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A mathematical model of mortality dynamics across the lifespan combining heterogeneity and stochastic effects ☆

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ABSTRACT

The mortality patterns in human populations reflect biological, social and medical factors affecting our lives, and mathematical modelling is an important tool for the analysis of these patterns. It is known that the mortality rate in all human populations increases with age after sexual maturity. This increase is predominantly exponential and satisfies the Gompertz equation. Although the exponential growth of mortality rates is observed over a wide range of ages, it excludes early- and late-life intervals. In this work we accept the fact that the mortality rate is an exponential function of age and analyse possible mechanisms underlying the deviations from the exponential law across the human lifespan. We consider the effect of heterogeneity as well as stochastic factors in altering the exponential law and compare our results to publicly available age-dependent mortality data for Swedish and US populations. In a model of heterogeneous populations we study how differences in parameters of the Gompertz equation describing different subpopulations account for mortality dynamics at different ages. Particularly, we show that the mortality data on Swedish populations can be reproduced fairly well by a model comprising four subpopulations. We then analyse the influence of stochastic effects on the mortality dynamics to show that they play a role only at early and late ages, when only a few individuals contribute to mortality. We conclude that the deviations from exponential law at young ages can be explained by heterogeneity, namely by the presence of a subpopulation with high initial mortality rate presumably due to congenital defects, while those for old ages can be viewed as fluctuations and explained by stochastic effects.

1. Introduction

Analysis of the dynamics of human mortality over the life course is of great importance. Demographic comparisons between populations may reveal clues into differences in causes of mortality that may be related to intrinsic and extrinsic factors. Study of mortality dynamics over age has a long story. Many researchers following the early works of Lexis (1878) and Pearson (1897) have considered mortality at different age intervals to be affected by different factors, with ageing to be at play only after sexual maturation (Gompertz, 1825). Early considerations of age dependent mortality were rather philosophical: according to Lexis (1878) everyone should live the same length of time – the normal length of life – but some die earlier due to accidents. He distinguished "normal" deaths which occur at the normal age of death or are randomly distributed around that age, from premature deaths of adults and, a fortiori, deaths of children. Pearson's (1897) approach was far more scientific: he considered death as a random event and his statistical analysis of age distribution of death in England (1871–1880) revealed five different phases described by different probabilities of death for five age groups. The reasons why probability of death (or mortality rate) depends on age and should follow different dynamics at different age intervals are not well understood. Recent studies of mortality dynamics over the life course attempt to understand the mechanisms of age-related mortality based on the underlying physiological, molecular and genetic processes. It is not surprising that a number of studies have been conducted to analyse mortality data as a function of age (de Magalhaes et al., 2005; Gavrilov and Gavrilova, 2003; Vaupel, 2005).

Mortality rate m_i at age i is defined as number of deaths of individuals of age i (ΔN_i) divided by the number of person-years (PY_i) calculated for individuals of age i in the population (Preston et al., 2000). If an average person who died at age i have died a years ($0 < a < 1$, i.e., a gives the fraction of a year) after his last birthday

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then $PY_i = N_i - (1 - a)\Delta N_i$ where N_i is the number of individuals who have reached age i. Thus:

$$m_i = \frac{\Delta N_i}{N_i - (1-a)\Delta N_i} \text{ or equally } \Delta N_i = \frac{m_i N_i}{1 + (1-a)m_i}. \quad (1)$$

If an average person who died at age i had died 6 months after his birthday then $a = 0.5$. Observations on mortality in human populations indicate that $a = 0.5$ (with very high precision) for all ages except for the age zero, $i = 0$, for which parameter a is considerably smaller (typically $a \approx 0.35$). Furthermore, the number of deaths of people aged i can be represented as:

$$\Delta N_i = N_i - N_{i+1} \quad (2)$$

where N_{i+1} represents the number of people who has reached the age $i + 1$.

For most of the human lifespan the Gompertz equation (Gompertz, 1825) depicting the exponential increase in mortality with age fits the data well and has been widely used. Mathematically the exponential dynamics of mortality rate is represented as:

$$m_i = m_0 e^{\beta i}, \quad (3)$$

where m_0 is the initial mortality when $i = 0$ (can be derived from the mortality at the age when mortality rates begin to climb) and parameter β defines the rate of demographic ageing or how quickly the mortality rate is changing.

Combining Eqs. (1–3) we have:

$$N_{i+1} = N_i - \Delta N_i = N_i - \frac{m_i N_i}{1 + 0.5 m_i} = \left(\frac{1 - 0.5 m_i}{1 + 0.5 m_i}\right) N_i = \left(\frac{1 - 0.5 m_0 e^{\beta i}}{1 + 0.5 m_0 e^{\beta i}}\right) N_i. \quad (4)$$

Eq. (4) shows how the number of individuals of age $i + 1$ is defined by the number of individuals of age i. Using the derivation from Eq. (4) multiple times we can find the size N_i as a function of the initial size N_0, initial mortality, m_0, and parameter β:

$$N_i = \left(\frac{1 - 0.5 m_0 e^{\beta(i-1)}}{1 + 0.5 m_0 e^{\beta(i-1)}}\right) N_{i-1} = \ldots = N_0 \prod_{k=0}^{i-1} \left(\frac{1 - 0.5 m_0 e^{\beta k}}{1 + 0.5 m_0 e^{\beta k}}\right). \quad (5)$$

Eqs. (1–5) represent a discrete counterpart of the continuous equations associated with the Gompertz law (Mueller et al., 1995).

Actual data on mortality in human populations can be found in different formats. Most commonly it is represented as a logarithm of mortality rate versus age (see Fig. 1) which can be interpolated by a linear plot if it is given by the exponential function as in the case of Eq. (3). Plots in Fig. 1 show that the mortality rate increases for most ages and this increase is approximately exponential. The deviations from the exponential law are observed in young (before 32) and old (after 102 in panel B) ages. The mortality plateau at late ages (Mueller and Rose, 1996; Pletcher and Curtsinger, 1998; Wachter, 1999) is one of particularly intriguing facets in human populations as well as in other non-human species.

A number of mathematical models have been developed and used to analyse observations on the mortality dynamics in human populations as well as in populations of other species (Vaupel, 2010; Yashin et al., 2000). Various explanations have been put forward for the peculiarities of mortality dynamics at young and old ages. For example, the proposed explanations for the late-age plateau include an assumption that the exponential law is not working at those ages and that the mortality dynamics should be described by logistic, quadratic or other mathematical functions (Gavrilov and Gavrilova, 2001; Kannisto et al., 1994; Pham, 2011). It has also been shown that the deviations from the exponential law can be explained by heterogeneity (Vaupel and Yashin, 1985; Vaupel et al., 1979), while heterogeneity can be explained and described using different models (Lebreton, 1996; Steinsaltz and Wachter, 2006). However, we feel that the systematic analysis of the mortality dynamics in heterogeneous populations is incomplete. Particularly, it would make an important exercise to construct a model of heterogeneous population with parameters fitting real observations as this could provide clues regarding biological, genetic and medical factors driving these mortality patterns. Another reason for deviations of mortality dynamics from Gompertz law can be associated with the random events affecting the longevity. The role of stochastic effects on the mortality dynamics as mediated by their impact on individual frailty have been addressed by many authors (Vaupel, 2010; Weitz and Fraser, 2001). And again the results of these studies have not been systematically compared with detailed observations available nowadays.

In this work, we aim to model mortality across the whole lifespan presuming that the rate of mortality changes over age according to the Gompertz law. Although many other models have been used to describe mortality dynamics over age (Pletcher, 1999) there is a genuine feeling that the fundamental processes underlying mortality

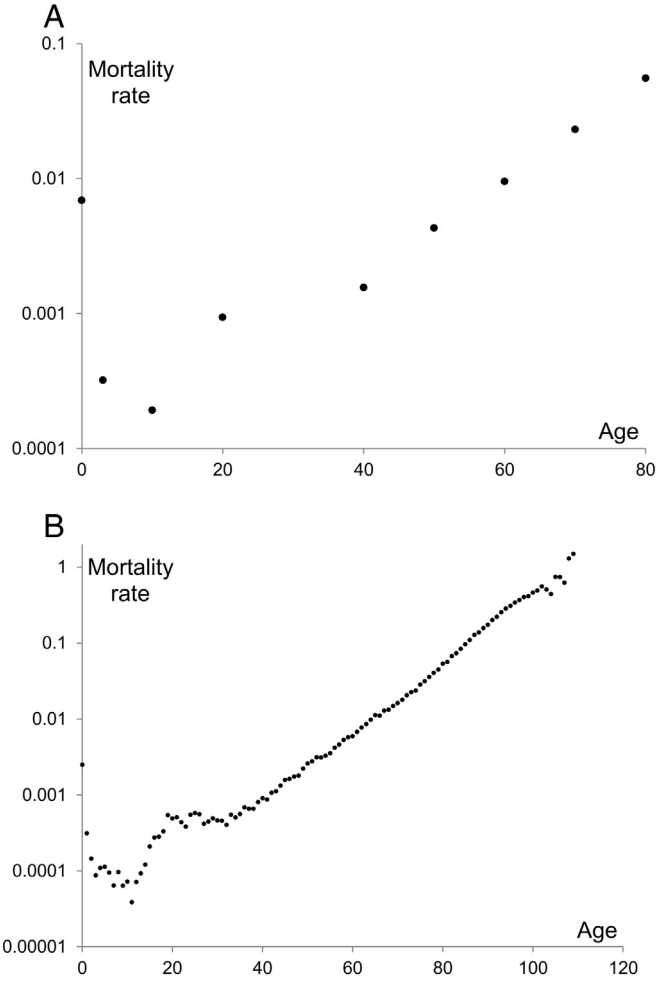


Fig. 1. Mortality rate versus age for the United States population in the year 2002 (Panel A) and for the Swedish population in the year 2007 (Panel B). The data presented in panel A is taken from the Centers for Disease Control and Prevention (http://www.cdc.gov/nchs/deaths.htm) and the data in panel B from the Human Mortality Database (http://www.mortality.org). Both panels represent the logarithm of mortality rate versus the age i. The data for the Swedish population is given for all ages while for the American population only selected ages are given. In both cases the data after the age of 25–30 fits into a straight line, i.e. indicates an exponential growth. The data for the Swedish population (which is more complete) shows the deviation from the exponential growth (which even includes drops in mortality rate) after the age of 100.

should result in exponential law (Yashin et al., 2000). Therefore we analyse whether the deviations from Gompertz law can be explained by the heterogeneity of populations while the mortality in each subpopulation is still described by the Gompertz law. Also assuming that the mortality dynamics is described by Gompertz law we check whether the deviations from this law can be explained by stochastic effects. In order to perform this analysis we developed mathematical models comprising the heterogeneity of the population and/or stochastic effects. We also aim to derive likely Gompertz parameters for the model so that it would fit the observation data used in this study and infer clues about biological, social or biomedical processes at work. We first focus on the young ages and then on the old ages to model and analyse the irregularities in the mortality dynamics using data both from Sweden and the US. This allows us to explain these irregularities and to reproduce the observed data in the model.

2. Study of heterogeneous populations

2.1. Mathematical model of heterogeneous populations

Each human population can be seen as consisting of a number of subpopulations which differ genetically and/or by life style (for example associated with gender or occupation). The parameters defining the mortality dynamics (m_0,β in Eq. (3)) of each subpopulation can be different, reflecting the variations in the genotype and life style (see (Vaupel et al., 1998) and references therein). Therefore, we can model the whole heterogeneous population in the following way. We consider the population as consisting of n subpopulations and assume that the mortality rate in each subpopulation is defined by the Gompertz equation, although the equation parameters are different for different subpopulations (Vaupel, 2010). Let us use the notation N_{j0} for the initial size, m_{j0} for the initial mortality rate, and β_j for the rate of mortality dynamics of subpopulation j. According to the Gompertz law the mortality rate of subpopulation j is:

$$m_{ji} = m_{j0}e^{\beta_j i}. \tag{6}$$

If the entire population consists of n subpopulations then Eq. (1) can be rewritten as:

$$m_i = \frac{\Delta N_{1i} + \Delta N_{2i} + \cdots + \Delta N_{ni}}{N_{1i} + N_{2i} + \cdots + N_{ni} - 0.5(\Delta N_{1i} + \Delta N_{2i} + \cdots + \Delta N_{ni})} = \frac{\sum_{j=1}^{n} \Delta N_{ji}}{\sum_{j=1}^{n} N_{ji} - 0.5\sum_{j=1}^{n} \Delta N_{ji}} \tag{7}$$

where sub-index i denotes the age and sub-index j — the subpopulation. Taking into account Eqs. (1) and (6), Eq. (7) can be rewritten as:

$$m_i = \frac{\sum_{j=1}^{n} \frac{N_{ji} m_{j0} e^{\beta_j i}}{1 + 0.5 m_{j0} e^{\beta_j i}}}{\sum_{j=1}^{n} N_{ji} - 0.5\sum_{j=1}^{n} \frac{N_{ji} m_{j0} e^{\beta_j i}}{1 + 0.5 m_{j0} e^{\beta_j i}}}. \tag{8}$$

In this equation the actual sizes of subpopulations can be replaced by their fractions. That is, we can define ρ_{ji} as the fraction formed by subpopulation j over the total population at any age i:

$$\rho_{ji} = \frac{N_{ji}}{N_i} = \frac{N_{ji}}{N_{1i} + N_{2i} + \cdots + N_{ni}} \text{ with } \sum_{j=1}^{n} \rho_{ji} = 1. \tag{9}$$

Then the Eq. (8) can be rewritten as:

$$m_i = \frac{\sum_{j=1}^{n} \frac{\rho_{ji} m_{j0} e^{\beta_j i}}{1 + 0.5 m_{j0} e^{\beta_j i}}}{1 - 0.5\sum_{j=1}^{n} \frac{\rho_{ji} m_{j0} e^{\beta_j i}}{1 + 0.5 m_{j0} e^{\beta_j i}}}. \tag{10}$$

The fractions ρ_{ji} in Eq. (10) are defined by the initial fractions ρ_{jo} by the equation similar to Eq. (5):

$$\rho_{ji} = \frac{\rho_{j0} \prod_{k=0}^{i-1} \left(\frac{1 - 0.5 m_{j0} e^{\beta_j k}}{1 + 0.5 m_{j0} e^{\beta_j k}} \right)}{\sum_{s=1}^{n} \left(\rho_{s0} \prod_{k=0}^{i-1} \left(\frac{1 - 0.5 m_{s0} e^{\beta_s k}}{1 + 0.5 m_{s0} e^{\beta_s k}} \right) \right)}. \tag{11}$$

We will use Eqs. (10–11) to define the mortality rate of the heterogeneous population as a function of age i and to examine the effect of model parameters on the dynamics of the mortality over age in the heterogeneous population. The continuous counterpart of Eq. (10) can be found in Vaupel and Yashin (1985).

2.2. Mortality dynamics in the model of heterogeneous populations

We start our study by considering a heterogeneous population consisting of two subpopulations (Fig. 2). The mortality of each subpopulation is described by Eq. (3) with parameters specific to the subpopulation. We can use Eq. (8) or Eq. (10) to analyse how the values of model parameters describing each subpopulation, namely initial sizes, N_{10} and N_{20} (or initial fractions ρ_{10} and ρ_{20}), initial mortalities, m_{10} and m_{20}, and parameters β_1 and β_2, defining ageing of subpopulations, affect the dynamics of the mortality rate of the entire population. Fig. 2A shows the influence of the initial mortality rate of a subpopulation on the dynamics of the total mortality rate. Here we consider the case when the subpopulations have equal initial sizes and equal slopes of ageing, i.e., $\beta_1 = \beta_2$. We can see that the value of the mortality rate for the entire population is initially in between (exactly in the middle for age $i = 0$) the mortality rates of the two subpopulations, but in the long run merges with the subpopulation that has the lower initial mortality. An increase in the difference in the initial mortality of subpopulations reduces the time needed for these to merge. The plot of mortality rate versus age has a single minimum that shifts down to smaller ages as the higher initial mortality is increased (compare red, green and blue solid lines in Fig. 2A).

We have also checked how the difference in the ageing slopes, β_1 and β_2, of subpopulations influences the dynamics of the mortality rate of a heterogeneous population (Fig. 2B). If the ageing slopes of subpopulations are different then the mortality rate of the entire population has a value in between the mortality rates of subpopulations. The total mortality increases at young ages, decreases for a short age interval and then increases again for old ages. In the long run the total mortality saturates to the level of the mortality rate of the subpopulation with the lower ageing coefficient, β. Generally, the graph of total mortality rate has a maximum and a minimum. They both are shifting to old ages when the difference between ageing slopes of subpopulations decrease.

The effect of variation in the initial sizes of subpopulations on the mortality dynamics of a heterogeneous population is shown in Fig. 2C. We have checked a general case of two subpopulations with different initial mortality rates ($m_{10} = 0.15$, $m_{20} = 0.02$) and different mortality coefficients ($\beta_1 = 0.0357$, $\beta_2 = 0.0556$) and varied the initial fractions ρ_{10} and ρ_{20} ($\rho_{20} = 1 - \rho_{10}$) of the subpopulations. The curves for the total mortality of the entire population (Fig. 2C) confirm the conclusions made after the analysis of the first two cases (shown in Fig. 2A and B). Generally, there is a single

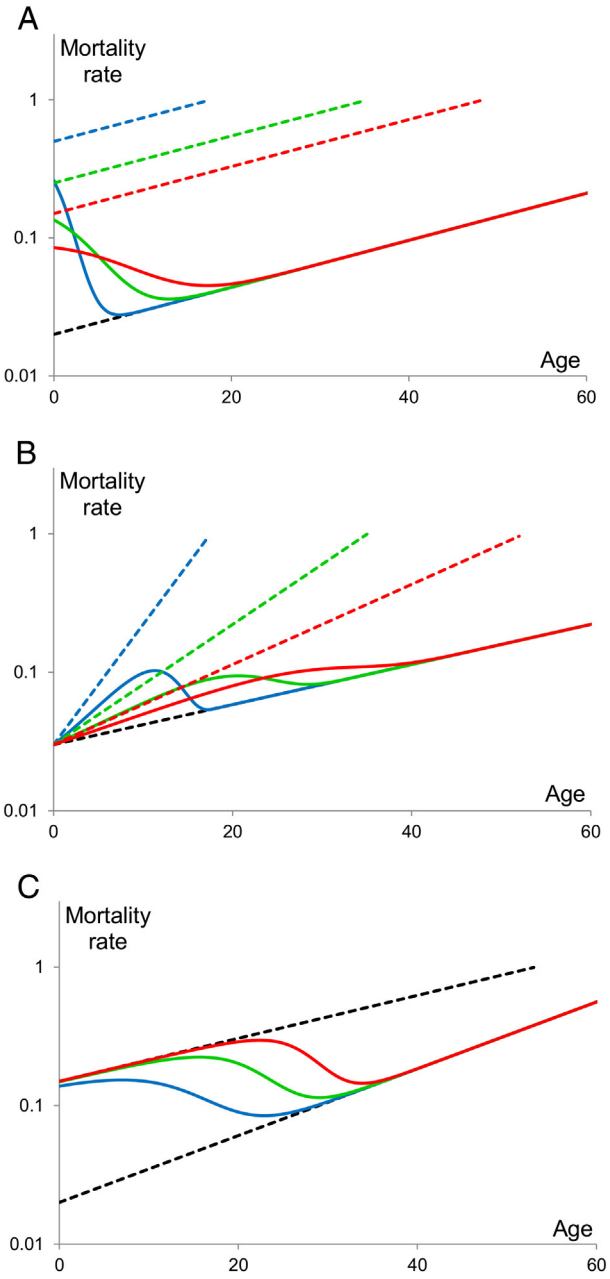


Fig. 2. The effect of varying model parameters on the mortality dynamics of a heterogeneous population consisting of two subpopulations.

A: The effect of varying the initial mortality rate for one of the subpopulations. Subpopulations have equal initial sizes ($\rho_{10} = \rho_{20} = 0.5$) and equal ageing slopes ($\beta_1 = \beta_2 = 0.039$). The initial mortality m_{10} takes the values 0.5, 0.25 and 0.15 for the blue, green and red dashed lines, respectively, while the initial mortality $m_{20} = 0.02$ is constant. The total mortality of the entire population is represented by a solid line with the colour of the corresponding dashed line (indicating the value of m_{10}).

B: The effect of varying the ageing slope. Subpopulations have equal initial sizes $\rho_{10} = \rho_{20} = 0.5$ and equal initial mortality rates $m_{10} = m_{20} = 0.03$. The rate of ageing β_1 takes the values 0.2, 0.1 and 0.067 for the blue, green and red dashed lines, respectively, while $\beta_2 = 0.033$ is constant. The total mortality of the entire population is represented by a solid line with the colour of the corresponding dashed line (indicating the value of β_1).

C: The effect of varying the initial size of the subpopulation. Two subpopulations (dashed lines) with different ageing slopes ($\beta_1 = 0.036$, $\beta_2 = 0.056$) and different initial mortality rates ($m_{10} = 0.15$, $m_{20} = 0.02$) are considered. Blue, green and red lines show the total mortality of a whole population where the initial fraction ρ_{10} is 0.9, 0.99 and 0.999 correspondingly.

minimum on the plot of the total mortality rate and this minimum shifts to old ages with the increase of the initial fraction of subpopulation 1 which displays both a higher initial mortality level and a slower mortality increase with age (i.e., lower β).

The analysis of simulations with varying parameters presented in Fig. 2 can be used for reproduction of two sets of mortality data presented in Fig. 1. Data on panel A of Fig. 1 is represented by a few points while data on panel B is much more detailed. We have picked up these two sets of data to demonstrate that the technique we use for fitting model parameters to observation data works equally well for sparse and extensive data sets. Fig. 1A gives the mortality data for the USA in the year 2002 taken from the Centres for Disease Control and Prevention http://www.cdc.gov/nchs/deaths.htm. Note, that this data could be interpolated either by a plot which has a single minimum (skipping the point at age 20) or by a plot with two minima. Our analysis (Fig. 2) indicates that in order to reproduce a plot of mortality rate with a single extreme point we need to consider two subpopulations. Since each subpopulation is described by three model parameters (initial mortality, m_0, rate of ageing, β, and fraction, ρ) and $\rho_1 + \rho_2 = 1$we need to find values of five parameters to fit the data in Fig. 1A. In the general case of n subpopulations the number of free (unknown) parameters is $k = 3n - 1$.

To find values for the free parameters that could minimize the sum of squared residuals (residual is a difference between the theoretical prediction and the observation data) and therefore to fit the data we have used the least squares (LS) method. This method was implemented using nonlinear regression algorithm (provided by the command *DataFit* in Maple which is included in the *DirectSearch* package). Using the LS method we have fitted parameters of the models for heterogeneous populations consisting of two (Fig. 3A) and three (Fig. 3B) subpopulations with the US data in Fig. 1A. The next task is to find out which of these two models is a better fit. The criterion we used for evaluation of how well the model fits the data is the Bayesian Information Criterion (*BIC*) (Schwarz, 1978) which is given by the formula:

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

where n_d is the number of data, $\hat{\sigma}_e^2$ is the sum of squared residuals divided by the number of data and k is the number of free parameters. The model with the lower value of *BIC* implies better fit to the data. Therefore, according to the *BIC*, the heterogeneous model with three subpopulations ($BIC = -44.06$) fits the US data better than the model with 2 subpopulations ($BIC = -13.01$). For the particular US data we cannot consider a population composed of four subpopulations because in that case we will need to calculate 11 free parameters while there are only 9 data points.

Now let us consider the data on the death rates in Sweden for the year 2007 presented in Fig. 1B (taken from the Human Mortality Database: http://www.mortality.org). This data is considerably more detailed compared to the US data presented in Fig. 1A. From Fig. 1B we see that the mortality rate is initially about 0.0025, and then declines to a minimum point at the age of 10 years, then increases until a local maximum value at the age of 25 years, drops slightly and advances exponentially (along a straight line on a logarithmic scale) from the age of 30 to about 100 years. At advanced ages, i.e., after approximately 100 years, the mortality data don't follow the monotonically increasing line. This can be explained either by fluctuations in mortality data or by the fact that the mortality rate starts to decline with age.

Fig. 4 shows three models of heterogeneous populations composed of 3 (panel A), 4 (panel B) and 5 (panel C) subpopulations fitting the data on the Swedish population presented in Fig. 1B. Compared by eye the plots on panels B and C seem to be better fits than the plot on panel A. The Bayesian Information Criterion indicates (see Fig. 4 legend)

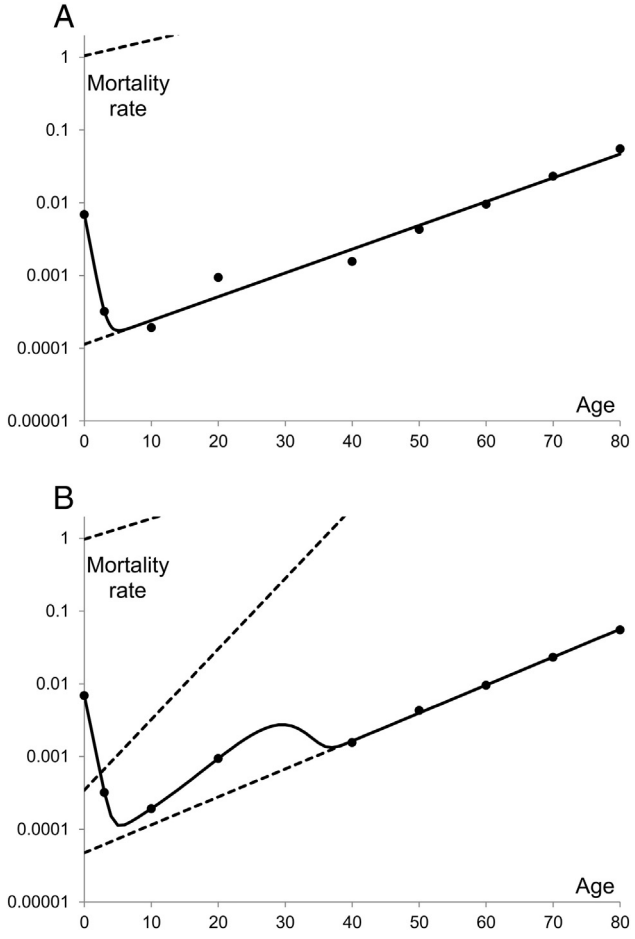


Fig. 3. Fitting the heterogeneous model to the US mortality data using the Least Squares Method. The data is denoted by the circle symbols, the mortality rates of modelled subpopulations are given by the black dashed lines and the mortality of the whole population by the solid black curve.

A: The heterogeneous population composed by two subpopulations. Model parameters:

1st subpopulation: $m_{10} = 1.052$, $\rho_{10} = 0.00978$, $\beta_1 = 0.0488$;
2nd subpopulation: $m_{20} = 0.00001133$, $\rho_{20} = 0.99022$, $\beta_2 = 0.0753$.
Sum of squared residuals: 0.625592.

B: The heterogeneous population composed by three subpopulations. Model parameters:

1st subpopulation: $m_{10} = 0.9748$, $\rho_{10} = 0.01038$, $\beta_1 = 0.065$;
2nd subpopulation: $m_{20} = 0.000345$, $\rho_{20} = 0.02486$, $\beta_2 = 0.223$;
3rd subpopulation: $m_{30} = 0.0000475$, $\rho_{30} = 0.96476$, $\beta_3 = 0.0885$.
Sum of squared residuals: 0.009544.

that the four-subpopulation model (panel B) fits to the data slightly better than the five-subpopulation model (panel C).

So far we assumed that $a = 0.5$ (see Eq. (1)) for all subpopulations in the heterogeneous model. Observations indicate that this is indeed true for all ages except the very first year ($i = 0$) for which the value of parameter a is significantly smaller. We have taken this observation into account by introducing an extra subpopulation for which the parameter a was predefined for age 0 to fit its observed value. The combination of Gompertz law and small parameter a causes this extra subpopulation to die entirely within the first year (at age 0), and therefore this subpopulation affects only the first ($i = 0$) modelled point. This lets us use the following improved procedure for fitting the heterogeneous population model to the observation data. We remove the first data point ($i = 0$) from consideration and find the best four-subpopulation fit for the remaining data similar to what was done for Fig. 4B. Then we add an extra subpopulation for which parameter a is small (i.e., $a = 0.3$ which is close to the observed value of a for age 0). As this subpopulation entirely disappears during the 1st year, we just need to adjust its size to have an ideal fit to the first data point ($i = 0$) which was removed from consideration earlier. Fig. 5A shows the outcome of the model, designed to fit the 2007 data for the Swedish population. It turns that this new model fits the data much better than models designed for Fig. 4.

We have used the procedure described above to fit a model comprising five-subpopulations to Swedish 1751 data (Fig. 5B). Although the 1751 data are considerably different from the 2007 data, the designed model also fits it remarkably well. A comparison of models for 1751 and 2007 data indicates that basically all parameters for all subpopulations did change over two-and-a-half century period. The most striking changes are the much higher initial mortality, m_{10}, in the main subpopulation in 1751 (>10 fold higher), and the fact that the main subpopulation, which comprises over 99% of the population in 2007, makes up less than half of the whole population in 1751. The latter observation also means that the other subpopulations (i.e., those with higher mortality) in 1751 were much larger. The detailed study of the evolution of model parameters could be done by making fits to the data for intermediate years, however this falls outside the scope of this study.

3. Study of fluctuations in mortality dynamics

The important observation we can make is that all models designed so far fail to describe the noisy pattern of observed data in early and late ages. This section will be devoted to the analysis of noise in mortality dynamics.

3.1. Modelling the stochastic effects

Assume that the probability to die, q_i, within a year for any individual depends only on his age. Then the number of death of individuals of age i is $\Delta N_i = q_i N_i$ where N_i is the number of people who reached their i-th birthday. Combining this with Eq. (1) we get $q_i = \frac{m_i}{1+0.5m_i}$ where m_i is presumed to follow the Gompertz law (Eq. 3). Furthermore, taking into account that if q_i is the probability to die then the probability to survive is $p_i = 1 - q_i$, we can find the probability that k out of N_i individuals survive (while $N_i - k$ individuals die) within a one-year interval. To find this probability we consider the following binomial expansion:

$$1 = [q_i + (1-q_i)]^{N_i} = \sum_{k=0}^{N_i} \frac{N_i!}{k!(N_i-k)!} q_i^{N_i-k}(1-q_i)^k. \quad (12)$$

Here the right-hand-side contains $N_i + 1$ terms (corresponding to values of k from 0 to N_i), each giving the probability for k individuals to survive or, correspondingly, the probability that $N_{i+1} = N_i - k$. Therefore we can use formulas for the mean and the variance of the stochastic process described by the binomial distribution and conclude that the mean value of ΔN_i is $\langle \Delta N_i \rangle = N_i q_i$ and its variance, $\sigma^2 = N_i q_i (1 - q_i)$ (see Allen, 2010; Morgan, 2000; Ross, 2002). The mortality error, Δm, can be defined as the standard deviation of the number of deaths divided by the mean number of person years lived at age i:

$$\Delta m_i = \frac{\sigma}{\langle PY_i \rangle} = \frac{\sqrt{N_i q_i (1-q_i)}}{N_i - 0.5 N_i q_i} = \sqrt{\frac{m_i(1-0.5m_i)}{N_i}}. \quad (13)$$

The fluctuations in mortality are observable when the mortality error is high relative to the mean mortality or when the relative

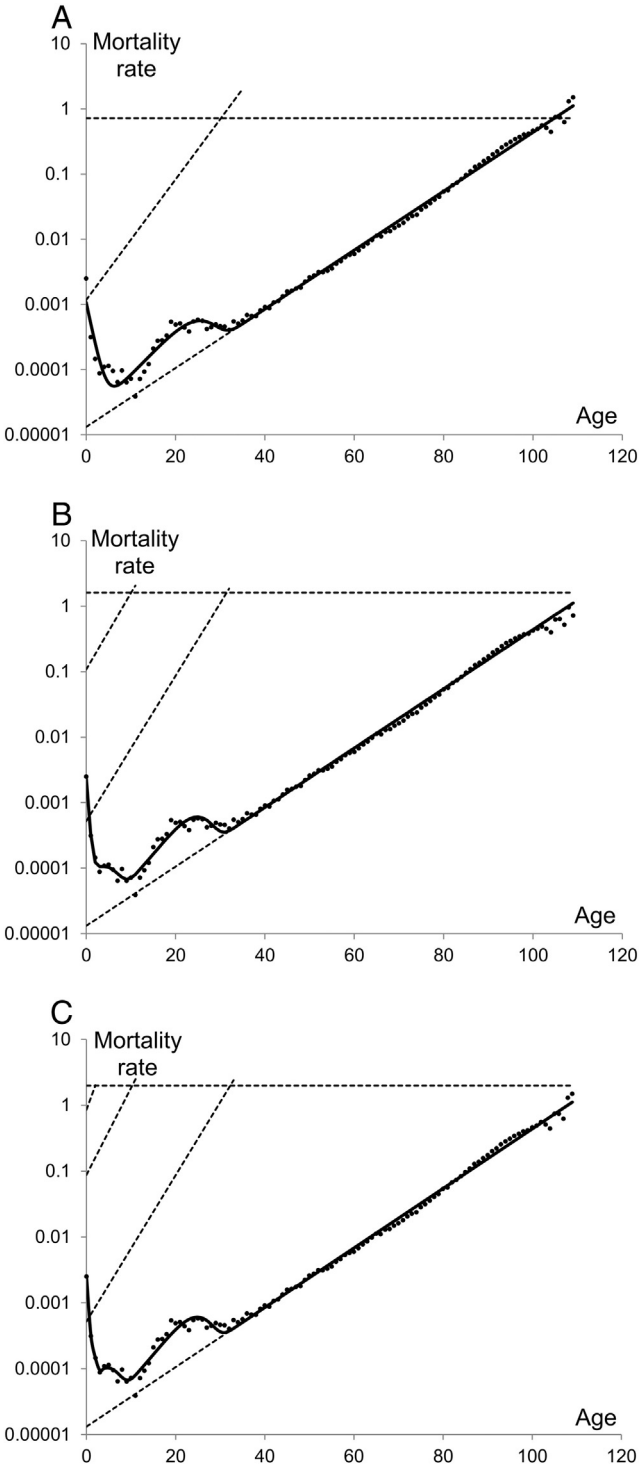
mortality error defined as the mortality error divided by the mean mortality is above some threshold, *Th*:

$$\frac{\Delta m_i}{m_i} = \sqrt{\frac{1-0.5m_i}{N_i m_i}} > Th. \tag{14}$$

Eq. (14) can be extended to the case of a heterogeneous population: the number N_i would represent the total size of the population (sum of all subpopulation sizes) and m_i represent the overall mortality of the heterogeneous population given by Eq. (10). The variables describing subpopulations in a heterogeneous population are independent and therefore the total variance, σ^2, for the whole population is a sum of the variances, σ_j^2, of the constituent subpopulations. Therefore, the mortality error for the entire heterogeneous population can be written in the form:

$$\frac{\Delta m_i}{m_i} = \frac{\left(\sum_{j=1}^{n}\sigma_{ji}^2\right)^{1/2}}{\langle PY_i\rangle m_i} = \frac{\left(\sum_{j=1}^{n} N_{ji}q_{ji}\left(1-q_{ji}\right)\right)^{1/2}}{m_i\sum_{j=1}^{n}\left(N_{ji}-0.5N_{ji}q_{ji}\right)} \tag{15}$$

where m_i is defined by Eq. 10).



3.2. Numerical implementations of the stochastic model

The direct implementation of Eq. (12) for computer simulations requires the comparison of random computer-generated numbers with terms on the RHS of Eq. (12). The binomial coefficients in Eq. (12) are found using the Pascal triangle. This algorithm is perfectly adequate if the size of the population is relatively small. However, for large populations, say when $N_i > 100$, we have to operate with extremely small numbers (like $q_i^{N_i}$ where $q_i < 1$) as well as extremely large numbers (like N_i !) hitting in both cases the computer limitations associated with handling real and integer numbers.

To overcome this difficulty we have used an alternative numerical algorithm which does not require Eq. (12). It is slow compared to the above algorithm but allows the consideration of populations of practically any size. If the number of individuals of age *i* is N_i then in order to find N_{i+1} we order the computer program to generate a set of N_i random numbers (each represented by a real number which is not less than zero and not more than one), i.e., one random number per each individual. Each of the generated random numbers is compared with the probability, $q_i, q_i = \frac{m_i}{1+0.5m_i}$ where m_i is defined by Eq. 3. The probability a random computer-generated number to be less than q_i is equal to q_i. Therefore, every time when the random number is less than q_i we conclude that one individual dies. Comparing N_i random numbers with q_i lets us make a decision (dies or stays alive) on each of N_i individuals and obtain the number of individuals N_{i+1} who

Fig. 4. Fitting the heterogeneous model to the Swedish mortality data using the Least Squares Method. The data is denoted by the circle symbols, the mortality rates of modelled subpopulations are given by the dashed lines and the mortality rates of the whole population by the solid curve.

A: The heterogeneous population composed by three subpopulations. Model parameters:

1st subpopulation: $m_{10} = 0.7211$, $\rho_{10} = 0.00198$, $\beta_1 = 0.67 * 10^{-5}$.
2nd subpopulation: $m_{20} = 0.001169$, $\rho_{20} = 0.00483$, $\beta_2 = 0.2129$;
3rd subpopulation: $m_{30} = 0.00001317$, $\rho_{30} = 0.99319$, $\beta_3 = 0.1041$
Sum of squared residuals: 5.715275; $BIC = -287.7033$.

B: The heterogeneous population composed by four subpopulations. Model parameters:

1st subpopulation: $m_{10} = 1.6139$, $\rho_{10} = 0.00266$, $\beta_1 = 0.67 * 10^{-5}$.
2nd subpopulation: $m_{20} = 0.108$, $\rho_{20} = 0.00057$, $\beta_2 = 0.2685$;
3rd subpopulation: $m_{30} = 0.00052$, $\rho_{30} = 0.00460$, $\beta_3 = 0.2558$;
4th subpopulation: $m_{40} = 0.000013146$, $\rho_{40} = 0.99217$, $\beta_4 = 0.1041$;
Sum of squared residuals: 3.229884; $BIC = -336.3785$.

C: The heterogeneous population composed by five subpopulations. Model parameters:

1st subpopulation: $m_{10} = 1.986$, $\rho_{10} = 0.002$, $\beta_1 = 0.67 * 10^{-5}$.
2nd subpopulation: $m_{20} = 0.859$, $\rho_{20} = 0.00074$, $\beta_2 = 0.4254$;
3rd subpopulation: $m_{30} = 0.088$, $\rho_{30} = 0.00052$, $\beta_3 = 0.3041$;
4th subpopulation: $m_{40} = 0.0005207$, $\rho_{40} = 0.00459$, $\beta_4 = 0.2558$;
5th subpopulation: $m_{50} = 0.00001316$, $\rho_{50} = 0.99215$, $\beta_5 = 0.1041$;
Sum of squared residuals: 3.173179; $BIC = -324.2254$.

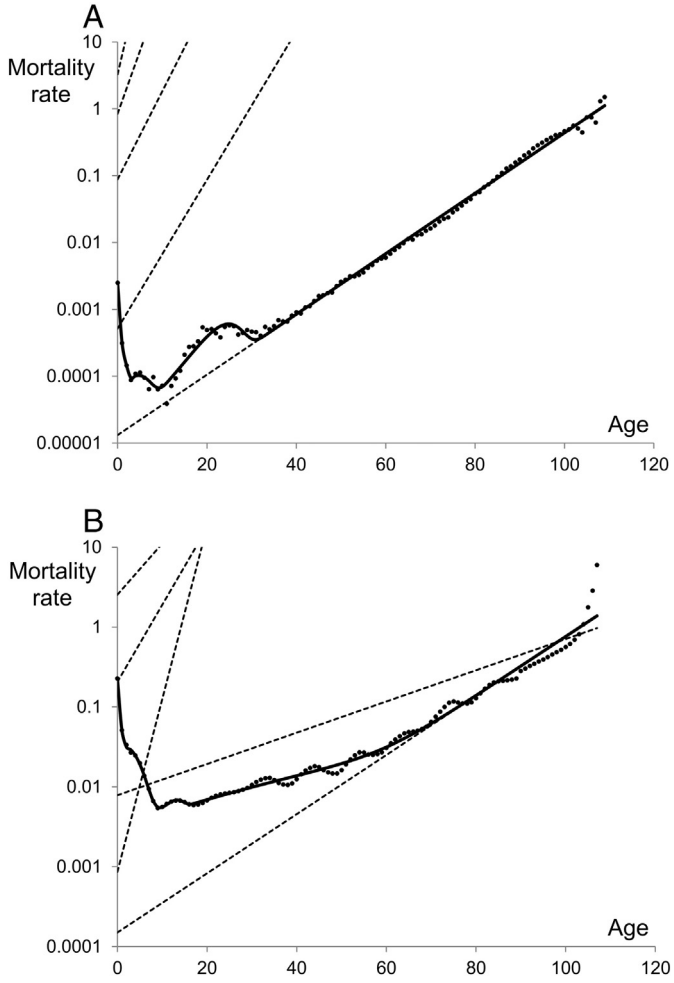


Fig. 5. Extension of the four-subpopulation heterogeneous model with extra-subpopulation to fit parameter a (in equation 1) in the Swedish mortality data for 2007 (panel A) and for 1751 (panel B). Since $a = 0.5$ at all ages except for the age zero the fitting was done in 2 steps. 1. The four-subpopulation model is composed to fit all data except the very 1st point; 2. Extra (fifth) population was added to fit parameter a (see Eq. (1)) and number of deaths for the 1st point. The data is denoted by the circle symbols, the mortality rates of modelled subpopulations are given by the dashed lines and the mortality rates of the whole population by the solid curve.

A: The heterogeneous population composed by five subpopulations. Model parameters:

1st subpopulation: $m_{10} = 3.28$, $\rho_{10} = 0.00122$, $\beta_1 = 0.0066$, $a_{10} = 0.3$.
2nd subpopulation: $m_{20} = 0.8477$, $\rho_{20} = 0.00072$, $\beta_2 = 0.4324$;
3rd subpopulation: $m_{30} = 0.08824$, $\rho_{30} = 0.00052$, $\beta_3 = 0.3034$;
4th subpopulation: $m_{40} = 0.0005179$, $\rho_{40} = 0.00459$, $\beta_4 = 0.2561$;
5th subpopulation: $m_{50} = 0.000013163$, $\rho_{50} = 0.99295$, $\beta_5 = 0.1041$;
Sum of squared residuals: 3.173157; $BIC = -324.2261$.

B: The heterogeneous population composed by five subpopulations. Model parameters:

1st subpopulation: $m_{10} = 2.544$, $\rho_{10} = 0.13045$, $\beta_1 = 0.1473$, $a_{10} = 0.32$.
2nd subpopulation: $m_{20} = 0.2054$, $\rho_{20} = 0.13239$, $\beta_2 = 0.2222$;
3rd subpopulation: $m_{30} = 0.007861$, $\rho_{30} = 0.28278$, $\beta_3 = 0.045$;
4th subpopulation: $m_{40} = 0.000862$, $\rho_{40} = 0.00587$, $\beta_4 = 0.4975$;
5th subpopulation: $m_{50} = 0.0001501$, $\rho_{50} = 0.44851$, $\beta_5 = 0.0853$;
Sum of squared residuals: 4.814607; $BIC = -270.3817$.

reach age $i + 1$. This procedure can also be extended to consider heterogeneous populations.

3.3. Fluctuations in the mortality dynamics in stochastic model

We have checked how the stochasticity affects the dynamics of mortality, which is presumed to follow the Gompertz law. Fig. 6 indicates that the amplitude of fluctuations depends on the model parameters such as the size of the population and its initial mortality. We can also see that fluctuations can appear and disappear in

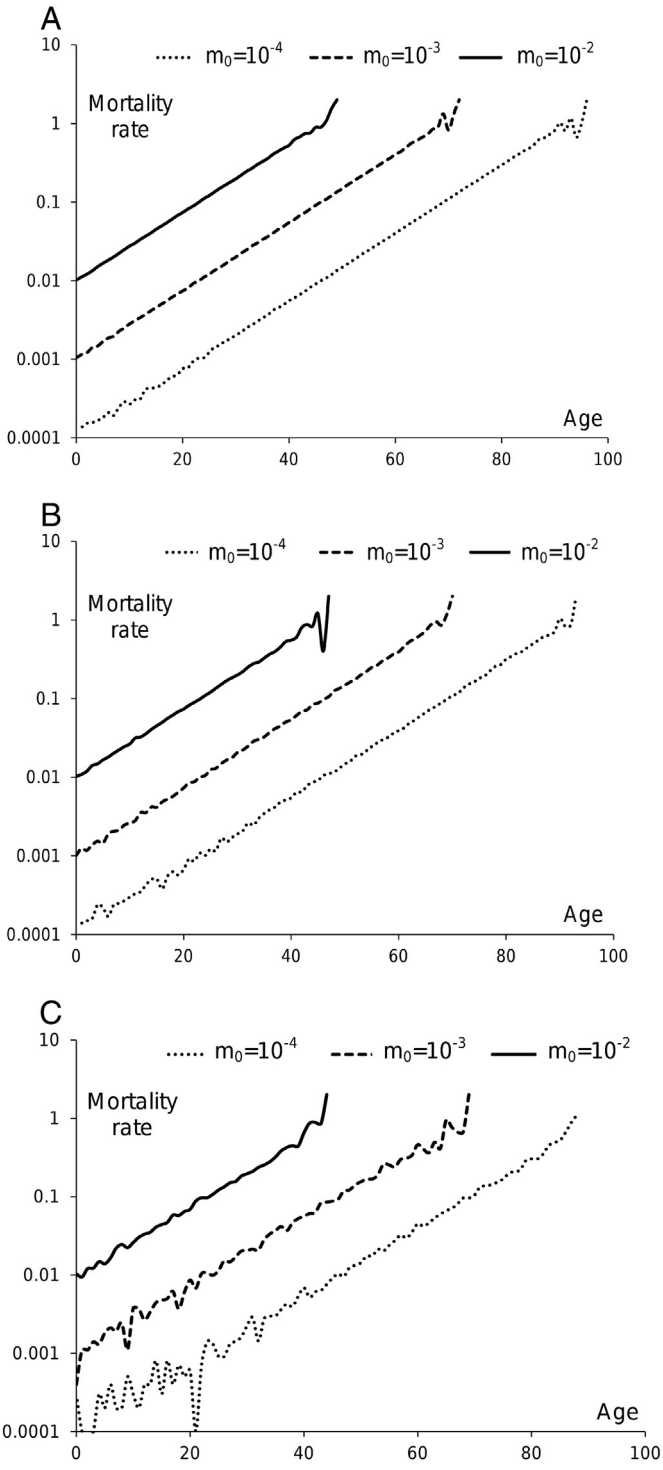


Fig. 6. The mortality dynamics in a stochastic model of a homogenous population. Implementation of stochasticity: the mortality rate (calculated according to the Gompertz law) is converted to a probability, q, for each individual to die. Whether the actual death event takes place or not is decided according to a computer-generated random number. Each plot shows the mortality dynamics for three populations having different initial mortality rates ($m_0 = 0.0001$, $m_0 = 0.001$, and $m_0 = 0.01$ shown by the dotted, dashed and solid lines respectively). Each panel corresponds to the different initial size of population: 10^6 on panel A, 10^5 on panel B and 10^4 on panel C. Each population has mortality coefficient, $\beta = 0.1$.

different parts of the same mortality plot. The fluctuations are generally observed at early and advanced ages. The occurrences of the fluctuations in Fig. 6 can be explained by Eq. (14), namely, we can claim that if the fluctuations in the mortality plot are due to stochastic effects, then they should become observable when the relative mortality error is high enough. Eq. (14) indicates that this error is inversely proportional to the mortality rate and to the size of the population. This implies that deviations from the theoretical mortality data can be observed on two sides of the mortality patterns, at the initial ages where the mortality, m_i, is small and at advanced ages where the number of individuals, N_i, is small. In both cases the fluctuations become observable since the total number of deaths is relatively small.

Eq. (14) states that the relative mortality error should be above a certain threshold (Th) for the fluctuations in mortality of a population to become observable. Fig. 7 shows the graphs of the relative mortality error (dashed lines) calculated for the mortality data (solid lines) presented in Fig. 6B. An analysis of these graphs indicates that the threshold value, Th, can be estimated by a number between 0.05 and 0.1 to reflect the transitions from observable to unobservable (and back) fluctuations on the mortality plots. As an example, the case of $Th = 0.06$ is shown in Fig. 7 where a horizontal solid black line represents this threshold. Intersections of the graphs of relative mortality error with this horizontal line correspond to the transitions from fluctuating to non-fluctuating behaviour in the mortality plots.

In practice, the term $1 - m_i$ in the numerator of the expression for the relative mortality error in Eq. (14) can be omitted (replaced by 1, as m_i is very small) at the transition point at young ages, and $Th = 0.06$ would represent the reciprocal of the square root of the product $N_i m_i$, $Th = 1/\sqrt{N_i m_i}$, or we could say that the young-age transition takes place when $N_i m_i = 1/Th^2 \approx 300$. The transition point at advanced age takes place when the mortality m_i is not very small and therefore some estimate of the size of population at this transition point can be made. For example, assuming that the transition takes place when $m_i = 0.6$ we get for the size of the population $N_i \approx 180$ (this is a case for the plot shown in Fig. 7A, when the fluctuations for the advanced ages start at age $i = 41$ for which the mortality $m_i = 0.6$ and the number of individuals $N_i = 149$).

Fig. 8 gives a few illustrations of the transition from non-fluctuating to fluctuating dynamics of mortality rate at advanced ages. The graph of mortality dynamics according to the Gompertz law is shown by the solid line while mortality in the stochastic model is shown by dashed line. Increase of the size of the population results in the disappearance of the fluctuations at early ages and further to the occurrence of fluctuations (the transition point) at progressively more advanced ages. Furthermore, despite the big differences in the initial sizes of the populations in all three shown simulations, the fluctuations start to become observable at the age represented by 150–180 individuals. The fluctuations affect the mortality dynamics in a random and unpredictable way which makes the shapes of mortality graphs after the transition points to be considerably different in all presented simulations.

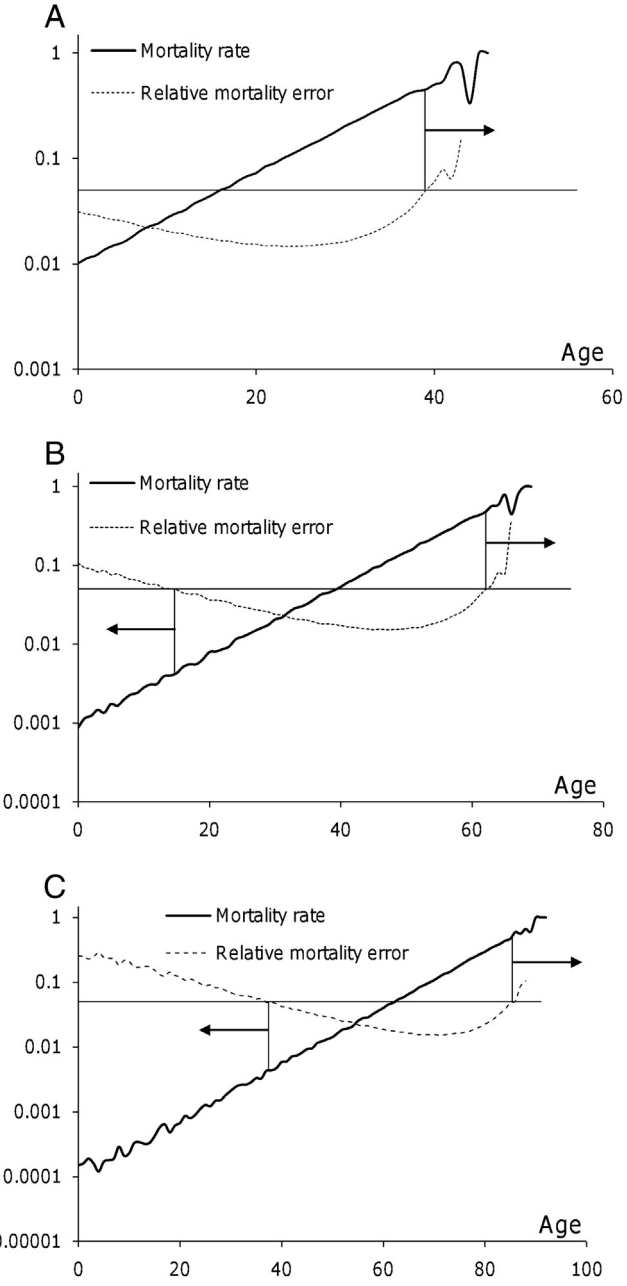


Fig. 7. Correlation between the fluctuations in mortality dynamics and the relative mortality error. Three graphs of mortality data from Figure 6B (solid lines) with the corresponding graphs of relative mortality error (dashed lines) are presented in three panels. When the relative mortality error is above the threshold (the dashed line is above the horizontal line) there are fluctuations in the mortality graphs, while when the error is below the threshold (dashed line below the threshold line), the fluctuations are not observed. Vertical lines indicate the ages when the error curves intersect the threshold line and the arrows show on what side of the vertical line the fluctuations are observed.

3.4. Fitting models to the observation data

Fig. 4 demonstrates that the model of a heterogeneous population indeed reproduces the dynamics of observed mortality data very well. However the observation data has a feature which is not captured by the model, namely the fluctuations. The noisy background of mortality records is especially expressed at young and old ages. Many authors have treated the noise at old ages as a deviation from the exponential law (Vaupel et al., 1998) either by considering this deviation as a plateau on the graph or even as a decline in mortality (Partridge and Mangel, 1999). Fig. 9A shows part of the data from Fig. 1B which is related to the elderly ages (solid black line). This data represent period data for the Swedish population for the year 2007 obtained from the Human Mortality Database (http://www.mortality.org). Dashed lines on the same panel in Fig. 9 give parts of the period data for a few other years (1994, 2001, 2009) which are taken from the same database. The plots indicate that the mortality dynamics for all shown cases exhibit roughly the same growing pattern and in all cases the fluctuations appear after the age of 102.

In order to check whether these fluctuations can be explained by the stochasticity in the dynamics of mortality we have performed computer simulations. Each time, we used the same model parameters (initial size of the population, and Gompertz parameters in Eq. (3)) but seeded different sets of random numbers to reproduce

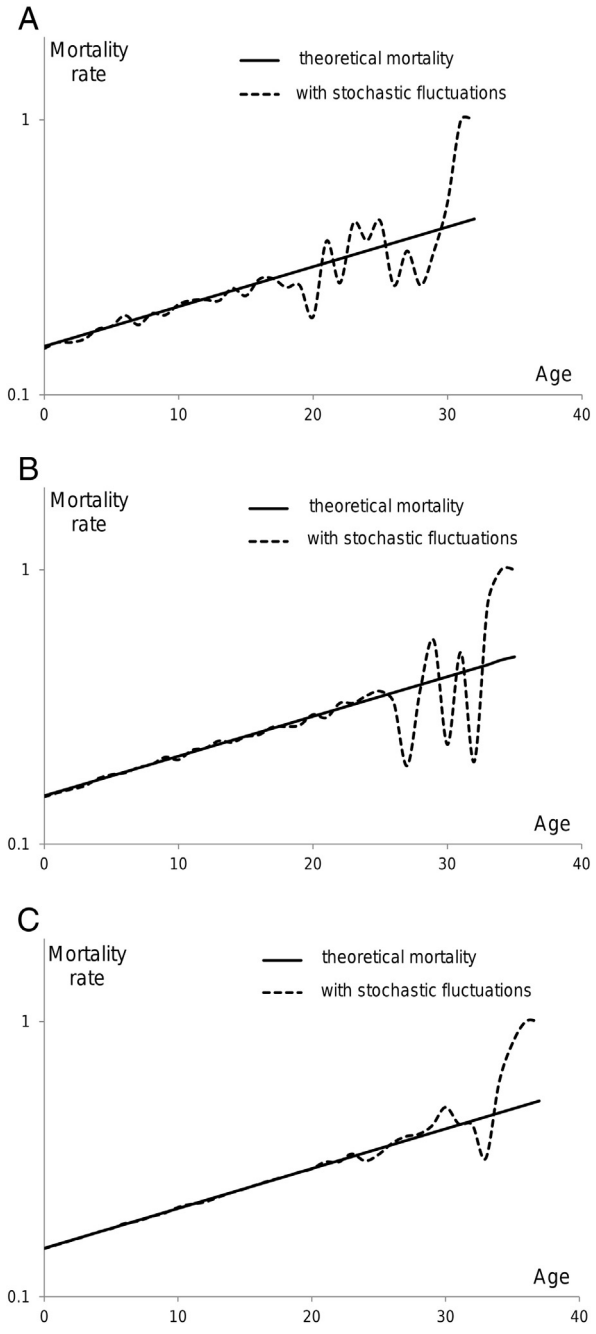


Fig. 8. Variations in the mortality dynamics due to stochastic effects. Plots of theoretical mortality (solid line) and actual mortality (dashed curve) for a population with initial mortality rate $m_0 = 0.15$ and mortality coefficient $\beta = 0.033$ are shown. The initial size of the population is 10^4 in panel A, 10^5 in panel B and 10^6 individuals in panel C.

death events. The initial mortality, m_0, and initial size of the population in the model was chosen to fit the first data point (at age 90) for the Swedish data for year 2007 and the rate of ageing β to fit the slope of the data points. Fig. 9B gives a few examples of computer simulated mortality dynamics (dashed lines) as compared with the actual data (black solid line). We can see that the simulations reproduce the data fairly well in a qualitative manner. However, the simulated mortality dynamics follows considerably different plots for different sets of random numbers generated by the computer. We can see that fluctuations on all presented plots (for simulated data as well as for the data taken from the database) take place after the age of 102 (when about 150 survivors are left in the population) and these fluctuations are the main reason for the deviation from the Gompertz dynamics.

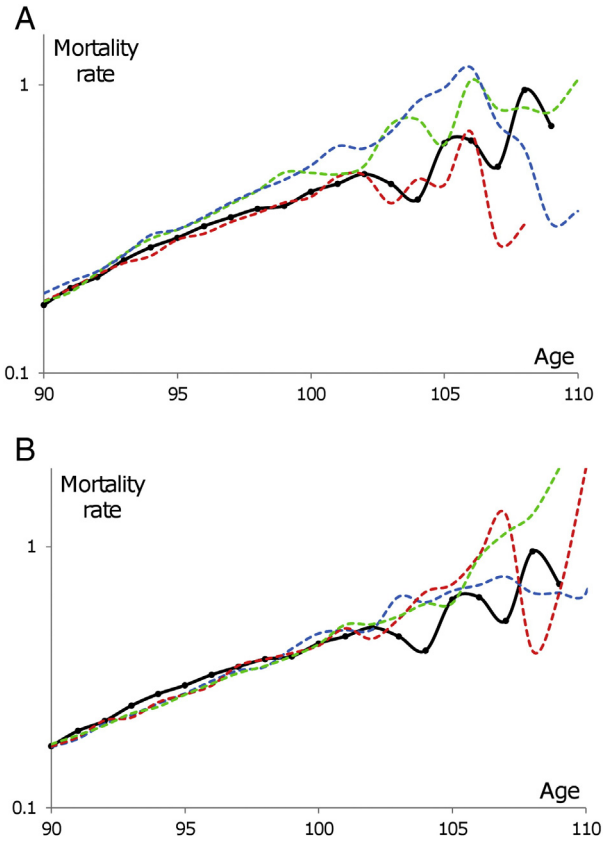


Fig. 9. Plots of mortality dynamics for the advanced ages in period data for Swedish population (A) in the stochastic model (B). The solid black line on both panels is the plot of the mortality rate for the advanced ages of the Swedish population in the year 2007 (part of the data from Fig. 1B). The red, blue and green dashed curves on panel A correspond to the period data on mortality for the Swedish population in 1994, 2001 and 2009. The red, blue and green dashed curves on panel B correspond to three simulations of mortality dynamics in the stochastic model for the different sets of random computer-generated numbers. All plots (period data and simulations) show the deviation from exponential growth in a very similar way, i.e., deviations are represented by fluctuations which start at age 102. Model parameters: $N_{90} = 18660$ $m_{90} = 0.172479$, $\beta = 0.0926$.

4. Model combining the heterogeneity of population with stochastic effects

Up to now we have considered either heterogeneous or stochastic models. Now we can combine these two models to reproduce the entire set of mortality data for the Swedish population presented in Fig. 1B. We have already modelled this data assuming that the Swedish population is heterogeneous and comprised of four subpopulations (Fig. 4B). Now we expand that model and introduce the stochastic effect to the mortality description of all four subpopulations. Fig. 10 shows the results of this simulation. We see that the simulated data (red triangles) exhibit noise, which is very reminiscent of the noise in the real data (blue circles). The noise in both cases is enhanced for young and advanced ages. We have calculated the relative mortality error in simulations (dashed line) and identified its threshold value ($Th = 0.05$ shown by the horizontal solid line) such that the fluctuations (noise) in the mortality are visible if the error is above this threshold. This is observed in two domains indicated by I (up to the age of 53) and III (above the age of 102) in the figure. The relative mortality error in the domain II (between the ages of 53 and 102) is less than the threshold and correspondingly the noise in the mortality data (both actual and simulated) is negligible in this domain.

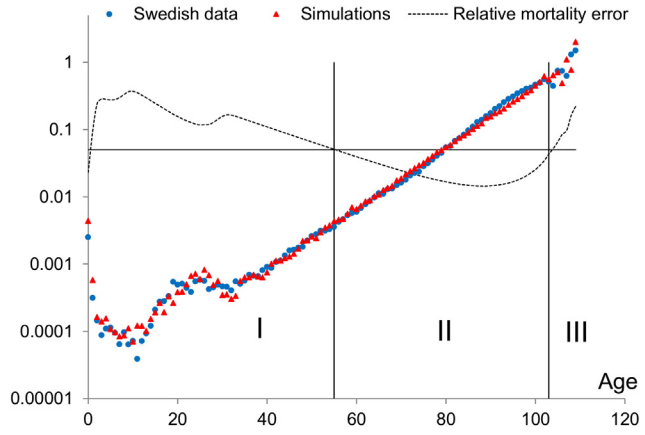


Fig. 10. Fitting the mortality data of the Swedish heterogeneous population with stochastic simulations. The blue circles represent the mortality data for the Swedish population from Fig. 1B while red triangles represent the simulation data. The model combining heterogeneity (the version used in Fig. 4B) and stochasticity (implemented in the same way as in Figs. 6–9) has been used. The graph of the relative mortality error for the simulated data is shown by the dashed line, the threshold level ($Th = 0.05$) is shown by the horizontal line. Vertical lines indicate ages at which the error graph crosses the threshold level. They divide the plot into 3 domains: domains I and III where the relative mortality error is above the threshold line (the fluctuations in both data sets are observed) and domain II where the relative mortality error is below the threshold line and both data sets are relatively free from the noise.

5. Discussion

Modelling the dynamics of human mortality has long been a focus of research. It could help understand the human ageing process and causes of mortality, possibly providing insights that may help to improve human health and to extend lifetime. Not surprisingly, a number of studies have assessed the impact of heterogeneity on the dynamics of mortality, in particular at later ages (Rossolini and Piantanelli, 2001; Vaupel, 2010; Vaupel et al., 1979). In this work we have developed a mathematical model which lets us reproduce and analyse the mortality dynamics across the entire human life span. Our model combines heterogeneity of population with stochastic effects and the model parameters can be easily tuned so that the simulated data fits well the actual data on mortality dynamics, as shown in Figs. 4, 9 and 10.

We have shown that our model is capable of reproducing the actual data on human population mortality fairly well. We had to consider only five subpopulations to reproduce with sufficient accuracy the detailed period data for Swedish populations in 1751 and 2007. Even though this is an underestimate of actual heterogeneity of human populations, it shows how a simple mathematical model can represent actual human mortality well. One intriguing observation from the values of model parameters is that the main subpopulation makes up over 99% of the whole population (Fig. 4), meaning that in modern populations heterogeneity is actually relatively low. A comparison of model parameters for 1751 and 2007 data (Fig. 5) shows that model parameters such as initial mortality, m_0, and rate of ageing, β, have dramatically changed, which is not surprising since the conditions of life have also dramatically changed. A more interesting point is that initial fractions of subpopulations, ρ, have also changed considerably. This, most likely, indicates that advances in medicine and hygiene over the last 250 years have caused fewer individuals to be susceptible or to be exposed to diseases, and infectious diseases in particular, essentially shifting individuals across the subpopulation. This argument can be rephrased in the following way. Each of the five considered subpopulations (say 1st level subpopulations) is also heterogeneous and composed of subpopulations (say 2nd level subpopulations). An improvement in life style over the last 250 years has caused for some of the 2nd level subpopulations to move across the 1st level subpopulations and contribute to the longer lasting fractions. This rearrangement has changed the fraction balance between the 1st level subpopulations.

Our simulations and analysis indicate that the contributions of heterogeneity and stochasticity are different at different ages. The effect of heterogeneity is profound when fractions formed by subpopulations are far from being zero or one. Our model suggests that at early ages a small subpopulation with high initial mortality explains the decline in mortality as this subpopulation gradually disappears. Generally, with an increased age the faster-ageing subpopulations are eliminated and the population starts to act more-and-more homogeneously as it would be composed by a single (having lowest mortality) subpopulation.

The leading causes of death in infants are congenital malformations, disorders related to short gestation and low birth weight, and sudden infant death syndrome (Kung et al., 2007). Therefore, a small subpopulation (the initial fraction comprised by the 1st subpopulation in the simulation shown in Fig. 4B, $\rho_1 = 0.00266$ which is 0.27% of the total population) with high initial mortality is in line with epidemiological data. On the other hand, it is not clear what the phenomenological differences between other modelled subpopulations are. Our preliminary simulations indicate that fitting the model to describe the mortality dynamics for males or for females will also require four subpopulations (roughly the same as in Fig. 4B) in both cases. Whether the modelled subpopulations are associated with different social groups has to be analysed in a follow-up study.

We also can identify a subpopulation (subpopulation 3 in Fig. 4B) which lets us reproduce the mortality peak at about age 20. While this fits the data well, this subpopulation can be considered somewhat artificial because this mortality peak in the teenage years is likely due to behaviour rather than intrinsic biological properties of a subset of individuals. It is possible, in fact, that the increase in mortality in teenage years is age-specific (goes up and down at a specific age range) and cannot be modelled by Gompertz law. Nonetheless, we speculate that risk-taking behaviour in a subset of individuals could make up such a hypothetical subpopulation.

In line with the results obtained earlier (Rossolini and Piantanelli, 2001; Vaupel, 2010; Vaupel et al., 1979) we conclude that the heterogeneity of a population is sufficient to explain the mortality plateaus observed at later ages. In addition, the size of the population declines with age and the effects of stochasticity become more pronounced. It seems that at later ages when the population is small the stochastic effects can explain the observed mortality plateaus as well as the high-amplitude fluctuations (high noise) in the mortality dynamics. Likewise, at earlier ages, when the number of death events is small, stochastic effects are also noticeable and cause the high-amplitude fluctuations in the mortality dynamics.

In conclusion, the assumption that the populations are heterogeneous and the mortality dynamics of each subpopulation follows the Gompertz equation with different parameters can account for observed deviations of the mortality dynamics (for the entire life course) from the Gompertz law. We also found that stochastic effects are important when relatively few individuals contribute to mortality. Our demographic modelling across the lifespan combining the effects of heterogeneity and stochasticity was successfully tested in simulations of human mortality data from populations in Sweden and the US.

Conflict of interest

The authors have no conflicts of interests.

Acknowledgements

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