RESEARCH ARTICLE

Long-term impact of mortality on population age structures

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Abstract

In this study, we tested the hypothesis that mortality has a greater influence than fertility on shaping population age structures in the long run and that recent mortality rates provide a satisfactory initial approximation for describing observed age structures in most empirical cases. In the theoretical part of this article, we elucidate a potential fallacy in the line of reasoning based on simulations and counterfactuals frequently used to attribute population aging to low fertility rates. The alternative view that we propose leads us to hypothesize that age structures conform, albeit not exclusively, to a standard derived from survival conditions: the age structure of a stationary population within a given period. We tested this hypothesis on all countries, using the data from the United Nations database (1951 – 2021) and specifically on 10 European countries using the data from the Human Mortality Database (1860 – 2019). The empirical results indicate that current survival conditions sufficiently explain a significant portion of the observed age structure across all examined countries and epochs. However, deviations from this underlying, long-term (mortality-driven) path exist, which our approach cannot fully explain. This is where the role of fertility arguably becomes more prominent. Several implications arise from our findings, including the debate on the relative role of fertility and mortality in shaping age structures in the long run, the theoretical meaning and practical use of cross-sectional life tables, and the notion and measure of demographic dividends.

Keywords: Age structure; Aging; Stationary population; Mortality; Fertility; Index of dissimilarity

1. Introduction

This article focuses on the determinants of population age structures and their evolution, with special regard to population aging. In this field, there is a significant divide between expert opinions, as shown in the excerpt below:

> "Why are populations of rich countries so much older today than they were a century or two ago?... Is the main driver falling mortality and lengthening life, or is it falling birth rates and slowing population growth? Common sense suggests that longer life is responsible for population aging, but decades ago, the work of demographers such as Coale (1956; 1957) and Keyfitz (1975) persuaded us that, in fact, fertility decline was more important. More recently, a new wave of demographic analysis suggests that mortality decline is the main demographic source of continuing population

aging. Here we... consider this possibility, but reject it." (Lee & Zhou, 2017, p.285-287)

Ignoring migration, which is indeed a minor force in this case, population aging may depend primarily on low fertility or low mortality. To assess which is the case, two main types of analysis have been proposed in the literature: (i) simulations/counterfactuals and (ii) empirical (decomposition) analysis. Simulations and counterfactuals, introduced by Coale in 1956 and subsequently adopted by various scholars such as Bengtsson & Scott (2005; 2010), remain a valid, possibly even the best approach to the topic (Lee & Zhou, 2017).

Simulations are typically done in four steps: (i) A population of the past is selected as a starting point (e.g., Sweden in 1860); (ii) one of its two demographic "behaviors" (e.g., fertility) is artificially kept constant, while the other (mortality) is, also artificially, forced to follow its observed historical path; (iii) after some time, three age structures are compared: the two observed ones, at the start and the end of the simulation period, and the hypothetical final one, obtained through simulation; and (iv) based on the distance between these age structures, conclusions are drawn on the relative structural impact of the two processes, fertility and mortality. The conclusion invariably drawn is that "equivalent changes" in fertility and mortality (equivalent in terms of the resulting growth rate, for instance) do not affect age structures in the same way: the former weighs considerably more than the latter. While this line of reasoning is correct to answer questions of the type "if … then …", it does not necessarily lead to valid conclusions when it comes to interpreting reality because it assumes that the conditions grouped in the premise (the "if") may in fact materialize, which may be questionable (e.g., Fernandes *et al.*, 2023; Murphy, 2017; 2021). In addition, the outcomes of counterfactuals and simulations depend heavily on the initial conditions, that is, on the starting date, which is arbitrary (Murphy, 2017).

One alternative to simulations is the decomposition analysis launched by Preston *et al.* (1989) and later applied by several other scholars (e.g., Caselli & Vallin, 1990; Fernandes *et al.*, 2023; Murphy, 2017; Preston & Stokes, 2012). In more recent studies, the typical steps are as follows: (i) selecting a synthetic indicator of the age structure, often the average age, A_t; (ii) observing its changes over time alongside fertility, mortality, and migration indicators (birth, death, and mortality rates, respectively); and (iii) evaluating factors (fertility, mortality, or migration) with the greatest influence on the variation of A_t. The typical conclusion of these studies is nuanced (Fernandes *et al.*, 2023): the influence of declining fertility was stronger in the past but lesser in recent times, when the role of mortality

has started to emerge, occasionally becoming prevalent, especially where the survival rate is high (Murphy, 2017; Preston *et al.*, 1989; Preston & Stokes, 2012). In all cases, migration was consistently found to be irrelevant.

We join the debate on the determinants of age structures advancing the hypothesis that survival is the main driving force at play, not just in recent times or developed countries, and that recent survival suffices to "explain" most of the dependent variable, the observed age distribution, at any point in time. To test our hypothesis, we compare two age structures, the observed and the "standard" one, the latter being the age structure of the stationary population associated with recent survival conditions. The comparison is conducted systematically for all the countries and periods for which reliable data are available. In Section 1.1, we outline our hypotheses in detail and the indicators used to corroborate them. In Section 2, we specify our sources and describe how we treated the data therein. In Section 3, we present our results, beginning with the case of China, considering all world countries over a relatively short period (1951 – 2021), and subsequently, we focus on a small group of countries with long time series data dating back to 1860. Section 4 discusses the theoretical and practical implications of our findings. Section 5 is devoted to the conclusions that can be derived from this study.

1.1. Hypothesis and indicators

Our hypothesis is that mortality (its level, not its variation) is the prevailing force that shapes population age structures. This hypothesis derives from the classical interpretation of the demographic transition, according to which the old demographic equilibrium (*ancien régime*), characterized by high birth and death rates, crumbled under the pressure of declining mortality, a process that started towards the end of the 18th century in Europe (Davis, 1963; Dyson, 2010; Kirk, 1996). In this interpretation, mortality is the leading force in the complex interplay of demographic variables; everything else adapts more or less rapidly to the constraints imposed by changing survival conditions. If this is true, mortality should also "explain" the age structure.

To test this expectation, (i) we ignore fertility and migration; (ii) we focus exclusively on mortality (or better, on its complement, survival, and in particular on the years of life lived, or L_x series, of a life table); (iii) we further restrict our attention to *recent* survival (i.e., we consider only a life table calculated either in the same year *t*, in which the population age structure is observed or in a preceding year, as close to *t* as possible); and (iv) we measure what share of the observed age structure

(P_x – population by age) can be "explained" using only the L_x series. A close correspondence between reality and model predictions (i.e., a high share of the population correctly classified by age, based only on a recent life table) is, in our interpretation, consistent with our claim that mortality is the most relevant force at play in shaping age structures.

To develop our approach, we introduce some notations. We denote vectors using bold font and define $\mathbf{P}_t = P_{x,t}$ and $\mathbf{L}_t = L_{x,t}$, as the population and years of life lived at age x at time t (where $\mathbf{L}_t$, signifies the period ending in year t). The $\mathbf{L}_t$ series, which depends exclusively on the current survival (or mortality) conditions, can also be interpreted as the stationary population associated with the life table of period t. Both $\mathbf{P}_t$ and $\mathbf{L}_t$ encompass a dimensional element that is to be eliminated, focusing exclusively on structures. This can be achieved by dividing both series by their corresponding totals (Equation I):

$$c_t = c_{x,t} = \frac{P_{x,t}}{\sum_x P_{x,t}} \quad \text{and} \quad c_t^* = c_{x,t}^* = \frac{L_{x,t}}{\sum_x L_{x,t}} \qquad (I)$$

where the asterisk denotes the stationary case, which we interpret as the standard of reference in the remainder of this article. Both c_t and c_t^* represent age structures at time t $\left(\sum c_x = \sum c_x^* = 1 \right)$, corresponding to the observed and stationary population, respectively.

As per the weak ergodicity theorem (Lopez, 1961), in all populations, the age structure that can be observed at instant t, denoted as $\mathbf{c}_t$, depends on a very long history of survival ($c_t^*, c_{t-1}^*, \ldots$), fertility (F_t, $F_{t-1}, \ldots$), and migration (M_t, $M_{t-1}, \ldots$) from periods ending in t, t-1,…

$$c_t = f(c_t^*, F_t, M_t; c_{t-1}^* F_{t-1}, M_{t-1}; \ldots) \qquad (II)$$

with recent years weighing more than remote ones. In this article, we argue that mortality is the main force at play in the long run. To prove our assertion, we simplify Equation II considerably, proposing Equation III:

$$c_t \approx c_t^* \qquad (III)$$

The equation implies that by ignoring fertility, migration, and also past mortality; we can achieve a fairly good approximation of reality.

Age structures are multidimensional, making comparisons difficult, especially over time, which can be considered an additional dimension of the problem. We circumvent this difficulty by transforming both age structures, c_t and c_t^*, into one-dimensional indicators, such as the old-age dependency index (OADI) (Equation IV):

$$OADI = \frac{P_{65+}}{P_{15-64}}; \; OADI^* = \frac{L_{65+}}{L_{15-64}} \qquad (IV)$$

or the average age of the population, A (Equation V):

$$A = \sum x c_x; A^* = \sum x c_x^* \qquad (V)$$

In both cases, the purpose is to compare the evolution of the asterisked indicator (which follows our hypothesis of Equation III and is assumed to be the driving force) with that of the corresponding non-asterisked empirically observed indicator. In practice, given the consistent behavior of these indicators (along with others not shown here), as discussed in Section 3.1, the focus will only be on one of them, the average age (A).

If our hypothesis holds, i.e., if Equation III is a reasonable approximation of the more complex reality represented by Equation II, what we expect to find with these indicators is exemplified in Figure 1. Figure 1A predicts that the evolution of the two indicators (same indicator but calculated separately on the stationary and the observed population) will be approximately the same, i.e., that their time paths will remain relatively close to each other. Figure 1B conveys the same message, but now time is implicit in the succession of observations (from left to right, denoting improved survival), and each point is expected to lie not far from the bisector, representing a theoretical case where the two indicators, standard and observed, possess identical values.

Comparing the standard and the observed population in this way has one disadvantage: it is difficult to evaluate the degree of approximation introduced by our hypothesis (Equation III) because there is no conventionally accepted "confidence interval" within which the distance between the two indicators should normally fall. Another minor drawback is the risk of "compensation": two age distributions may occasionally result in similar synthetic indicators (e.g., almost the same average age) even if the original distributions differ. To circumvent both shortcomings, we computed the index of the dissimilarity, ID (Equation VI), which provides the proportion of units of either distribution that should be moved to a different age groups to make the two distributions identical.

$$ID = \frac{1}{2} \sum_x \left| c_x - c_x^* \right| \qquad (VI)$$

In our case, without loss of generality, we assume that the c_t^* series, derived from the stationary age structure, acts as a standard and that only the units in $\mathbf{c}_t$ can and must be relocated, so that, ultimately, $c_t = c_t^*$. ID ranges from 0,
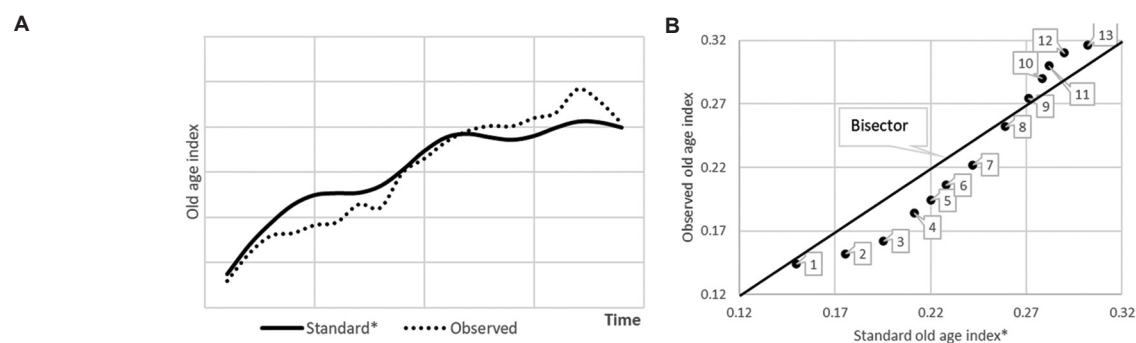
A

B

Figure 1. (A and B) Illustrative example of the evolution of a structural indicator (e.g., an old age index) calculated on the standard* and on the observed population in the same periode.

Notes: The numerical values in Figure 1B have the only purpose of highlighting that as time passes (from the first to the last observation, a total of 13 of them), the indicator evolves, e.g., because of population aging. The continuous lines represent the bisector of the figure; all data points would lie on the bisector if the observed age structure coincides with the standard at all times. (*) means a standard indicator is calculated on the L_x series of the life table of the same period.

when the two distributions are identical, to 1, when they never overlap. For instance, if ID = 15%, the compared distributions overlap by 85%, which means that 85% of the units in $\mathbf{c}_t$, are correctly classified into their respective age groups, assuming that $\mathbf{c}_t^*$ is the appropriate standard.

2. Data sources and data organization

We obtained our data from two renowned sources: the Human Mortality Database (HMD), available at https://www.mortality.org/, and the database of the World Population Prospects 2022, accessible at https://population.un.org/wpp/(United Nations, 2022). Both are freely accessible, with a large set of well-controlled data from different countries and epochs. To minimize data-related issues:

(i) For the United Nations (UN) case, the analysis was restricted to relatively large countries (each with a population of at least 1 million people in all the years between 1951 and 2021) to reduce the influence of random variations. We also excluded two countries, Cambodia and North Korea, due to exceptionally high mortality during the wars of 1976 and 1951, respectively. This left us with 131 countries (and, separately analyzed, six regions: Africa, Asia, Europe, Latin America and the Caribbean, Northern America, and Oceania), each observed 15 times at 5-year intervals from 1951 to 2021.

(ii) For the HMD case, the analysis was focused on relatively recent data (post-1860), aiming at countries with the longest possible series: Belgium, Denmark, Finland, France, Italy, Norway, the Netherlands, Spain, Sweden, and Switzerland. This selection strikes a reasonable compromise between data quality (generally very high in the HMD, but somewhat lower for very remote years), length of series, and sample size.

In both cases, we used the two series of data presented above, $\mathbf{P}_t$ and $\mathbf{L}_t$, and transformed them into relative values, $\mathbf{c}_t$ and $\mathbf{c}_t^*$, respectively. Age was consistently grouped into 5-year intervals: x = 0–4; 5–9;…; 95–99; 100+. However, time t was treated slightly differently in the two cases: (i) for UN data, $\mathbf{P}_t$ and $\mathbf{L}_t$ referred to the population of specific years, spaced by 5 years. We selected those ending in 1 and 6 (1951, 1956,…, 2021), resulting in 15 observations for each country or region; (ii) for HMD data, both $\mathbf{P}_t$ and $\mathbf{L}_t$ represented averages over 5-year intervals (e.g., t = 1860–64; 1865–69;…). This provided a total of 32 potential observations for each country, except that not all of them were present at all times (see Section 3.3). We decided to work in 5-year intervals with both datasets, partly to preserve symmetry with age groups and partly because the phenomena that we observe (changes in the age structure) are not sufficiently dynamic to justify an analysis using a single calendar year.

3. Results

3.1. China as an example

To clarify the issue, our approach, and our measures, China was considered as an example. China served as a good candidate owing to its large population and rapid demographic transition, starting in the second half of the 20th century. This was believed to counter our hypothesis because its abrupt fertility decline has greatly affected its age structure in the recent past and to this day. Only for the Chinese case (not for the global analysis of the next sub-sections, referred to as all world countries), we extended our analysis to 2051 using UN projections (medium variant). With a limited margin of uncertainty, this permitted us to better appreciate the long-term consequences of such an accelerated demographic transition.

Figure 2 presents the evolution of two synthetic indicators of age structure: the average age of the Chinese population, *A* (panels on the left), and the OADI (panels on the right). Both indices were calculated twice: first on the observed population (or projected one, for the years 2026 – 2051) and then on the standard (stationary) population of the same period. Both indices are presented twice: as a time series (top panels) and as a scatter diagram (bottom panels). In the latter case, the bisector is drawn; it represents the theoretical case when the two indexes (observed and standard) give the same result.

A few insights can be learned from this example. First, both structural measures convey the same message, and in the following sections, only the average age (A) is utilized. Second, the scatter point representation (bottom panels) saves space, which is useful when the dataset increases (this type of representation is used in the next sections). With the omission of tags (for reasons of space), the time dimension is lost, but it can be imagined as a rightward movement because as time passes, survival conditions improve, and this makes the standard (stationary) population older. Based on our hypothesis, this is the main driving force behind population aging, and this is precisely the third aspect that emerges from the Chinese example: empirical data evolved more or less in accordance with our expectations. In the Chinese case, to be sure, the difference between model predictions and observed data is larger

than in Figure 1, but the general tendency is the same: there is an underlying "normal" value for each chosen indicator (the standard one, with an asterisk). Shocks may, and usually do, hit populations, driving the age structure and its indicators away from their usual shape and levels: be it a war, demographic transition, or economic crisis. In the following years, however, the effects of these shocks tend to be reabsorbed, and little by little, things tend to get back to normal. However, the standard has changed because it is determined by the constantly evolving survival conditions.

The same conclusions emerged from the analysis of the dissimilarity (ID) index. Firstly, it should be noted that it is always low: 23% in the worst year (1976), 16% on average over the past 70 years (1951 – 2021), and likely to be even lower in the future (12%; 2026 – 2051; Figure 3). This means that the share of Chinese who are classified correctly by age (5-year age groups) using the corresponding stationary population (i.e., assuming that current mortality is the only force at play) is about 84% on average and never below 77%, even in the worst year. This means that all other factors combined (previous mortality, fertility, and migration) compete to explain only about 16% of the Chinese age structure on average.

Figure 4 displays the observed and standard (stationary) Chinese age structures in selected years. At all times, the effects of past waves of fertility (high until the 1960s and
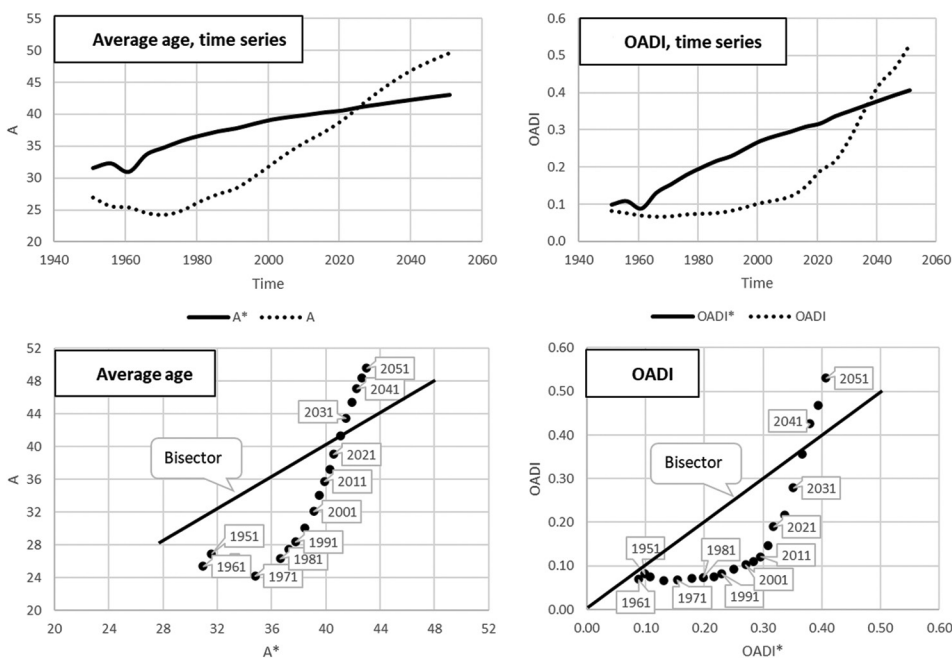

Figure 2. Structural indicators of the observed (or projected) population and the standard (stationary) population (*) of China, 1951 – 2051 (United Nations (2022).

Note: Standard values [*] are calculated for the stationary population. Abbreviations: A: Average age of population (Equation V); OADI: Old-age dependency index (Equation IV).

very low nowadays) are clearly visible. Yet, despite these rather extreme variations, current survival conditions, as expressed by the L_x series, "explain" a large share of the observed age structure, at least 78% in the worst year (1981), and much more in periods of more gradual change.

3.2. Results for all world countries (1951 – 2021)

In this section, not just China but all world countries with at least one million inhabitants were considered. Figure 5 (left panel) reveals the association between the standard average age (A*) of the corresponding stationary population and the observed average age (A). Quadratic interpolation provided an insight into how the relationship has evolved for different values of A*, or, in practice, over time, because higher values of A* correspond to better survival conditions. Most

countries went through their demographic transition in the period under observation (1951 – 2021), and this explains why most of the observed points are under the bisector, which means that populations are younger than they "should" be if mortality were the only force at play. However, the results also suggest that this "unbalanced" phase is temporary: the distance from the bisector increased at first (until A* reaches approximately 36 years, corresponding to a life expectancy [e_0] of approximately 60 years) but tends to decrease over time. The points can be imagined as "moving" rightward (toward better survival conditions), forming a sort of wave that oscillates around the bisector, where A = A*.

The same tendency, with less "noise," emerges in the right panel of Figure 5, displaying world regions. In both cases, the underlying pattern seems to be the same as that observed in China (Figure 2) and is hypothesized in our model (Figure 1). Most of the data points in Figure 5 fall below the bisector, but this is due to the demographic peculiarities of the observation period. As good demographic data are generally available only for the recent past, in most cases after the beginning of the demographic transition, the bulk of the information that we get refers to the "first wave" of the scheme of Figure 1 (right panel), where the data points are below the bisector. In Figure 5 and the following sections, we do not include projections for the future because their validity may be questioned, even when they come from authoritative institutions, and because, in all cases, projections cannot be treated as observations. Had these projected data points been plotted in Figure 5, the resulting scheme would have been even closer to that shown for China (Figure 2, bottom panels), with data points both above and below the bisector.
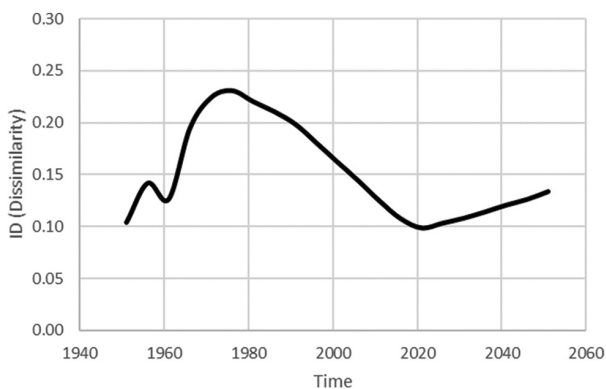

Figure 3. Index of dissimilarity (ID) between the standard (stationary) and the actual age structure (China, 1951 – 2021) (United Nations, 2022). Note: The formula for the ID index is given in Equation VI.
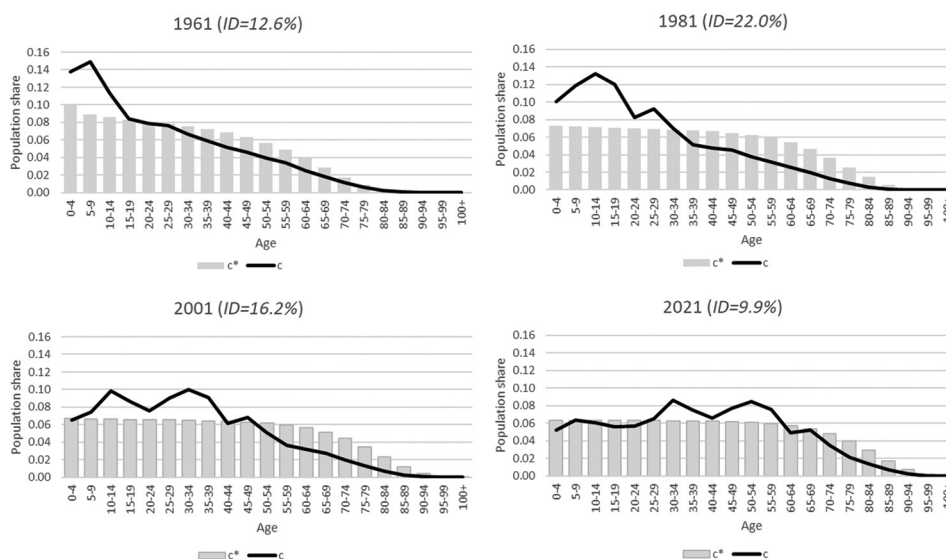

Figure 4. Observed (c) and standard stationary (c*) age structures in China for selected years (United Nations, 2022). Abbreviation: ID: Index of dissimilarity.
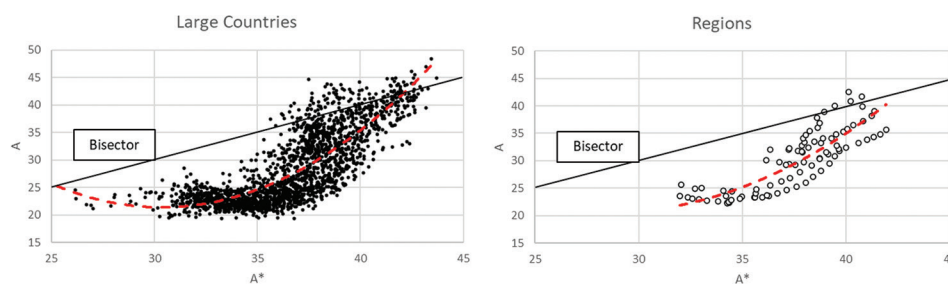
Figure 5. Observed (A) and standard, or stationary (A*) average age, by countries and regions, from 1951 to 2021 (United Nations, 2022).
Notes: There were 131 countries, only those with at least one million inhabitants, excluding Cambodia and North Korea, because of their high mortality during the war years (1967 – 1975 and 1950 – 1953, respectively). There are six regions: Africa, Asia, Europe, Latin America and the Caribbean, Northern America, and Oceania. In both panels, each case was observed 15 times: in 1951, 1956,…, 2021. If our predictions were 100% accurate, the age structure of the observed populations would coincide with that of their standard (the stationary population), and all data points would lie on the bisector. The quadratic interpolation (dotted red line) gives the general tendency of the scatter and suggests that points may indeed be moving in waves around the bisector, as survival conditions improve.

The share of the population that is misallocated (by 5-year age group) using our approach is presented in Figure 6. On average, this share is below 18% and never exceeded 36%. This means that using only information on recent mortality, age structures can be described with a modest margin of error: they are 82% correct on average, and at least 64% correct in the worst case. Similar to previous observations, using regions instead of individual countries reduces random variations and improves the precision of the model estimates: ID declines to 15% on average, with a peak of only 25%. In both cases, the parabolic interpolation suggests that after reaching a peak when e_0 is close to 55/60 years (i.e., in the midst of the demographic transition), ID tends to decline and return to the extremely small values observed before the transition started.

3.3. Results for 10 countries in the HMD

The same results, but with closer adherence to model predictions, emerge with reference to a different period (starting in 1860) and a different set of countries: the developed countries included in the HMD, of which we took the 10 with the longest time series available (Figure 7). As in the case of Figure 5, the initial phase of the demographic transition breaks the (presumed) original equilibrium (i.e., drives the points to the right, far from the bisector); however, once the process matures, the cloud of points tends to converge towards the bisector, where A = A*, as predicted by the model.

The share of misclassified individuals is less than 9% on average and never above 16% (Figure 8). Once again, a quadratic interpolation provides insight into how things evolve over time, suggesting that the worst case for our model is when A* is about 36 years (e_0 is close to 55/60 years), i.e., in the middle of the demographic transition. Even then, however, the explicatory power of

recent mortality (i.e., its capability of predicting the shape of the age distribution) is remarkably high, and only a small fraction of individuals fall into an age group different from that predicted by our model.

4. Discussion

The main result of this paper is that the hypothesis that we set out at the beginning, and in Equation III, that current survival conditions determine a large share of the observed age structures, seems to hold remarkably well. Not surprisingly, the model performs worse in the most turbulent phases of the demographic transition, but even these cases fit well with the general pattern that we sketched in our initial hypothesis. The observed age structures tend to resemble those of their corresponding standard (the stationary population), with occasional shocks, such as the demographic transition, that drive the observed age structure away from its expected shape (the stationary case). However, after the shock is absorbed, the standard shape tends to resurface.

This holds in all the cases that we could investigate with our datasets: The HMD and the UN database, both including several countries in different epochs and conditions. Incidentally, this result is consistent with the dynamic analysis that we conducted elsewhere on the same topic, proving that the observed age structures "move" over time following the evolution of the L_x series (De Santis & Salinari, 2023). It is worth noting that our analysis included only the observed or estimated data up to 2021. If we had included population forecasts, as demonstrated by Fernandes *et al.* (2023), for instance, using UN (2022) demographic projections until the year 2100, the results, although not reported here, would have been even better, with a closer correspondence between (forecasted) reality and (forecasted) stationary populations (the L_x series of predicted life tables).
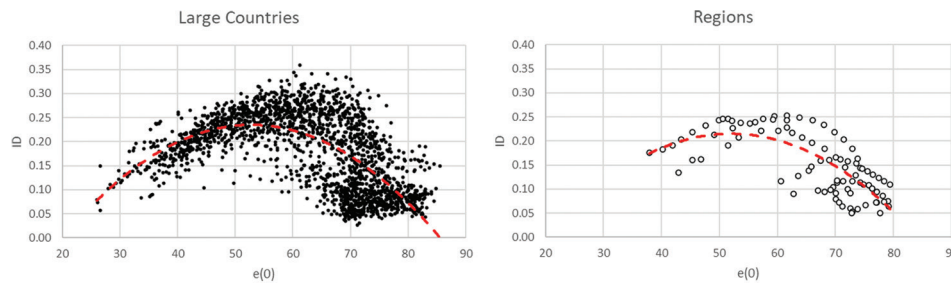
Figure 6. Index of dissimilarity (ID) by average length of life (e_0) across various countries and regions, from 1951 to 2021 (United Nations, 2022).
Notes: There are 131 countries that only include those with at least 1 million inhabitants, excluding Cambodia and North Korea because of their high mortality during the war years (1967 – 1975 and 1950 – 1953, respectively). Regions are six: Africa, Asia, Europe, Latin America and the Caribbean, Northern America, and Oceania. In both panels, each case is observed 15 times, corresponding to the years 1951, 1956,…, 2021. The quadratic interpolation (dotted red line) provides the general tendency of the scatter and suggests that data points may indeed tend to return to their initial low values (ID close to zero) after the distortions in the age structure caused by the demographic transition have been absorbed.
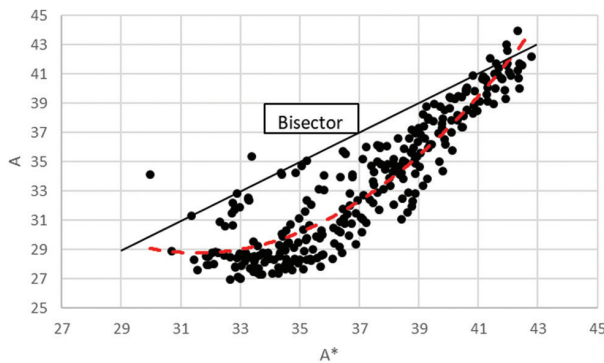

Figure 7. Observed (A) and standard, or stationary (A*) average age, in selected developed countries (circa 1860 to 2019) (Human Mortality Database).
Notes: The countries (with the chosen starting year) are Belgium (1920), Denmark (1860), Finland (1880), France (1860), Italy (1875), the Netherlands (1860), Norway (1860), Spain (1910), Sweden (1860), and Switzerland (1880). If our predictions were 100% accurate, the age structure of the observed populations would coincide with that of their standard (the stationary population), and all dots would lie on the bisector. The quadratic interpolation (dotted red line) gives the general tendency of the scatter, and suggests that points may indeed be moving in waves around the bisector, as survival conditions improve.

Figure 8. Index of dissimilarity (ID) by average length of life (e_0) in selected developed countries (circa 1860 to 2019) (Human Mortality Database).
Notes: Countries (with the starting year chosen for this analysis, or earliest available) are: Belgium (1920), Denmark (1860), Finland (1880), France (1860), Italy (1875), the Netherlands (1860), Norway 1860), Spain (1910), Sweden (1860), and Switzerland (1880). The quadratic interpolation (dotted red line) gives the general tendency of the scatter, and suggests that data points may indeed tend to get back to their initial low values (ID close to zero) after the shocks caused by the demographic transition have been absorbed.

After all, the reason we can observe individuals living up to 40 years, for instance (which is not the case for mosquitoes), but not to the age of 1000 (as it happens with sequoias), is that human mortality has certain characteristics, which translate into and shape population age structures. These mortality characteristics do not remain constant over time, but their evolution is typically gradual, which explains why even the use of just one piece of mortality information – a recent cross-sectional life table – is generally sufficient to provide a good approximation of reality. The incipient second demographic transition will probably trigger a new cycle of declining and aging populations. These phases cause waves in the age structures
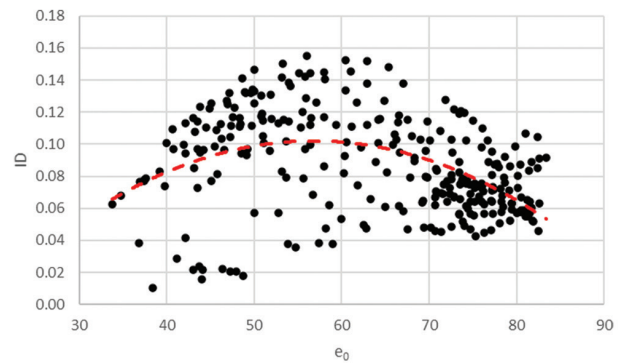
of the affected countries. Our prediction is that the cycle will repeat itself: standard and observed age structures will temporarily diverge, but the former will still be capable of "explaining" a large share of the latter, and the latter will eventually converge on the former after some years.

Mortality is slow and steady, and this is how it eventually "wins the race" (gradually shaping the age structure). It erodes its base (a birth cohort) gradually but consistently over several years, never stopping, and always in the same direction, like a water drop gradually hollowing a stone. Other forces, such as fertility and migration, are frequently stronger, more variable, and more clearly visible in the short run, but are less consistent in strength and direction; therefore, their structural effects tend to diminish over

time. For this reason, our model is not very effective in predicting short-term changes in age structures, and analyses of the determinants of such changes (and notably those on the causes of population aging) may result in the opposite conclusion that fertility matters more than mortality. In the simplest terms, these analyses involve regressions of the following type (Equation VII):

$$\Delta c = f\left(\Delta c^{*}, \Delta F, \Delta M, \varepsilon\right) \qquad \text{(VII)}$$

where the deltas indicate variations, and ε is the error term. In Equation VII, a variation in the age structure Δ**c** is thought to be caused by variations in survival, fertility, and migration (Δ**c***, Δ**F**, and Δ**M**, respectively), and a decomposition analysis of some sort will attempt to assess the relative role of each of these forces. Short-term variations in survival, however, are generally modest and may even be non-existent; in Equation VII, this may well result in a lesser role estimated for survival in determining population aging. However, if our hypothesis is correct, this is nonetheless consistent with the predominant role of survival in shaping population age structures in the long run.

This should help explain why several demographers, following Coale (1956; 1957), tend to think that it is mainly fertility that causes population aging (Bengtsson & Scott, 2005; 2010; Keyfits, 1975; Lee & Zhou, 2017), although exceptions for developed countries have been frequently noted (Fernandes *et al.*, 2023; Murphy, 2017; Preston *et al.*, 1989; Preston & Stokes, 2012). As mentioned, our claim is that mortality is the main driver of the shape of age pyramids in the long term, although its action is slow and may remain in the background, especially in times of rapid change, such as demographic transition.

Our findings may influence the debate regarding the advantages and disadvantages of cross-sectional life tables. Some demographers (e.g., Borgan & Keilman (2019) and Keilman (2019) are skeptical about their theoretical and practical utility and argue that they are likely to convey biased results in periods of mortality change (i.e., almost always). Our study indicates that they are useful both in theory and practice.

In the same spirit, our findings may prompt demographers to reconsider the notion and measurement of "demographic bonus" or "dividend." Until now, to the best of our knowledge, the "window of opportunity" has been defined in terms of improvement over the recent past. For example, Lee & Mason (2010) call it a "phase of … three to five decades … [when] support ratios rise well above their pre-transition levels", while Crombach & Smits (2022) describe it as "a period in which the working-

age population is large and the dependent population … is small." Our proposition is that a comparison should be made with the standard (stationary) age structure. In this sense, a demographic dividend (or the "first demographic dividend," in Lee and Mason's words) can be considered present as long as the observed age structure is "better" than that of the corresponding stationary population. In Figure 2, for instance, the old age dependency index of China (OADI, right panels) started to worsen (i.e., to increase) since the 1980s and is currently undergoing rapid deterioration. However, until approximately 2036, the observed OADI in China will be lower than its standard equivalent OADI*. In our interpretation, this means that until then, China will still benefit from a demographic bonus, although this will become a bit smaller every year.

The question may be asked in more general terms: When looking at the age structure of a population, what should observers expect to find and against what implicit standard do they asses the current situation? Our answer is that (excluding exceptional cases, such as an ongoing war), the best possible expectation should be based on the stationary age structure of the period. All relevant aspects of the observed age structure (peaks and troughs, larger or smaller bases, etc.) can be better appreciated compared to this standard.

Our findings clarify some of the issues behind the frequently re-surfacing question, "Are immigrants substitutes for births?" (United Nations, 2000). Those who reject this notion typically take some observed structural index (e.g., the OADI or its reciprocal, the support ratio) and simulate the number of immigrants needed to preserve that value forever—frequently, but not surprisingly, arriving at implausibly high values (e.g., Coleman [2008]). In light of our findings, this question appears to be misleading. The data points outside the bisector (e.g., Figure 5), suggest that the demographic structure is biased (i.e., far from its standard) and that this situation will not last: things will eventually get back to "normal." Only standard-consistent structural targets can be pursued in the long term, and, with this more modest target in mind, simulations (not shown here) indicate that immigrants can be quantitative substitutes for births unless fertility drops to extremely low levels.

Finally, it is noteworthy that due to mortality changes, all target values move over time (notably the OADI of Figure 2 [right panel]), unless improvements in survival are neutralized by offsetting adjustments in threshold ages, such as higher retirement ages. In other words, policy measures of this type, while adopted under the pressure of circumstances (budget imbalances in pension systems) and wearily defended by reluctant policymakers, may find theoretical support in our approach, which is consistent

with the evolution of the underlying standard (stationary) age structure.

The approach we suggest here is extremely simple: it can be regarded as the static version of the dynamic and considerably more complex model we recently proposed to analyze the combined evolution of the two age structures, the stationary and the observed ones (De Santis & Salinari, 2023). Precisely because of its simplicity, our model has its limitations, and, in particular, it cannot adequately describe all empirical cases (all countries in all years). What it indicates is the likely direction of future changes: An empirical age structure that is far from its stationary counterpart will likely tend to get closer to it in the future. The force of attraction exerted by the stationary age structure on the observed one is small but persistent; in the short run, other forces, and especially fertility variations, may affect the observed age structure in a much stronger way (which explains occasional cases of poor fit with its stationary counterpart). In the long run, the prevailing role of survival emerges.

5. Conclusion

Age structures evolve over time, under the influence of fertility, mortality, and migration. Demographers have long debated the relative role played by each of these forces, focusing in particular on the variations of the age structure or any of its possible synthetic indicators (average age, OADI, etc.). The conclusion has frequently been that fertility is the main driving force of change, although with exceptions among mature populations, where mortality matters more. In this paper, we focus on the shape of the age structure and we show how close it is to that of the corresponding stationary population; therefore, we conclude that mortality (or, better yet, its complement: survival) plays a significant role in shaping age structures.

We reached this conclusion by combining data from several countries over several periods. Although there are variations and exceptions, the general scheme seems to hold: observed age structures tend to follow the path traced by their standards, that is, the corresponding stationary populations.

This finding has both theoretical and practical implications. Theoretically, this study contributes to the debate on the relative importance of the forces that drive population aging. Our interpretation is that, in the long run, due to its relatively modest but consistent and persistent action, mortality matters more than anything else, and that recent mortality is generally enough to "explain" a large fraction of the observed age distribution of any population at any time.

Regarding practical implications, our findings may be relevant, especially in the pension debate. Most pension arrangements adjust their parameters based on recent life tables and survival conditions. Our findings suggest that this practice is correct and should be more widespread.

Conflict of interest

The authors declare no conflict of interest.

Author contribution

Conceptualization: All authors
Formal analysis: All authors
Investigation: All authors
Methodology: All authors
Writing – original draft: Gustavo De Santis
Writing – review & editing: All authors

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Availability of data

The data used in this study are accessible to the public.

Further disclosure

Some findings of this study were presented at a congress (Population Days, AISP [Associazione Italiana per gli Studi di Popolazione] held in Rome, Italy, 1-3 January 2023.

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