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Healthy Lifespan Statistics Derived From Cross-Sectional Prevalence Data Using the Sullivan Method are Informative Summary Measures of Population Health*

Magdalena Muszyńska-Spielauer, Tim Riffe, Martin Spielauer

Abstract: Health expectancy (HE), commonly derived from cross-sectional prevalence data using the Sullivan method, serves as the most frequently used summary measure of population health. Like lifespan distribution statistics, which are often discussed alongside life expectancy (LE) in demographic studies, analogous statistics on healthy lifespans can provide valuable information on population health. We examine whether healthy lifespan distribution statistics beyond HE can be estimated based on cross-sectional prevalence data and the life table, the data inputs of the Sullivan method. To do so, we treat the Sullivan method as an extension of the stationary population model to health and distinguish between health conditions with and without recovery from the state of decreased health. Our empirical demonstration is based on the prevalence of chronic diseases in selected European countries in 2017 from the Survey of Health, Ageing and Retirement in Europe (SHARE), as well as on life tables from EUROSTAT.

We find that the Sullivan method, when considered as an extension of the stationary population model to health, allows for the estimation of a healthy survival distribution and its statistics, beyond HE, for health characteristics with no recovery from the state of decreased health. We show that for such health conditions, the method requires that the number of persons in full health in a stationary population does not increase with age. We argue that for such health dimensions, HE conditional on being in good health at the life table radix age is of relevance for health policy interventions.

In our empirical application, we show that the conditional and unconditional measures of HE can give substantially different pictures of population health. Furthermore, we show that across European countries, in contrast to the negative

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relationship between LE and lifespan inequality, higher HE is associated with greater inequality in healthy years lived when conditional on being healthy at age 50.

Overall, the Sullivan method, when considered as an extension of the stationary population model, proves to be a valuable tool for deriving summary statistics of population health beyond HE, which are highly relevant to public policy.

Keywords: Population health · Health expectancy · The Sullivan method · Healthy survival · Healthy lifespan

1 Introduction

Health expectancy (HE) is the most common summary measure of population health and is most often derived using the Sullivan method. Despite its well-discussed limitations (*Barendregt et al*. 1994, 1997; *Laditka/Hayward* 2002; *Rogers et al.* 1990), the Sullivan method remains the most widely used method to estimate HE due to its minimal data requirements and computational simplicity. The method is based on cross-sectional health prevalence data combined with the stationary population distribution of a period life table. Other methods for deriving HE are double decrement life tables, multistate life tables, multistate Markov chain models with rewards, and microsimulation models. Some of the solutions of the Sullivan method have previously been used to derive measures of healthy lifespans other than HE. First, *Caswell* and *Zarulli* (2018) propose a Markov chain with rewards model to derive the first three moments of the healthy longevity distribution. The first three moments allow, in addition to HE, to estimate the variance and skewness of the distributions of healthy longevity. Second, *Permanyer et al.* (2022) use Sullivan data inputs to derive "age-at-disability onset distributions" (p.3). From these distributions, the authors derive HE and inequality in the age of disability onset, quantified by the Gini coefficient. Finally, based on health-adjusted life expectancy (HALE) values from the Global Burden of Diseases Study (GBD), *Permanyer et al.* (2023) and *Zarulli* and *Caswell* (2022) reconstruct healthy lifespans and estimate healthy lifespan inequality statistics.

In this study, we revisit the Sullivan method and show that, when considered as a stationary population model, it gives the theoretical foundation needed to derive healthy lifespan distributions in period life tables. We identify the limitations of the above-mentioned previous studies and show that our method significantly improves their solutions. We also identify the necessary assumptions and limitations of our method and apply it to a comparative study of the distribution of years lived in full health in selected European countries in 2017.

2 Methods

2.1 The Sullivan method basics

Research questions answered by the Sullivan method refer to the average experience of a synthetic life table cohort. The Sullivan method, however, is based on the stationary population model. The link between the stationary population model and the synthetic life table cohort is the period life table, from which they both derive (*Heuveline* 2023; *Preston et al.* 2000). According to the Sullivan method, the number of persons alive in each age group in the stationary population, as implied by a period life table, is partitioned into subgroups by health state according to the age-specific probabilities of being in each health state. These probabilities are estimated from the observed age-specific prevalence of health states in cross-sectional data, usually a survey. The resulting number of persons alive at age x in a given health state i in a stationary population ($L_{x,i}$, using life table notation) is then interpreted as the statistic of the corresponding life table synthetic cohort of the total years lived in a given age interval [x, $x + n$) and health state i (*Cambois et al.* 1999; *Rogers et al.* 1990). The HE of persons alive at age x is then derived by summing the years lived in good health at ages x and above.[1]

Imai and *Soneji* (2007) provide statistical proof that, to derive an unbiased and consistent estimator of HE, in addition to the standard assumptions of the life table stationary population model, the requisite assumption under the Sullivan method is that the age-specific prevalence of health conditions remains constant over time long enough for the population to become stationary. The authors refer to this assumption as "stationarity of age-specific disability prevalence" (*Imai*/*Soneji* 2007: 1203). The prevalence of a health state is a stock variable, resulting from flows between health states, and all assumptions of the stationary population model concern population flows. Therefore, the extension of the stationary population model to health states requires there to be the assumption that the transition rates between health states result in a constant age-specific probability of being in each of the selected health states. Furthermore, the lifespans of individuals by health status can only be derived from life table mortality rates and health prevalence data if the Sullivan method is considered as an extension of the stationary model to health status.[2] In the following sections of the paper, "Sullivan method" means "the Sullivan method considered as an extension of the stationary population model".

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1 This method, known as the Sullivan method, actually differs from the one originally proposed by *Sullivan* (1971). In the original method, the number of years lived free of disability in an age group x was derived by redistributing the number of years lived in an age group x in a life table synthetic cohort in accordance with the average share of disability days in a study year per person aged x, as observed in a study population.

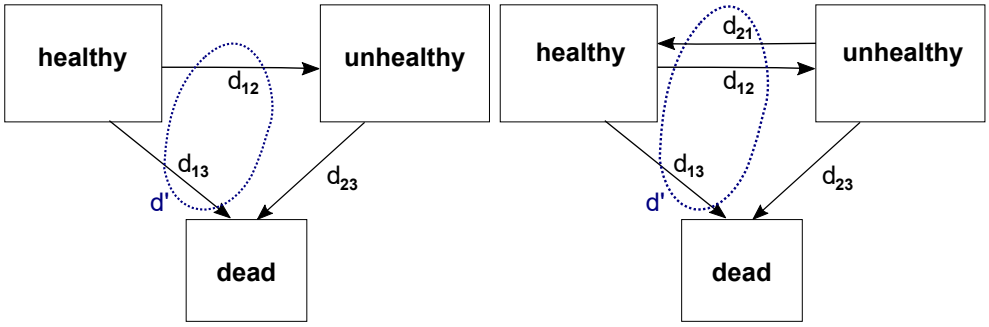
2 Alternatively, the Sullivan method can be considered as a solution to derive HE as the multiplication of the average number of years of life of the life table cohort (LE) by the average healthy period per year of life.

2.2 Types of health dimensions and life table notations

In this paper, we focus on the Sullivan method applied to health conditions with a binary specification of health states, i.e. full or decreased health, which is the most common in demographic studies. Our method can be extended to health dimensions with more than two health states, and other specifications of health dimensions as in *Caswell* and *Zarulli* (2018), as long as the requirements specified in the next sections are met. The Sullivan method is based on the prevalence of decreased health by age. As in any population, prevalence at age *x* is implicitly an outcome of transitions between health states in ages below *x*. Accounting for these transitions, we distinguish between health conditions with an irreversible (Fig. 1a) and reversible state of decreased health (Fig. 1b).

Fig. 1: Diagrams of the population stocks and flows between health states in two types of health dimensions with a binary specification of health state

(a) Irreversible state of decreased health (b) Reversible state of decreased health



Notes: The specific transitions in the diagrams are highlighted in order to facilitate the explanation of the methods in the text.

Source: Own design

In Table 1, we define the notations used throughout this paper. The notations are defined for an age interval [*x, x* + *n*) from an abridged life table, where *n* defines the width of the age interval.

2.3 Stationary population by health state in a single-age life table

Since the Sullivan method derives the number of persons alive and healthy in each age group in the stationary population of a period life table, it also provides an estimate of the average number of persons healthy in each age group in this population.

According to the Sullivan method, the number of persons in full health in a stationary population at age *x* at any point in time is a subset of the number of

Tab. 1: Notations for population stocks and flows in the stationary population and the synthetic cohort models of an abridged life table*

Variable	Stationary Population	Synthetic Cohort
${}_nL_x$	Number of persons alive at any point in time between ages x and $x + n$	Person-years lived between ages x and $x + n$
${}_nL'_x$	Number of persons healthy at any point in time between ages x and $x + n$	Person-years lived in full health between ages x and $x + n$
${}_na_x$	Mean time elapsed at death since x*th* birthday for deaths occurring between ages x and $x + n$ in a calendar year	Mean person-years lived between ages x and $x + n$ by those dying in the age interval
$x + {}_na_x$	Mean age at death for deaths occurring between ages x and $x + n$ in a calendar year	-
$l_{x + {}_na_x}$	Average number of persons alive at any point in time between ages x and $x + n$ in a calendar year**	Number of persons left alive at age $x + {}_na_x$
$l'_{x + {}_na_x}$	Average number of persons who are healthy at any point in time between ages x and $x + n$ in a calendar year**	Number of persons in full health at age $x + {}_na_x$
${}_n\pi_x$	Share of persons who are unhealthy among those alive between ages x and $x + n$	Average share of years lived as unhealthy out of the total person-years lived between ages x and $x + n$
${}_nd_x$	Annual number of deaths between ages x and $x + n$	Number of persons dying between ages x and $x + n$
${}_nd'_x$	*Models with an irreversible state of decreased health*	
	Annual number of persons leaving the stationary population by a decrease in health or death between ages x and $x + n$	Number of persons becoming unhealthy or dying between ages x and $x + n$
	Models with a reversible state of decreased health	
	Annual difference in the number of persons recovering and persons becoming unhealthy plus deaths between ages x and $x + n$	Difference in the number of persons recovering and persons becoming unhealthy or dying between ages x and $x + n$

* for a single-age life table: $n = 1$, ${}_na_x = 0.5$, the notations are simplified to L_x, L'_x, $l_{x + 0.5}$, $l'_{x + 0.5}$, π_x, d_x, d'_x, accordingly;

** this is a novel interpretation of the value of $l_{x + {}_na_x}$ and follows the explanations provided in Section 2.4.

Source: Own specifications based on *Preston et al.* (2000: 54, 57), *Jagger et al.* (2014)

persons alive at that age, proportional in size to the probability that a person alive at age x is in full health $(1 - \pi_x)$:[3]

$$L'_x = (1 - \pi_x)\, L_x \tag{1}$$

where the probability that a person alive at age x is in full health is estimated from the proportion of respondents who are in full health out of the total number of respondents at age x in a survey, or other source.

In a single-age life table, it is commonly assumed that deaths are evenly distributed across the age intervals, with the exception of the first age and the last open interval. Under this assumption, the period life table relies on the trapezoidal rule to provide a discrete approximation of the underlying continuous age distribution of the stationary population. The trapezoidal rule is routinely used in calculus to estimate the definite integral of a continuous function as the sum of the areas of trapezoids that approximate it in small intervals. The area of a trapezoid is half the sum of the lengths of its bases multiplied by its height. As shown in Figure 2b, the area of the trapezoid in the age interval $[x, x + 1)$ equals L_x, i.e. the number of persons alive at age x in a stationary population of a single-age period life table. Since the base of the trapezoid is the length of the age interval, its area is calculated as half of twice the length of the age interval multiplied by $l_{x + 0.5}$, which simplifies to:

$$L_x \approx l_{x + 0.5} \tag{2}$$

where $l_{x + 0.5}$ is the number of persons who survive to the middle of the age interval, which, assuming that deaths are evenly distributed over the age interval, is also the average number of persons alive in the age interval $[x, x + 1)$. Similarly, in a single-age life table, the number of those in full health at age x (L'_x) is equal to the average number of persons who are healthy at age x, which is the number of healthy individuals in the middle of the age interval ($l'_{x + 0.5}$). Since the Sullivan method allows us to derive the number of healthy individuals at age x using equation (1), we can also apply it to calculate the average number of people who are healthy at this age:

$$l'_{x + 0.5} = (1 - \pi_x)\, l_{x + 0.5} \tag{3}$$

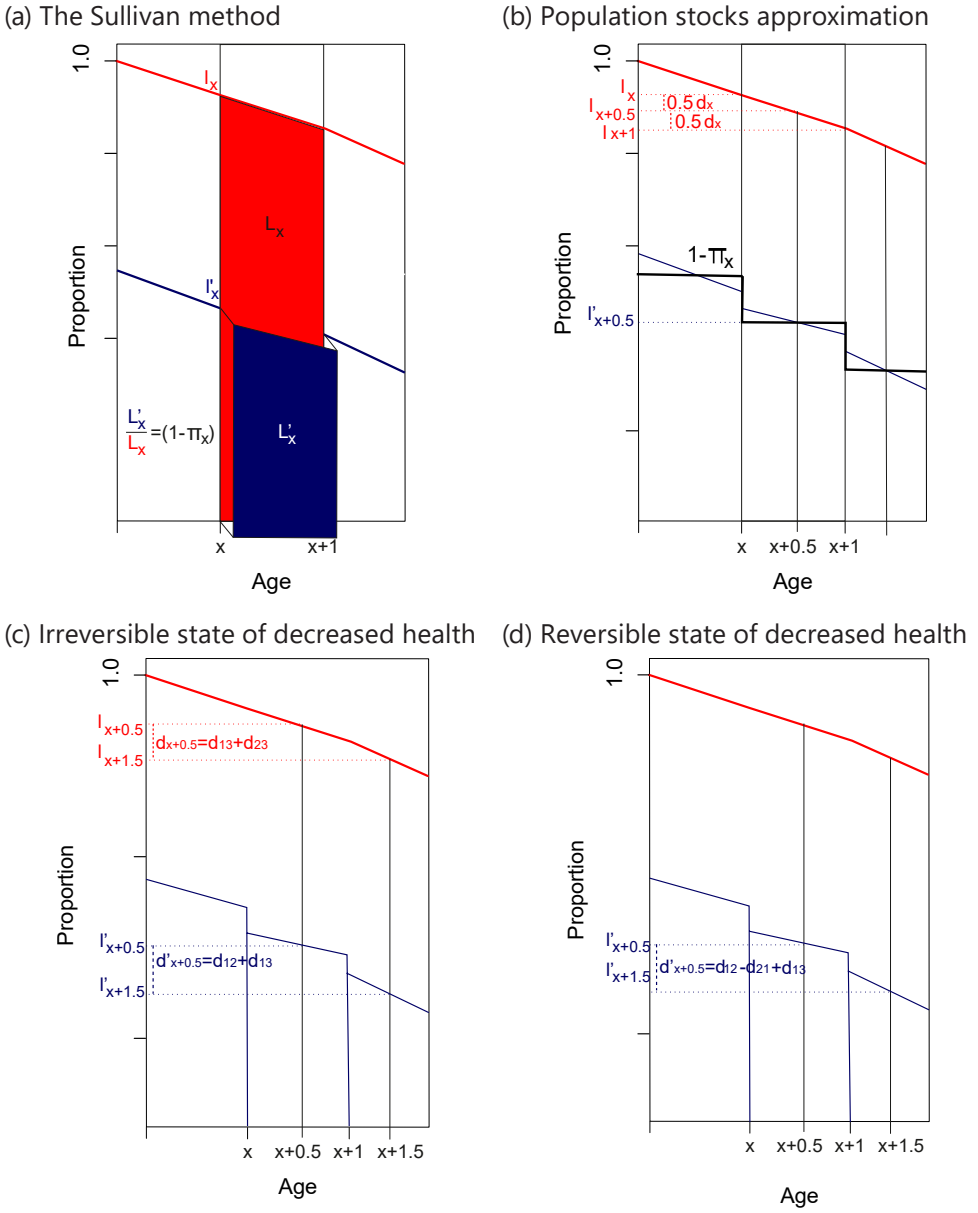
Compare Figures 2a and 2b for a graphical explanation of these relationships.

2.4 Stationary population by health state in an abridged life table

In an abridged life table, the average number of years lived by persons who die in an age interval $[x, x + n)$, denoted as ${}_n a_x$, is not well-approximated by the interval midpoint. For the case of abridged life table data, we presume that ${}_n a_x$ is either

[3] In a single-age life table, we refer to the age interval [x,x + 1) as "age x".

Fig. 2: Stationary populations in a single-age life table and the flows between health states



Source: Own design

given as a life table column or, if it is not given, it can be derived from other life table columns. The average number of persons alive in the age interval $[x, x + n)$ is approximately equal to the number of persons aged $x + {}_na_x$ (denoted as $l_x + {}_na_x$).

Accordingly, the number of persons alive in a stationary population of a period life table at age [x, $x + n$) is approximated by (see Fig. 3b)

$$ {}_nL_x \approx n \cdot l_{x+{}_na_x} \tag{4} $$

When ${}_na_x > 0.5n$ the distribution is right skewed and vice versa. In the example in Figure 3b, ${}_na_x > 2.5$, which implies that $d_{x,1} > d_{x,2}$. Here, $d_{x,1}$ denotes deaths that occur in the first part of the age interval, [x, $x + {}_na_x$), and $d_{x,2}$ denotes deaths in the second part of the age interval, i.e. [$x + {}_na_x$, $x + n$). In Figure 3b, the total number of years lost in the first sub-interval [x, $x + {}_na_x$) by persons who die in this sub-interval is denoted by $D_{x,1}$ and derived as:

$$ D_{x,1} = \frac{d_{x,1}\,{}_na_x}{2} \tag{5} $$

Similarly, years lost upon death in the second sub-interval [$x + {}_na_x$, $x + n$) by persons who die in this sub-interval is denoted by $D_{x,2}$ and derived as:

$$ D_{x,2} = \frac{d_{x,2} \cdot [n - {}_na_x]}{2} \tag{6} $$

According to the trapezoidal rule, the sum of the number of years lost by persons who die in the two age sub-intervals, i.e. [x, $x + {}_na_x$) and [$x + {}_na_x$, $x + n$), is equal ($D_{x,1} = D_{x,2}$). It therefore corresponds to the equations (5) and (6), with the total number of deaths in the age interval [x, $x + n$) denoted as $d_x = d_{x,1} + d_{x,2}$, where $d_{x,1}$ is the number of deaths in the age interval [x, $x + {}_na_x$) and derived as:

$$ d_{x,1} = \left[1 - \frac{{}_na_x}{n}\right] d_x \tag{7} $$

Therefore, survivors to age $x + {}_na_x$, and the average number of persons alive in the age interval [x, $x + n$) is approximated as

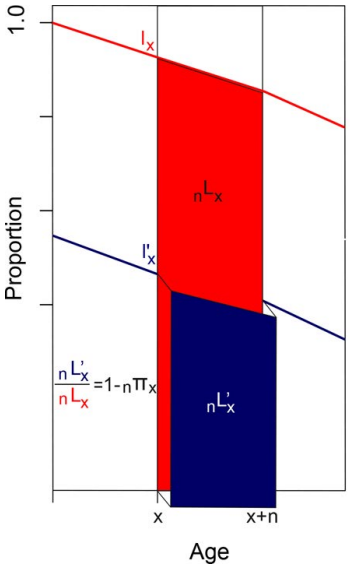
$$ l_{x+{}_na_x} = l_x - \left[1 - \frac{{}_na_x}{n}\right] d_x \tag{8} $$

According to the Sullivan method, the number of persons alive and in full health in a stationary population at age [x, $x + n$) is a subset of the total number of persons alive in that age interval, and its size is proportional to the prevalence of full health in that age interval ($1 - {}_n\pi_x$) :

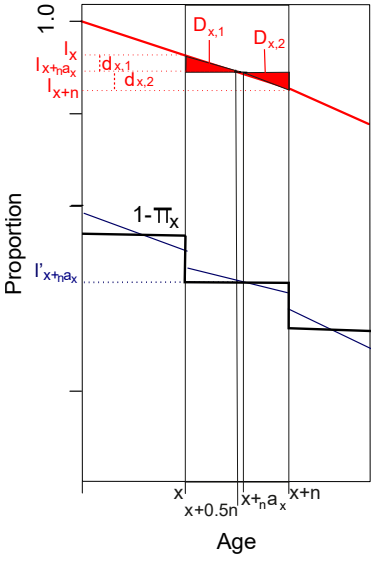
$$ {}_nL'_x = (1 - {}_n\pi_x)\,{}_nL_x \tag{9} $$

Fig. 3: Stationary populations in an abridged life table and the flows between health states

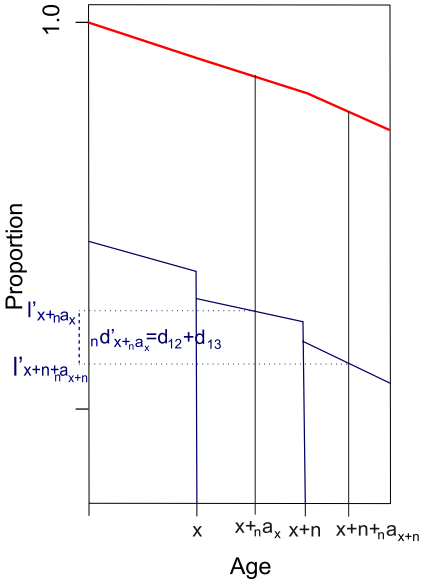
(a) The Sullivan method



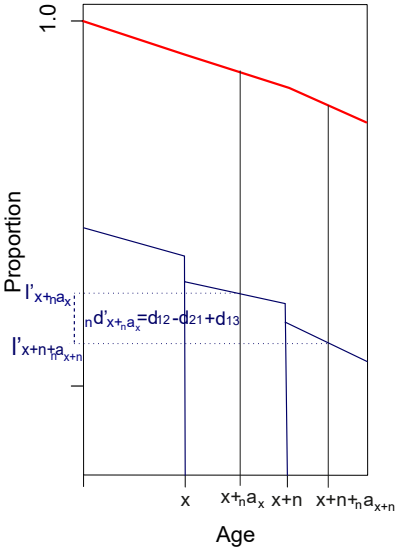
(b) Population stocks approximation



(c) Irreversible state of decreased health



(d) Reversible state of decreased health



Source: Own design

Hence, the number of persons who are healthy at age $x + {}_n a_x$, and, at the same time, the average number of persons who are healthy in an age interval $[x, x + n)$, is derived as:

$$l'_{x+n a_x} = (1 - {}_n\pi_x)\, l_{x+n a_x} \quad , \tag{10}$$

where $l_{x+n a_x}$ follows from equation (8).

2.5 An additional requirement for extending the stationary population model to health status

When using the empirical prevalence data, as in the empirical example of this study, an increase in the average number of persons who are healthy between two neighbouring age groups is sometimes observed (${}_n l'_{x+n} > {}_n l'_x$). This is impossible in health models based on health characteristics with an irreversible state of decreased health, and by extension, is not possible in the corresponding stationary population model.[4] In the case of a model with a reversible state of decreased health, an increase in the number of persons in full health from one age group to the next can only occur if the recovery rates are higher than the incidence, but this situation is rather unlikely. As shown, for example, by *Guillot* and *Yu* (2009) and *Lièvre et al.* (2003), the incidence of disability increases with age, and recovery from disability decreases with age. As the Sullivan method has not been commonly seen as an extension of the stationary population model to health, to our knowledge, this is the first time that this additional requirement has been recognised.[5]

The problem of an increase in the number of healthy individuals between two adjacent age groups can be resolved by any of the methods for data smoothing, for example, as presented in *di Lego* and *Sauerberg* (2023) in this special issue. In our empirical application, rather than making a greater intervention in the data by smoothing the entire survival curves, we choose to correct only individual observations where the number of healthy individuals in a given age group is higher than in a younger age group. In such cases, the number of individuals who reach a given age in full health is replaced by the average of those who reach the age group before the study group in full health and those who reach the age group after the study group in full health, i.e. $l'_y = \frac{l'_{y-n} + l'_{y+n}}{2}$.

4 However, an increase in the prevalence of full health from one age group to the next is possible. This can occur if the mortality of those experiencing diminished health is much higher than that of those in full health and the transitions from full to decreased health do not compensate for this difference in mortality.

5 The Sullivan method commonly applies the total number of persons who are healthy in an age interval (${}_n L'_x$). An increase in the number of healthy persons from one age interval to the next, is equivalent to an increase in the average number of healthy persons between two neighbouring age intervals of the same length (${}_n l'_{x+n} > {}_n l'_x$). Therefore, an increase in the total number of healthy persons from one interval to the next is not possible either.

2.6 Statistics of the healthy lifespan distribution

Based on period life tables and cross-sectional health prevalence data, we can derive the population stocks (denoted as $l_{x+0.5}$ and $l'_{x+0.5}$ in Figures 2c and 2d, or as $l_{x+n}a_x$ and $l'_{x+n+n}a_{x+n}$ in Figures 3c and 3d). The period life tables also give us the total number of deaths at age *x*. However, we do not have information on the exact number of transitions between health states (denoted as d_{ij} $i \in \{1,2\}$, $j \in \{1,2,3\}$, in Figures 1a and 1b).

For a health model with an irreversible state of decreased health, the healthy stock in a stationary population (l'_x) is equivalent to the healthy survivorship in a synthetic cohort of the same life table (see Table 1). From the healthy survivorship, we infer attrition from full health, either through death (d_{13} in Figure 1a) or health deterioration (d_{12}). In a single-age life table, the number of persons who cease to be in full health in the age interval [$x + 0.5$, $x + 1.5$) is denoted as $d' = d_{12} + d_{13}$ in Figure 1a and derived as (see Figure 2c):[6]

$$d'_{x+0.5} = l'_{x+0.5} - l'_{x+1.5} \tag{11}$$

In an abridged life table, the number of persons who cease to be in full health in the age interval [$x + {}_na_x$, $x + n + {}_na_{x+n}$) is derived as (see Figure 3c):

$${}_nd'_{x+na_x} = l'_{x+na_x} - l'_{x+n+na_{x+n}} \tag{12}$$

For a health dimension with a reversible state of decreased health, the value of $d'_{x+0.5}$ (or ${}_nd'_{x+na_x}$) gives the number of "net" transitions from a state of full health ($d' = d_{12} - d_{21} + d_{13}$ in Figure 1b), or in other words, a difference between outflows to and inflows from the state of decreased health ($d_{12} - d_{21}$) plus deaths of healthy people (d_{13}). The number of useful summary statistics that can be derived for the distribution of d' for a reversible state of decreased health is limited to HE. Since inflows and outflows are not observed separately for the Sullivan input data, it is not possible to derive a distribution of healthy and unhealthy lifespans for individuals when return to full health is possible, and by extension, one cannot estimate statistics of inter-individual inequality in healthy lifespans. Furthermore, it is not possible to derive the inflows and outflows according to health status at the threshold age. Nor is it possible to estimate the number of healthy years lived by persons who are healthy at the threshold age for these health dimensions. As result, HE that are conditional on being healthy at the threshold age cannot be derived for health dimensions with a reversible state of decreased health. All statistics in the following sections are derived for health dimensions with an irreversible state of decreased health.

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6 The proposed method of deriving the quantities l'_x and d'_x for a health model with an irreversible state of decreased health differs from the double-decrement model (see, for example, *Katz et al.* (1983)), as the latter is derived based on transition rates between health states.

Below, we provide solutions to derive statistics for data from abridged life tables, as these formulas can be easily adapted to a single-age life table. A statistic of HE conditional on being healthy at age *x* for a synthetic cohort of an abridged life table is estimated as

$$e'h_x \approx e'h_{x+na_x} = \frac{1}{l'_{x+\,{}_na_x}} \sum_{z=x}^{\omega} L_z \pi_z \tag{13}$$

Since the distribution of healthy individuals by age can only be inferred at the exact ages $x + {}_na_x$, the remaining HE of persons who are healthy at age *x* can only be approximated by the statistic at age $x + {}_na_x$. This statistic differs from the standard HE, derived as

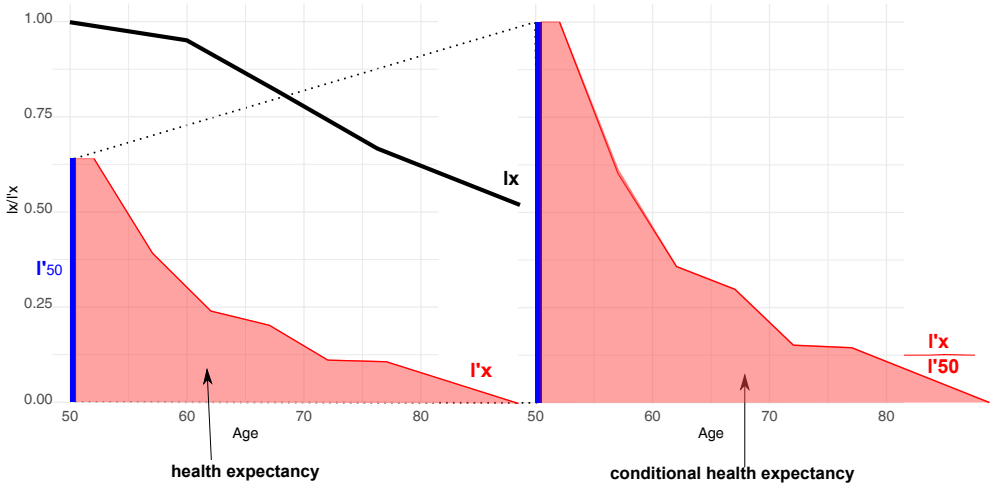
$$eh_x = \frac{1}{l_x} \sum_{z=x}^{\omega-n} L_z \pi_z = \frac{1}{l'_x + l''_x} \sum_{z=x}^{\omega} L_z \pi_z \tag{14}$$

where $l''_{x\,+\,na_X}$ is the average number of persons who are unhealthy at any point in time between ages *x* and *x+n* in the stationary life table population and, at the same time, the number of persons in a decreased health status at age $x + {}_na_x$ in the synthetic life table cohort.

While the conditional HE ($e'h_x$) represents the mean number of healthy years remaining among persons who are healthy at age x, the standard HE (eh_x) represents the mean number of healthy years remaining among persons who are alive at age *x*, regardless of their initial health status. In the case of a health dimension with an irreversible state of decreased health, persons who are unhealthy at age *x* have no healthy life years ahead of them. Thus, the standard statistic of HE averages the remaining healthy years between the two subgroups: healthy persons, who could potentially accumulate the healthy years in their lives, and persons who are already unhealthy, who cannot. The conditional statistic of HE averages the healthy years ahead only over the group of healthy people who could potentially live those years, in the same way as remaining life expectancy (LE) at age *x* is conditional on survival to age *x*. HE conditional on being healthy in the presence of irreversible disease can be interpreted as the mean age of decline in health, similar to LE being interpreted as the mean age of death in a stationary population. Figure 4 shows the difference between HE and HE conditional on being healthy at age $50 + {}_5a_{50}$. LE at age 50 is conditional on survival to this age and is equal to the area under the survival curve l_x (*Preston et al.* 2000: 69) in Figure 4a. HE is the area under the healthy survival curve l'_x in Figure 4a. HE conditional on survival to age $50 + {}_5a_{50}$ is equal to the area under the healthy survival curve in Figure 4b. The healthy survival curve, denoted as $\frac{l'_x}{l'_{50}}$ in Figure 4a, is derived by dividing the number of healthy persons at any age by the number of healthy persons at the initial age $50 + {}_5a_{50}$.

In this study, we quantify healthy lifespan inequality using the standard deviation. However, it is also possible to estimate any additional statistic of lifespan disparities for a distribution of healthy survival in health dimensions with an irreversible state of

Fig. 4: Health expectancy (left panel) and health expectancy conditional on being healthy at age 50 (right panel)



Source: Own design

decreased health (for example, compare the statistics of lifespan variation discussed in *Wilmoth* and *Horiuchi* (1999)). For a synthetic cohort of an abridged life table, the standard deviation of healthy lifespans conditional on being healthy at the threshold age x is estimated as:

$$S'h_x \approx S'h_{x+\,{}_n a_x} = \sqrt{\frac{1}{l'_{x+\,{}_n a_x}} \sum_{z=x}^{\omega-1} (z - [e'h_x + x])^2 \;\; {}_n d'_z} \tag{15}$$

where

$$z = x + \frac{d_{x,2}\,{}_n a_x + d_{x+1,1} \cdot {}_n a_{x+n}}{d_{x,2} + d_{x+1,1}} \tag{16}$$

approximates the average age at death in the interval $[x + {}_n a_x,\ x + n + {}_n a_{x+n})$, which is also assumed to equal the average age at which a person stops being healthy. d_{x2} denotes the number of deaths that occurred in the age sub-interval $[x + {}_n a_x,\ x + n)$, and $d_{x+1,1}$ denotes the number of deaths that occurred in the age sub-interval $[x + n,\ x + n + {}_n a_{x+n})$ (compare equations (5)-(7)). $l'_{x+\,{}_n a_x}$ is the number of people who reach age $x + {}_n a_x$ in full health, ${}_n d'_{y+\,{}_n a_y}$ is the total number of transitions from full health between ages $x + {}_n a_x$ and $x + n + {}_n a_{x+n}$, as defined in equations (3) and (10) (see Fig. 2c and 3c). The conditional standard deviation at age x is approximated by this statistic for age $x + {}_n a_x$ x.

2.7 Improvements over previous methods

Caswell and Zarulli (2018) propose using Markov chain models with rewards to derive various statistics of healthy lifespans based on prevalence data. The proposed inequality statistic is the variance of healthy lifespans. This statistic accounts for the variance due to stochasticity in survival and due to the random outcome of the probabilities of collecting the reward of a year of healthy life. In the model of *Caswell* and *Zarulli* (2018), due to the limitations imposed by the health prevalence data, the distribution of the probability of collecting a reward of a year of healthy life, as well as the probability of death, are identical for healthy and unhealthy individuals.[7] Hence, years of life and years of healthy life are assigned randomly to the living individuals, independent of current health status. In this article, we show that for a health dimension with an irreversible state of decreased health, the healthy life years of individuals belonging to a stationary population can actually be derived from information on survival and prevalence of decreased health.

Life tables commonly use the standard trapezoidal rule to approximate the survival curve at each age interval. In our study, and also in the study undertaken by *Permanyer et al.* (2023), we derive healthy survival distributions using the same approximations as those used in the period life tables. This improves the solution proposed by *Permanyer et al.* (2022), in which the healthy survival curve is estimated based on the assumption that transitions between health states occur at the beginning of each age interval.

In this study, we distinguish between health dimensions with an irreversible and a reversible decreased health state and demonstrate that healthy life years can be deconstructed only for the former. This distinction was not formally made in these prior studies. Furthermore, in the empirical demonstrations of all these studies, the health dimensions applied are all reversible health conditions (including the study of *Zarulli* and *Caswell* 2022).

3 Data

The health prevalence data is estimated based on cross-sectional data from the Survey of Health, Ageing and Retirement in Europe (SHARE) (*Börsch-Supan* 2020; *Börsch-Supan et al*. 2013). To construct our full sample, we combine respondents observed in wave 7 with respondents who dropped out of the panel sample and whose health status at wave 7, including the status of being dead, was imputed in a microsimulation model. This imputation procedure and its implications are discussed in detail in *Muszyńska-Spielauer* and *Spielauer* (2022). Similar to the original method of deriving cross-sectional individual weights in the SHARE survey (*De Luca/Rosetti* 2019), we derive cross-sectional individual weights for our full sample by raking to

[7] The probability of collecting a reward of a year of healthy life depends on the current health status in the incidence-based models of *Caswell* and *van Daalen* (2021).

sex, 10-year age groups and NUTS-1 population margins from *EUROSTAT* (2022), using the function *anesrake* from the *anesrake* package in R (*Pasek/Pasek* 2018).

We include 13 European countries that participated in wave 7 and had non-missing information on NUTS-1 place of residence. Additionally, to avoid random variation in prevalence due to small sample sizes, only countries with a sample of at least 2,000 respondents per sex were included in the study. The survey was conducted in the study countries in 2017. We also use the 2017 abridged life tables from *EUROSTAT* (2022).

Health state is measured across 13 irreversible chronic diseases. A person with at least one of these conditions is considered to be in a decreased state of health. A list of the diseases included in the study can be found in the Online Appendix in Table A1.

Tab. 2: Total* and observed sample size, by country and by sex

		Women		Men	
	Country	Total	Observed	Total	Observed
1	Belgium	5518	2720	4472	2153
2	France	4868	1930	3581	1378
3	Italy	4739	2514	3763	2043
4	Czech Republic	4631	2523	3204	1679
5	Germany	4309	2024	3605	1777
6	Spain	4169	2619	3273	2063
7	Estonia	3953	3113	2497	1945
8	Sweden	3469	1724	2803	1463
9	Greece	3209	1768	2498	1292
10	Slovenia	3121	2127	2413	1532
11	Austria	3117	1876	2168	1297
12	Poland	3056	2595	2391	2071
13	Denmark	2742	1760	2320	1474

* The total sample consists of respondents observed in wave 7 and respondents who were not observed in wave 7 because they had dropped out of the panel sample prior to this wave. The health state at wave 7 of attrited respondents is derived in a microsimulation model as described in *Muszyńska-Spielauer* and *Spielauer* (2022).

Notes: Countries are ranked by the size of the total sample of female respondents.

Source: Own estimations based on data from SHARE (*Börsch-Supan* 2020; *Börsch-Supan et al.* 2013)

4 Results

Figure 5 shows the healthy survival distributions. For this specific example, we select the five countries with the largest total samples in SHARE wave 7, as shown in Table 2. The reason for this selection is that we intend to show the cases where an increase in the number of persons in full health from one age to the next in the stationary population is a systematic pattern and not a random fluctuation due to a small

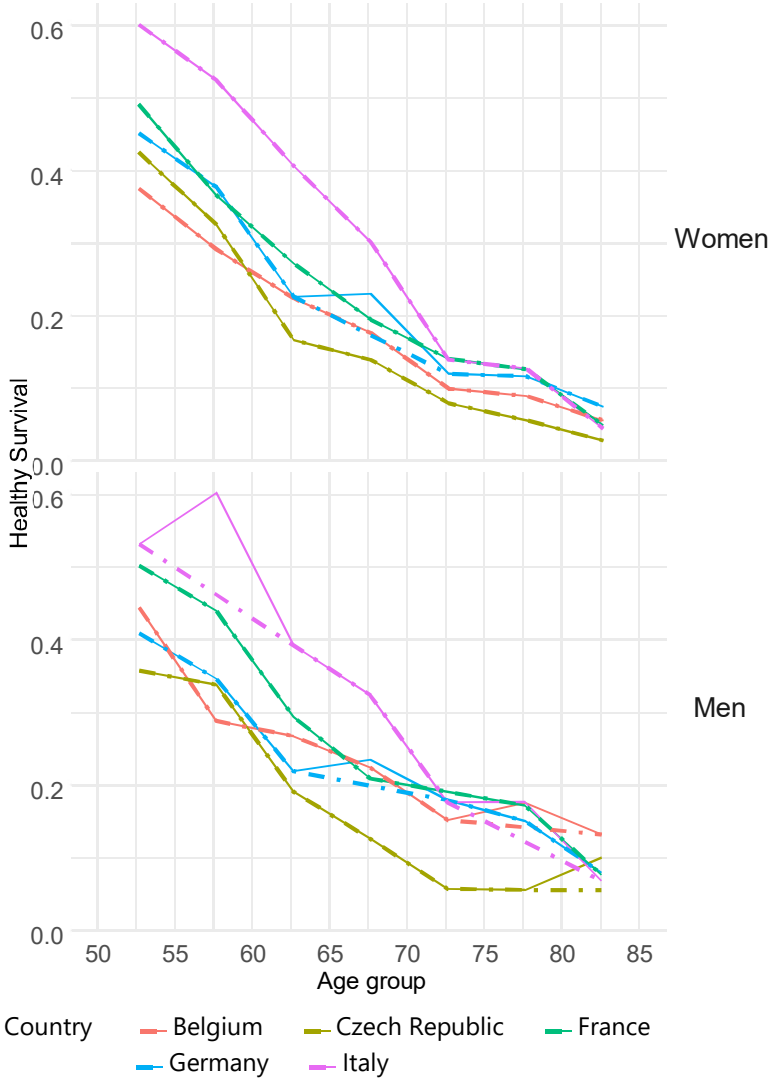
sample size. In this study, following the simple method described in the Methods section, we correct individual observation points of a higher average number of persons in full health than in a previous age group in the selection of countries. The number of persons in full health was corrected for German men and women in the age group [65,70), Italian and Belgian men aged [55,60) and men in the Czech Republic at age [80,85). As far as the men in the Czech Republic are concerned, since no values of l'_x for the age group 85+ can be derived based on the SHARE data, we assume a constant healthy survival after the age group [75,80). The newly derived number of persons who reach a given age in full health by sex (shown as dashed lines in Fig. 5) replaces the corresponding number in the healthy survival curve (solid lines) and is then used to derive the number of healthy years lived (L'_x) in estimating health expectancies in accordance with the standard Sullivan method. The corrected counts are further applied to derive the number of persons who cease to be in full health (d'_x). Table A1 in the Supplementary Material shows the number of persons in full health by age and sex in all 13 countries studied, according to the raw and smoothed estimates of l'_x.

Table 3 presents statistics of HE at age 50 for years lived before age 85. We approximate HE conditional on being in good health at age 50 using the average number of healthy years lived between ages $50 + a_{50}$ and $80 + a_{80}$ of persons who were healthy at the exact age $50 + a_{50}$. Where $a_{50} \in [2.7,2.8]$ and $80 + a_{80}$ ($a_{80} \in [2.5,2.8]$, a_{50} and a_{80} vary between the study countries). The three statistics of HE are estimated for the same age interval, i.e. $[50 + a_{50}, 80 + a_{80}]$. The age restriction is related to the fact that the SHARE survey covers respondents of age 50+, and the EUROSTAT population data required to adjust survey weights has an open age interval of 85+. To simplify the presentation, we also refer to the standard statistic of HE as "HE at age 50", and shorten the name "HE at age 50 conditional on reaching age 50 in full health" to "conditional HE at age 50". All the statistics are based on the adjusted l'_x data, i.e. healthy survival distributions corrected for the increasing number of persons in full health from one age group to the next.

HE at age 50 is on average a year lower than the same statistic estimated on the basis of the raw l'_x data, and variation in the gap between the two statistics across the countries is small. The largest gap is of 1.6 years for Italian men and is due to the large difference in the number of persons in full health in the age group [55,60] between the raw and corrected data, as shown in Figure 5. For women, the largest difference between the two HE is of 1.3 years in Greece and Spain.

The gap between conditional HE at age 50 and HE at age 50 depends on the difference between survival to age 50 (l_{50}) and healthy survival (l'_{50}), but is also proportional to the total number of years lived in full health above age 50. The average HE at age 50 in the study countries is 8.3 years for women and 8.1 for men, and the average conditional HE at age 50 is 15.5 for women and 15.8 for men. This implies that the HE for persons who are healthy at age 50 is almost twice as high as for all persons who are alive at age 50. The largest absolute difference in the HE variants is for women in Belgium (10.5 years) and for men in Spain (13 years). These differences are the result of a very high conditional HE value coexisting with the lowest values of standard HE. Coefficients of variation in the statistic, i.e. disparities

Fig. 5: Fraction of persons surviving in full health, by age and sex in selected countries



Note: Solid lines represent the estimated number of people in full health, while dashed lines represent the same number, but smoothed.

Source: Own estimations based on data from SHARE (*Börsch-Supan* 2020; *Börsch-Supan et al.* 2013) and *Eurostat* 2022

between countries relative to the average value of the statistic, are only slightly higher for HE than for conditional HE, and show no notable differences between the sexes. As shown in Table 4, different conclusions are reached for men when studying population health based on the ranking of countries according to the conditional

Tab. 3: Health expectancy (HE) based on raw data (*eh*), HE based on smoothed data ($\widehat{eh}$), HE conditional on being healthy at age 50 (*e'h*), and the difference between the last two HE (*e'h* − $\widehat{eh}$), by sex in selected European countries in 2017

	Women					Men				
Country	*eh*	$\widehat{eh}$	$\widehat{eh} - eh$	*e'h*	*e'h* − $\widehat{eh}$	*eh*	$\widehat{eh}$	$\widehat{eh} - eh$	*e'h*	*e'h* − $\widehat{eh}$
Austria	10.7	9.9	-0.8	18.7	8.7	11.5	10.3	-1.1	14.2	3.8
Belgium	6.9	6.4	-0.5	16.9	10.5	8.0	7.3	-0.6	16.4	9.0
Czech Republic	6.6	5.9	-0.7	13.6	7.7	5.7	5.1	-0.6	14.2	9.1
Denmark	11.3	10.4	-0.9	17.3	6.9	10.1	9.3	-0.8	16.2	6.9
Estonia	8.9	8.0	-0.9	15.3	7.3	8.9	8.2	-0.7	15.1	6.9
France	8.7	7.9	-0.9	15.9	8.0	8.9	8.1	-0.8	16.0	7.9
Germany	8.5	7.4	-1.1	16.2	8.8	7.6	6.9	-0.7	16.8	9.9
Greece	9.5	8.2	-1.3	12.0	3.8	9.3	7.9	-1.4	11.1	3.1
Italy	11.2	10.1	-1.1	16.6	6.5	11.0	9.3	-1.6	17.5	8.1
Poland	7.1	6.3	-0.8	13.4	7.2	7.3	6.4	-0.9	12.8	6.4
Slovenia	9.9	8.7	-1.2	15.9	7.2	9.4	8.4	-1.0	16.0	7.6
Spain	8.6	7.3	-1.3	11.4	4.1	8.4	7.6	-0.8	20.6	13.0
Sweden	12.0	10.9	-1.0	17.8	6.9	11.4	10.6	-0.8	18.9	8.3
Mean	9.2	8.3	-1.0	15.5	7.2	9.0	8.1	-0.9	15.8	7.7
Standard Deviation	1.7	1.6	0.2	2.1	1.7	1.6	1.5	0.3	2.4	2.4
100*CV	18	19	-23	14	24	18	18	-33	15	32

Notes: CV = Coefficient of variation. The statistics are estimated at age 50 + $a_{50} \in [52.7 - 52.8]$, with the value of a_{50} differing between the countries. 50 + a_{50} is the average age at death within the age interval [50, 55).

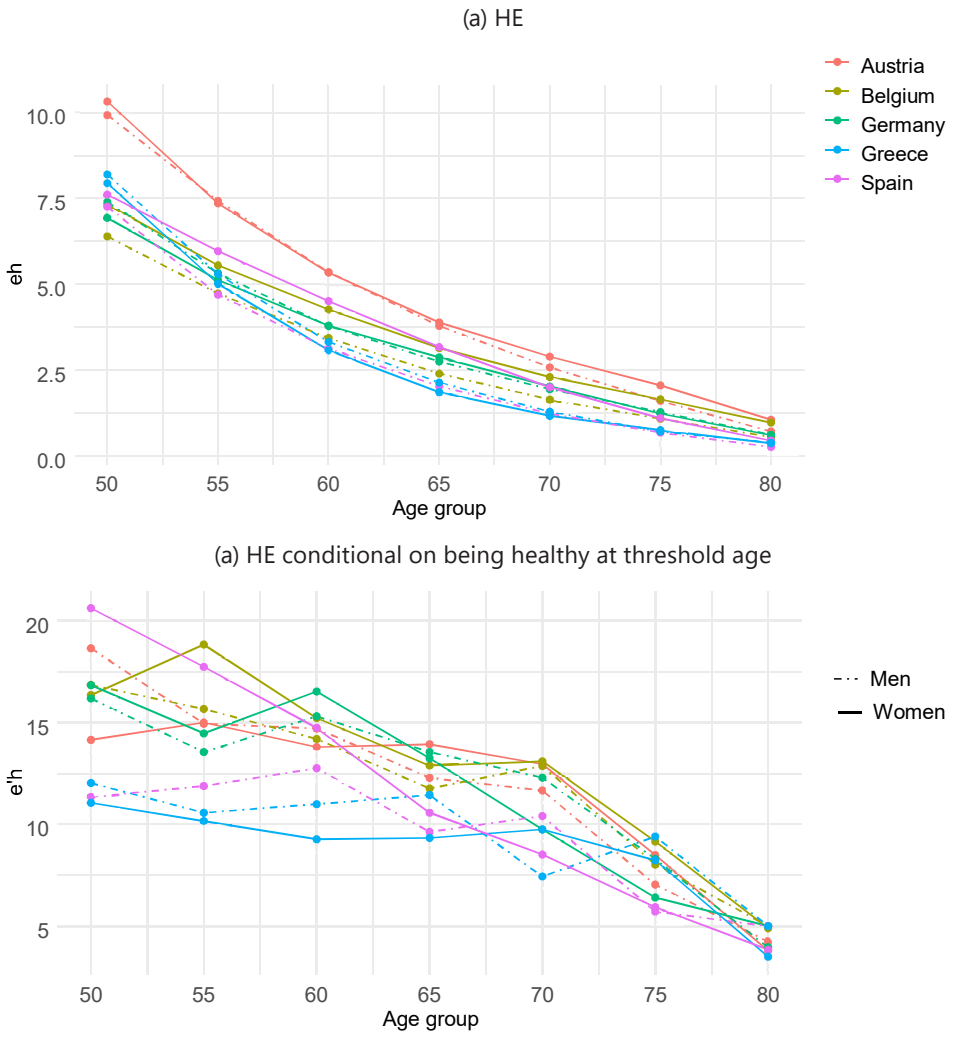
Health expectancy refers to the expected number of healthy years lived between age 50 + a_{50} and 80 + a_{80}, where 80 + $a_{80} \in [82.5,82.8]$, depending on the study country.

Source: Own estimations based on data from SHARE (*Börsch-Supan* 2020; *Börsch-Supan et al.* 2013) and *Eurostat* 2022

HE at age 50 and the ranking according to HE at age 50, as these rankings are not correlated (the Spearman correlation coefficient is insignificant). For women too, differences emerge in the rankings. However, a positive and significant correlation between the ranking of countries according to the two HE values is observed for women.

Figure 6 shows HE and HE conditional on being healthy at a given age, by age and sex. For this presentation, we chose five countries with the highest and lowest differences between the two statistics at age 50, following Table 3. In all countries, we observe a decrease in HE with age, but not necessarily a decrease in HE conditional on being healthy at a given age. Such a universal decline in the conditional HE only starts at age 70. The exceptions are Spanish and German men, for whom the decrease in the statistic begins in the youngest age groups already. For the remaining country-sex observations, the statistic remains relatively stable until age 70.

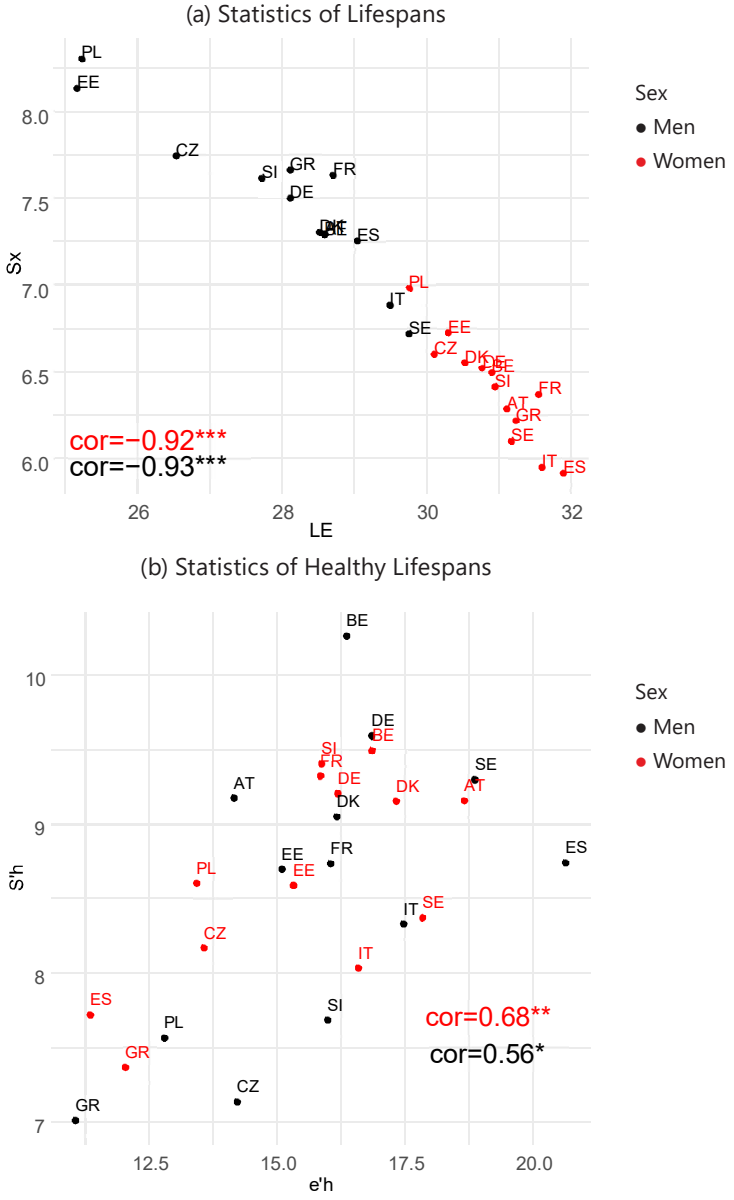
Fig. 6: Health expectancy (HE) and HE conditional on being healthy at a given age, by age and sex in selected European countries in 2017



Source: Own estimations based on data from SHARE (*Börsch-Supan* 2020; *Börsch-Supan et al.* 2013) and *Eurostat* 2022

The values of the standard deviation of healthy lifespans conditional on being healthy at age 50 are presented in Figure 7b, with the exact numbers listed in Table 5 in the Supplementary Material. The average value of the statistic in the study countries is 8.6 years for women and 8.7 years for men, and its level is similar across the study countries, as indicated by a small standard deviation of the statistic (0.7 for women and 0.9 for men). The largest disparity in healthy lifespans is found in Belgium, where the standard deviation of conditional healthy lifespan at age 50 is 9.5

Fig. 7: Life expectancy (LE) and lifespan inequality (Sx) at age 50, prior to age 85 (a), health expectancy (*e'h*) and healthy lifespan inequality (*S'h*) conditional on being healthy at age 50* (b), by sex in selected European countries in 2017



* Statistics are estimated at age 50 + $a_{50} \in [52.7 - 52.8]$, depending on country. Both statistics are estimated for healthy years between age 50 + a_{50} and age 80 + $a_{80} \in [82.5,82.8]$.

Source: Own estimations based on data from SHARE (*Börsch-Supan* 2020; *Börsch-Supan et al.* 2013) and *Eurostat* 2022

Tab. 4: Ranking of the study countries based on an increasing value of health expectancy (HE) at age 50 (*eh*) and on an increasing value of HE conditional on being healthy at age 50 ($e^{'}h$), by sex

	Women		Men	
Rank	*eh*	$e^{'}h$	*eh*	$e^{'}h$
1	Czech Republic	Spain	Czech Republic	Greece
2	Poland	Greece	Poland	Poland
3	Belgium	Poland	Germany	Austria
4	Spain	Czech Republic	Belgium	Czech Republic
5	Germany	Estonia	Spain	Estonia
6	France	France	Greece	Slovenia
7	Estonia	Slovenia	France	France
8	Greece	Germany	Estonia	Denmark
9	Slovenia	Italy	Slovenia	Belgium
10	Austria	Belgium	Denmark	Germany
11	Italy	Denmark	Italy	Italy
12	Denmark	Sweden	Austria	Sweden
13	Sweden	Austria	Sweden	Spain
Spearman cor. coeff.	0.62**		0.24	

***α < 0.01, **α < 0.05, *α < 0.1

Source: Own estimations based on data from SHARE (*Börsch-Supan* 2020; *Börsch-Supan et al.* 2013) and *Eurostat* (2022)

years for women and 10.3 years for men. The smallest disparity in healthy lifespans is observed in Greece, with 8.7 and 8.9 years for women and men respectively. The distributions of the mean and standard deviation of years lived and healthy years lived across the study countries are presented in Figure 7. In the 13 study countries, a higher LE coincides with larger inter-individual differences in longevity. For both sexes, the correlation coefficient between LE and lifespan disparity (both estimated for ages between 50 and 85 years) is significant and the relationship is almost linear. However, the relationship between HE and healthy lifespan inequality is positive in the study countries, i.e. higher average healthy lifespans are associated with higher inter-individual differences in healthy lifespans within the countries. The correlation coefficient between the two healthy lifespan statistics is significant and positive for both sexes (Fig. 7b). Both statistics are conditional on being healthy at age 50.

5 Summary and discussion

We propose a method to derive healthy survival distributions by extending the stationary population model to health status using the Sullivan method. We discuss the method's assumptions and conclude that the method is only valid for health models with an irreversible state of decreased health. For these models, we identify an additional requirement of the method, namely that the number of healthy

individuals cannot increase from one age to the next. For health models with an irreversible state of decreased health, in addition to HE, we introduce summary statistics of population health derived from healthy survival and conditional on being healthy at the threshold age: health expectancy (HE) and healthy lifespan inequality. Our empirical application is based on the prevalence of chronic diseases in selected European countries in 2017, utilising health data from the SHARE cross-sectional study and the EUROSTAT life tables.

We conclude that, when health is measured across irreversible diseases, the indicator of HE conditional on being healthy at a given age is a more informative measure for health policy interventions, particularly those aimed at delaying the onset of health conditions, than the standard HE. The reason is that persons who are already unhealthy have zero potential for healthy years lived and the standard measure of HE is an average of their HE and that of persons who are healthy and thus still have some healthy years ahead of them. In the case of irreversible diseases, policies to improve the health of the population would potentially affect only the latter group, and therefore only the HE of this group is potentially of interest. Policymakers should consider using HE conditional on being healthy at a selected threshold age as a key measure of population health, particularly when targeting interventions to improve healthy ageing. The importance of discussing the policy relevance of conditional HE is further underscored by the results of this study, which show that, for men, different conclusions can be drawn from examining population health based on the ranking of countries according to conditional HE versus standard HE at age 50. Furthermore, the two HEs show different age patterns: a decreasing pattern for the standard HE, and a relatively stable level of the conditional HE until age 70, only then followed by a rapid decline with age. Additionally, in the 13 European countries studied, the HE of persons who are healthy at age 50 is almost twice as high as the standard HE, i.e. HE for all persons alive at age 50 irrespective of their health status.

Across the European countries studied, in contrast to the well-known negative relationship between LE and lifespan inequality (e.g. *d'Albis et al.* 2014; *Smits/Monden* 2009; *Vaupel et al.* 2011), higher HE coexists with larger disparities in healthy years between individuals (both statistics conditional on being healthy at age 50). The positive relationship between HE and healthy lifespan inequality for health dimensions with an irreversible health state of chronic disease, means that higher HE is achieved in countries where the onset of a disease is postponed to older age groups for a fraction of individuals. Countries where chronic disease onset is concentrated at earlier ages are also characterised by lower HE. This result differs from that reported by *Permanyer et al.* (2022), where higher conditional HE at age 35 is associated with lower inequality in healthy lifespans across educational groups in Spain, but is consistent with the findings of *Permanyer et al.* (2023) who report a positive relationship between the HALE statistic and the healthy lifespan inequality statistic.

The limitations of the proposed method are the same as the well-recognised problems of the Sullivan method for deriving HE, and arise from the limitations of health prevalence data (see, for example, *Barendregt et al.* 1994, 1997; *Laditka/*

Hayward 2002; *Rogers et al.* 1990). The method proposed in this article is based on approximations of several quantities related to the average age of health deterioration in an interval, resulting in complicated formulas. The method proposed by *Permanyer et al.* (2022) to approximate the number of persons who are alive and healthy at the beginning of the age interval leads to simpler formulas than those proposed in the article. If the bias introduced by the *Permanyer et al.* (2022) approximation is small, it is better to choose this approximation – even if it is less accurate than that proposed in this article – because it reduces formula complexity. As the bias depends on the prevalence of decreased health and years lived at each age interval, it needs to be assessed for each empirical study. Therefore, even if it were assessed on the basis of the data in this article, it would not be possible to draw general conclusions about its level.

This study improves on previously developed methods for deriving healthy life distribution statistics in addition to HE from cross-sectional health prevalence data and period life tables, by showing that the Sullivan method – when considered as an extension of the stationary population model to health – provides a solution for deriving additional statistics of healthy survival distributions for health dimensions with an irreversible state of decreased health.

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