

Not all females outlive all males:

A new perspective on lifespan inequalities between sexes

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Abstract

Differences in lifespan between populations, e.g. between females and males, are often measured by differences in summary statistics, such as life expectancy, which generally show an advantage of females over males across the whole age span. However, such statistics ignore the fact that two lifespan distributions are generally not mutually exclusive and that not all females outlive all males. Here we use a novel measure of inequality in lifespans: the outsurvival probability, which is interpreted as the probability of males to outlive females. The measure accounts for the similarities in lifespan between populations. It also considers the interaction between the mean and variance of two lifespan distributions and their combined effect on between-populations inequalities. Our results show that the probability of males outliving females varied between 25% and 50%, across 44 countries and regions since the middle of the 18th century. Thus, despite the usually male lower life expectancy and higher death rates at all ages, males have a substantial chance of outliving females. Our suggested approach is generalizable to any pair of populations.

Keywords: Lifespan, Inequality, Sex differences, Outsurvival probability

1. INTRODUCTION

The female survival advantage has been observed over time across many human populations and is rooted in a complex combination of biological and behavioral factors (Austad & Fischer, 2016; Crimmins et al., 2019; Gjonça et al., 2005; Preston & Wang, 2006; Rogers et al., 2010). Females have been found to have longer survival and lower death rates than men in most modern populations (Austad & Fischer, 2016; Barford et al., 2006; Beltran-Sanchez et al., 2015; Gjonça et al., 2005; Luy & Gast, 2014) and even under extreme mortality conditions (Zarulli et al., 2018). In addition, females experienced lower lifespan variation than males (Aburto et al., 2020; Colchero et al., 2016). Sex differences in mortality have often been identified by comparing life expectancy and lifespan variation between females and males, which respectively summarize the average length of life and the spread of lifespans within populations. However, the use of life expectancy and lifespan variation ignores the fact that lifespan distributions are generally not mutually exclusive. Indeed, two lifespan distributions can overlap, such that individuals can have similar lifespans even if they belong to different populations. Despite females having higher life expectancy and lower lifespan variation than males, not all females outlive all males. In addition, while the degree of overlapping between two lifespan distributions largely depend on the mean and on the variation around it, life expectancy and lifespan variation are generally analyzed independently, overlooking their combined effect on inequalities between sexes.

To overcome these shortcomings, previous research has suggested investigating how different are two lifespan distributions, using, for example, the Kullback-Leibler divergence (Edwards & Tuljapurkar, 2005). Stratification indexes, based on how much two lifespan distributions overlap, have also been used to study mortality differences between socioeconomic groups (Shi et al., 2020; Zhou & Wodtke, 2019). The interpretation of these indexes can, however, be cumbersome and not demographically meaningful.

In this article, we use a novel and straightforward measure, the *outsurvival probability* (Vaupel et al., 2020), which quantifies the probability that individuals in one population outlive those in another population, for randomly paired individuals. We show that this measure considers both the overlap between two lifespan distributions and the interaction between the mean and variance of each distribution. We computed the outsurvival probability to study sex differences in mortality in 44 populations covering over 200 years of data. Our results highlight that, despite sometimes large differences in life expectancy, there are important similarities between males' and females' lifespan distributions.

2. METHOD

2.1 THE CONCEPT

Consider two populations under the four scenarios based on lifespan distributions with mean and standard deviation (SD) defined in Figure 1. When looking at scenario A, the first population (in red) has a smaller mean lifespan and larger SD than the second population (in blue). An inference from these summary statistics would be that individuals in the first population are worse off than individuals in the second. However, more individuals survive to (and die at) high ages in the first population, as illustrated by the red band to the right of the figure, suggesting a certain advantage in health and mortality at older ages. At the same time, the first population has a disadvantage at younger ages. Thus, only some individuals in the first population are worse off than some individuals in the second. Randomness plays a salient role in the mortality process and many individuals in both populations might end up having similar lifespans. The mean and SD statistics tend to provide a dichotomic perspective on inequalities between two populations and neglect the similarities and overlaps in lifespan between populations. The outsurvival probability, φ , instead, captures these dimensions by measuring the probability that an individual from a population with high mortality will

outlive an individual from a population with low mortality (Vaupel et al., 2020). In scenario A, this statistic is 48%. If both distributions were equal, φ would be 50%, meaning that individuals in both populations have an equal probability to outlive each other.

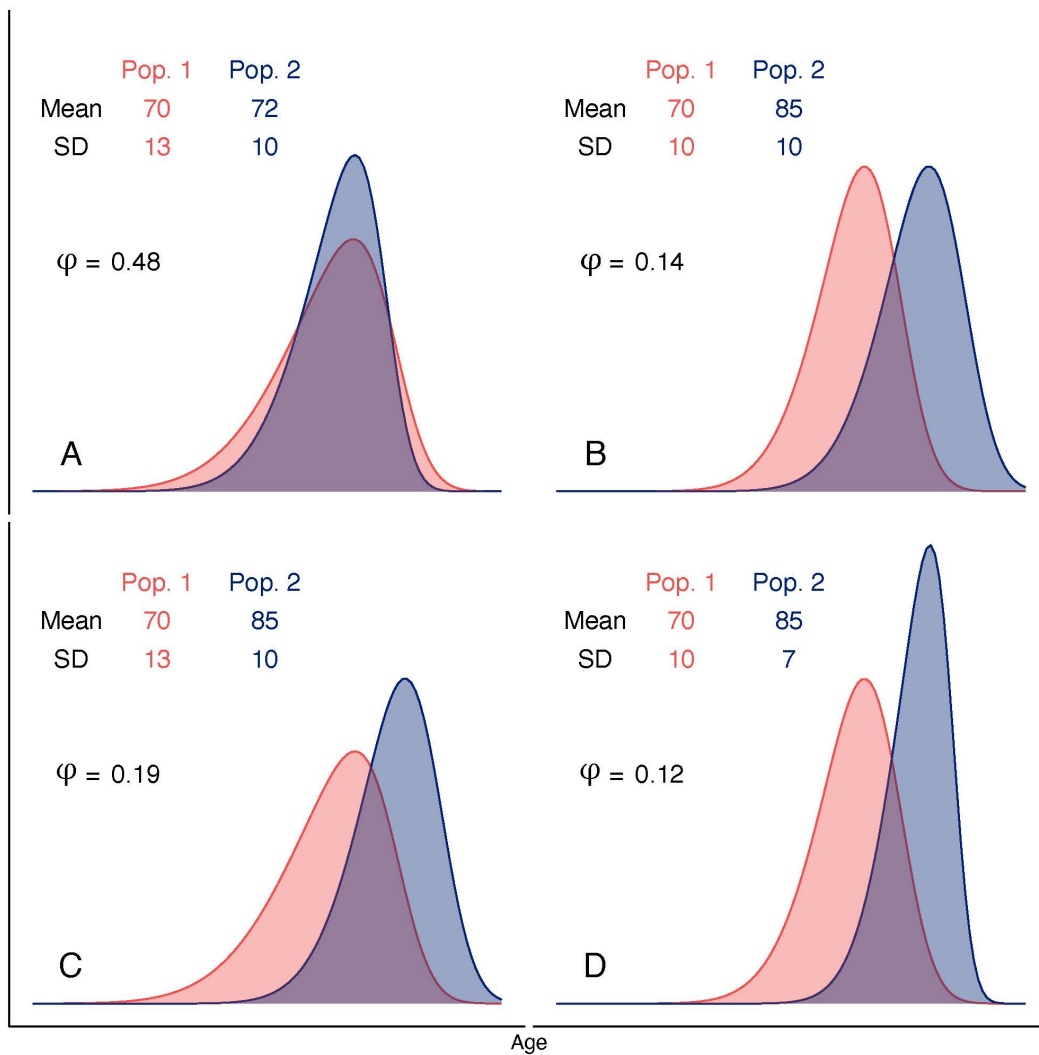


Fig. 1 Four scenarios of interactions between lifespan distributions and corresponding statistics.

We also show that values of φ depend on both the differences in life expectancies and the spread of the lifespan distributions. Consider the two populations in scenarios B and C. The difference in mean lifespan is the same in both scenarios, i.e. 15 years. However, in scenario C the first population

has a larger SD, which implies more individuals surviving to older ages, despite greater inequalities, and thus a greater potential to outlive individuals from the second population. Indeed, φ is higher in scenario C (19%) than in scenario B (14%).

Now compare scenario B to scenario D. This time, the second population in D has a smaller SD, with fewer individuals dying at younger ages, making it more difficult for individuals in the first population to outlive them. This reduces φ to 12%.

The last two comparisons highlight that for the same difference in life expectancy, larger lifespan variation in both populations generally results in larger φ . The comparison of scenarios A and C also show that small differences in life expectancy leads to larger value of φ .

2.2 FORMALIZING THE APPROACH

Let $d_i(x)$, $i = 1, 2$, denote the lifespan distribution at age x in two populations. The cumulative distributions are represented by $D_i(x)$, such that $D_i(x) = \int_0^x d_i(x)dx$ and the survivorship is denoted by $\ell_i(x)$, with $\ell_i(x) = 1 - D_i(x)$. The probability that the individual from the first population will outlive the individual from the second population is (Vaupel et al., 2020):

$$\varphi = \int_0^{\infty} d_2(x)\ell_1(x)dx. \quad (1)$$

It can be shown that this statistic relates to the joint probability density function of two lifespan distributions, which gives the probability of realizations of two lifespans and thus is related to the overlap of the two distributions. Assume two populations of individuals, with age at death x and y , respectively. Assume the two populations are independent, meaning that the length of life x does not depend on the length of life y and vice versa. This implies that the joint probability density function, $d_{1,2}(x, y)$, equals the product of the marginal densities so that $d_{1,2}(x, y) = d_1(x) d_2(y)$. We are interested on calculating the probability (φ) of individuals in the first population outliving those in the second population. This implies that $0 \leq y < x$ so:

$$\begin{aligned}
\varphi &= \int_0^{\infty} \int_0^x d_{1,2}(x,y) dy dx = \int_0^{\infty} d_1(x) \int_0^x d_2(y) dy dx \\
&= \int_0^{\infty} d_1(x) D_2(x) dx \\
&= \int_0^{\infty} d_1(x) [1 - l_2(x)] dx = 1 - \int_0^{\infty} d_1(x) l_2(x) dx \\
&= \int_0^{\infty} d_2(x) \ell_1(x) dx.
\end{aligned} \tag{2}$$

More details about equation (2) and its relation to equation (1) are provided in Appendix B. Equation (2) is equivalent to matching at random individuals from each population and calculating the proportions of individuals from the first population outliving the paired individual from the second. We performed such analysis via simulation of individuals from a specific lifespan distribution and estimated the corresponding statistics (see Appendix C). Equivalent results were found.

Equation (2) is also equivalent to the expected failure probability in stress-strength interference (SSI) model, which assesses the probability that the stress (population 1) exceeds the strength (population 2) of a material (An et al., 2008). If the distributions of both populations follow a Normal distribution with mean μ_i and standard deviation s_i , SSI model has shown that the probability of failure is $P(Z)$ with $Z = -\frac{\mu_2 - \mu_1}{\sqrt{s_1^2 + s_2^2}}$ (EL-Sayed S & Constantin, 2011). This relation formalizes what is illustrated in section 2.1: φ is sensitive to the difference in the means and to the level of variation in both distributions. However, lifespan distributions are not normally distributed and additional moments could also affect the value of φ .

2.3 DISCRETE APPROXIMATION

In a discrete time setting, similar equivalences can be found. Let ${}_n d_x^i$ be the life table deaths between age x and $x+n$ in population i and ${}_n D_x^i$ the cumulative distribution. For a given age-group width of n ,

the probability of individuals in the first population outliving those in the second population can be found by:

$$\varphi \approx \sum_{x=0}^{\omega} {}_n d_x^1 {}_n D_{x-n}^2 + \bar{d} = \sum_{x=0}^{\omega} {}_n d_{x-n}^2 {}_n l_x^1 + \bar{d} \quad (3)$$

with $\bar{d} = \frac{\sum_{x=0}^{\omega} {}_n d_x^1 {}_n d_x^2}{2}$ and $\sum_{x=0}^{\omega} {}_n d_x^1 {}_n d_x^2$ being the probability that individuals in both populations died in the same age-group. The latter statistic is sensitive to the width of the age-groups such that smaller age-groups result into smaller values, with $\lim_{n \rightarrow 0} \sum_{x=0}^{\omega} {}_n d_x^1 {}_n d_x^2 = 0$. In the Appendix C, we compared the discrete and continuous approaches and find that both approaches yield comparable results.

3. DATA

We used life tables by sex for all available countries and years from the Human Mortality Database (HMD, 2020). Subnational data were used for Germany with separate analysis for East and West Germany; and the United Kingdom for England-Wales (total population), Scotland and Northern Ireland, totalizing 44 populations. The earliest year with available data was 1751 (for Sweden). Information about the available populations and years are provided in Appendix A. We compared females and males' life tables in each country/region.

4 RESULTS

Figure 2 shows the outsurvival probability of males over females (φ) since 1850 for all HMD countries. The probability of males outliving females has, in all points in time and across all populations, varied between 25% and 50%, with only one exception: Iceland in 1891 (51.3%), an exceptional year when female life expectancy was lower than male life expectancy. Before the First World War, φ was slowly decreasing, on average from 47.3% in 1850 to 46.0% in 1913. Afterwards,

φ declined faster. In 1930, the mean φ across populations was 45.4% (ranging from 42.8% (France) to 48.4% (Netherlands)). By 1985, the mean φ was 35.5% (ranging from 31.2% (Russia) to 42.8% (Israel)). φ started increasing around the 1980s for some countries, but continued to decrease in others until the 2000s, especially in Eastern European countries. The mean in 2017 was 37.1%, with values varying between 28.7% (Belarus) and 42.5% (Iceland).

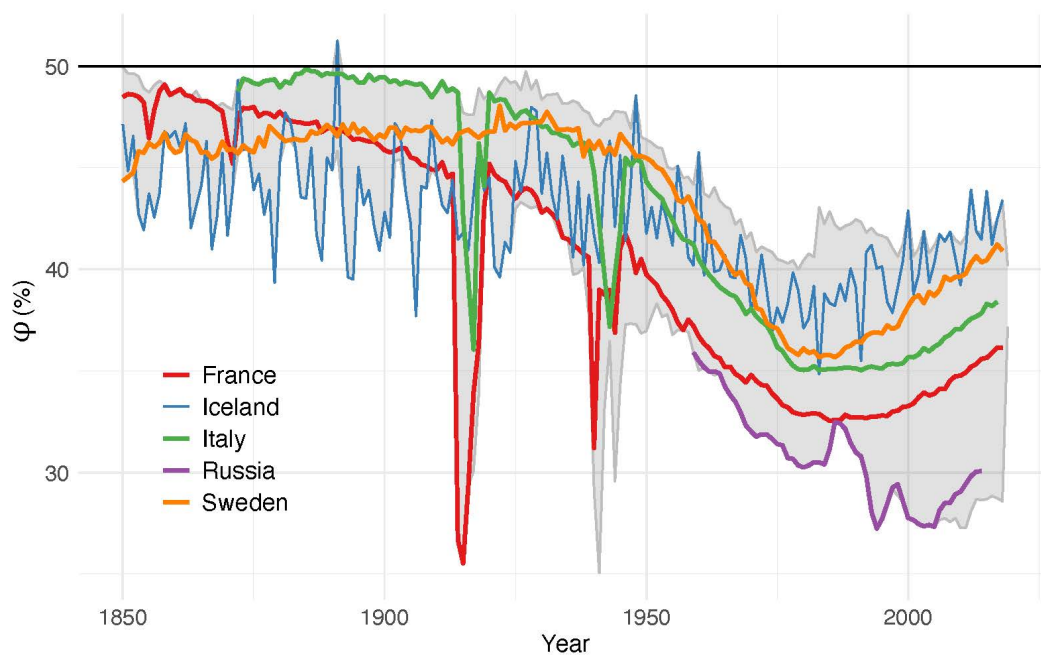


Fig. 2 Probability of males outliving females since 1850 for five countries and the range for all countries in the HMD in grey.

Figure 3 shows that φ is negatively correlated with the differences in life expectancy and positively correlated with females' standard deviation (similar results were found when males' standard deviation was used, due to the strong correlation between females and males' standard deviation). Thus, the smaller the difference in life expectancy and the larger the standard deviation, the higher φ would be. The correlation between φ and the standard deviation is weaker in recent years, due to reduction in sex differences in life expectancy, which is also driving changes in φ . Even

though both life expectancy and lifespan variation affect φ , the statistic appears more sensitive to the differences in life expectancy than to the level of lifespan variation. We found similar results for cohort data (see Appendix D).

The same φ value can then be found for different combinations of sex differences in life expectancy and levels of lifespan variation. For example, the same φ of 36.3% was found in France in 1961 and in 2017 (Figure 3). However, the sex differences in life expectancy was 6.9 in 1961 and 5.8 in 2017 and the standard deviation for females was 18.3 in 1961 and 13.6 in 2017. Thus, due to smaller lifespan variation in recent years, smaller sex differences are required today to have the same φ as in the past.

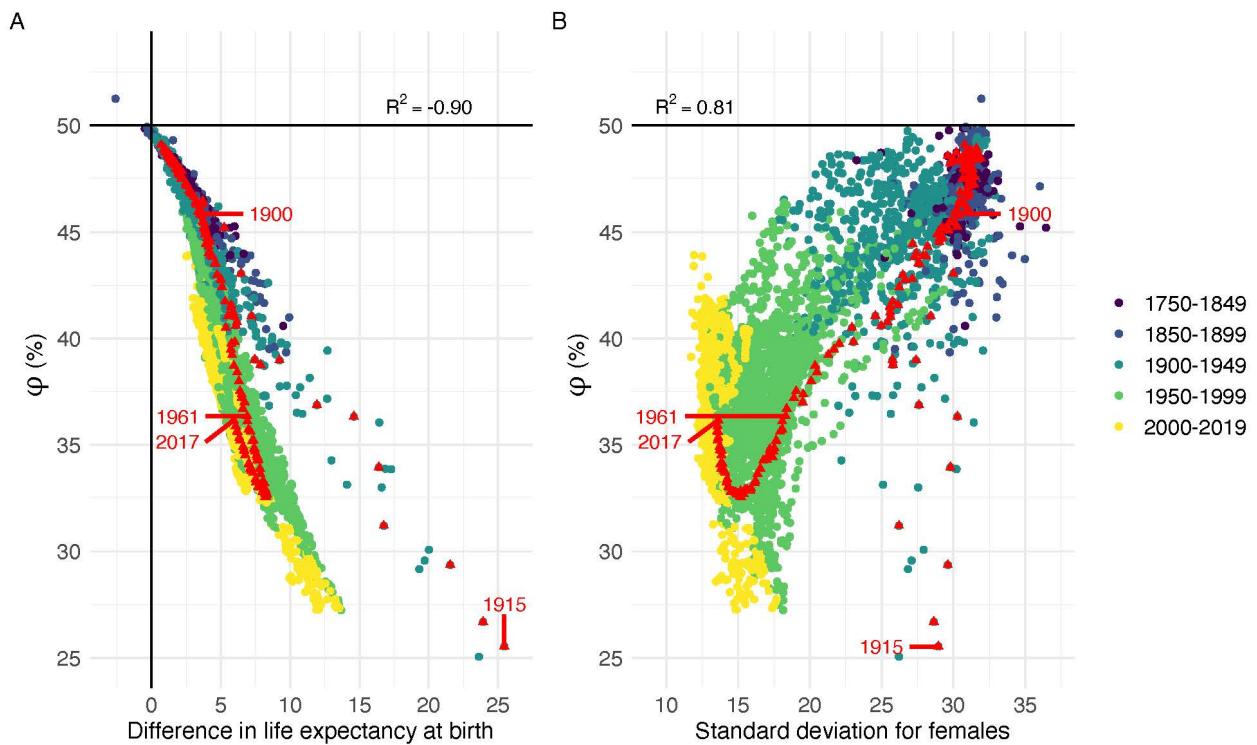


Fig. 3. Relation between φ and (a) the sex differences in life expectancy and (b) the standard deviation for females for HMD period data, with France highlighted (red triangles).

Figure 4 shows the same relations as shown in Figure 3 but for survivors to age 50. Lifespan variation at age 50 has stayed roughly constant over time (Engelman et al., 2014) and comparing φ from this age can help assessing the sensitivity of the measure to changes in lifespan variation. The relation between φ and differences in life expectancy is stronger and more linear from age 50 (correlation coefficient of -0.99) than when using the full age-range, increasing predictive ability. For example, for a difference in life expectancy at age 50 of 3 years, males have around 42% probability to outlive females. Noteworthy, φ in France was 36.2% in 1961 and 36.4% in 2017.

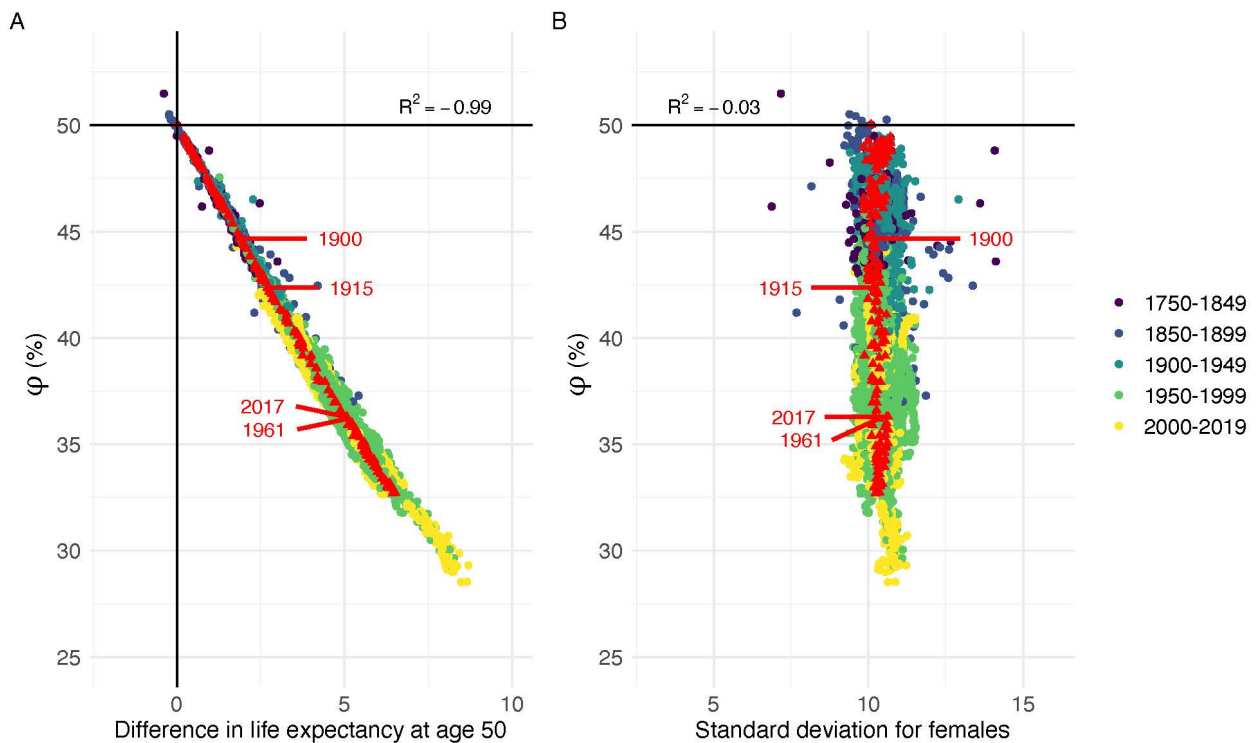


Fig. 4 Relation between φ and (a) the sex differences in life expectancy and (b) the standard deviation for females for HMD period data, conditional to survival to age 50, with France highlighted (red triangles).

Similar to the distribution from birth, the probability of males outliving females from age 50 has, in almost all periods and populations, varied between 28% and 50%, with only few exceptions. In recent years, the φ statistics from birth and from age 50 are similar.

5. DISCUSSION

Our analysis highlights the importance of looking at the randomness of the mortality process and reveals important similarities between the distribution of lifespans of females and males. Due to a mixture of cultural, social, epidemiological and biological factors, males tend to die earlier, on average, compared to females (Crimmins et al., 2019; Rogers et al., 2010). Still, we found that in almost all points in time, between one and two men out of four outlived a randomly paired woman. When the analysis only relies on statistics such as life expectancy and lifespan variation such an important aspect of the mortality process is overlooked.

Another major result of our analysis is that the smaller the difference in life expectancy and the larger the standard deviation, the higher the probability that males outlive females. On the one hand, the narrowing sex difference in mortality in the last decades (Glei & Horiuchi, 2007) would lead to bigger proportions of males outliving females. On the other hand, the important reduction in lifespan variation observed over time for both sexes (Aburto et al., 2020; Vaupel et al., 2011) reduces the probability of males outliving females. Therefore, within a same country and for a same sex difference in life expectancy, recent φ are often smaller than for earlier years, due to smaller lifespan variation observed in recent years. The φ statistics could also be sensitive to other moments than the mean and variance and more work is needed to assess this relationship.

The reduction in lifespan variation represents a major achievement of the mortality improvement process that has reduced inequalities between individuals. However, the reduction of lifespan inequality has also made it less likely for males to outlive females. This is partly explained

by the fact that lifespan variation reduction has been driven by mortality declines at younger ages (Aburto et al., 2020). When looking at the lifespan distribution (as in Figure 1, scenario D), survival improvements at younger ages narrowed the left tails of the distribution for both sexes. By reducing the left tail of female distribution, without increasing the right tail of the male distribution, the overlapping area is reduced. In other words, as the number of short-lived females, which are easier to outlive, decreases over time, males have to increasingly shift their distribution to higher ages to be able to outlive females.

Trends over time in φ are consistent with the reversed trends in sex differences in life expectancy (Glei & Horiuchi, 2007): the probability of males outliving females decreased until the 1970s, after which it gradually increased in all populations. Beltran-Sanchez et al. (2015) showed that the increase in sex differences in mortality emerged in cohorts born after 1880, which is consistent with our analysis of φ (see Appendix D).

As previously discussed, the metric we use expresses the proportion of males outliving females among randomly paired individuals and assumes independence between populations. However, males and females in a population are generally not random pairs but couples, whose health and mortality patterns have been found to be positively correlated due a strong effect of social ties on health and longevity (Rasulo et al., 2005). Coupled individuals also influence each other's health (Perelli-Harris et al., 2018), and this is particularly true for males, who benefit more than females from being in a stable relationship (Staehelin et al., 2012). Unfortunately, the HMD data and the φ statistic do not permit the estimation of the probability of males outliving females for not randomly paired individuals.

There are always some males living longer than some females. This implies that inequalities in lifespan between sexes are attributable to some part of (each) population and not to the whole. Indeed, Luy and Gast (2014) found that male excess mortality is mainly caused by some specific

subpopulation of males with particularly high mortality. Given the sex differences in mortality within a population, being able to better identify the characteristics of the short-lived men could help tackle more efficiently male-female inequality. The method we proposed is applicable to other (sub-)populations or to a combination of them. For example, differences in life expectancy between females and males tend to decrease with increasing number of education years (Molla et al., 2004). Knowing the probability of males outliving females in a specific educational group can contribute to developing more informed policies aimed at reducing specific education inequalities in mortality between sexes.

Our results show that there are more important similarities between females and males' lifespans than indicated by an analysis that relies only differences in life expectancy and lifespan variation. To get a better picture about inequalities, the φ statistics is then an important complement to life expectancy and lifespan variation in any study of inequalities between populations.

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APPENDIX

A. DATA

Table 1. Countries/ regions and years with available data in the HMD

Country\region	Years	Country\region	Years
Australia	1921-2018	Japan	1947-2018
Austria	1947-2017	Latvia	1959-2017
Belarus	1959-2018	Lithuania	1959-2017
Belgium	1841-2018	Luxembourg	1960-2017
Bulgaria	1947-2017	Netherlands	1850-2018
Canada	1921-2016	New Zealand	1948-2013
Chile	1992-2008	Norway	1846-2018
Croatia	2001-2018	Poland	1958-2018
Czechia	1950-2018	Portugal	1940-2018
Denmark	1835-2019	Republic of Korea	2003-2018
Estonia	1959-2017	Russia	1959-2014
Finland	1878-2019	Slovakia	1950-2017
France	1816-2018	Slovenia	1983-2017
Germany-East	1956-2017	Spain	1908-2018
Germany-West	1956-2017	Sweden	1751-2018
Greece	1981-2017	Switzerland	1876-2018
Hong Kong	1986-2017	Taiwan	1970-2014
Hungary	1950-2017	UK – England and Wales	1841-2018
Iceland	1838-2018	UK- Scotland	1855-2018
Ireland	1950-2017	UK- Ireland	1922-2018
Israel	1983-2016	USA	1933-2018
Italy	1872-2017	Ukraine	1959-2013

B. PROOF

In the main manuscript, we showed that the probability (φ) of individuals in the first population outliving those in the second population is:

$$\begin{aligned}
 \varphi &= \int_0^{\omega} \int_0^x d_{1,2}(x,y) dy dx \\
 &= \int_0^{\omega} d_1(x) \int_0^x d_2(y) dy dx \\
 &= \int_0^{\omega} d_1(x) D_2(x) dx.
 \end{aligned} \tag{B1}$$

Following the same approach, we can find the complement of φ , labeled φ' , which is the probability of individuals in the second population to outlive those in the first:

$$\begin{aligned}
\varphi' &= \int_0^\omega \int_0^y d_{1,2}(x,y) dx dy \\
&= \int_0^\omega d_2(y) \int_0^y d_1(x) dx dy \\
&= \int_0^\omega d_2(y) D_1(y) dy \\
&= \int_0^\omega d_2(y) [1 - l_1(y)] dy \\
&= 1 - \int_0^\omega d_2(y) l_1(y) dy.
\end{aligned} \tag{B2}$$

From Equations (B1) and (B2) it can be shown that $\varphi + \varphi' = 1$. Thus, φ is also equal to:

$$\begin{aligned}
\varphi &= 1 - \varphi' \\
&= 1 - \left[1 - \int_0^\omega d_2(x) l_1(x) dx \right] \\
&= \int_0^\omega d_2(x) l_1(x) dx.
\end{aligned} \tag{B3}$$

Equation (B3) is the same as equation (1) in the main manuscript.

C. SIMULATIONS AND DISCRETE APPROXIMATION

We simulated age at death distributions, using the Gompertz model, using various scale (M) and shape (β) parameters (Missov et al., 2015). The distributions were first found using an age width (n) of 0.0001, after which the data were aggregated within 1-year and 5-years age-groups. The probability that individuals in both population died within the same age-group, $\sum_{x=0}^\omega n d_x^1 n d_x^2$, was then redistributed between φ and φ' based on two assumptions: equal (equation C1) and proportional redistributions (equation C2). The results are presented in Table 2.

$$\varphi \approx \sum_{x=0}^{\omega} n d_x^1 n D_{x-n}^2 + \frac{\sum_{x=0}^{\omega} n d_x^1 n d_x^2}{2} \quad (C1)$$

$$\varphi \approx \sum_{x=0}^{\omega} n d_x^1 n D_{x-n}^2 + \sum_{x=0}^{\omega} n d_x^1 n d_x^2 * \frac{n d_x^1 n D_{x-n}^2}{n d_x^1 n D_{x-n}^2 + n d_x^2 n D_{x-n}^1} \quad (C2)$$

The simulations show that equally redistributing $\sum_{x=0}^{\omega} n d_x^1 n d_x^2$ between the two other statistics provide very similar results to the continuous data ($n=0.0001$), especially for the 1-year age-group. More differences are found when aggregating by 5-years age-groups, but the difference in φ between the different age-width remains less than 1 percentage point, when equally redistributing $\sum_{x=0}^{\omega} n d_x^1 n d_x^2$.

Table 2. Assumptions to redistribute $\sum_{x=0}^{\omega} n d_x^1 n d_x^2$ for different mortality scenarios.

	φ	φ'	$\sum_{x=0}^{\omega} n d_x^1 n d_x^2$	Eq. C1	Eq. C2
Gompertz: $M_A = 61, M_B = 65, \beta_A = 0.12, \beta_B = 0.14$					
Continuous	36.3	63.7	0.0	-	-
1-year	34.8	62.2	3.0	36.3	35.9
5-years	28.2	55.8	15.0	36.7	34.3
Gompertz: $M_A = 61, M_B = 70, \beta_A = 0.10, \beta_B = 0.14$					
Continuous	23.6	76.4	0.0	-	-
1-year	22.5	75.2	2.3	23.6	23.0
5-years	18.5	70.0	11.3	24.2	20.9
Gompertz: $M_A = 68, M_B = 70, \beta_A = 0.13, \beta_B = 0.14$					
Continuous	42.8	57.2	0.0	-	-
1-year	41.2	55.5	3.3	42.8	42.6
5-years	34.9	48.8	16.3	43.0	41.7
Gompertz: $M_A = 69, M_B = 70, \beta_A = 0.10, \beta_B = 0.12$					
Continuous	46.1	53.9	0.0	-	-
1-year	44.7	52.6	2.7	46.1	46.0
5-years	39.4	47.2	13.4	46.1	45.5

To further test the model and the redistribution of $\sum_{x=0}^{\omega} n d_x^1 n d_x^2$, we simulated 100,000 individual lifespans from an exponential distribution with piece-wise constant rates (Willekens,

2009). We performed this procedure for every population and by sex using as an input empirical death rates retrieved from the HMD (2020). Then we randomly paired males and females and calculated the proportions of males outliving the paired female. Table 3 compares the discrete approach introduced in the main document (eq. C1) and the continuous approach based on simulations. Both approaches provided very similar results.

Table 3. Proportions of males outliving females based on a discrete and continuous approach (simulations).

	% males outliving females		% females outliving males	
	Continuous	Discrete	Continuous	Discrete
Denmark				
1850	46.1	46.4	53.9	53.6
1900	45.8	45.8	54.2	54.2
1950	46.2	46.3	53.8	53.7
2016	40.7	40.6	59.3	59.4
France				
1850	48.6	48.5	51.4	51.5
1915	25.6	25.5	74.4	74.5
1950	39.8	39.8	60.2	60.2
2016	35.9	36.0	64.1	64.0
Japan				
1950	44.1	44.2	55.9	55.8
2016	33.8	33.7	66.2	66.3
Russia				
1960	35.6	35.5	64.4	64.5
2014	30.2	30.0	69.8	70.0

D. COHORT ANALYSIS

Similar relations as those for period data were also found for cohorts (Figure 5). In the HMD, life table for cohorts were only available for 11 countries: Denmark, England and Wales, Finland, France, Iceland, Italy, Netherlands, Norway, Scotland, Sweden and Switzerland. For cohorts with complete mortality history, the proportions of males outliving females varied between 35% and 49%. Only small changes in φ were observed for cohorts born prior to 1870-1890, with φ varying around 46.5%.

For the cohorts born afterwards, φ decreases, reaching a mean of 38.4% for the cohort born in 1925, with values varying between 35.3% (Finland) and 40.4% (Scotland).

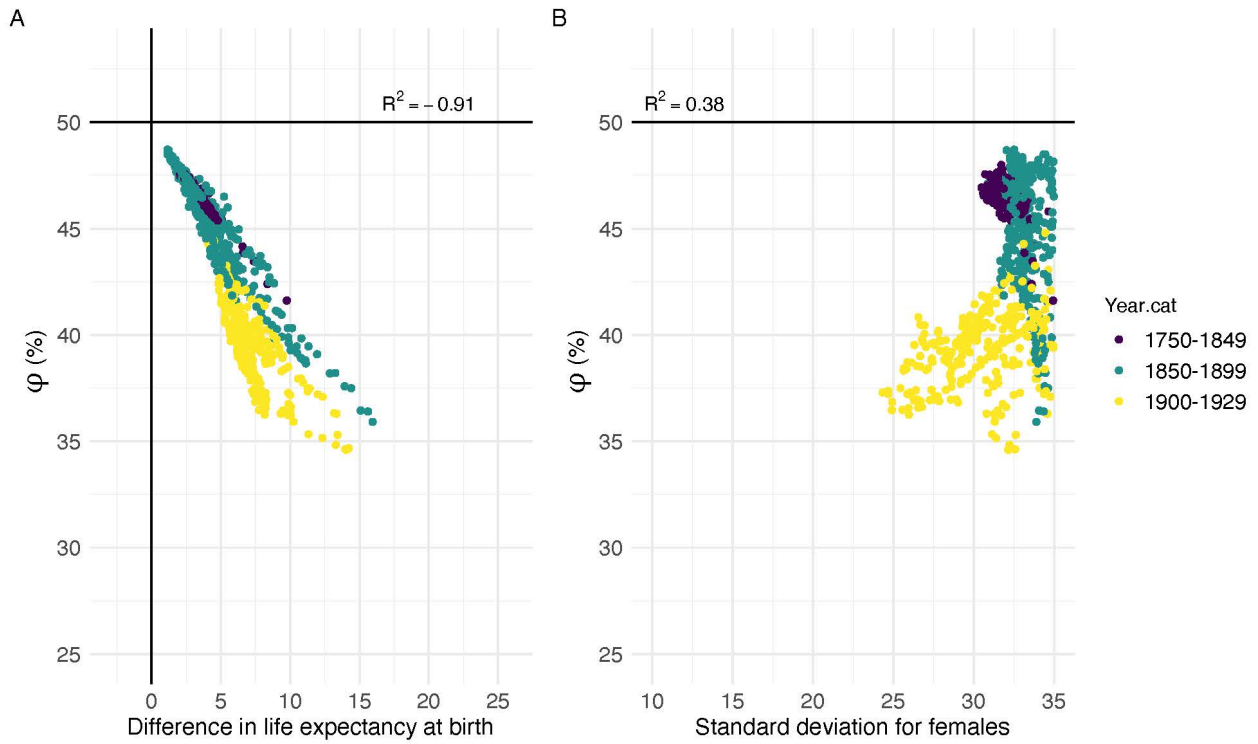


Fig. 5 Relation between φ and (a) the sex differences in life expectancy and (b) the standard deviation for females for HMD cohort data.