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In a Stationary Population, the Average Lifespan of the Living Is a Length-biased Life Expectancy

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In a stationary population, the average lifespan of the living is a length-biased life expectancy

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ABSTRACT:
What is the average lifespan in a stationary population viewed at a single moment in time? Even though periods and cohorts are identical in a stationary population, we show that the answer is not life expectancy, but a length-biased version of life expectancy. That is, the distribution of lifespans of the people alive at a single moment is a self-weighted distribution of cohort lifespans, such that longer lifespans have proportionally greater representation. This result connects stationary population lifespan measures to a well-developed body of statistical results; provides new intuition for established demographic results; generates new insights into the relationship between periods, cohorts, and prevalent cohorts; and offers a framework for thinking about mortality selection more broadly than the concept of demographic frailty.

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How long, on average, will the people who are currently alive live? It turns out that, in a stationary population, this "average lifespan of the living" (ALL) can be interpreted as a length-biased life expectancy—meaning, a transformation of life expectancy in which lifespans are re-weighted by their own values. We will show that this has several important implications, such as that period life expectancy is always less than the average lifespan of the people alive in that period, and provides intuition for a number of previous results about stationary populations.

Length bias, also known as size bias or a self-weighted distribution, occurs when units are observed in proportion to their size (e.g., Correa and Wolfson 1999, Patil 2005, Lann and Falk 2005). Demographers are likely to be most familiar with length-biased sampling in the context of Preston's (1976) analysis of the family sizes of children vs. women. A survey that asks gestational parents how many children they have will receive one report per parent, while a survey that asks children how many children are in their family will receive one report from each one-child family, but six reports from each six-child family, and so forth (Bytheway 1974, Preston 1976, Patil and Rao 1978, Ruggles 2012, Song and Mare 2014). Similarly, a length-biased—or self-weighted—lifespan distribution is a distribution of lifespans that is weighted by lifespan, such that the longer-lived are more likely to be observed, in proportion to their longer lifespans. We will show that, in a stationary population, the average lifespan of the living (ALL) is such a length-biased lifespan.

1. Length-Biased Life Expectancy: Proof and Intuition

a. Length Bias

Consider a non-negative real-valued random variable $Y \geq 0$—lifespans or family sizes, for example—with probability density function $f(y)$ and mean $E[Y]$. The length-biased distribution arising from $f(y)$ has the density:

$$f_{lb}(y) = \frac{yf(y)}{E[Y]} \tag{1}$$

and the mean of this length-biased distribution is:

$$E_{lb}[Y] = \frac{E[Y^2]}{E[Y]}. \tag{2}$$

This length-biased mean can be re-expressed, by using the definition of the variance $\sigma_Y^2 = E[Y^2] - E[Y]^2$, as a function of the coefficient of variation, $cv_Y^2 = \frac{\sigma_Y^2}{E[Y]^2}$:

$$\begin{aligned} E_{lb}[Y] &= \frac{\sigma_Y^2 + E[Y]}{E[Y]} \\ &= 1 + \frac{\sigma_Y^2}{E[Y]} \\ &= E[Y](1 + cv_Y^2) \end{aligned} \tag{3}$$

These equations describing length-biased samples are well-known in the sampling statistics literatures (e.g., Cochran 1977: 249-255, deCarvalho 2016).

b. Length-Biased Life Expectancy

Consider a stationary population—one with constant birth and death rates, zero net migration, and zero population growth—in which the number of survivors at any age x is $l(x)$, such that the cohort survivorship is $l(x)/l(0)$ and the population at any moment in time has size $\int_0^\omega l(x)$ where ω is the oldest attainable age. Let the number of deaths at each age be denoted $d(x)$, so that the density of ages at death is given by $f(x) = d(x)/l(0)$. The average lifespan (life expectancy at birth) of this cohort, $e(0)$, is:

$$e(0) = \frac{\int_0^\omega l(x)dx}{l(0)} = \frac{\int_0^\omega xd(x)dx}{\int_0^\omega d(x)\,dx} \tag{4}$$

In this population, the lifespan distribution of the living, $f_l(x)$, is a length-biased transformation of the lifespan distribution of each cohort (or period) $f(x)$:

$$\begin{aligned} f_l(x) &= \frac{xd(x)}{\int_0^\omega l(x)\,dx} \\ &= \frac{xf(x)/l(0)}{e(0)/l(0)} \\ &= \frac{xf(x)}{E[X]} \end{aligned} \tag{5}$$

The first line of Eq. (5) reflects that, among the people currently alive, the number of

people who will die at exact age x is the product of the per-cohort deaths at age x, $d(x)$, and the x cohorts that have future deaths at age x; and the density that will die at exact age x is the ratio of those $xd(x)$ deaths to the size of the full living population, which is $\int_0^\omega l(x)$. Since Eq. (5) instantiates Eq. (1), Eq. (5) establishes that the distribution of lifespans in the living population is a length-biased sample of the lifespans in the stationary population's cohort or period.

Similarly, Eq. (5), along with Eq. (2) and (3), implies that the average lifespan of the living is:

$$\begin{aligned} ALL &= \frac{\int_0^\omega x^2 d(x)dx}{\int_0^\omega xd(x)dx} \\ &= \frac{E_{f(x)}[x^2]}{E_{f(x)}[x]} \\ &= e(0) + \frac{\sigma_x^2}{e(0)} \end{aligned} \tag{6}$$

An alternative derivation of these expressions for the ALL, not relying on Eq. (2) and (3) but derived directly from the life table functions, is given in Appendix 1.

c. Intuition for the Result

The results in Eq. 5 and 6 connect lifespan demography to well-developed areas of statistics and provides intuition for other results about stationary populations. The intuition for this result is simple. By definition, the living population dies at an age older than its current age. This has the consequence that older ages of death are disproportionately likely among the living population, compared to its original birth cohorts. This selective sample of lifespans is illustrated in Figure 1, which shows a Lexis diagram in which the living population is defined by a vertical line and their future deaths are only those deaths included in the triangle on the right of this line. The two horizontal bands reflect two example ages at death, illustrating that older ages at death will be experienced by more currently-living cohorts than younger ages at death will. This concordance between age at death and the number of cohorts that can still reach that age at death produces length bias.

A practical application of this result is that, if age-specific death rates are

unchanging over time, the lifespan of the population alive in a period will necessarily be greater than the period life expectancy.[1] A conceptual implication—recalling the familiar family size example—is that lifespans cluster time the way that families cluster children.

Length bias is not the only perspective in which to view these results. For example, an alternative proof begins from a decomposition, provided by Cohen (2015), of life expectancy at birth into survivorship to any prior age and life expectancy at that age. We present this alternative proof in Appendix 2. In the remainder of this article, we use the length-biased interpretation of the ALL as a length-biased sample to develop new insights and connect these results to other concepts in demography and other fields.

2. Empirical illustration: Life expectancy, variation in the age at death, and the ALL

The expression for the ALL given in the last line of Eq. 6 generates useful insights into the relationship between the ALL, life expectancy, and variance in the age at death. It implies that the ALL is always greater than life expectancy (except in the special case that everyone dies at the same age, in which case the ALL equals life expectancy). More generally, Eq. 6 shows that, holding life expectancy fixed, a population with more variable ages at death will have an older ALL that is more divergent from life expectancy. Conversely, holding the variation in the ages at death fixed, a population with a larger life expectancy will have a smaller ALL that is more similar to life expectancy.

The relationships between life expectancy, variation in the age at death, and the ALL are illustrated by calculating the ALL implied by model life tables.[2] As a simple illustration, Table 1 summarizes four such life tables, which form two pairs. The first pair are two life tables with identical life expectancy (60 years) but divergent variance (represented in the table as the standard deviation, for ease of interpretation). The one with the smaller variance (the UN's male Far East Asian life table) has an ALL that is 8 years above its life expectancy, while the one with the larger variance (the Coale-

[1] This implication assumes that everybody does not die at the same age, as we explain below.

[2] UN Extended Model Life Tables were downloaded from https://www.un.org/en/development/desa/population/publications/mortality/model-life-tables.asp on October 22, 2020. Specifically, we used the complete (non-abridged) life tables in one-year age increments.

Demeny female South life table) has an ALL that is more than 13 years above its life expectancy. The second pair are two life tables with nearly-identical variance but radically different life expectancy. In this case, the life table with the larger life expectancy (the UN's female Latin American life table at life expectancy 67) generates an ALL that is less than 10 years above life expectancy, while the low-lifespan table (Coale and Demeny's male North life table at life expectancy 21) generates an ALL that is more than 30 years above life expectancy. In this last population, the combination of relatively large variance and very small life expectancy generate an extreme discrepancy between the lifespan of the population alive in cross-section and the lifespan of a cohort.

Figure 2 illustrates how this divergence between life expectancy and the ALL occurs by showing the age at death distribution for the living population (hollow bars) and for birth cohorts (filled bars) implied by these four model life tables. As is well-known, deaths at young ages have an outsized effect on life expectancy. Figure 2 shows that these deaths are dramatically underrepresented in the living population's lifespans. For example, someone who dies at 1 month old would need to appear in the living population at age less than 1 month, and the population contains few people in this narrow age band. More generally, the distribution of ages at death is systematically pulled upward among the living, compared to the cohorts from which they spring.

Figure 3 takes a more global view of these relationships, across the full set of UN Extended Model Life Tables. (The life tables marked in gold *X*s are the four example life tables just discussed.) Panels A and B show that, at low levels of life expectancy, the ALL diverges widely from life expectancy, while at high levels, it diverges very little. This relationship between the ALL and life expectancy is not only driven by life expectancy, but also by life expectancy's historical relationship with variance in the age at death. Panel C illustrates that relationship for these model life tables. This historical relationship between life expectancy and variation in the age at death can be roughly periodized into three phases. First, the earliest increases in life expectancy (away from the levels experienced by early human societies) may also have increased variation in the age at death, relative to a context where most deaths were in childhood. Second, in the past few centuries, large increases in life expectancy were driven by declining mortality at young ages when such deaths were less common than in early human societies, and these changes tended to substantially reduce variation in the age at death.

Third, in high-longevity populations, more recent increases in longevity are concentrated at older ages and may tend to reduce variation in the age at death only a small amount, and sometimes increase it (Engelman et. al. 2010, Tuljapurkar 2010). Since the ALL will diverge from life expectancy the most when the variance is high and life expectancy is low (Eq 6), these relationships help to explain why, as Panels A and B showed, the ALL is maximally divergent from life expectancy when life expectancy is roughly in the age range 20-40, and converges rapidly toward life expectancy once life expectancy reaches roughly age 50. Panel D shows the resulting relationship between the variance in the age at death and the ALL. Even though, fixing life expectancy, a larger variance means a larger divergence of the ALL from life expectancy, the historical relationship between life expectancy and variance complicates the overall relationship between variance and the ALL. As life expectancy increases across these model life tables, the ALL travels along the arcs shown in Panel D, from the uppermost values (representing low life expectancy contexts) then out to the right, then down toward the bottom left.

A few examples help to calibrate expectations about how much longer the living population will live, compared to birth cohorts. As Figure 3 implies, even in stationary populations, this additional lifespan can differ dramatically across populations. In a comprehensive review of hunter-gatherer societies, Gurven and Kaplan (2007) suggest that life expectancy at birth in such societies ranges from roughly 21-37; the model life tables in that range of life expectancy estimate average lifespans of the living that are 18-35 years older than life expectancy. On the other hand, for low-mortality populations, the divergence is much smaller. Recent U.S. life expectancy values are 76 for men and 81 for women. Model life tables at those values generate ALLs that are, respectively, 2.9-5.7 years and 2.1-4.3 years older than life expectancy. For hypothetical populations with life expectancy of 95 or older, in these models, the ALL diverges from life expectancy by less than one year.

3. The ALL, the average age, and the average remaining life

The last line of Eq. 6, which represented the ALL as a function of life expectancy and the variance in the cohort age at death, also provides the core intuition for a well-known, but somewhat inscrutable, formula for the mean age of a stationary population, denoted

A. The formula, given by Ryder (1975: 8) and Preston et al. (2001: 112), is:

$$A = \frac{e(0) + \frac{\sigma_X^2}{e(0)}}{2} \tag{7}$$

This formula follows from two properties of stationary populations. One is the property shown here: that the average lifespan of their living members is a length-biased life expectancy. The second distinctive feature of stationary populations is that the distribution of lifetimes lived so far—that is, age—equals the distribution of lifetimes still to come—that is, remaining life expectancy (Müller et al. 2004, 2007; Vaupel 2009; Villavicencio and Riffe 2016).[3] This property can be considered a form of time symmetry in stationary populations, implying that in a stationary population observed at a specific moment in time individuals are equally likely to be observed at any point in their lives, and on average are observed halfway through their lives (Kim and Aron 1989, Goldstein 2009). Thus, the average age of the population and the average remaining lifespan are each half of the ALL. In combination, these two properties imply that the average age and average remaining lifespan in a stationary population each equal one half of the length-biased life expectancy, generating Eq. 7.[4]

This perspective similarly provides intuition for a proof given by Finkelstein (2008: 268) that a stationary population with a larger life expectancy than a second stationary population need not also have a larger average remaining lifespan: thus, it is possible for $e_1(0) > e_2(0)$ while $A_1 < A_2$ (where A, which we used to denote mean age, also

[3] Specifically, Eq. (7) draws on the fact that the average age in a stationary population equals the average expected lifespan. This result was shown in a demographic context by Kim and Aron (1989) and Goldstein (2009), with elaborated historical context in Goldstein (2012). It was broadened to the more general claim about stationary populations referenced here—that the distribution of ages equals the distribution of past lifespans—in Vaupel (2009) and is generally considered to have been independently discovered in work by Brouard (1989) [which the authors are unable to read in its original French] and Carey (Müller et al. 2004, 2007) and subsequently (Villavicencio and Riffe 2016) dubbed the Carey-Brouard inequality. An alternative proof of the broader claim is presented in Rao and Carey (2015) and amended and corrected in Villavicencio and Riffe (2016). Finally, exploration of these time symmetries has been extended to other measures in stationary populations (Riffe 2015) and modified for stable populations (Vaupel and Villavicencio 2018).

[4] Ryder (1975: 8-11) discusses implications of Eq. (7) for the relationship between life expectancy, the coefficient in the variation in the age at death, and the mean age of a stationary population. His discussion is an intellectual forerunner to our discussion in Section 3, above.

equals mean remaining lifespan). Finkelstein's clever proof, which involves making a succession of changes to a survival curve, does not (to our mind) provide a clear intuition as to the mechanism by which a cohort with a larger life expectancy can have a smaller remaining lifespan. Given that average remaining lifespan equals average age in a stationary population, Eq. 6 and Eq. 7 clarify that this will be true if the variation in the age at death in the second cohort is large enough to offset its smaller life expectancy. In that circumstance (and only that circumstance), a randomly-selected member of this second cohort at a single moment in time will have a longer lifespan than a randomly-selected member of the reference cohort, even though a randomly-selected member at birth will have a shorter lifespan.

4. Other Implications: Cohorts, periods, and prevalent cohorts

a. Cohort Questions and Period Data

In epidemiology, the upper triangle in Figure 1—representing the deaths that contribute to the lifespan of the living—is called a *prevalent cohort* (e.g., Törner et al. 2011). The results illustrated here offer new perspective on the relationship between cohorts, periods, and prevalent cohorts.

Cohort life expectancy takes everyone who starts their lives at a single moment in time, irrespective of their lifespans, and follows that unselected sample across time, weighting everyone equally. Period perspectives take everyone alive in a moment, regardless of when they began. Because their units are time (not people), period perspectives count people in proportion to the time they spend in the population—which is why the average age in a period is more than half of the life expectancy of the underlying cohorts—but stay within that single moment in time. Prevalent cohorts, whose lifespan is the ALL, are distinct from both the cohort and the period perspectives. Like periods, they first *select* people on their longevity but then, like cohorts, *follow* them through their own lifespans. Thus the length bias arises because the ALL is asking a cohort question about a period slice of the data.

One implication is that other contexts that define 'cohort' membership through cross-sectional membership in some category will produce similarly length-biased estimates of the duration of category membership. For example, epidemiological research designs that begin by selecting people with some incurable medical condition

at a particular time point, and then follow those people as a cohort to see how long they live—a prevalent cohort study design—generate length-biased lifespan estimates analogous to the bias in the ALL (Zelen and Feinleib 1969). The results here underscore that demographers can conceptualize living populations and their relationship to underlying birth cohorts with the same analytical tools that epidemiologists use to represent prevalent cohort samples and their relationship to disease incidence (e.g., Alho 1992, Addona et al. 2009, Carone et al. 2012, Keiding et al. 2019).

b. Mortality Selection Without Frailty

By highlighting the *inherent* bias in lifespan measures that begin with a population defined by a period, the length-biased lifespan in Eq. (5) also gives a somewhat different perspective on mortality selection than demographers' and biostatisticians' traditional perspective based on frailty modeling. Frailty is a construct representing systematic and sustained individual differences in longevity (Manton et al. 1979, Vaupel and Yashin 1985, Vaupel and Missov 2014). It implies that, if the frailer people who die young did instead live to old age, their old-age mortality would be higher than that of the robust people who actually do survive to old age. In other words, the concept of frailty implies that there are stable differences in individuals' expected longevity, and, therefore, differences in actual longevity select the population by continually removing those with the lowest expected longevity.

Yet recent theoretical and empirical investigations (Steiner and Tuljapurkar 2012; Caswell 2014; Hartemink, Missov, and Caswell 2017) suggest that the vast bulk of heterogeneity in lifespans may be due to stochastic differences in individual luck, rather than stable frailty. The results here highlight the importance of lifespan variability in generating mortality selection, whether or not there is any such frailty in the population. Indeed, no concept of frailty is needed to generate any of the results in this article. Imagine that everyone in the population has exactly the same age-specific hazards and lifespans differ purely by chance. Even in this situation, the ALL reflects a length-biasing selection on individual differences in actual longevity—even though those differences in actual longevity do not reflect differences in individuals' expected longevity. Viewing the population in a cross-section intrinsically means viewing individuals in proportion to their lifespan. The cross-section selects cohort members, not on frailty (expected longevity), but on *actual* longevity.

c. Longevity of the living population vs. longevity of living cohorts: Comparison with the Cross-Sectional Average Lifespan (CAL)

The ALL is part of "a family of mortality indicators that make use of cohort information but refer to only one period" (Guillot and Payne 2019: 418). One member of that family deserves special mention because, like the ALL, it uses cohort mortality to describe the longevity of cohorts alive during a particular period. That measure is the cross-sectional average lifespan (CAL), proposed by Brouard (1986) and developed by Guillot (2003). A comparison between the ALL and CAL is informative about both measures.

The CAL at time t is defined in terms of the cohort-specific survivorship $p_c(x, t-x) = l_c(x)/l_c(0)$, the survivorship of cohort c at age x, as:

$$CAL(t) = \int_0^{\omega} p_c(x, t-x)dx$$

Thus, "$CAL(t)$ is the sum of proportions of survivors among the various cohorts present in the population at time t" (Guillot 2003: 42). We note that this implies that the CAL summarizes lifespans using only the deaths included in the left-hand triangle of our Fig. 1 (past deaths of living cohorts), in contrast to the ALL, which uses only the deaths included in the right-hand triangle (future deaths of living people).[5]

This key contrast between the CAL and the ALL—whether past or future deaths of living cohorts comprise the lifespans that the measure summarizes—also means that the two measures describe different population units: the ALL describes the (future) longevity of living *people*, while the CAL describes the (past) longevity of living *cohorts*. The relationship of living people to their current cohort survivorships—reflecting the mortality that such people did *not* succumb to—may or may not proxy meaningful aspects of their own lives. In many contexts, being a rare survivor of a cohort with high past mortality, compared to a survivor of a cohort with lesser mortality, might capture something quite meaningful about the survivor (such as the intensity of the disease exposures each may have endured). On the other hand, in highly unequal and

[5] This restriction to past deaths of living cohorts generates one of the key practical advantages of the CAL as a period longevity indicator: while it is based on genuine cohort, rather than synthetic cohort, mortality (unlike period life expectancy), it requires no data on the future (unlike cohort life expectancy or the ALL).

segregated contexts, high past mortality concentrated in a particular (disadvantaged) subpopulation might not be a meaningful descriptor of the experiences of survivors drawn largely from a different (advantaged) subpopulation. In contrast to most other longevity measures, the ALL describes living populations directly, rather than the cohorts into which they were born.

6. Conclusion

We have shown that, in a stationary population, the lifespans of the living population form a length-biased sample of the cohort (and period) lifespan distribution. This insight connects demographic lifespan measures with a well-developed body of statistics (e.g., Cochran 1977: 249-255, deCarvalho 2016), including many epidemiological applications (e.g., Hill et al. 2003, Asgharian et al. 2006, Törner et al. 2011), and provides new intuition for existing demographic results. It implies that, when death rates are unchanging, the average lifespan of the living always exceeds period life expectancy, and exceeds it by more years when variation in the age at death is large and life expectancy is low.

These results are relevant whenever the population of interest is the population that currently experiences a state, rather than the population that ever experiences a state. Here, we considered the state of being alive, comparing the lifespan of the living to the lifespan of a cohort. The same results would apply when characterizing the expected length of current marriages (Alho 2016), disease durations among those who currently have a disease (Zelen and Feinleib 1969), or incarceration (Patterson and Preston 2008) or unemployment (Beach and Kaliski 1983) spells among those currently incarcerated or unemployed. Each of these applications involves what we termed "asking a cohort question about a period slice of the data," introducing length bias.

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TABLES AND FIGURES

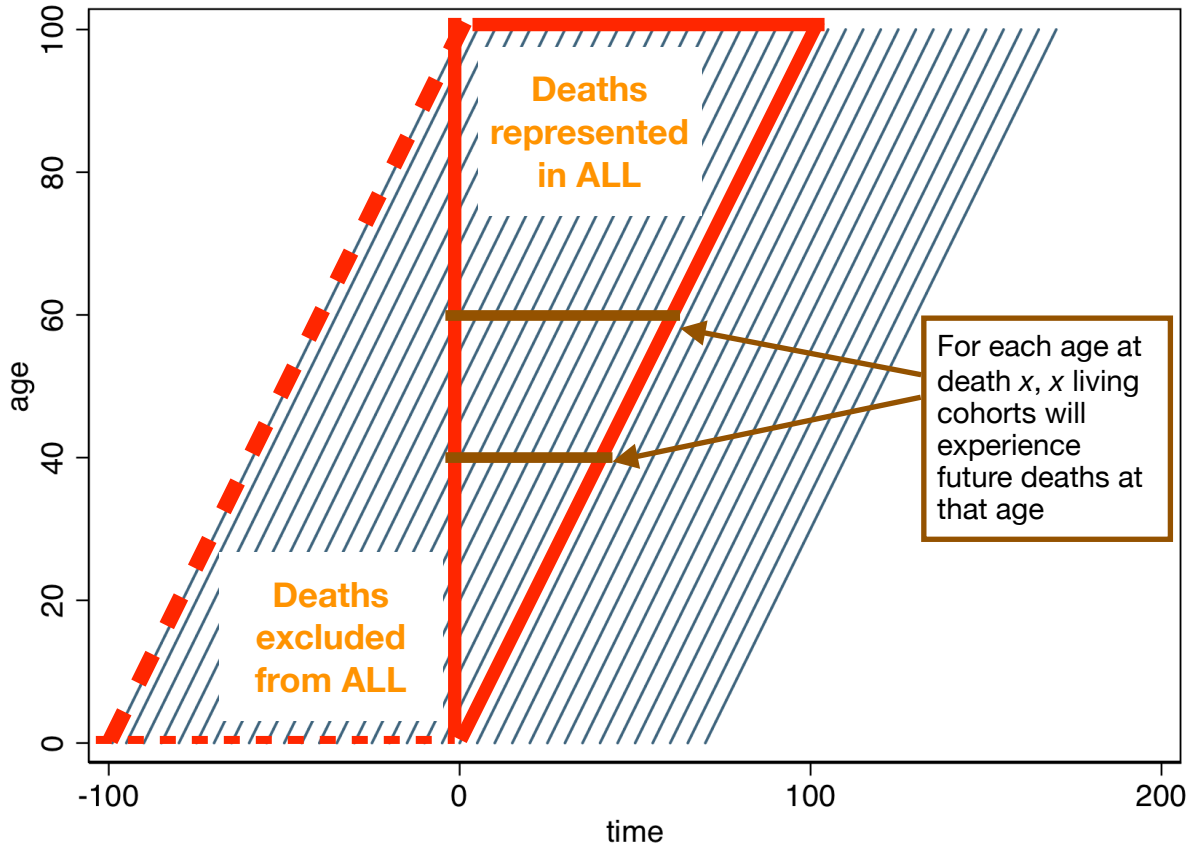

Figure 1. The average lifespan of the living (ALL) is the average of the lifespans that end in the upper right triangle. These deaths represent the future deaths of the living population. The deaths in the left triangle reflect the past deaths of living cohorts. The horizontal bands illustrate the unequal number of cohorts that contribute deaths at different ages at death.

Life Table Family & Gender	Life Expectancy	Standard Deviation of the Age at Death	Average Lifespan of the Living (ALL)	ALL – life expectancy divergence
UN Far East Asian, Male	60	22.14	68.17	8.17
Coale & Demeny South, Female	60	28.81	73.84	13.84
UN Latin, Female	67	25.43	76.65	9.65
Coale & Demeny North, Male	21	25.43	51.74	30.74

Table 1. Average lifespan of the living and its divergence from life expectancy for four model life tables. The first two life tables share a life expectancy; the second two share a variance (reported here as the standard deviation) in the age at death.

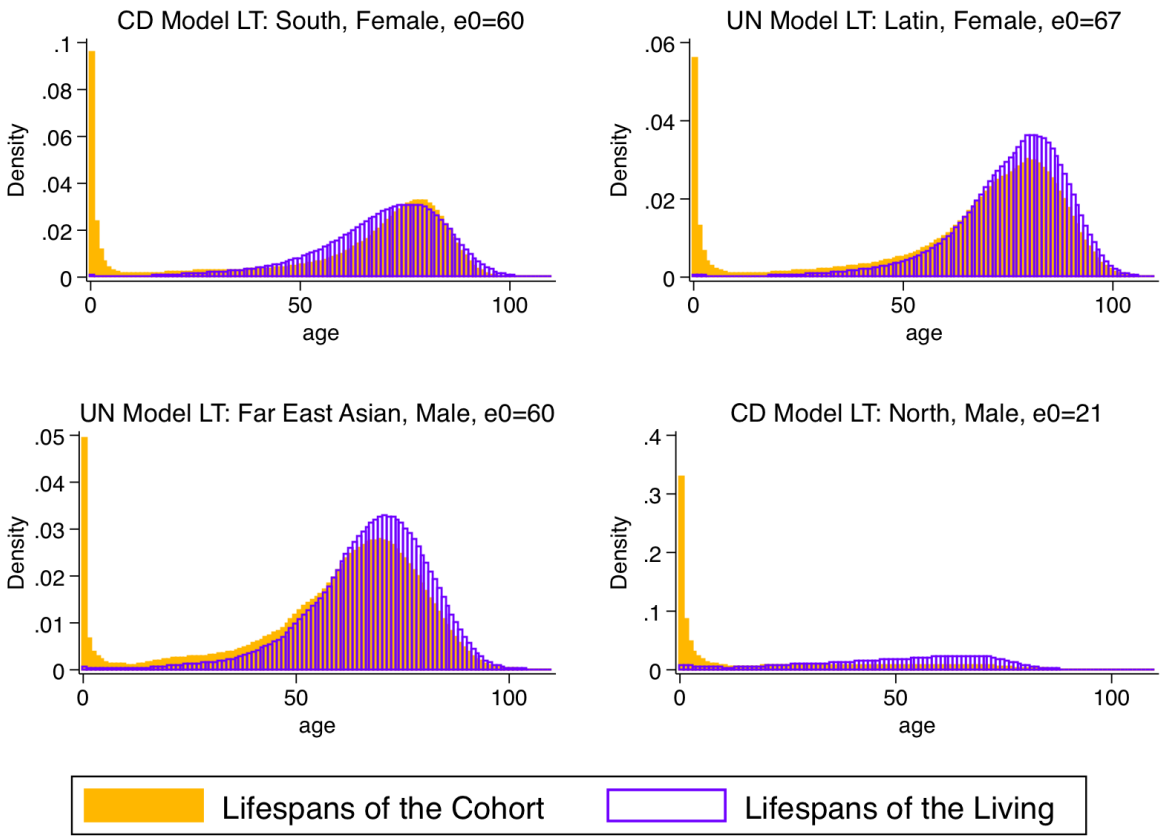

Figure 2. Distribution of lifespans in a life table (solid bars) and its associated living population (hollow bars), corresponding to the life tables shown in Table 1. The living population's lifespans are systematically selected to be older than the life table's. The distributions are displayed to age 110 (the model life tables extend to age 130). Note that, in the upper left panel, the living population appears visually to have a younger distribution of ages of death than the life table; this is a consequence of the relative absence of very young deaths among the living population creating proportionately more deaths at middle ages. Note also that the visually small peaks in the lower right panel result from the extremely high infant mortality of the life table, which distorts the graph scale.

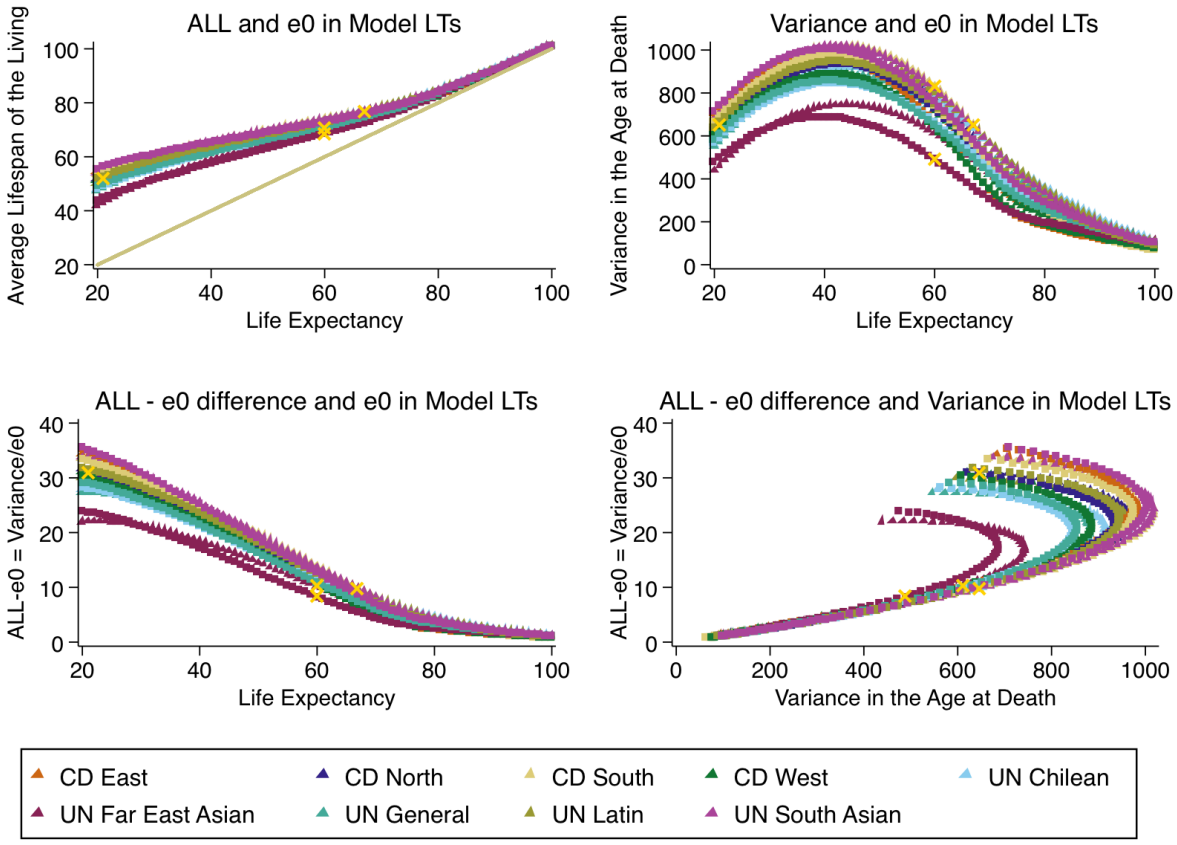

Figure 3. ALL, life expectancy, and variance in the age at death in the full set of UN Extended Model Life Tables. Gold Xs distinguish the four life tables portrayed in Table 1 and Figure 2. (A) The average lifespan of the living (ALL) as a function of life expectancy. (B) The divergence of the ALL from life expectancy as a function of life expectancy. (C) Variance in the age at death as a function of life expectancy. (D) The divergence of the ALL from life expectancy as a function of variance in the age at death.