

Death Expectancy H_1

An Alternative Measure for Longevity

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Abstract

We introduce death expectancy H_1 , an alternative measure for longevity. It is the age when the cumulative hazard is one, i.e. the age at which an individual could expect to have lived exactly one life, if death were a repeatable event. Standard statistical relationships reveal that this age is reached when the probability of survival is about 36.8%. In the special case of identical mortality rates at all ages, H_1 and life expectancy are equal, but we demonstrate using other mortality laws that this is not true in general. Using data from the Human Mortality Database, we show, for instance, that H_1 is similar to the modal age at death in recent decades and about 5 years higher than life expectancy. We demonstrate that the latter result could be expected in a “true” Gompertz setting. We suggest that H_1 could be used as a dynamic threshold age for the oldest-old.

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1 Introduction

1.1 Background / Motivation

“How long will *I* live?” is a question probably everyone has asked themselves. But nobody has *the* answer. Even the question “How long will *we* live *on average*?” does not have a straightforward answer, even if age-specific mortality does not change in the future. Mean, median and mode are traditional statistical measures of such a central tendency. Applied to mortality, they correspond to life expectancy, the median length of life and the modal age at death. During the past 20 years several new measures were introduced and passionately discussed. Some prominent examples are “tempo adjusted life expectancy” or the cross-sectional average length of life “CAL” (e.g., Barbi et al., 2008; Bongaarts and Feeney, 2002, 2003; Guillot, 2003; Luy, 2006; Vaupel, 2002). Apparently, demographers have not yet found or agreed upon *the* measure to describe the average length of life.

Our contribution will not end the discussion nor is it our aim. Instead, we want to introduce another measure. We think that our new concept *death expectancy*, tentatively denoted by H_1 , addresses a different theoretical dimension than the other concepts, is simple to measure, has interesting implications, and yields insightful empirical results.

1.2 Idea and Notation

We consider a situation in which individuals, like proverbial cats or video game characters, could have more than one life. In this model, which demographers have used to investigate improvements in longevity (Finkelstein, 2005; Schmertmann, 2020; Vaupel and Yashin, 1987), an individual who dies at age x receives *minimal repairs* (Finkelstein, 2005) and is returned to the population to live another life that starts at age x .

In this “revival” model life expectancy e_0 is the average age at which first lives end. Here we address a different question: “At what age can we expect to have used up exactly one life?”. This age can be estimated using the cumulative hazard: The cumulative hazard until time point t has the “nice interpretation as the expected number of deaths in $(0, t]$ per unit at risk.” (Rodríguez (2005), p. 5, see also Schmertmann (2020), p. 498). Thus, the age when the cumulative hazard has a value of one can be interpreted as the age at which an individual can expect to have “used up” exactly one life. Because the cumulative hazard is usually denoted by H , we denote this *death expectancy* by H_1 .¹

¹ H_1 has appeared, under different names, in other formal demographic analyses. For example, Schmertmann (2020) found that it is the age above which deaths would increase if all individuals had two lives instead of one. Wagner (2010) discovered that H_1 is the age at which a mortality decrease would lead to the largest possible increase in life inequality, as measured by e^\dagger .

2 Definition and Estimation of the Cumulative Hazard $H(x)$ and Death Expectancy H_1

Death Expectancy H_1 is the age x , at which the cumulative hazard $H(x) = \int_0^x h(u)du = 1$. Or, “the number of times we would expect (mathematically) to observe failures over a given period, if only the failure event were repeatable” (Cleves et al., 2008, p. 13). This means the age x , which corresponds to a cumulative hazard $H(x) = 1$ is the age at which an individual can expect to have exhausted exactly one life.

Integration, such as in this case of the cumulative hazard from birth until age x , implies infinitesimally small time/age units. Empirical data are necessarily discrete, though. At best, demographers encounter those aggregate level data at a granularity of one age-/calendar-year in the form of period or cohort life tables. The discrete version of the hazard $h(x)$ —demographers tend to use $\mu(x)$ —is usually represented by the central death rate $m(x)$ in life tables. Thus, we could use the cumulative sum of death rates to approximate the cumulative hazard. Knowing that the cumulative hazard can be also expressed by the survival function (e.g., Klein and Moeschberger, 1997):

$$H(x) = -\log S(x) \tag{1}$$

we actually estimate the cumulative hazard by the number of life table survivors, typically denoted by $l(x)$, but here with a radix of 1 instead of the canonical choice of 100,000. Consequently, H_1 corresponds to a survival function value of $S(x) \approx 0.368$.²

For the sake of simplicity we use η for this constant. This means that H_1 is the age x where the cumulative hazard equals 1 or the age x when $\approx 36.8\%$ of the population is left.

It is extremely unlikely that H_1 is observed at an exact integer age. Therefore, we need to estimate a more precise age H_1 numerically. We do this by linear interpolation between the two integer ages surrounding a value of 1 for the cumulative hazard.

3 Analytical Relationships for Parametric Mortality Models

Following Lotka’s (1938, see also Section B, p. 26) advice to cultivate formal and empirical methods side by side, we present first some analytical relationships for H_1 . This will demonstrate, for instance, that life expectancy and death expectancy can be identical but it is rather an exception than the rule. We will then proceed with empirical estimates in Section 4.

3.1 Exponential Hazard

The simplest parametric mortality model is arguably represented by the exponential distribution with one parameter, which is the constant hazard $h(x) = \lambda$. The cumulative hazard is simply $H(x) = \lambda x$. The age x when $H(x) = 1$ is, after rearranging, $H_{1,\text{exponential}} = \frac{1}{\lambda}$, which

² $H(x) = -\log S(x) \Rightarrow S(x) = e^{-H(x)} \Rightarrow S(x) = e^{-1} \approx 0.368$.

is equivalent to the mean (age at death; i.e. life expectancy) in the case of an exponential distribution (see, for instance, Klein and Moeschberger, 1997). With survival function $S(x)$, the median age at death with exponentially distributed lifetimes is:

$$S(x) = e^{-\lambda x} = 0.5; \quad \Rightarrow \frac{-\log(0.5)}{\lambda}.$$

Hence, life expectancy and death expectancy are both necessarily larger than the median age at death (by a factor of about $1 / -\log(0.5) \approx 44\%$). The modal age at death is 0 because the exponential distribution has a constant hazard, leading to a strictly monotonically declining density ($f(x) = \lambda e^{-\lambda x}$).

3.2 de Moivre

Probably the oldest mortality law has been developed by Abraham de Moivre in 1725. It also has just only one parameter to estimate: ω , the highest attainable age.

Translated into a modern notation, the survival function can be represented as:

$$S(x) = 1 - \frac{x}{\omega} \tag{2}$$

Consequently, the age x of $H_{1,\text{deMoivre}}$ can be derived if we equal Eq. 2 to η and solve for x :

$$H_{1,\text{deMoivre}} = \omega(1 - \eta) \approx 0.6321206\omega \tag{3}$$

Median life expectancy is 0.5ω as well as life expectancy:

$$e_{0,\text{deMoivre}} = \int_0^{\omega} S(x)dx = \int_0^{\omega} \left(1 - \frac{x}{\omega}\right) dx = \frac{\omega}{2} \tag{4}$$

Consequently, $H_{1,\text{deMoivre}} = 0.632/2 \approx 32\%$ higher than life expectancy or median life expectancy in this case.

The distribution function $F(x) = 1 - S(x) = 1 - \left(1 - \frac{x}{\omega}\right) = \frac{x}{\omega}$ results in a uniform density function $f(x) = \frac{dF(x)}{dx} = \frac{1}{\omega}$. Thus, there is no modal age at death, because death counts are the same at each age.

Summarizing: In the case of a constant hazard (exponential distribution) life expectancy and H_1 are equal, whereas life expectancy and median age at death are equivalent in the case of a constant/uniform density function (De Moivre).

3.3 Gompertz

De Moivre published his theory in 1725. Exactly 100 years later Gompertz proposed a law of mortality, which has received more attention for human populations than any other. It needs two parameters and applies primarily to adult ages. The hazard $h(x)$ of Gompertz's law is exponentially increasing $h(x) = ae^{bx}$ with the initial level of mortality a and the proportional increase per unit of time b , with $a, b > 0$. The survival function $S(x) = e^{\frac{a}{b}(1-e^{bx})}$ implies a

cumulative hazard of $H(x) = -\frac{a}{b}(1 - e^{bx})$. After setting the cumulative hazard function $H(x)$ equal to $-\log(\eta)$, we obtain:³

$$H_{1,\text{Gompertz}} = \frac{\log \left[1 + \frac{-\log(\eta)b}{a} \right]}{b} \quad (5)$$

The median age at death in a Gompertz distributed case is, consequently:

$$x_{0.5,\text{Gompertz}} = \frac{\log \left[1 + \frac{-\log(0.5)b}{a} \right]}{b} \quad (6)$$

Not surprising since both concepts refer to different levels on the survival curve, this implies that $H_{1,\text{Gompertz}}$ has to be greater than $x_{0.5,\text{Gompertz}}$.

The modal age at death in Gompertz distributed mortality data is (see Missov et al., 2015):

$$x_{\text{mode,Gompertz}} = \frac{\log \left(\frac{b}{a} \right)}{b} \quad (7)$$

If H_1 and the modal age at death in a Gompertz scenario were identical, equations 5 and 7 need to be equivalent. After simplifying we obtain: $1 + \frac{b}{a} \neq \frac{b}{a}$. Hence, H_1 is *always* larger than the modal age at death, with $a, b > 0$. But with the secular decline in mortality, resulting in decreasing values of a , and a rather immutable value of b (e.g., Ebeling et al., 2021; Oeppen and Vaupel, 2002; Rau and Vaupel, 2014; Vaupel, 2010), the ratio b/a becomes larger and larger, yielding a difference between Eq. 5 and Eq. 7, which tends to zero.

Gompertz life expectancy is (Lenart and Missov, 2010):⁴

$$e_{0,\text{Gompertz}} = \frac{e^{\frac{a}{b}} E_1 \left(\frac{a}{b} \right)}{b} \quad (8)$$

where E_1 is the exponential integral. We were unable to describe the relationship between H_1 and e_0 analytically (so far). To see whether $H_{1,\text{Gompertz}}$ and $e_{0,\text{Gompertz}}$ can be identical, we estimated the difference Δ between H_1 and e_0 from Equations 5 and 8 for simulated values a and b . The ranges for a and b were set intentionally larger than typically observed in any human population in the past, present, and probably also in the future: a ranges from 0.000001 to 0.001 and b from 0.001 to 0.5. Although both parameters are not statistically independent from each other—the Strehler-Mildvan correlation posits a negative relationship between a and b (Strehler and Mildvan, 1960; Zheng et al., 2011)—we simply estimated e_0 and H_1 for all possible combinations. The results are plotted in Figure 1. The x -axis denotes parameter a on a \log_{10} scale; the y -axis refers to parameter b . We would have plotted any negative values, i.e. when e_0 is larger than H_1 , in blue. But there weren't any. Identical values would have been plotted in red. To allow numerical inaccuracies we deliberately used an interval for Δ

³Obviously, we could have set $H(x) = 1$. But when comparing H_1 to the median of a Gompertz distribution in the next step, it hopefully becomes apparent why we did *not* do that.

⁴We are aware of Castellares et al. (2020) who point out that the equations of Lenart and Missov (2010) are not correct. This applies not to life expectancy at birth, though. After simplification the equations of both groups of authors turn out to be identical.

between -0.01 and 0.01 to depict identical values of H_1 and e_0 . But there were not any either. All values were positive. The smallest value denoted a difference Δ of 1.13 years. Thus, we conclude for now that H_1 is always larger than e_0 . Please note that the contour lines indicate that the difference in years is rather insensitive to changes in a . The green horizontal reference line has been added at a value of 0.11, which is a typical value for the observed population level increase of mortality with age. This means that in a “perfect” Gompertz setting in human population, we should observe a difference of about 5 years.

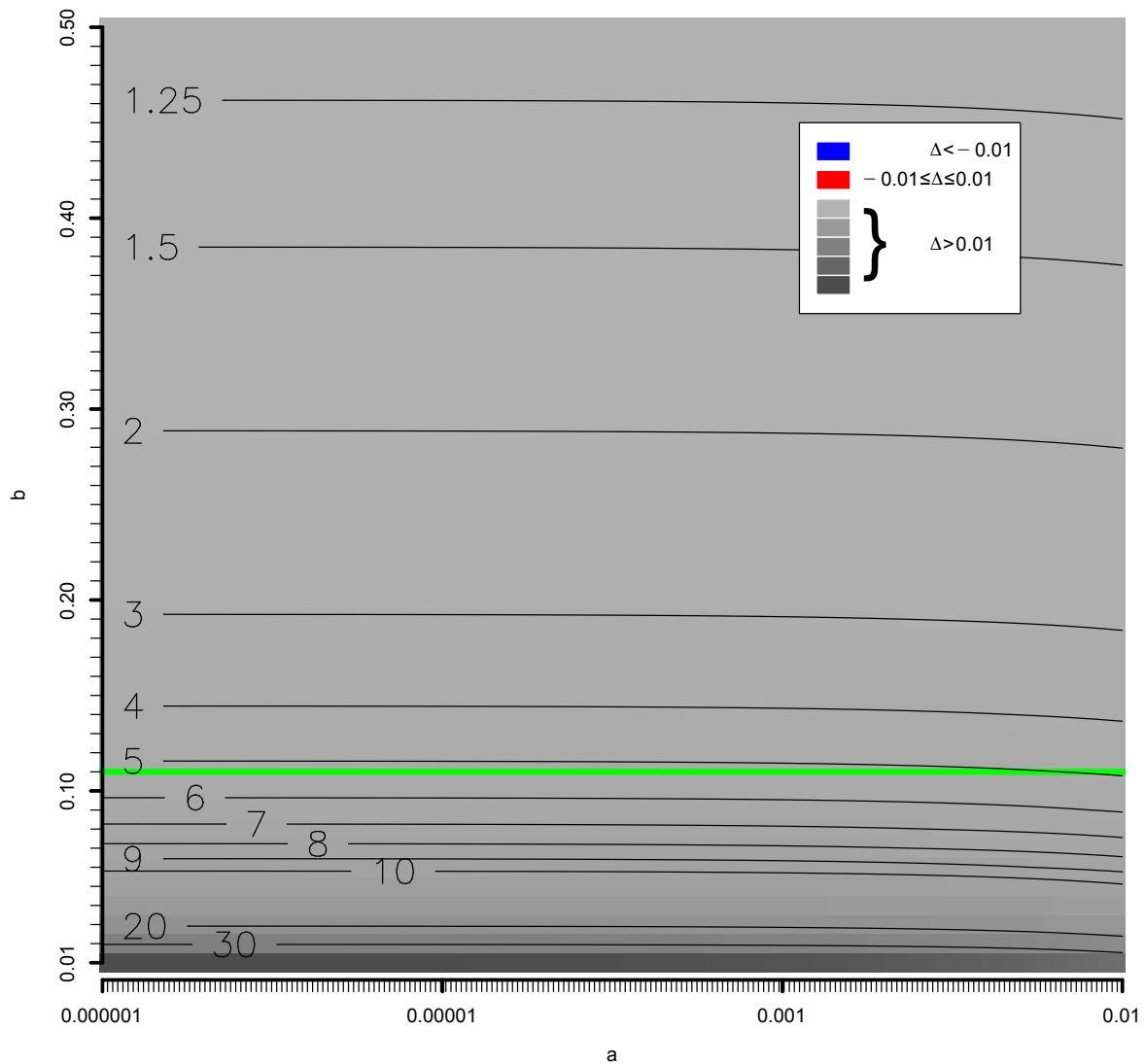


Figure 1: Difference Δ between H_1 and e_0 in a Gompertz setting for various values of parameters a and b . Source: Own illustration, based on simulated values.

3.4 Gamma-Gompertz

The Gompertz distribution can be considered as a special case of the Gamma-Gompertz-distribution where all individuals are identical, i.e. share the same individual hazard. It has been

argued, however, that “[s]ome individuals are frailer than others, innately or because of acquired weaknesses. The frail tend to suffer high mortality, leaving a select subset of survivors” (Vaupel et al., 1998, p. 858). The distribution across the frailer and the more robust individuals is often described by a Gamma-distribution with an initial mean of one, used as a multiplicative factor for the Gompertz hazard (e.g., Vaupel et al., 1979).

According to Vaupel and Missov (2014), the survival function $S(x)$ for Gamma-Gompertz distributed data can be expressed as:

$$S(x) = \left[1 + \frac{a\gamma}{b} (e^{bx} - 1)\right]^{-\frac{1}{\gamma}} \quad (9)$$

Consequently:

$$H(x) = \frac{\log \left[1 + \frac{a\gamma}{b} (e^{bx} - 1)\right]}{\gamma} \quad (10)$$

Substituting $H(x)$ with $-\log(\eta)$ and solving for x , H_1 in a Gamma-Gompertz distributed case is:

$$H_{1,GG} = \frac{\log \left[\frac{b(e^{-\log(\eta)\gamma} - 1)}{a\gamma} + 1 \right]}{b} \quad (11)$$

... more to come here still ...

4 Empirical Findings

4.1 H_1

We used life table data from the Human Mortality Database (2021) to estimate H_1 . We selected the year 2017 for our cross-sectional perspective and went back until 1850 for our temporal perspective.⁵

4.1.1 H_1 in 2017

Death expectancy H_1 in the year 2017 ranged for men from 76.01 years (Belarus) to 87.95 years (Hong Kong). In the same year H_1 ranges for women from 84.81 years (Bulgaria) to 93.48 years (Hong Kong). Across the selected countries, the age at which the average individual has used exactly one life can be expected for men around 84.49 years and 88.95 years for women. The median H_1 for men is around 85.47 years and 89.12 years for women. This implies a left-skewed distribution of H_1 for men and (less left skewed) for women. Figure 2 shows the distribution of H_1 for all included HMD countries for men and women. The death expectancy is higher for women than for men. Figure 3 shows that the skewness seems to emerge from Eastern European countries, where we find the lowest values of H_1 .

⁵We included the following countries: Australia, Austria, Belgium, Bulgaria, Belarus, Canada, Chile, Croatia, the Czech Republic, Denmark, England & Wales, Spain, Estonia, Finland, France, Germany (East, West, and combined since 1990), Great Britain, Greece, Hong Kong, Hungary, Iceland, Italy, Ireland (Republic and Northern Ireland), Japan, Latvia, Lithuania, Luxembourg, the Netherlands, Norway, Poland, Portugal, Scotland, Slovakia, Slovenia, South Korea, Sweden, Switzerland, Taiwan and the United States of America.

H_1 - Distribution in 2017 for Men and Women

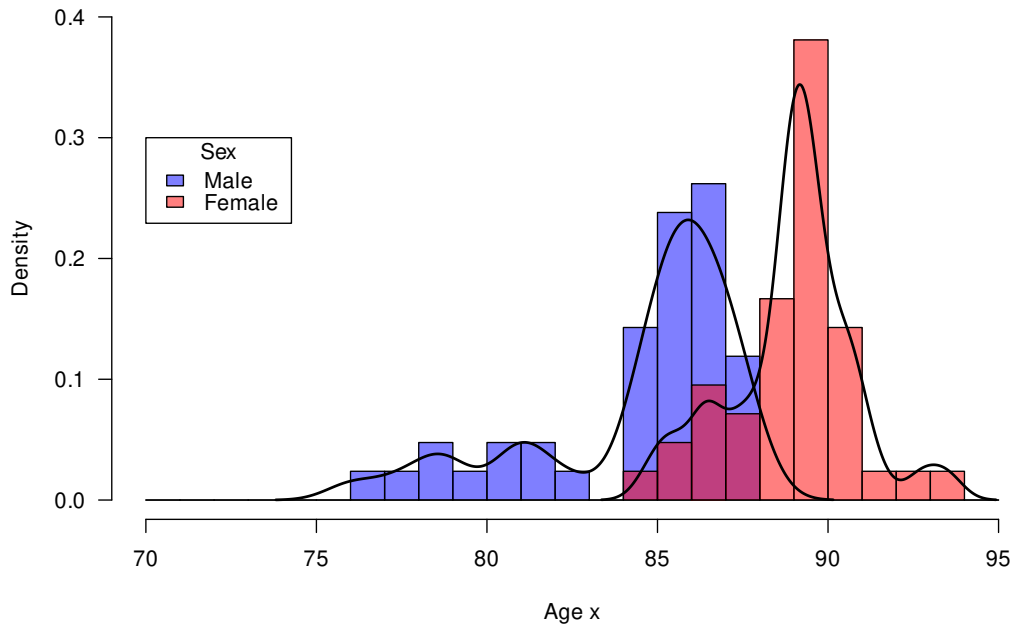


Figure 2: Empirical distribution and density of H_1 for women and men in each country from the Human Mortality Database in 2017. Source: Own illustration and estimation, based on data from the Human Mortality Database (2021)

4.1.2 H_1 over time

Figures 4 and 5 show the trend for H_1 over time. We opted to visualize the distribution by boxplots. The median is depicted inside the rectangles, which denote the interquartile range. The whiskers stretch to 1.5 times the interquartile range. The legend features only those countries which were outside the boxplot whiskers.

Overall, we see an upward trend of H_1 over time due to improved survival chances. We are also able to see major historical events that affected mortality in the past: Outliers and longer whiskers are usually observed in crisis years such as the two world wars and the Spanish Flu, especially for males. For the First World War we find especially high effects on H_1 for Italian and French males. The second world war had notably high impact on H_1 for Spanish People and Finnish, French and Italian men. The Spanish Flu is recognizable for men and women, but the impact has been bigger for men in general and for Spanish and Italian women. In the years around the millennium and beyond we find relative low values of H_1 in Eastern European Countries. It should also be highlighted that Japanese and Hong Kong women exhibit particularly high values H_1 during recent years.

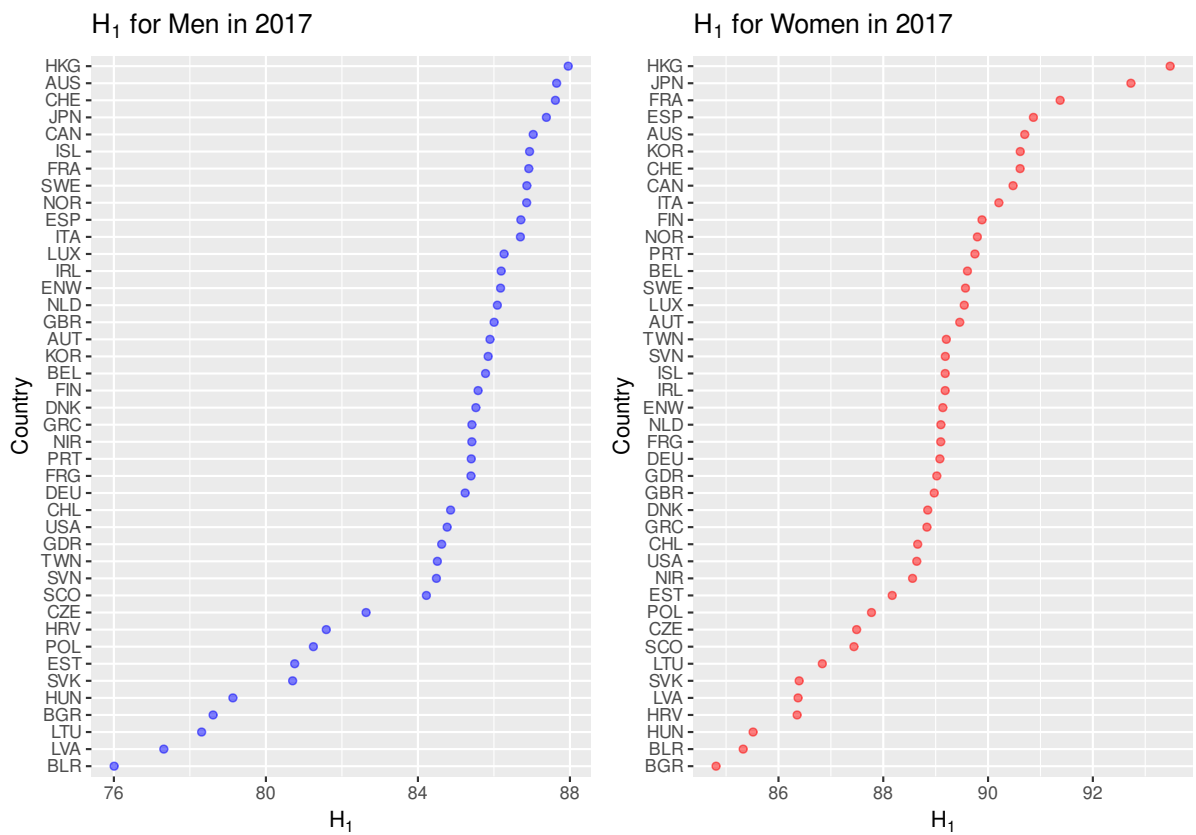


Figure 3: Distribution of H_1 as a sorted dot-plot for women and men in each country from the Human Mortality Database in 2017. Source: Own illustration and estimation, based on data from the Human Mortality Database (2021)

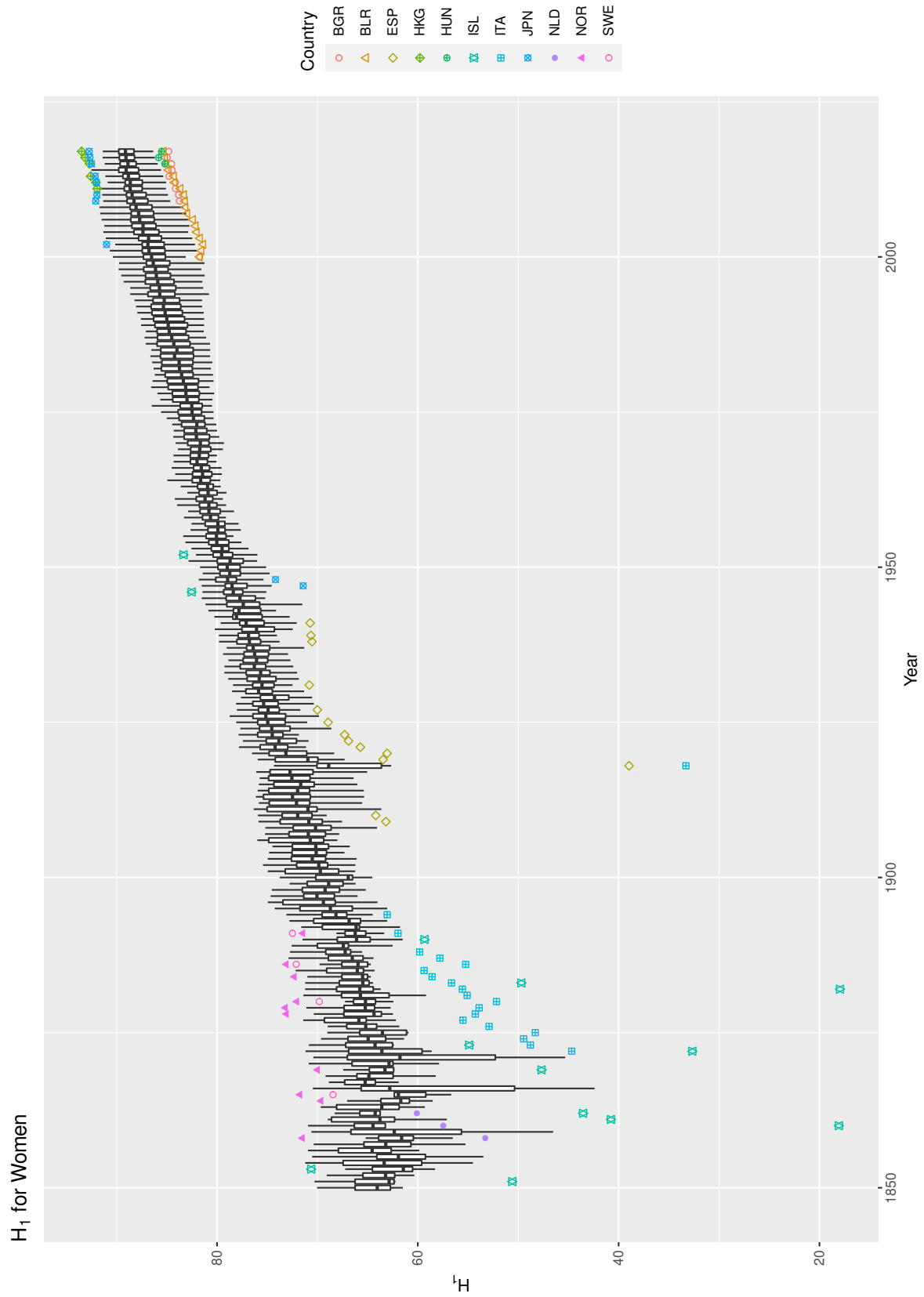


Figure 4: H_1 over time for women for all included countries. Only countries that were outside the 1.5 times interquartile range are listed in the legend. Source: Own illustration and estimation, based on data from the Human Mortality Database (2021)

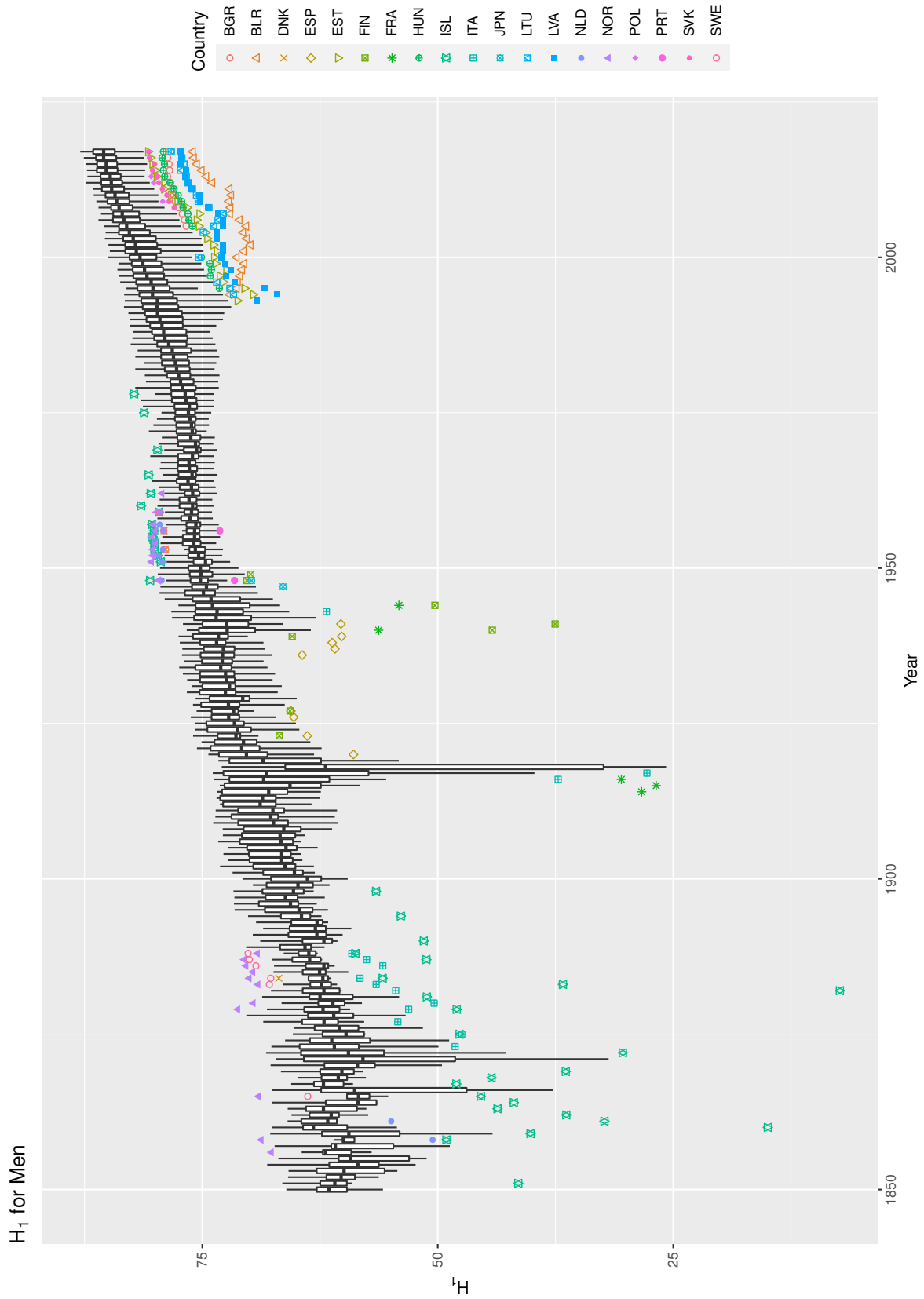


Figure 5: H_1 over time for men for all included countries. Only countries that were outside the 1.5 times interquartile range are listed in the legend. Source: Own illustration and estimation, based on data from the Human Mortality Database (2021)

4.2 H_1 vs. e_0

Figures 6 and 7 show the relationship between life expectancy at birth e_0 and H_1 for women and men, respectively. A thick diagonal line has been plotted on the 45° line to depict identical values of H_1 and e_0 . Results above this line indicate higher values of H_1 and vice versa. The grey reference lines above and below the thick diagonal line were drawn for 5, 10, 15, 20, and 25 years of difference in either direction.

We observe that H_1 is in almost every case bigger than e_0 . Exceptions are Iceland 1860 and 1882, French males (1914–1916), Italian males (1917) and British males (1918). These exceptions could be linked to infectious diseases and the First World War. During the first 100 years we observe an increase in the difference between the two measures followed by a decline. In more recent years we observe an almost linear increase, relatively close to the 45-degree line depicting values for H_1 , which are 5 years higher than e_0 . Please note that this pattern and the numerical difference resembles the “perfect” Gompertz setting (green horizontal line in Figure 1) very closely.

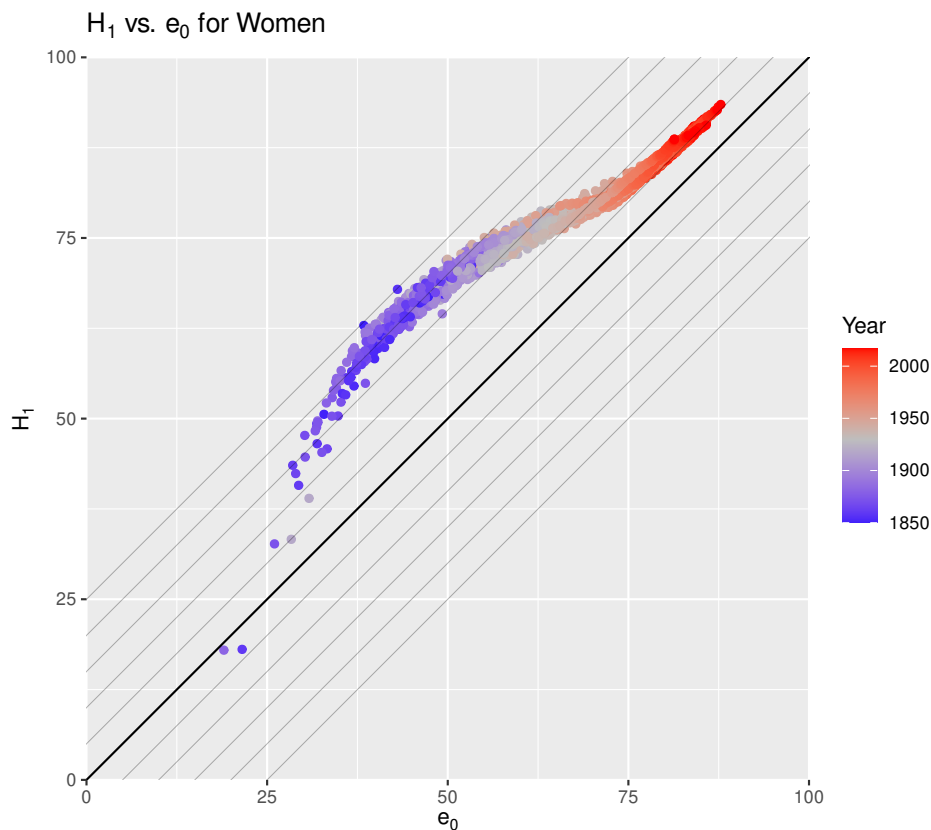


Figure 6: Scatterplot of H_1 vs. e_0 over time for women in all included countries. The black 45-degree line corresponds to identical values. The parallel gray lines have a distance of 5 years each. The coloring starts from blue (1850) over grey (1930) to 2017 (red). Source: Human Mortality Database (2021), own estimation and visualization.

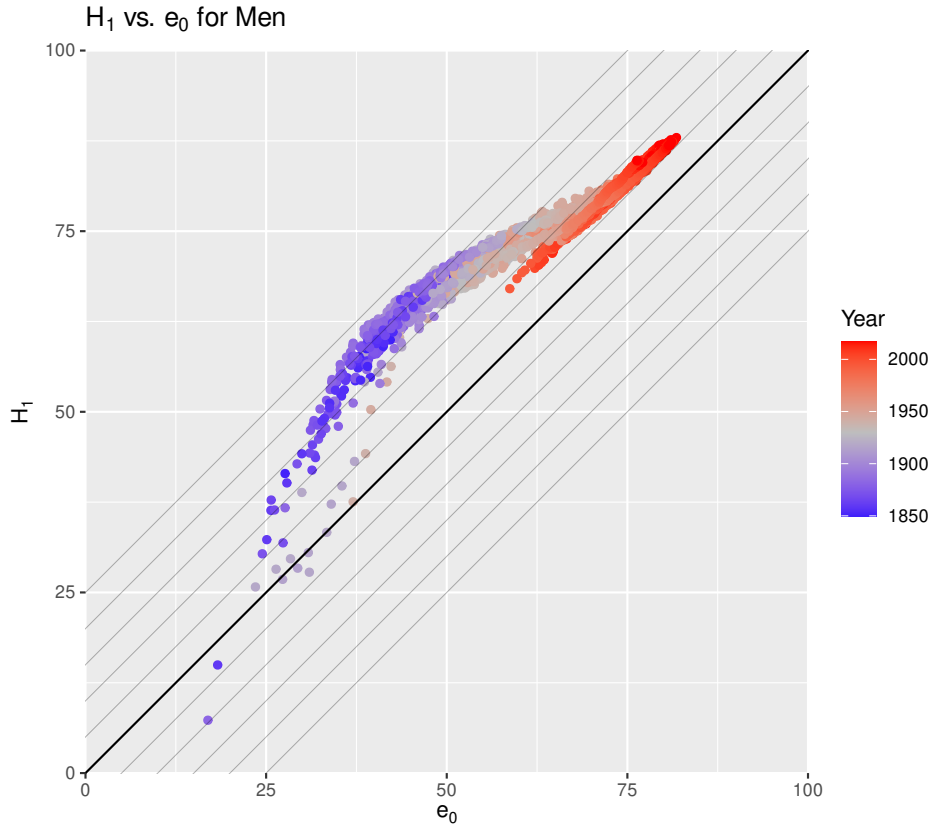


Figure 7: Scatterplot of H_1 vs. e_0 over time for men in all included countries. The black 45-degree line corresponds to identical values. The parallel gray lines have a distance of 5 years each. The coloring starts from blue (1850) over grey (1930) to 2017 (red). Source: Human Mortality Database (2021), own estimation and visualization.

4.3 H_1 vs. Median Life Expectancy

H_1 and median life expectancy both depict a certain level of the survival curve, namely $\approx 36\%$ alive and 50% alive, respectively. Hence, they can not be identical, unless we observe a single age where the survival curve drops instantaneously from 0.5 to 0.36. In all realistic cases, H_1 needs to be larger than the median. This is also shown in Figures 8 and 9 for women and men. We do not detect the increase and decrease in the difference as we did in the case of H_1 and e_0 . Despite large variability in the first decades of our time-frame, we generally see a decline. The past decades show only a minor shrinking, though. This means that there were not any major survival advances between the 50th and 63rd percentile in recent years.

4.4 H_1 vs. Modal Age at Death

We estimated the modal age at death, i.e. the highest density of deaths, using P -splines under the assumption of Poisson distributed deaths (see, for instance, Horiuchi et al., 2013). To avoid the distortion of high infant and childhood mortality, we only looked at ages 30 and above. This explains the few vertical dots at age 30 in Figures 10 and 11. Generally speaking, the modal age at death has been higher than H_1 before World War II. After that it seems that H_1 and the modal age at death closely resemble each other. An explanation for this can be

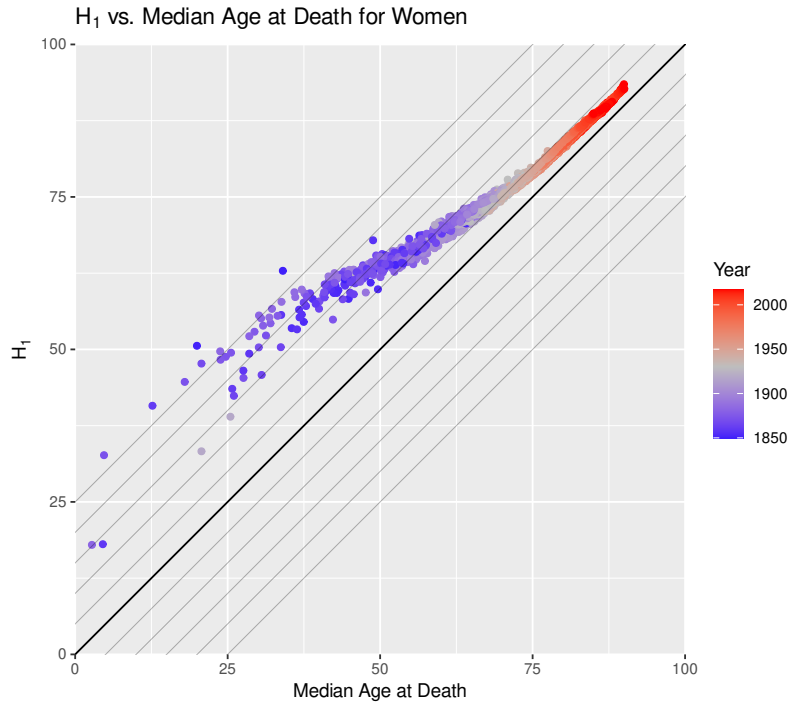


Figure 8: Scatterplot of H_1 vs. median life expectancy over time for women in all included countries. The black 45-degree line corresponds to identical values. The parallel gray lines have a distance of 5 years each. The coloring starts from blue (1850) over grey (1930) to 2017 (red). Source: Human Mortality Database (2021), own estimation and visualization.

provided by the Gompertz model. As pointed out in Section 3.3, H_1 is always larger than the modal age at death in a Gompertz setting. But a is declining as mortality is declining. With a quasi-constant value of b , the difference between the two measures tends to zero in a Gompertz setting.

5 Extensions

5.1 H_1^\dagger

5.1.1 Idea

Inequalities in the age at death can be measured via the average number of live-years lost, usually denoted by e^\dagger (e.g., Vaupel and Romo, 2003). This measure has become more popular during the past 10 years (e.g., van Raalte, 2011; van Raalte et al., 2018; Vaupel et al., 2011).

e^\dagger can be defined as:

$$e^\dagger = \int_0^\omega e(x)f(x)da \quad (12)$$

where $e(x)$ is remaining life expectancy at age x and $f(x)$ denotes the density of deaths, given survival until age x . Analogously to the number of life years lost defined for life expectancy, we can define the number of life years lost for H_1^\dagger as:

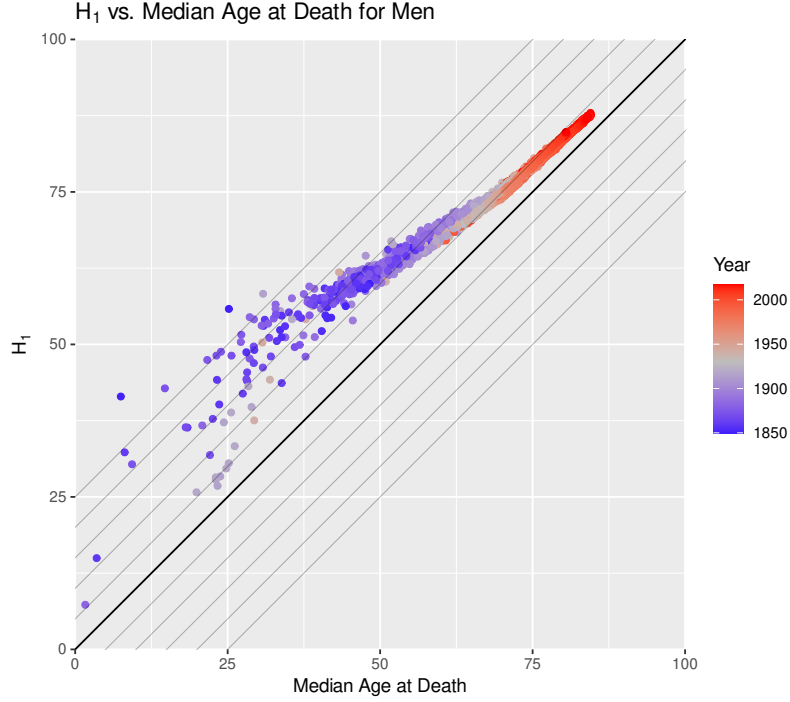


Figure 9: Scatterplot of H_1 vs. median life expectancy over time for men in all included countries. The black 45-degree line corresponds to identical values. The parallel gray lines have a distance of 5 years each. The coloring starts from blue (1850) over grey (1930) to 2017 (red). Source: Human Mortality Database (2021), own estimation and visualization.

$$H_1^\dagger = \int_0^\omega [H_1(x) - x] f(x) da \quad (13)$$

$H_1(x)$ denotes H_1 given survival until age x . Thus, $[H_1(x) - x]$ in our application is the equivalent of $e(x)$, i.e. remaining life expectancy at age x in the conventional analysis of life expectancy.

5.1.2 Empirical Results

5.1.2.1 Empirical Findings H_1^\dagger Figure 12 and Figure 13 show the evolution of H_1^\dagger from 1850 to 2017 for women and men, respectively. These boxplots follow the same principle as the H_1 over time (Section 4.1.2) plots. We observe decreasing inequalities for H_1 for women and men over time. Historic events are also clearly visible by bumps and higher whiskers such as during the Spanish flu and World War II. Trends in H_1^\dagger appear to be similar for women and men before the second world war. After that H_1^\dagger evolves in favor for females. Also the range from minimum to maximum per year seems to be smaller for women than for men since the 1950s. Additionally, we see that males in Eastern European countries are often outliers with a higher inequality of H_1 since the 1970s compared to other countries. We observe the same for females for a very narrow time period after the dissolution of the Soviet Union.

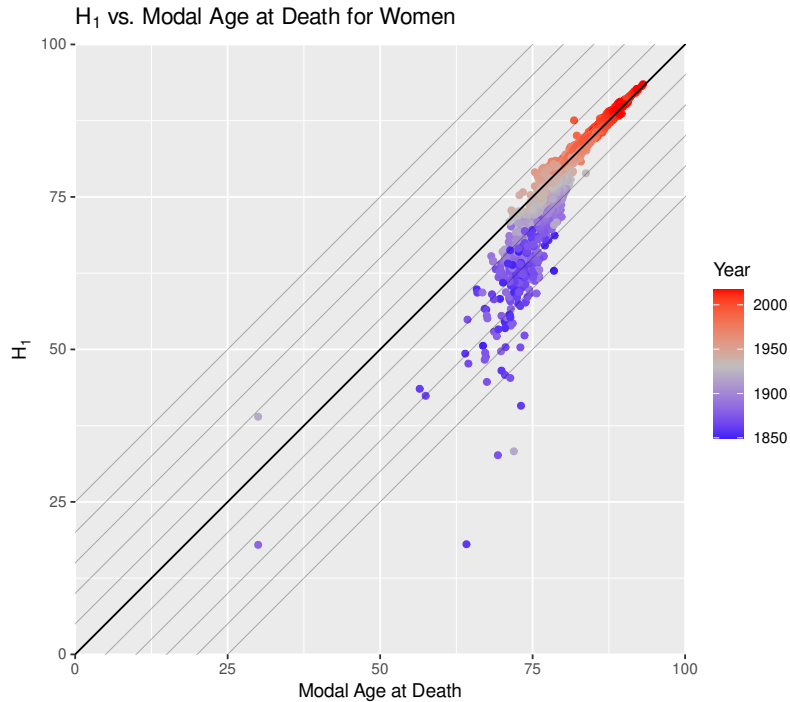


Figure 10: Scatterplot of H_1 vs. modal age at death over time for women in all included countries. The black 45-degree line corresponds to identical values. The parallel gray lines have a distance of 5 years each. The coloring starts from blue (1850) over grey (1930) to 2017 (red). Source: Human Mortality Database (2021), own estimation and visualization.

5.1.2.2 H_1^\dagger vs. e^\dagger We compare H_1^\dagger with e^\dagger in Figures 14 and 15 for women and men, respectively. In almost all cases H_1^\dagger is larger than e^\dagger . Exceptions are French males in 1915 and Icelandic males in 1882. Over time H_1^\dagger and e^\dagger are moving towards the 45-degree line for women as well as for men.

5.2 H_2, H_3, \dots

... more to come here still ...

6 Discussion

We introduced a new measurement H_1 which we tentatively called “death expectancy”. It should not replace life expectancy, median life expectancy or the modal age at death as scalars describing mortality in a population. But we think it provides a novel theoretical and empirical perspective. It is the age when the cumulative hazard equals the value one. The rationale for this choice is that this would be the age when a standard individual could expect to have lived exactly one life. Death expectancy is different from life expectancy: Geometrically speaking, life expectancy is the area under the survival curve. In contrast, death expectancy refers to a certain level/“height” of the survival curve since the cumulative hazard can be also expressed as $-\log S(x)$. We denoted this level of the survival curve as η , corresponding to a value of 0.368. To illustrate this point: If one third of the population was extremely long-lived,

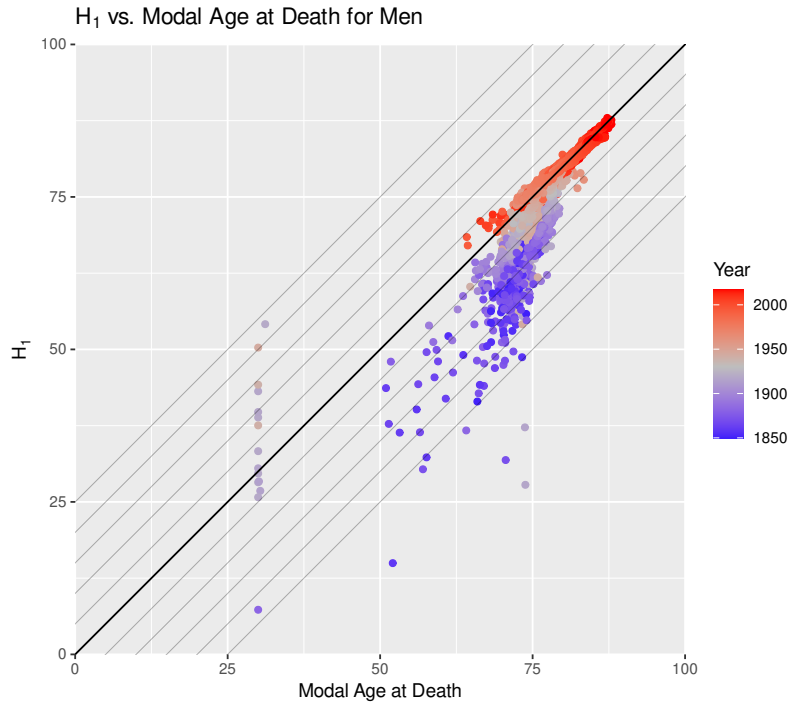


Figure 11: Scatterplot of H_1 vs. modal age at death over time for men in all included countries. The black 45-degree line corresponds to identical values. The parallel gray lines have a distance of 5 years each. The coloring starts from blue (1850) over grey (1930) to 2017 (red). Source: Human Mortality Database (2021), own estimation and visualization.

H_1 would remain unaffected as the cut-off proportion is 36.8% whereas the area under the survival curve, life expectancy, would be influenced. Thus, H_1 and median life expectancy share the positive characteristic to be more robust in the presence of extreme outliers than life expectancy — at the cost of not incorporating the whole age range.

In our section on the mathematical relationships we have shown for several “mortality laws” how H_1 , life expectancy e_0 , median life expectancy and the modal age at death are related and sometimes are even equivalent.

It is probably not surprising that we found in our empirical applications of H_1 that many modern population resemble closely what one would expect from a “true” Gompertz-like mortality experience.

We also introduced the measure H_1^+ , which is the equivalent to e^+ , the average number of life-years lost, as H_1 is to e_0 . In contrast to life expectancy, the median age at death and the modal age at death, H_1 can be extended to H_2 or H_3 or even generalized to H_n . They denote the ages when a person could expect to be dead a second time, a third time, ... At first, this might sound counterintuitive: If I am dead, I can not die a second or third time. While this is true, we would like to remind the reader that the expected age of the first death is when 36% of the population are still alive. The equivalent numbers for the second and third death are 13.5% and 5%, respectively.

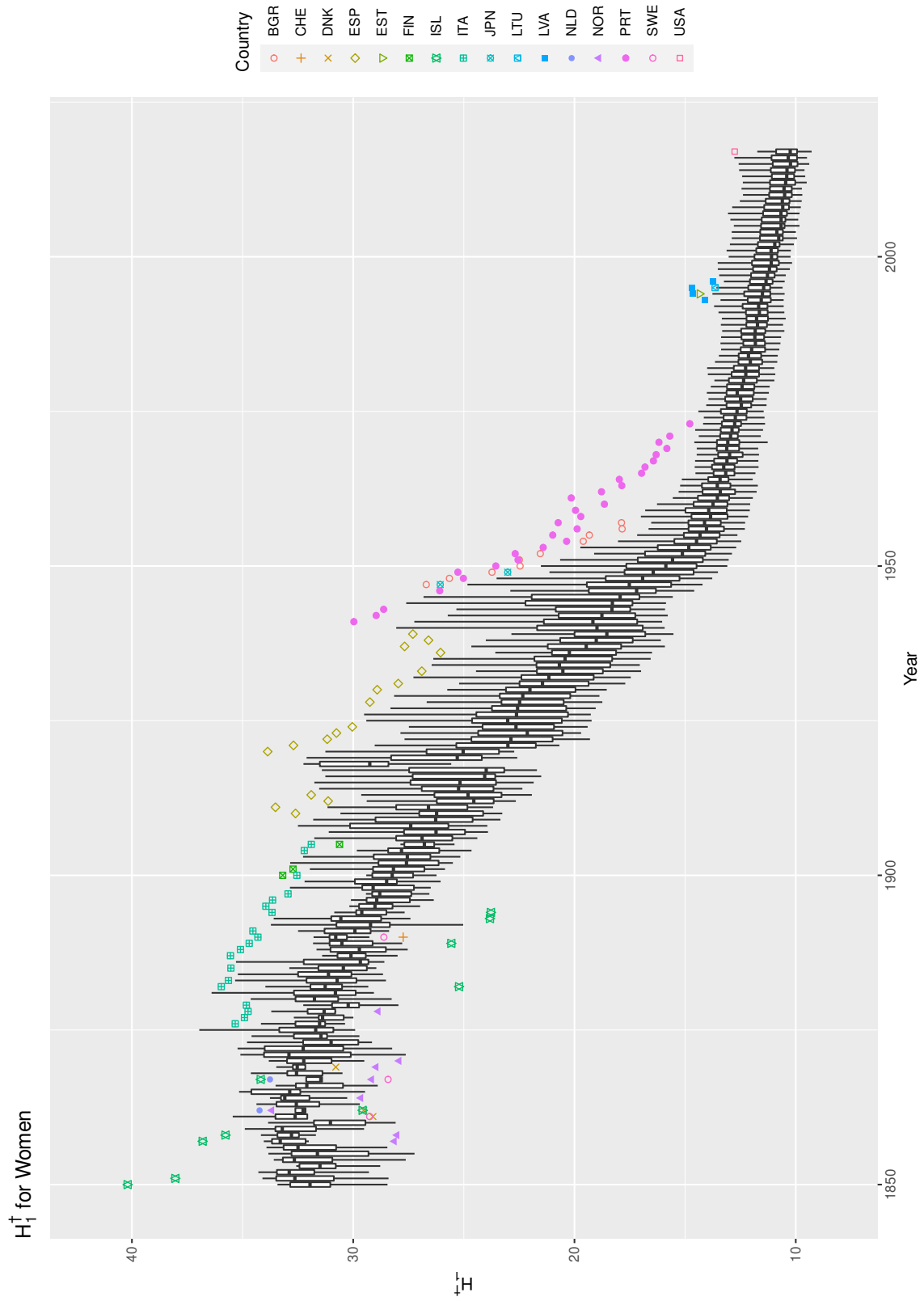


Figure 12: H_1^\dagger over time for women for all included countries. Only countries that were outside the 1.5 times interquartile range are listed in the legend. Source: Own illustration and estimation, based on data from the Human Mortality Database (2021)

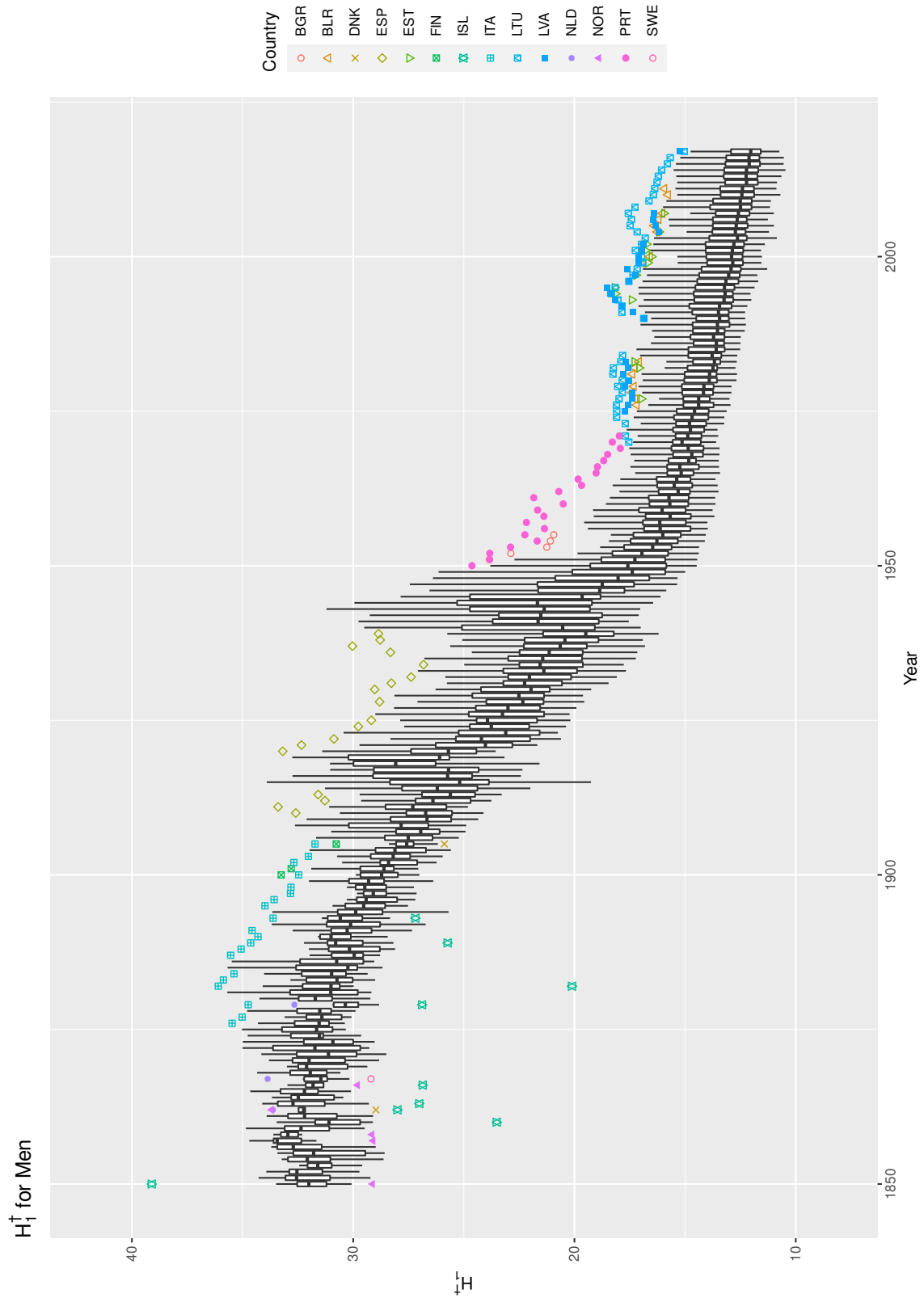


Figure 13: H_1^\dagger over time for women for all included countries. Only countries that were outside the 1.5 times interquartile range are listed in the legend. Source: Own illustration and estimation, based on data from the Human Mortality Database (2021)

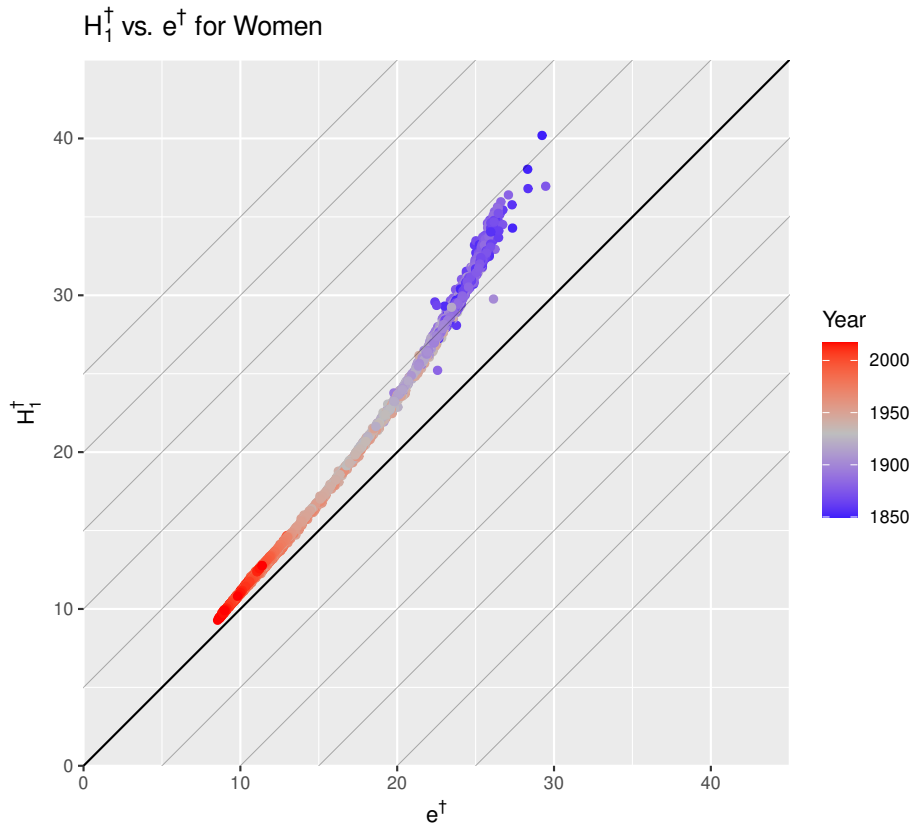


Figure 14: H_1^\dagger vs. e_0^\dagger for women for all included countries and years. Source: Own illustration and estimation, based on data from the Human Mortality Database (2021)

We argue that H_1, H_2, \dots could be used as dynamic indicators to measure the beginning of old-age, the oldest-old or similar “threshold” ages. This would be in contrast to traditional fixed threshold ages such as 80, for instance, for the oldest-old (e.g., Kannisto, 1994). We are not the first ones to propose such a dynamic age. As far as we know, Ryder was the first in 1975 to suggest a definition for old age which was related to the mortality experience of a population. In the section “A new index of old age” of his paper, he suggests to use the age when remaining life expectancy is 10 years, acknowledging that this is, of course, “some arbitrary length of time” (p. 16). This idea was successfully resuscitated and slightly modified during the past 15 years (e.g., Lutz et al., 2008; Sanderson and Scherbov, 2005, 2007, 2010). An important distinction between their approach(es) and ours is that by looking at remaining life expectancy they are rather “forward-looking”, whereas we are “backward-looking”, using the mortality experience of the population until this indicator age.

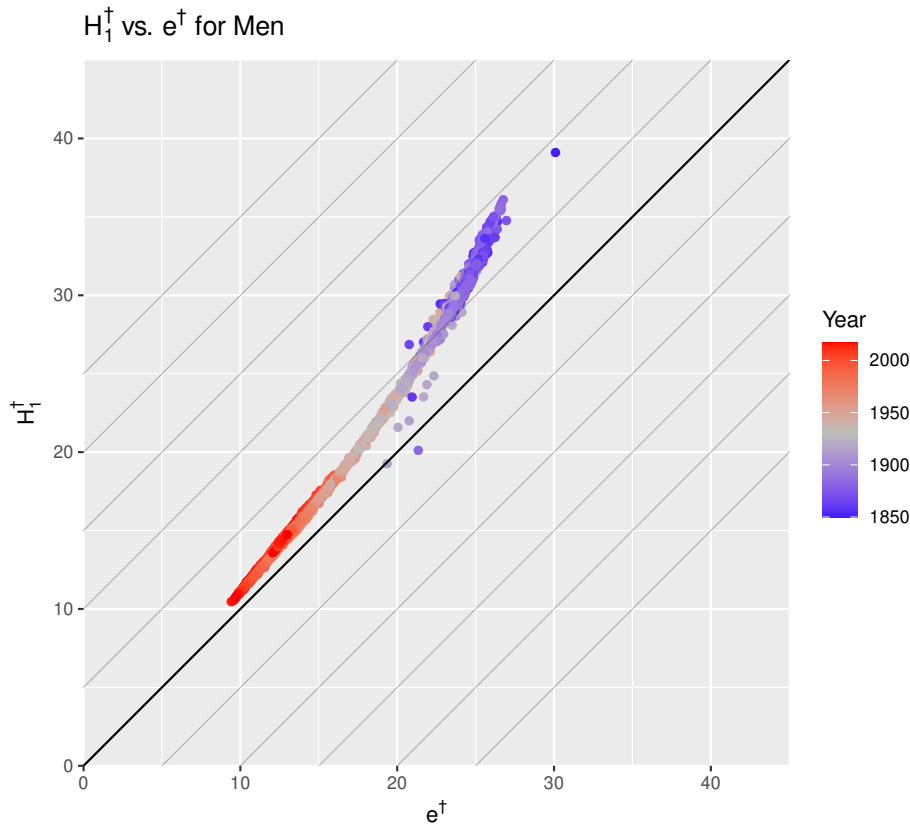


Figure 15: H_1^\dagger vs. e_0^\dagger for men for all included countries and years. Source: Own illustration and estimation, based on data from the Human Mortality Database (2021)

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A Notation

We use the following notation and remind the reader of some standard relationships (e.g., Klein and Moeschberger, 1997):

Notation	Explanation / Relationship
\log	natural logarithm; i.e.: $\log e^1 = 1$.
x	Age
$S(x)$	Survival function; Probability to survive to age x ; corresponds to $l(x)$ in (discrete-time) standard life table notation but here with a radix of 1.
$f(x) = -dS(x)/dx$	Density function; corresponds to $d(x)$ in (discrete-time) standard life table notation, the distribution of deaths by age.
$h(x) = f(x)/S(x) = -d \log S(x)/dx$	Hazard function; corresponds to $m(x)$ in (discrete-time) standard life table notation, the central death rates, or to $\mu(x)$ in continuous perspective.
$H(x) = \int_0^x h(t)dt = -\log S(x)$	Cumulative hazard
H_1	Age when $H(x) = 1$.
$\eta = e^{-1} \approx 0.368$	Value of the survival function at H_1 .
ω	Highest attainable age.
$e_0 = \int_0^{\omega} S(x)dx$	life expectancy at birth
M	Modal age at death

B Quote by Lotka

Alfred J. Lotka wrote in 1938, p. 164:

“The study of quantitative demography or population analysis can be undertaken from two points of view or by two methods the empirical method and the rational or formal method. The rational method is possible through the fact that between the various demographic characteristics there exist certain necessary relations, that is, relations imposed by the laws of physics or the laws of logic. But the rational method is not only possible, it is indispensable if we wish to obtain an entirely satisfactory understanding of population phenomena. Undoubtedly the ideal process is to cultivate both methods side by side. According to our predilections, the empirical data will then be for us concrete illustrations of the abstract principles that mainly interest us; or, on the contrary, the formal relations will serve us as guides in the examination and interpretation of the empirical data which, in the case, will be our fundamental interest.”