Chapter

Mortality Analysis with a Life Table

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Abstract

This paper presents the basic features of mortality analysis using period life tables. While life table construction is outside the aims of this paper, the elements analyzed are the life expectancy at birth, probabilities of death, death, and survival curves. Therefore, an attempt is made here to present an overall picture of the study of the mortality phenomenon. However, due to the multitude of different approaches, this picture will be short and comprehensive, failing to cover all aspects of the phenomenon and the entire literature in a limited space. All modes of analysis will be accompanied by corresponding examples, which will assist the researcher in a more complete understanding of the analytical methods presented. The epilogue summarizes the analytical scheme and briefly mentions new research efforts that may occur in the future.

Keywords: mortality, life expectancy, probabilities of death, death curve, survival curve, dispersion measures, gini coefficient, e-dagger, a-dagger

1. Introduction

The mortality patterns in a population result from very complex processes. Of course, everyone is subject to the risk of death; that is why people die at different ages. However, this risk varies according to gender, age, and other conditions and situations. In other words, mortality depends on a series of biological and environmental factors, rules, values, standards of living, and lifestyles, and it is directly connected with the socio-economic situation and the health support system in a population.

This paper aims to demonstrate the major aspects of mortality analysis in a population based on the well-known life tables. In this context, a brief description of the life tables and their basic elements for the analysis will be given in the introductory section. All these elements will be presented later in the text, in such a way that the reader will develop a comprehensive picture of the analysis of the phenomenon. Note, of course, that this is a challenging task, as hundreds if not thousands of papers about mortality have been published. Naturally, it is impossible to cover all of them in a paper of limited size. On the contrary, a brief but at the same time comprehensive approach to the phenomenon is presented here, clearly emphasizing that its complete coverage would require the size of a volume or even more.

1.1 The analytical framework

After the notorious epidemic of the Black Death hit London, the Bills of Mortality were created during the outbreaks of the plague to record the thousands of victims. In

1662, John Graunt tried to address several questions about the numbers of deaths, survival health, sex ratio, family, population age structure and growth, etc. (see at http://www.edste-phan.org/Graunt/bills.html), forming in that way a framework for the modern demography and mortality statistics (See [1]). The next significant contribution to the field was made by Edmond Haley in [2], the famous astronomer who studied data from the Wroclaw (Breslau of Hamburg Empire) by further developing the famous life table. Since then, life tables have been improved significantly, and they effectively and accurately describe the mortality status in a population (see ([3], pp. 38–91) and [4]).

A life table summarizes the age-specific mortality rates operating on an actual or hypothetical cohort of individuals, and it can be produced in various ways. Taking into consideration that the scope of this paper is not to describe the assumptions needed and the procedures used for its calculation, a period life table is organized in the following columns (for the calculations, see [3]):

P_x: the midyear population of age x.

D_x: the number of births observed in a population.

a_x: the proportion of years lived by those who have died in an age interval x and x + 1.

m_x: the age-specific mortality rates.

q_x: the probability that a person living at the age x will die before age x + 1.

l_x: the number of people surviving at the exact age x. For x = 0 (infants), l_0 is usually a power of 10 (100.000, 1.000.000, etc.), and it is called the "radix" of the life table.

d_x: The number of deaths in the age interval x to x + 1.

L_x: the total number of years lived by people in the age group x to x + 1.

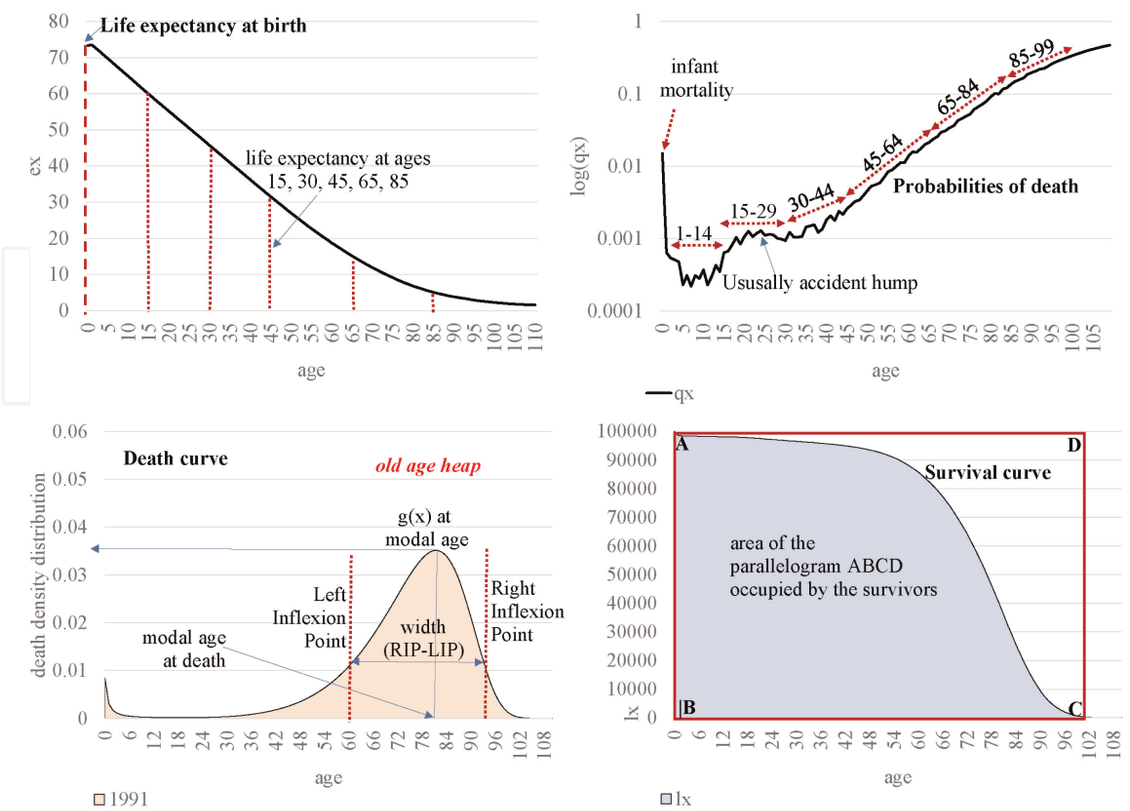

Figure 1.
The most essential elements of a life table.

$\mathbf{T_x}$: total number of years lived by those alive at age x and after that.

$\mathbf{e_x}$: the life expectancy at age x.

Note that a life table can appear in its full form, consisting of age classes of 1 year long, or in its abridged form, consisting of age classes of several years long. Then, a life table often contains unapparent information. On the contrary, some further processing of the data in the table is needed so that they can be displayed effectively and finally describe the prevailing mortality profile. **Figure 1** depicts the most essential elements of this information.

During the life table analysis, four curves mainly arise: life expectancy at birth, probabilities of death, death curve, and survival curve. As seen in **Figure 1**, an age-specific component always affects their levels. Life expectancy at birth and the survival curve decreases with age. On the contrary, the death probabilities are high for infants (aged less than a year old) and remain low in childhood to increase rapidly during adolescence and early adulthood. Then they increase continuously. The death curve is more complex as it presents a particular formation at old ages, the well-known "old-age heap". A brief description of the characteristics of this curve follows.

2. Life expectancy at birth

An example of the temporal trends of life expectancy at birth is portrayed in **Figure 2** (life expectancy at birth) and **Figure 3** (Life expectancy at the age of 65) for the population of Greece. Several conclusions can be drawn from **Figure 2**, while analogous ones can be drawn from **Figure 3**. The most important of them follow:

a. Life expectancy at birth e0, i.e. the mean duration of time a liveborn is expected to live if throughout its life mortality will have the same pattern seen in a year, increases in both genders. However, a more precise analysis revealed that this occurs at different genders' paces (see [5]).

b. Females live longer than males. In **Figure 2**, the term "gender gap" represents the difference in female and male life expectancy. In **Figure 2**, this gap is not constant and tends to increase until a one-time point and to decrease afterwards. That is an expected situation in all human populations. If the

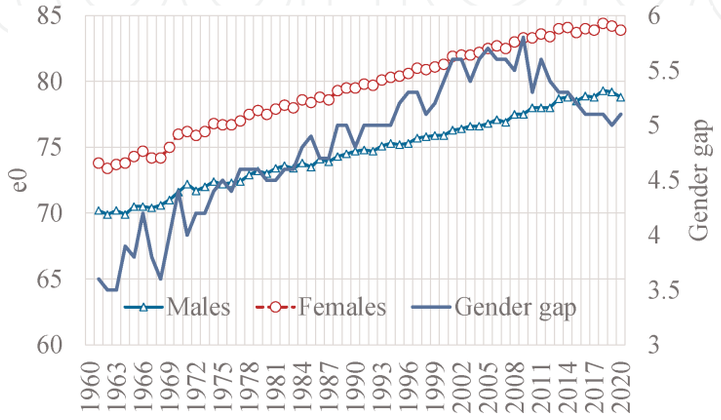

Figure 2.
Life expectancy at birth and gender gap. Greece, 1961–2020. Data source: EUROSTAT DATABASE (https://ec.europa.eu/eurostat/data/database). Own calculations.

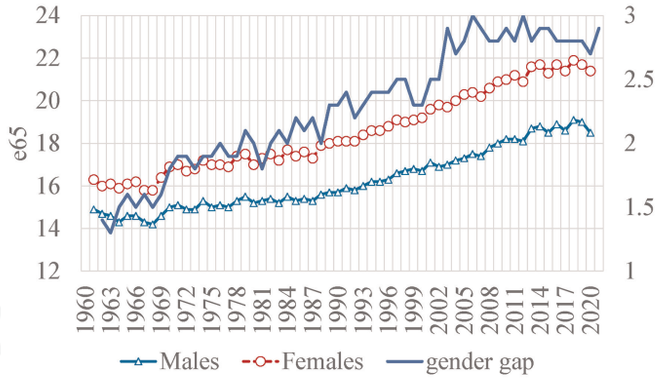

Figure 3.
Life expectancy at the age of 65 and the relevant gender gap. Greece, 1961–2020. Data source: EUROSTAT DATABASE (https://ec.europa.eu/eurostat/data/database). Own calculations.

opposite happens, i.e. males' e0 is larger than females' e0, after checking the data, one should suspect that there are problems in the population's standard of living, health and health care, conditions during childbirth, and the perinatal period. In any case, in Europe, the gender gap has varied a lot recently (3.2 years in the Netherlands to 9.9 years in Latvia), which is evidence of male excess mortality, a finding confirmed since the middle of the eighteenth century when the first life tables were constructed separately for each gender [6]. In Western Europe, female longevity has been higher than male longevity at least since 1751 in Sweden, 1835 in Denmark, and 1841 in England and Wales [7]. Genetic, anatomic, and physiological factors are responsible for the female survival advantage, known—besides humans—in most animal species. Despite that, women experience higher rates of disability and poorer health than men, the well-known male-female health-survival paradox (see [8]).

Of course, life expectancy at birth (e0) is an age-standardized measure of mortality, and thus its interpretation is straightforward (see [9]). However, when comparing the two genders or populations over time, it must be seriously taken into consideration that any e0 differences result from the differential mortality throughout the human life span. Therefore, *"a change in life expectancy (at any age) does not necessarily mean that mortality rates change in the same magnitude, or even in the same direction at all ages,"* as Arriaga [10] notices for the e0 changes between two-time points. An example of this situation comes from Canada. When Auger et al. [11] studied the e0 differences between Quebec and the rest of Canada, they demonstrated that almost equal life expectancies at birth conceal excessive mortality inequality.

Then, the question is how to solve this problem, i.e., when comparing life expectancies at birth, how to consider all the differences in mortality patterns. For this reason, many methods have been developed like those of Andreev [12], Pollard [13, 14], Pressat [15], Arriaga [10, 16], and [17]; see also [18]). The Arriaga method [10, 16] will be presented here, as it is relatively simple and straightforward.

According to this method, the e0 differences between two-time points are coming under the effects of two factors. "*The direct effect on life expectancy is due to the change in life years within a particular age group as a consequence of the mortality change in that age group*". The indirect effect *"consists of the number of life years added to a given life expectancy because the mortality change within (and only within) a specific age group will*

produce a change in the number of survivors at the end of the age interval". Another effect comes from the interaction between the exclusive effect of each age group and the overall effect.

The direct effect, named ${}_iDE_x$, is calculated as:

$$ {}_iDE_x = \frac{l_x^t}{l_a^t}\left(\frac{T_x^{t+n} - T_{x+i}^{t+n}}{l_x^{t+n}} - \frac{T_x^t - T_{x+i}^t}{l_x^t}\right) \tag{1}$$

The indirect effect, named ${}_iIE_x$, is given by:

$$ {}_iIE_x = \frac{T_{x+i}^t}{l_a^t}\left(\frac{l_x^t l_{x+i}^{t+n}}{l_{x+i}^t l_x^{t+n}} - 1\right) \tag{2}$$

The interaction ${}_iI_x$ is given by:

$$ iI_x = {}_iOE_x - {}_iIE_x \tag{3}$$

and

$$ {}_iOE_x = \frac{T_{x+i}^{t+n}}{l_a^t}\left(\frac{l_x^t}{l_x^{t+n}} - \frac{l_{x+i}^t}{l_{x+1}^t}\right) \tag{4}$$

In these equations, the terms x, $x + i$ refer to age groups, t and $t + n$ correspond to time points (years), l to the number of survivors at an exact age, and T the number of person-years lived by the members of a population beyond that age. The algebraic sum of these effects gives the overall e0 difference.

A paradigm of this method follows in **Figure 4**. If women's mortality per age or age group is lower, the contribution to mortality differences is positive. The opposite happens when the mortality rates are higher in them.

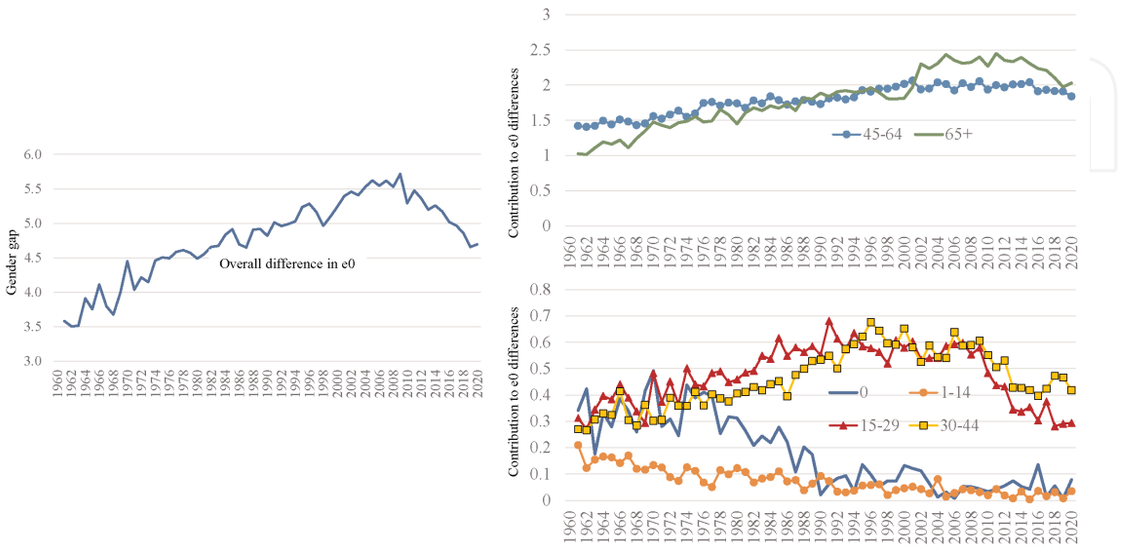

Figure 4.
Gender differences in e0 (females-males) in large age groups in Greece, 1961–2020. Data source: EUROSTAT DATABASE (https://ec.europa.eu/eurostat/data/database). Own calculations.

In this figure, it is evident that old age (65+) and late adulthood (45–64 years) mortality govern the gender differences in this case, while the other ages play a smaller role. Note the small contribution of ages 1–14 because of the low-mortality rates and also that the effects are not constant over time.

Up to this point, the life expectancy at birth and Arriaga's decomposition procedure were presented. The next step in mortality analysis is to check the probabilities of death and their characteristics.

3. Probabilities of death

This paper's introductory section has already given some information about the changes in the probabilities of death that occur throughout the human life span. Infant mortality is high, and afterwards, the probabilities of death become very low in childhood. A sharp increase occurs in the juvenile phase of the human life cycle and early maturity. It is the accident hump (see [19]) due to traffic accidents and lifestyle reasons (use of drugs, alcohol consumption, etc.). Some diseases may also play a minor role. After this hump, mortality constantly increases.

That is portrayed in **Figure 5**, which is evident that at almost all ages, the probabilities of death become smaller over time in both genders. Note that the phenomenon of "mortality rotation" is observed in many developed countries, as over time, a decline in mortality occurs in the younger ages, while an acceleration occurs in the older ones. This rotation may also occur in developing countries as they attain high life expectancies [20].

An open question remains: How can we describe the mortality curve or smooth it many times? One solution is to apply the Heligman-Pollard method [21] as modified by Kostaki [22]. That is a parametric model that can describe relatively accurately the age changes in mortality. Also, all of its parameters have a demographic interpretation. A shortcoming is the high number of parameters used, and the deviations that may occur when applying the model to modern empirical data.

The odds of mortality according to the Heligman-Pollard formula (**Figure 6**, [21]) can be given as:

$$\frac{q_x}{p_x} = A^{(x+B)^C} + De^{-E(lnx-lnF)^2} + GH^x \tag{5}$$

where x is the age and A, B, C, D, E, F, G, and H are the model parameters. The odds of mortality at age x are the sum of three components.

1st component: It describes the fall in mortality during early childhood as the child adapts to its new environment and gains immunity from diseases from the outside world. Parameters: A, B, and C.

A: measures the level of mortality.

C: measures the rate of mortality decline in childhood.

B: represents the location of infant mortality within the range (q1, ½), but in practice it is close to 0 in modern times.

2nd component: It describes the accident hump between ages 10 and 40, appearing either as a distinct hump in the mortality curve or at least as a flattening out of the mortality rates. Parameters: D, E, and F

F: the location of the accident hump,

E: its spread.

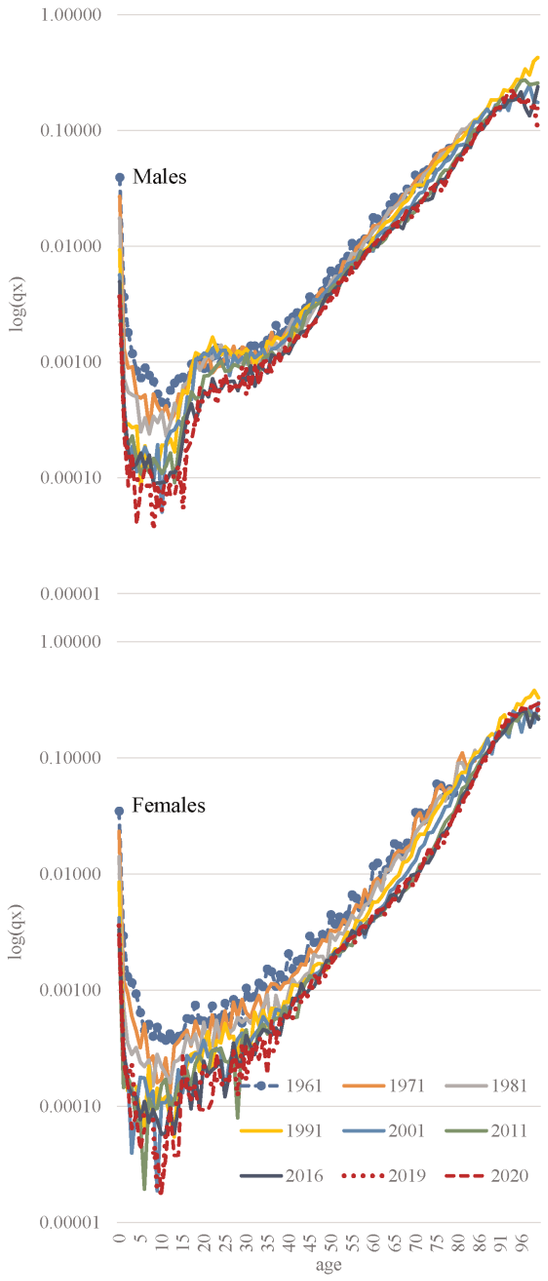

Figure 5.
Probabilities of death by age and gender in Greece, 1961–2020. Data source: EUROSTAT DATABASE (https://ec.europa.eu/eurostat/data/database). Own calculations.

D: its severity.

3rd component: a Gompertz [23–25] exponential, representing the aging or the deterioration of the body. Parameters: G and H.

G: the base level of senescent morality.

H: the rate of increase of that mortality.

Kostaki [22] modified this procedure as follows:

$$\frac{q_x}{p_x} = \begin{cases} A^{(x+B)^C} + De^{-E_1(lnx-lnF)^2} + GH^x, for\ x \le F \\ A^{(x+B)^C} + De^{-E_2(lnx-lnF)^2} + GH^x, for\ x > F \end{cases} \quad (6)$$

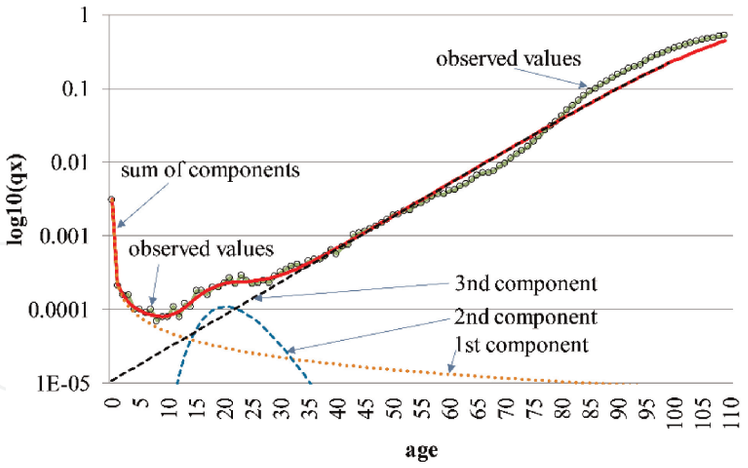

Figure 6.
The probabilities of death [log10(qx)] and the Heligman-Pollard formula. Greece, females, 2010–2013. Own elaboration. Data Source: Human Mortality Database. www.mortality.org.

The formulas described above differ in the parameter E, which has been replaced with the relevant parameters E1 and E2, representing the spread of the accident hump to the left and right of its top (its location denoted by the parameter F), respectively.

Because of the deviations seen in **Figure 6**, Zafeiris and Kostaki [19] combined the modified procedure with three successive cubic splines of the form:

$$\hat{q}_i = \hat{q}_x + a_k(x_i - x) + b_k(x_i - x)^2 + c_k(x_i - x)^3 \tag{7}$$

where k = 1 ... 3 the number of splines, x is the age and $\hat{q_x}$ is the fitted value at the beginning of the spline and x_i stands for a specific age within that spline. Thus, the difference between x_i and x represents a particular point in the set of points included in the spline. The end of each spline is the beginning of the next one, while the knots are dynamically chosen to achieve the best fit of the process.

However, this is a very complex problem in the analysis of mortality, and several scholars have either proposed new procedures or modified existing ones to smooth the mortality curves or to express a law for mortality. Some examples follow.

Abraham De Moivre [26] proposed that the survival function changes linearly and the force of mortality is:

$$\mu_x = \frac{1}{\omega - x} \tag{8}$$

The probability of survival is:

$$xp_0 = \left(1 - \frac{x}{\omega}\right) \tag{9}$$

ω is the maximum age a person can reach in a population, thought those days could be 86 years.

Babbage [27] also proposed a quadratic formula for survival probabilities. The most famous approach is that of Gobertz [23–25], as mentioned above. According to

him [25] "*... the one, chance, without previous disposition to death or deterioration; the other, a deterioration, or an increased inability to withstand destruction. If, for instance, there be a number of diseases to which the young and old were equally liable, and likewise which should be equally destructive whether the patient be young or old, it is evident that the deaths among the young and old by such diseases would be exactly in proportion of the number of young to the old; provided those numbers were sufficiently great for chance to have its play; and the intensity of mortality might then be said to be constant; and were there 130 other diseases but such as those, life of all ages that would be of equal value, and the number of living and dying from a certain number living at a given earlier age, would decrease in geometrical progression, as the age increased by equal intervals of time ...* ".

Thus, the force of mortality increases geometrically as:

$$\mu_x = Bc^x \tag{10}$$

where x is the age and B a constant. Note that this is a mathematical formula described differently in the literature.

Makeham [28] modified the Gobertz law by adding a constant element as:

$$\mu_x = A + Bc^x \tag{11}$$

which was finalized as:

$$\mu_x = A + Hx + Bc^x \tag{12}$$

Weibull [29] proposed that the force of mortality is:

$$\mu_x = Ax^B \tag{13}$$

where x is the age and A and B parameters.

Siler [30, 31] modified the Gompertz model to include a negative Gompertz function and the Gompertz-Makeham-method, proposing a three-component model. The first for the prematurity period, including a novel exponentially decreased hazard. The second represents a constant hazard, dominant during maturity. The third is a conventional Gompertz hazard, dominant during senescence.

Delaportas et al. [32] used a parametric model of Heligman-Pollard and applied a Monte Carlo simulation to process the results further. Sharrow et al. [33] also used Bayesian methods along with the Heligman-Pollard model to investigate mortality in the rural population in South Africa. Peristera and Kostaki [34] used the logistic model (see [35]); others used P-splines [36], etc. That is a highly complex topic, and many scholars have proposed several other methods, which are impossible to present here, either because of their complexity or because of the length limitation of this chapter.

The next step in mortality analysis is to examine the life table's death and survival curves and their variability, along with several measures needed for this purpose.

4. The death curve and the survival curve

The life tables' death curve is always bimodal. The first mode corresponds to infant mortality, and the second mode corresponds to the old-age heap, a death aggregation in the older ages of the human life span, i.e. the old-age mortality. In the past, this high

infant mortality resulted in a significant excess of deaths compared to the other ages, as portrayed in **Figure 7**. That phenomenon (see also [37]) reversed over time in the low-mortality countries, and most of the deaths occur in the old-age heap while the number of infant deaths is minimal. The question arises is how to describe the mortality curve, especially in modern times.

One simple but incomplete way to answer this question is by calculating the modal age at death. Canudas-Romo [38] gives the following formula:

$$Md(t) = x + \frac{[0.5 - l(x,t)]}{[l(x+1,t) - l(x,t)]} \tag{14}$$

where t is the year, x and x + 1 are the interval ages at which the number of survivors equals 50%, and l represents the number of survivors. Such a calculation is affected by infant, child, and reproductive-adult mortality and thus fails to interpret old-age mortality accurately.

A solution to this problem could be the modal age at death, which may portray mortality changes more accurately, as longevity in modern low-mortality countries comes after the improvements in old-age mortality (see [39]). The modal age at death, i.e. the age at which most deaths occur at the old-age heap, is given [38, 40, 41] by:

$$M(t) = x + \frac{[d(x,t) - d(x-1,t)]}{[d(x,t) - d(x-1,t)] + [d(x,t) - d(x+1,t)]} \tag{15}$$

where t is the year, x is the age where the maximum number of deaths occurs (except for infant mortality), and d represents the number of deaths.

The Kannisto C-Family indicators are also quite helpful. The C-family indicators C10, C25, and C50, respectively, are the narrowest age intervals in which 10, 25, and 50% of all deaths occur. The procedure for the calculations is the one described in

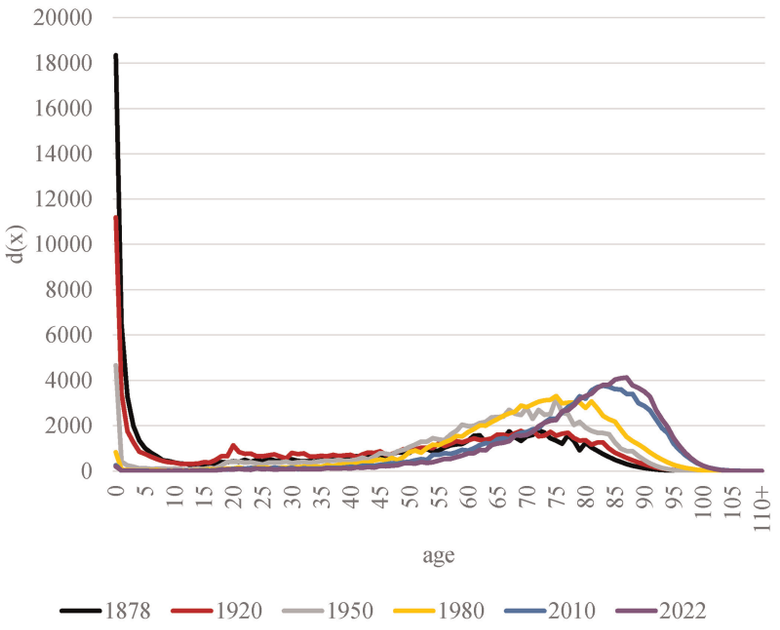

Figure 7.
The Life Tables' death curve (dx). Finland. Males. Own elaboration. Data Source: Human Mortality Database. www.mortality.org.

Kannisto's paper [42]. Thus, we may know the width of the old-age heap, even approximately.

Another method can be proposed here, based on dynamic measurement of this width and other death curve characteristics. First, the death density distribution is calculated as:

$$g_{(x)} = m_{(x)} EXP\left(-\sum_{x=0}^{x} m_x\right) \tag{16}$$

Then, it is normalized to sum one so the findings can be comparable among all populations. The formula for this is:

$$g_{(x,n)} = x_{(x)} / \sum_{x=0}^{\omega} g_x \tag{17}$$

where x and ω are the first and the last ages of a life table.

Afterwards, the following line is fitted on the data (for the proof and the relevant calculations, see: [43–46]):

$$g(x) = k\ (l + (c-1)(bx)^c)\left(x^{-3/2}\, e^{-\frac{(l-(bx)^c)^2}{2x}}\right) \tag{18}$$

The almost perfectly smoothed death density distribution serves for calculating the following:

i. Modal age at death

ii. The old-age death heap's height or mode: corresponds to the g(x) value at the modal age at death (see [5]).

i. The width of the old-age heap. After estimating the formula's derivatives above, this procedure identifies this curve's left and right inflection points (see **Figure 8**). Note that in mathematical terms, an inflection point corresponds to a smooth curve point where the curvature changes sign. The first derivative is called the "speed of the death distribution". The second derivative will be the rate of change of the speed of death distribution, called "acceleration". The second derivative is 0 in the left and right inflection points. The age distance between the left and the right inflection points (RIP-LIP) will estimate the width of the mortality curve at the old-age heap (for the whole procedure, see [47]).

One can apply the g(x) formula to ages with two decimal precisions to avoid mathematics for the relevant calculations. A paradigm of the application not discussed in detail here is seen in **Figure 9**. One can see the increase in the modal age and mode described previously over time, along with the decrease in the width of the old-age heap.

The survival curve is the direct product of the death curve, and many scholars have tried to model both of them (see, for example, [35, 48–52], etc.). Cheung et al. [53] described three properties of the survival curve:

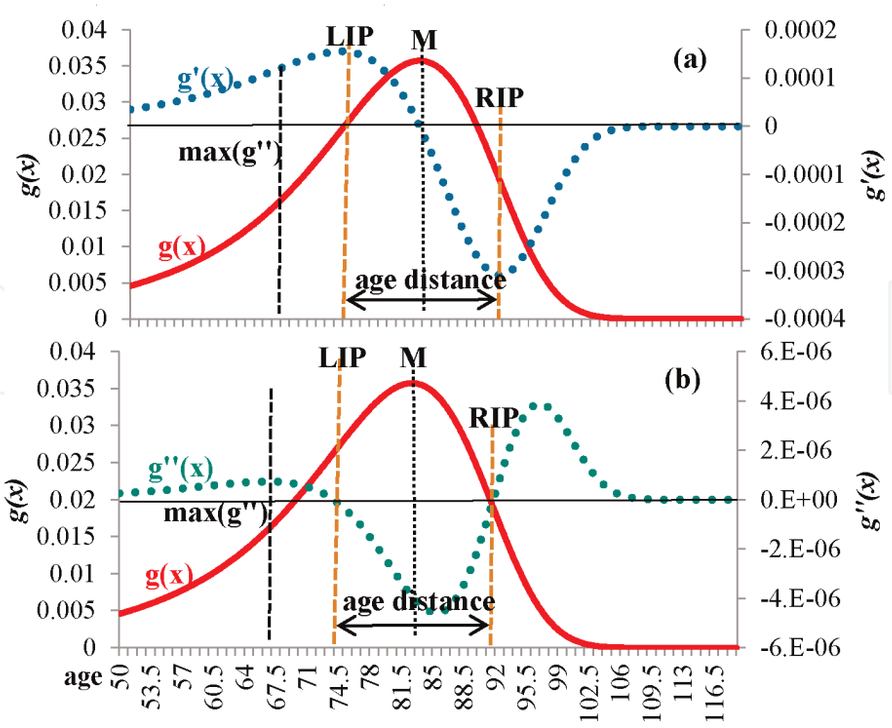

Figure 8.
Left and right inflection points of the death density distribution. Source: Zafeiris and Skiadas [47].

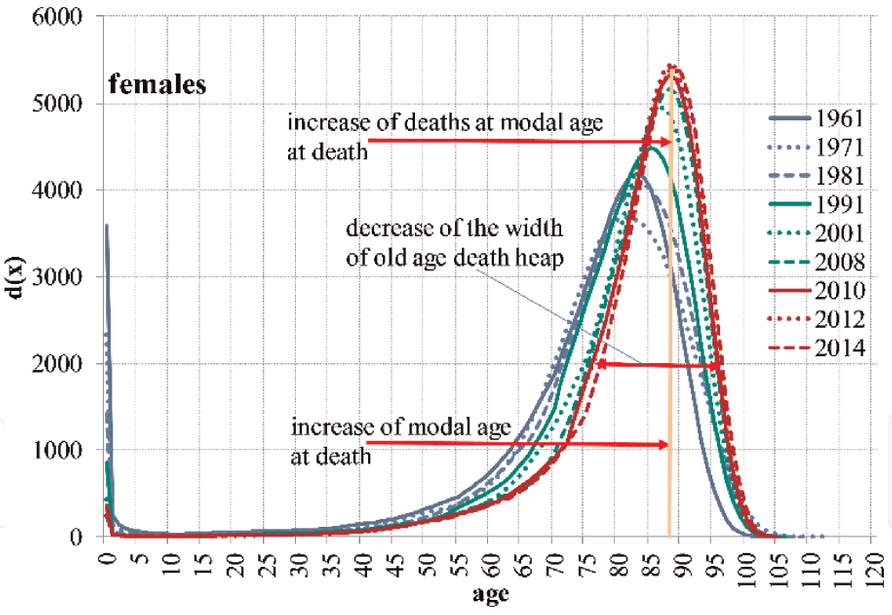

Figure 9.
The d(x) distribution in selected years. Females. Greece. Source: Zafeiris and Kostaki [19].

i. Horizontalization, i.e. "*how long a cohort and how many survivors can live before aging related deaths decrease the proportion of survivors*".

ii. Verticalization, i.e., the amount of concentration of deaths around the modal age at death.

iii. Longevity extension. "*corresponds to how far the highest normal life durations can exceed*".

Many indicators, including those described previously for the death curve, can be used for the study of survival curves; however, the published literature is once again enormous and in a limited space paper, one cannot entirely refer to it (some examples are: [42, 51, 52, 54]; and [55]).

Suppose any of the developed models or approaches is applied. In that case, the temporal evolution of survival curves indicates the rectangularization process, as seen clearly in **Figure 10**: over time, the curves become more rectangular. In other words, as life expectancy increases, the survival curve in a life table tends to become more "steep" (i.e., declines very steeply) at older ages. That occurs because as longevity increases, deaths accumulate in older ages (the old-age heap). In that way, the diversity of the life table decreases, and e0 has a strong negative correlation with this diversity.

However, as Shkolnikov et al. [56] note, in some countries after the 1970s, while life expectancy continues to rise, the diversity in the age of death remains stable or increases (see also [57]). This phenomenon is complex and—among other things—may be because mortality at younger ages has already decreased a lot, and consequently, it is challenging to decline further. Alternatively, deaths are "expanding" at older ages. As Canudas-Romo [40] notes, when mortality is "compressed" (mortality compression), more and more people die at the same ages, and diversity decreases. However, mortality may shift to older ages (the shifting mortality hypothesis), as the shape of the death curve does not change over time but "shifts" at these ages, a phenomenon that can be described by the modal age of death (modal age at death). Many measurements have been developed to evaluate the variation in ages of death. Among them are the Gini coefficient [58, 59], the standard deviation of the ages of death, and the coefficient of variation (see Edwards and Tuljapurkar [60] and others).

As a measure of the diversity of the ages of death, the interquartile range [52] as well as the so-called "lifetime losses", known in the literature as the e-dagger (e†, [61, 62]), are well known. The characteristics of these two measures and another one,

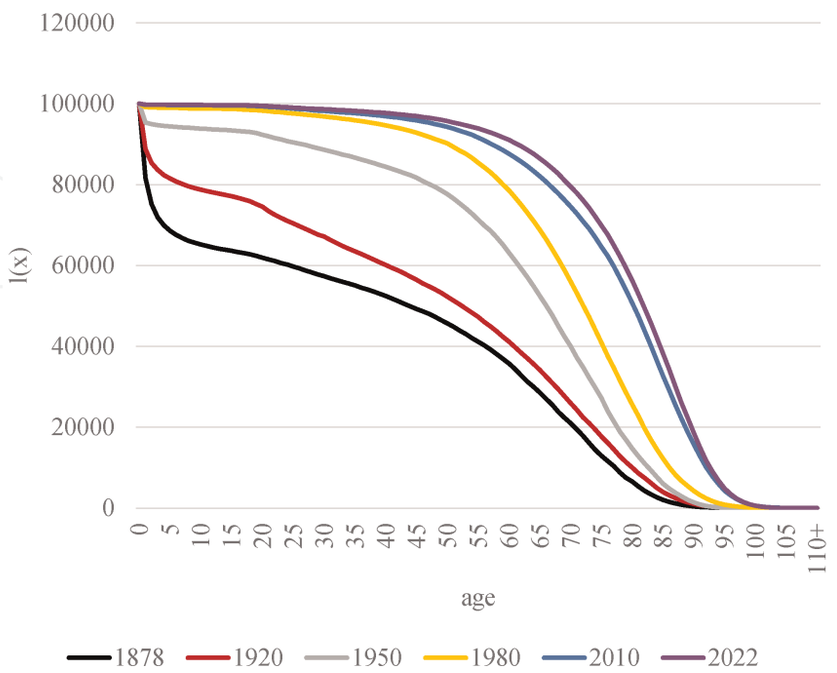

Figure 10.
The Life Tables' survival curve (lx). Finland. Males. Own elaboration. Data Source: Human Mortality Database. www.mortality.org.

the α-dagger (α†, [63]), which estimates the age at which early and late deaths are separated, will be presented in the following paragraphs.

The interquartile range [52] is:

$$IQR = Q_{25} - Q_{75} \tag{19}$$

The Q25 and Q75 points correspond to the ages where the survival curve lx bears the values 0.25 and 0.75, respectively. However, as Shkolnikov et al. [58] noted, the interquartile range does not consider the changes observed between quartiles, limiting its analytic power.

That is not a problem of e† [57]. As said above, this measurement concerns "lifetime losses" and goes back to the time of Keyfitz [61]. According to Vaupel and Canudas-Romo [62], e† corresponds to the average number of person-years lost due to deaths in a life table. According to Shkolnikov and Andreev [64], the e-dagger is calculated as:

$$e_x^{\dagger} = \frac{1}{l_x} * \sum_{y=x}^{\omega-1} \lfloor d_x \left(e_{y+1} - a_y\right\rfloor + \frac{l_\omega}{2\lambda_x} e_\omega \tag{20}$$

The Keyfitz [61] entropy is:

$$H_x \cong \frac{e_x^{\dagger}}{e_x} \tag{21}$$

where x and ω are the ages, e the life expectancy or life losses, l the survivors at the beginning of each age x (or ω), and α_x, the percentage of person-years lived at an age.

The well known from Physics entropy, as a measure of the disorder of a system, in demography, is used to describe changes in the average life span associated with changes in the age-specific mortality pattern (see [65]). Taking into account the above two equations, it is evident that the entropy Hx of a life table is the proportional expression of e† to life expectancy. e† by quantifying average life expectancy losses at birth measures the variation in age at death as the weighted average of differences between individuals. Thus, it studies the variation in life expectancy losses between countries either longitudinally, over time, or cross-sectionally. Vaupel et al. [66] found that an increase in average life span was accompanied by a decrease in lifespan inequalities between individuals, i.e. e†.

Moreover, as observed by Fernadez and Beltrán-Sánchez [65] e† is a necessary parameter to calculate an age cutoff α† (α-dagger), which separates early from late deaths (see [63]). If the entropy of the survival matrix is less than unity, the age limit α† is given by the formula:

$$e^{\dagger}(\alpha) = \mathrm{e(a)} * (1 - \mathrm{H(a)}) \tag{22}$$

where α is the age limit and H is the system's entropy at that age. The age α†, that is, is calculated by linear interpolation between two known ages of the life table where the difference between the two terms of the above equation becomes zero. Of course, as Keyfitz [61] said, every death is early. Nevertheless, the importance of separating early from late deaths based on this method is important because, as Vaupel et al. [66] observed, reducing early deaths reduces lifespan diversity, while when it occurs in late

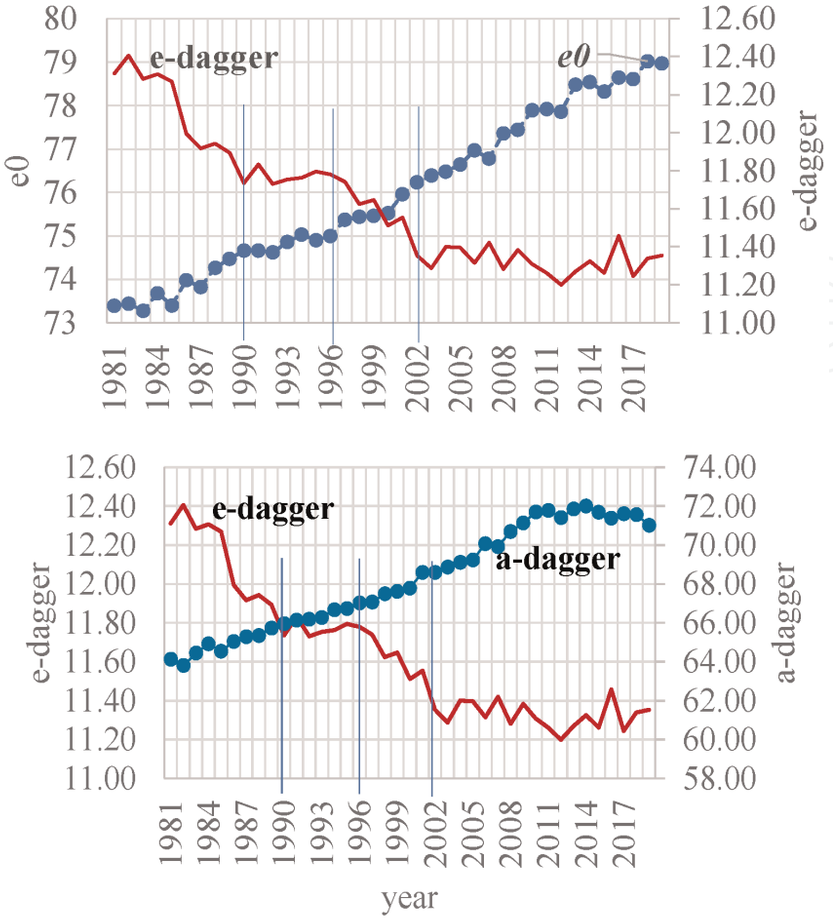

Figure 11.
The Life Tables' survival curve e-dagger and a-dagger. Greece. Males. Own calculations. Data Source: Human Mortality Database. www.mortality.org and EUROSTAT.

ones, it increases it. Deaths are characterized as late or early according to a population's mortality level and in no other way.

e† differences can also be decomposed according to Andreev et al. [18] and Shkolnikov and Andreev [67]. The analysis is based on an algorithm that allows the stepwise decomposition by age at any value of a life table, so that similar to the method of Arriaga [10, 16] described above, the changes in the values of e† are the result of changes in the age-specific mortality pattern between the 2 years under consideration.

An example of this procedure is given in **Figure 11**, where, generally speaking, it is evident that the increase in e0 is accompanied by a decrease in e-dagger and an increase in the a-dagger.

5. Epilogue

The study of mortality through life tables is a challenging venture. Many scholars have published numerous studies to describe this phenomenon and evaluate its changes over time. Naturally, these approaches differ significantly from each other and can often lead to contradictory data.

A severe limitation of mortality analysis is that it requires good-quality data. If this does not exist, indirect but less accurate methods should be used to analyze it. The differences in the calculation methods of the various branches of science dealing with this phenomenon should also be emphasized. Examples of these are formal demography, actuarial science, and paleodemography. Moreover, there is no single way of analysis. All methods have their own advantages and limitations. In this sense, this article is not a mortality analysis manual. It simply suggests some of the dozens of ways this could take place.

Thus, the major elements of life table data used for mortality analysis were briefly described. The first ones are the age-specific mortality rates and the probabilities of death. Their temporal trends over time and the age-specific mortality pattern occurring in a period are the first indications of the development of mortality patterns in a population. The same happens with the probabilities of death. The very high infant mortality in the past gave way to the very low one today in developed countries. The same happens with children's mortality. Mortality in the accident hump is more challenging to predict, as it is connected with lifestyle and infrastructure effects. Mortality tends to increase towards the old-age heap, and the same happens with mortality in the older ages. However, since the time of Gompertz towards the new era, several departures from the relevant law of mortality have created new problems and opportunities for studying the phenomenon.

For this reason, various approaches have been developed today. However, this is an issue that is open to further research. It should not be forgotten that there may be variations in the existing mortality patterns in the future. Indeed, one cannot predict the future accurately. Still, the developments in living standards, the socio-economic status of populations, and medical technology may significantly alter the situation.

On the other hand, one must consider that the existing mortality transition in developed countries came about as a result of limiting infectious diseases, and the leading causes of death became the diseases of human civilization and degenerative diseases. Shockingly, the recent COVID-19 pandemic reminded people that it is a hybris to forget the infectious diseases in our prediction. A similar situation will undoubtedly occur in the future.

For now, life expectancy at birth and other ages, except the period of recent pandemics, continued to increase, but at a slower pace than previously. That is expected because, in low-mortality countries, where life expectancy at every age is already high, any more gains are more difficult to make. However, this is another matter of concern for future mortality trends.

For now, we know that the once bimodal mortality curve turns unimodal in low-mortality countries due to the vast decrease in infant mortality. That gives this unique scheme in the existing death curves, which needs to be described accurately. Some methods were referred to in this paper, but this is still another issue that requires further research. The same happens with the survival curve. Will future deaths "expand" at older ages, or will we see more vertical survival lines? The question remains: how can we describe this phenomenon with precision? Various ways of studying survival or death curves and measures of diversity of these curves have been developed to date. A few have already been mentioned here. Indeed, others will be created in the future that will be flexible enough to describe an existing situation and consider the peculiarities of each human population. That also applies to the entire study of mortality, as it is already apparent from the text that it is a highly complex issue. The way is open to developing an efficient method to accurately describe this phenomenon in the various populations and the inherent diversity. Let us see.

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