

# Renewal and stability in populations structured by remaining years of life

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## Abstract

A unisex model of population renewal for populations structured by thanatological age is presented in both continuous and discrete form. Various stable and transient properties populations are compared and related when viewed by chronological versus thanatological age. Results from the two age perspectives are conformable if the starting population is stable, but are otherwise divergent.

\*This is a work in progress. All findings are preliminary at this time, so please don't cite without permission of the author.

In this paper, I explore some formal demographic consequences of a particular redefinition of age. Instead of counting age as the time passed since birth, consider age as the amount of time left until death<sup>1</sup>. The first kind of age is called chronological age and the kind of age explored in this paper is called thanatological age. Individuals in this case move in the same direction along imaginary life lines, but the reference point for age is now at the end of the life line instead of at the beginning. For individuals, the timing of events in life is identified exactly using either of the two definitions of age, but aggregate patterns differ. The models of demography are prefaced by the observation that demographic phenomena vary over age and time in empirically regular ways. Some such phenomena are best described in the aggregate as a function of time since birth, and others of time until death, while still others can be a function of both to some degree (Riffe, T. et al. 2015). This observation ought to motivate the formal demographic base by incorporating this aspect of time in into models.

I describe the Lotka-Euler-Leslie renewal model when structured by thanatological age. The renewal model relates fertility, mortality, and population structure in a parsimonious form, revealing the long term consequences of a particular set of conditions. All diverse lines of contemporary demographic research are relatable to the renewal model. Some might say that stable population theory is not relevant to everyday demography, since populations are always changing. Even if change precludes the notion of stability as a

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<sup>1</sup>This quantity is referred to as *residual* lifetime in the reliability literature, or just time-to-death (TTD) elsewhere.

prediction, models of long-run consequences still give a useful measure of the demographic force implied by a given set of rates. In this and other ways, stability is never far away. That population projections lead into a stable state means that some form of stability is implied by the routine practice of demography. Stability or even stationarity are imaginable for the world population of humans one day. Models of stationary populations are easily applied by analogy to closed or nearly-closed birth cohorts. Finally, stable population theory is relevant to other non-human structured populations, such as stars.

To present the renewal model based on thanatological age is not necessarily a suggestion for a better way to model or project population. Rather, the thanatological renewal model represents an alternative and coherent way to describe the process of population renewal by relating renewal to a death flow rather than to a birth flow. The chronological-age classified renewal model and the thanatological renewal model both approximate the movement of population stocks over time, but from opposite vantage points. Specifying a model of thanatological renewal expands the toolbox available to approach complex temporal population structure. The next section of this article describes the lifetable method of transforming age-classified data into thanatological age classes. I then derive the continuous version of the thanatological renewal model, and some other stable properties. This is followed by the matrix version of the model, which is explained alongside the lifecycle graph.

## A lifetable approximation of thanatological age

Direct information on the timing of demographic transitions with respect to death is available retrospectively from linked population registers or panel surveys with mortality follow-ups. Some surveys also ask respondents in various ways about their perceived future lifetime, which may underly those demographic transitions governed to some degree by volition. The present inquiry draws only from lifetable-projected remaining lifetime, which is intended to approximate actual remaining lifetime under the strong assumption of homogenous populations. Chronological age-classified counts are redistributed over future death times according to a fixed mortality schedule. This allows us to make statements about the remaining lifetime distribution within a stock of population, under certain assumptions.

A lifetable approach to transforming chronologically classified data into thanatologically classified data is valid when the given lifetable accurately describes the future mortality of age-classified population. To make a projective statement about a current stock of population, one does well to factor in future changes in mortality, and to allow the trajectory of changes to vary over ages and cohorts. In the case of a stable population model, mortality is assumed invariant over time, which means that the same survival pattern underlies each birth cohort. This is the case we explore, and so the following formulas assume a single lifetable pattern.

The basic transformation to thanatological age proceeds by defining a deaths density function, similar the lifetable  $d(a)$ , but over two dimensions: chronological age attained,  $a$ , and remaining years of life,  $y$ . This

function we denote  $f(y|a)$  — The density distribution of thanatological age conditional on chronological age. This is essentially the same notion as the familiar  $d(a)$ , but rescaled as a function of chronological age. For ages higher than 0, simply condition on survival:<sup>2</sup>

$$f(y|a) = \mu(a+y) \frac{\ell(a+y)}{\ell(a)} \quad . \quad (2)$$

A convenient discretization of (2) is to simply work with the  $d_a$  column of the lifetable (here with single ages):

$$f_{y,a} = \frac{d_{a+y} + d_{a+y+1}}{L_a + L_{a+1}} \quad , \quad (3)$$

where  $L_a$  is lifetable exposure.<sup>3</sup> One produces in this way a probability density function over future death times for each chronological age,  $a$ . The  $f(y|a)$ - weighted average of  $y$  for a given  $a$  returns the familiar remaining life expectancy column of the lifetable,  $e(a)$ . If  $P(a)$  is a chronological age-classified population count, we can derive  $P(y)$ , a thanatological age-classified population count using

$$P(y) = \int_0^\infty P(a) f(y|a) da \quad . \quad (4)$$

Since  $1 = \int_0^\infty f(y|a) dy$  for each  $a$ , this density is useful for decomposing data classified by chronological age. For example, we can break down a population pyramid into thanatological age classes. Figure 1a shows this exercise for 2010 US data, assuming the 2010 period mortality schedule remains constant. When looking from the chronological age perspective, this decomposition reveals thanatological heterogeneity, but when viewed from the thanatological perspective (Figure 1a) it reveals chronological age heterogeneity and the overall thanatological age profile, the future death flow of the current population. Figure 1b shows this recomposition for the same 2010 US data.

Brouard (1986) applied this method to highlight regional differences in French age structure, at times combining this projective method with historical stocks. Brouard (1989), and later Vaupel (2009), showed that in stationary populations the chronological and thanatological age structures are identical, and this provides a limited basis for comparison between the two perspectives. Wachter (2014) hints at, and Vaupel (2014) elaborates on how to make chronological and thanatological age structure commensurate under a constant growth rate,  $r$ . These results will also follow from the following specification of a thanatological

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<sup>2</sup>In the reliability literature, our concept of  $d(y|a)$  is denoted by

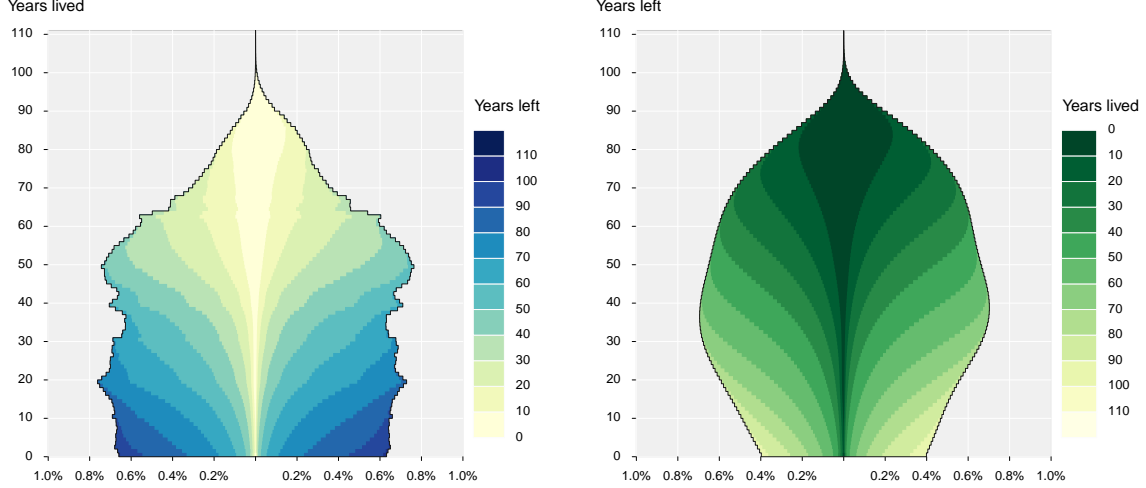
$$X - t | X > t \quad (1)$$

where  $X$  is the total lifespan and  $t$  is the current chronological age attained.

<sup>3</sup>Equation (3) will incur some error depending on the method used to derive  $L_a$ . To remove this error, rescale over the  $a$  margin so that each distribution conditioned on  $a$  sums to 1. Working with  $\ell_a$  rather than  $L_a$  eliminates error and yields similar results, but is not necessarily better.

Figure 1: 2010 US population structure

- (a) Chronological age-structure (years lived) decomposed by thanatological age (years left). (b) Thanatological age-structure (years left) decomposed by chronological age (years lived).



\*Population and mortality data from the HMD.

renewal model.

It bears repeating that lifetable-derived thanatological age structure is probabilistic until after death, since it refers to the future according to an assumed mortality pattern. As such, Figure 1b is projective in nature, a forward-looking glance at population attrition given the population stock and lifetable of a particular moment, whereas Figure 1a is reflective in nature, since a population's chronological age-structure is mostly the fruit of past fertility, but also migration and to a lesser degree attrition. Any count classified by chronological age can be reclassified in this way given a corresponding lifetable. Exploiting this, we derive thanatological fertility rates,  $\gamma(y)$ , by applying (4) to age-classified birth counts,  $B(a)$ , to get  $B(y)$  and again to exposure-to-risk,  $E(a)$  (here we take exposures from all ages), to get  $E(y)$  and then dividing

$$\gamma(y) = \frac{B(y)}{E(y)} \quad . \quad (5)$$

We are interested to use thanatological fertility rates,  $\gamma(y)$  in models of population renewal,<sup>4</sup> rather than to explicitly study the nature of these rates. Nonetheless it is best not to throw such rates into a model blindly, so we offer a schematic overview of some of their characteristics. Figure 2b represents the full variety

<sup>4</sup>This is probably premature, but helps to understand the nature and provenance of model components.

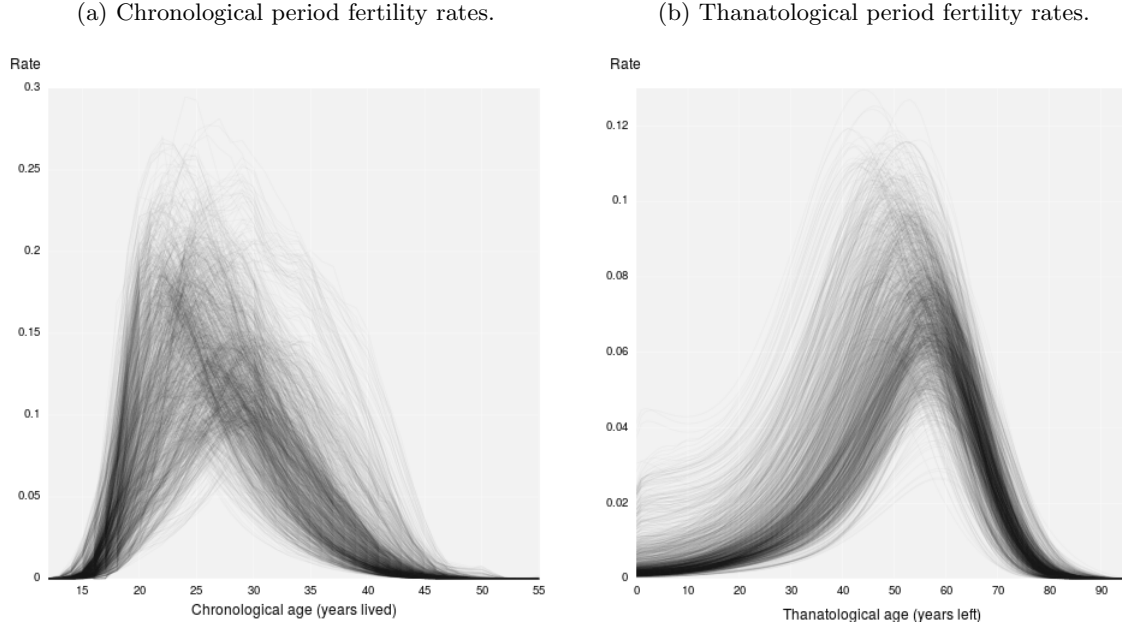
in female thanatological period fertility rates that can be found for all years of data that overlap in the HFD and HMD.<sup>5</sup> Figure 2a gives ASFR for the same populations and years as a more familiar reference, but note that both scales are different. With no indication of particular populations or time series, one already concludes that period thanatological fertility rates have a characteristic shape and are not random, erratic or informationless: There is a pattern to fertility rates by remaining years of life, and it varies over time and between populations within some range of normality. Thanatological fertility rates have a wider distribution than do chronological rates. Note that this spaghetti plot includes both fertility booms and busts, as well as some mortality crises (1918, WWII). Some patterns to note, but which we do not separate graphically here, are that the left tail (a gauge of how orphan-prone a population is) has tended to fall over time. All populations have shown a rightward shift in both the mean and modal mother's thanatological age at childbearing (TAC) over time. Several populations now show modal TACs of over 60 years. Thanatological total fertility rates (TTFR) track standard period total fertility rates (PTFR) rather closely, but tend to be somewhat higher (not shown).

In general, thanatological fertility rates will not be useful for purposes of projection, unless the demographer believes that their empirical regularity is somehow stronger than typical ASFR. This is a question we do not seek to answer in the present treatment. There are alternative ways of defining thanatological fertility rates, for instance by transforming the birth and population vector from a stable population. As proven in appendix B, thanatological fertility rates derived from a stable population imply a certain symmetry with stable populations from the chronological model. First let us define the basic model.

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<sup>5</sup>There are as of this writing 1933 population-years of overlap between the HMD and HFD, including a wide variety of fertility and mortality combinations.

Figure 2: Chronological and thanatological fertility rates, all 1600 country-year combinations present in both the HFD and HMD.\* Note different x and y scales.



\*AUT, 1951 – 2010; BGR, 1947 – 2009; BLR, 1964 – 2012; CAN, 1921 – 2009; CHE, 1932 – 2011; CHL, 1992 – 2005; CZE, 1950 – 2011; DEUTE, 1956 – 2011; DEUTNP, 1990 – 2011; DEUTW, 1956 – 2011; ESP, 1922 – 2012; EST, 1959 – 2011; FIN, 1939 – 2009; FRATNP, 1946 – 2013; GBR\_NIR, 1974 – 2011; GBR\_NP, 1974 – 2011; GBR\_SCO, 1945 – 2011; GBRTENW, 1938 – 2011; HUN, 1950 – 2009; IRL, 1955 – 2009; ISL, 1963 – 2010; JPN, 1947 – 2012; LTU, 1959 – 2011; NLD, 1950 – 2009; NOR, 1967 – 2009; PRT, 1940 – 2012; RUS, 1959 – 2010; SVK, 1950 – 2009; SVN, 1983 – 2009; SWE, 1891 – 2011; TWN, 1976 – 2010; UKR, 1959 – 2009; USA, 1933 – 2010

## The thanatological renewal model

For the renewal model that follows, we are most interested in using the kind of fertility rates shown in Figure 2b, and we refer to a closed, unisex population based on female vital rates. Assuming constant vital rates, the births for the present year are given by

$$B(t) = \int_0^\infty P(y, t) \gamma(y) \, dy = \int_0^\infty P(a, t) m(a) \, da \quad , \quad (6)$$

where  $a$  indexes chronological age,  $y$  indexes thanatological age,  $P(a), P(y)$  are population counts, and  $\gamma(y), m(a)$  are exact specific fertility probabilities (rates), best imagined as the fertility rates of females born to females. The thanatological integral can be broken down back in terms of chronological age:

$$= \int_{y=0}^{\infty} \int_{a=0}^{\infty} \gamma(y) \frac{P(a, t) d(a + y)}{\ell(a)} da dy \quad , \quad (7)$$

where  $d(a)$  is the continuous life-table death distribution with radix of 1, so  $d(a)/\ell(0)$ . We can relate the present population to past births with  $P(a, t) = B(t - a)\ell(a)$ :

$$= \int_{y=0}^{\infty} \int_{a=0}^{\infty} \gamma(y) B(t - a) d(a + y) da dy \quad . \quad (8)$$

Eventually strong ergodicity will assert itself, and  $B(t)$  will be related to  $B(t - a)$  according to a constant factor  $e^{ra}$ , where  $r$  is the familiar intrinsic rate of growth:

$$= \int_{y=0}^{\infty} \int_{a=0}^{\infty} \gamma(y) B(t) e^{-ra} d(a + y) da dy \quad . \quad (9)$$

Divide out  $B(t)$  to get back a familiar-looking renewal equation:

$$1 = \int_{y=0}^{\infty} \int_{a=0}^{\infty} \gamma(y) d(a + y) e^{-ra} da dy \quad . \quad (10)$$

Now compare this to Lotka's chronological formulation

$$1 = \int_{a=0}^{\infty} m(a) l(a) e^{-ra} da \quad , \quad (11)$$

which can be expressed as well as

$$= \int_{a=0}^{\infty} \int_{y=0}^{\infty} m(a) d(a + y) e^{-ra} dy da \quad , \quad (12)$$

and note that (12) and (10) are really quite similar, since  $\int_{y=0}^{\infty} d(a + y) da = l(a)$ . For intuition, notice that  $l(a)$  is here split up into pieces of  $d(a)$ , and imagine a 2D surface of these, where one axis is chronological age and the other axis is thanatological age. For the chronological case (11), we multiply chronological age-specific fertility rates,  $f(a)$ , over the chronological age margin, and for the thanatological case we multiply  $f^*(y)$  over the thanatological age margin.

There are gaps in the above line of development, since the jump from (8) to (9) (strong ergodicity) is

unproven, although it is rather intuitive, given the much greater density of connections within the model; persons from nearly any thanatological age can produce offspring that can have any other thanatological age.<sup>6</sup> In this sense, the smoothing mechanism at play as the population passes through time must be much stronger than that for chronological age, at least in most cases. The mechanisms at play unfold in the same way as those so intuitively described by Arthur (1982), and said proof may apply here without further modification. Later in this paper I note how strong ergodicity is guaranteed given the properties of the thanatological projection matrix. A proof of the uniqueness of the solution to (10) is given in Appendix A. A proof that the chronological and thanatological renewal models must yield the same  $r$  if the starting population is already stable is given in Appendix B. A fast-converging iterative method for finding  $r$  from equation (10) is given in Appendix C

If the thanatological fertility rates do not derive from a stable population, as will typically be the case, then the two age perspectives will, unless by coincidence, yield divergent stable models. There is a strong parallel here with the case of two-sex age-specific fertility rates. As in the case of divergence between male and female single-sex models, there will virtually always be divergence between single-sex models under chronological versus thanatological age, unless the starting population is stable. Even though the modeled population stocks are in a way commensurable, the rates used here,  $f(a)$  versus  $f^*(y)$  are calculated on the basis of differently distributed denominators  $E(a)$  versus  $E(y)$ .

Once one finds  $r$  from (10), other familiar stable population parameters can be calculated. For instance, we may calculate the mean thanatological generation time,  $T^*$ :

$$T^* = \frac{\int_{y=0}^{\infty} \int_{a=0}^{\infty} y e^{-ra} d(a+y) f^*(y) da dy}{\int_{y=0}^{\infty} \int_{a=0}^{\infty} e^{-ra} d(a+y) f^*(y) da dy} . \quad (13)$$

Literally, this is the mean of the remaining lifespans of new mothers in the stable population. The net reproduction rate,  $R_0$  is related by, e.g.,

$$R_0 = e^{rT^*} \quad (14)$$

The birth rate,  $b$ , is given by

$$b = \frac{1}{\int_{y=0}^{\infty} \int_{a=0}^{\infty} e^{-ra} d(a+y) da dy} , \quad (15)$$

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<sup>6</sup>I say *nearly* because the very highest thanatological ages tend to be composed of pre-menarchical females, so these can be thought of as structural zeros. I am uncertain if it is a record, but it is certainly an extreme case useful for illustration: Jeanne Calment, who lived to 122, had a daughter at age 22, which means she was about thanatological age 100 ([http://en.wikipedia.org/wiki/Jeanne\\_Calment](http://en.wikipedia.org/wiki/Jeanne_Calment)). If the lifetable used to transform to thanatological closes out at age 110+, as is the case with HMD data, then fertility rates for thanatological ages 101-110+ would be structural zeros.



the denominator of which is the inside of equation (10) less  $f^*(y)$ . This simplifies to

$$= \frac{1}{\int_{a=0}^{\infty} e^{-ra} l(a) da} \quad , \quad (16)$$

which is exactly the same as that valid for chronological age in the Lotka-Euler setup, except that  $r$  here comes from the thanatological renewal model. If the stable age structure,  $c^*(y)$ , is known, then we may take the sum of hypothetical births over thanatological age:

$$= \int_{y=0}^{\infty} f^*(y) c^*(y) dy \quad . \quad (17)$$

The stable thanatological age structure,  $c^*(y)$ , is the proportion of the stable population with remaining years to live  $y$

$$c^*(y) = b \int_{a=0}^{\infty} e^{-ra} d(a+y) da \quad , \quad (18)$$

or, given the stable chronological age structure,  $c(a)$ , and a lifetable,

$$= \int_{a=0}^{\infty} c(a) d(y|a) da \quad (19)$$

$$= \frac{\int_{a=0}^{\infty} d(a+y) e^{-ra} da}{\int_{a=0}^{\infty} l(a) e^{-ra} da} \quad . \quad (20)$$

It has previously been shown that when  $r = 0$  and  $y = a$ , that  $c(a) = c^*(y)$  (Brouard 1989, Vaupel 2009), and now we can arrive at the same conclusion directly by equating the chronological and thanatological renewal equations. For small non-zero magnitude values of  $r$  and survival patterns typical of humans, it is also the case that  $c^*(y|r) \approx c(a|-r)$ . This could make a useful heuristic, and the relationship is asymptotically exact as  $r$  approaches zero, but the exact relationship is to be found in equation (19). Further stable population quantities may be estimated by similarly translating the various common definitions (e.g., in the glossary of Coale (1972)) to the present perspective. We will focus on the main model rather than on these.

## The thanatological projection matrix

These descriptions can be made more explicit, and in some ways more tractable, by hashing out the projection matrix that corresponds to the thanatological renewal model. As with the chronological age-structured Leslie matrix, the thanatological projection matrix,  $\mathbf{Y}$ , is square and of dimension  $y \times y$ , where  $y$  is the number of thanatological age classifications on which the population is structured. The matrix contains elements for survival and elements for fertility. Unlike Leslie matrices,  $\mathbf{Y}$  is not sparse, but is instead populated primarily with positive entries greater than zero. In the following, I illustrate using a  $6 \times 6$  matrix.

Mortality occurs in only the population class with zero remaining years of life. The population of thanatological age 1 in year  $t$  moves to 0 in year  $t + 1$  and dies in the course of that year. Thus, rather than in the subdiagonal, survival elements are located in the superdiagonal. All survival values are 1, since there is no decrement until after living through age 0. The survival component of  $\mathbf{Y}$  is organized as in Matrix 0.1. To imagine a lifecycle graph, each age decrements by one through each lower age in successive order until being absorbed by death after completing thanatological age zero.

Matrix 0.1: Survival component of unisex thanatological projection matrix,  $\mathbf{Y}$

$$\begin{array}{c} e_y \\ 0_{t+1} \\ 1_{t+1} \\ 2_{t+1} \\ 3_{t+1} \\ 4_{t+1} \\ 5_{t+1} \end{array} \begin{pmatrix} 0_t & 1_t & 2_t & 3_t & 4_t & 5_t \\ 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix}$$

Fertility inputs to the matrix are derived from single-sex thanatological fertility and the life table  $d_a$  distribution, where  $a$  indexes chronological age and is equated to  $y$  remaining years of life for members just born. It is simpler to imagine  $d_a$  in this case as indexing the future lifespan distribution of newborns. Fertility in a thanatologically structured human population occurs in all but the very highest remaining years classes, which can be thought of as structural zeros for simplicity, as they only contain pre-menarchical females that will have very long lives. For our  $6 \times 6$  example, say that fertility is observed in thanatological classes 0-4, while the final class has no fertility, where  $f_y^*$  indicates the fertility probability for class  $y$  in the year  $t$  entering population (in the matrix columns). Each  $f_y^*$  is then distributed out over rows according to  $d_a$ . The fertility entry in row  $m$  and column  $n$  of  $\mathbf{Y}$  will therefore be  $f_n^* \cdot d_m$ . One can assume that those dying over the course of year  $t$  (the first column) are exposed to fertility for half of the year,<sup>7</sup> and so discount the fertility entry accordingly. Further, infant mortality,  $f_y^* \cdot d_0$ , located in the first row, must also be discounted, since part of the mortality will occur in the same year  $t$  and the rest in year  $t + 1$ . The

<sup>7</sup>One might be tempted to not allow for fertility at all for females dying in year  $t$ , but recall that fertility is measured in the moment of birth, and not conception.

first row of fertility must be further discounted by a factor,  $\lambda$ , in order to account for the fact that infant mortality is higher in the lower Lexis triangle than in the upper. Of those infants who die in the first year of life, a proportion equal to  $\lambda$  do not make it to December 31st of the calendar year in which they were born.<sup>8</sup> The fertility component of  $\mathbf{Y}$  is then composed as in Matrix 0.2.

Matrix 0.2: Fertility component of unisex thanatological projection matrix,  $\mathbf{Y}$

$$\begin{array}{c} e_y \end{array} \quad \begin{array}{cccccc} 0_t & 1_t & 2_t & 3_t & 4_t & 5_t \end{array} \\
\begin{array}{c} 0_{t+1} \\ 1_{t+1} \\ 2_{t+1} \\ 3_{t+1} \\ 4_{t+1} \\ 5_{t+1} \end{array} \left( \begin{array}{cccccc} (1-\lambda)\frac{f_0^*d_0}{2} & (1-\lambda)f_1^*d_0 & (1-\lambda)f_2^*d_0 & (1-\lambda)f_3^*d_0 & (1-\lambda)f_4^*d_0 & 0 \\ \frac{f_0^*d_1}{2} & f_1^*d_1 & f_2^*d_1 & f_3^*d_1 & f_4^*d_1 & 0 \\ \frac{f_0^*d_2}{2} & f_1^*d_2 & f_2^*d_2 & f_3^*d_2 & f_4^*d_2 & 0 \\ \frac{f_0^*d_3}{2} & f_1^*d_3 & f_2^*d_3 & f_3^*d_3 & f_4^*d_3 & 0 \\ \frac{f_0^*d_4}{2} & f_1^*d_4 & f_2^*d_4 & f_3^*d_4 & f_4^*d_4 & 0 \\ \frac{f_0^*d_5}{2} & f_1^*d_5 & f_2^*d_5 & f_3^*d_5 & f_4^*d_5 & 0 \end{array} \right)$$

The survival and fertility components of  $\mathbf{Y}$  add together elementwise, thus the full  $6 \times 6$  matrix is composed as in Matrix 0.3.

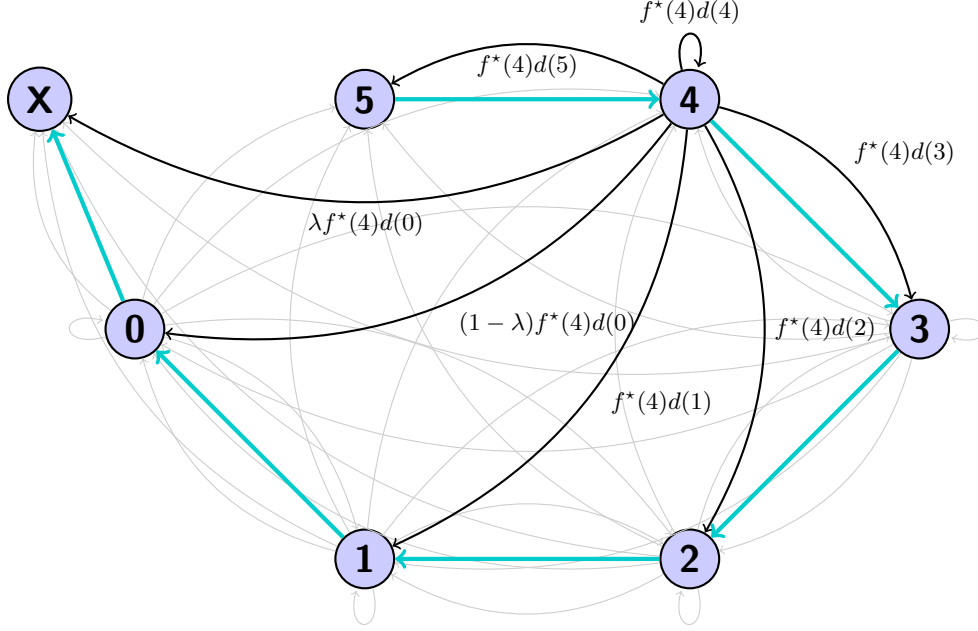
Matrix 0.3: A full unisex thanatological projection matrix,  $\mathbf{Y}$

$$\mathbf{Y} = \begin{array}{c} e_y \end{array} \quad \begin{array}{cccccc} 0_t & 1_t & 2_t & 3_t & 4_t & 5_t \end{array} \\
\begin{array}{c} 0_{t+1} \\ 1_{t+1} \\ 2_{t+1} \\ 3_{t+1} \\ 4_{t+1} \\ 5_{t+1} \end{array} \left( \begin{array}{cccccc} (1-\lambda)\frac{f_0^*d_0}{2} & (1-\lambda)f_1^*d_0 + 1 & (1-\lambda)f_2^*d_0 & (1-\lambda)f_3^*d_0 & (1-\lambda)f_4^*d_0 & 0 \\ \frac{f_0^*d_1}{2} & f_1^*d_1 & f_2^*d_1 + 1 & f_3^*d_1 & f_4^*d_1 & 0 \\ \frac{f_0^*d_2}{2} & f_1^*d_2 & f_2^*d_2 & f_3^*d_2 + 1 & f_4^*d_2 & 0 \\ \frac{f_0^*d_3}{2} & f_1^*d_3 & f_2^*d_3 & f_3^*d_3 & f_4^*d_3 + 1 & 0 \\ \frac{f_0^*d_4}{2} & f_1^*d_4 & f_2^*d_4 & f_3^*d_4 & f_4^*d_4 & 1 \\ \frac{f_0^*d_5}{2} & f_1^*d_5 & f_2^*d_5 & f_3^*d_5 & f_4^*d_5 & 0 \end{array} \right)$$

Figure 3 depicts the projection matrix  $\mathbf{Y}$  in the form of a lifecycle graph. In this graph, each thanatological age is a node, and death is the absorbing state, denoted with an “X”. Population members are born into

<sup>8</sup> $\lambda$  can be derived directly from death counts data classified by Lexis triangles. If the demographer does not have information to derive  $\lambda$  directly, ad hoc or semidirect methods may be used to assign a reasonable proportion, such as 0.9 for contemporary low mortality populations.

Figure 3: The thanatological lifecycle graph



any of the thanatological age classes, and then follow clockwise around the graph on the thick blue paths in order until finally being absorbed into death (the node labeled “X”, not included in the projection matrix). The light gray paths represent fertility. These originate from any age class that has a fertility rate greater than zero, which for this toy matrix are all age classes except the 5th (highest). The  $y^{th}$  age class is subject to the fertility rate  $f^*(y)$ , and these births distribute out to all other age classes according to the lifespan distribution from the lifetable,  $d_a$ . Hence, the rate intensity of a fertility path is determined by the fertility rate of the origin age and probability of having a lifespan equal to the order of the destination node. A fraction of the fertility destined for infant mortality equal to  $\lambda$  leads straight to the absorbing state of death. Fertility paths from the 4th thanatological age class have been highlighted. These correspond to the fifth column of the example matrix  $\mathbf{Y}$ , plus an additional path direct to death for the fraction of infant mortality prior to December 31st in year  $t$ . Paths that loop back into the same age class simply indicate those offspring that are destined to die in the same year as their mother. It is perhaps clearer to see from the density of this graph and by recalling that thanatological fertility distributions are relatively wide (see Figure 2b) that there is a high degree of mixing of thanatological age within populations via reproduction – a strong tendency toward stability.

Thanatological age-classes will ideally terminate at the highest value permitted by data. For the data used in this paper, there are 111 total age classes, which translate to 111 total remaining-years classes (0-

110+). In practice  $\mathbf{Y}$  becomes a  $111 \times 111$  matrix, with most entries non-zero (nearly complete connectivity, such as in Figure 3). Construction may appear tedious for this reason. However, note that the bulk of fertility entries can be derived as the outer (tensor) product  $d_a \otimes f_y$ , leaving only the first row and first column mortality discounting followed by the addition of the survival superdiagonal. In most statistical programming languages constructing  $\mathbf{Y}$  entails only a couple more lines of code than constructing a Leslie matrix.

Thanatological projection matrices may be manipulated using standard matrix techniques applicable to the Leslie matrix. Where  $\mathbf{p}$  is a population vector classified by thanatological age, projection proceeds by multiplying  $\mathbf{Y}$  from the left:  $\mathbf{p}(t+1) = \mathbf{Y}\mathbf{p}(t)$ .

For rate schedules typical of human populations, thanatological projection matrices are filled with non-negative values, mostly greater than zero. Raising the matrix to some not-very-large power,  $k$ , will make all entries greater than zero. This observation, or else by noting that the lifecycle graph is strongly connected, lets us conclude that the matrix is irreducible and primitive. By the Perron-Frobenius theorem, the matrix will always have a unique, dominant, positive real eigenvalue, the natural log of which is the intrinsic growth rate,  $r$ , and strong ergodicity is assured. In other words, given a fixed matrix and enough time, the population will conform to some stable thanatological age distribution. Strong ergodicity was taken for granted in jumping from equation (8) to (9), but the presently described properties of the matrix model should, albeit unrigorously, satisfy lingering uncertainty on that step. The eigenvector corresponding to the dominant eigenvalue gives this stable thanatological age structure. If the fertility rates placed in the matrix are from the stable population, then the growth rate from the thanatological projection matrix is equal to that of the standard Leslie matrix.<sup>9</sup> The square of the, or the pace of convergence to stability (the ratio of the 1st to the 2nd eigenvalues).<sup>10</sup>

## Stable age structure

## Some preliminary empirical findings

The thanatological renewal equation and the discrete projection matrix can be put to work with data. In this case a few options are available for determining what kind of thanatological fertility rates to use. The two obvious choices are to derive rates from the stable population implied by the chronological renewal model, or to derive rates such as those from Figure 2b, based on a particular stock of population.

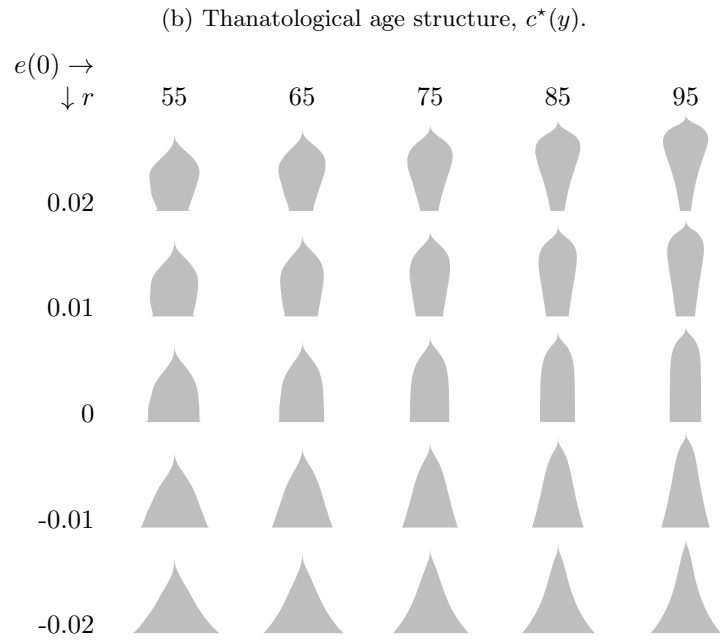
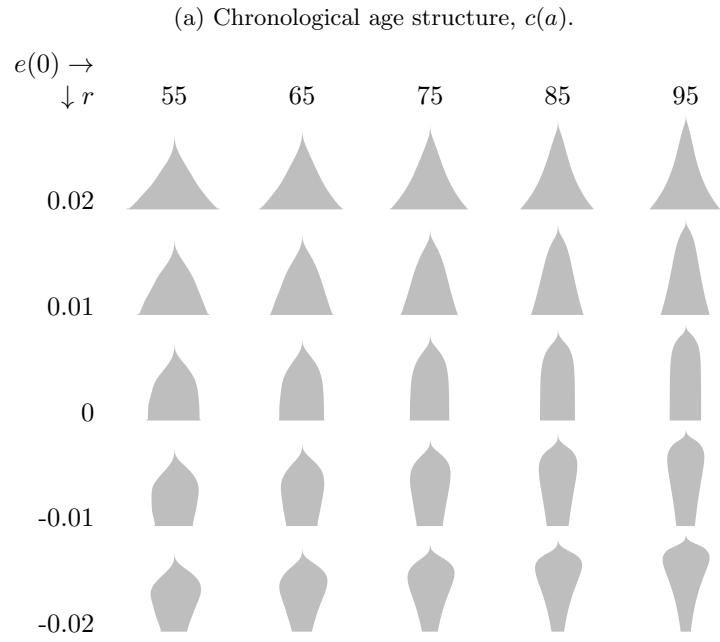
Of the 1834 population-years of data on hand, we optimize  $r$  from both (10) and (11). In this sample, both versions of  $r$  are only plausibly equal in a single instance. Usually thanatological  $r$  is greater than

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<sup>9</sup>Some care needs to be taken in order to demonstrate this point, since common approximations and adjustments used in matrix construction can throw things off. R code is available from the author to demonstrate this point. See also Appendix B for the corresponding proof from the continuous model.

<sup>10</sup>See Caswell (2001, p.86-87).

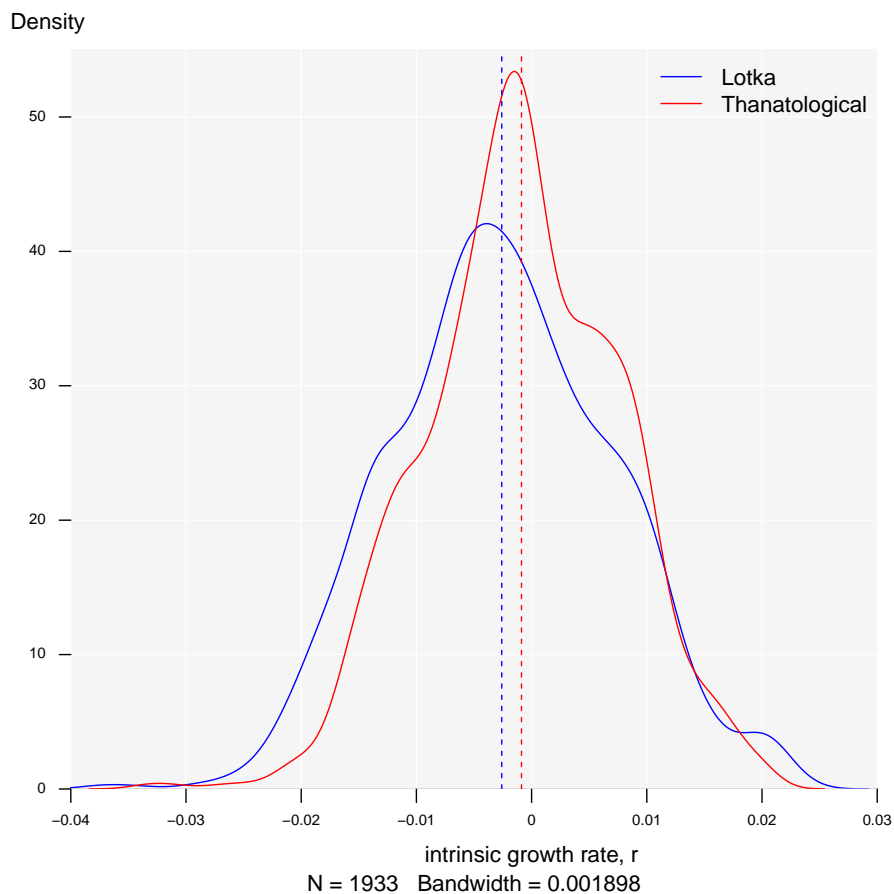
Figure 4: Stable age structures by life expectancy,  $e(0)$ , and growth rate,  $r$ .\*



\*Underlying mortality pattern based on 2010 USA (HMD)

Lotka's  $r$  (1373 cases). When Lotka's  $r$  is positive (693 cases), thanatological  $r$  is greater just over 50% of the time (356), but when Lotka's  $r$  is negative, thanatological  $r$  is the greater of the two around 90% of the time (1017 cases). These two approximations of  $r$  are of opposite sign 138 times. We provide a comparison of the  $r$  distributions in Figure 5. Mean locations for each distribution are indicated with vertical dashed lines; thano. -0.0010; chrono. -0.0027. The distribution of thanatological  $r$  is more compact than for chronological  $r$ , with the ratio of variances (thano./chrono.) of about 0.75. The two theoretical values of  $r$  covary strongly, but thanatological  $r$  is the less erratic of the two, and it usually paints a less dire picture when both are negative.

Figure 5: Distribution of  $r$ , chronological (Lotka) and thanatological\*.



\* Data from HMD and HFD. Countries and years listed in Figure 2.

The differences described here are not due primarily to rounding errors in the data, but rather to the way in which  $f^*(y)$  has been calculated. Specifically, in this case we have transformed fertility rates from empirical data with a particular chronological age structure. If the chronological age structure is far from its stable distribution, then it may be hard to imagine that  $f^*(y)$  will remain fixed over time. When holding chronological-age classified fertility rates fixed, the assumption is just the opposite.

From the projection matrix, the ratio of the largest to the second largest eigenvalue, the damping ratio, is an indicator of the *springiness* of the stable population structure,  $c^*(y)$  or  $c(a)$ , if perturbed from the state of stability. A higher damping ratio means that the population structure oscillates back to its stable state faster, i.e., that oscillations decrease in size more rapidly. The thanatological damping ratio was greater than the Leslie damping ratio for all 1834 population-years included in our empirical analysis. Leslie damping ratios ranged from 1.01258 to 1.0518, while thanatological damping ratios ranged from 1.0455 to 1.0868. Again, this was for the raw data, and I am not sure whether this consistent finding is a natural property of the model or an artifact of the unstable starting state of the data used to derive thanatological fertility rates. Intuitively, the thanatological smoothing process should be an order of magnitude stronger than the chronological smoothing process because each thanatological age class (node) – except for the oldest-old – is connected directly to each other thanatological age class in both directions. Again, I think contrived examples will be necessary to shed more light on this finding.

## 1 Discussion

The thanatological renewal model is valid, but this perspective may take some time to gestate before accepting that it is also a sound description of how populations renew. What should one imagine under the model of thanatological population renewal? A useful mnemonic bases itself on Figures 1a and 1b. In the chronological age-structured model, new generations appear at the bottom of the pyramid, and move up one rung per year. All age-classes are subject to attrition, which is spread out over ages and not readily visible in the pyramid. In the thanatological *leaf*, each birth cohort increments to the population over the whole range of thanatological age according to  $d(a)$ , as seen in (10), becoming the shaded layers seen in Figure 1b. Each horizontal step is a death cohort, and these move one step down the pyramid each year without any decrement (indeed incrementing due to births) until reaching the very bottom. In short, the locations of increment and decrement, and the direction of movement (when so visualized) are all switched. The chronological and thanatological renewal models are almost perfectly opposite descriptions of the same process.



## A Unique solution for thanatological $r$

This appendix contains a brief proof that the real solution for the intrinsic growth rate,  $r$ , is unique for the case of the thanatological renewal model, (10), and can be proven so in essentially the same fashion as those in existence for the Lotka-Euler model, (11). This proof follows that given in Pressat (1973). Define a convenience function,  $I(r)$ , for the integrand of (10) for a given  $r$  and fixed  $f^*(y)$  and  $d(a)$ :

$$I(r) = \int_{y=0}^{\infty} \int_{a=0}^{\infty} f^*(y) d(a+y) e^{-ra} da dy \quad (21)$$

Since the death distribution function,  $d(a)$ , and fertility function,  $f^*(y)$ , are continuous and non-negative,  $\lim_{r \rightarrow +\infty} I(r) = 0$  and  $\lim_{r \rightarrow -\infty} I(r) = \infty$ . If  $r_2 > r_1$ , then  $I(r_1) > I(r_2)$ .  $I()$  is therefore a continuous and monotonically decreasing function of  $r$  with boundaries that include the value 1 of (10), and necessarily only obtain this value once. As with the Lotka-Euler equation, there will be more complex conjugate solutions for  $r$  in the thanatological model, and these are not explored in this paper.

## B Equivalence in stability

This appendix contains a proof that the thanatological renewal equation implies the same intrinsic growth rate,  $r$ , as the Lotka-Euler model if the starting population is stable, given a particular set of thanatological fertility rates. This is identical to claiming that the right side of the renewal equation is equal given the same  $r$ . Since there is a unique real solution, demonstrated in the previous appendix, then it is sufficient to show that the two integral equations are equal under these conditions. The basic relationship is:

$$\int_{a=0}^{\infty} l(a) e^{-ra} f(a) da = \int_{y=0}^{\infty} \int_{a=0}^{\infty} d(a+y) e^{-ra} f^*(y) da dy \quad (22)$$

when

$$f^*(y) = \frac{b^*(y)}{c^*(y)} \quad (23)$$

$$b^*(y) = \int_{a=0}^{\infty} b(a) \mu(a+y) \frac{l(a+y)}{l(a)} da \quad (24)$$

$$c^*(y) = \int_{a=0}^{\infty} c(a) \mu(a+y) \frac{l(a+y)}{l(a)} da \quad (25)$$

Note that:

$$c(a) = \frac{l(a)e^{-ra}}{\int l(a)e^{-ra} da} \quad (26)$$

$$b(a) = f(a)c(a) \quad (27)$$

Replacing  $f^*(y)$  with the full expanded expression and plugging into the thanatological renewal equation gives:

$$= \int_{y=0}^{\infty} \int_{a=0}^{\infty} d(a+y)e^{-ra} \frac{\frac{\int_{t=0}^{\infty} f(t)l(t)e^{-rt}\mu(a+y)\frac{l(t+y)}{l(t)} dt}{\int_{t=0}^{\infty} l(t)e^{-rt} dt}}{\frac{\int_{t=0}^{\infty} l(t)e^{-rt}\mu(t+y)\frac{l(t+y)}{l(t)} dt}{\int_{t=0}^{\infty} l(t)e^{-rt} dt}} da dy \quad (28)$$

The denominator of  $c(a)$  cancels out:

$$= \int_{y=0}^{\infty} \int_{a=0}^{\infty} d(a+y)e^{-ra} \frac{\int_{t=0}^{\infty} f(t)l(t)e^{-rt}\mu(t+y)\frac{l(t+y)}{l(t)} dt}{\int_{t=0}^{\infty} l(t)e^{-rt}\mu(t+y)\frac{l(t+y)}{l(t)} dt} da dy \quad (29)$$

Some  $l(a)$ 's also cancel out:

$$= \int_{y=0}^{\infty} \int_{a=0}^{\infty} d(a+y)e^{-ra} \frac{\int_{t=0}^{\infty} f(t)e^{-rt}\mu(t+y)l(t+y) dt}{\int_{t=0}^{\infty} e^{-rt}\mu(t+y)l(t+y) dt} da dy \quad (30)$$

Now  $d(a+y) = \mu(a+y)l(a+y)$ , so we can cancel the inner integral with the denominator:

$$= \int_{y=0}^{\infty} \int_{a=0}^{\infty} f(a)e^{-ra}\mu(a+y)l(a+y) da dy \quad (31)$$

Note also that  $l(a) = \int_{=a}^{\infty} d(x) dx$  (present livings are future deaths), which brings us back to the chronological formulation:

$$= \int_{a=0}^{\infty} e^{-ra}l(a)f(a) da \quad (32)$$

This finding essentially proves that in the stable population there is at least one thanatological fertility rate schedule that will satisfy the constraints of the lifespan distribution and  $r$ . However, it is not necessary to derive the thanatological fertility distribution in the way prescribed here, and indeed an infinite number of such fertility distributions would satisfy the same constraints. Imagine these fertility rates cross-classified in both age dimensions, where two marginal sums give the thanatological and chronological rates, as they

would be calculated over the corresponding cross-classified exposures. The shape of this rate surface can be shifted around in infinitely many ways that would preserve a given growth rate and lifespan distribution, and the above proof shows one such mapping.

## C An iterative method to find the thanatological $r$

Coale (1957) proposed a fast-converging iterative approach to estimate the intrinsic growth rate for the Lotka-Euler equation. For the thanatological renewal model, a similar approach may be taken, with some slight modifications to Coale's original. The following steps can be followed to estimate  $r$  from Equation (10):

1. Derive a first rough estimate of the mean remaining years of life at reproduction,  $\widehat{T}^*$ , akin to Lotka's mean generation time,  $T$ . To start, a good-enough guess is to just assume  $r = 0$ :

$$\widehat{T}^* = \frac{\int_{y=0}^{\infty} \int_{a=0}^{\infty} y d(a+y) f^*(y) da dy}{\int_{y=0}^{\infty} \int_{a=0}^{\infty} d(a+y) f^*(y) da dy} \quad (33)$$

2. A first rough guess at the net reproduction rate,  $R_0$  is given by

$$R_0 = \int_{y=0}^{\infty} \int_{a=0}^{\infty} d(a+y) f^*(y) da dy \quad (34)$$

3. A first rough estimate of  $r$ ,  $r^0$ , is given by

$$r^0 = \frac{\ln(R_0)}{\widehat{T}^*} \quad (35)$$

4. Plug  $r^0$  into Equation (10) to calculate a residual,  $\delta^0$ .
5. Use  $\delta^0$  and  $\widehat{T}^*$  to calibrate the estimate of  $r$  using

$$r^1 = r^0 + \frac{\delta^0}{\widehat{T}^* - \frac{\delta^0}{r^0}} \quad (36)$$

6. Repeat step (4) to to derive a new  $\delta^i$ , then step (5) to refine  $r^i$ , until converging on a stable  $r$  after some 20 or so iterations, depending on the degree of precision desired ( $\widehat{T}^*$  is not updated in this process).

The above procedure is more computationally efficient than minimizing the absolute residual of Equation (10) using a generic optimizer. Alternatively, one could use the method of cumulants to estimate  $r$ , but this would entail less precision than the above (unless one goes beyond, say, five cumulants), and this has not yet been worked out at this time.

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