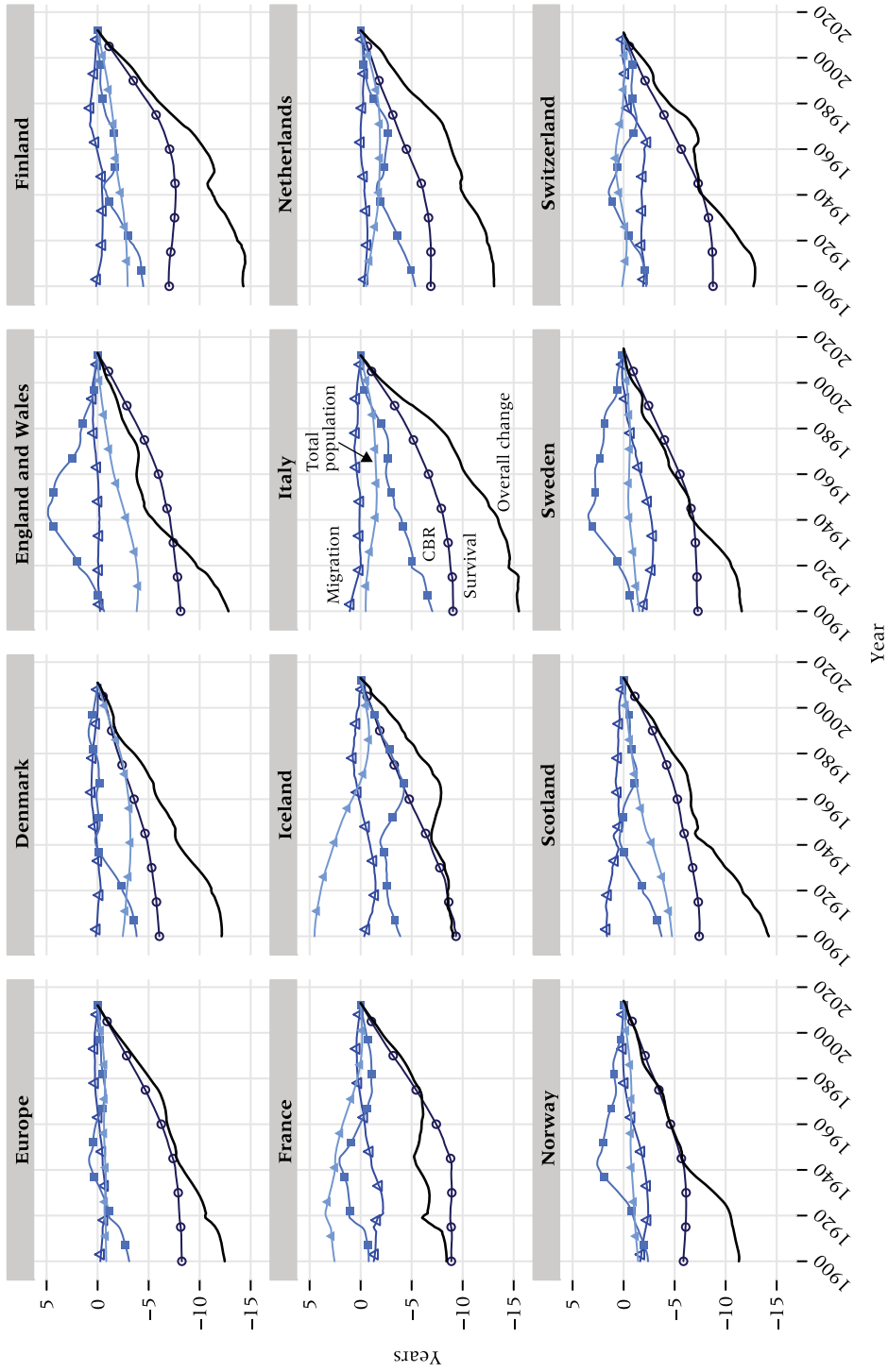
FIGURE 5   Relationship of population growth and change in mean age between initial and final year
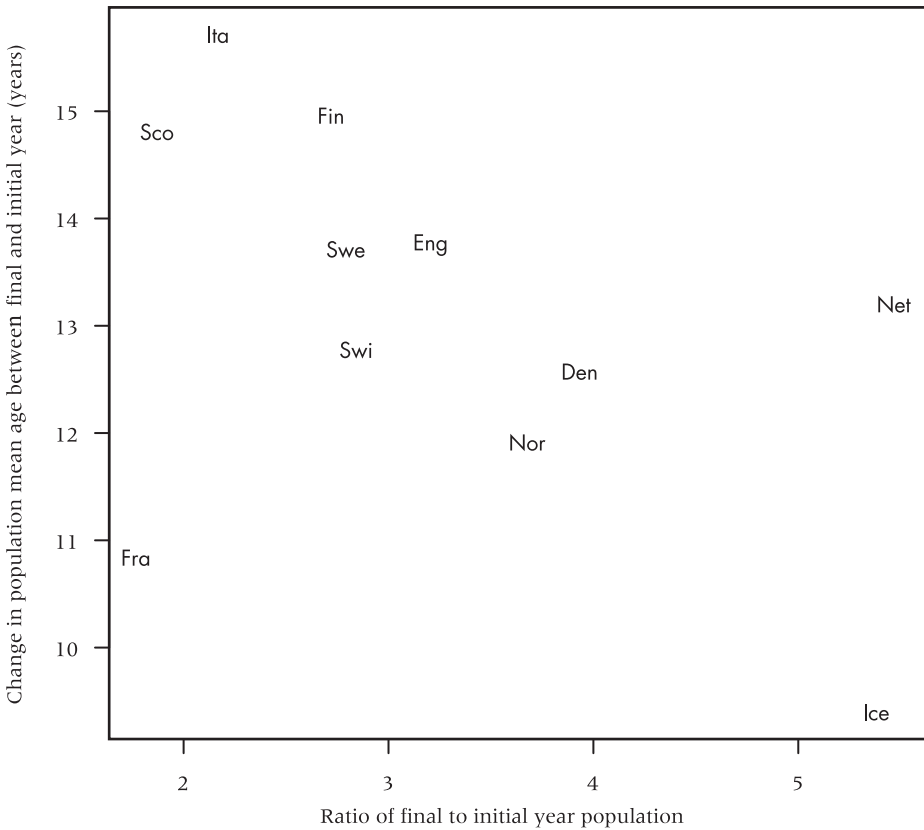
SOURCE: Author's analysis of Human Mortality Database.

most to have the lowest levels of population aging (Figure 5). Most countries grew between a factor of two and four over the period 1850 (or first available year if later) to the present. On average, this corresponds to an expected change of about 13 years in mean age over the period. This is not inevitable, however: at the extremes of the growth distribution, since 1850 France grew by only 80 percent, whereas the Netherlands grew by 450 percent, but mean age actually increased less in France than the Netherlands, the opposite of what might have been expected.

Summary and conclusion

Mean age has advantages as an indicator of population aging. It is the natural statistic for modeling the components of population dynamics.[6] However, the relative importance of fertility and mortality for population aging is unrelated to the choice of index of aging.

Approaches using population projections might appear to be more straightforward, and the data required are both more readily available and sometimes considerably less substantial. Nevertheless, results with this approach require a number of decisions for which there is no obvious rationale. Some analyses are based on projections with counterfactual assumptions from a given time point and a comparison with actual outcomes from that date (for example, Hermalin 1966). Other approaches apply their assumptions for long periods of time before comparing the results and actual values. Lee and Zhao (2017) apply the alternative assumptions for a century before examining differences in population aging over a five-year period. This latter approach is more consistent with the PHE model, but also requires information for about a century before comparisons are available.

A model like PHE appears to have major advantages for elucidating the process of population aging compared with alternative methods, for reasons set out earlier. Some of the concerns about the interpretation of results from the PHE approach may turn out to be less important with these additional findings. The analysis presented here tracks the determinants of population aging in 11 European countries for well over a century, including over the period of demographic transition relevant to population aging.[7] The PHE approach provides an interpretation of aging trends using explicit outputs as opposed to subjective criteria—apart from the choice of fertility indicator, which appears to have little influence. In the most recent period, mortality is the dominant determinant of population aging, and since 1950 fertility and birth cohort size have no effect on population aging other than a slight inhibiting effect. This statement could be qualified by inserting "direct" in front of determinants, but I have shown that the unallocated (indirect) component is small and does not affect the main conclusions about the relative importance of fertility and mortality over this period. This approach also provides precise estimates of timing, identifying the period 1945–50 as a key moment when mortality overtook fertility as the driver of population aging in Europe, a position it seems unlikely to relinquish in the foreseeable future.

The finding that mortality improvement has had a dominant role in population aging in these European countries since the middle of the twentieth century is not surprising, given that fertility had been relatively low for the whole lifetime of those now alive. In Britain, the total fertility rate is almost the same as it was nearly a century ago, 1.9 in 2010 compared with 2.0 in 1926–30 (OPCS 1987; Office for National Statistics 2015). The contribution of fertility change to population aging in Europe was confined largely to changes in a period of a couple of decades around the start of the twentieth century. Like the tortoise and the hare, the steady improvement in mortality eventually overwhelms the volatile fertility component. We also note that the contribution of net migration to population aging was

both small and transient (although over this period, its main component was often emigration rather than immigration).

These results also provide a clearer chronology for the development of population aging. We can identify the point at which mortality replaces fertility as a primary determinant of population aging as just after the end of World War II. The importance of the postwar baby boom in these societies is also noteworthy. These results confirm the initial pre-eminent role of fertility being superseded by mortality in these high-income countries, a pattern that will plausibly be followed by low- and middle-income countries in due course. I emphasize that these results are specific to Europe and possibly to some other high-income countries, although in the initial period covered by the analysis they were at an early stage of demographic transition. However, the much more rapid and substantial reduction in fertility in a country such as China, where the total fertility rate fell from 6.3 to 1.5 in a generation between in 1965–70 and 1995–2000, produces a shock wave that will propagate for a century or more into the future, with major socio-demographic implications (United Nations Department of Economic and Social Affairs 2015). The postwar baby boom in the West, which retarded population aging and eased the inevitable aging transition, was a luxury that will not be available to such emerging economies.

While population aging has moved to the top of the social, economic, and political agenda in much of the world, the mechanisms underpinning it—in particular, the relative long-term contributions of fertility, mortality, and migration—remain unclear. I have attempted to show how the process unfolded over an extended time period in a single continent using a particular decomposition approach. The results are broadly similar to those based on other approaches, but suggest that the role of mortality improvement has attracted less attention than it deserves.

Notes

1 Counterfactual projections, which conventionally fix fertility or mortality at an initial value and compare projection results with later actual values, are sometimes used to identify the contributions of fertility and mortality to population aging. However, this approach fails to provide useful information over the extended time scales such as those considered here. If the effect of fertility change on population structure is assessed by a projection with fertility fixed at around 1850 levels, the projected population would be about eight times larger than the actual population by 2015 and it would have a very young age structure. On the other hand, if mortality is fixed at 1850 levels, the projected population would be about one quarter of the actual size. Thus conclusions are based on comparisons of actual with unrealistic projections. With shorter projection periods, an additional problem is that the results can

be very sensitive to choice of the starting date. For example, if such an exercise were undertaken over a period of about 40 years in Britain starting from the mid-1960s, baseline fertility (TFR in England and Wales of 2.93 in 1964) was much higher than the average over the next four decades. The current observed population structure would be considerably older than the projected population, leading to the interpretation that fertility change in recent decades had made the population older. On the other hand, if the same analysis had been started 30 rather than 40 years ago (TFR 1.66 in 1977, thus lower than the average over the subsequent period), the actual population would be younger than the projected one, and the interpretation would be that fertility change in that period had made the population younger.

2 These points had been emphasized by Horiuchi (1991, p. 42): "It is important to distinguish direct and indirect effects of mortality changes on population growth. The present method [using age-specific growth rates $r(a,t)$] is concerned with direct mortality effects only. Mortality reduction, however, has some indirect effects. … Such indirect mortality effects working through fertility are difficult to assess when the present method is adopted." Preston and Stokes (2012, p. 224) noted that: "The answer supplied by this accounting approach [PHE model] is not necessarily the same as what would be supplied by models or by counterfactual simulations." Lee and Zhou (2017) compare counterfactual population projections based on constant fertility and/or mortality from 1900 with actual values in India and the more developed countries (MDCs) over the period 2005–10, the period chosen for direct comparison with the findings of Preston and Stokes (2012), to identify the determinants of population aging. They show that with this model, fertility decline was the main factor in population aging. This is consistent with the findings of Bengtsson and Scott (2010) for Sweden over the same period and with the conventional explanation as summarized by Wilmoth (2015). There appear to be different answers to what is apparently the same question: what is the relative contribution of fertility and mortality to contemporary population aging? Since this issue is closely tied to the allocation between direct and

indirect pathways, I consider this issue in more detail.

3 Apart from, for example, decisions about how to implement a formal model based on continuous function formulation when data are available only in discrete form. This means that there are some minor discrepancies between the change in observed mean age and the sum of the individual components, but these are substantively unimportant. There may also be decisions about how the requirement for a 100-year lead-in period may be relaxed as done by Preston and Stokes (2012), who devote considerable attention to this issue since they use United Nations data available only from 1950.

4 However, assumptions of constant mortality and zero migration before the first available year produce estimates that are biased toward zero before 1900. Constant age-specific mortality and migration before the start date means that the first derivatives of the corresponding terms in equation (2) are constrained to be zero at the start date. In addition, one must recognize the possibility of imprecision for data close to the initial year in estimates of net migration based on the difference between overall and natural population change. However, since population aging was limited or even absent in the nineteenth century, differences between estimates to the present starting in 1850 or 1900 are likely to be small. Biases become larger for start years in the twentieth century, both because population aging had started and because the preceding demographic regime was changing substantially. This suggests that estimates in such cases will require a longer lead-in time or further adjustment. To the extent that mortality and migration trends were less marked in developing countries in the twentieth century, these findings should not be regarded as invalidating their use in such contexts, although more detailed approaches such as those of Preston and Stokes (2012) may be necessary.

5 Note that the migration component includes only the contribution of first-generation migrants. As with the indirect effect of mortality, their descendants are classified as native-born children who therefore contribute to the birth cohort term.

For discussion of models that estimate the long-term implications of migration on population size and structure, see Murphy (2016a).

6 While not discussed here, the same approach can be confined to sub-populations to investigate, for example, aging within the older population, or separately for men and women or for different socio-demographic groups.

7 This excludes the first half of the nineteenth century (Lee 2003), but there was little sign of population aging until well after 1850.

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