All You Can Fit: Estimating a Fixed Rate of Aging on Human Mortality Surfaces

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Abstract

The individual rate of aging is defined as the relative derivative of one's risk of death by senescent causes with respect to one's age. The *b*-hypothesis, formulated by Vaupel (2010), suggests that all humans might share the same individual rate of aging. This can be true if and only if the aging process is captured by a Gompertz curve. Assuming that the *b*-hypothesis holds, we estimate the individual rate by fitting a two-dimensional gamma-Gompertz frailty model on human mortality surfaces. We present several statistical approaches, their advantages and shortcomings, as well as some preliminary conclusions.

Introduction

Lifetable adult mortality data (death counts and exposures in the absence of explanatory variables) are usually fit parametrically by a gamma-frailty model with a Gompertz-Makeham baseline (Beard 1959; Vaupel et al. 1979). This is a model for cohorts, but its

straight application to cohort mortality data produces dubious estimates for the individual rate of aging (Gompertz' b) as it does not incorporate improvements in age-specific mortality rates that occur yearly (see, for example, Tuljapurkar et al. 2000). Vaupel (1986) proposed a model that accounts for mortality progress over period assuming, though, one and the same improvement at each age and in every single year. Using Japanese data from HMD (2014), Missov and Lenart (2011) showed on a 3D-scatterplot for mortality reduction over age and year that this assumption is quite strong (see Missov and Lenart 2011: p.461, Figure 2). However, an extension of the model by Vaupel (1986), accounting for the different rates of mortality progress over age and year, results in a statistically unidentifiable model as the number of parameters to estimate exceed the number of data points. As a result, in order to assess the individual rate of aging properly, it is necessary to design adequately and fit accordingly statistical models for mortality surfaces instead of single cohorts.

A Gamma-Gompertz Model for Mortality Surfaces

Suppose in a population the *force of mortality* for an *individual* aged x in year y is given by

$$\mu(x, y \,|\, Z(x_0, y-x)\,) = Z(x_0, y-x) \cdot \mu(x, y \,|\, 1)\,, \tag{1}$$

where *frailty* $Z(x_0, y-x)$ of individuals in the $(y-x)$-cohort is a random variable that stays fixed from their adult age x_0 onwards. In this way we allow one's frailty to change from birth to age x_0, but not thereafter. We assume age x_0 is also big enough, so that the effect of the Makeham term is negligible. The density $\pi(z \,|\, x_0, y-x)$ characterizes the initial distribution of frailty, i.e. among individuals aged x_0 in year $y-x+x_0$. Here and throughout the entire article we assume that $x_0 \leq x$. The hazard $\mu(x, y \,|\, 1)$, which we will address as the *baseline hazard*, characterizes the mortality mechanism for the "standard" individual, i.e. an individual with unit frailty. Note that $\mu(x, y \,|\, Z(x_0, y-x)\,)$ characterizes a distribution conditional upon $Z(x_0, y-x)$. As frailty is unobserved, model (1) cannot be directly fit to

mortality data. Since the latter are usually aggregated for the entire population age- and year-wise, an adequate model for their study is the marginal distribution of (1) with respect to $Z(x_0, y-x)$. The *marginal* (or *population*) *force of mortality* of individuals aged x in year y is given by

$$\bar{\mu}(x,y) = \bar{z}(x, y-x) \cdot \mu(x, y \,|\, 1)\,, \tag{2}$$

where $\bar{z}(x, y-x)$ is the *expected* (we will also use the term *average*) frailty among survivors of the $(y-x)$-cohort to age x in year y.

As already pointed out, we assume that after x_0 mortality is predominantly senescent, i.e. $\mu(x, y \,|\, 1)$ for $x \geq x_0$ follows a Gompertz curve. Then the hazard $\mu(x, y \,|\, Z(x_0, y-x)\,)$ for an individual aged x in year y is given by

$$\mu(x, y \,|\, Z(x_0, y-x)\,) = Z(x_0, y-x) \cdot a(x_0, y) \cdot e^{b(x-x_0)}\,, \tag{3}$$

where $a(x_0, y)$ is the initial (at age x_0) baseline (for $Z(x_0, y-x) = 1$) hazard level in year y (to account for mortality progress from year $y-x$ to year $y-x+x_0$), and

$$b = \frac{\partial}{\partial x} \ln \mu(x, y \,|\, Z(x_0, y-x)\,)$$

is the individual rate of aging.

Using (2) and (3), we can express the marginal hazard $\bar{\mu}(x, y)$ as

$$\bar{\mu}(x,y) = \bar{z}(x, y-x) \cdot a(x_0, y) \cdot e^{b(x-x_0)}\,. \tag{4}$$

Suppose that individual frailty follows a gamma distribution with unit frailty and squared coefficient of variation γ, i.e. $Z(x_0, y-x) \sim \Gamma(1/\gamma, 1/\gamma)$. Then we can express the population force of mortality as

$$\bar{\mu}(x,y) = \bar{z}(x_0, y-x) \cdot [\bar{s}(x,y)/\bar{s}(x_0, y-x+x_0)]^{\gamma} \cdot a(x_0,y) \cdot e^{b(x-x_0)}\,, \tag{5}$$

where $\bar{s}(x,y)$ is the survivorship to age x for the cohort born in year $y-x$. This general outcome means that the population's force of mortality $\bar{\mu}(x,y)$ at age x in year y depends on the following quantities

(i) the average frailty $\bar{z}(x_0, y-x)$ of survivors to age x_0 in the $(y-x)$-cohort and the survivorship from age x_0 to age x in it

(ii) the initial (at age x_0) level of mortality $a(x_0,y)$ in year y

(iii) the rate of aging b (assumed to be constant)

As (i) vary across cohorts, (ii) varies across years, and $e^{b(x-x_0)}$ varies age-wise, (5) is an age-period-cohort model, which is unidentifiable unless we fix the behavior of the right-hand side on one of the three axes.

Statistically Feasible Models

Losing part of the generality in (5), we can deduce three special cases, in which, on the one hand, we are able to overcome the age-period-cohort unidentifiability problem, and, moreover, get a demographic insight from actual datasets. For conciseness we define the survivorship from age x_0 to x within the $(y-x)$-cohort by $\bar{\boldsymbol{S}} = [\bar{s}(x,y)/\bar{s}(x_0, y-x+x_0)]^{\gamma}$. Note that the product $\bar{z}(x_0, y-x) \cdot a(x_0,y)$ cannot be statistically disentangled when estimating model (5) or any of its simplifications that we further present – it is always estimated together on a log-scale as an intercept of the Poisson regression. Thus we are not able to assess separately the effect of selection $\bar{z}(x_0, y-x)$ to age x_0 and the effect of mortality improvement on the level of mortality $a(x_0,y)$ at the starting age in year y. All statistically feasible models deduced from (5) with their associated assumptions can be classified into the following three groups:

1. **Simple model**: The simplest case is the one, in which both the average frailty among survivors and the initial baseline hazard level do not change over cohorts and years:

$$\bar{\mu}(x, y) = \bar{z}(x_0, y_0 - x_0) \cdot a(x_0, y_0) \cdot \bar{\boldsymbol{S}}^{\gamma} \cdot e^{b\,\boldsymbol{x}}\,.$$

   Obviously this over-simplistic model is unrealistic given the mortality progress made in the last decades. Note that in this special case we would not be able to distinguish between the average frailty and the initial level of mortality. We can thus simplify the model as it follows:

$$\bar{\mu}(x, y) = \bar{w}(x_0) \cdot \bar{\boldsymbol{S}}^{\gamma} \cdot e^{b\,\boldsymbol{x}}\,, \tag{6}$$

   where $\bar{w}(x_0)$ denotes the starting level of mortality at age x_0 which is the same for each cohort and in every year due to the absence of mortality progress. Because of the latter this model does not advance our knowledge of estimating b and, thus, it can only serve as an example of the simplest statistically feasible two-dimensional gamma-Gompertz setting.

2. **Cohort model**: In the second special case we assume that the average frailty among survivors changes across cohorts. As a result we are not able to estimate $a(x_0, y)$. Model (5) reduces to

$$\bar{\mu}(x, y) = \bar{z}(x_0, y - x) \cdot \bar{\boldsymbol{S}}^{\gamma} \cdot e^{b\,\boldsymbol{x}}\,. \tag{7}$$

   Thus, we incorporate all period mortality improvements in the change of $\bar{z}(\cdot)$ over cohorts.

3. **Period model**: The last option is based on the assumption that $a(\cdot)$ captures the change in mortality over y. In this way we lose information about the average frailty among survivors. Formally:

$$\bar{\mu}(x,y) = a(x_0,y) \cdot \bar{\boldsymbol{S}}^{\gamma} \cdot e^{b\,\boldsymbol{x}}\,. \tag{8}$$

This model generalizes the approach proposed by Vaupel (1986), in which the mortality progress follows a specific parametric structure, i.e. $a(x_0,y) = a_0 \cdot e^{-\rho y}$.

Estimation Procedure

Formally, let $D(x,y)$ and $E(x,y)$ denote, respectively, the number of deaths and exposure at age x in year y. We can assume that death counts are Poisson-distributed $D(x,y) \sim \mathcal{P}\left[E(x,y) \cdot \bar{\mu}(x,y)\right]$. A common feature of all models in the previous section is that the log-force of mortality can be represented as a linear combination of a model matrix and a set of parameters: $\ln\left[\texttt{vec}(\bar{\mu}(x,y))\right] = \boldsymbol{X}\boldsymbol{\beta}$, where:

	$\boldsymbol{X}$	$\boldsymbol{\beta}$
Simple model	$[\mathbf{1} : \texttt{vec}(\ln(\bar{\boldsymbol{S}})) : \texttt{vec}(\boldsymbol{x}\,\mathbf{1}_n)]$	$[\ln(\bar{w}(x_0))\,;\,\gamma\,;\,b]$
Cohort model	$[\boldsymbol{\Psi} : \texttt{vec}(\ln(\bar{\boldsymbol{S}})) : \texttt{vec}(\boldsymbol{x}\,\mathbf{1}_n)]$	$[\ln(\bar{z}(x_0,y-x))\,;\,\gamma\,;\,b]$
Period model	$[\texttt{diag}(n) \otimes \mathbf{1}_m : \texttt{vec}(\ln(\bar{\boldsymbol{S}})) : \texttt{vec}(\boldsymbol{x}\,\mathbf{1}_n)]$	$[\ln(\bar{a}(x_0,y))\,;\,\gamma\,;\,b]$

The elements ψ_{ij} of $\boldsymbol{\Psi}$ are equal to 1, if row i belongs to cohort j, and zero otherwise. $\mathbf{1}_m$ and $\mathbf{1}_n$ are vectors of 1s, whose lengths m and n correspond to the number of ages and years, respectively, and $\otimes$ denotes the Kronecker product. This aids estimating all models using (penalized) iteratively re-weighted least-squares

$$(\boldsymbol{X}'\tilde{\boldsymbol{W}}\boldsymbol{X} + \boldsymbol{P})\tilde{\boldsymbol{\beta}} = \boldsymbol{X}'\tilde{\boldsymbol{W}}\tilde{\boldsymbol{z}}\,, \tag{9}$$

where $\boldsymbol{W}$ and $\tilde{\boldsymbol{z}}$ are derived from the Poisson assumption (McCullagh and Nelder 1989). Instead of enforcing parametric structure, we assume that both average frailty among survivors and mortality progress change smoothly over cohorts and years, respectively. This is captured in strategies 2. and 3. by the penalty term $\boldsymbol{P}$, which measures the roughness of

$\bar{z}(x_0, y - x)$ and $a(x_0, y)$ with differences of order d, weighted by a positive regularization parameter (Camarda 2012).

Application

We illustrate the performance of each strategy on Swedish female mortality data (HMD 2014) for years 1955-2000 and ages 80-104. Figure 1 (right panel) shows the outcomes over ages for selected years. While the first strategy fails to describe mortality developments, the other two models seem to be equally correct. We can discriminate between strategies 2. and 3., by computing the Bayesian Information Criterion (Schwarz 1978): the model in which mortality progress is captured by the parameters $a(x_0, y)$ outperforms the others (see left panel of Figure 1). Figure 2 illustrates the estimated parameters (with 99% confidence bounds) for the selected strategy.

Strategy	Dev	ED	BIC
1.	29722	3.0	29743
2.	2677	16.2	2791
3.	2429	14.1	2528

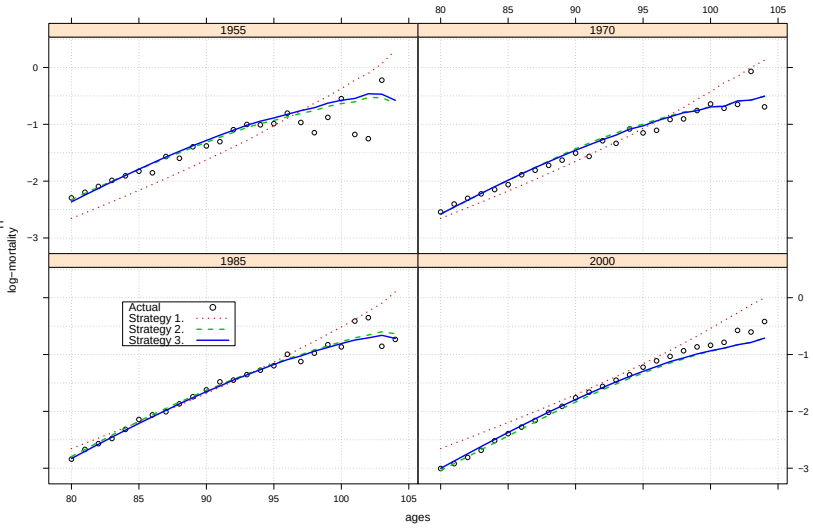

Figure 1: Left panel: Deviance, Effective Dimension and Bayesian Information Criterion. Right panel: Actual and fitted death rates, in log scale.

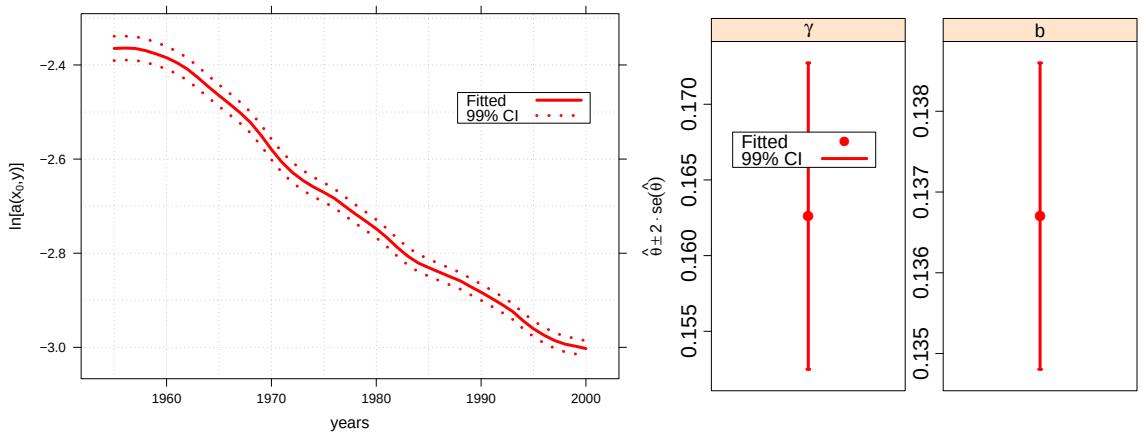

Figure 2: Estimated parameters from strategy 3. as well as the associated 99% confidence intervals.

Possible Model Extensions

In order to reduce the number of estimated parameters and overcome the age-period-cohort unidentifiability problem in (5), one can use auxiliary information and apply formal demographic relationships. One option would be to incorporate information about the human mortality plateau reached at a level of 0.7 (see Gampe 2010). In a gamma-Gompertz multiplicative setting this implies fixing $b/\gamma = 0.7$, which eliminates γ. Note that this approach is applicable to strategies 1.-3. from the previous sections if and only if we assume that γ is one and the same for all periods and cohorts. Nevertheless different cohorts $y - x$ could also have different $\gamma = \gamma(y - x)$. This assumption generalizes (5) since heterogeneity in frailty is allowed to change over cohorts. While the resulting parameter-vector leads again to the problem of model unidentifiability, the corresponding generalization of (5) reduces to a number of additional special cases, in which the resulting models could be feasible.

In order to solve the age-period-cohort unidentiability problem, one could also make use of some formal demographic relationships. For example, when $a(y)$ has a parametric structure as in Vaupel (1986), we can use such relationships to express $\bar{\mu}(x, y)$ just as a function of a_0 and γ. Missov et al. (2014) show that the auxiliary knowledge we need is just about the modal age at death and the observed period life expectancy increase over year.

This approach could be implemented, though, just in strategy 3. from the previous sections and only when $a(x_0, y) = a_0 \cdot e^{-\rho y}$.

We plan to explore these new approaches and estimate the presented class of models to different countries to shed new light on the estimation of the human rate of aging.

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