

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

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## **Structured abstract**

### **Background**

The Lotka-Leslie renewal model is the core of formal demography. This model is structured by age, and it does not account for time until death.

### **Objective**

I derive a specification of the classic renewal equation that is structured by years left rather than by years lived. I give both continuous and discrete variants of the derived model, and relate these to the Lotka-Leslie renewal model.

### **Results**

In stability, the years lived and left renewal models are commensurable, implying identical intrinsic growth rates. I demonstrate approximate symmetry between years lived and left

age structure in stability when subject to intrinsic growth rates equal magnitude and opposite sign.

## **Conclusions**

Birth-death renewal processes can be expressed as death-birth processes, and vice versa.

## **Contribution**

The years left renewal model offers a new perspective on population renewal, and it is valid more generally as an aspect of birth-death processes.

## **Introduction**

Contemporary demography is built upon a small set of empirically regular age patterns. The models and methods of demography are in varying degrees prefaced on such regularity. There is evidence that many demographic phenomena are best described in the aggregate as a function of time since birth, and others of time until death, while others can be a function of both to some degree (Riffe et al. 2015, Wolf et al. 2015). Further, aggregate indices motivated by measures of remaining lifetime have also become widely-used indicators of ageing (Sanderson and Scherbov 2007). These observations motivate incorporating time-to-death into formal demographic methods and models.

In this paper, I explore some formal demographic consequences of a particular re-definition of age. Instead of counting age as the time passed since birth, consider the

amount of time left until death.<sup>1</sup> Individuals in this case move in the same direction along imaginary life lines, but the reference point for measurement is switched from birth to death. For individuals, the timing of events in life is exactly identified using either of years lived or left, but aggregate patterns differ.

The renewal model relates fertility, mortality, and population structure in a parsimonious form, revealing the long term consequences of a set of vital rates. All lines of contemporary demographic research are relatable to the renewal model, and by extension to stable population theory. The purpose of this paper is to describe the Lotka-Leslie renewal model when structured by years of life left. The years left 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. I have described a limited case of this perspective on renewal for the case of stationary populations (Riffe 2015), and here provide a broader treatment allowing for growth in the population. The years lived renewal model and the years left renewal model both describe the movement of population stocks over time, but from opposite vantage points.

I couch the present inquiry in terms of aggregate renewal of human populations, but the renewal model is more generally a description of the birth-death process (Cox 1962, Feller 1941), and so may be valid for other kinds of renewable aggregates. The present inquiry establishes the validity of the model, but does not argue for its empirical practicality or soundness. The years lived and left renewal models imply one another in the state of stability. We therefore present the years left model as a property implied by the standard Lotka-Leslie renewal model, as two sides of the same coin. The objective in this paper is to deepen our understanding of the Lotka-Leslie renewal model, and to

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<sup>1</sup>Elsewhere this quantity is referred to as *residual* life, time-to-death (TTD), prospective age (Sander-son and Scherbov 2007), or thanatological age (Riffe 2015).

offer an extension of stable population theory.

The next section of this article reviews the lifetable method of transforming age-classified data into remaining years classes. I then derive the continuous version of the years left renewal model, and some other stable properties. This is followed by the matrix version of the model, which is explained alongside the lifecycle graph. Finally, I explore patterns in stable age structure compared between the two models. I conclude that years left renewal offers a new perspective on the familiar Lotka-Leslie model.

## Requisites of a years left renewal model

The Lotka-Leslie renewal model (Leslie 1945, Sharpe and Lotka 1911) is situated in a closed, unisex, homogenous population framework. With parameters equated, the continuous form of the model contains a component for survival,  $\ell(a)$ , a scaling factor for growth,  $e^{-ra}$ , and a component for fertility,  $m(a)$ :

$$(1) \quad 1 = \int_{a=0}^{\infty} \ell(a) e^{-ra} m(a) da \quad .$$

Each of these elements is structured by age,  $a$ . The model can be approximated by observed data because age is typically known. Age in the growth factor,  $e^{-ra}$ , pertains to the passage of time more than it does to chronological age (these are synchronous for birth cohorts). The product of this growth factor and  $\ell(a)$  gives a function proportional to the stable age structure,  $c(a)$ , and it is often intuitive to imagine these two elements together as one for this reason. Female fertility rates,  $m(a)$ , are based on daughters born to mothers in this limited single-sex model. This model lends itself to commonly collected

data because age is typically known, and can be asked.

Remaining lifetime is different in this respect because we do not know when we will die— it is only knowable retrospectively or probabilistically. Under a set of simple assumptions, the same lifetable used to estimate  $\ell(a)$  can be used to partition and recombine counts observed by age into estimates classified by years of life left. Our objective is then to estimate a population structure component, similar to  $\ell(a)e^{-ra}$ , and a fertility component similar to  $m(a)$ , but each for the years left case. Taken together, these components yield the years left renewal model.

## A lifetable approximation of life left

The present inquiry approximates years left in the aggregate using lifetable-projected remaining lifetime, which is intended to approximate remaining lifetime under the strong assumptions of homogenous populations und fixed vital rates. Under these assumptions, each birth cohort undergoes the same pattern of attrition.

The basic transformation to years left starts with the well-known remaining years density function,  $f(y|a)$ .

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

where  $\mu(a)$  is the force of mortality. The  $f(y|a)$ - weighted average of  $y$  for a given  $a$  returns the remaining life expectancy column of the lifetable,  $e(a)$ .  $f(y|a)$  is also useful for decomposing age-classified data, such as the population pyramid, into remaining years classes. If  $P(a)$  is an age-classified population count, we can derive the years left version  $P(y)$ , using<sup>2</sup>

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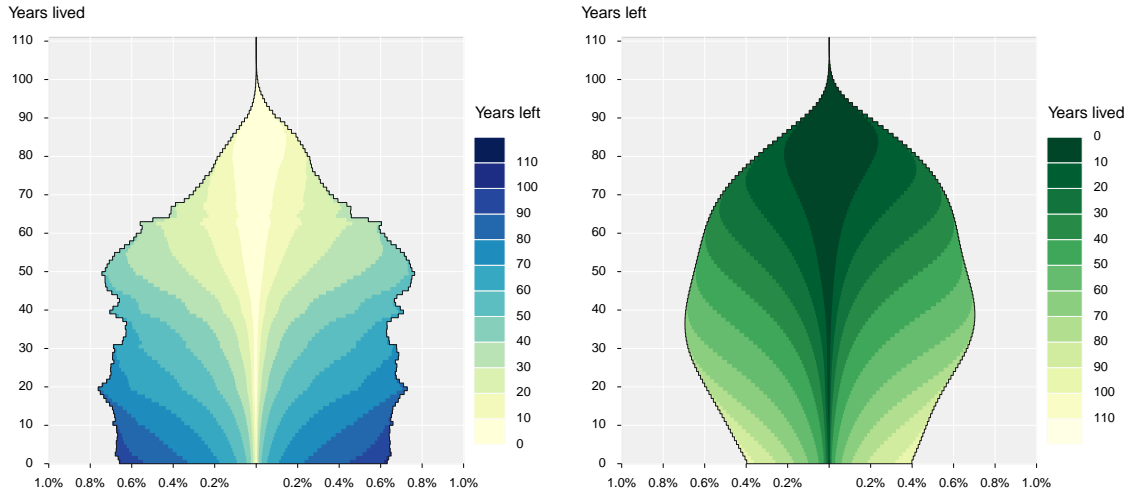
<sup>2</sup>An identical definition is found in Brouard (1989) and illustrated in Brouard (1986).

$$(3) \quad P(y) = \int_0^\infty P(a)f(y|a) \, da \quad .$$

Figure 1 shows this exercise for 2010 US data (Human Mortality Database), assuming homogeneity and that the 2010 period mortality schedule is held fixed. When looking from the age perspective (Figure 1a), this decomposition reveals projected years left heterogeneity within a stock of known age, but when viewed from the years left perspective (Figure 1b) it reveals age heterogeneity and the projected overall years left profile—the future death flow of the current population,  $P(y)$  under our assumptions.

Figure 1: 2010 US population structure

- (a) Age structure (years lived) decomposed by years left.      (b) Years left structure decomposed by years lived.



\*Population and mortality data from the HMD.

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 Vaupel (2009), showed that in stationary populations the marginal chronological and thanatological age structures are identical, and this provides a limited basis for comparison between the two perspectives.

Lifetable-derived thanatological age structure is probabilistic until after death in several senses. In this case, note that counts from a given age class are distributed over a range of higher ages according to a given mortality rate schedule; in this case a period mortality pattern is used. 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 the fruit of past demographic forces.

## 0.1 Thanatological fertility rates.

Any count classified by chronological age can be reclassified as in equation (3) given a pertinent lifetable. To derive thanatological fertility rates under these assumptions,  $\gamma(y)$ , apply (3) to chronological age-classified birth counts,  $B(a)$ , to get  $B(y)$  and again to exposure-to-risk,  $E(a)$ , to get  $E(y)$  and then divide in the usual way:

$$(4) \quad \gamma(y) = \frac{B(y)}{E(y)} \quad .$$

Figure 2b represents the full variety in female thanatological period fertility rates that can be found for all years of data that overlap in the HFD and HMD.<sup>3</sup> I show  $\gamma(y)$  calculated in this way because it enters into the renewal model here studied. Figure 2a

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<sup>3</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.

gives ASFR for the same populations and years as a more familiar reference, but note that both the x and y axes are different. The shape of thanatological fertility curves is speculative and due to the above-mentioned strong assumptions. Nonetheless it is best not to include such rates into a model blindly, so we offer this schematic overview of some of their characteristics.

Period thanatological fertility rates estimated in this way have a characteristic shape. The distribution is wider than that of chronological fertility rates. The range of post-childbearing lifespans stretches from zero, due e.g., to maternal mortality, to at least 100.<sup>4</sup> This spaghetti plot includes both fertility booms and busts, as well as some mortality crises (1918, WWII). Some patterns in the data (not highlighted in the figure) include that the left tail (a gauge of how orphan-prone a population is) has tended to fall over time. All populations have shown an increase in both the mean and mode of thanatological age at childbearing over time. Several contemporary populations now show modes of over 60 years. Period thanatological total fertility rates track standard period total fertility rates closely, but tend to be somewhat higher (not shown).

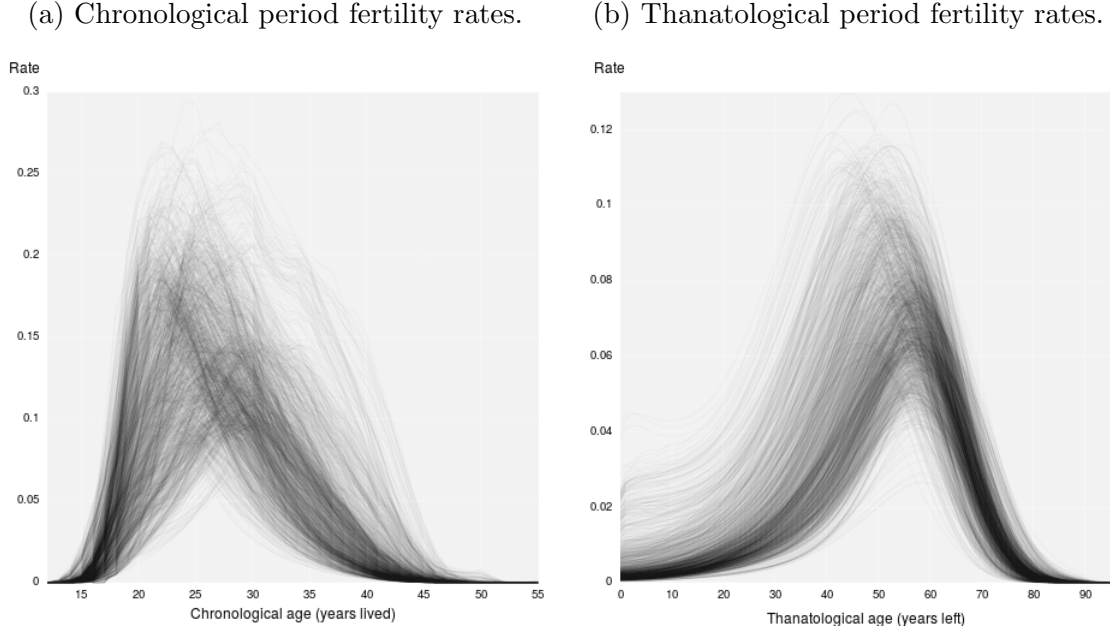
In general, thanatological fertility rates will not be useful for purposes of projection, unless their empirical regularity is stronger than typical ASFR. This is a question I do not seek to answer in the present treatment, but in any case such rates are not susceptible to direct measurement. There are 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.

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<sup>4</sup>For instance, Jeanne Calment lived for another 100 years after giving birth to her daughter.



Figure 2: Chronological and thanatological fertility rates, all 1933 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

The renewal model that follows uses thanatological fertility rates,  $\gamma(y)$ , the form of which is suggested in Figure 2b, and we refer to a homogenous, closed, unisex population based on female vital rates. Assuming constant vital rates, the births for the present year are given by

$$(5) \quad B(t) = \int_0^\infty P(y, t) \gamma(y) \, dy = \int_0^\infty P(a, t) m(a) \, da \quad ,$$

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

$$(6) \quad = \int_{y=0}^{\infty} \int_{a=0}^{\infty} \gamma(y) P(a, t) f(y|a) \, da \, dy \quad ,$$

where  $f(y|a)$  is defined per equation (2), so  $d(a)/\ell(0)$ . We can relate the present population to past births with  $P(a, t) = B(t - a)\ell(a)$ :

$$(7) \quad = \int_{y=0}^{\infty} \int_{a=0}^{\infty} \gamma(y) B(t - a) d(a + y) \, da \, dy \quad .$$

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:

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

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

$$(9) \quad 1 = \int_{y=0}^{\infty} \int_{a=0}^{\infty} \gamma(y) d(a + y) e^{-ra} \, da \, dy \quad .$$

Now compare this to Lotka's chronological formulation in Equation (1), which can be expressed as well as:

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

and note that (10) and (9) are really quite similar, since  $\int_{y=0}^{\infty} d(a+y) da = l(a)$ . For intuition, notice that  $l(a)$  is here decomposed into  $d(a)$ . Imagine a matrix of this decomposition, where one margin is chronological age and the other margin is thanatological age. For the chronological case (1), we multiply chronological age-specific fertility rates,  $m(a)$ , over the chronological age margin, and for the thanatological case we multiply  $\gamma(y)$  over the thanatological age margin.

There are gaps in the above line of development, since the jump from (7) to (8) (strong ergodicity) is assumed for the moment.<sup>5</sup> The step has some intuition, due to 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 (9) 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 (9) 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-

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<sup>5</sup>The step to exponential stability is proven for the discrete version of the model.

<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.

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  $\gamma(y)$  are calculated on the basis of differently distributed denominators  $E(a)$  versus  $E(y)$ .

Once one finds  $r$  from (9), other familiar stable population parameters can be calculated. For instance, we may calculate the mean thanatological generation time,  $T^*$ :

$$(11) \quad T^* = \frac{\int_{y=0}^{\infty} \int_{a=0}^{\infty} y e^{-ra} d(a+y) \gamma(y) \, da \, dy}{\int_{y=0}^{\infty} \int_{a=0}^{\infty} e^{-ra} d(a+y) \gamma(y) \, da \, dy} \quad .$$

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

$$(12) \quad R_0^* = e^{rT^*}$$

The birth rate,  $b$ , is given by

$$(13) \quad b = \frac{1}{\int_{y=0}^{\infty} \int_{a=0}^{\infty} e^{-ra} d(a+y) \, da \, dy} \quad ,$$

the denominator of which is the inside of equation (9) less  $\gamma(y)$ . This simplifies to

$$(14) \quad = \frac{1}{\int_{a=0}^{\infty} e^{-ra} l(a) \, da} \quad ,$$

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:

$$(15) \quad = \int_{y=0}^{\infty} \gamma(y) c^*(y) \, dy \quad .$$

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

$$(16) \quad c^*(y) = b \int_{a=0}^{\infty} e^{-ra} d(a+y) \, da \quad ,$$

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

$$(17) \quad = \int_{a=0}^{\infty} c(a) f(y|a) \, da$$

$$(18) \quad = \frac{\int_{a=0}^{\infty} d(a+y) e^{-ra} \, da}{\int_{a=0}^{\infty} l(a) e^{-ra} \, da} \quad .$$

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 (17). 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. I 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  $\omega \times \omega$ , where  $\omega$  is the number of equal-interval thanatological age classes into 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 populated primarily with non-zero positive entries. 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  $\mathbf{Y}$ ,  $\mathbf{S}$ , 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,  $\mathbf{S}$ , of unisex thanatological projection matrix.

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

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 (Riffe 2015). Fertility in a thanatologically structured human population occurs in all but the very highest thanatological age classes, which can be thought of as structural zeros, 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  $\gamma_y$  indicates the fertility probability for class  $y$  in the year  $t$  entering population (in the matrix columns). Each  $\gamma_y$  is then distributed over rows according to  $d_a$ . The fertility entry in row  $m$  and column  $n$  of  $\mathbf{Y}$  will therefore be  $\gamma_n \cdot d_m$ . 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,  $\gamma_y \cdot d_0$ , 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 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 survive to December 31st of the calendar year in which they were born.<sup>8</sup> The fertility component of  $\mathbf{Y}$ ,  $\Gamma$ , is then composed as in Matrix 0.2.

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<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.

<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.

Matrix 0.2: Fertility component,  $\Gamma$ , of unisex thanatological projection matrix.

$$\begin{array}{c} e_y \end{array} \begin{array}{cccccc} 0_t & 1_t & 2_t & 3_t & 4_t & 5_t \end{array} \\
 \begin{array}{c} 0_{t+1} \\ 1_{t+1} \\ 2_{t+1} \\ 3_{t+1} \\ 4_{t+1} \\ 5_{t+1} \end{array} \left( \begin{array}{cccccc} (1-\lambda)\frac{\gamma_0 d_0}{2} & (1-\lambda)\gamma_1 d_0 & (1-\lambda)\gamma_2 d_0 & (1-\lambda)\gamma_3 d_0 & (1-\lambda)\gamma_4 d_0 & 0 \\ \frac{\gamma_0 d_1}{2} & \gamma_1 d_1 & \gamma_2 d_1 & \gamma_3 d_1 & \gamma_4 d_1 & 0 \\ \frac{\gamma_0 d_2}{2} & \gamma_1 d_2 & \gamma_2 d_2 & \gamma_3 d_2 & \gamma_4 d_2 & 0 \\ \frac{\gamma_0 d_3}{2} & \gamma_1 d_3 & \gamma_2 d_3 & \gamma_3 d_3 & \gamma_4 d_3 & 0 \\ \frac{\gamma_0 d_4}{2} & \gamma_1 d_4 & \gamma_2 d_4 & \gamma_3 d_4 & \gamma_4 d_4 & 0 \\ \frac{\gamma_0 d_5}{2} & \gamma_1 d_5 & \gamma_2 d_5 & \gamma_3 d_5 & \gamma_4 d_5 & 0 \end{array} \right)$$

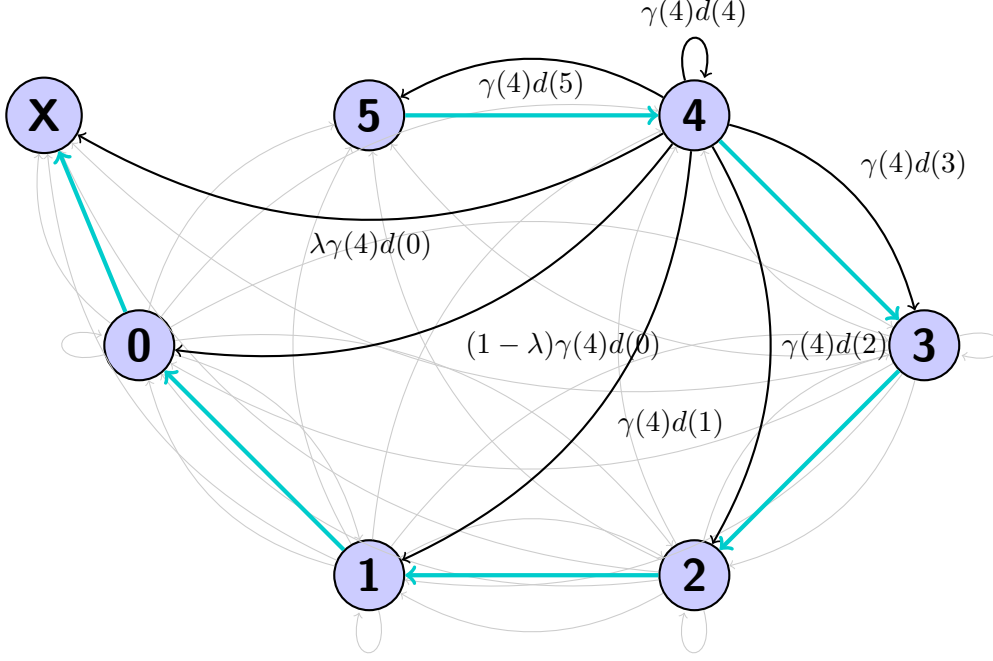
The survival matrix,  $\mathbf{S}$ , and the fertility matrix,  $\Gamma$  sum to create the thanatological projection matrix,  $\mathbf{Y}$ :

$$(19) \quad \mathbf{Y} = \mathbf{S} + \Gamma$$

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 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 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  $\gamma(y)$ , and these births distribute out to all other age classes according to the lifespan distribution from the life table,  $d_a$ . 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



Figure 3: The thanatological lifecycle graph



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 are 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 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 (7) to (8), 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>

## Stable age structure

The thanatological stable age structure, as given in equation (16), displays some regular patterns worthy of mention. In Figure 4 the same underlying mortality pattern, based on US males and females from 2010 (HMD) is rescaled to different mortality levels and growth rates. Figure 4a shows stable age structures by chronological age, while Figure 4b shows stable age structure of the same population by thanatological age. Rows indicate growth rates, descending from positive to negative, while columns indicate the both-sex

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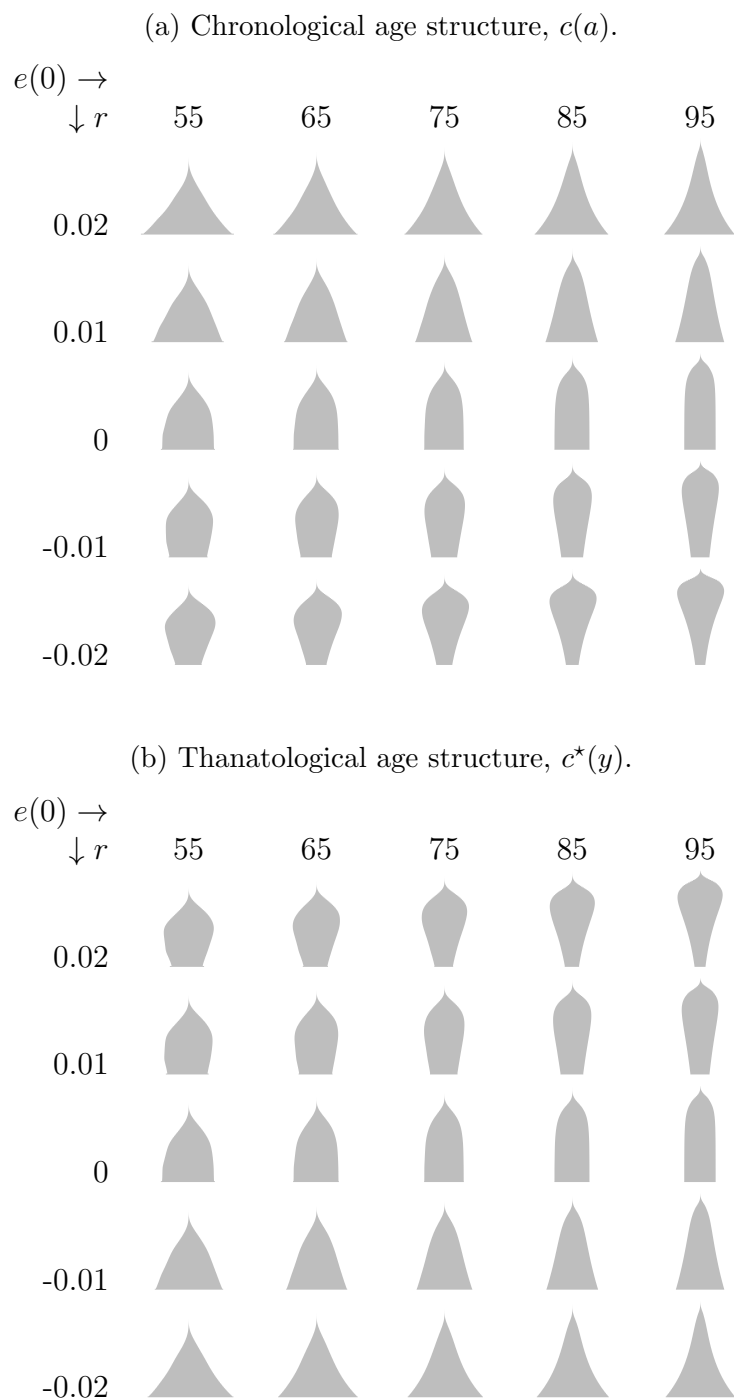
<sup>9</sup>Some care needs to be taken in order to demonstrate this point, since common approximations and adjustments used in matrix construction can throw things off. R code is available from the author to demonstrate this point. See also Appendix B for the corresponding proof from the continuous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

mean life expectancy,  $e(0)$ , to which 2010 US mortality is scaled. The rows and columns of Figures 4a and 4b are organized in identical fashion, each element referring to the same intrinsic growth rate and average  $e(0)$ .

The Brouard-Carey equality is visible by noting that the middle rows from the chronological and thanatological matrices are identical. In comparing any other rows, however, it is as if the thanatological matrix were flipped: a growing population in the chronological perspective looks like a shrinking population in the thanatological perspective, and vice versa. While the bottom row of Figure 4a looks like the top row of Figure 4b, the profiles are not rigorously identical, and the symmetry is only noteworthy as rule of thumb. In thinking of the birth flow and the death flow, the approximate reflection of age structure over the  $r$ -axis does make sense: in a shrinking population new birth cohorts are smaller than old birth cohorts, which means that relatively fewer people are born, and relatively more are in older ages, closer to dying. In this case, the base of the chronological pyramid is relatively thin, while the base of the thanatological leaf is relatively thick. The same holds in reverse for growing populations.

While this heuristic applies to stable populations, but it does not necessarily hold for real observed populations under changing mortality. Further, the observation is only valid for the period perspective in stability. In the cohort perspective, i.e., within closed birth cohorts, the analogy to stationary populations is spot on— That is, within birth cohorts the Brouard-Carey equality is exactly true when applied to the lifespan distribution.

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



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

## Discussion

The thanatological renewal model is valid, but I do not expect the reader to accept that it is also a sound description of the fundamental forces of population renewal. Specifically, I expect that the fertility rates are best described in the margin by chronological age and not by thanatological age. The main contribution of this inquiry is to demonstrate a transformation of the Lotka-Leslie renewal model, and to highlight a parallel aspect of renewal that occurs irrespective of its empirical regularity. That is, it is the case that in the moment of birth, both progenitor and baby have a certain number of remaining years of life, and that the range of potential values for both is great. The thanatological renewal model therefore is an abstraction of a real process, and not merely an adornment of the chronological renewal model.

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 class 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 (9), 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 swapped. The chronological and thanatological renewal models are almost perfectly opposite descriptions of the same process.

This symmetry is visible in comparing the chronological and thanatological renewal

equations (10) and (9), and it is also seen in the approximate symmetry between chronological and thanatological age structure profiles under intrinsic growth rates of equal magnitude but opposite sign. The thanatological projection matrix may be thought of as a sort of dual to the Leslie matrix— a twin construct. The thanatological perspective on renewal I present is a hitherto undescribed property of the Lotka-Leslie renewal model. Possible applications of this perspective on renewal are mentioned in Riffe (2015), the only difference in the present inquiry is that we now account for constant growth rates in the population. The present treatment is broader, and potentially applicable to a wider range of birth-death processes. In the first place, we offer a deeper understanding of the Lotka-Leslie renewal models.

## 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, (9), and can be proven so in essentially the same fashion as those in existence for the Lotka-Euler model, (1). This proof follows that given in Pressat (1973). Define a convenience function,  $I(r)$ , for the integrand of (9) for a given  $r$  and fixed  $\gamma(y)$  and  $d(a)$ :

$$(20) \quad I(r) = \int_{y=0}^{\infty} \int_{a=0}^{\infty} \gamma(y) d(a+y) e^{-ra} \, da \, dy$$

Since the death distribution function,  $d(a)$ , and fertility function,  $\gamma(y)$ , 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 (9), 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:

$$(21) \quad \int_{a=0}^{\infty} \ell(a) e^{-ra} f(a) \, da = \int_{y=0}^{\infty} \int_{a=0}^{\infty} d(a+y) e^{-ra} \gamma(y) \, da \, dy$$

when

$$(22) \quad \gamma(y) = \frac{b^*(y)}{c^*(y)}$$

$$(23) \quad b^*(y) = \int_{a=0}^{\infty} b(a) \mu(a+y) \frac{\ell(a+y)}{\ell(a)} \, da$$

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

Note that:

$$(25) \quad c(a) = \frac{\ell(a)e^{-ra}}{\int \ell(a)e^{-ra} da}$$

$$(26) \quad b(a) = m(a)c(a)$$

Replacing  $\gamma(y)$  with the full expanded expression and plugging into the thanatological renewal equation gives:

$$(27) \quad = \int_{y=0}^{\infty} \int_{a=0}^{\infty} d(a+y)e^{-ra} \frac{\frac{\int_{t=0}^{\infty} m(t)\ell(t)e^{-rt}\mu(a+y)\frac{\ell(t+y)}{\ell(t)} dt}{\int \ell(t)e^{-rt} dt}}{\frac{\int_{t=0}^{\infty} \ell(t)e^{-rt}\mu(t+y)\frac{\ell(t+y)}{\ell(t)} dt}{\int \ell(t)e^{-rt} dt}} da dy$$

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

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

Some  $\ell(a)$ 's also cancel out:

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

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

$$(30) \quad = \int_{y=0}^{\infty} \int_{a=0}^{\infty} m(a)e^{-ra}\mu(a+y)\ell(a+y) da dy$$



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

$$(31) \quad = \int_{a=0}^{\infty} e^{-ra} \ell(a) m(a) \, da$$

This proof establishes 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 (9):

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  $r = 0$ :<sup>10</sup>

$$(32) \quad \widehat{T}^\star = \frac{\int_{y=0}^{\infty} \int_{a=0}^{\infty} y d(a+y) \gamma(y) \, da \, dy}{\int_{y=0}^{\infty} \int_{a=0}^{\infty} d(a+y) \gamma(y) \, da \, dy}$$

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

$$(33) \quad R_0^\star = \int_{y=0}^{\infty} \int_{a=0}^{\infty} d(a+y) \gamma(y) \, da \, dy$$

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

$$(34) \quad r^0 = \frac{\ln(R_0^\star)}{\widehat{T}^\star}$$

4. Plug  $r^0$  into Equation (9) to calculate a residual,  $\delta^0$ .

5. Use  $\delta^0$  and  $\widehat{T}^\star$  to calibrate the estimate of  $r$  using

$$(35) \quad r^1 = r^0 + \frac{\delta^0}{\widehat{T}^\star - \frac{\delta^0}{r^0}}$$

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 ( $\widehat{T}^\star$  is not updated in this process).

The above procedure is more computationally efficient than minimizing the absolute residual of Equation (9) 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 is not explored.

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<sup>10</sup>Using the Brouard-Carey equality, the denominator could also be:  $\int_{y=0}^{\infty} \ell(y) \gamma(y) \, dy$

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