Study on the dynamics of human ageing and mortality

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Contents

Abstract

This dissertation is devoted to the mathematical modelling of dynamics of mortality in human populations. Human population consists of many subpopulations with different characteristics, which affects the feature of the whole population. In the particular study we will focus on the dynamics of human ageing. A general definition for the mortality rate is that it is a measure of the number of deaths in a population, scaled to the size of that population, per unit of time Δt. Let us assume that the number of deaths is M and the size of a population is N. Then, the mortality rate m expressed by the equation

$$m = \frac{M}{N\Delta t}. \tag{1}$$

One of the important features of the mortality rate is that it depends on the age of individuals. This dependence is referred as ageing. It looks that ageing for the wide range of ages can be described by the Gompertz exponential function:

$$m(t) = Ae^{t/\tau}. \tag{2}$$

Difference between this exponent and real data on the mortality rate versus age can be explained in different ways (i.e. questioning the exponent). However, one of the attractive hypothesis to explain this discrepancy is to consider the entire population as heterogeneous and consisting of a few subpopulations, each ageing exponentially but with different mortality parameters. By this consideration we can study ageing and mortality for the entire population and check whether the modelling data can fit the observations. Furthermore, another important hypothesis for the study on the dynamics of ageing and mortality is the consideration of stochasticity to explain some fluctuations which are observed in the pattern of mortality rates at advanced ages of human life.

On this dissertation we will study the mortality rate of a whole population consisting of subpopulations with different parameters and we will explain some pecularities which observed at some ages and seen in the mortality rate's curve. Therefore we separate our research into two parts where we study the effects of heterogeneity and stochasticity on the ageing dynamics respectively.

Chapter 1

Introduction

1.1 Main causes of death

To begin with, we will describe the main causes that lead humans to death. Generally, many deaths occuring in older people beacuse ageing causes some syndromes or illnesses. Elderly people are more prone to death because they are more vulnerable to illnesses than the rest part of a population. However, a lot of diseases or other causes of death which affect the elderly, also affect younger people.

There is a big variety of life threatening diseases which differ among the populations. When mortality in a population is high, a large extent of deaths are caused by infectious diseases such as tuberculosis (TB) and HIV/AIDS, as well as by maternal and nutritional conditions, while a smaller extent of deaths are caused by non-infectious diseases, which include cardiovascular diseases and several types of cancer. In low-mortality populations, the majority of deaths are due to non-infectious diseases. In developed countries, whose populations are generally considered by low mortality, just 6 per cent of the deaths that occured in 2004 were due to infectious diseases, whereas 86 per cent by non-infectious causes. In the countries that were least developed, where both infectious and non-infectious diseases contribute to high mortality, 63 per cent of all deaths in 2004 were the result of infectious diseases, while 30 per cent were caused by non-infectious diseases.

Besides disease, injury is a major category for causes of death worldwide and include those caused by road accidents. Rarely, we can observe an increased mortality rate in countries where natural disasters are more likely to happen such as earthquakes, floods, tsunamis and hurricanes. In 2004, injuries accounted for 10 per cent of deaths worldwide, ranging from a 3 per cent in a number of countries to an increased 40 per cent in Sri Lanka as a result of the tsunami that hit the country at the end of the year.

Below, table 1.1 presents the top 10 causes of death as recorded in the website of World Health Organization (WHO) for the year 2004, [1].

Table 1.1: Top 10 causes of death for 2004

Causes of deaths	Deaths in millions	% of deaths
Coronary heart diseases	7.2	12.2
Stroke and other cerebrovascular diseases	5.71	9.7
Lower respiratory infections	4.18	7.1
Chronic obstructive pulmonary diseases	3.02	5.1
Diarrhoeal diseases	2.16	3.7
HIV/AIDS	2.04	3.5
Tuberculosis	1.46	2.5
Trachea, bronchus, lung cancers	1.32	2.3
Road traffic accidents	1.27	2.2
Prematurity and low birth weight	1.18	2.0

As it can be seen from table 1.1, the main reason for mortality was cardiovascular diseases which include coronary heart disease, as nearly 7.2 million people died in 2004. According to the table 1.1 later comes stroke and cerebrovascular diseases which affect a large number of the population. Following this pattern, lower respiratory infections (i.e. pneumonia), chronic obstructive pulmonary diseases such as chronic bronchitis and emphysema, diarrhoeal diseases, HIV/AIDS, Tuberculosis, Trachea-bronchus-lung cancers, road traffic accidents and prematurity, make up the top 10 causes of death in 2004.

The mortality rate changes each year depending on the number of deaths from each cause. However, the rate of deaths by cause, differ each year and sometimes new causes affect the total mortality. A recent example, is the Swine Flu virus (H1N1) which emerged the last 2 years as a flu pandemic. It is estimated that a 0.02% percentage of deaths was caused from this pandemic.

Also, reasons which cause deaths vary between separate countries and regions. So we can compare two groups of people from different areas to see the influences of some particular causes. An example is the comparison of the number of deaths caused by AIDS between two economically different countries. In third world countries a larger percentage of people is observed which are carriers of AIDS and therefore the mortality rate for this disease is different from the same mortality rate of a country that is economically developed. Another example, is the comparison of two groups of people, from the same country but different areas, assuming that the first one living in an industrial area with many factories and air-pollution and the other in a better environment with clean air and better life conditions i.e. healthy nutrition and less polluted air. From this comparison we can deduce that people from the first group are more vulnerable to respiratory diseases or types of cancer than people from the second group which have much less probability to acquire these diseases.

1.2 Mortality variation by ages

An important feature of the mortality rate is that it depends on age of humans. We can compare mortality rates of people from different age groups. Firstly, we can classify people by age and study the mortality rate for each age group, and then we can study the parameters and the reasons that cause deaths. For example, we can analyse separately, the mortality rates for infants, children, teenagers, adults and elderly people.

Infant mortality is defined as the number of infant deaths which are one year of age or younger. In previous years, the most common reason for infant deaths worldwide was dehydration by diarrhoea. However, the percentage of these deaths started to decrease considerably, while the information about Oral Dehydration solution which is a mixture of salts, sugar and water, became popular amongst the mothers. Nowadays the main cause of infant mortality is pneumonia and some other diseases such as malnutrition, malaria, congenital malformation, infections and SIDS (Sudden Infant Death Syndrome). Furthermore, in some countries, other common phenomena which increase the infant mortality are infanticide, child abuses, child abandonment and neglect.

In previous years there were high percentages of infant mortality, however the rates have significantly declined in recent years, due to the fact that improvements have been made in basic health care as well as high technology medical advances have been achieved.

A recent research (April, 2010) by the World Health Organization [2], states that the deaths of millions of infants and mothers could easily be prohibited by widely adopting simple practises like hand washing and immunizations. According to the same report it is estimated that 3.6 million newborns do not survive until their first month whereas 300,000 - 500,000 women die in child birth each year. A large percentage (82%) of those deaths occur in Sub-saharan Africa and South Asia. According to the WHO many infant deaths can be avoided with the help of a program for global health care improvement. An important part of the report is the estimation that up to three million newborns can be saved each year with simple approaches, like cutting the umbilical cord with a clean blade or the use of antibiotics to treat infections.

Poverty plays a major role for high infant and maternal mortality rates in some countries. Major causes such as malaria, unsafe abortions, HIV/AIDS, preterm births and obstructed labours are difficult to be faced efficiently in poor societies.

Child mortality is maintained at the same levels as infant mortality mainly in developing countries. About 29,000 children under the age of five die every day from causes that could easily be avoided. A report from UNICEF [3] states that more than 70 per cent of nearly 11 million child deaths every year are deducted from six main causes: infections, malaria, diarrhoea, pneumonia, measles and malnutrition. These causes are also the same for infant mortality but most of the children die before they reach their fifth birthday. Moreover, lack of clean water and sanitation contributes to half of all those deaths.

The mass of the infant and child deaths, could be prevented with maternal and neonatal care programs and better hygiene methods. Two thirds of these deaths could be prevented by cost-effective ways such as vaccines, antibiotics, insecticide-treated bed nets, improved family care and breastfeeding methods. In addition, education could also be given to mothers about how they can make simple changes to living conditions, for example, improved hygiene in order to increase the health of their children.

Another percentage of the population, teenagers, accounts a large proportion for mortality. Mainly, teenagers which are also in a more sensitive state than the remaining population, usually die from motor vehicle accidents, homicides and suicides, violence and risky behaviour including alcohol, drug use and risky sexual behaviours.

The risk of motor vehicle accidents is higher between 16 to 20 year olds than any other age group. In fact, per mile driven, teen drivers aged 16 to 20 are four times more likely than older drivers to crash. Immaturity is a contributing factor to the high rate of auto crashes and deaths among teenagers. For instance, high speeding and not using safety belts are often danger habits. Besides the immature behaviour of teenagers, the lack of driving skill and the inexperience are the main factors to cause an accident on the road.

In addition, a considerably important fact is teen violence. Unfortunately, teens are likely to involve in violent fights or crimes which often result to death. Homicides, suicides and violence are usually consequences of low education and poor support to teens from families, schools and generally the whole society. Secondary factors which play an important role are the use of drugs and alcohol, the exposure to media violence (violent movies and video games), the emotional problems with the lack of self-control from teens, and the lack of economic opportunities for the teenager's future (unemployment or low income).

The remaining part of a population, adults and elderly, are affected mainly by age related diseases. After sexual maturity, some biological changes contributes significantly in human mortality. While the people grow up, the process of ageing contribute to make their organisms weak, more vulnerable to many diseases and difficult to face them. Thus ageing renders human beings progressively more likely to die.

1.3 Human Ageing

Ageing is the main reason that leads elderly people towards death. Ageing is an important part in human life as it reflects biological changes that occur throughout time. As people grow older their physical state and health declines and the organism cannot "repair" these changes anymore. As a definition of ageing we can say that it is the accumulation of changes in an organism over time. Particularly for humans, ageing refers to a multidimensional process of biological, psychological and social changes. One characteristic of ageing in humans is an age-related increase in

mortality rates (figure 1.1).

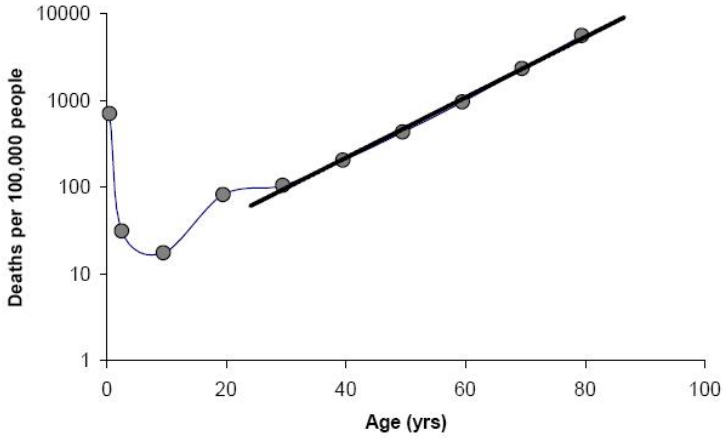


Figure 1.1: Mortality rates, expressed in deaths per 100000 people, as a function of age for the 2002 US population [4]. The black line represents the Gompertz function extrapolated from the mortality rates after maturity.

In figure 1.1 we see that the curve for the mortality data of the US population, begins from the value of initial mortality rate, suddenly declines to a minimum point at the age of 10 years, then increases until the age of 20 and produces a tiny plateau in the part from 20 to 30 years. In the interval from the age of 30 years and onward mortality rate advances exponentially and fits in a straight line. This part of the mortality curve is reffered to as ageing. Mathematically, ageing can be quantified using the exponential Gompertz function

$$m(t) = Ae^{Gt}, \tag{1.1}$$

where $m(t)$ is the mortality rate as a function of time or age t, A is the extrapolated constant to birth or maturity, and G is the exponential (Gompertz) mortality rate coefficient. From figure 1.1 it is possible then to estimate the Gompertz equation for a human population by a simple regression analysis after maturity [4], by

$$m(t) = 8.84e^{0.0800t}. \tag{1.2}$$

From this equation we can derive the initial mortality rate, which is the mortality rate independent of ageing, often calculated from the mortality rate prior to its exponential increase with age. In this case, the initial mortality rate is equal with 0.0002/year since that is the mortality rate at ages 10-20. Another important variable taken from the Gompertz equation is the mortality rate doubling time (MRDT) given by MRDT$= 0.693/G$. Hence, MRDT $= 0.693/0.0800 = 8.66$ years. In fact, human populations have a MRDT of about 8 years. This means that after our sexual peak, or roughly age 30, our chances of dying double about every 8 years.

The process of ageing is significantly affected by the variation of the considerable parameters. If we take into account the hypothesis that the populations are heterogeneous and consisting by various subpopulations with slightly different mortality parameters we can derive conclusions about how these differences, affect the total mortality of the entire population. Besides the heterogeneity, even genetically identical populations have differences, because some individuals are frailer than others. The frail tend to suffer high mortality, leaving a select subset of survivors. An advanced research can be done about the mortality rate at more advanced ages, i.e. after the age of 80 years. It is fact that the population of old age people has increased substantially since 1950. Death rates seems to decelerate with age for humans and other species. The expansion of the older population is due to the fact that new generations have delayed ageing and also that the chance of surviving to old age is increasing. The elderly are living longer because of remarkable, largely reductions in mortality at older ages. If there were an impending limit to further decline in death rates at older ages, countries with low levels of mortality would tend to show slow rates of reduction.

The reduction in death rates at older ages has increase the size of the elderly population considerably. From figure 1.1, we see that the mortality curve in ageing (from the age of 30 years until 80) fits in a straight line and is presented by the Gompertz function. However, studying the mortality rate at specific ages after 80 mainly, we can observe that the mortality decelerate and after a particular age declines. The deceleration of human mortality occurs after age 80 and the levelling off or decline after age 110. In figure 1.2, the death rates increase at a slower rate after age 80 [5].

The figure 1.2 shows the death rates from age 80 to 122. The red line is for an aggregation of 14 countries (Japan and 13 Western European countries) with reliable data, over the period from 1950 to 1990 for ages 80 to 109 and to 1997 for ages 110 and over. The exponential (Gompertz) curve that best fits the data at ages 80 to 84 is shown in blue line. A logistic curve fits the entire data set best and is shown by light blue line. A quadratic curve (that is, the logarithm of death rate as a quadratic function of age) was fit to the data at ages 105 and higher and it is shown by green line.

The leveling off and even decline of mortality can be entirely accounted for by models in which the chance of death for all individuals in the population rises at a constant or increasing rate with age. A frailty model applied to data on the lifespan of Danish twins suggests that mortality for individuals of the same genotype and with the same no genetic attributes (such as educational achievement and smoking behaviour) at some specified age may increase even faster than exponentially after that age. On the other hand, mortality deceleration could result from behavioural and physiological changes with age [5].

In a further step of our research we will consider a stochastic model of ageing to observe the behaviour of the mortality curve at advanced ages where a small subset of people is still alive.

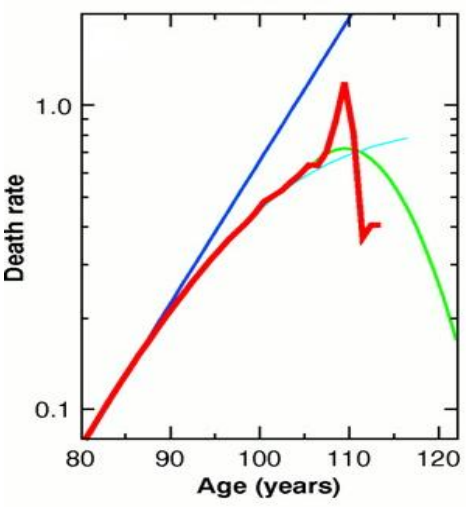


Figure 1.2: Death rates from age 80 to 122 for human females [5]. The exponential (Gompertz) curve that best fits the data at ages 80 to 84 is shown in blue line. A logistic curve (light blue) that fits the data well from age 80 to 105 indicates that death rates may reach a plateau. A quadratic curve (green) fit to the data at ages 105+ suggests a decline in mortality after age 110.

1.4 Longevity-the postponement of ageing

Scientists, demographers and epidemiologists have shown that in recent years, humans have a longer life expectancy, because ageing is delayed and they reach old age healthier. Evolutionary biologists believed that ageing was inevitable for humans, but genetic and other interventions might slow the process. Further evolution is to be made on that, as years progress.

Improved life conditions as well as medicine have managed to increase average life of people and delay any signs of ageing. Debility, which is one of the signs of ageing and often appears at the last years of human's life, seems to have been delayed. Furthermore, mortality resulting from ageing has been postponed significantly as a result of improving health. The future seems uncertain, but it is very possible, the younger people that are alive today to have longer life expectancy.

It is possible to reduce the risk of age related diseases by medical improvement, and to cover the signs of ageing, however, it is impossible for humans to grow younger. This would require reversing the deterioration of molecular reliability which is one of the most important parts of human ageing. Even though scientists would be able to do the impossible breakthrough, to replace or fix cells, tissues and organs in a human's biological system which means the bypass of the ageing process, the phenomenon of growing younger would still not be possible.

The postponement of ageing is delay and not deceleration. This is because age-

ing results from a cumulative imbalance between "damage" and "repair". For the difference in the balance between these two acts, the improvement of health has an important role. The progress in reducing damage, for example, by public-health efforts to improve living conditions and to prevent diseases, as well as the progress in increasing repairs i.e. by medical interventions is the two fundamental causes of health improvement. Thus it might be thought, that with these progresses would decelerate the rate of weakening so that the debilitation of humans that was appearing between ages 70 and 80 would occur between ages 70 and 85 and the debilitation that occur between ages 80 and 90 would occur between ages 80 and 100. However, this is not the case. Evidence by studies indicates that deterioration, instead of being decelerated, is being delayed. Thus, mortality rates and other signs of ageing like the debility, that were recorded between people aged about 70 years old or 80 years old, now are presented at age 80, and 90 years respectively [6].

Besides the medical improvements and the better life conditions which result to reduce the risk of age related diseases, we should mention about anti-ageing. Many products and medicines currently being sold seem like the future of immortality, most of the times they misrepresent the true science behind it. All those products have no proof of efficacy, have not been scientifically accepted and in many cases they might turn out to be harmful. Medical actions for age related diseases do result in an increase in life expectancy, but none of these have been proven to modify the process of ageing. The use of cosmetics, cosmetic surgery, hair dyes, and similar means for covering up signs of ageing may be effective in hiding age changes, but they do not slow, stop, or reverse ageing at any one time.

A significant result of the postponement of ageing is that, the delay of death is fuelling a large, rapid increase in the numbers of centenarians. Centenarians, the people who lives more than 100 years, were rare the previous years. However, the number of this part of population has increased rapidly the last 50 years at a faster rate than any other age group, indicating the results of the postponement of ageing and the progress of life expectancy.

The following example is very characteristic for the increasing of the centenarian's number. The figure 1.3, which presented in the paper "Biodemography of human ageing" by J. W. Vaupel [6], shows the numbers of females aged 100 and over in Sweden from 1861 to 2008 and aged 105 and over in Japan from 1947 to 2007.

The figure 1.3, shows that from the year 1950 and later the number of centenarians females aged 100 and over has increased in Sweden. Over the period 1861 to 2008 it is estimated that the number of female centenarians has increased, from only few tens in 1861 to 1,300 approximately in 2008. This increase it seems that has not been constant across the period. Growth was slowest between 1861 and 1950. Over this 89 years period, the number of female centenarians in Sweden increased by less than 100. In comparison, the female centenarian population in this country became by 1,300 over the 58 years from 1950 to 2008. Similar consequences are observed for the females age 105 ond over in Japan. Between 1947 and 2007, the number of female centenarians grew from less than 100 to 1,900, an increase of 1,800 and more Japanese female centenarians over the short period of 50 years.

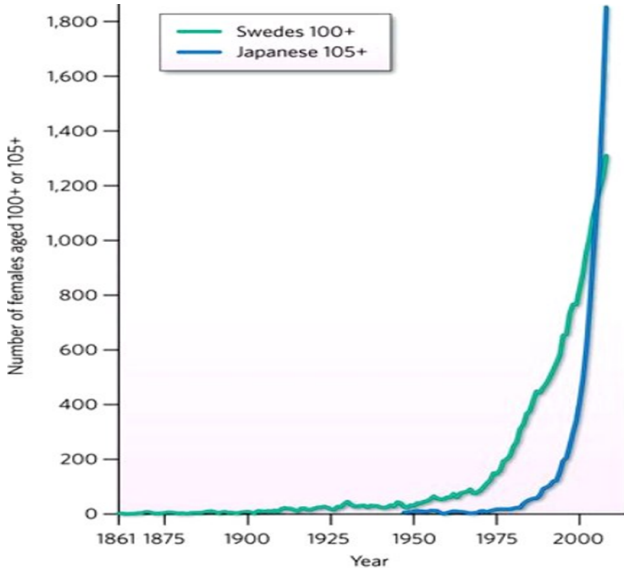


Figure 1.3: The numbers of females aged 100+ in Sweden from 1861 to 2008 and aged 105+ in Japan from 1947 to 2007. The figure is presented in [6] where the data are taken from the Kannisto Thatcher Database on old age mortality and are supplemented with data from the Statistics Sweden and Japanese Ministry of Health.

The increasing number of centenarians and generally the process being made in expansion of lifespan and the postponement of ageing the last years, are results of the improvement of medical treatment and public health efforts, the rising housing and living standards, the healthier nutrition, better education and more healthy lifestyles. If these medical developments and human habits progress over time, the lifespan of people may expand more in the future.

1.5 The impact of heterogeneity on the dynamics of mortality

Each human has different risk of dying from the others, due to the different behaviours and the different influences by diseases on their organisms. These differences can produce patterns of mortality for the population as a whole that are particularly different from the patterns for subpopulations or individuals. For the reason that heterogeneity between the individuals in a population is very important, we must take it into account studying the dynamics of human ageing and mortality. As it has be mentioned at section 1.3 about human ageing, the mortality curve after sexual maturity (after the age of 25-30 years) increases exponentially and fits in a straight line on a logarithmic scale graph (see figure 1.1). This part of mortality curve is the human ageing and is presented by the Gompertz function (1.1). At ad-

vanced ages (after the age of 80-85 years) it is observed a deceleration and a decline on mortality rate (see figure 1.2). The pecularities at initial ages and the exponential growth at ageing, can be explained by the hypothesis that the human populations are heterogeneous and consists some subpopulations with different mortality components.

A cohort's rate of death could be measured by the mortality (or hazard) rate m. At age x and time y the mortality rate is given by

$$m(x,y) = -\frac{dN(x,y)/dx}{N(x,y)} \tag{1.3}$$

where $N(x,y)$ is the proportion of the cohort born x years ago that is surviving at time $y = y_0 + x$, and y_0 is the year when the cohort was born. It is obvious that in a heterogeneous population the mortality rate $m(x,y)$ vary between the individuals of age x in year y while this rate is the same for all individuals of age x in year y in a homogeneous population.

A heterogeneous population consists of various subpopulations which are differs in some parameters. Therefore, the age patterns of mortality for a heterogeneous population can be qualitatively different from the age patterns of mortality for the subpopulations that comprise it. The figure 1.4 shows these differences between the mortality rates for humans at advanced ages, of heterogeneous population (red curve) and the subpopulations (blue lines) [6].

To discuss about the figure 1.4, firstly we need to rearrange the model which describes the dynamics of mortality rate for each subpopulation and it is given by the exponential equation

$$m_i = m_0 e^{i/\tau}, \tag{1.4}$$

where m_0 is the initial mortality rate, τ is the mortality coefficient and i is the age in years. Then, the equation (1.4) can be written in the form

$$ln(m_i) = ln(m_0) + \frac{i}{\tau}. \tag{1.5}$$

Therefore, putting the vertical axis on a logarithmic scale the mortality rate is presented by a straight line (blue lines in figure 1.4) which has slope $1/\tau$ and point of intersection with the vertical axis, the initial mortality m_0.

The graph on the left in figure 1.4, depicts a population that consists of subpopulations with different initial mortalities m_0 but with the same mortality coefficients τ. Therefore, the three straight lines have the same slopes. The subpopulation with the highest level of mortality dies out first, then follows the second subpopulation and last the third. If there is a continuous range of subpopulations, with the three blue lines representing illustrative cases, then the total mortality rate for the population as a whole follow a pattern like the one shown by the red curve.

The graph on the right is similar, but there the subpopulations differ in the mortality coefficients τ (the blue lines have different slopes), and also differ in the initial mortalities m_0. The mortality of a population as a whole, which consisting by

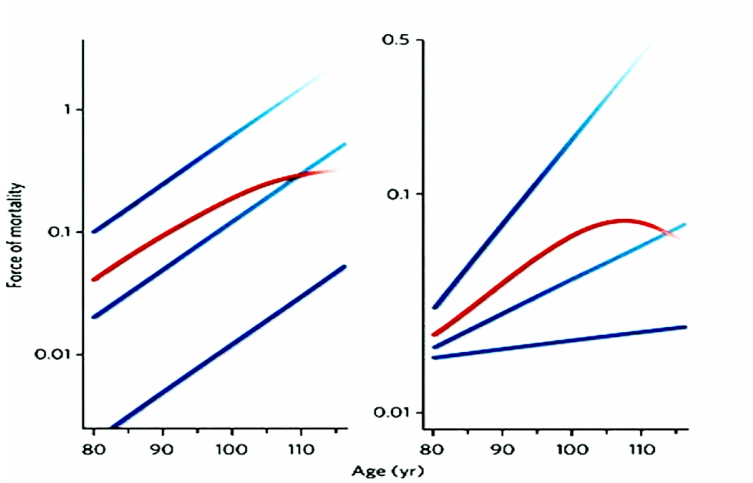


Figure 1.4: Dynamics of mortiality in the model of heterogeneous populations [6]. The red curve shows the total mortality of heterogeneous population which consists three subpopulations and the blue lines are the mortality rates of each subpopulation. The vertical axis is on a logarithmic scale.

subpopulations with different initial levels of mortality decline as indicated by the red curve, despite the magnitude of the differences in the initial rates.

1.6 A model of individual differences in frailty

A systematic way of describing heterogeneity is by an unobserved quantity called frailty, entering the hazard multiplicatively. The studies about mortality rates vary between subpopulations, by age and over time. In recent years scientists and demographers include in their analyses a third component, the frailty variable which plays a significant role to studying the mortality.

We assume that $m_j(x, y, z)$ denotes the mortality choosing a human from the subpopulation j at age x, at some instant in time y, and with a frailty of z [7]. This frailty variable could be defined by the following relationship

$$m_j(x, y, z) = z m_j(x, y, 1). \tag{1.6}$$

An individual with a frailty $z = 1$ often called standard individual. Comparing two people with different values of frailty we can imply the differences of the probabilities for death for each other. For instance, an individual with a frailty $z = 2$, is twice likely to die at any particular age and time than the standard individual, while an individual with a frailty $z = 1/2$ has half probability to die than the standard individual.

From the definition of frailty we can make the assumption that frailty for individuals is constant for their life. We can assume that each individual is born at a certain level of frailty and stays at this level all his or her life. In addition, we cannot assume that individuals with the same level of frailty are identical, even if they are members in the same subpopulation. This is due to the fact that unless the frailty level, mortality and the probability of death at an exact time for individuals among the same population, are determined by several of individual differences such as age, dates of birth, etc.

Another measurement which affected by frailty level is the hazard of mortality. The expression $h_j(x, y, z)$ can be denotes the hazard of mortality of a person aged x whose belong in a subpopulation j, of frailty level z and born at time $y - x$. This hazard of mortality is given by the following integral

$$h_j(x, y, z) = \int_0^x m_j(t, y - x + t, z)dt. \tag{1.7}$$

Studying the frailty levels z, we can use more simple notations. For example, we can write the mortality $m_j(x, y, z)$ as $m(z)$. So the equation (1.6) takes the form

$$m(z) = zm(1), \tag{1.8}$$

and similarly, the equation (1.7) reduces to

$$h(z) = zh(1). \tag{1.9}$$

Let $s_j(x, y, z)$ be the probability that an individual in some population j of frailty z, will survive to age x. Using the simplified notation we have the expression

$$s(1) = e^{h(1)}, \tag{1.10}$$

and from the equation (1.9) we imply that

$$s(z) = (s(1))^z. \tag{1.11}$$

As a consequence, we can compare individuals with different frailty levels to estimate the probability to survive at some time. For example, if a standard individual (frailty level $z = 1$) has a 50% probability to survive at a particular age, another individual with a frailty level $z = 2$ has a 25% probability of surviving to this age, and an individual with a frailty level $z = 3$ has only a 12,5% chance.

1.7 Stochastic processes

Since we have studied the impact of heterogeneity on the dynamics of ageing and mortality, now we will focus on the modelling and analysis of stochastic processes. In this section we will describe the birth and death stochastic processes, where the probability of a birth or death depends on the population size at time t, (for further details the reader can consult [8] and [9]). For instance in a death process, if there

are more individuals in a population, the possibility of a death is bigger than the same possibility of a population with smaller number of members.

Birth and death processes are processes in continuous time and referred to as Markov processes which are characterized by the condition that future development of the processes depends only on their current states and not their whole history up to that time. In other words, on death process for example, the probability of death at time t depends on what happens in the previous step, at time $t-1$, and is independent of the actions of deaths in the previous times. To explain the processes we use the assumption that could not observed multiple births (or deaths) so at the next time-step, the population size can increase by one for a birth or can decrease by one for a death, respectively in the two processes. In the following subsections we will present the two processes separately and then we will describe a general combination of them.

The birth process

In the birth process we assume that there are no deaths (everyone lives forever) and the population size increases throught the time (new births). Also we assume that the probability that a birth occurs in a population of size n, is $\lambda n \delta t$ where λ is the birth rate. Let $p_n(t)$, be the probability that the size of a population is n at time t. If the initial size of the population is $n_0 \geq 1$ at time $t = 0$, then

$$p_{n_0}(0) = 1, \text{ and } p_n(0) = 0 \text{ for } n > n_0. \tag{1.12}$$

By the birth process, a population of size n at time $t + \delta t$ can arise either from a population of size $n-1$ at time t when a birth occurs with probability $\lambda(n-1)\delta t + o(\delta t)$ or throught no event, which can occur with probability $1 - \lambda n \delta t + o(\delta t)$. So that for $n \geq n_0 + 1$,

$$p_n(t+\delta t) = p_{n-1}(t)[\lambda(n-1)\delta t + o(\delta t)] + p_n(t)[1 - \lambda n \delta t + o(\delta t)] \tag{1.13}$$

$$\Rightarrow \frac{p_n(t+\delta t) - p_n(t)}{\delta t} = \lambda(n-1)p_{n-1}(t) - \lambda n p_n(t) + o(1). \tag{1.14}$$

If the population has the initial size $n = n_0$, since no birth is possible at $n = n_0 - 1$ then,

$$p_{n_0}(t+\delta t) = p_{n_0}(t)[1 - \lambda n_0 \delta t + o(\delta t)] \tag{1.15}$$

$$\Rightarrow \frac{p_{n_0}(t+\delta t) - p_{n_0}(t)}{\delta t} = \lambda n_0 p_{n_0}(t) + o(1). \tag{1.16}$$

Let $\delta t \to 0$ then we derive the following system of differential equations:

$$\frac{dp_{n_0}(t)}{dt} = \lambda n p_{n_0}(t), \tag{1.17}$$

$$\frac{dp_n(t)}{dt} = \lambda(n-1)p_{n-1}(t) - \lambda n p_n(t), \ (n \geq n_0 + 1). \tag{1.18}$$

Since this is a birth process it follows that $p_n(t) = 0$ for $n < n_0$. Starting from $n = n_0$, the equation (1.17) becomes

$$\frac{dp_{n_0}(t)}{dt} = \lambda n_0 p_{n_0}(t) \tag{1.19}$$

and has the solution

$$p_{n_0}(t) = e^{-\lambda n_0 t}, \tag{1.20}$$

since $p_{n_0}(0) = 1$. Putting $n = n_0 + 1$ in equation (1.18) and using the solution (1.20) we derive the equation:

$$\frac{dp_{n_0+1}(t)}{dt} - \lambda(n_0 + 1)p_{n_0+1}(t) = \lambda n_0 p_{n_0}(t) = \lambda n_0 e^{-\lambda n_0 t}. \tag{1.21}$$

The solution of the second differential equation (1.21), is given by

$$p_{n_0+1}(t) = e^{-\lambda n_0 t}(1 - e^{-\lambda t}), \tag{1.22}$$

since $p_{n_0}(0) = 0$. Let us consider the probability generating function

$$G(s, t) = \sum_{n=0}^{\infty} p_n(t)s^n. \tag{1.23}$$

For continuous time stochastic processes, the probability generating function can be defined as a power series in a dummy variable s, in which the coefficients in the series are the probabilities $p_n(t)$, (see equation (1.23)). The partial derivatives of the generating function are

$$\frac{\partial G(s, t)}{\partial t} = \sum_{n=0}^{\infty} \frac{dp_n(t)}{dt} s^n, \tag{1.24}$$

and

$$\frac{\partial G(s, t)}{\partial s} = \sum_{n=0}^{\infty} np_n(t)s^{n-1}. \tag{1.25}$$

Then we need to express the system of differential equations (1.17), (1.18) in terms of the probability generating function $G(s, t)$ and its derivatives. For the second equation (1.18), we multiply both sides by s^n and sum from the lowest value of n to infinity as appropriate. Thus,

$$\sum_{n=0}^{\infty} \frac{dp_n(t)}{dt} s^n = \lambda \sum_{n=2}^{\infty} (n - 1)p_{n-1}(t)s^n - \lambda \sum_{n=1}^{\infty} np_n(t)s^n. \tag{1.26}$$

On the right hand side of equation (1.26) we can rewrite the two terms as

$$\sum_{n=2}^{\infty} (n - 1)p_{n-1}(t)s^n = \sum_{n=1}^{\infty} np_n(t)s^{n+1} = s^2 \frac{\partial G(s, t)}{\partial s}, \tag{1.27}$$

and

$$\sum_{n=1}^{\infty} np_n(t)s^n = s\frac{\partial G(s,t)}{\partial s}. \tag{1.28}$$

As a result, the function (1.26) takes the form

$$\frac{\partial G(s,t)}{\partial t} = \lambda s^2\frac{\partial G(s,t)}{\partial s} - \lambda s\frac{\partial G(s,t)}{\partial s} = \lambda s(s-1)\frac{\partial G(s,t)}{\partial s}, \tag{1.29}$$

which is a partial differential equation. To solve this equation we use the initial condition $p_{n_0}(0) = 1$, which becomes

$$G(s,0) = s^{n_0} \tag{1.30}$$

for the generating function.

For the solution of partial differential equation (1.29) with the initial condition (1.30), we use the method of changing a variable to remove the term $\lambda s(s-1)$. Let,

$$\frac{ds}{dz} = \lambda s(s-1) \tag{1.31}$$

and we assume that $0 < s < 1$. Thus, we have a first order differential equation which is solved by separating the variables and integrate. Therefore,

$$\int \frac{ds}{s(1-s)} = \int -\lambda dz \tag{1.32}$$

$$\Rightarrow \int \Big(\frac{1}{s} + \frac{1}{1-s}\Big) = \int -\lambda dz \tag{1.33}$$

$$\Rightarrow ln\Big(\frac{s}{1-s}\Big) = -\lambda z \tag{1.34}$$

(we assume that any constant of integration has zero value).

Hence, the solution of differential equation is,

$$\frac{s}{1-s} = e^{-\lambda z} \Rightarrow s = \frac{1}{e^{\lambda z}+1}. \tag{1.35}$$

Let

$$Q(z,t) = G(s,t) = G(1/(1+e^{\lambda z}),t). \tag{1.36}$$

We can use the chain rule in differentiation to derive that

$$\frac{\partial Q(z,t)}{\partial z} = \frac{\partial G(1/(1+e^{\lambda z}),t)}{\partial z} = \frac{\partial G(s,t)}{\partial s}.\frac{ds}{sz} = \lambda s(s-1)\frac{\partial G(s,t)}{\partial s}. \tag{1.37}$$

As a result the partial differential equation (1.29) becomes

$$\frac{\partial Q(z,t)}{\partial t} = \frac{\partial Q(z,t)}{\partial z}. \tag{1.38}$$

The general solution of this equation is any differentiable function of $z+t$, so we can say that $Q(z,t) = w(z,t)$. Using the initial condition (1.30) and the expression (1.35) for s, we obtain that

$$G(s,0) = s^{n_0} = \Big(\frac{1}{1+e^{\lambda z}}\Big)^{n_0}. \tag{1.39}$$

Also we know that,

$$G(s,0) = Q(z,0) = w(z). \tag{1.40}$$

Thus, by the initial condition we can determine the function w which, in this case is

$$w(z) = \frac{1}{(1+e^{\lambda z})^{n_0}} \tag{1.41}$$

$$\Rightarrow w(z,t) = \frac{1}{[1+e^{\lambda(z+t)}]^{n_0}}. \tag{1.42}$$

Therefore, the probability generating function $G(s,t)$, for the simple birth process is given by

$$G(s,t) = Q(z,t) = w(z,t) = \frac{1}{[1+e^{\lambda(z+t)}]^{n_0}} = \frac{1}{[1+\frac{(1-s)}{s}e^{\lambda t}]^{n_0}} \tag{1.43}$$

$$\Rightarrow G(s,t) = \frac{s^{n_0}e^{-\lambda n_0 t}}{[1-(1-e^{-\lambda t})s]^{n_0}}. \tag{1.44}$$

The individual probabilities are the coefficients of s^n in the power series expansion of equation (1.44), which can be obtained by applying the binomial theorem to the denominator to derive a power series in s. Thus,

$$\begin{aligned} G(s,t) &= \frac{s^{n_0}e^{-\lambda n_0 t}}{[1-(1-e^{-\lambda t})s]^{n_0}} \\ &= s^{n_0}e^{-\lambda n_0 t}\Big[1+\frac{n_0}{1!}(1-e^{-\lambda t})s + \frac{n_0(n_0+1)}{2!}(1-e^{-\lambda t})^2 s^2 + \cdots\Big] \\ &= s^{n_0}e^{-\lambda n_0 t}\sum_{m=0}^{\infty}\binom{m+n_0-1}{n_0-1}(1-e^{-\lambda t})^m s^m \end{aligned} \tag{1.45}$$

and putting $m = n - n_0$, we get

$$G(s,t) = e^{-\lambda n_0 t}\sum_{n=n_0}^{\infty}\binom{n-1}{n_0-1}(1-e^{-\lambda t})^{n-n_0}s^n, \tag{1.46}$$

where the binomial coefficient is given by the formula

$$\binom{n-1}{n_0-1} = \frac{(n-1)!}{(n_0-1)!(n-1-(n_0-1))!}. \tag{1.47}$$

If $n_0 = 1$, then

$$\binom{n-1}{0} = 1, \tag{1.48}$$

for all $n \geq 1$, since 0! is defined to be 1. Finally, from equation (1.46) the coefficients of the powers of s imply that, since the leading power is s^{n_0}, then

$$p_n(t) = 0 \text{ for } n < n_0, \tag{1.49}$$

and

$$p_n(t) = \binom{n-1}{n_0-1} e^{-\lambda n_0 t}(1-e^{-\lambda t})^{n-n_0} \text{ for } n \geq n_0. \tag{1.50}$$

At the birth process which is a continuous time random process we have defined the generating probability function as a power series in a dummy variable s, in which the coefficients in the series are the probabilities $p_n(t)$. By that, we can express the mean value at time t, in terms of the generating probability function. Let as set the mean function by $\tilde{\mu}(t)$ then,

$$\tilde{\mu}(t) = \sum_{n=1}^{\infty} n p_n(t) = \Big[\frac{\partial G(s,t)}{\partial s}\Big]_{s=1} = G_s(1,t). \tag{1.51}$$

Using the equation (1.44) of generating function for the birth process, we can derive an expression for the mean population size at time t,

$$\begin{aligned}
\tilde{\mu}(t) = G_s(1,t) &= \frac{\partial}{\partial s}\Big[\frac{s^{n_0}e^{-\lambda n_0 t}}{[1-(1-e^{-\lambda t})s]^{n_0}}\Big]_{s=1} \\
&= \Big[\frac{n_0 s^{n_0-1}e^{-\lambda n_0 t}}{[1-(1-e^{-\lambda t})s]^{n_0}} + \frac{n_0 s^{n_0}e^{-\lambda n_0 t}(1-e^{-\lambda t})}{[1-(1-e^{-\lambda t})s]^{n_0+1}}\Big]_{s=1} \\
&= n_0(1-e^{-\lambda t})e^{\lambda t} + n_0 \\
&= n_0 e^{\lambda t}.
\end{aligned} \tag{1.52}$$

As a result, we imply that the mean population size increases exponentially with time.

The death process

In the death process we assume that there are no births and the size of population declines throught deaths. Also we assume that the probability that any individual dies in a short time interval δt is $\mu\delta t$ where μ is the death rate and the probability that a death occurs in a population of size n is $\mu n\delta t$. Similar to the birth process, we express the probabilities for the death process by

$$p_0(t+\delta t) = [\mu\delta t + o(\delta t)]p_1(t), \tag{1.53}$$

$$p_n(t+\delta t) = [\mu(n+1)\delta t + o(\delta t)]p_{n+1}(t) + [1-\mu n\delta t - o(\delta t)]p_n(t), \ (1 \leq n \leq n_0 - 1). \tag{1.54}$$

If the initial size of the population is n_0, then $p_n(t) = 0$ for $n > n_0$ for all t, and since this is a death process

$$p_{n_0}(t+\delta t) = [1-\mu n_0\delta t + o(\delta t)]p_{n_0}(t). \tag{1.55}$$

We rearrange the above three expressions for the probabilities and we take the following forms

$$\frac{p_0(t+\delta t)-p_0(t)}{\delta t}=\mu p_1(t)+o(1), \tag{1.56}$$

$$\frac{p_n(t+\delta t)-p_n(t)}{\delta t}=\mu(n+1)p_{n+1}(t)-\mu n p_n(t)+o(1) \text{ with } (n\geq 1), \tag{1.57}$$

and

$$\frac{p_{n_0}(t+\delta t)-p_{n_0}(t)}{\delta t}=-\mu n_0 p_{n_0}(t)+o(1). \tag{1.58}$$

If we let $\delta t\to 0$, we get the following system of differential equations for the death process

$$\frac{dp_0(t)}{dt}=\mu p_1(t), \tag{1.59}$$

$$\frac{dp_n(t)}{dt}=\mu(n+1)p_{n+1}(t)-\mu n p_n(t),\ (1\leq n\leq n_0-1) \tag{1.60}$$

and

$$\frac{dp_{n_0}(t)}{dt}=-\mu n_0 p_{n_0}(t). \tag{1.61}$$

If the initial size of the population is n_0 at time $t=0$, then $p_{n_0}(0)=1$. By the same method we have done in the birth process, we multiple respectively the above differential equations for the death process by s^n as appropriate, and sum over $0\leq n\leq n_0-1$. After the operations the differential equation (1.60) becomes

$$\sum_{n-0}^{n_0}\frac{dp_n(t)}{dt}s^n=\mu\sum_{n=0}^{n_0-1}(n+1)p_{n+1}(t)s^n-\mu\sum_{n=1}^{n_0}np_n(t)s^n. \tag{1.62}$$

Then we define again the probability generating function $G(s,t)$, but now this generating function is a finite series:

$$G(s,t)=\sum_{n=0}^{n_0}p_n(t)s^n. \tag{1.63}$$

From this function we derive its partial derivatives as

$$\frac{\partial G(s,t)}{\partial s}=\sum_{n=0}^{n_0}np_n(t)s^{n-1}, \tag{1.64}$$

and

$$\frac{\partial G(s,t)}{\partial t}=\sum_{n=0}^{n_0}\frac{dp_n(t)}{dt}s^n. \tag{1.65}$$

Also we need to express the equation (1.60) in terms of the generating function and its derivatives. On the left hand side of equation (1.60) the term is the partial derivative $\partial G(s,t)/\partial t$. On the right hand side we can rewrite the two series as

$$\sum_{n=0}^{n_0-1}(n+1)p_{n+1}(t)s^n=\frac{\partial G(s,t)}{\partial s} \tag{1.66}$$

and

$$\sum_{n=1}^{n_0} np_n(t)s^n = \sum_{n=0}^{n_0} np_n(t)s^n = s\sum_{n=0}^{n_0} np_n(t)s^{n-1} = \frac{\partial G(s,t)}{\partial s}. \tag{1.67}$$

As a result the expression (1.60) takes the form of the partial differential equation:

$$\frac{\partial G(s,t)}{\partial t} = \mu\frac{\partial G(s,t)}{\partial s} - \mu s\frac{\partial G(s,t)}{\partial s} = \mu(1-s)\frac{\partial G(s,t)}{\partial s}. \tag{1.68}$$

To solve this partial differential equation we assume that,

$$\frac{ds}{dz} = \mu(1-s). \tag{1.69}$$

Therefore,

$$\int \frac{ds}{1-s} = \int \mu dz \tag{1.70}$$

$$\Rightarrow -ln(1-s) = \mu z \quad \Rightarrow \quad s = 1 - e^{-\mu z}, \tag{1.71}$$

for $0 < s < 1$.

For the death process we let

$$Q(z,t) = G(s,t) = G(1-e^{-\mu z}, t), \tag{1.72}$$

where $Q(z,t)$ now satisfies the partial differential equation

$$\frac{\partial Q(z,t)}{\partial t} = \frac{\partial Q(z,t)}{\partial z}. \tag{1.73}$$

We see that is the same partial differential equation as for the birth process, so the solution is

$$G(s,t) = w(z+t). \tag{1.74}$$

If the initial population size is n_0, then

$$G(s,0) = s^{n_0} = (1-e^{-\mu z})^{n_0} = w(z) = Q(z,0). \tag{1.75}$$

Hence,

$$\begin{aligned} G(s,t) = Q(z,t) = w(z+t) &= \left(1-e^{-\mu(z+t)}\right)^{n_0} \\ &= [1-e^{-\mu t}(1-s)]^{n_0} \\ &= (1-e^{-\mu t})^{n_0}\left(1+\frac{se^{\mu t}}{1-e^{-\mu t}}\right)^{n_0}. \end{aligned} \tag{1.76}$$

We can continue by the same method as for the birth process (using the binomial theorem), to find the individual probabilities.

Moreover, we can express the mean population size $\tilde{\mu}(t)$ at time t, for the death process by

$$\begin{aligned} \tilde{\mu}(t) = G_s(1,t) &= \frac{\partial}{\partial s}\Big[(1-e^{-\mu t}(1-s))^{n_0}\Big]_{s=1} \\ &= n_0 e^{-\mu t}\Big[(1-e^{-\mu t}(1-s))^{n_0-1}\Big]_{s=1} \\ &= n_0 e^{-\mu t}. \end{aligned} \tag{1.77}$$

The combined birth and death process

In this section we combine the two previous processes into one. We denote again the birth rate by the letter λ and the death rate by the letter μ. Using similar arguments as to how a population of size n can arise at time $t + \delta t$, we get the probabilities

$$p_0(t + \delta t) = [\mu\delta t + o(\delta t)]p_1(t) + [1 + o(\delta t)]p_0(t) \tag{1.78}$$

and

$$\begin{aligned} p_n(t + \delta t) = {} & [\lambda(n-1)\delta t + o(\delta t)]p_{n-1}(t) + [1 - (\lambda n + \mu n)\delta t + o(\delta t)]p_n(t) \\ & + [\mu(n+1)\delta t + o(\delta t)]p_{n+1}(t), \text{ for } n \geq 1. \end{aligned} \tag{1.79}$$

In the limit $\delta t \to 0$, we have

$$\frac{dp_0(t)}{dt} = \mu p_1(t) \tag{1.80}$$

and

$$\frac{dp_n(t)}{dt} = \lambda(n-1)p_{n-1}(t) - (\lambda + \mu)np_n(t) + \mu(n+1)p_{n+1}(t) \tag{1.81}$$

Since birth occurs we have defined the probability generating function as an infinite series (equation (1.23)). We multiply the expression (1.81) by s^n and sum over $n \geq 0$. Using the similar method as in the birth and death processes, we obtain the partial differential equation

$$\frac{\partial G(s,t)}{\partial t} = \lambda s(s-1)\frac{\partial G(s,t)}{\partial s} + \mu(1-s)\frac{\partial G(s,t)}{\partial s} \tag{1.82}$$

$$\Rightarrow \frac{\partial G(s,t)}{\partial t} = (\lambda s - \mu)(s-1)\frac{\partial G(s,t)}{\partial s}. \tag{1.83}$$

We assume that the birth rate is unequal to death rate, $\lambda \neq \mu$. By the method of changing the variable we set that,

$$\frac{ds}{sz} = (\lambda s - \mu)(s-1). \tag{1.84}$$

Solving this differential equation we get the solution

$$z = \frac{1}{\lambda - \mu} ln\Big(\frac{1-s}{\frac{\mu}{\lambda} - s}\Big), \tag{1.85}$$

and solving respect to the variable s, we take

$$s = \frac{\lambda - \mu e^{(\lambda-\mu)z}}{\lambda - \lambda e^{(\lambda-\mu)z}}. \tag{1.86}$$

We let $Q(z,t) = G(s,t)$, so that $Q(z,t)$ satisfies

$$\frac{\partial Q(z,t)}{\partial t} = \frac{Q(z,t)}{\partial t}, \tag{1.87}$$

with the general solution $Q(z,t) = w(z+t)$.

If the initial size of the population is n_0, then

$$G(s,0) = s^{n_0} = \Big[\frac{\lambda - \mu e^{(\lambda-\mu)z}}{\lambda - \lambda e^{(\lambda-\mu)z}}\Big]^{n_0}. \tag{1.88}$$

Additionally,

$$G(s,t) = Q(z,t) = w(z+t) = \Big[\frac{\lambda - \mu e^{(\lambda-\mu)(z+t)}}{\lambda - \lambda e^{(\lambda-\mu)(z+t)}}\Big]^{n_0}. \tag{1.89}$$

Also from the expression (1.85) we have that,

$$e^{(\lambda-\mu)z} = \frac{1-s}{\frac{\mu}{\lambda} - s} = \frac{\lambda(1-s)}{\mu - \lambda s}. \tag{1.90}$$

As a result, the equation (1.89) takes the form

$$G(s,t) = \Big[\frac{\mu(1-s) - (\mu - \lambda s)e^{-(-\lambda-\mu)t}}{\mu(1-s) - (\mu - \lambda s)e^{-(-\lambda-\mu)t}}\Big]^{n_0}. \tag{1.91}$$

For this combined birth and death process, the mean population size at time t (for $\lambda \neq \mu$) is given by

$$\begin{aligned}\tilde{\mu}(t) &= \sum_{n=1}^{\infty} n p_n(t) = G_s(1,t) \\ &= \frac{n_0(-\mu + \lambda e^{-(\lambda-\mu)t})}{-(\mu-\lambda)e^{-(\lambda-\mu)t}} - \frac{n_0(-\mu + \lambda e^{-(\lambda-\mu)t})}{-(\mu-\lambda)e^{-(\lambda-\mu)t}} \\ &= n_0 e^{(\lambda-\mu)t}.\end{aligned} \tag{1.92}$$

Moreover, for this process we must study the case when $\lambda = \mu$. In that case, the equation (1.83) becomes

$$\frac{\partial G(s,t)}{\partial t} = \lambda(1-s)^2 \frac{\partial G(s,t)}{\partial s}. \tag{1.93}$$

To change the variable we let the differential equation

$$\frac{ds}{dz} = \lambda(1-s)^2, \tag{1.94}$$

which has the solution

$$z = \frac{1}{\lambda(1-s)} \tag{1.95}$$

$$s = \frac{\lambda z - 1}{\lambda z}. \tag{1.96}$$

Therefore

$$w(z) = s^{n_0} = \Big(\frac{\lambda z - 1}{\lambda z}\Big)^{n_0}, \tag{1.97}$$

and the probability generating function for this case in which the birth rate is equal to death rate is given by

$$G(s,t) = \Big[\frac{\lambda(z+t) - 1}{\lambda(z+t)}\Big]^{n_0} = \Big[\frac{1 + (\lambda t - 1)(1-s)}{1 + \lambda t(1-s)}\Big]^{n_0}. \tag{1.98}$$

1.8 A stochastic model of ageing to explain deviations from exponential growth

In this section we will describe a stochastic model of ageing to explain the deviations from exponential growth in mortality rates. These deviations are observed at advanced ages where a small subset of people is still alive (in contradiction to the magnitude of the initial size of that population). Therefore the consideration of stochasticity of the model, takes into account the influence of cohort size. The model which is described here, was proposed by Joshua S. Weitz and Hunter B. Fraser in the paper "Explaining mortality rate plateaus" [10].

Consider a population of size N with a distribution of viabilities, $v_i \geq 0$ where $v_i = 0$ means death. The dynamics of an individual viability is described by the model

$$v_i(t+1) = v_i(t) - \varepsilon + \sigma\chi_i(t), \tag{1.99}$$

where $\varepsilon > 0$ is a constant drift, $\sigma > 0$ is the standard deviation of the fluctuations and $\chi_i(t)$ is an uncorrelated Gaussian random variable with zero mean and unit standard deviation. The inclusion of stochasticity at the individual level implies that equation (1.99) may be consider a changing frailty model as opposed to a fixed frailty model. A fixed frailty model preserves any heterogeneity in v throughout each individual lifespan.

We consider the limit of vanishing noise (when $\sigma \to 0$) and the limit of vanishing drift (when $\varepsilon \to 0$). When $\sigma \to 0$, means that the individuals move in a step where death is inevitable. The mortality rate, $\mu(t)$ at $t > 0$, for any initial distribution of viabilities, $n_0(v)$ is

$$\mu(t) = \frac{D(t)}{N_0 - \sum_{t'=0}^{t-1} D(t')}, \tag{1.100}$$

where N_0 is the initial number of individuals and $D(t)$ is the number of people that die at time t and is given by the integral

$$D(t) = \int_{\varepsilon(t-1)}^{\varepsilon t} n_0(v)dv. \tag{1.101}$$

For the initial viabilities, $0 < v_i(0) < 1$, the mortality rate reduces to

$$\mu(t) = \frac{\varepsilon}{1 - \varepsilon t}, \tag{1.102}$$

which is

$$\mu(t) \approx \varepsilon e^{\varepsilon t}, \text{ for } \varepsilon t \ll 1. \tag{1.103}$$

As a consequence, in the limit of slow drift the mortality rate $\mu(t)$, grows exponentially for small t (similar conclusions for the Gompertz model), but at advanced ages is not increasing exponentially.

By considering the other limit (when $\varepsilon \to 0$) of equation (1.99), we can explain the fluctuations at intermediate ages. During the process an individual viability

$v_i(t)$, follows a random walk that ends when $v \leq 0$. As the time is increasing, the average viability increases and the mortality rate decreases. So, as the people of the population die over time, the mortality rate demonstrates fluctuations, until the last individual die.

To simplify the analytical calculation of hazard rates we rewrite equation (1.99) in the case of continuous time,

$$dv_i = -\varepsilon dt + \sigma dW_i(t), \tag{1.104}$$

where $W_i(t)$ is a continuous time stochastic process which is called Wiener process [11]. The probability of dying in the interval between t and $t + dt$ is given by

$$P(t|v_0) = \frac{v_0}{\sqrt{2\pi\sigma^2 t^3}} exp\Big(- \frac{(v_0 - \varepsilon t)^2}{2\sigma^2 t}\Big). \tag{1.105}$$

The mortality rate $\mu(t)$, in the continuous model (1.104) for an initial viability $n_0(v)$ is given by

$$\mu(t) = \frac{D(t)}{N_0 - \int_0^t D(t')dt'}, \tag{1.106}$$

where

$$D(t) = \int_0^\infty n_0(v) P(t|v) dv \tag{1.107}$$

is the density of individual dying as a function of age.

For heterogeneous populations we can find $D(t)$ with analytical or numerical calculations. For a homogeneous population, with $v_i(t) = v_0$ and N_0 individuals then, $D(t) = N_0 P(t, v_0)$. In this case if $v_0 = 1$ for all individuals at time $t = 0$, then the mortality rate can be expressed analytically by

$$\mu(t) = \frac{\sqrt{\tau_r/2\pi t^3} exp(-\frac{\tau_r (t-\tau)^2}{2\tau^2 t})}{1 - H(\sqrt{\tau_r/2t}(1 - t/\tau))/2 - e^{2\tau_r/\tau} H(\sqrt{\tau_r/2t}(1 + t/\tau))/2}, \tag{1.108}$$

where τ is the time corresponds to the mean lifetime, τ_r the time corresponds to the mean time for an individual to change its viability by v_0 through fluctuations and $H(x)$ is the complementary error function. The two time scales are given by $\tau = v_0/\varepsilon$ and $\tau_r = {v_0}^2/\sigma^2$.

The figure 1.5 shows the mortality rate curves according to the equation (1.108), where the solid curve is for $\tau = 10$ and $\tau_r = 2$, the dashed curve is for $\tau = 10$, $\tau_r = 50$, and the dot-dashed curve for $\tau = 10$ and $\tau_r = 150$.

From the figure 1.5 we imply that, if $\tau_r \gg \tau$, the system dominated by drift and we observe that the mortality curves after a brief delay at initial stages of t, increases rapidly until a level off (dashed and dot-dashed curves). If $\tau_r \ll \tau$, the system is dominated by fluctuations and we observe that the mortality rate (solid curve), decline with age after a brief increase. When $\tau_r > \tau$, but still of the same order of magnitude, the mortality curve shows an initial increase followed by a plateau.

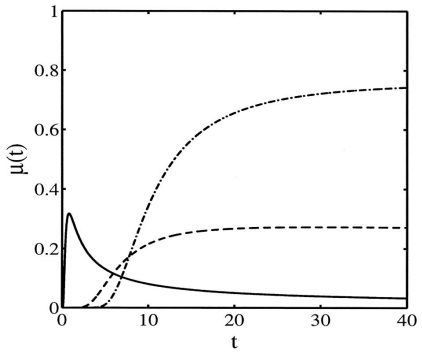


Figure 1.5: Mortality rates according to the equation (1.108) with $\tau = 10$ and $\tau_r = 2,\ 50$ and 150 corresponding to the solid, dashed, and dot-dashed curves respectively. The figure is presented in the paper "Explaining mortality rate plateaus" [10].

The asymptotic mortality rate for the inverse Gaussian distribution is nonzero, i.e. $lim_{t\to\infty}\mu(t) > 0$. However, for finite size populations the fluctuations lead to the eventual decline of the entire population, and therefore $\mu(t) = 1$ at some finite value of t. The results of numerical simulations of equation (1.99) can be found in figure 1.6.

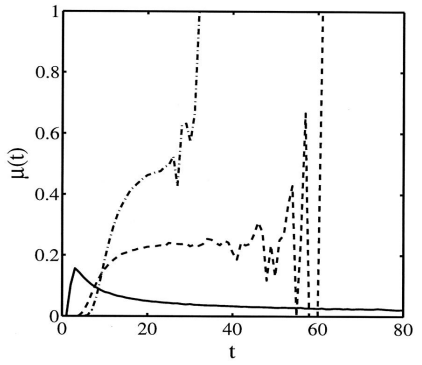


Figure 1.6: Mortality rates obtained via numerical simulations of a homogeneous population of $N = 10^6$ organisms, the dynamics of which is that of equation (1.99), with $v_0 = 1, \tau = 10$, and $\tau_r = 2$, 50 and 150 corresponding to the solid, dashed and dot-dashed curves respectively. Note that $\varepsilon = 1/\tau$ and $\sigma = 1/\sqrt{\tau_r}$. The figure is taken from [10].

Generally, the shapes of the curves in figures 1.5 and 1.6, are similar to each other, but the presence of fluctuations becomes important as the size of cohorts decline.

Chapter 2

Modelling the dynamics of ageing and mortality

2.1 Mathematical Model

Mathematically the dependance of mortality rate on age can be modelled by the exponential Gompertz function

$$m_i = m_0 e^{i/\tau}, \tag{2.1}$$

where m_i is the mortality rate for age i, m_0 is the initial mortality (the mortality for age $i = 0$) and τ is the mortality rate coefficient. We assume that for this model the time takes discrete values, i.e. the value of i gives age in years (integer values). Let N_i be the number of people of age i and ΔN_i the number of deaths of people aged i with

$$\Delta N_i = N_i - N_{i+1}. \tag{2.2}$$

From the definition of mortality for each age, as the number of deaths of people aged i per total number of people of this age, we can have the following expression for the mortality m_i

$$m_i = \frac{\Delta N_i}{N_i}. \tag{2.3}$$

Also, we can count the number of people of age $i + 1$, if from the people who were alive in the previous year (people of age i) substract the number of people who have died that year.

$$N_{i+1} = N_i - \Delta N_i = N_i - m_i N_i = (1 - m_i)N_i = (1 - m_0 e^{i/\tau})N_i \tag{2.4}$$

$$\Rightarrow N_{i+1} = (1 - m_0 e^{i/\tau})N_i. \tag{2.5}$$

Each human population consists by various subpopulations each ageing exponentially but with different parameters, such as the initial mortality rates, the mortality coefficients and the initial sizes of the subpopulations.

Let use the notations N_{j0} for the initial size, m_{j0} for the initial mortality rate, and τ_j for the mortality rate coefficient of the j subpopulation. The equations for the mortality rates are given by

$$m_{ji} = m_{j0}e^{i/\tau_j}, \tag{2.6}$$

If we assume that the entire human population consists n subpopulations, i.e. $j = 1, 2, \ldots, n$ then the total mortality rate can be expressed by

$$m_i = \frac{N_{1i}m_{1i} + N_{2i}m_{2i} + \ldots + N_{ni}m_{ni}}{N_{1i} + N_{2i} + \ldots + N_{ni}} \tag{2.7}$$

$$\Rightarrow m_i = \frac{N_{1i}m_{10}e^{i/\tau_1} + N_{2i}m_{20}e^{i/\tau_2} + \ldots + N_{ni}m_{n0}e^{i/\tau_n}}{N_{1i} + N_{2i} + \ldots + N_{ni}} \tag{2.8}$$

$$\Rightarrow m_i = \frac{\sum_{j=1}^{n} N_{ji}m_{j0}e^{i/\tau_j}}{\sum_{j=1}^{n} N_{ji}}. \tag{2.9}$$

Also we can define ρ_j as the fraction of the size of j subpopulation over the total population size N,

$$\rho_j = \frac{N_j}{N} = \frac{N_j}{N_1 + N_2 + \ldots + N_n}, \tag{2.10}$$

with

$$\sum_{j=1}^{n} \rho_j = 1. \tag{2.11}$$

From the definition of the mortality (2.3), we can express the mortality rate of each subpopulation as

$$m_j = \frac{\Delta N_j}{N_j}. \tag{2.12}$$

Then the total mortality m is given by

$$m = \frac{\Delta N_1 + \Delta N_2 + \ldots + \Delta N_n}{N_1 + N_2 = \ldots + N_n} = \frac{m_1N_1 + m_2N_2 + \ldots + m_nN_n}{N_1 + N_2 + \ldots + N_n} \tag{2.13}$$

and substituting the fractions (2.10) into (2.13) we have

$$m = m_1\rho_1 + m_2\rho_2 + \ldots + m_n\rho_n = \sum_{j=1}^{n} m_j\rho_j. \tag{2.14}$$

We will use the equation (2.9) of the total mortality and expressions (2.6) for the mortality rates of each subpopulation to plot the mortality rate respect to age i, taking into account the heterogeneity of the entire population, to examine the behaviour of the total mortality for a variation of the mortality parameters.

2.2 Analytical solution of the continuous model

In this section we will derive analytical solutions for a continuous model describing heterogeneous populations. To simplify our analysis, we assume that a human heterogeneous population consists only two subpopulations (methods are similar for more than two subpopulations). We replace the discrete time i by continuous time t.

To derive the function of total mortality, firstly we need to find expressions for N_1 and N_2, depending on the initial mortality rates, mortality coefficients and time t. To achieve this, we assume the continuous model for mortality rate of the first subpopulation

$$m_{1t} = \frac{-\Delta N_1}{N_1 \Delta t}. \tag{2.15}$$

Then,

$$\frac{dN_1}{N_1} = -m_{1t}dt \Rightarrow ln(N_1) = -\int m_{10}e^{t/\tau_1}dt. \tag{2.16}$$

Solving the integration we get

$$N_1 = Ae^{-m_{10}\tau_1 e^{t/\tau_1}}, \tag{2.17}$$

where A is a constant and for the initial value of time $t = 0$,

$$N_{10} = Ae^{-m_{10}\tau_1} \Rightarrow A = N_{10}e^{m_{10}\tau_1}. \tag{2.18}$$

This means that the expression for N_1 depends on the initial mortality m_{10}, the coefficient τ_1 and time t is given by

$$N_1 = N_{10}e^{m_{10}\tau_1(1-e^{t/\tau_1})}. \tag{2.19}$$

Similarly for N_2 we have that

$$N_2 = N_{20}e^{m_{20}\tau_2(1-e^{t/\tau_2})}. \tag{2.20}$$

Hence we can rewrite the expression for the total mortality as

$$m = m_{20}e^{t/\tau_2} + (m_{10}e^{t/\tau_1} - m_{20}e^{t/\tau_2})\frac{N_{10}e^{m_{10}\tau_1(1-e^{t/\tau_1})}}{N_{10}e^{m_{10}\tau_1(1-e^{t/\tau_1})} + N_{20}e^{m_{20}\tau_2(1-e^{t/\tau_2})}}. \tag{2.21}$$

To compare the continuous model with the discrete model of mortality we can consider values of analytical solutions for integer values of time $t = i$.

2.3 The stochasticity on the dynamics of ageing

At advanced ages of human life a small subset of people is still alive in contrast to the magnitude of the initial population size. For this situation we will analyse the idea of stochasticity on the dynamics of ageing.

At a particular age t, we have the value of the mortality rate by the exponential function (2.1). This value is always between 0 and 1. The mortality rate give us the probability for how many people will die until the next time-step, i.e. if the mortality rate at time t is 0.5 and there are n people, therefore it is possible the half of that people to die before time $t+1$.

Let us begin with an example to understand easier the stochasticity on the process of ageing. We assume that at time (age) $t = 80$, n people are alive and that the mortality rate at this age is $m = 0.2$. Thus the probability to die before the age $t = 81$, a person is $p = 0.2$ equal to the mortality rate, and to survive is $1 - p = 0.8$. Then,

$$[m + (1 - m)]^n = 1, \tag{2.22}$$

or we can write

$$[p + (1 - p)]^n = 1. \tag{2.23}$$

Using the binomial expansion we have that

$$[p + (1 - p)]^n = \sum_{k=0}^{n} \binom{n}{k} p^{n-k}(1 - p)^k, \tag{2.24}$$

where the binomial coefficients are given by the formula

$$\binom{n}{k} = \frac{n!}{k!(n - k)!}. \tag{2.25}$$

For the simplest case that only one people is alive at time t where the mortality rate is $m = 0.2$, there is a probability $p = 0.2$ to die before the age $t + 1$, and a probability $p = 0.8$ to survive.

Let us assume that at time t the mortality rate is $m = 0.2$ and there are two alive individuals, $n = 2$. Then we separate the probabilities into three cases: to none deaths, one death or two deaths. The probabilities for the three cases are

$$\text{two deaths: } P(X_t = 0) = (0.2)^2 = 0.04$$

$$\text{one death: } P(X_t = 1) = 2(0.2)(0.8) = 0.32$$

$$\text{none deaths: } P(X_t = 2) = (0.8)^2 = 0.64$$

where X_t denotes the number of people which survive in the age interval between t and $t + 1$. The values of probabilities are taken from the terms of the binomial expansion

$$1 = (0.2 + 0.8)^2 = (0.2)^2 + 2(0.2)(0.8) + (0.8)^2. \tag{2.26}$$

We have three cases so that, we divide the probability range $[0, 1]$, into three intervals. The first interval is from 0 to 0.04, the second from 0.04 to $0.04 + 0.32 = 0.36$ and the third one from 0.36 to $0.36 + 0.64 = 1$. Then we consider a random generating number between 0 and 1. The interval where the random number belongs indicates how many people die before the next age.

By the same way, for $n = 3$ survived people at time t, with the same value of mortality rate $m = 0.2$, we have the binomial expansion

$$1 = (0.2 + 0.8)^3 = (0.2)^3 + 3(0.2)^2(0.8) + 3(0.2)(0.8)^2 + (0.8)^3. \tag{2.27}$$

Therefore we can derive the following probabilities:

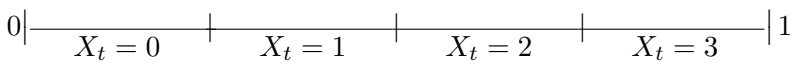
three deaths (zero alives at time $t + 1$): $P(X_t = 0) = (0.2)^3 = 0.008$

two deaths (1 alive at time $t + 1$): $P(X_t = 1) = 3(0.2)^2(0.8) = 0.096$

one death (2 alives at time $t + 1$): $P(X_t = 2) = 3(0.2)(0.8)^2 = 0.384$

none deaths (3 alives at time $t + 1$): $P(X_t = 3) = (0.8)^3 = 0.512$

We divide the probabilities which take values from zero to one, into four intervals



Then, we assume a generating random number between 0 and 1. Let us consider that for the particular example the generating random number is 0.3. This random number belongs to the third interval (between the values $0.008 + 0.096 = 0.104$ and $0.104 + 0.384 = 0.488$), therefore we imply that one individual dies and two survive up to age $t + 1$. So at time $t + 1$ there are two alive individuals. By the same way, at time $t + 1$ we have the value of the mortality rate, we assume a new random generating number and we imply how many of the alive people die before $t + 2$.

In the general case where the size of population is n at time t, we know the mortality rate, then we find the binomial coefficients using the Pascal triangle and finally considering a generating random number we imply how many people survive before the next time, $t + 1$. In this way, we progress the algorithm until all people of the population die.

Chapter 3

Numerical results

3.1 Case studies for heterogeneous populations

Studying heterogeneous populations which consists two or more subpopulations, we can derive results on the changes in the total mortality rate which are produced by the variation of the mortality parameters of each subpopulation. We will analyse each one of the mortality parameters separately, and we will deduce conclusions about how their variations affect the results. The results of the study of heterogeneity are presented into the following random examples where the values of the parameters are taken arbitrary.

Example 1:

In the first example let us assume that we have one heterogeneous population which include two subpopulations with equal initial sizes $N_{10} = N_{20} = 1000$, same initial mortality rates, $m_{10} = m_{20} = 0.03$, but different mortality coefficients, $\tau_1 = 15,\ \tau_2 = 30$.

The figure 3.1 shows the mortality rates for the two subpopulations (dashed lines) which are given by the equations (2.6), and the total mortality (solid curve) which is given by (2.21). The vertical axis is on a logarithmic scale so we have two straight lines for the mortality of the two subpopulations. The two lines have the same point of intersection with the vertical axis which is the value of initial mortality and have different slope due to the fact that the subpopulations differ in the coefficients τ. The age i where the mortality rate takes the final value equal to 1, is the age when the last individual of each subpopulation is dying. For this example, the last individual of the frailer subpopulation dies at the age of 53 years old and the last individual of the more robust subpopulation dies at the age of 107 years. The curve of the total mortality begins at age $i = 0$ from the initial mortality value 0.03, increases steadily over time somewhere between the two mortality rates and after the age $i = 40$ follows the mortality level of the more robust subpopulation.

As a result, if we have two subpopulations with same initial mortality rates but different coefficients τ, we conclude that the people of a frailer subpopulation

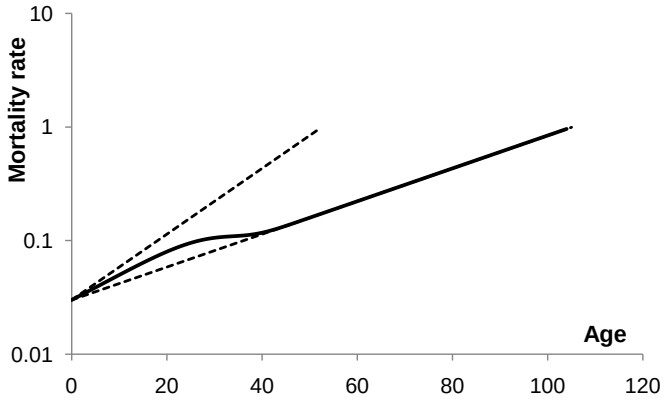


Figure 3.1: Heterogeneous population consisting of two subpopulations with equal initial sizes ($N_{10} = N_{20} = 1000$), same initial mortality rates ($m_{10} = m_{20} = 0.03$), but different mortality coefficients ($\tau_1 = 15,\ \tau_2 = 30$). The solid curve indicates the total mortality of the whole population and the dashed lines the mortality rates of each subpopulation. The vertical axis is on a logarithmic scale.

(smaller coefficient τ,) have shorter lifespan (are dying faster) than the people of a more robust subpopulation with bigger mortality coefficient.

Let us consider that we choose more individuals from the frailer subpopulation to see how the initial size of each subpopualtion affect the pattern of mortality. We keep constants the values $\tau_1 = 15,\ m_{10} = 0.03$ and $\tau_2 = 30,\ m_{20} = 0.03$. We assume that $N_{20} = 10$ and N_{10} has 100, 1000 and 10000 individuals respectively. Then we have three different curves for the total mortality in figure 3.2.

The curve of the total mortality starts from the initial mortality value 0.03, increases steadily on the mortality of the first subpopulation (faster dying), suddenly declines and then starts increasing again at a slower rate through the mortality line of the second subpopulation. When the initial size of the first subpopulation is increased, the extrema points are shifted up and right and observed a sharper drop from maximum to minimum point. The sudden decline in the total mortality rate is produced by the rapid extinction of the frailer subpopulation. Until the point of decline, the frailer subpopulation experiences death rates that are relatively low. Then, due to the exponential increase in the force of mortality, the death rates become sufficiently large that within a few years almost all of the frailer subpopulation dies. After a particular age, the total mortality follows the exponential growth of the robust subpopulation because only members of this subpopulation are still alive.

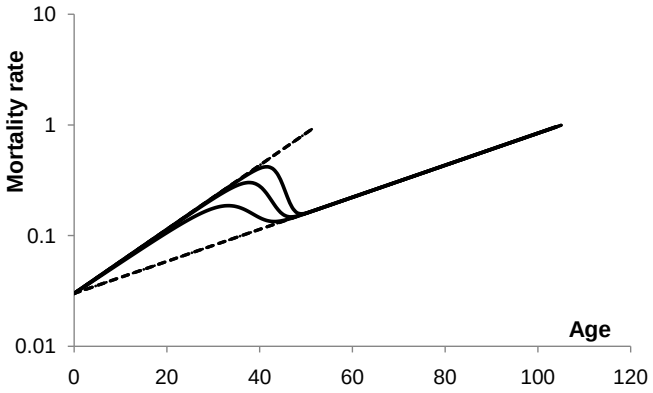


Figure 3.2: Two subpopulations with same initial mortality ($m_{10} = m_{20} = 0.03$) and different coefficients ($\tau_1 = 15,\ \tau_2 = 30$). The total mortality of the whole population follows first the mortality of the frailer subpopulation (individuals with shorter lifespan), then declines to a level of mortality rate for the more robust subpopulation (individuals with longer lifespan) and still increased in that level. The three solid lines, from left to right, shows the total mortality of a whole population which consists of the two subpopulations where the more robust has 10 individuals and the frailer subpopulation has 100, 1000 and 10000 individuals respectively.

Example 2:

We assume that we have two subpopulations with the same coefficient $\tau_1 = \tau_2 = 25.5$, but different initial mortality $m_{10} = 0.15,\ m_{20} = 0.02$. Thus, the two lines which denote the two mortality rates have the same slope and different point of intersection with the vertical axis (dashed lines in figure 3.3). Also we assume that $N_{20} = 10$ and N_{10} is 100, 1000 and 10000 individuals respectively.

The last individual of the first subpopulation (with $m_{10} = 0.15$), dies at the age of 50 years old, and the last individual of the other subpopulation (with $m_{20} = 0.02$), dies at the age of 100 years old. As a result, from the comparison of two subpopulations with same mortality coefficients but different initial mortalities, we imply that the subpopulation with smallest initial mortality consists individuals with longer lifespan than the second subpopulation. The curve of total mortality begins from the initial mortality of the frailer subpopulation, has a maximum point, then decline to a minimum point and finally after the age of 35-40 years old continues on the mortality line of the more robust subpopulation. Besides that the frailer subpopulation has more individuals, the whole population after a particular age follows the mortality rate of the more robust subpopulation (smaller initial size). When the initial size of the frailer subpopulation increases the extrema points are shifted up and some years later.

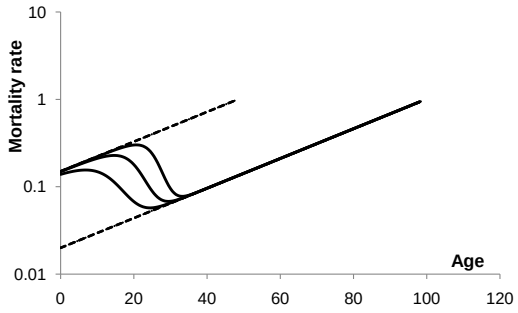


Figure 3.3: Two subpopulations with same coefficient ($\tau_1 = \tau_2 = 25.5$) and different initial mortality ($m_{10} = 0.15,\ m_{20} = 0.02$). The three solid lines, form left to right, shows the total mortality of the whole population which consists two subpopulations with $N_{20} = 10$ and N_{10} is 100, 1000 and 10000 individuals respectively.

Example 3:

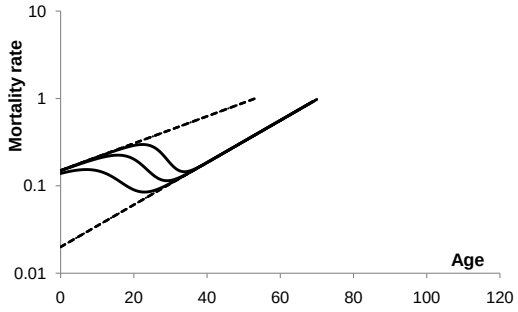


Figure 3.4: Two subpopulations (dashed lines) with different coefficients ($\tau_1 = 28,\ \tau_2 = 18$) and different initial mortality rates ($m_{10} = 0.15,\ m_{20} = 0.02$). The three solid lines, form left to right, shows the total mortality of a whole population which consists the two subpopulations with constant $N_{20} = 10$, and N_{10} is 100, 1000 and 10000 respectively.

We assume that we have two subpopulations with different initial mortality rates $m_{10} = 0.15,\ m_{20} = 0.02$ and different mortality coefficients $\tau_1 = 28,\ \tau_2 = 18$. We keep constant the initial size of the second subpopulation, $N_{20} = 10$ and we consider that the first subpopulation has initial size N_{10} =100, 1000 and 10000 individuals respectively. The curves for the total mortality of the entire population are presented in figure 3.4 where the two dashed lines are the mortality rate for each subpopulation and have different slopes and different point of intersection. The conclusions about

the curves of the total mortality rates are similar to the conclusions of the first two examples.

Therefore, at the first three examples we have studied the changes of total mortality curve for a variation of the initial subpopulations sizes. The discrepancy of initial sizes can be expressed by a variation of the fractions ρ_1 and ρ_2. At the following examples we will examine the behaviour of total mortality with a variation of the two other parameters, initial mortality and mortality coefficient.

Example 4:

We consider a population with two subpopulations, of equal initial sizes $N_{10} = N_{20} = 1000$ and same initial mortality rates $m_{10} = m_{20} = 0.03$. Also we assume that the coefficient $\tau_2 = 30$ is constant, and choosing different values for τ_1 we will see how this parameter change the total mortality.

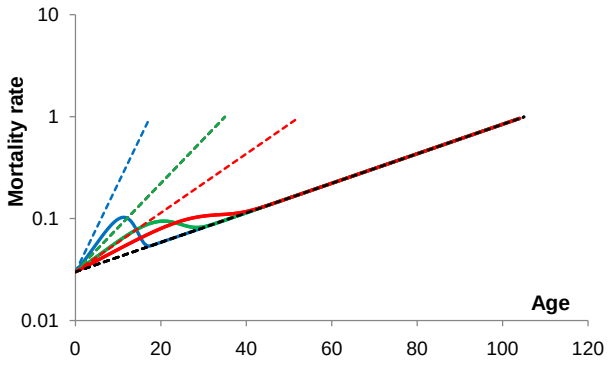


Figure 3.5: The change on mortality dynamics with change of mortality coefficient for one of the subpopulations. We consider a population with two subpopulations, of equal initial sizes $N_{10} = N_{20} = 1000$ and same initial mortality rates $m_{10} = m_{20} = 0.03$. Also, the coefficient $\tau_2 = 30$ is constant and the coefficient τ_1 takes the values 5, 10 and 15 for the blue, green and red dashed lines respectively. The total mortality of the entire population is presented in a solid line. Each colour corresponds to the mortality of a population which consists the robust subpopulation (black dashed line) and one of the frailer subpopulations (dashed line with the same colour as the total mortality curve, in each case).

In figure 3.5 we compare the second subpopulation (black dashed line) with the first subpopulation where τ_1 takes the values 5 (blue dashed line), 10 (green dashed line) and 15 (red dashed line) respectively. Each solid line corresponds to the total mortality of a population which consists the first subpopulation with the similar colour dashed line and the second subpopulation (black dashed line). In each case the curve of total mortality, increases steadily between the two mortality rates, then declines and increases again to a level of the mortality rate of the more robust

subpopulation (with bigger mortalitry coefficient τ). When the coefficient τ_1 takes smaller values the maximum point of the total mortality is observed in younger age.

Example 5:

We consider two subpopulations with equal initial values of individuals $N_{10} = N_{20} = 1000$, equal mortality coefficients $\tau_1 = \tau_2 = 25.5$ and different initial mortality rates. We keep constant the value $m_{20} = 0.02$ and choosing different values for m_{10} we see the changes in the pattern of total mortality. We assume that m_{10} takes the values 0.5 (blue dashed line), 0.25 (green dashed line) and 0.15 (red dashed line) respectively.

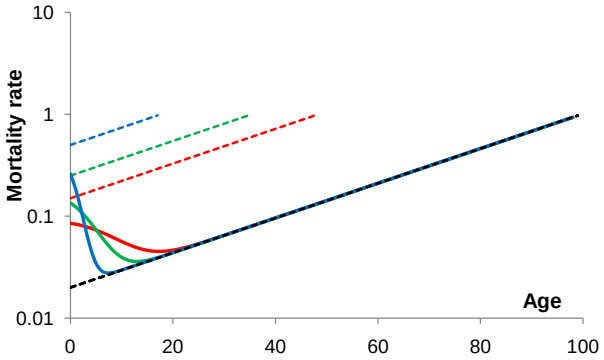


Figure 3.6: The change on mortality dynamics with change of initial mortality rate for one of the subpopulations. We consider a population with two subpopulations, of equal initial sizes $N_{10} = N_{20} = 1000$ and same mortality coefficients $\tau_1 = \tau_2 = 25.5$. Also, we consider the initial mortality $m_{20} = 0.02$ is constant, and the initial mortality m_{10} takes the values 0.5, 0.25 and 0.15 for the blue, green and red dashed lines respectively. The total mortality of the entire population is presented in a solid line. Each colour corresponds to the mortality of a population which consists the robust subpopulation (black dashed line) and one of the frailer subpopulations (dashed line with the same colour as the total mortality curve, in each case).

From figure 3.6 we see that in each case the curve of the total mortality begins in a point somewhere between the two mortality rates, declines in a minimum point and then increases again at the level of the mortality rate of the robust subpopulation. When the initial mortality of the frailer subpopulation increases, the drop in the total mortality curve become sharper, and the minimum point shifted in younger age.

3.2 Extrema points in solutions of heterogeneous model

To study the heterogeneity, we have assumed that a human population consists of some subpopulations. Therefore, if we have two subpopulations the model might has one or two extrema points as we have seen at the previous cases of heterogeneous populations. To examine the shifts of two extrema points (maximum and minimum), we need to differentiate the function of total mortality respect to time t and find the roots of the derivative in each case. The derivative of (2.21) is given by

$$\begin{aligned}\frac{dm}{dt} &= \frac{m_{20}e^{t/\tau_2}}{\tau_2} + \frac{\left(\frac{m_{10}e^{t/\tau_1}}{\tau_1} - \frac{m_{20}e^{t/\tau_2}}{\tau_2}\right) N_{10}e^{m_{10}\tau_1(1-e^{t/\tau_1})}}{N_{10}e^{m_{10}\tau_1(1-e^{t/\tau_1})} + N_{20}e^{m_{20}\tau_2(1-e^{t/\tau_2})}} \\ &\quad - \frac{\left(m_{10}e^{t/\tau_1} - m_{20}e^{t/\tau_2}\right) N_{10}m_{10}e^{t/\tau_1}e^{m_{10}\tau_1(1-e^{t/\tau_1})}}{N_{10}e^{m_{10}\tau_1(1-e^{t/\tau_1})} + N_{20}e^{m_{20}\tau_2(1-e^{t/\tau_2})}} \\ &\quad + \frac{\left(m_{10}e^{t/\tau_1} - m_{20}e^{t/\tau_2}\right) N_{10}e^{m_{10}\tau_1(1-e^{t/\tau_1})}\left(N_{10}m_{10}e^{t/\tau_1}e^{m_{10}\tau_1(1-e^{t/\tau_1})}\right)}{\left(N_{10}e^{m_{10}\tau_1(1-e^{t/\tau_1})} + N_{20}e^{m_{20}\tau_2(1-e^{t/\tau_2})}\right)^2} \\ &\quad + \frac{\left(m_{10}e^{t/\tau_1} - m_{20}e^{t/\tau_2}\right) N_{10}e^{m_{10}\tau_1(1-e^{t/\tau_1})}\left(N_{20}m_{20}e^{t/\tau_2}e^{m_{20}\tau_2(1-e^{t/\tau_2})}\right)}{\left(N_{10}e^{m_{10}\tau_1(1-e^{t/\tau_1})} + N_{20}e^{m_{20}\tau_2(1-e^{t/\tau_2})}\right)^2}.\end{aligned} \tag{3.1}$$

If the derivative equated with zero we will have up to two solutions corresponding to maximum and minimum values.

We will examine the behaviour of the extrema points for different initial sizes of the two subpopulations. From the previous section we choose example 2 where we have one maximum and one minimum point. In that example we have a heterogeneous population consisting of two subpopulations with different initial mortality rates ($m_{10} = 0.15,\ m_{20} = 0.02$) and equal mortality coefficients ($\tau_1 = \tau_2 = 25.5$). We assume that the initial size of the second subpopulation is constant, $N_{20} = 10$ individuals, and choosing indicative values for the initial size N_{10} of the first subpopulation (i.e. different values of the fraction ρ_1) we record the extrema points on the table 3.1.

For only one individual in the first subpopulation, the total mortality of the entire population has not a maximum point but has a minimum point at the age of 4 years (The function has a maximum point for negative value of i but we didn't mention it because we study only the positive values of human age i). The first positive maximum point appears at the age of 1 year if we choose 23 individuals for the initial size of the first subpopulation. The two extrema points are shifted exponentially over time (figure 3.7). If we choose a huge initial number of individuals of the frailer subpopulation ($N_{10} > 10^{19}$), the total mortality of the entire population is increasing at the level of the mortality rate of the frailer subpopulation, until the age of 49 years, and then is increasing at the level of the mortality rate of the more

Table 3.1: Maxima and minima points for different values of the fraction ρ_1 for the total mortality of a heterogeneous population consisting of two subpopulations with $m_{10} = 0.15,\ m_{20} = 0.02$ and $\tau_1 = \tau_2 = 25.5$

N_{10}	ρ_1	max point i	max point m_i	min point i	min point m_i
1	0.090909091	no max	no max	4	0.031049916
10	0.5	no max	no max	17	0.045110564
22	0.6875	no max	no max	20	0.049386802
23	0.696969697	1	0.110667377	20	0.049634757
30	0.75	2	0.11849251	21	0.051023368
100	0.909090909	7	0.155064587	24	0.057213983
500	0.980392157	12	0.205597464	28	0.064806518
1000	0.99009901	15	0.227776566	29	0.068070245
5000	0.998003992	19	0.279261506	32	0.074926523
10000	0.999000999	21	0.300930181	33	0.077809815
10^5	0.99990001	25	0.372181815	36	0.086797281
10^6	0.99999	29	0.441196777	39	0.094926506
10^7	0.999999	32	0.505559911	41	0.102288808
10^9	0.99999999	37	0.624782762	44	0.114880202
10^{10}	0.999999999	39	0.678929605	45	0.120551866
10^{13}	1	44	0.822234195	48	0.131815051
10^{15}	1	46	0.895635694	49	0.136633328
10^{17}	1	47	0.944745897	49	0.136633328
10^{19}	1	48	0.983673705	49	0.136633328

robust subpopulation because after this age only members of that subpopulation are still alive.

From the figure 3.7 we see that if we keep constant the initial size N_{20} of the robust subpopulation and increase the initial size N_{10} of the frailer subpopulation there is an exponential "movement" of the etrema points. The vertical axis in figure 3.7 is on a logarithmic scale so the shifts of the extrema points are shown by straight lines. For the particular example, the trend line for the maxima points is

$$m_i = 0.1146e^{0.0454i}, \tag{3.2}$$

and similar for the minima points is

$$m_i = 0.0251e^{0.0345i}. \tag{3.3}$$

By this way, we can work for all the previous examples or generally for heterogeneous populations consisting of two subpopulations with known mortality parameters of each subpopulation.

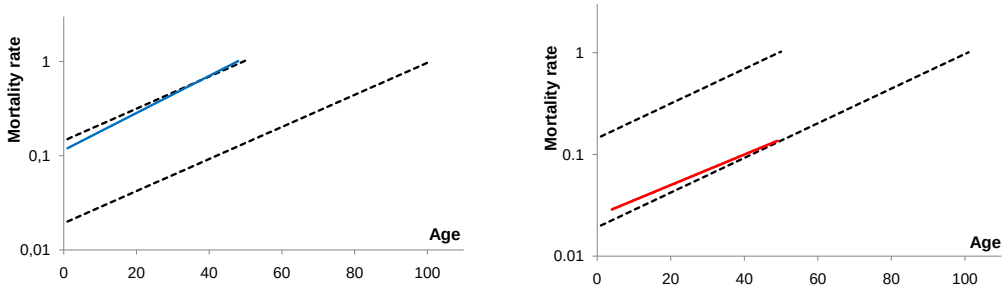


Figure 3.7: The lines corresponds to the shifts of the extrema points of the total mortality for one heterogeneous population consisting two subpopulations, with different initial mortality and same mortality coefficients. The blue (maxima) and red (minima) lines indicate the dynamics of extrema with an increase of the fraction ρ_1 (from left to right).

3.3 Adjusting the model parameters to fit to the mortality data of a human population

As we have seen the mortality rate depends on the age i of each individual. The curve of mortality rates for each population begins from the value of initial mortality at age $i = 0$, declines in a minimum point somewhere near the age of 10 years old, then fits in a straight line until the age of 90 almost, and finally shows a slight drop until all individuals in the population die. Thus, the simple case of the mortality curve of a population, has three extrema points and to achieve that, we assume that the entire population consisting by three subpopulations at least.

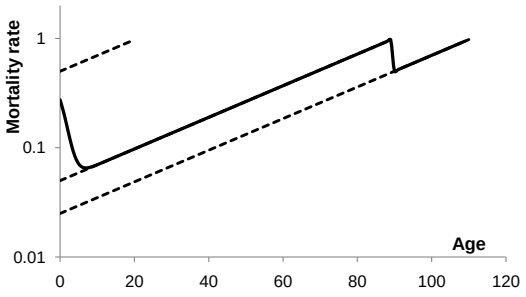


Figure 3.8: A model for the mortality rates of a human population. Mainly, the mortality curve of a human population exhibit a minimum point somewhere between 10 and 25 years, then advanced exponentially until a peak at the age of 80 roughly, and finally has a behaviour depends of the number of people who still alive.

The figure 3.8 shows a model of this simple case where the mortality curve has a minimum point somewhere between 10 and 25 years, then advanced exponentially until a peak at the age of 80 roughly, declines slightly and increase again until all the individual of the population are died. The behaviour of the mortality curve at advanced ages depends on the number of people who still alive at this age interval. Therefore, we can observe a slight fall, fluctuations or a plateau until all the people of the population die.

Example 1: United States population data for the year 2002

We have the observed mortality data for the United States population for the year 2002. The mortality rates lies in a curve (see figure 1.1) where there is a minimum value of the mortality at the age of 10 years almost, and also there is a part of mortality which advances exponentially and fits in a straight line. This part is the interval from 30 years to 85 and as we have seen is referred as the process of ageing. The data of US population are taken from CDC (Centers for Diseases Controls and Prevention) [12], and are given in the table 3.2.

Table 3.2: Mortality rates for the 2002 US population

Age (years)	Deaths per 100000 people	Death Rates
0	687.8	0.006878
3	32	0.00032
10	19.2	0.000192
20	93.7	0.000937
40	155.8	0.001558
50	430.1	0.004301
60	952.3	0.009523
70	2311.9	0.023119
80	5529.8	0.055298

We present the US data in the figure 3.9 where the vertical axis is on a logarithmic scale and denotes the mortality rate, and the horizontal axis is the age in years.

If we assume that we skip the fourth point (where the mortality rate is 0.000937 at the age of 20 years old), we observe that the mortality curve has only one extremum point (minimum). To fit the data for one extremum point we need a population consisting by two subpopulations. To achieve this we need to know the three mortality parameters of each subpopulation. If we know the initial mortality, the mortality coefficient τ, and the fraction ρ of the first subpopulation and choosing arbitrary values for the parameters of the other subpopulation, we achieve to have a minimum point but the solution is not unique. For known fraction ρ_1, directly we have the value of the fraction ρ_2 by the identity $\rho_1 = 1 - \rho_2$, if the total size of the entire population is known. Thus, we need to know another one parameter of the second subpopulation to achieve the right fit (unique solution).

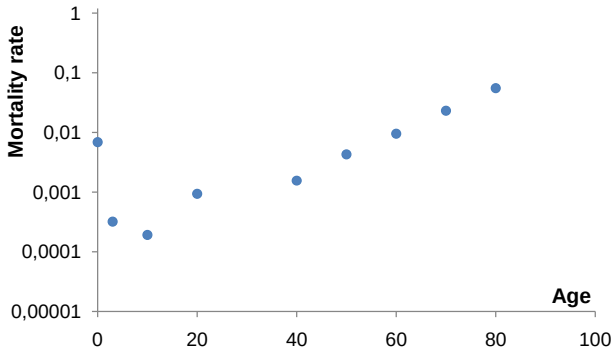


Figure 3.9: Mortality rates over time (years) for the United States population for the year 2002. The data are taken from the website of Centers for Diseases Controls and Prevention [12]

Recall again that we skip the fourth point. We assume that the two subpopulations have mortality parameters which are given in the table 3.3, where j denotes each subpopulation.

Table 3.3: Mortality parameters of the subpopulations that needed to fit the United States data if we skip the fourth data point

subpopulation j	N_{j0}	ρ_j	m_{j0}	τ_j
1	45	0.009	0.6	30
2	5000	0.991	0.00005	11.2

For the above parameters we achieve a good fit for the data as it shown in figure 3.10, where the solid line fits the data points except the point at 20 years which it is shown by a cross symbol.

By the same way, we can skip the second and the third point (the death rates for the ages 3 and 10 years respectively). Again, the mortality curve has one minimum point, therefore we need at least two subpopulations to fit the data. To achieve a good fit we assume that the first subpopulation contains $N_{10} = 50$ people at the age $i = 0$, has initial mortality $m_{10} = 0.11$ and mortality coefficient $\tau_1 = 59$. The second subpopulation has initial mortality $m_{20} = 0.00006$, mortality coefficient $\tau_2 = 12$ and the initial size of that subpopulation is $N_{20} = 1000$ people. We can say, that $\rho_1 = 50/1050 = 0.048$ and $\rho_2 = 1000/1050 = 0.952$. As a result, the new fit for the data is shown in figure 3.11, where the data are denoted by circle symbols, the two points we have skipped are shown with cross symbols, the mortality rates of each subpopulation are given by the dashed lines and the total mortality of the whole population by the solid line which is a good fit for the data points.

Finally, for the US morrtality data, we take into account all the points from the figure 3.9. Now, we need to fit the data by creating two extrema points and

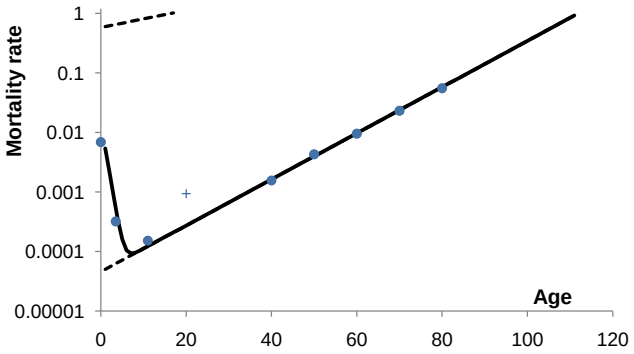


Figure 3.10: Fit of the US mortality data if we skip the point which denoted by cross symbol. To achieve the plot where there is only one minimum point at the mortality curve, we have considered a population consisting by two subpopulations with mortality parameters $m_{10} = 0.6, \rho_1 = 0.009, \tau_1 = 30$ and $m_{20} = 0.00005, \rho_2 = 0.991, \tau_2 = 11.2$ respectively.

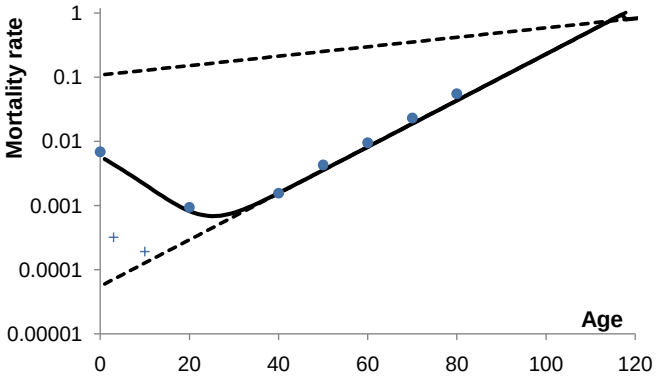


Figure 3.11: Fit of the US mortality data if we skip the two points which denoted by cross symbol. To achieve the plot where there is one minimum point at the mortality curve, we have considered a population consisting by only two subpopulations with mortality parameters $m_{10} = 0.11, \rho_1 = 0.048, \tau_1 = 59$ and $m_{20} = 0.00006, \rho_2 = 0.952, \tau_2 = 12$ respectively.

to achieve the essential result we assume that three subpopulations belongs to the entire population. The table 3.4 gives the parameters that needed for a good fit.

Table 3.4: Mortality parameters of the three subpopulations that needed to fit the United States data

subpopulation j	N_{j0}	ρ_j	m_{j0}	τ_j
1	250	0.008	0.7	29
2	420	0.014	0.0015	5.5
3	30000	0.978	0.00006	11.5

Using the above parameters for the three subpopulations, we take the figure 3.12 where there observed a good fit (solid curve) for the data. To achieve a better fit we can consider that the US population consists more than three subpopulations.

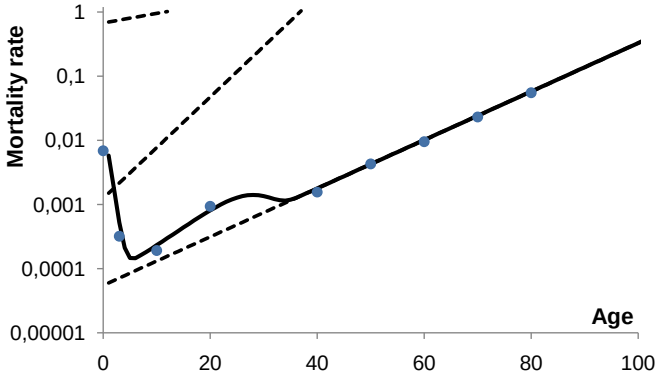


Figure 3.12: Fit of the United States mortality data using a population consisting by three subpopulations. The mortality rates of each subpopulation are presented by dashed lines and the mortality rate of the entire population by the solid line which fit the data (blue points). The mortality parameters of the three subpopulations are $m_{10} = 0.7, \rho_1 = 0.008, \tau_1 = 29$, $m_{20} = 0.0015, \rho_2 = 0.014, \tau_2 = 5.5$ and $m_{30} = 0.00006, \rho_3 = 0.978, \tau_3 = 11.5$ respectively.

Example 2: Swedish death rates for the year 2007

In that example we used the data for the death rates of Sweden for the year 2007. The data which are taken from the Human Mortality Database (HMD) [13], are more complete and accurate than the US population data because the Swedish death rates are recorded for each age in years (discrete values of time) until the last person of the population is died. The figure 3.13 presents the data which are taken from [13].

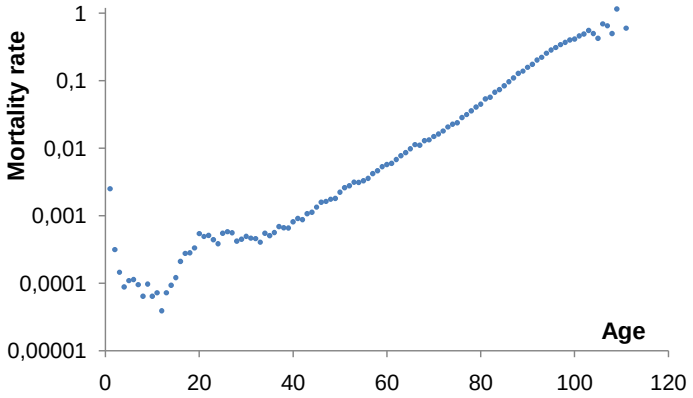


Figure 3.13: Swedish death rates for the year 2007. The data are taken from the website of Human Mortality Database [13]

From the figure 3.13 we see that the mortality data has initial mortality 0.0025 approximately, declines and create a minimum point at the age of 10 years, then increase until a local maximum value at the age of 25 years, drops slightly and advanced exponentially from the age of 30 to 100 years. The exponential growth at the part of ageing, fits in a straight line when the vertical axis is on a logarithmic scale. At advanced ages, i.e. after 100 years approximately, we observe a part where the mortality curve has fluctuations. Let assume that at this part the mortality leads a peak at the age of 100 years then decline and advanced exponentially again, until the last point. Thus, we have three extrema points and to fit the mortality curve we need at least 4 subpopulations. The mortality parameters of the four subpopulations that were used to fit the data are given in the table 3.5, where j denotes each subpopulation.

Table 3.5: Mortality parameters of the four subpopulations that needed to fit the Swedish data

subpopulation j	N_{j0}	ρ_j	m_{j0}	τ_j
1	150	0.00489	0.5	80
2	130	0.00424	0.0014	5.2
3	30000	0.97783	0.0000165	10
4	400	0.01304	0.0000165	10.7

The figure 3.14, shows the Swedish data (blue points), the mortality rates for the four subpopulations (dashed lines) and the mortality curve of the whole population which consists the four subpopulations (solid line). The mortality rate of the entire population forms a good fit for the data. To achieve a better fit on the data we can use more than four subpopulations.

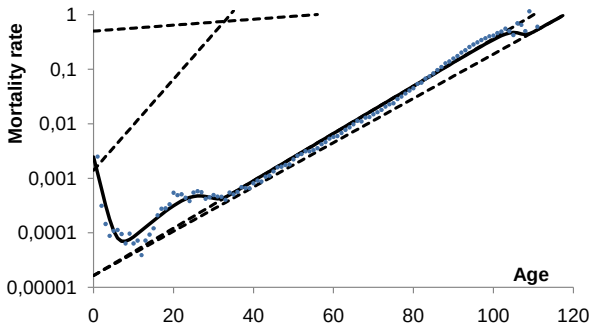


Figure 3.14: Fit of the Swedish mortality data using a population consisting by four subpopulations with mortality parameters $m_{10} = 0.5, \rho_1 = 0.00489, \tau_1 = 80$, $m_{20} = 0.0014, \rho_2 = 0.00424, \tau_2 = 5.2$, $m_{30} = 0.0000165, \rho_3 = 0.97783, \tau_3 = 10$ and $m_{40} = 0.0000165, \rho_4 = 0.01304, \tau_4 = 10.7$ respectively. The mortality rates of each subpopulation are presented by dashed lines and the mortality rate of the entire population by the solid line which fits the data (blue points).

3.4 Study of stochasticity on ageing problem

If we make a bigger focus at advanced ages of the figure with the Swedish data we observe some noises which are shown in figure 3.15. The mortality data after the age of 102 years, diverge from the exponential growth and create some fluctuations.

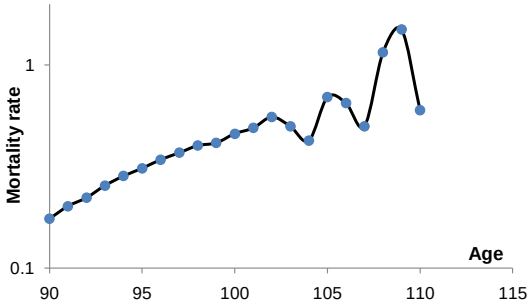


Figure 3.15: A focus on the Swedish data at advanced ages. The mortality curve after the age of 102 years, gets away from the exponential growth and create some fluctuations.

As we have mentioned before, the effects of stochasticity on the dynamics of mortality are visible when a small group of people is alive. Therefore, studying human populations which consists huge number of individuals, some fluctuations

are observed at advanced ages where few people are survive. To derive results of stochasticity, we must make an analysis to find from what size of population we observe the deviation from exponential growth of the mortality.

To achieve the essential results we have used the C^{++} programme to study the mortality taking into account the stochasticity. We have create a source code, for given the mortality parameters, to calculate the theoretical mortality rate which is given by the Gompertz exponential function and the actual mortality due stochasticity which is the number of deaths per number of size for each age (time) t. Although, using C^{++} code we have produced plots of theoretical and actual mortality over time to observe the differences. Two of that plots are given in figure 3.16, where we have assumed a population of ten thousand people (graph on the left) and a population of one hundred thousand people (graph on the right). The two populations have initial mortality $m_0 = 0.15$ and mortality coefficient $\tau = 30$.

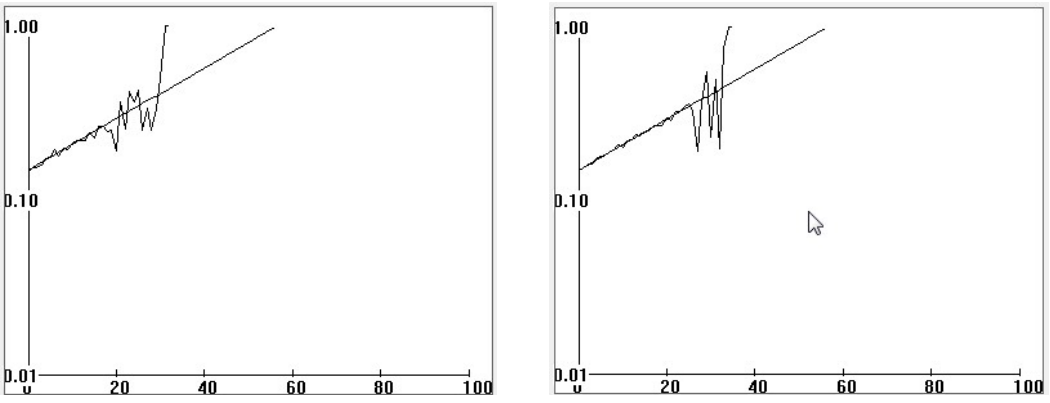


Figure 3.16: Plots of theoretical mortality (straight line) and actual mortality (fluctuations) for populations of sizes 10000 individuals (left graph) and 100000 individuals (right graph). The two populations have the same initial mortality $m_0 = 0.15$, and the same mortality coefficient $\tau = 30$.

From figure 3.16 we observe that, the theoretical mortality of a population advanced exponentially over time (straight line in a logarithmic scaled vertical axis). However, the actual mortality, which is counted dividing the number of deaths per number of alive individuals for each discrete value of time, creates some fluctuations (noises) which becomes visible when a small subset of people remain alive.

The following part of source code has used to place the vertical axes of the plots in a logarithmic scale:

```
for (double ord=-2.; ord<0.1; ord+=1.)
{
r.y=R.BottomRight().y-0.05*R.Height()-0.9*R.Height()*(ord+2.)/2.;
r.x=R.TopLeft().x+0.05*R.Width()+5;
```

```
dc.MoveTo(r.x, r.y);
r.x=R.TopLeft().x+0.05*R.Width()-5;
dc.LineTo(r.x,r.y);
str.Format("%4.2f", powf(10.,ord));
dc.TextOutA(r.x-15.,r.y-7.,str);
}
```

Furthermore, to plot the mortality rate for a population, which is given by the exponential function (2.1), we have create the following part of source code:

```
r.x=R.TopLeft().x+0.05*R.Width();
r.y=R.BottomRight().y-0.05*R.Height()-0.9*R.Height()*(log10(Mort1[0])+2.)/2.;
dc.MoveTo(r.x, r.y);
for (i=1; i<100; i++)
{
Mort1[i]=Mort1[0]*exp(i/tau1);
r.x=R.TopLeft().x+0.05*R.Width()+0.9*R.Width()*i/100;
r.y=R.BottomRight().y-0.05*R.Height()-0.9*R.Height()*(log10(Mort1[i])+2.)/2.;
if(Mort1[i]<1) dc.LineTo(r.x,r.y);
}
```

To take into account the stochasticity and calculate the actual mortality for each discrete value of time we haven't used a code to count the binomial coefficients (Pascal triangle) as the method we have described in section 2.3. This is because, for big size populations (i.e. big value of n), the binomial coefficients might be very large numbers and can't be declared as double numbers in C^{++}.

Therefore, we have made a code for an algorithm which take the current size for each time-step, consider a random generating number and count how many individuals survived before the next time. The following part of source code produces a table with sizes, the theoretical and actual mortality for each age until all individuals die, and draws the actual mortality over time:

```
srand(1);
Size1A=Size1[0];
float DeathRate;
float current_mortality=Mort1[0];
int current_size=1;

r.x=R.TopLeft().x+0.05*R.Width();
r.y=R.BottomRight().y-0.05*R.Height()-0.9*R.Height()*(log10(Mort1[0])+2.)/2.;
dc.MoveTo(r.x, r.y);

for(i=0;(i<100 && current_size>0);i++)
{
current_size=int(Size1A);
```

```
for (int ind=0; ind<current_size; ind++)
{
if((float)rand()/RAND_MAX<Mort1[i]) Size1A-=1.;
}
if(current_size>0) DeathRate=(float)(current_size-Size1A)/current_size;
current_mortality=0.75*DeathRate*exp(1/tau1)+0.25*Mort1[i];
r.x=R.TopLeft().x+0.05*R.Width()+0.9*R.Width()*i/100;
r.y=R.BottomRight().y-0.05*R.Height()-0.9*R.Height()*(log10(DeathRate)+2.)/2.;
dc.LineTo(r.x,r.y);

str.Format("time=%d size=%d\ mortality=%5.3f ActualMortality=%6.4f \n",
                                        i,current_size, Mort1[i], DeathRate);
fFile.Write(str, str.GetLength());
}
```

Using our code for various sizes of populations we transferred some tables in Excel Worksheets to derive conclusions about the impact of stochasticity on the dynamics of ageing, (from what sizes of population we observe differences between theoretical and actual mortality). We present some of these examples in the plots of the figure 3.17.

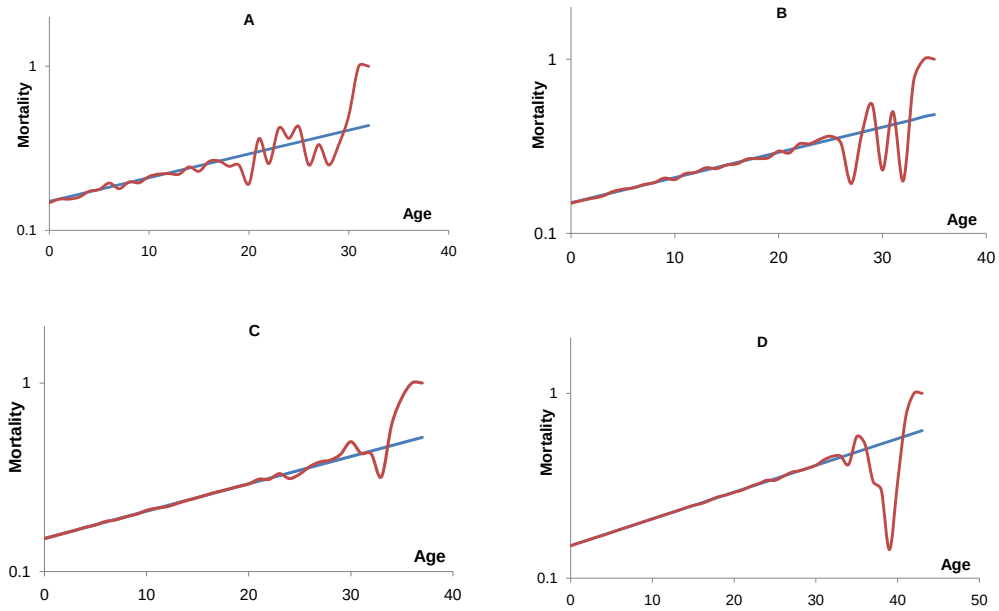


Figure 3.17: Theoritical mortality (blue line) and actual mortality (red curve) of a population with initial mortality rate $m_0 = 0.15$, mortality coefficient $\tau = 30$ and initial sizes **A:** 10000, **B:** 100000, **C:** 1000000 and **D:** 10000000 individuals.

In figure 3.17 we have consider populations with initial mortality rate $m_0 = 0.15$ and mortality coefficient $\tau = 30$. We assumed that the initial size is **A:** 10000, **B:** 100000, **C:** 1000000 and **D:** 10000000 individuals respectively. The plots of figure 3.17, indicate that from some age the actual mortality declines from exponential growth (theoritical mortality) and create some fluctuations. By the algorithm which takes into account the stochasticity, that we have made using C^{++}, we imply that the fluctuations begin when a small subset of people of each population is remain alive. For figure 3.17 A, we have that the fluctuations begins at age 18 where there are 175 individuals alive. For 3.17 B the fluctuations starts after the age of 25 years where 133 individuals are still alive. Also, for figure 3.17 C, the deviation from exponential growth observed after the age of 30 where there are 129 alive individuals and for figure 3.17 D, after the age of 34 where only 131 people are still alive from the huge population of 10 million people.

As a consequence, the stochasticity can explain the deviations from exponential growth at advanced ages. From the above examples, we imply that, for huge differences between the initial sizes of the populations the fluctuations start to observed at similar period each time, when almost less than 150-180 people are still alive.

3.5 Fitting the stochastic model to the mortality data

For real population data we can make similar observations with the figure 3.17 but the fluctuations on the mortality curve are exhibit at advanced ages of human life (i.e. after the age of 100 years). An example with real data is figure 3.13 which are the mortality data for the population of Sweden for 2007 and the focus at advanced ages of them in figure 3.15.

To study this part of human mortality we need to take into account the stochasticity on the dynamics of ageing to fit the data. Using our C^{++} code we have made different simulations with different set of random numbers to derive some fits for the fluctuations of figure 3.15. Some of these simulations are shown in figure 3.18.

The red, purple and green curves in figure 3.18 shows actual mortality due stochasticity which are taken asuuming different sets of random numbers. Some of these simulations can fit the mortality data (blue curve) well, at advanced ages.

From Human Mortality Database [13], we take the numbers of deaths for each age for the year 2007. From that numbers we can calculate and plot the mortality at advanced ages. We observe different fluctuations at advanced ages, so some values of the death rates from [13] might be wrong. This result can explain the two rates for the ages 108 and 109 which have values more than 1.

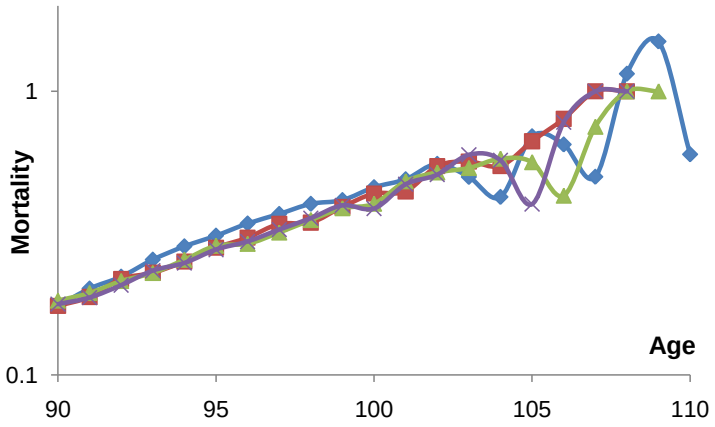


Figure 3.18: The blue curve is the mortality for advanced ages of Swedish population for the year 2007. The red, purple and green curves shows actual mortality due stochasticity which explain the deviation from exponential growth. Some simulations of stochasticity can fit the data well.

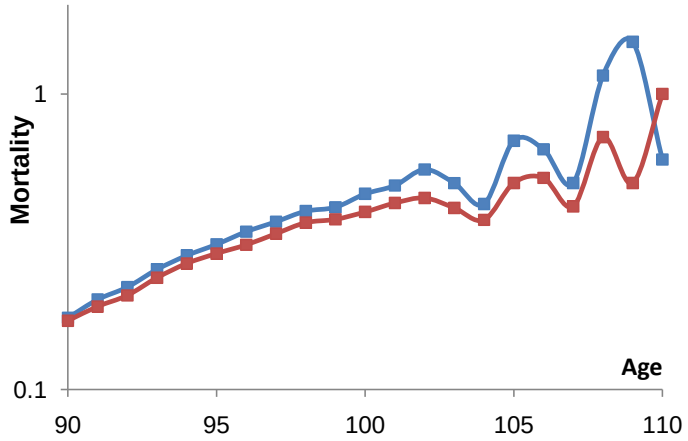


Figure 3.19: The blue curve shows the death rates and the red curve the calculated mortality (with known number of deaths for each age) for advanced ages of Swedish population for the year 2007. The data for death rates and number of deaths are taken from Human Mortality Database [13]. Some values of the death rates might be wrong (where the mortality is more than one), therefore we can assume that the red curve is the correct for the real data of Sweden.

Chapter 4

Conclusion

In this paper we have studied the dynamics of mortality for human populations. We have proposed a mathematical model that describes the change of the mortality rate over time (age). The model we have used, which is known as Gompertz model is the exponential function

$$m_i = m_0 e^{i/\tau}. \tag{4.1}$$

As we have seen, the exponent describes the behaviour of the mortality at the part after sexual maturity which referred as ageing. At the interval of ageing the exponent fits the mortality data in a straight line.

Furthermore we have assumed that the difference between the actual data and this exponent is explained by heterogeneity of the population. We have checked what kind of differences between exponential ageing dynamics and total ageing dynamics of heterogeneous population can be observed for a simplest case when the population consists only of two subpopulations each ageing exponentially with slightly different mortality parameters (initial mortality rate, mortality coefficient and initial size of each subpopulation). This approach can be used to consider the effect of each category of people on the dynamics of overall mortality rate. The difference on the ageing dynamics for each cohort of humans can be taken into account, by the hypothesis of heterogeneity of the population.

Moreover we have seen that at advanced ages of ageing the mortality curve exhibit some deviations from the exponential growth. Then, the exponential function which proposed by Gompertz fail to describe the behaviour in mortality of populations at advanced ages. Therefore we have assumed the stochasticity of ageing to explain a decline, a plateau or some fluctuations which are observed at intermediate ages.

Generally, we have examined the behaviour of the total mortality curve of a human population. The curve of total mortality indicates how many people are dying in the particular population each year, from childhood to the sexual maturity, where in this period some modulating is produced, the period of ageing where the mortality rates increases exponentially (Gompertz function) and advanced ages (after 80-85 years) where a small subset of people is still alive and the mortality curve produces

some fluctuations. Thus a general plot of the mortality rate for a human population is like the following figure.

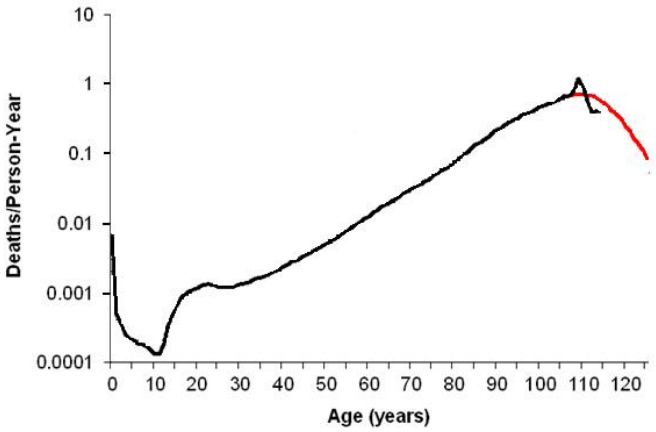


Figure 4.1: General case of plot for the mortality rates of a human population. At the initial stages of life, there are some modulations, at the part of ageing the rates are fit in a straight line and at more advanced ages (after 100 years), there is a deviation from the exponential growth (fluctuations). The red line indicates that there is a decline in mortality at ages after 105, and that a quadratic curve can fit the data better at these ages.

In this study we have derived numerical results for both parts of our research. Firstly, using the hypothesis of heterogeneity, we derived an expression for the total mortality of the entire population depending on the parameters of the subpopulations. We have made conclusions for the effects of the total mortality rate on the parameters of the subpopulations and we have presented the results throught random examples with arbitrary values of the parameters. Also, we have used the model for the total mortality rate, to fit real mortality data of two populations (Swedish for the year 2007 and United States population for the year 2002). Furthermore, we have consider a stochastic model of ageing to derive results about the behaviour of the mortality curve at advanced ages.

From this study we conclude that the pecularities at initial stages of human life can be explained by the hypothesis of heterogeneity, (a human population consists different subpopulations) and the pecularities at advanced ages can be explained by the consideration of stochasticity (at advanced ages few people are still alive). Further research can be done for a combination of the two hypotheses. Moreover, we can say that the quatratic curve which is shown in figures 4.1 and 1.2, can't fit the data at advanced ages because we observe fluctuations and not only a decline. Therefore, a stochastic model fits the data at these ages.

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