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The Triangular Life Table: A unified framework for the study of mortality and morbidity

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Introduction

Over the past two centuries, populations around the globe have experienced a remarkable increase in the average length of life (Riley, 2001; Oeppen and Vaupel, 2002). Whether this is a normatively desirable outcome or not depends, *inter alia*, on the health quality in which those longer lives are lived. In fact, living longer does not necessarily imply living more years in a healthy state, and the relationship between mortality and morbidity has been the subject of a longstanding debate with fundamental implications for the sustainability of pension and health care systems all over the world (Grunenberg, 1977; Fries, 1980; Manton, 1982).

Unfortunately, currently existing methods to investigate the intertwined relationship between mortality and morbidity have typically ignored the number of years individuals spend unhealthy. A good example is the Sullivan method, which combines disease/disability *prevalence* data with mortality information to estimate the average number of years individuals are expected to live in "good" or "less-than-good" health (Sullivan, 1971). In this paper, we propose an extension to the classic life table (Preston et al., 2001), the so-called "triangular life table", with the aim of taking into account not only the ages at which individuals die, but also those in which they cease to be in full health (i.e., the age at morbidity onset). Importantly, this novel approach allows to incorporate duration (i.e., the time spent in different states) and investigates how survival and morbidity jointly evolve across all possible ages.

Methodology

We consider a three-state model (see Figure 1) with two "living" states, *healthy* (H) and *unhealthy* (U), and a "dead" state (M - for *mortem*). We assume individuals are born healthy and cannot experience transitions between U and H, meaning that if their health deteriorates, no recovery is possible. Adopting this perspective, we aim at modelling the onset of major chronic diseases, which are the leading causes of death and disability in most low-mortality countries. If we denote with x the length of life, h the amount of years spent in H, and u the amount of years spent in U, the relationship $x = h + u$ will hold and the model will translate graphically

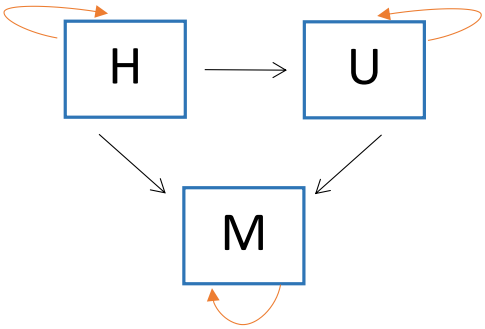

Figure 1. Our three-state model: healthy H, unhealthy U, dead M. We assume no transition is possible between U and H, implying that recovery is not contemplated.

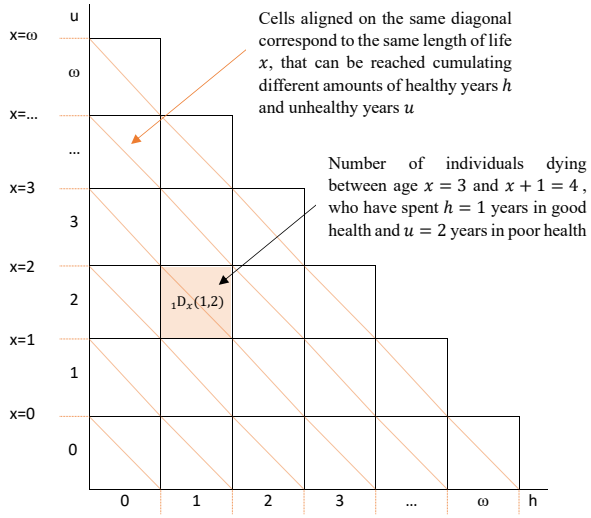

Figure 2. Example of a column in the new life table. Here presented the case of observed deaths ${}_1D_x(h,u)$. The symbol ω denotes the maximal attainable lifespan.

in two different trajectories on a (h,u) plane: one being horizontal, indicating sustained health throughout one's life, and the other resembling a "mirrored-L", indicating the emergence of health issues at some point in one's life.
We propose a new period life table, where we follow a synthetic cohort of individuals throughout their lives, assuming that at every age they are exposed not only to the observed mortality pattern of a population, but also to its morbidity experience. The various quantities of the classic life table are age-specific. Here, they depend on the amount h of years of life spent in a healthy state, and the amount u of years spent in an unhealthy state. Instead of calculating rates, probabilities, person-years, and other metrics for each specific age x, they are computed for different combinations of h and u, such that $x = h + u$. In this way, the "original" life table columns become triangular tables, as exemplified in Figure 2. For simplicity, we consider single-age intervals and assume transitions between H and U happen at the beginning of the interval.

Implementation

The crucial step in constructing a period life table involves transforming the observed age-specific death rates into age-specific probabilities of dying. In our model, the are two possible trajectories to death: never getting unhealthy and then dying $(H \to M)$, and getting unhealthy at some point in the lifespan and then dying $(H \to U \to M)$. This implies that supplementary information is needed to compute the new life table: transition rates, from H to U, to be converted into the corresponding transition probabilities. In this section, we present how we derived these rates and probabilities, following Preston et al. (2001). In the classic framework, the number of individuals in the synthetic cohort dying between age x and

$x+1$ ($_1d_x$) is computed as

$$_1d_x = \ell_x - \ell_{x+1} \tag{1}$$

where ℓ_x is the proportion of individuals who survived to age x, ℓ_{x+1} to $x+1$. In this new setting it becomes

$$_1d_x(h,u) = \ell_x(h,u) - \ell_{x+1}(h+1,u) - \ell_{x+1}(h,u+1) \tag{2}$$

In essence, the number of deaths in the cohort between ages x and $x+1$ for individuals who have spent h years in good health and u years in poor health ($h+u=x$) can be calculated by subtracting the count of those who survive to age $x+1$ with either an additional year of good health, $\ell_{x+1}(h+1,u)$, or an additional year in poor health, $\ell_{x+1}(h,u+1)$, from the population alive at age x with h years spent in good health and u years in poor health, $\ell_x(h,u)$.[1]

Let $_1L_x(h,u)$ denote the number of person-years lived by the cohort between ages x and $x+1$ with h years spent healthy, and u years spent unhealthy. Then, the death rates $_1m_x(h,u)$ between ages x and $x+1$, for individuals with h years spent in health and u with a health condition are

$$_1m_x(h,u) = \frac{_1d_x(h,u)}{_1L_x(h,u)} \tag{3}$$

and the corresponding probability of dying is

$$_1\pi_x(h,u) = \frac{_1d_x(h,u)}{\ell_x(h,u)}. \tag{4}$$

It is worth mentioning that, depending on the value of u, this formula provides the probability of both possible transitions to death. In fact, if $u=0$, Eq. (4) returns the probability of dying in good health at age $x=h$; for $u>0$, it represents the chance of dying at age $x=h+u$, having spent an initial h years healthy and the remaining u years unhealthy. Instead, the transition rates $_1w_x(h)$ from H to U, at age $x=h$ are given by

$$_1w_x(h) = \frac{\ell_{x+1}(h,1)}{_1L_x(h,0)} \tag{5}$$

and the probability of becoming unhealthy after h years spent in health is

$$_1\pi_x^{HU}(h,0) = \frac{\ell_{x+1}(h,1)}{\ell_x(h,0)}. \tag{6}$$

Now

$$_1L_x(h,u) = \ell_{x+1}(h+1,u) + \ell_{x+1}(h,u+1) + {}_1a_x(h,u)\,{}_1d_x(h,u) \tag{7}$$

where $\ell_{x+1}(h+1,u)=0$ for $u>0$, and $_1a_x(h,u)$ is the average number of person-years lived by members of the cohort who died between ages x and $x+1$ having spent h years healthy, and u unhealthy.

[1] Note that, since U is an absorbing state, $\ell_{x+1}(h+1,u)$ will be zero if $u>0$.

Emulating Preston et al. (2001), combining (2) and (7) we obtain the two following conversion formulae

$$ {}_1\pi_x(h,u) = \frac{{}_1m_x(h,u)}{1+(1-{}_1a_x(h,u))\cdot {}_1m_x(h,u)} \tag{8} $$

$$ {}_1\pi^{HU}_x(h,0) = \frac{{}_1w_x(h)}{1+(1-{}_1a_x(h,0))\cdot {}_1m_x(h,0)} \tag{9} $$

that allow us, from the observed death and $H \to U$ transition rates, to compute all the remaining columns of the life table. The next section outlines the steps to be followed.

Constructing the Period Triangular Life Table

The new framework we propose decomposes the length of life x in the sum of years spent in a healthy state h, and the amount of years spent in an unhealthy state u. Consequently, both the inputs and the outputs of the table will need to be derived for all the possible combinations of h and u, such that $x = h + u$.
Before proceeding, we want to point out that this has an impact on the terminal age interval. In this context, an open-ended interval from a certain age x^* becomes less straightforward than in the one-dimensional case, as it would cover the whole positive surface above the triangle with vertices $(0,0)$, $(0,x^*)$ and $(x^*,0)$ in the $h-u$ plane. For instance, if $x^* = 90$, where should an individual aged 95 with $h = 91$ and $u = 4$ be allocated? Since the answer to this type of questions is not clear, we exclude all the observations with age older than a set value ω.
Three observed quantities are needed to produce the period triangular life table. With the only difference that they now depend on h and u, the first two are shared with the traditional approach: the mid-year population in age interval x to $x+1$, denoted as ${}_1N_x(h,u)$, and the number of deaths between ages x and $x+1$, ${}_1D_x(h,u)$. The third is specific to this setting and consists in the number of transitions $H \to U$ between ages $x = h$ and $x+1$, ${}_1U_x(h)$.
From this data, the observed mortality rates, ${}_1M_x(h,u)$, and the observed transition rates, ${}_1W_x(h)$, are obtained as

$$ {}_1M_x(h,u) = \frac{{}_1D_x(h,u)}{{}_1N_x(h,u)} \qquad\qquad {}_1W_x(h) = \frac{{}_1U_x(h)}{{}_1N_x(h,0)} $$

Then, the procedure to compute the main columns of the life table can be outlined in a total of twelve steps.

1. Calculate the set of age-specific death rates ${}_1m_x(h,u)$ for every $x = h+u$. Assume that ${}_1m_x(h,u) = {}_1M_x(h,u)$.

2. Calculate the set of age-specific $H \to U$ transition rates ${}_1w_x(h)$ for every $x = h$. Assume that ${}_1w_x(h) = {}_1W_x(h)$.

3. Adopt a set of ${}_1a_x(h,u)$.

4. Compute the probability of dying ${}_1\pi_x(h,u)$, as

$$ {}_1\pi_x(h,u) = \frac{{}_1m_x(h,u)}{1+(1-{}_1a_x(h,u))\cdot {}_1m_x(h,u)}. $$

5. Compute the probability of becoming unhealthy ${}_1\pi_x^{HU}(h,0)$

$$ {}_1\pi_x^{HU}(h,0) = \frac{{}_1w_x(h)}{1+(1-{}_1a_x(h,0))\cdot {}_1m_x(h,0)}. $$

6. Compute the remaining probabilities

   - The probability of surviving healthy between ages $x=h$ and $x+1$

   $$ {}_1\pi_x^{HH}(h,0) = 1 - {}_1\pi_x^{HU}(h,0) - {}_1\pi_x(h,0). $$

   - The probability of surviving unhealthy between ages $x=h+u$ and $x+1$

   $$ {}_1\pi_x^{UU}(h,u) = 1 - {}_1\pi_x(h,u). $$

7. Choose a value of l_0, the radix of the life table.

8. Working sequentially from the youngest age to the oldest, calculate

$$ \ell_{x+1}(h+1,0) = \ell_x(h,0)\,{}_1\pi_x^{HH}(h,0) $$
$$ \ell_{x+1}(h,u+1) = \ell_x(h,u)\,{}_1\pi_x^{U}(h,u) $$

   where ${}_1\pi_x^{U}(h,u) = {}_1\pi_x^{HU}(h,u)$ for $u=0$, and ${}_1\pi_x^{U}(h,u) = {}_1\pi_x^{UU}(h,u)$ for $u>0$.

9. Derive

$$ {}_1d_x(h,u) = \ell_x(h,u) - \ell_{x+1}(h+1,u) - \ell_{x+1}(h,u+1). $$

10. Derive the person-years lived between ages x and $x+1$ with h years spent in health and u with a chronic condition as

$$ {}_1L_x(h,u) = \ell_{x+1}(h+1,u) + \ell_{x+1}(h,u+1) + {}_1a_x(h,u)\,{}_1d_x(h,u). $$

11. Derive the person-years lived above age $x=h+u$

   - If $u=0$

   $$ T_x(h,0) = \sum_{a=h}^{\omega} {}_1L_a(a,0) + \sum_{a=1}^{\omega} {}_1L_{a+h}(h,a). $$

   - If $u>0$

   $$ T_x(h,u) = \sum_{a=u}^{\omega} {}_1L_{a+h}(h,a). $$

12. Derive life expectancy at age $x=h+u$, with h years spent healthy and u years spent unhealthy as

$$ e_x(h,u) = \frac{T_x(h,u)}{\ell_x(h,u)}. $$

    This formula divides the number of person years that will be lived above age x by the number of individuals who will live them.

Contribution

The life table is one of demography's pillars. When facing the necessity to jointly study mortality and morbidity, three different life table models come to mind: prevalence based life tables, double decrement life tables (DDLT) and multistate life tables (MSLT) (Rogers et al., 1990; Schoen, 1988).
The Sullivan method (SM) (Sullivan, 1971) is an alternative name of the first. Notwithstanding all its acknowledged limitations (Rogers et al., 1990; Barendregt et al., 1997), it is still widely employed due to its simplicity, both in intelligibility and data requirements. The triangular life table (TLT) and the SM differ on multiple aspects, the most important being the perspective they adopt, dictated by the input they require. The TLT utilises occurrence-exposure rates, while the SM relies on prevalence rates. This implies the need of longitudinal data for the first, while cross-sectional surveys are enough for the second. Both methodologies do not admit recovery, even if one could argue that Sullivan's prevalence orientation implicitly permits it from one observation time point to the next, although not directly modelling it.
The triangular life table shares more ground with double decrement life tables: both need the same inputs and, again, exclude health improvements. However, in DDLTs individuals exit the population not only when they die, but also when their health deteriorates. This does not happen in our framework. When they transition from health to less than good health ($H \rightarrow U$), individuals start to accumulate unhealthy years (quantified by u) that will then influence their remaining life.
Many scholars indicate the multistate life table as the most accurate method to measure longevity and morbidity. When built on the same state space as ours, it models transitions including recuperation of health ($U \rightarrow H$), making it a more realistic representation of the the human life course. Like the triangular life table, it computes age-specific transition probabilities from incidence rates. Nevertheless, as the previously mentioned methodologies, multistate life tables implicitly assume an underlying Markov process governing these transitions, and the probability that an individual will leave a state depends only on the state and the age of the individual, not on the time spent in that state over the years. We believe the main strength of the life table proposed in this paper is the ability to overcome this assumption and incorporate duration, and all the information it carries. Attempts to relax the Markov assumption can be traced back to more than thirty years ago, when Wolf (1988) developed a modification of MSLTs to accommodate for duration dependency. The so-called multistate life table with duration-dependence (DDMSLT) is a multistate model where dependency is converted in a categorical variable and included in each state. The triangular life table can be considered a simpler and more intuitive version of the DDMSLT, with the nice addition of innovative graphics to help understand the studied phenomena.
In theory, the TLT does not require more data than the MSLT, but it exploits it more. We record not only when transitions between two states happen, but also the time elapsed before they happen. Indeed, as already pointed out multiple times, the triangular life table, at its current development, does not permit recovery. This is a feature we intend to investigate and incorporate in the future, since the recuperation of health plays a strong role in extending healthy life (Rogers

et al., 1990). However, the definition of "unhealthy" as the emergence of a chronic condition justifies the exclusion of a $U \to H$ transition.
One of the main goals when computing a life table is the derivation of life expectancy (LE). It is a simple metric to understand, both for scientists and the general public, and it can be used to effectively inform policy makers. The expectancies calculated via Sullivan, double decrement and multistate life tables summarise information related to the health states *separately*: healthy life expectancy (HLE) and unhealthy life expectancy (ULE), to give an example. From the triangular setting, an indicator reflecting the whole health trajectory experienced (combinations of h and u) can be extracted, incorporating both dimensions of health *simultaneously*.
Apart from the "usual suspects" discussed above, it is worth to also mention multiple time scales models. Carollo et al. (2023) recently demonstrated the method using the same basic illness-death model we adopt, resulting in a triangular representation similar to the one presented in this paper. However, our objectives and approaches differ significantly: we develop a life table-oriented technique, while they lean towards an event history analysis direction.

Data

The empirical data we will have access to and that will be used in the complete version of the paper is extracted from the mortality and health records for the entire population of Denmark (roughly 5.8 Million inhabitants) which have been updated yearly since 1986. Such records capture the ages at which individuals residing in the country die or are diagnosed from one of the following major chronic diseases: diabetes; myocardial infarction; angina pectoris; other diseases of the heart; stroke; chronic bronchitis/chronic obstructive pulmonary disease/emphysema; cirrhosis of the liver; malignant tumor; parkinsonism; Alzheimer's disease and chronic renal failure. Linking mortality and health information, we are able to compute age-at-first-diagnosis and age-at-death for all individuals dying at a given year, from which we infer the corresponding values of x, h and u.

Future Outlook

The paper will feature an application of the developed methodology using the data previously described for the years between 2000 and 2020. This empirical section has a twofold objective. Firstly, we are interested in the study of two surfaces that can be produced with the triangular life table: the survival function $\ell_x(h, u)$ and the age-at-death distribution ${}_1d_x(h, u)$. Through identifying their properties, potential shapes, and observing their changes over time, our goal is to provide new insights into the evolution of mortality and morbidity. Figure 3 presents stylized/simplified examples of graphs we expect to create for the survival function $\ell_x(h, u)$ (analogous figures can be easily created for the corresponding age-at-death distributions ${}_1d_x(h, u)$). While our current dataset is limited to Denmark, our objective is to initiate the collection of technical information on these two surfaces.

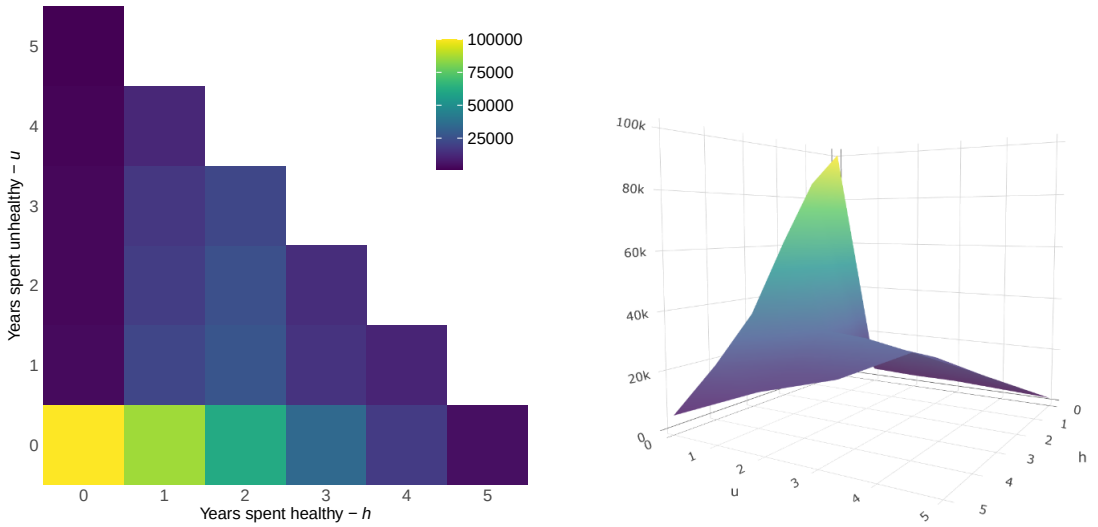

Figure 3. Example of possible plots for $\ell_x(h,u)$. Data manually generated. Maximum lifespan $\omega = 5$.

Looking ahead, we aspire to investigate whether they exhibit recurring patterns or behaviours across countries.

Secondly, the triangular life table can be used to address fundamental questions regarding the dynamics of mortality and morbidity. We intend to compare different time periods, to see, for instance, if remaining life expectancy at a certain age x, with a certain amount of years spent with a chronic condition u, has increased, remained stable or, even, decreased. Likewise, we will explore the relationship between the number of years individuals have lived in good and in less-than-good health (i.e., h and u) at time at death. Finally, we plan to construct separate triangular life tables for males and females to conduct further analyses on sex differences.

Relevance

Studies investigating mortality dynamics typically assume that gains in longevity are desirable no matter what. However, the fact that a non-negligible and potentially large and increasing fraction of individuals' lifespans are composed of years spent in less-than-good health questions the validity of this assumption. The trade-offs between the quantity of years of life and the "health quality" of those years could affect our assessments of populations' and individuals' health performance.

The tools presented in this paper allow estimating how individuals' lifespans are composed of years spent in good and in less-than-good health at time at death. Analytically, the possibility of breaking down individuals' length of life (x) as the sum of time spent in different health states ($h+u$) is a major breakthrough with respect to currently existing frameworks to investigate (healthy) population ageing. The new approach opens the possibility of going beyond state-of-the-art methods to advance our knowledge about the complex interplay between mortality and morbidity.

In particular, it allows revisiting under a new light the longstanding 'compression vs expansion of morbidity' debate (Grunenberg, 1977; Fries, 1980; Manton, 1982). Rather than relying on the comparison of average-based indicators that ignore the amount of time that individuals spend in "less-than-good" health (like Life Expectancy and Healthy Life Expectancy (Jagger et al., 2020)), the method proposed here takes into consideration the different ages at which individuals' health starts deteriorating, thus offering the chance to get a more comprehensive understanding of contemporary health and mortality dynamics.

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