Variation and Vulnerability: Unobserved Heterogeneity in the Course of Mortality Transitions

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Abstract

The dramatic increase in life expectancy in most industrialized countries has been accompanied by a similarly striking compression in the variance of ages at death. We show that mortality variation in later life has nonetheless followed a contrasting pattern, with survivors to older ages becoming increasingly heterogeneous in their mortality risk. We argue that delayed mortality selection may be a result of ongoing improvements in survival at younger ages, and investigate the extent to which frailty models that account for changes in population composition over time capture both the temporal trend and age-pattern of mortality variability. We incorporate gamma-distributed frailty into a Siler trajectory representing the mortality hazard across the lifespan, and use maximum likelihood methods to simultaneously estimate the parameters of the resulting model. Our findings indicate that the distribution of frailty at older ages has been growing as survivorship increases, potentially accounting for the observed variability patterns.

Introduction: The Age-Pattern of Variability Trends

Over the past century, the dramatic increase in life expectancy in most industrialized countries has been accompanied by a similarly striking reduction in the variance of ages at death. Numerous indicators are available for characterizing variability in the distribution of deaths (Wilmoth and Horiuchi 1999; Cheung et al. 2005), including measures that explicitly focus on aging populations by conditioning on survival past childhood. While conditional measures exclude some information on deaths at younger ages (Robine 2001) they are advantageous in revealing patterns in mortality variation that are otherwise obscured by measures weighted towards early life (Edwards and Tuljapurkar 2005).

Using life tables from national populations with at least five decades of data (Human Mortality Database 2009), we examined variability patterns in the complete distribution of ages at death as well as in distributions conditioning on survival to successively older ages. The standard deviation of the mortality distribution for survivors to age a at time t is the square root of the variance, and is given by:

$$s_{a,t} = \sqrt{\frac{\int_a^\omega (x-a)^2 d(x)\,dx}{l(a)} - (e_a)^2}, \tag{1}$$

where x represents age at death and the life table function describing the distribution of deaths by age is denoted by $d(x)$. For the distributions conditional on survival to age a, remaining life expectancy is e_a, and $l(a)$ represents the population of survivors to age a. Finally, ω is the last age attained by a person in the life table. For the HMD life tables used in this analysis, $\omega = 110$, and all deaths at or above age 110 are included in this final category. Note that this general formula applies to the complete (unconditional) mortality distribution when $a = 0$. **Figure 1** traces the trend over time in s_0, s_{50}, and s_{75} in 24 countries, highlighting the trajectory of Sweden.

In order to juxtapose trends in each measure on a single scale, we standardized each age-specific standard deviation $s_{a,t}$ in year t to its value in 1900, when variation in the full mortality distribution began its visible decline and tracked the trend in the relative ratio, $r_{a,t}$, given by:

$$r_{a,t} = \frac{s_{a,t}}{s_{a,1900}} \tag{2}$$

Figure 2 illustrates the full range of age-specific trends for Swedish females using a filled contour plot. The division of the plot into distinct upper blue and lower red segments demonstrates that variability trends proceed in opposite directions for the young and old. While the distributions including younger people are becoming increasingly homogeneous, distributions encompassing only the growing older population show rising heterogeneity, especially among the oldest old.

Given that mortality rates have been declining at all ages including the oldest (Rau et al. 2008) why has the variation in later-life mortality not followed the temporal pattern of variation in overall mortality? Combining observations

about historical mortality transitions with concepts of selection and heterogeneity gives rise to the expectation that, in cohorts experiencing lower mortality at younger ages, a larger proportion of vulnerable individuals will survive to later ages. This, in turn, may be reflected in the growing variability of mortality within the older population. Because the trends at any given age may be a function of changes in the composition of successive cohorts reaching that age, we use frailty models and cohort life tables in the analyses described below to explore changes in unobserved heterogeneity over time.

The Siler Mortality Trajectory

We assume mortality on the individual level follows a Siler (1979) trajectory. We chose this model, rather than the more commonly used Gompertz (1825) because the latter includes information only on adult mortality, whereas the Siler model includes an exponentially declining hazard describing mortality in childhood, an exponentially increasing hazard characterizing mortality in adulthood, and a constant background component. Representing the full age range is key for our purpose, because we are primarily interested in how reductions in early life mortality influences the distribution of frailty and the subsequent variation in later-life mortality. The Siler model is given by:

$$\mu(x) = \alpha_1 e^{-\beta_1 x} + \alpha_2 e^{\beta_2 x} + \alpha_3, \tag{3}$$

where the α constants describe the hazard levels and the β parameters represent fixed rates of mortality decline and increase over age. Note that the cumulative hazard function $H(x)$ under a Siler model is given by:

$$H(x) = \frac{-\alpha_1}{\beta_1}(e^{-\beta_1 x} - 1) + \frac{\alpha_2}{\beta_2}(e^{\beta_2 x} - 1) + \alpha_3 x. \tag{4}$$

Modeling Changing Frailty

By introducing parameters meant to reflect individual differences in vulnerability, frailty models (Vaupel et al. 1979, Vaupel and Yashin 2006) address variance more explicitly than models focusing solely on the age trajectories of mortality hazards. Tuljapurkar and Edwards (2009) demonstrate that adding gamma-distributed frailty to the Gompertz model amplifies the calculated variance in age of death, capturing the observed trend more accurately than the standard model. Still, they note, that "temporal change in frailty has not been a feature of mortality models."

Changes in the distribution of frailty during the course of mortality transitions are, however, predicted by the theory of heterogeneity (Vaupel et al. 1979, Vaupel and Yashin 1985). In particular, progress in reducing past mortality rates allows a greater proportion of individuals (including frail ones) to survive to older ages, resulting in a population that is frailer on average than the past

population. Note that this expansion of frailty should become especially apparent at older ages (when survival changes are substantial enough to alter the population composition), and only if progress in reducing mortality at older ages is not sufficient for counterbalancing the effect of improved survival at younger ages. A steady but slow pace of survival improvement at older ages may have fostered a dynamic with gradually declining mortality rates at older ages and variability trends that hint at the changing population composition.

We thus examine the connection between frailty in mortality and variance in length of life, with special attention to how frailty models of mortality may be able to represent the pattern of changes in mortality variability across both age and time. The proportional-hazard (relative risk) formulation of the frailty model (Vaupel et al. 1979) depicts the age-specific mortality hazard of any individual at age x with frailty z relative to the hazard of a standard individual as follows:

$$\mu(x, z) = z\mu(x). \tag{5}$$

Frailty is often assumed to follow a gamma distribution with the marginal probability density function:

$$f_z(z) = \frac{\lambda^\kappa z^{\kappa-1} e^{-\lambda z}}{\Gamma(\kappa)}, \tag{6}$$

with mean $\bar{z} = \frac{\kappa}{\lambda}$, and variance $\sigma^2 = \frac{\kappa}{\lambda^2}$. For a model of gamma-distributed frailty with $\kappa = \lambda$, mean $\bar{z}(0) = 1$ and variance σ^2, the mean frailty for survivors to age x can be expressed as (Vaupel and Yashin 2006):

$$\bar{z}(x) = \left(1 + \sigma^2 \int_0^x \mu(t)\, dt\right)^{-1}. \tag{7}$$

Note also that the observed population trajectory can be shown to be a function of mean frailty in the population:

$$\bar{\mu}(x) = \bar{z}(x)\mu(x). \tag{8}$$

Combining the Siler model in equation (3) with the gamma-distributed age-specific frailty in equation (7), the observed population trajectory of mortality described in equation (8) may thus be represented via the logistic-like function that we call the Siler-gamma model:

$$\bar{\mu}(x) = \frac{\alpha_1 e^{-\beta_1 x} + \alpha_2 e^{\beta_2 x} + \alpha_3}{1 + \sigma^2 \left(\frac{-\alpha_1}{\beta_1}(e^{-\beta_1 x} - 1) + \frac{\alpha_2}{\beta_2}(e^{\beta_2 x} - 1) + \alpha_3 x\right)}. \tag{9}$$

Preliminary Results

Using a binomial likelihood function (where the probability of death is based on the Siler-gamma model) and life tables for Swedish females, we obtained maximum likelihood estimates of all model parameters for cohorts born between

1751-1915 via an iterative estimation procedure. **Figure 3** shows the observed pattern of mortality decline for several cohorts and the estimated trajectories based on the Siler-gamma model.

Figure 4 presents plots of the gamma distribution of frailty among Swedish females at four selected ages. Each plot includes curves representing the distribution of frailty among women aged x during four points in time, and each curve is normalized to a probability mass equal to the survivorship proportion at age x, $l(x)$. Each figure was prepared using the procedure described by Manton et al. (1981) and using the coefficient of variation estimated via the Siler-gamma model discussed above. Manton et al. (1981) showed that within individual cohorts, the distribution of frailty contracts with age, as selective mortality removes the frailest from the population and leaves a more homogeneous group of robust survivors. Our results show that as successive cohorts age, the distribution of frailty at ages 45, 60, 75, and 80 appears to change over successive periods. Each age-specific plot indicates that the mode of the frailty distribution has shifted to the right, indicating slightly higher mean frailty at every age, even while the distributions seem more concentrated around this mode than in the past.

Next Steps

The Siler model can be modified to include two parameters for change over time in the age-specific mortality hazard. We plan to incorporate these parameters into the model and re-estimate the parameters to see whether this alternate specification affords more insight into changes in population composition, particularly as expressed in the mean and variance of age-specific frailty.

After identifying the Siler-based frailty model with the best fit for the overall mortality pattern, we will translate the hazard trajectories into their associated life tables. We will then calculate successive truncated variances and examine their age pattern and time trend via contour plots to determine the extent to which they reflect the trends observed in the empirical life tables from the HMD. Finally, we will test the evidence for a cycle of influence, whereby reductions in early life mortality rates influence the later distribution of frailty, which in turn influences later mortality variability among the old. These analyses will be conducted for all national populations in the HMD with a sufficiently long time-series of cohort life tables, including the nations of Scandinavia, Northern and Western Europe, Australia, New Zealand (non-Maori), the U.S. and Canada. Analyses will be conducted separately for men and women and compared.

As mortality declines, selections reduced influence on early-life mortality may be replaced by frailtys growing manifestation in shaping profiles of morbidity and disability among aging populations (see Yashin et al. 2008 for modeling approaches using longitudinal health data). Mortality declines at every age potentially lead to a less selected older population, and this paper aims to trace the extent to which life tables that span the course of 20th century demographic transitions provide evidence in support of this hypothesis.

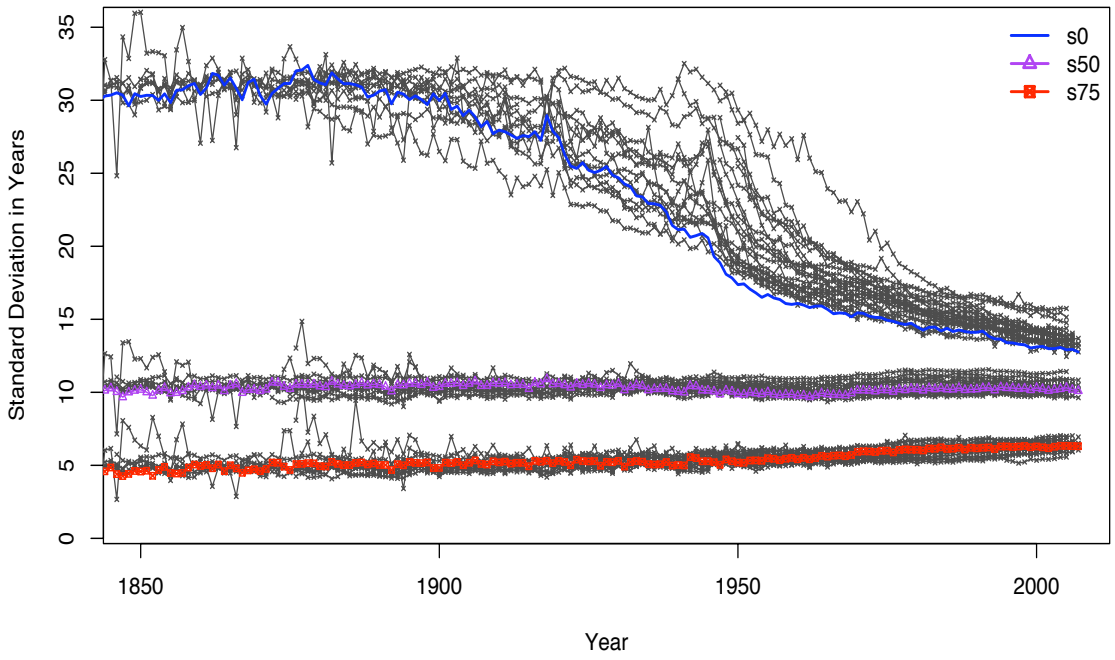

Figure 1: Trends in standard deviations for mortality distributions: full population (s_0) and survivors to ages 50 (s_{50}) and 75 (s_{75}). Calculated using life tables for males in 24 countries, 1850-2006. Measures for Sweden are highlighted. Source: HMD 2009.

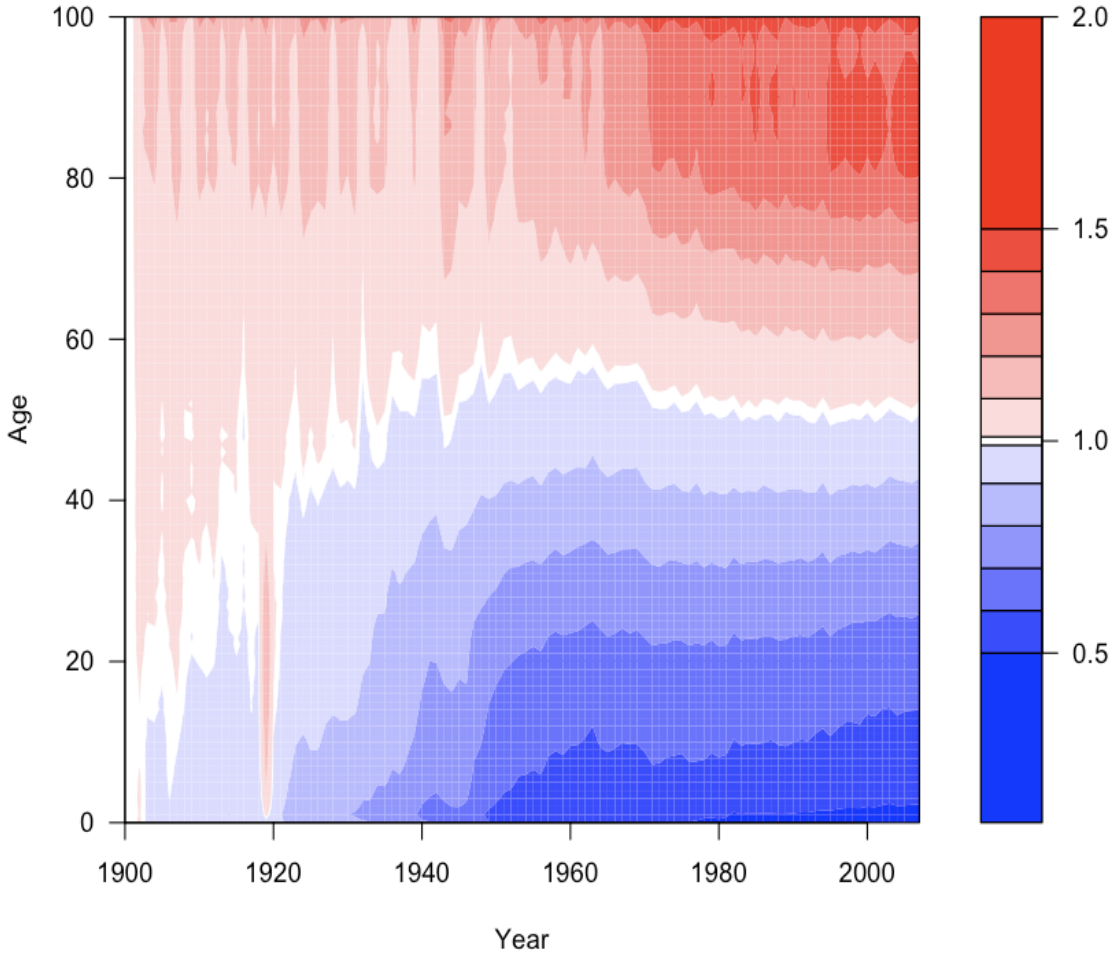

Figure 2: Trends in age-specific standard deviations of the mortality distribution relative to their 1900 values. Calculated using life tables for females in Sweden, 1900-2006. Color is assigned according to the ratio of the standard deviation in the distribution of mortality for survivors to a given age (y-axis) in a given year (x-axis), relative to the age-specific value in 1900. White represents a ratio of 1 (no change); successively darker blues represent declining values less than 1; successively darker reds represent increasing values greater than 1. Source: HMD 2009.

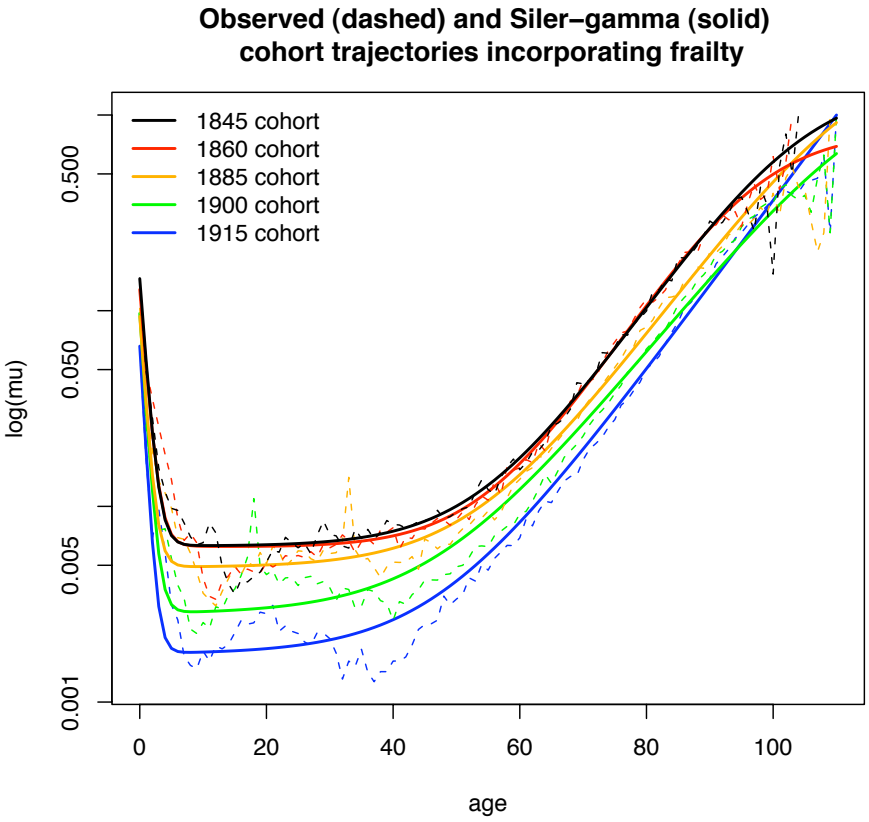

Figure 3: Observed logged mortality hazard trajectories and model trajectories based on maximum-likelihood estimates. Calculated using life tables for females in Swedish cohorts 1845-1915. Source: HMD 2009.

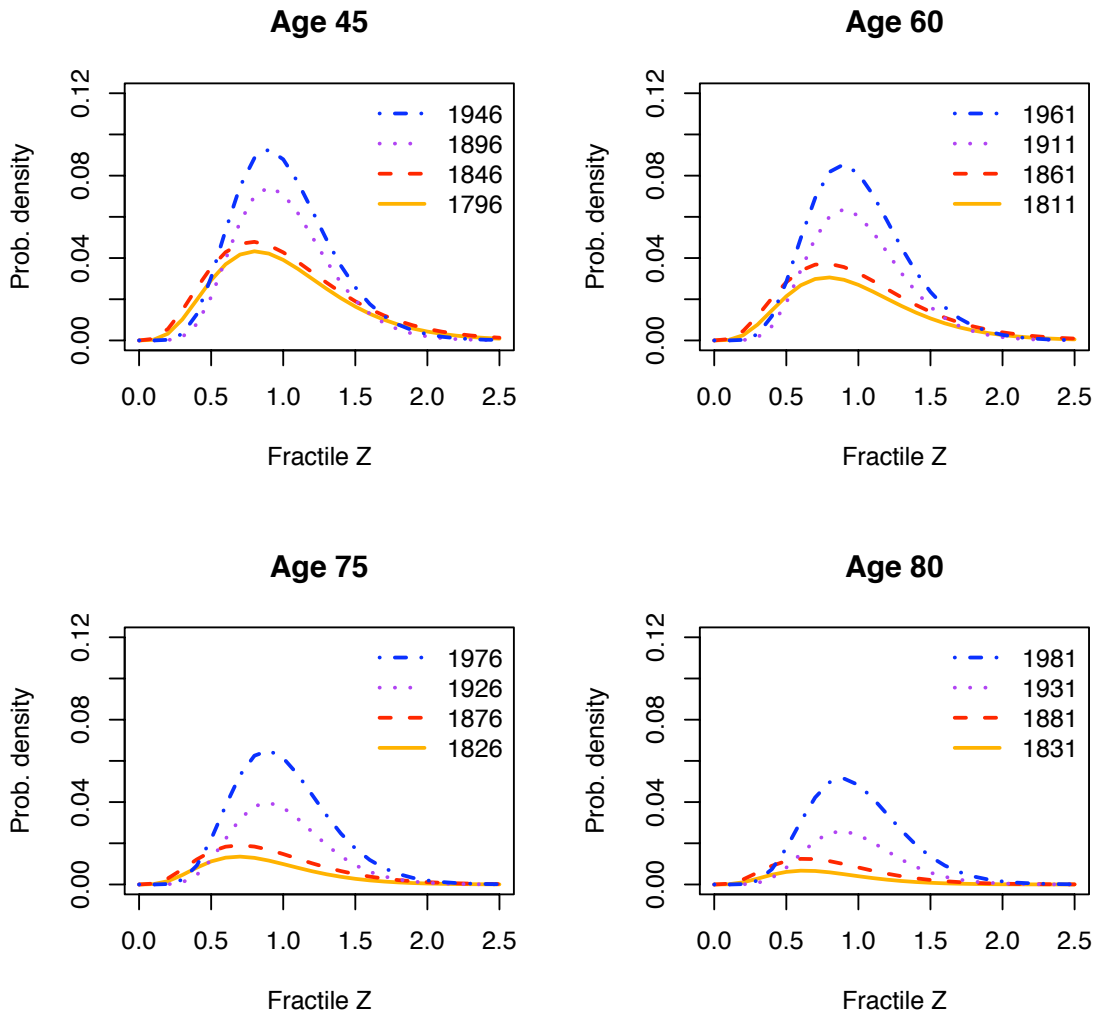

Figure 4: Age-specific frailty distributions for Swedish females in successive periods, calculated from life tables for the 1751-1901 cohorts. Source: HMD 2009.

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