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Descriptive Finding

The role of reductions in old-age mortality in old-age population growth

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Abstract

BACKGROUND
The variable-r model provides demographers with a way to explore the contributions of demographic components (fertility, mortality, migration) to changes in populations' age structures. However, traditional variable-r methods require extremely long mortality series to explore growth at oldest-old ages.

OBJECTIVE
Our goal is to disentangle the old-age growth rate into two main components: the growth rate at some younger age, and reductions in mortality between the younger and older ages.

METHODS
We focus on an adaptation of the variable-r model that can use shorter mortality series to explore population growth between two ages.

RESULTS
Using data from the Human Mortality Database, we explore how these two components are driving the growth rate of 100-year-olds. Observed growth of those reaching age 100 results primarily from the high growth rates when those cohorts were 80-year-olds, and from time reductions in cohort mortality between ages 80 and 100. However, the latter component behaves differently across populations, with some countries experiencing recent slowdowns in cohort mortality declines or increases in mortality between ages 80 and 100.

CONCLUSIONS
We find great diversity in the level of old-age mortality improvements across populations, and heterogeneity in the drivers of these improvements. Our findings highlight the need

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to closely monitor the underlying reasons for the changes in old-age mortality across populations and time.

CONTRIBUTION

We present illustrations of the use of the variable-r method to monitor demographic change in an online interactive application, estimated even when only short historical series of demographic data are available.

1. Introduction

In nearly every country in the world, populations are living longer today than ever (He, Goodkind, and Kowal 2016). Worldwide, individuals alive today can expect to live a decade longer than the average person in their parents' generation, and two decades longer than the average person in their grandparents' generation. Though advances in infant and child mortality have driven a considerable portion of this change in the past, mortality rates have also declined substantially at older adult ages. These shifts in early-life survival, combined with reductions in adult mortality, have led to rapid growth of the global oldest-old population (those aged 80+). The pace of growth of these age groups is unprecedented, and current rates of growth of the oldest-old population are three times higher than the rate of global population growth (United Nations Population Division 2017b). Growth of even older populations, such as centenarians, has been even more rapid (Medford et al. 2019; Robine and Caselli 2005). Uncertainty remains as to whether longevity increases will maintain their current pace in coming decades (Dong, Milholland, and Vijg al. 2016; Oeppen and Vaupel 2002), and great heterogeneity in old-age mortality persists within populations, with increasing disparities observed between socioeconomic statuses in the USA (Currie and Schwandt 2016) and education groups in Sweden and Finland (Zarulli, Jasilionis, and Jdanov 2012). However, there is widespread agreement that future longevity gains in high-income countries will come primarily from reductions in old-age mortality (Vaupel 2010).

A considerable body of demographic analysis has sought to understand the factors contributing to population aging, seeking to disentangle the relative contributions of demographic components (fertility, mortality, migration) to changes in populations' age structures (Coale 1956; Horiuchi 1991; Lee and Zhou 2017; Preston 1974; Preston, Himes, and Eggers 1989; Preston and Stokes 2012). In recent years, many of these efforts have relied on the variable-r method to quantify the contribution of demographic components to changes in age structure (Horiuchi and Preston 1988; Preston and Stokes 2012). This type of analysis was developed by Preston and Coale (1982) and Arthur and

Vaupel (1984), who defined the mathematical relationships existing between age-specific population growth and age-specific rates of fertility, mortality, and migration. A lively debate is still ongoing as to whether the current trends in population aging seen throughout the world are predominantly driven by changes in fertility (Lee and Zhou 2017) or changes in mortality (Preston and Stokes 2012).

However, a significant drawback of these methods emerges when they are used for the analysis of old-age population growth. Using traditional variable-r methods to explore growth at oldest-old ages requires long mortality series (Preston and Stokes 2012). Furthermore, as pointed out by Lee and Zhou (2017), disentangling the contribution of mortality and fertility components is a complex quantification involving the reverberations of past cohorts in the current population. Finally, the high-quality data needed to quantify age-specific migration within cohorts from birth to old age is largely absent for extant cohorts, and the limited data available are often not comparable across countries.

These limitations mean that previous work has struggled to explain the determinants of old-age growth rates in the majority of global populations, which lack extensive, high-quality historical data. In this paper we apply the variable-r model, focusing specifically on the relative role of changes in old-age mortality and changes in population growth rate at some younger age in explaining the growth rate at an older age. Rather than trying to explain whole-population change, we narrow the focus to explaining age-compositional differences occurring between two ages over time. Our analyses aim to answer a simple, clear question: Is the observed growth rate at a given age a consequence of the high growth rate at some younger age, or is this growth due to progress in reducing mortality between the two ages? For example, does the observed growth of 100-year-olds result from high growth rates of 80-year-olds or from reductions in cohort mortality between ages 80 and 100 over time? This simplified approach avoids the need for long time series of mortality and the complexity of involving information from previous cohorts to disentangle their fertility, mortality, and migration contributions. We illustrate our approach by estimating the components of change for the population growth rate at age 100 for industrialized countries.

2. Data

Our analyses use population and life table data from the Human Mortality Database (HMD 2021). The HMD contains high-quality historical data that combines vital statistics and census counts or official population estimates, and applies standard methods to all populations over time to ensure comparability (Wilmoth et al. 2017; Barbieri et al. 2015). All populations with at least 40 years of mortality data between 1950 and 2021

(34 of 41 populations in the HMD) were included in the analysis. Population and death counts by single age were obtained from the HMD to calculate the components of growth rate at age 100.

3. Methods

The population growth rate at older ages, for example age 100, is disentangled into three distinct parts:

1) The population growth rate at a younger age, e.g., 80,
2) The contribution of cohort mortality changes between two ages, e.g., 80 and 100, and
3) Net migration between the ages.

To do so, we use the variable-r method (Preston and Coale 1982; Arthur and Vaupel 1984) to directly obtain the observed increase at the old-age population and to calculate the contribution of old-age mortality to this change. Let $r_x(t,t+n)$ be the age-specific growth rate at age x between times t and $t+n$ in a population (average annual growth over the period). This growth rate can be decomposed into (1)–(3) as

$$r_x(t, t+n) = r_y(\tau, \tau+n) + \Delta S^{t-x}(y, x) + \Delta M^{t-x}(y, x), \quad (1)$$

where $r_y(\tau, \tau+n)$ is the age-specific growth rate at the earlier age y calculated from time $\tau = t - x + y$ and $\tau + n$; the change in probabilities of surviving is denoted as $\Delta S^{t-x}(y, x) = ln\frac{S^{t+n-x}(y,x)}{S^{t-x}(y,x)}$ corresponding to the survival from age y to x for birth cohort t+n-x and between those same ages for birth cohort t-x; and finally $\Delta M^{t-x}(y, x)$ corresponds to the net migration rate with similar notation as for the probabilities of survival.

According to Preston and Stokes (2012), the net migration effect $\Delta M^{t-x}(y, x)$ can be estimated as a residual term from Equation (1). Our approach differs from that of Preston and Stokes in that Equation (1) aggregates all the previous demographic changes in the earlier growth rate $r_y(\tau, \tau+n)$. Disentangling the determinants of the growth rate at this earlier age would require accurate information on all of those components (mortality, migration, and birth counts) for many years back in time (e.g., 80 years in our illustrations below), which are not available for most populations. As such, the growth rate at a younger age in Equation (1) hides all the past demographic information, but the procedure allows us to assess the mortality effects on growth at older ages. Furthermore,

as pointed out by Lee and Zhou (2017), in the original Horiuchi (1991) and Preston and Stokes (2012) the change in cohort birth counts, captured by the birth growth rate, can also be decomposed into mortality and fertility components. For example, Murphy (2017) disentangles those birth counts as the product of an age-aggregated fertility and population at risk terms. By contrast, the shorter version of the variable-r in Equation (1) changes the focus, exploring whether the observed growth between two cohorts to an advanced age (e.g., age 100) results from increases in cohort growth at an earlier age (e.g., age 80) or is due to differentials in survival between the cohorts from age 80 to 100.

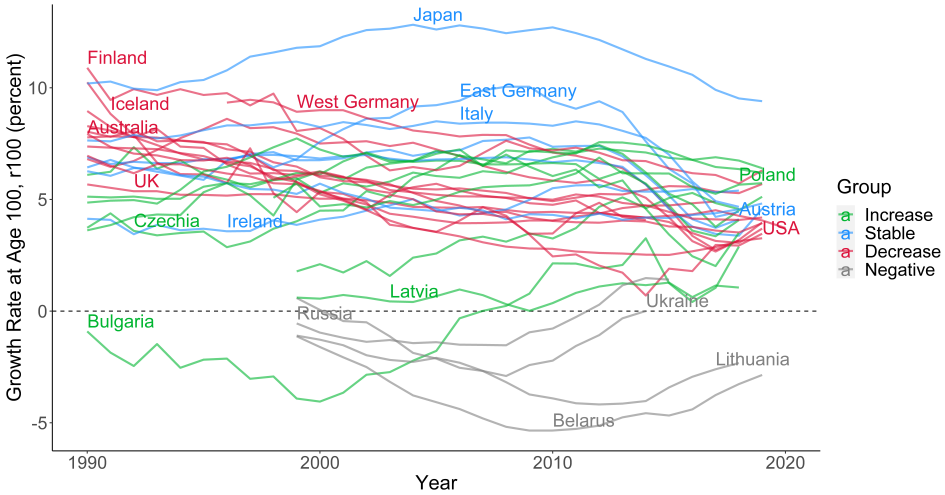
Similar to Preston and Stokes (2012), we estimate the migration effect $\Delta M^{t-x}(y,x)$ as the residual element, as opposed to including country-specific data on actual migration flows. In practice, international migrations tend to be quite rare at older-adult ages in the high-income countries under study (United Nations Population Division 2017a).

All the calculations in this study were carried out using 'R' software (R Core Team 2021). The interactive shiny online application created for this study includes detailed decomposition of r_{100} for each country and gender, for (1) developed countries using HMD (2021), and (2) for all regions in the world using the World Population Prospects (UNPD 2019), as well as (3) specifics of Equation (1) in continuous notation and on its estimation procedure. The online application allows the user to select across countries, decide the time span of analysis (e.g., changing from 20 to 5 years) and the age (e.g., changing from ages 80 to 100 to ages 60 to 90): https://demo268.shinyapps.io/Growth/.

4. Results

Figure 1 presents the trends in female population growth rate at age 100 (r_{100}) for populations included in the HMD. Given the importance of the survival component ($\Delta S^{t-x}(y,x)$ in Equation (1) in driving changes in growth rates, we classified countries into four groups (increase, stable, decrease, negative) based on the time trend in this survival component (additional details in the online interactive application). Overall, we find substantial heterogeneity across countries in the HMD in terms of time trends in r_{100}. Broadly, a number of countries in Eastern Europe (e.g., Poland, Czechia, Latvia, Bulgaria) are seeing steady increases in r_{100} and survivorship between ages 80 and 100. By contrast, countries such as the United States, Australia, Denmark, and the Netherlands have seen a slowdown in r_{100}, driven largely by a slowing of survivorship improvements. Another group of countries, including Japan, Italy, and Ireland, have seen relative stability in survivorship across cohorts, and steady r_{100} over time. Finally, a cluster of former Eastern Bloc countries is experiencing negative growth of 100-year-olds over time, and consistently negative trends across cohorts in survivorship between ages 80 and 100.

Figure 1: 100-year-olds' growth rates for HMD countries, classified by time trend of survival component



Source: Authors calculations based on HMD (2021).

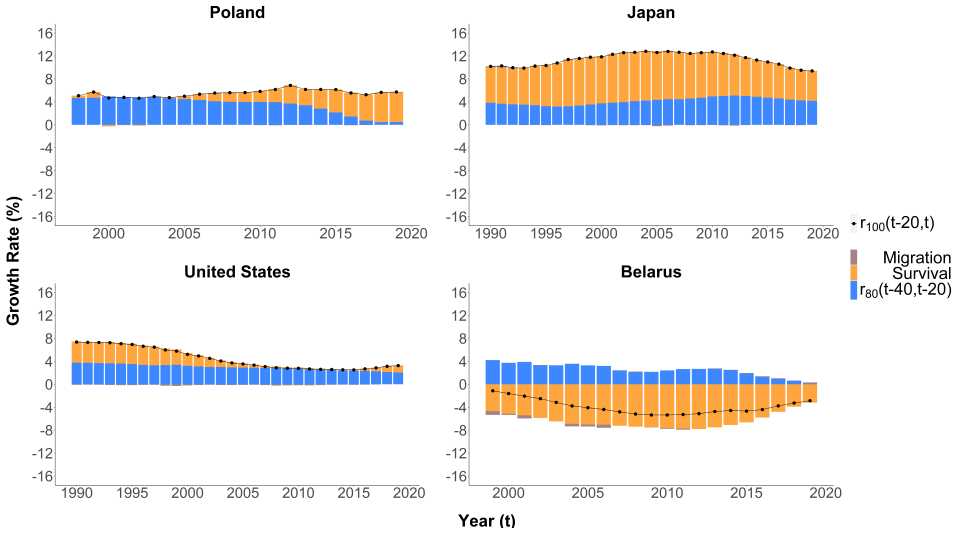
To illustrate our findings in more depth, a representative country from each group was taken to further study the contribution of the growth rate components: stable (Japan), increasing (Poland), decreasing (United States), and negative (Belarus). These countries were selected to represent the observed heterogeneity in the components of change of the old-age-population growth rate. Trends in female growth rates at age 100 in these countries, and the underlying components driving these trends, are displayed in Figure 2 (figures for males and the remaining countries are available in the online application). In Figure 2 the continuous line corresponds to the average annual population growth rate at age 100 (r_{100}) between years t and $t+n$, or $r_{100}(t, t+n)$. For example, the first data point for the United States (in 1990) displays the average annual growth rate r_{100} between 1970 and 1990, showing that American females aged 100 grew at an average annual rate of 7.37% between these two years (indicated by the dot in 1990). Correspondingly, the three colours of the columns in Figure 2 provide the contribution of the three components of change in this growth rate between 1970 and 1990. Following Equation (1), $r_{100}(1970,1990)$ in American females is decomposed into three parts:

1) The contribution of the population growth rate at age 80 between 1950 and 1970 (for American females $r_{80}(1950,1970)$ = 3.77% annual increase, blue bar),
2) The contribution of cohort mortality changes between ages 80 and 100 in the 1870 and 1890 birth cohorts

($\Delta S = ln\frac{S^{1890}(80,100)}{S^{1870}(80,100)} = 3.70\%$, annual increase, orange bar), and

3) The contribution of migration changes between cohorts ($\Delta M = -0.1\%$, estimated as the residual from Equation (1), gray bar).

Figure 2: 100-year-olds' growth rates and their components: the growth rate at age 80, and survival and migration between these ages, for selected countries between 1990 and 2019



Source: Authors calculations based on HMD (2021).

Continuing with the example of American females, the growth rate of 100-year-olds increased by 7.37% annually between 1970 and 1990. Decomposing this increase shows that more than half of this increase in the growth rate came from survival progress across cohorts between ages 80 and 100, while the rest is explained by the already sizeable observed growth rate at age 80. Migration between ages 80 and 100 plays only a negligible role. Positive values of $r_{100}(1985, 2005)$ to $r_{100}(1995, 2015)$ (representing 100-year-olds' growth from 1985–2005 to 1995–2015) were almost entirely due to growth rates at age 80, with almost no contribution from cohort survival improvements between 80 and 100. In recent years a slight recovery of this component is observed.

By contrast, in Japan the growth of 100-year-old females was driven primarily by survival improvements. Polish females transition from negligible, or even negative, survivorship improvements over time to survivorship becoming the main component of

change in population growth at age 100. However, for Belarus, r_{100} remained negative in all studied periods, as the small positive growth rates of 80-year-olds could not make up for deterioration in old-age survival. Again, we find that the migration contribution at these ages is negligible for all observed countries.

5. Discussion

In this study we apply a variable-r-based method for explaining population growth at older ages that obviates two limitations of prior approaches: the need for extensive historical data on demographic trends (Preston and Stokes 2012), and the intensive modeling needed to account for the lagged effects of past cohorts in a population (Lee and Zhou 2017). Our approach provides clear answers to a key question in the study of population change – "What explains population growth at a given age?" – by decomposing this growth into interpretable components of mortality change, migration change, and changes in population growth at some earlier age. In our application of this method to substantive data, we focused on explaining changes in the growth rate of 100-year-olds. Although the benefits of avoiding the need for extensive mortality histories are most pertinent when studying old-age mortality, the variable-r method can be used to estimate growth between any two ages (Nepomuceno and Turra 2020). We believe this provides useful information on the drivers of growth between two ages in a population, while avoiding some of the 'thornier' issues that face analysts conducting full variable-r decomposition analyses.

Our substantive findings show that there is considerable cross-national heterogeneity in both the levels of population growth at age 100 (r_{100}) and the components driving this growth. We find that in most populations the population growth rate at age 80 (r_{80}) acts to increase the growth rate at age 100. The role of changing cohort mortality is more varied, with different countries experiencing improvements or declines. We also find evidence of recent changes in the pace of mortality declines in some developed countries, with a number of countries showing a slower pace of progress in reducing mortality at the older ages in recent years. These findings highlight the need to closely monitor the underlying reasons for the changes in old age mortality across populations and time.

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