Mathematical study of mortality dynamics in heterogeneous population composed of subpopulations following the exponential law

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Abstract. Many features of biological populations can be described in terms of their heterogeneity by taking into account variations among individuals and cohorts in the population. In demography, the heterogeneity of populations can explain various features of age-dependent demographic observations including those related to mortality dynamics. Mortality dynamics is underlined by the Gompertz law stating that the mortality rate increases exponentially between sexual maturity and considerably old ages (i.e. between 20 and 80 years old). Deviations from the exponential increase are observed at early- and late-life intervals. Different models (i.e Heligman-Pollard model) were developed over the past decades to describe and explain these deviations. These models postulate that a few different processes take place in the population and affect its mortality dynamics. In this study we present a model based on an assumption that mortality dynamics is indeed underlined by the exponential law and the irregularities at young and very old ages are due to the heterogeneity of human population. We demonstrate that the model is capable of reproducing the entire pattern of mortality and explaining the deviations from the exponential growth. The model fitted to Swedish age-dependent mortality rates indicates that the population should be composed of four subpopulations each following the exponential law of mortality increase over age. We also expand the idea of heterogeneity to probability density and survival functions, that is we adjust the model to the number of Swedish deaths and survivors instead of mortality rates.

Keywords: Gompertz law, Heterogeneity, Mathematical model, Model fitting, Probability density, Survival function.

New Trends in Stochastic Modeling and Data Analysis (*pp.* 159-171)
Raimondo Manca – Sally McClean – Christos H Skiadas (Eds)

1 Introduction

Analysis of the human mortality dynamics over the life-course is of great importance for many reasons including understanding the mechanisms of ageing and developing ways to control and extend the duration of lifespan. The mathematical modelling of the dynamics of human mortality makes a significant contribution to these studies. A number of studies have been performed to model (Makeham[21]; Siler[20]; Heligman and Pollard[12]; Lee and Carter[15]) and analyse (Gavrilov and Gavrilova[13]; de Magalhaes *et al.*[7]) mortality data as a function of age. Age-dependent mortality data are tabulated in life tables that contain essential information for the age-structure of a population (Preston *et al.*[17]).

Two of the basic quantities of interest tabulated in a human life table are the probability of death and the mortality rate. Probability of death, q_i, is the probability for an individual aged i to die before reaching age $i+1$ and is expressed as the ratio of the number of deaths of people aged i, ΔN_i, divided by the number of individuals alive at exact age i, N_i. Death (or mortality) rate m_i is defined as the number of deaths of people of age i divided by the average number of individuals of age i:

$$m_i = \frac{\Delta N_i}{0.5(N_i + N_{i+1})} \tag{1}$$

where the number of deaths of people aged i is represented as:

$$\Delta N_i = N_i - N_{i+1}. \tag{2}$$

The average number of survivors within one-year age interval approximately coincides with the number of survivors at the centre of the interval and therefore the mortality rate is commonly referred as central death rate.

Data on mortality rates can be found in two different formats depending on the way the data are recorded. Data recording deaths of individuals born the same year and growing up together (in the sense that they will celebrate their *i*-th birthday exactly i years after their birth) form the cohort data. Data recording deaths occurring during a specific year form the period data. In order to illustrate the difference between the period and cohort data, we briefly introduce the Lexis diagram. The Lexis diagram (Lexis[19]) outlines the stocks and flows of a population and the occurrence of demographic events (such as deaths) over age and time. It is a two-dimension graph (Fig. 1) in which the vertical axis represents the age and the horizontal axis the time, both measured in same units (e.g. years). Deaths occurring in a parallelogram formed by two diagonal lines in Fig. 1 contribute to cohort mortality, while the deaths occurring in a rectangle outlined by two vertical lines in Fig. 1 - to period mortality.

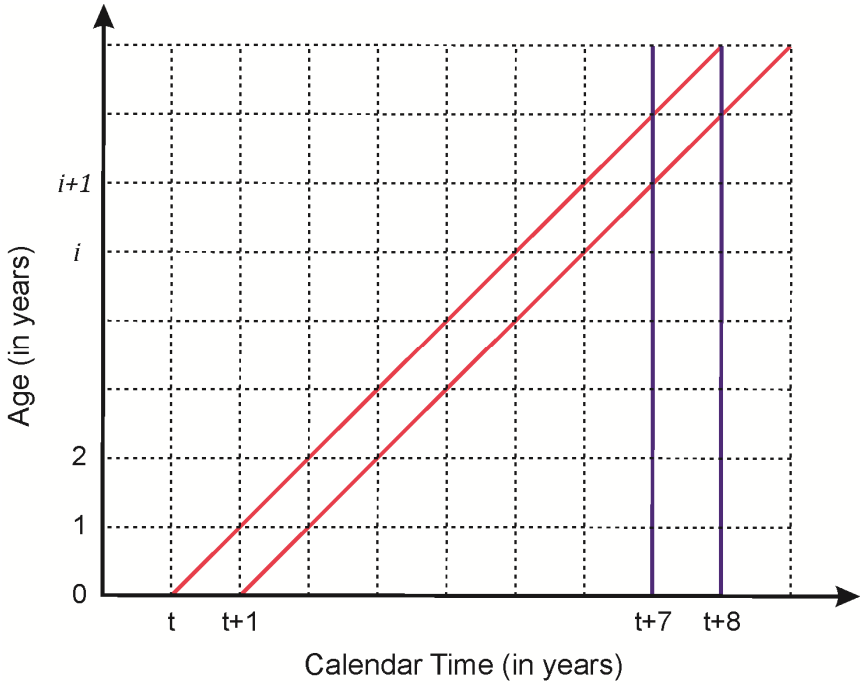

Fig. 1. Lexis diagram

The diagram illustrates demographic events as distributed over age and time. Cohort mortality rates refer to the deaths of a cohort that are occurring in a parallelogram formed by two diagonal lines. Period mortality rates refer to deaths occurring within a period outlined by two vertical lines.

The mortality rate of human populations (and other species as well) advances exponentially with age (i.e. follows the Gompertz law of mortality (Gompertz[1])) for a significant part of the age range starting from the period of reproductive maturity (age ~35) up to extreme old ages (age ~100). Mathematically, the Gompertzian dynamics of mortality is expressed as

$$m_i = m_0 e^{\beta i}, \tag{3}$$

where m_0 is the initial mortality at age $i = 0$ and parameter β defines the rate of change of mortality with age (usually called rate of ageing or Gompertz slope).

Graphically, mortality data are most frequently plotted in semi-logarithmic graphs (logarithm of mortality versus age) and therefore their exponential increase with age, as expressed by the Gompertz law of mortality (equation (3)), is represented with a straight line. Fig. 2 presents data (dots) on period mortality rates for the Swedish 2010 population together with the solid line representing the Gompertz function fitting the presented data. Even if the exponential growth accurately represents most of the ages, some peculiarities are observed in young (before 35) and extremely old (after 100) ages.

A number of mathematical models have been developed and used to analyse the human mortality dynamics and to clarify the deviations from the exponential growth. Various explanations have been given to the peculiarities of mortality at young and old ages. For example, the proposed explanations for the late-life mortality plateau include an assumption that the Gompertz law (exponential function) is not valid at those ages and that the mortality dynamics should be described by logistic, quadratic or some other mathematical functions (Gavrilov and Gavrilova[14]; Kannisto *et al.*[18]; Pham[5]). Other explanations take into account the heterogeneity of a population and its impact on the dynamics of mortality (Vaupel *et al.*[11]; Vaupel and Yashin[8]). The heterogeneity can be explained in different ways and can be described by different models (Lebreton[6]; Steinsaltz and Wachter[3]).

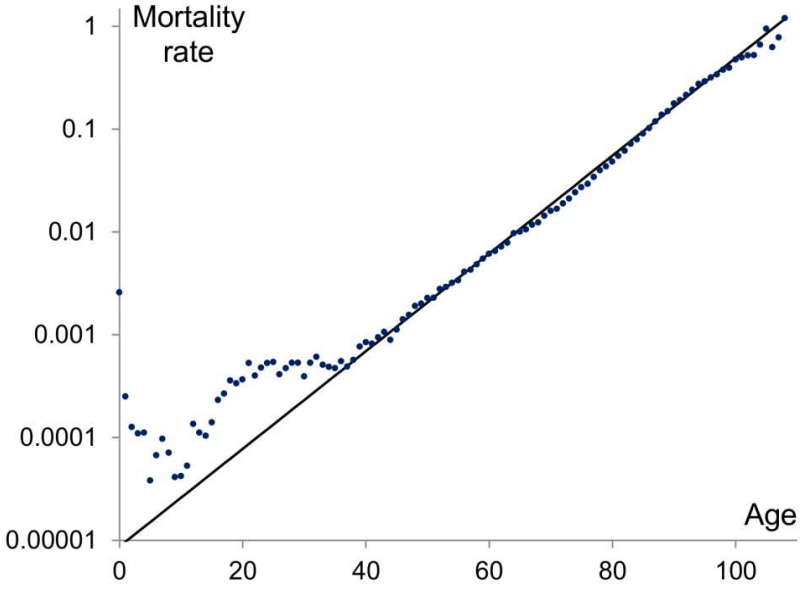

Fig. 2. Mortality rates of the 2010-period Swedish population set in a semi-logarithmic scale

The data are taken from the Human Mortality Database (http://www.mortality.org). The Gompertz function with parameters $m_0 = 8.7 \cdot 10^{-6}$ and $\beta = 0.109$ fits the data very well after the age of 35. Deviations from the exponential growth are observed at young (before 35) and considerably old (after 100) ages.

In this work, we aim to analyse the dynamics of mortality in human populations using the mathematical model that associates the exponential law for mortality dynamics with the heterogeneity of populations. We also develop the model for continuous age, which complements the discrete model developed in Avraam *et al.*[2]. Both, the discrete and continuous models, can reproduce and explain the pattern formed by period or cohort mortality rates across the

entire lifespan and are able to explain the deviations from the exponential growth. The model is fitted to Swedish period data and it is shown that a theoretical heterogeneous population composed by four subpopulations can reproduce the actual data fairly well. The model proposed in Avraam *et al.*[2], is then reformulated for the analysis of the probability density and survival functions of the population.

The remainder of this paper is structured as follows. In Section 2, the theoretical models in discrete and continuous age are introduced and their probability density and survival function for heterogeneous populations developed. Section 3 presents the fitting procedure we used. The models presented in Section 2 are applied to Swedish mortality rates in 2010 in Section 4 and obtained results are discussed in Section 5.

2 Mathematical model

2.1. Discrete model of mortality in heterogeneous populations

The main assumption of the model is that human populations are heterogeneous and composed of a number of subpopulations or individuals, which differ genetically and/or by life style factors (Vaupel *et al.*[10]; Vaupel[9]). The model that combines the heterogeneity with the Gompertz law of mortality (Avraam *et al.*[2]) has a further assumption that the mortality rate in each subpopulation grows exponentially (i.e. in the same way as in Gompertz law) with different mortality parameters (m_0, β) for each subpopulation, reflecting the variations in the genotype and life style. The notations N_{j0}, m_{j0} and β_j are used for the initial size, initial mortality rate and rate of ageing of the *j*-th subpopulation respectively. The mortality or the central death rate of the *j*-th subpopulation at age i is then expressed by the exponential function:

$$m_{ji} = m_{j0} e^{\beta_j i}. \tag{4}$$

Using the definition of mortality rate (equation (1)), the mortality of the entire heterogeneous population composed by n subpopulations is given by:

$$m_i = \frac{\sum_{j=1}^{n} \Delta N_{ji}}{0.5\left(\sum_{j=1}^{n} N_{ji} + \sum_{j=1}^{n} N_{j,i+1}\right)}, \tag{5}$$

with N_{ji} and ΔN_{ji} representing the number and the number of death of persons of age i in subpopulation j. By taking into account equations (1) and (4), equation (5) is rewritten as:

$$m_i = \frac{\sum_{j=1}^{n} \frac{N_{ji} m_{j0} e^{\beta_j i}}{1 + 0.5 m_{j0} e^{\beta_j i}}}{\sum_{j=1}^{n} N_{ji} - 0.5 \sum_{j=1}^{n} \frac{N_{ji} m_{j0} e^{\beta_j i}}{1 + 0.5 m_{j0} e^{\beta_j i}}}. \quad (6)$$

When dealing with period data the number of individuals aged i is constant for a stationary population and therefore the mortality rate is defined as the number of deaths ΔN_i divided by the actual size N_i. Thus, the model of mortality (equation (6)) for period data is simplified and can be expressed as a sum of weighted exponential terms:

$$m_i = \frac{\sum_{j=1}^{n} \Delta N_{ji}}{\sum_{j=1}^{n} N_{ji}} = \sum_{j=1}^{n} \rho_{ji} m_{ji} = \sum_{j=1}^{n} \rho_{ji} m_{j0} e^{\beta_j i}, \quad (7)$$

where each weight ρ_{ji} represents the proportion of the j-th subpopulation in the whole population at age i:

$$\rho_{ji} = \frac{N_{ji}}{N_i} \text{ with } \sum_{j=1}^{n} \rho_{ji} = 1.$$

2.2. Continuous model of mortality in heterogeneous populations

In the continuous model the age is defined by a real number x (continuous age) rather than by the integer number i. For continuous age, the instantaneous mortality, μ_x at age x (force of mortality) of a homogeneous population is defined as:

$$\mu(x) = \lim_{\Delta x \to 0} \frac{-\Delta N}{N(x) \Delta x} = \frac{-1}{N(x)} \frac{dN}{dx}. \quad (8)$$

Substituting the Gompertz law in the LHS of equation (8) and solving the differential equation results in:

$$N(x) = A e^{-\frac{\mu_0}{\beta} e^{\beta x}}, \quad (9)$$

where the constant of integration A is equal to $N_0 e^{\mu_0 / \beta}$ as estimated by the initial condition $N(x = 0) = N_0$. This means that the expression for the population size N at age x depends on the initial mortality, μ_0, and the mortality coefficient β:

$$N(x) = N_0 e^{\frac{\mu_0}{\beta}\left(1 - e^{\beta x}\right)}. \quad (10)$$

With heterogeneous populations, formula (10) is used to describe the size of each subpopulation at age x. Therefore, the subscript j is added in each parameter. As a result, the mortality of the entire population in continuous age is formulated by:

$$\mu(x) = \frac{\sum_{j=1}^{n} \mu_j(x) N_j(x)}{\sum_{j=1}^{n} N_j(x)} = \frac{\sum_{j=1}^{n} \mu_{j0} e^{\beta_j x} N_{j0} e^{(\mu_{j0}/\beta_j)(1-e^{\beta_j x})}}{\sum_{j=1}^{n} N_{j0} e^{(\mu_{j0}/\beta_j)(1-e^{\beta_j x})}}. \tag{11}$$

By solving equation (11) at integer values of age ($x = i$), equation (6) is found, providing then a link between the dynamics of mortality in the continuous and discrete models.

2.3. Probability density and survival function in heterogeneous populations

The consideration of heterogeneity in human population can be used for the derivation of models for other mortality-related variables that exist in human life tables. Such variables are the number of survivors and the number of deaths at age x. In this section, the models of probability density and survival function for heterogeneous populations are developed in continuous time.

In a homogeneous population, $S(x+\Delta x)$ denotes the probability of an individual to survive at age $x+\Delta x$ (usually called survival function) and is calculated as the difference between the probability to survive at age x and the probability to die between x and $x+\Delta x$:

$$S(x+\Delta x) = S(x) - S(x)\mu(x)\Delta x \tag{12}$$

$$\Rightarrow \frac{S(x+\Delta x) - S(x)}{\Delta x} = -\mu(x)S(x). \tag{13}$$

The limit of LHS of equation (13) when Δx tends to 0, is the derivative of $S(x)$ with respect to x :

$$\lim_{\Delta x \to 0} \frac{S(x+\Delta x) - S(x)}{\Delta x} = \frac{dS(x)}{dx}, \tag{14}$$

and therefore equation (13) can be written as the differential equation

$$\frac{dS(x)}{dx} = -\mu(x)S(x). \tag{15}$$

The solution of the differential equation (15) when the force of mortality $\mu(x)$ follows the Gompertz law, is

$$S(x) = A \exp\left(-\frac{\mu_0}{\beta} e^{\beta x} \right), \tag{16}$$

where the constant of integration A, is given by the initial condition $S(x=0) = 1$ and is equal to $A = e^{\mu_0/\beta}$.

By multiplying the survival function with the initial size of the population N_0, we find the number of individuals alive at age x. Therefore, for the heterogeneous population, the theoretical number of survivors at age x is given by:

$$N(x) = N_0 S(x) = N_0 \sum_{j=1}^{n} \rho_{j0} \exp\left(\frac{\mu_{j0}}{\beta_j} \left(1 - e^{\beta_j x} \right) \right). \tag{17}$$

The probability density function $f(x)$, of a heterogeneous population is obtained similarly. The probability $q(x)$ of an individual to die by age x is the complement of the probability to survive at the same age (i.e $q(x) = 1 - S(x)$) and therefore the probability density function is obtained by differentiating the cumulative distribution function $q(x)$ with respect to x:

$$f(x) = q'(x) = \mu_0 \exp\left(\beta x - \frac{\mu_0}{\beta} \left(e^{\beta x} - 1 \right) \right). \tag{18}$$

By multiplying the probability density function with the size of the initial population, we have the theoretical distribution of deaths across the lifespan, $\Delta N(x) = N_0 f(x)$.

For the case of a heterogeneous population composed by n subpopulations, the distribution of deaths is given by the sum of the number of deaths of individuals from each subpopulation:

$$\Delta N(x) = \sum_{j=1}^{n} N_{j0} f_j(x) = N_0 \sum_{j=1}^{n} \rho_{j0} \mu_{j0} \exp\left(\beta_j x - \frac{\mu_{j0}}{\beta_j} \left(e^{\beta_j x} - 1 \right) \right). \tag{19}$$

3 Fitting Procedure

The practical and commonly-used Least Squares Method was performed for the estimation of the model parameters that minimize the sum of the squared residuals between the theoretical and observed values. Log-Linear regression was used for the comparison between the logarithm of actual mortality rates and the logarithm of the theoretical mortality rates (logarithm of equation (6) or (11)), while Linear-regression was used to compare the actual number of deaths and survivors with the theoretical number of deaths given by equation (19) and theoretical number of survivors given by equation (17) respectively. In order to select the model with the optimal number of subpopulations, we used the Bayesian Information Criterion (BIC) (Schwarz[4]) which is given by the formula

$$BIC = n_d \ln\left(\hat{\sigma}_e^2 \right) + k \ln\left(n_d \right), \tag{20}$$

where n_d is the number of data points, $\hat{\sigma}_e^2$ is the sum of squared residuals divided by the number of data points and k is the number of free parameters. The model with the lowest BIC value represents the optimum. Note that each subpopulation is characterised by three parameters (initial mortality, rate of

ageing and its size or proportion with respect to the whole population) and also the sum of the subpopulations fractions is equal to unity. Therefore, the model of heterogeneous population composed by n subpopulations contains $k = 3n - 1$ unknown parameters.

4 Results

The theoretical heterogeneous population model is fitted to three different sets of mortality-related data (mortality rates, number of deaths and number of survivors) for the 2010 period Swedish data for the entire population including males and females. The data come from the website of Human Mortality Database, (http://www.mortality.org). We first fit the model to the mortality rates introduced in Fig. 2.

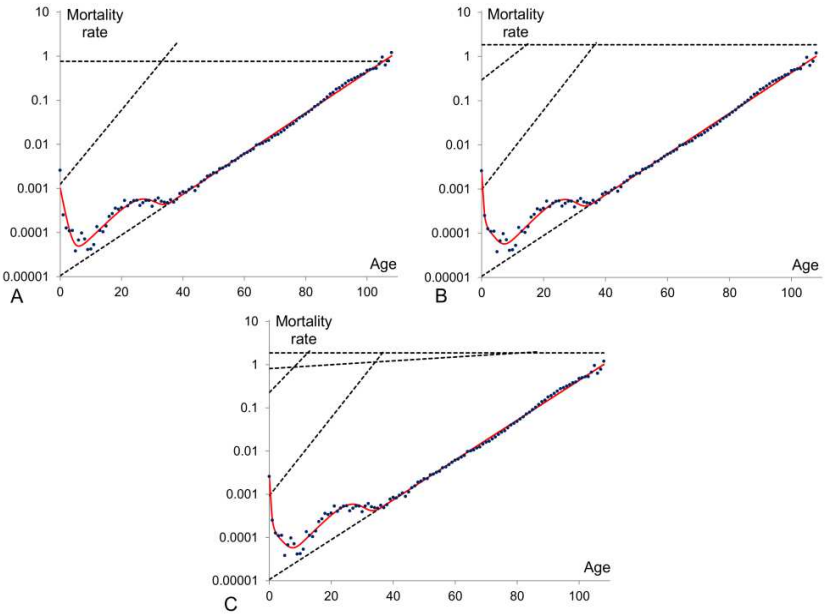

Fig. 3. The model of heterogeneous population fitted to the 2010 Swedish mortality rates

The heterogeneous population composed by three (panel A), four (panel B) and five (panel C) subpopulations are presented. The observed mortality rates are denoted by the dot points, the mortality dynamics of the subpopulations are given by the dashed lines and the total mortality of the whole population by the solid curve.

Fig. 3 presents the data and the fitted model composed by three (Fig. 3A), four (Fig. 3B) and five (Fig. 3C) subpopulations. The BIC values reveal that the population composed by four subpopulations ($BIC = -334.07$) fits the 2010 period Swedish data better than the model of three ($BIC = -302.06$) subpopulations and slightly better than the five-subpopulation model

($BIC = -315.73$). In the four-subpopulation model (Fig. 3B), the first subpopulation considered as the frailest (the subpopulation with the highest initial mortality) explains the sharp decline of mortality pattern at infant ages. The second subpopulation (with initial mortality closed to 0.3) mainly forms the left part of the local minimum that is observed at young ages (ages 2-7). The third subpopulation with initial mortality around 0.001 forms the local hump that appears over the reproductive period (ages 20-30). This hump is frequently called the accidental hump since it reflects external death factors such as accidents (for both sexes) and maternal mortality (for females). The fourth subpopulation is the most robust (having the lowest initial mortality) and has the biggest initial fraction. It explains the exponential growth of mortality at the period of ageing.

The fitting procedure is then applied to the numbers of deaths and survivors taken for the 2010 Swedish population, with equation (19) and equation (17) respectively. The BIC values indicate that the best fit to the observed numbers of deaths and survivors is obtained in both cases with a model composed by four subpopulations (Fig. 4).

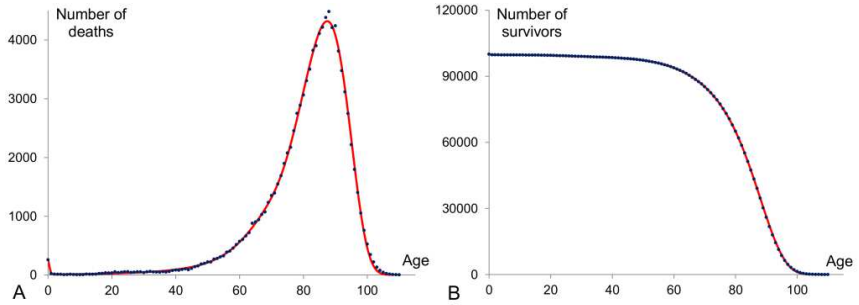

Fig. 4. The model of heterogeneous population fitted to the 2010 Swedish number of deaths and number of survivors

A: The density function of heterogeneous population composed by four subpopulations is fitted to the actual numbers of deaths and B: The survival function of heterogeneous population composed by four subpopulations is fitted to the actual numbers of survivors.

Consequently, the analysis shows that the assumption of population heterogeneity provides mathematical models that fit the mortality-related data (Fig. 3 and 4) better than a model of homogeneous population. On the other hand, the three attempts of fitting mortality-related data for the same population do not give the same values for the mortality parameters. The model for mortality rates of heterogeneous population provides the parameters that shape the mortality pattern of the entire lifespan, since by using the logarithm of mortality rates during the fitting procedure we increase the weight of young ages. The other two models (equations (17) and (19)) provide parameters that minimize the residuals mainly at adulthood span, since the differences between theoretical values and observations at young and extreme old ages are negligible. Besides, the theoretical relationships between equations (6), (11), (17) and (19) developed in Section 2 are valid only for cohort data with no

migration where the number of persons alive at age $i+1$ (N_{i+1}) in year t are equivalent to the number of persons alive at age i in year $t-1$ minus the number of persons who died at age i in year $t-1$, $N_i - \Delta N_i$. However, since we do not fit cohort data but period data and since the Swedish population is subject to migration flows, this relation does not hold, explaining partly the observed differences between the values of the parameters of the three fitted models. The mortality rates of the entire population resulting from the model applied to the three different sets of Swedish data are shown in Fig. 5. The dotted and dashed curves indicate that the parameters obtained by fitting the numbers of deaths and survivors, fail to accurately model the peculiarities of mortality pattern at early and extreme old ages. However they both create a smooth dip at around age 75 and thus better capture the mortality pattern at adult age than the curve of mortality obtained by fitting mortality rates (solid curve in Fig. 5).

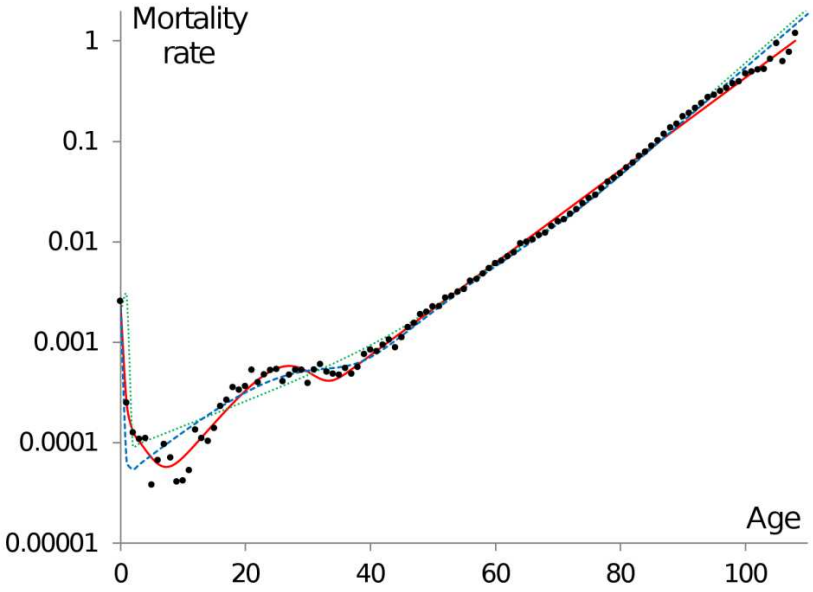

Fig. 5. Different fits of four-subpopulation heterogeneous model to 2010 Swedish mortality data

The solid (red) curve represents the mortality pattern resulting from the heterogeneous model fitted to the mortality rates (same pattern as in Fig. 3B) while the dotted (green) and dashed (blue) curves show the mortality pattern resulting from the model fitted to the numbers of deaths and the numbers of survivors respectively. (For interpretation of the references to colour in this figure legend, the reader is referred to the electronic version of this book.)

Conclusions

Modelling the dynamics of human mortality has long been the focus of various studies aiming an understanding the ageing processes and the causes of mortality at different ages. A number of studies have assessed the impact of heterogeneity on the dynamics of mortality, in particular at young and extremely old ages. The assumption that the population is heterogeneous combined with the assumption that the mortality dynamics of each subpopulation follows the exponential law, have been used to model the observed mortality dynamics and particularly to explain the deviations of mortality dynamics from the exponential growth (Avraam *et al.*[2]). In this work, we extended the model developed in Avraam *et al.*[2], from discrete to continuous time and we use it to reproduce and analyse the mortality dynamics across the entire human lifespan. The model contains meaningful demographic parameters and is capable of reproducing the actual data of a human population fairly well. The heterogeneity of a population is also used to derive models reproducing the patterns formed by the numbers of deaths and survivors.

The model reveals that we need to consider only four subpopulations to reproduce with sufficient accuracy the Swedish period mortality-related data (Fig. 3B and 4). The four-subpopulation model appears to be the optimum in all three fitted models we developed, that are 1) fitted model to mortality rates, 2) fitted model to the number of deaths and 3) fitted model to the number of survivors. Even though it probably underestimates the real heterogeneity of human populations, it shows how a simple mathematical model can well represent actual human mortality dynamics. Our analysis indicates that the contribution of heterogeneity differs across ages. The mortality model suggests that a small subpopulation with high initial mortality explains the decline in mortality at young ages as this subpopulation gradually disappears. Generally, the faster-ageing subpopulations are eliminated with increasing age and the entire population starts to act more-and-more homogeneously, as if it was composed by a single (with the lowest mortality) subpopulation.

The model presented in this study allows many future developments, such as an analysis of the time evolution of the Gompertz parameters. Indeed, such study could help to better understand past mortality evolutions, such as the ageing process, and could provide a new approach to forecast mortality trends of human populations. By comparing these projections with traditional forecasting techniques currently used in practice, such as the Lee-Carter and the Heligman-Pollard models (see for example Gaille[16]), the analysis of potential future mortality developments will be enhanced.

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