The statistics of health and longevity: a dynamic analysis of prevalence data

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Abstract

Increases in human longevity have made it critical to distinguish healthy longevity from longevity without regard to health. We present a new method for calculating the statistics of healthy longevity which extends, in several directions, current calculations of health expectancy (HE) and disability-adjusted life years (DALYs), from data on prevalence of health conditions. Current methods focus on binary conditions (e.g., disabled or not disabled) or on categorical classifications (e.g. in good, poor, or very bad health) and report only expectations. Our method, based on Markov chain theory, applies to both binary and continuous measures, and provides not only the expectation but also the variance, coefficient of variation, skewness and other distributional properties of longevity. We apply the method to 9 European countries using the SHARE survey data on disability and on grip strength. The method can extend DALY calculations to produce information on variance as well as expectations.

1 Introduction

Increases in human longevity, driven by improvements in nutrition, public health, medical care, and medical technology have dramatically changed the prospects of future life for the elderly. This has led to the desire to distinguish *healthy* longevity from longevity without regard to health, concept first introduced by **?**. The interaction of population structure (especially age structure) with changes in mortality and morbidity has important sociological, ethical, and economic implications.

Our goal in this paper is to present a new methodology for calculating the statistics of healthy life. Our method subsumes, and extends in several important directions, currently used calculations for health expectancy (HE), healthy-adjusted life expectancy (HALE), and disability-adjusted life years (DALYs). We have separated analyses based on prevalence of health conditions from those based on the incidence of, and transitions between, health states. This paper focuses on prevalence data.

The most commonly used approach to incorporating prevalence data into health longevity is the so-called Sullivan method (**?**). It is based on age-specific prevalence of a binary condition (e.g., disabled or non-disabled). The survivorship to each age, multiplied by the prevalence, and integrated over age, gives the expected number of years lived with the condition. Our method extends this in several ways:

1. It is applicable to both age-classified demography and to models incorporating other dimensions (e.g., multistate models; we will refer to "stages" to indicate these more general categories; the familiar age calculations are a special case).

2. It is not restricted to binary conditions: we will consider binary, nominal, and interval measures of health. As we will see, this greatly extends the possibilities for measuring the elusive concept of "health."

3. We will provide calculations not only of the *expectation* of healthy life, but also the variance, skewness, and related statistics. Such measures of inter-individual variability have been largely ingored in the literature on health and longevity, but they provide potentially valuable additional insights into the future prospects of a group of individuals, as well as inter-individual variation.

4. Because our analysis is based on a matrix formulation, it is directly amenable to sensitivity analyses using methods from matrix calculus. Such sensitivity analyses have recently been applied to a variety of demographic models and outputs (**???????**).

Our approach relies on recently developed demographic theory using the theory of Markov chains with rewards (**????**). The model characterizes the life cycle as a discrete-time, finite-state absorbing Markov chain, with death as an absorbing state. At each transition, an individual accumulates a random reward, in this case, some measure of health. A system of equations (**?**) provides the moments of the accumulated amount of healthy life.

Notation: Matrices are denoted by upper-case bold symbols (e.g., $\mathbf{P}$), vectors by lower-case bold symbols (e.g., $\boldsymbol{\rho}$). Some block-structured matrices are denoted by, e.g., $\mathbb{P}$. Vectors are column vectors by default. The transpose of $\mathbf{P}$ is $\mathbf{P}^{\mathsf{T}}$. The vector $\mathbf{1}$ is a vector of ones. The diagonal matrix with the vector $\mathbf{x}$ on the diagonal and zeros elsewhere is denoted $\mathrm{diag}\,(\mathbf{x})$. The expected value is denoted by $E(\cdot)$, the variance by $V(\cdot)$, the coefficient of variation by $CV(\cdot)$ and the skewness by $Sk(\cdot)$. The Hadamard, or element-by-element, product of matrices $\mathbf{A}$ and $\mathbf{B}$ is denoted by $\mathbf{A} \circ \mathbf{B}$. Transition matrices of Markov chains are written in column-to-row orientation, and hence are column-stochastic.

2 Survival as a Markov process

We suppose the life cycle to be composed of a set of states. In our applications, these will represent age classes $1, \ldots, \omega$. However, the method applies equally to life cycles classified by stages (e.g., employment status, marital status) or to multistate models combining stages and age classes.

Let $\mathbf{U}$ represent the transition matrix among age classes:

$$\mathbf{U} = \begin{pmatrix} 0 & 0 & 0 & 0 \\ p_1 & 0 & 0 & 0 \\ 0 & p_2 & 0 & 0 \\ 0 & 0 & p_3 & 0 \end{pmatrix} \tag{1}$$

(shown here for $\omega = 4$).

Death appears in the life cycle as an absorbing state or, in some cases, a set of absorbing states (e.g., death classified by cause of death). Arranging the absorbing states to come after the transient states gives the Markov chain transition matrix

$$\mathbf{P} = \left(\begin{array}{c|c} \mathbf{U} & 0 \\ \hline \mathbf{M} & \mathbf{I} \end{array}\right) \tag{2}$$

The matrix $\mathbf{M}$ contains the probabilities of death for each age class. The identity matrix in the lower right assures that the dead remain in their states. The matrix $\mathbf{U}$ is the transient matrix (dimension $\omega \times \omega$) describing transitions among the living states. We will assume throughout that the dominant eigenvalue of $\mathbf{U}$ is less than 1, so that an individual beginning in any transient state will eventually be absorbed (i.e., will eventually die) with probability 1. We assume that individuals in the absorbing state receive no rewards. Thus $r_{ij} = 0$ for any j in the set of absorbing states.

2.1 The approach: Markov chains with rewards

The method used here was introduced in **?**. An absorbing Markov chain is used to describe the life cycle, and a "reward" is associated with each possible transition among the states of the Markov chain. An individual moving from state j to state i collects a reward r_{ij}. Previous demographic analyses (**???**) have considered rewards as reproductive output, and as economic accumulation of income or expenditures. In the present application, the reward corresponds to a measure of health.

Markov chains with rewards were introduced by Howard **?** to analyze Markov decision processes. In his development, the reward r_{ij} was a fixed quantity. Here, however, the r_{ij} are random variables with specified statistical properties **??**. Fixed rewards follow as a special case.

3 Analytical methods

As an individual moves through its life cycle, it accumulates health rewards. The goal of our analysis is to calculate the statistical properties (mean, variance, skewness) of the accumulated lifetime reward. The solution to this problem is provided by an simple set of recurrence relations.

Define $\boldsymbol{\rho}$ as the vector (dimension $(\omega+1)\times 1$) of accumulated rewards as a function of the initial stage of the individual. The vector of kth moments of the entries of $\boldsymbol{\rho}$ is denoted $\boldsymbol{\rho}_k$, where

$$\boldsymbol{\rho}_k = \left(\; E\left[\rho_i^k\right] \; \right). \tag{3}$$

The rewards r_{ij} are random variables. The matrix of the kth moments of the r_{ij} is denoted $\mathbf{R}_k$:

$$\mathbf{R}_k = \left(\; E\left[r_{ij}^k\right] \; \right). \tag{4}$$

Notation alert. The subscripts on the vectors $\boldsymbol{\rho}_k$ and the matrices $\mathbf{R}_k$ denote the order of the moments. When referring to the entries of the vector or the matrix, subscripts refer to the location in the matrix and the order of the moments migrates to become a parenthetical superscript. That is, the ith entry of $\boldsymbol{\rho}_k$ is $\rho_i^{(k)}$ and the (i,j) entry of $\mathbf{R}_k$ is $r_{ij}^{(k)}$.

The calculation of the accumulated rewards proceeds in the "backwards" fashion familiar from dynamic programming; e.g., **?**. Choose some terminal time T, define t as the time remaining until this terminal time, and let $\boldsymbol{\rho}(t)$ be the reward yet to be accumulated at t. At the terminal time, no more rewards will be accumulated, so $\boldsymbol{\rho}(0)=0$.

Caswell **?** proved that the moment vectors $\boldsymbol{\rho}_i$ can be calculated recursively as follows. Let $\mathbf{P}$ be the transition matrix of the Markov chain, let $\mathbf{R}_k$ be the matrix of kth moments of the transition-specific rewards. Calculations are referenced to a terminal time T. The first three moments of the accumulated reward satisfy

$$\boldsymbol{\rho}_1(t+1) = (\mathbf{P}\circ\mathbf{R}_1)^{\mathsf{T}}\mathbf{1} + \mathbf{P}^{\mathsf{T}}\boldsymbol{\rho}_1(t) \tag{5}$$

$$\boldsymbol{\rho}_2(t+1) = (\mathbf{P}\circ\mathbf{R}_2)^{\mathsf{T}}\mathbf{1} + 2\,(\mathbf{P}\circ\mathbf{R}_1)^{\mathsf{T}}\boldsymbol{\rho}_1(t) + \mathbf{P}^{\mathsf{T}}\boldsymbol{\rho}_2(t) \tag{6}$$

$$\boldsymbol{\rho}_3(t+1) = (\mathbf{P}\circ\mathbf{R}_3)^{\mathsf{T}}\mathbf{1} + 3\,(\mathbf{P}\circ\mathbf{R}_2)^{\mathsf{T}}\boldsymbol{\rho}_1(t) + 3\,(\mathbf{P}\circ\mathbf{R}_1)^{\mathsf{T}}\boldsymbol{\rho}_2(t) + \mathbf{P}^{\mathsf{T}}\boldsymbol{\rho}_3(t) \tag{7}$$

for $t = 0, \ldots, T-1$, with $\boldsymbol{\rho}_1(0) = \boldsymbol{\rho}_2(0) = \boldsymbol{\rho}_3(0) = 0$. In general, the mth moments of accumulated rewards are given by

$$\boldsymbol{\rho}_m(t+1) = \sum_{k=0}^{m} \binom{m}{k} \left(\mathbf{P} \circ \mathbf{R}_{m-k}\right)^{\intercal} \boldsymbol{\rho}_k(t) \tag{8}$$

with $\boldsymbol{\rho}_m(0) = 0$. The combination of the assumptions that $\mathbf{P}$ has the structure (2) and that $r_{ij} = 0$ for all absorbing states j means that every individual will eventually be absorbed in a state in which future rewards are zero; thus $\boldsymbol{\rho}_1(t)$ will converge to a limit as $T \to \infty$; this limit is the expectation of lifetime rewards calculated over the entire lifetime of every individual. See **?** for proofs and further references.

The first moment $\boldsymbol{\rho}_1$ gives the mean lifetime accumulated health for individuals of each age. This accumulation might be in units of years of life without disability, years of life weighted by some quantitative maeasure of health, or years of life lost to some disease. The variance, standard deviation, coefficient of variation, and skewness of lifetime reproductive output are calculated from the moment vectors

$$\begin{aligned}
V(\boldsymbol{\rho}) &= \boldsymbol{\rho}_2 - \boldsymbol{\rho}_1 \circ \boldsymbol{\rho}_2 && (9)\\
SD(\boldsymbol{\rho}) &= \sqrt{V(\boldsymbol{\rho})} && (10)\\
CV(\boldsymbol{\rho}) &= \operatorname{diag}\left(\boldsymbol{\rho}_1\right)^{-1} SD(\boldsymbol{\rho}) && (11)\\
Sk(\boldsymbol{\rho}) &= \operatorname{diag}\left[V(\boldsymbol{\rho})\right]^{-3/2} \left(\rho_3 - 3\boldsymbol{\rho}_1 \circ \boldsymbol{\rho}_2 + 2\boldsymbol{\rho}_1 \circ \boldsymbol{\rho}_1 \circ \boldsymbol{\rho}_1\right). && (12)
\end{aligned}$$

The skewness, which is dimensionless, measures the symmetry of the distribution of healthy life. Positive skewness implies a long tail of positive values, and vice versa.

4 Quantifying health rewards

4.1 Categorical health status measures

These measures partition the continuum of health states in a set of mutually exclusive states, ordered by one or more health dimensions. The area under the survival curve is divided into two components (or more, when a non-dichotomous health classification is adopted): one component for the time lived in full health state and one component for the time lived in a state of less than full health (or in the other states with different levels of health). Total life expectancy is the sum of the areas under the survival curve, each of them spent in a specific health state.

Examples of binary measures are disability free life expectancy and dementia free life expectancy. In these cases the total life expectancy is divided into two components: years lived without disability or dementia and years lived with disability or dementia.

Examples of measures that use a more disaggregated set of health states are active life expectancy, when several levels of activity limitations in the daily functions are considered: non-limited, limited, severely limited.

Two types of information are needed to compute these health expectancies: an age-specific mortality schedule (from age specific death rates or life tables) and an age-specific prevalence rates of the health condition under study (usually from health surveys).

4.2 Quantitative health status measures

These measures of health look at quantitative continuous dimensions of health such as grip strength, body mass index or blood pressure.

These variables in the field of demography of health are not very commonly used. When these dimensions are considered, they are usually grouped into categories like low-medium-high BMI or weak-medium-normal hand grip, thus going back to the nominal variable case. Alternatively the analysis focus on the average value by age.

We use a different approach. By keeping the variable as a continuous one, for example grip strength, what we compute is the future life in terms of "strength-years". At every age, this is the remaining units of grip strength from that age until the end of life.

Another way to think of it is in terms of money. Suppose individuals are entered in a grip contest every year, and they win an amount of money equal to their grip strength. Then what we calculate is the mean, the standard deviation, the coefficient of variation and the skewness of the amount of money they would win in the contest for the rest of their life.

4.3 Disability-adjusted life years

Disability-adjusted life years (DALYs) play a major role in quantifying healthy longevity in the Global Burden of Disease project (**??**). DALYs integrate two different measures of health condition; we will show how to calculate the statistics of DALYs from the Markov chain model in Section 7.1 below.

5 Data

For the age-specific prevalence of disability we used data from the Survey of Health, Ageing and Retirement in Europe (**?**). For the age-specific mortality schedule we used data from the Human Mortality Database (**?**).

SHARE is a longitudinal survey containing information on more than 85,000 individuals, aged 50 and over, in 20 European countries. It comprises several waves and ad-hoc modules on specific topics, which make it a very complex database suitable for studying a wide range of research questions. A simplified version of the data is represented by *easySHARE* (**?**). This includes the same number of observations as the main release of SHARE but it is restricted to a subset of variables covering the following topics: demographics, household composition, social support and network, childhood conditions, health and health behavior, functional limitation indices, work and money.

From easySHARE we selected data for the most recent available wave (wave 4), corresponding to year 2011, and for the nine countries for which a mortality schedule in the year 2011 was available on the HMD. These are: Germany, Sweden, France, Denmark, Switzerland, Belgium, Czech Republic, Portugal and Estonia. Table 1 reports the sample size by country. We analyzed ages from 55 (in order to avoid the several 0 prevalences of disability observed at ages younger than 55) until 110 (the last available age in the HMD [1]).

[1]The last age for which prevalence data were available differ from country to country. When this age was younger than 110, all the other ages until 110 were assumed to have the last observed prevalence of

	female	male
Belgium	2937	2363
Czech Republic	3542	2576
Denmark	1240	1036
Estonia	4080	2748
France	3345	2512
Germany	836	736
Portugal	1185	895
Sweden	1057	894
Switzerland	2068	1682

Table 1: SHARE wave 4: Sample size of the respondents in the countries selected for the analysis.

For the analysis of a binary health measure we applied our method to the activity of daily living variable *adla*, defining as healthy the individuals with no activity limitation (*adla*=0) and unhealthy the individuals that showed any level of limitation (*adla* from 1 to 5).

Let v_j denote the prevalence of disability in age class j. Then the reward r_{ij} for a binary disability variable satisfies

$$r_{ij} = \begin{cases} 0 & \text{with probability } v_j \\ 1 & \text{with probability } 1 - v_j \end{cases} \tag{13}$$

The moments of these rewards satisfy

$$E\left(r_{ij}^k\right) = 1 - v_j \qquad \text{for all } j \tag{14}$$

As a quantitative health measure, we chose to use the variable measuring the grip strength *maxgrip*. This variable reports the information in Kg-strength units as measured by a dynamometer. We calculated the first three moments of *maxgrip* directly from the SHARE data and used these as the age-specific rewards.

6 Results

In the following pages we show a gallery of the main results by gender and country: expected values, standard deviations, coefficients of variation and skewness for the binary case (healthy/unhealthy life expectancy based on the distinction between non-limited and limited in daily activities) and for the quantitative health measure (the grip strength over the life time). Differences and ratios between the indicators were also computed but the sake of brevity they are not reported here.

Figures 1 and 2 show total and healthy life expectancies. As we could expect, women live longer than men but have higher proportion of years with disability. At age 55 they can expect to live about 30 years more in all the analyzed countries, while men have less years to live. On the other hand, the sex difference in healthy life expectancy is smaller,

disability.

indicating that women are likely to spend more years with disability than men. Only in Sweden and Denmark are the number of years with disability is similar between the two sexes.

Figures 3 and 4 show the decreasing standard deviation of healthy and total life expectancy over age. As they age, both men and women see their inter-individual variation in the expected years of life left decrease from about 9-10 years at the age 55 to about 1-2 years at the end of their life. Moreover, the plots show that the variation in healthy life expectancy is lower than in total life expectancy.

Figures 5 and 6 show the CV of life and healthy life. After about age 80, the CV of healthy life becomes much greater than the CV for overall longevity. The skewness of longevity increases from slightly negative to distinctly positive.

Figures 9 and 10 show the expected values of strength-years of life by age for women and men respectively. To help in the interpretation of the curves we can focus, for example, on men from Belgium. At age 55 they have an average hand grip of 50 kg and a remaining life expectancy of about 25 years. If their grip would stay the same for the next 25 years, they would have a total of 1250 strength-years of life left. However, the computed value is lower (1053 strength-years) because it takes into account the uncertainty of the future and the fact that their grip strength is going to decrease with age.

Just as the binary measure based on disability re-scales a year of life (to 0 if disabled, to 1 if not disabled), the quantitative measure rescales a year of life to the quality of that life; in this case, measured by grip strength.

7 Discussion

7.1 Calculation of DALYs

Considered as a health measure, DALYs differ in three ways from the rewards considered previously. First, they view the glass as half empty rather than half full: when DALY is large, that means that health is poor. Second, DALYs are a measure of health gap, which means that they quantify the difference between the actual health of a population and a stated ideal health level, a sort of golden standard for the health of a population. Third, they combine two different kinds of rewards, by including two different dimensions (one for mortality and one for disability) in the calculation of the years of life lost (**?**).

1. Years lost due premature mortality (compared to the an ideal-standard life expectancy). The standard survival schedule is the female Japanese population, the currently longest living human population. When an individual dies, it loses some number of years of remaining life. The expectation of that loss is just the life expectancy at the age at death. But the other moments of remaining years of life are also easily calculated, and can be treated as moments of the reward resulting from the transition to the absorbing state.

2. Years lost due to disability. The prevalence rates for all the known diseases are multiplied by a disease-specific severity of disability weight that ranges between 0 and 1 based on how disabling the disease is. One year spent in a severely disabling condition , with a weight close to 1, would cause the almost complete loss of that

year. On the contrary, one year spent in a lightly disabling condition, whose weight is close to 0, would cause a minor loss in terms of year-time.

Summing the two components and integrating them over age will give global burden of disease of a population, expressed in the total number of years of good health lost due to either death or disability.

Our method can carry out DALY calculations; by doing so we can extend the results to include measures of variation among individuals. We start with Figure 17, which shows a piece of an age-classified life cycle with two causes of death. Suppose that Cause 1 is the one we are interested in, and Cause 2 represents all other causes. The transition matrix for this Markov chain is

$$\mathbf{P} = \left(\begin{array}{c|c} \mathbf{U} & \mathbf{0} \\ \hline \mathbf{M} & \mathbf{I} \end{array}\right) \tag{15}$$

$$= \left(\begin{array}{cccc|cc} 0 & 0 & 0 & 0 & 0 & 0 \\ p_1 & 0 & 0 & 0 & 0 & 0 \\ 0 & p_2 & 0 & 0 & 0 & 0 \\ 0 & 0 & p_3 & 0 & 0 & 0 \\ \hline m_{11} & m_{12} & m_{13} & m_{14} & 1 & 0 \\ m_{21} & m_{22} & m_{23} & m_{24} & 0 & 1 \end{array}\right) \tag{16}$$

where p_j is the survival probability of age class j and m_{ij} is the probability of death from cause i in age class j.

Computation of DALYs requires two kinds of rewards. Transitions m_{1j} represent death due to cause 1. These transitions accumulate a reward equal to the number of years of life lost due to this death. The GBD study uses the life expectancy of a standard population (Japan) as this number; however, any population, including the one under study, could be used.

Let η_j be the longevity of an individual of age j. The expectation of η_j is the familiar life expectancy, but η_j is a random variable, and its moments are calculated directly from the matrix $\mathbf{U}$ (**???**)

$$\mathbf{N}_1 = (\mathbf{I} - \mathbf{U})^{-1} \tag{17}$$

be the fundamental matrix (its entries give the mean time spent in each transient state) for the standard population (e.g., Japan). Then the vectors giving the first three moments of longevity satisfy

$$\boldsymbol{\eta}_1^{\mathsf{T}} = \mathbf{e}^{\mathsf{T}}\mathbf{N}_1 \tag{18}$$

$$\boldsymbol{\eta}_2^{\mathsf{T}} = \boldsymbol{\eta}_1^{\mathsf{T}}(2\mathbf{N}_1 - \mathbf{I}) \tag{19}$$

$$\boldsymbol{\eta}_3^{\mathsf{T}} = \boldsymbol{\eta}_1^{\mathsf{T}}\left(6\mathbf{N}_1^2 - 6\mathbf{N}_1 + \mathbf{I}\right) \tag{20}$$

These values will provide part of the reward matrices $\mathbf{R}_i$. The calculation of DALYs, however, requires calculation of years lost due to disability.

Transitions p_j represent survival. Some fraction of those survivors will be disabled due to cause 1, and that disability is assigned a severity. Let v_j be the prevalence of disability, due to cause 1, in age class j, and let s_j be the severity. Then the reward accumulated for the survival transition from age j to age $j+1$ is

$$r_{j+1,j} = \begin{cases} s_j & \text{with probability } v_j \\ 0 & \text{with probability } 1 - v_j \end{cases} \tag{21}$$

Under this model, the matrices that give the moments of the transition-specific rewards are:

$$\mathbf{R}_1 = \left(\begin{array}{cccc|cc} 0 & 0 & 0 & 0 & 0 & 0 \\ v_1 s_1 & 0 & 0 & 0 & 0 & 0 \\ 0 & v_2 s_2 & 0 & 0 & 0 & 0 \\ 0 & 0 & v_3 s_3 & 0 & 0 & 0 \\ \hline E(\eta_1) & E(\eta_2) & E(\eta_3) & E(\eta_4) & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{array}\right) \tag{22}$$

$$\mathbf{R}_2 = \left(\begin{array}{cccc|cc} 0 & 0 & 0 & 0 & 0 & 0 \\ v_1 s_1^2 & 0 & 0 & 0 & 0 & 0 \\ 0 & v_2 s_2^2 & 0 & 0 & 0 & 0 \\ 0 & 0 & v_3 s_3^2 & 0 & 0 & 0 \\ \hline E(\eta_1^2) & E(\eta_2^2) & E(\eta_3^2) & E(\eta_4^2) & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{array}\right) \tag{23}$$

$$\mathbf{R}_3 = \left(\begin{array}{cccc|cc} 0 & 0 & 0 & 0 & 0 & 0 \\ v_1 s_1^3 & 0 & 0 & 0 & 0 & 0 \\ 0 & v_2 s_2^3 & 0 & 0 & 0 & 0 \\ 0 & 0 & v_3 s_3^3 & 0 & 0 & 0 \\ \hline E(\eta_1^3) & E(\eta_2^3) & E(\eta_3^3) & E(\eta_4^3) & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{array}\right) \tag{24}$$

Given the Markov chain matrix $\mathbf{P}$ and the reward matrices $\mathbf{R}_i$, the calculation of the moments of the lifetime accumulated reward would be calculated just as we have for binary and quantitative measures of health.

This computation would provide not only the *expected* DALYs, but also the moments, variances, and skewness of disability-adjusted life years, for individuals of any age class. We will apply this to disability data in a subsequent analysis.

8 Figures

8.1 Disability analysis with binary variable

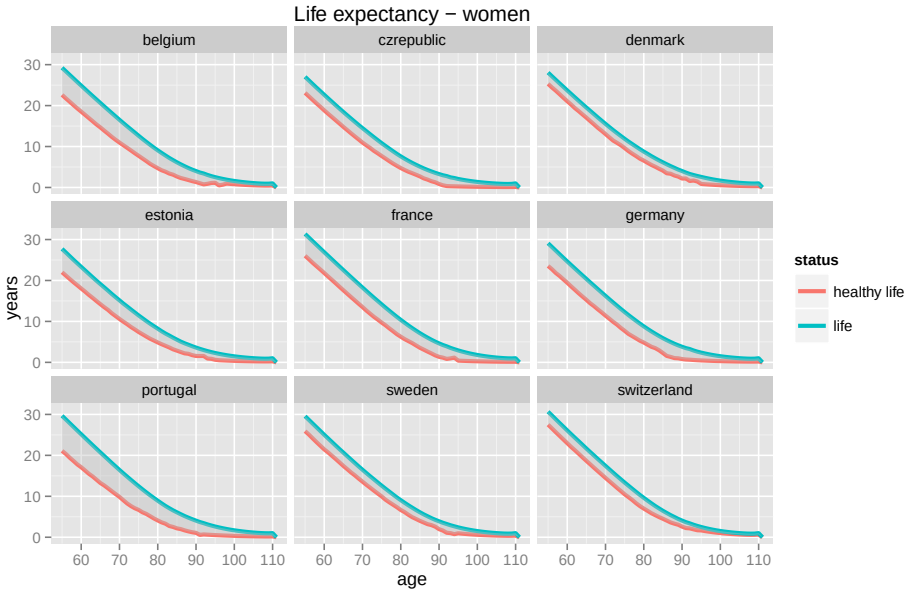

Figure 1: Expectation of life and healthy life for women in nine countries, based on disability data from the SHARE study (see Methods).

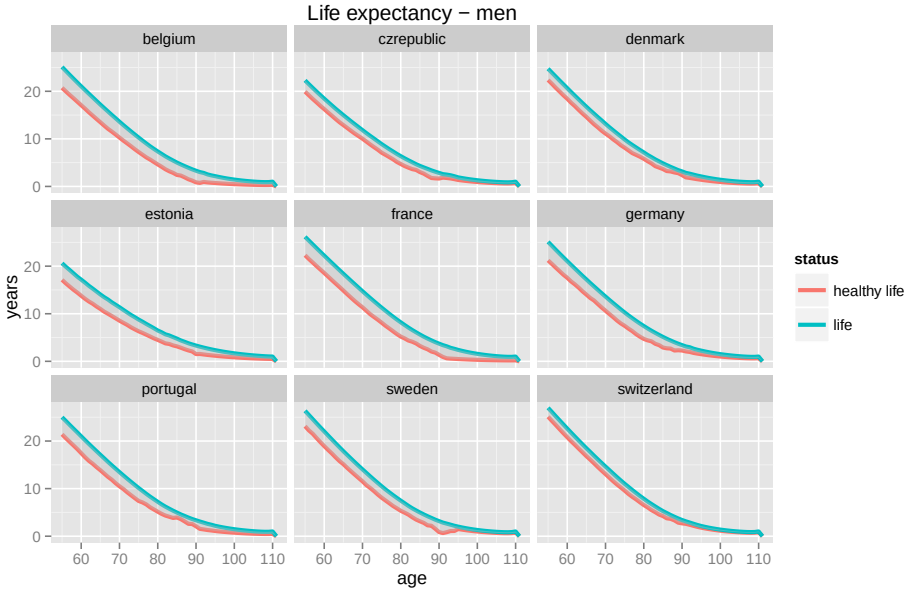

Figure 2: Expectation of life and healthy life for men in nine countries, based on disability data from the SHARE study (see Methods).

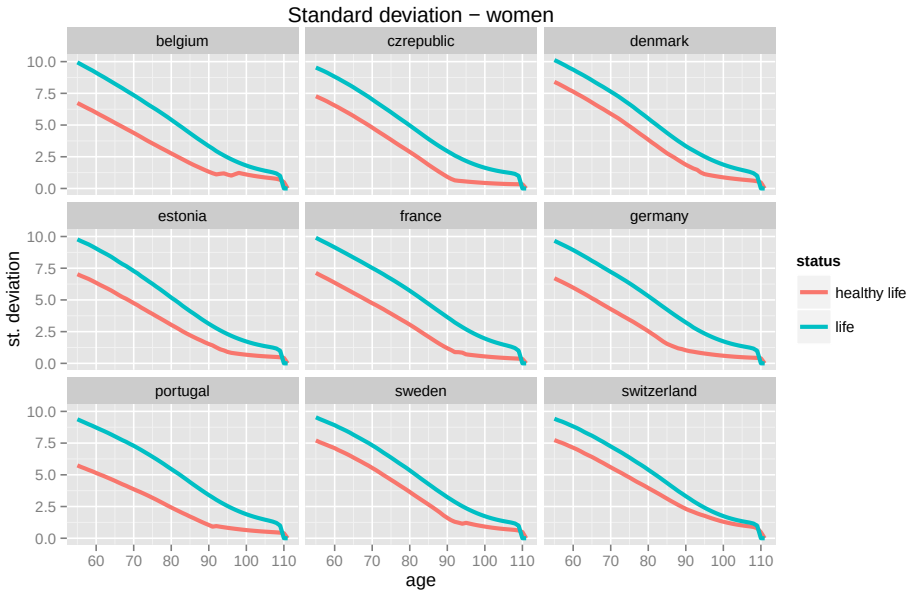

Figure 3: Standard deviation of life and healthy life for women in nine countries, based on disability data from the SHARE study (see Methods).

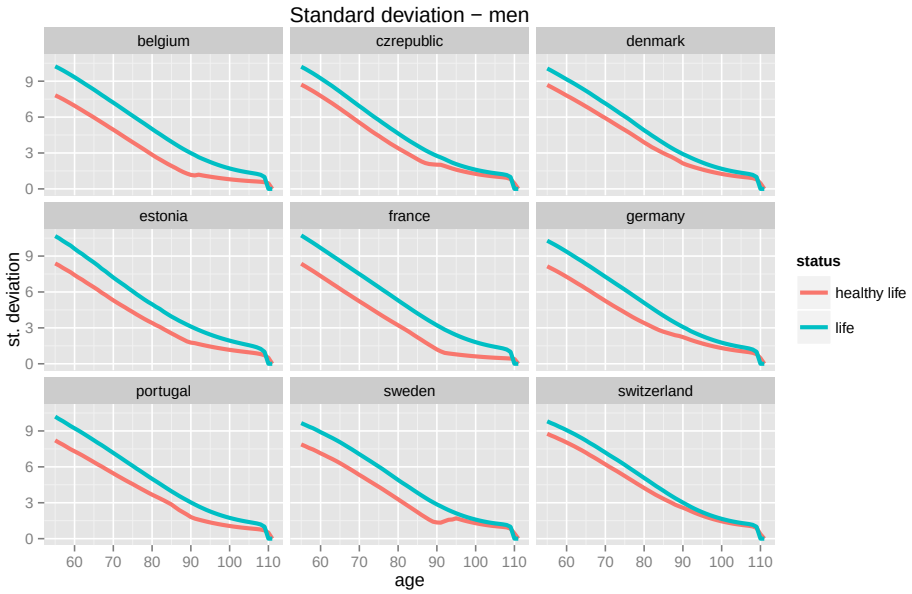

Figure 4: Standard deviation of life and healthy life for men in nine countries, based on disability data from the SHARE study (see Methods).

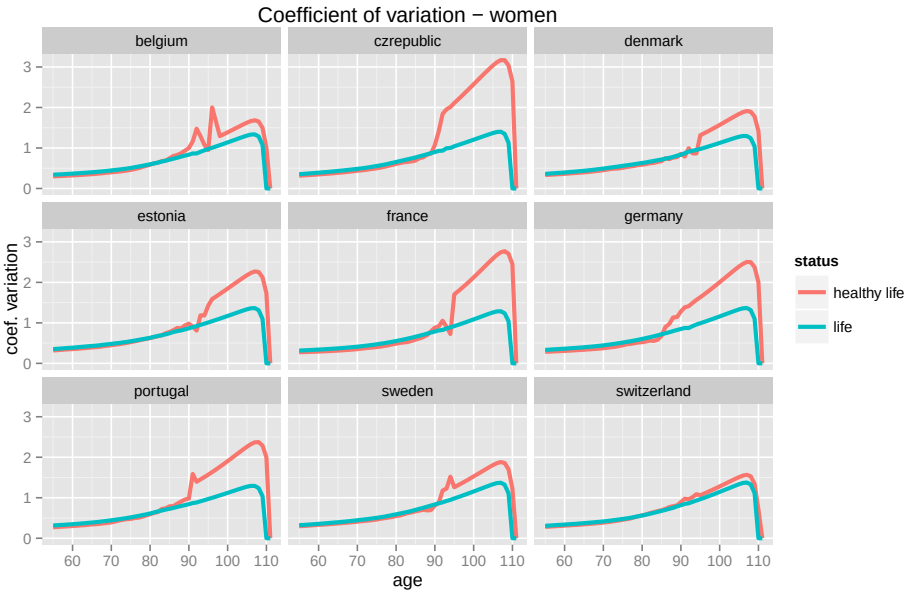

Figure 5: Coefficient of variation (CV) of life and of healthy life for women in nine countries, based on disability data from the SHARE study (see Methods).

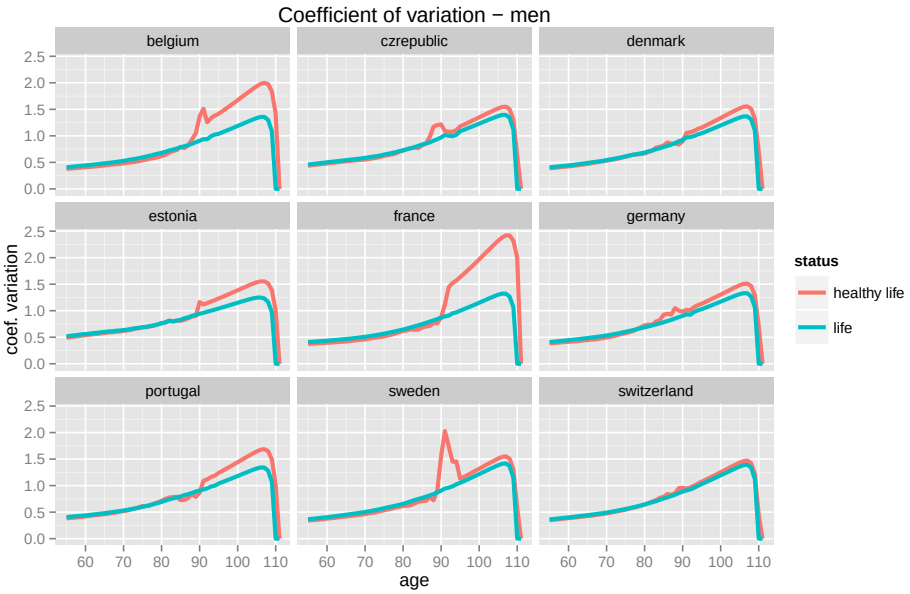

Figure 6: Coefficient of variation (CV) of life and of healthy life for men in nine countries, based on disability data from the SHARE study (see Methods).

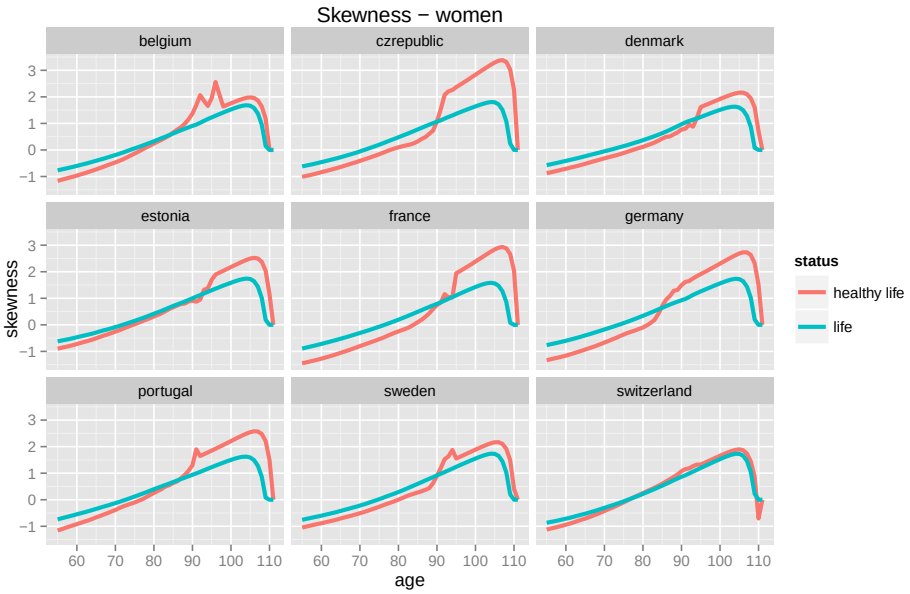

Figure 7: Skewness of life and of healthy life for women in nine countries, based on disability data from the SHARE study (see Methods).

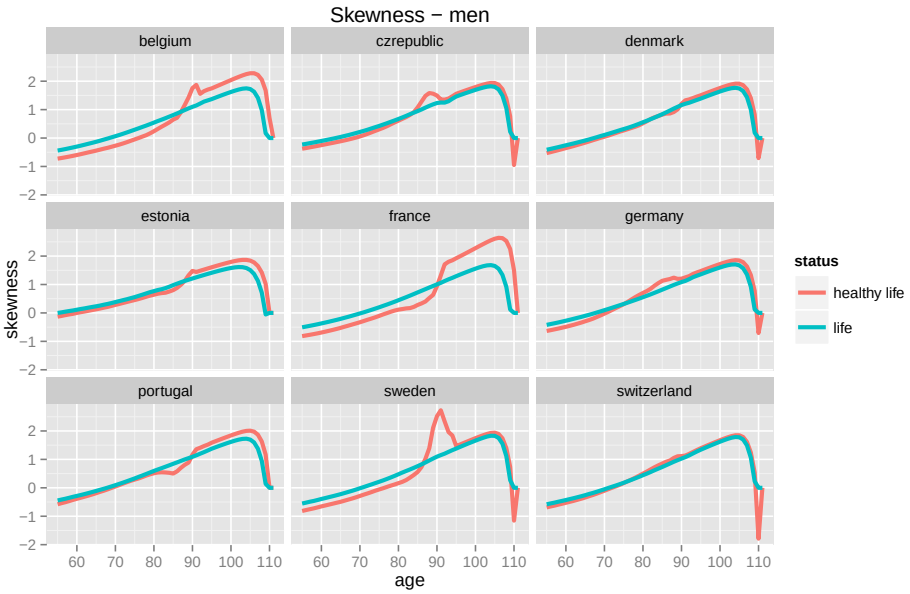

Figure 8: Skewness of life and of healthy life for men in nine countries, based on disability data from the SHARE study (see Methods).

8.2 Grip strength as a quantitative health measure

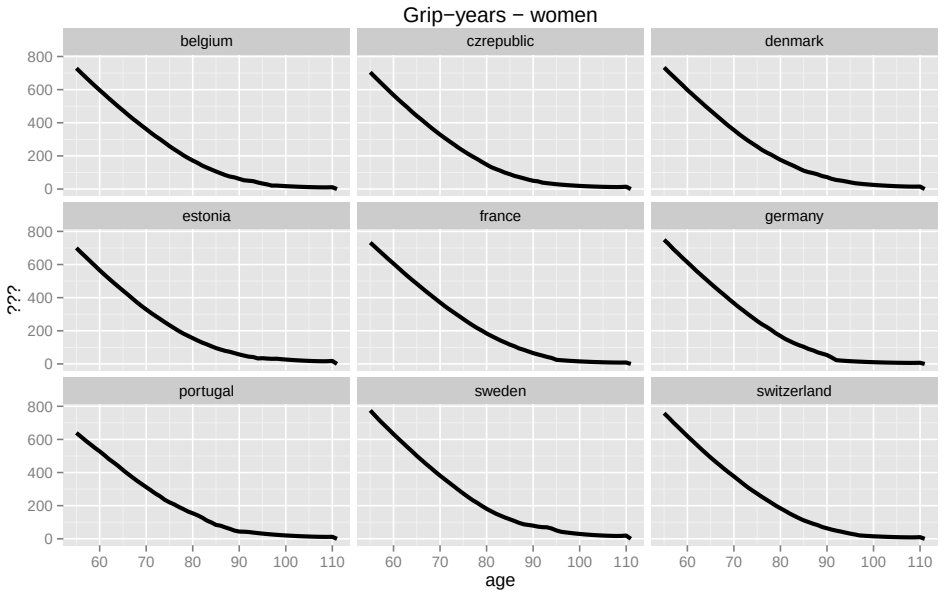

Figure 9: Expectation of healthy life, where health status is coded by grip strength, for women in nine countries, based on grip strength data from the SHARE study (see Methods).

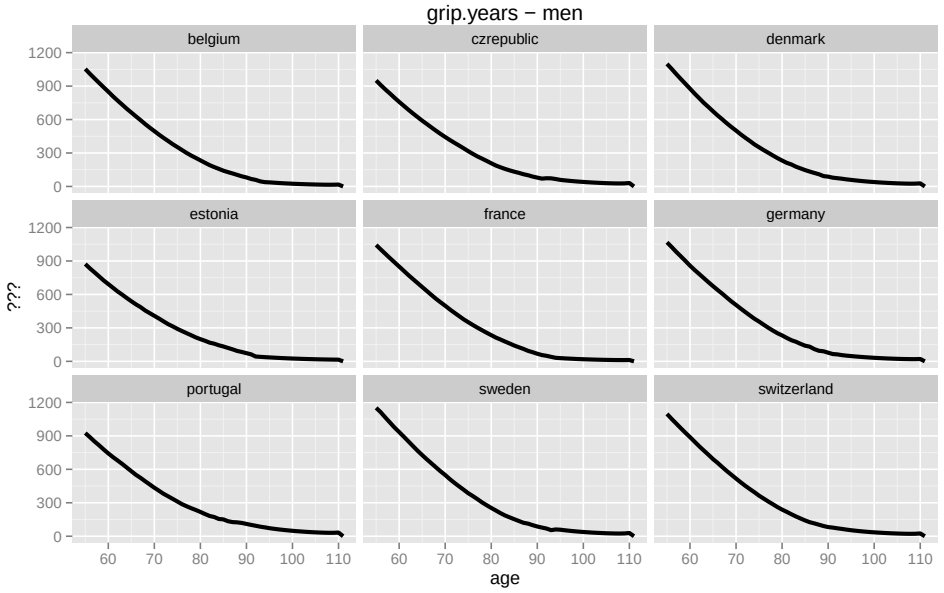

Figure 10: Expectation of healthy life, where health status is coded by grip strength, for men in nine countries, based on grip strength data from the SHARE study (see Methods).

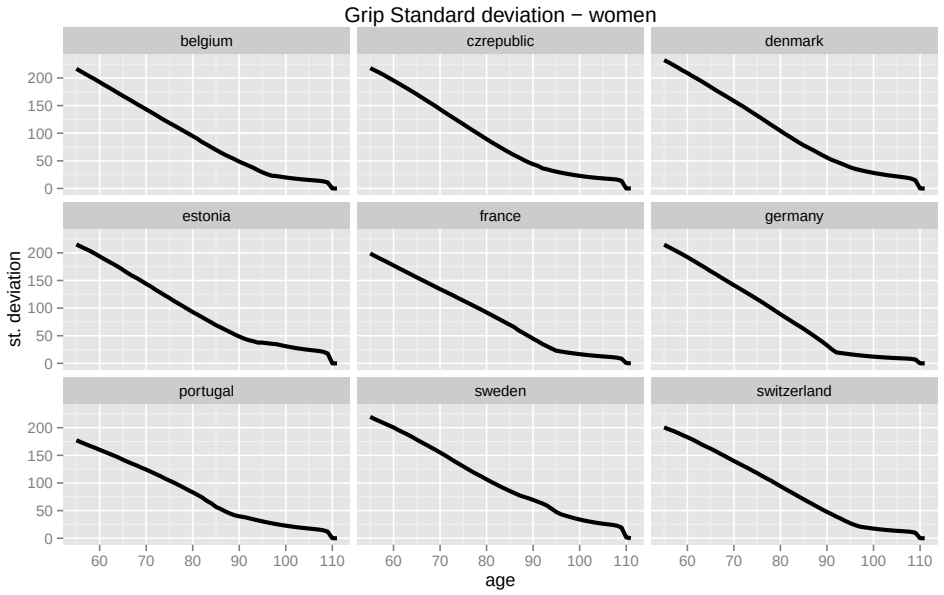

Figure 11: Standard deviation of healthy life, where health status is coded by grip strength, for women in nine countries, based on grip strength data from the SHARE study (see Methods).

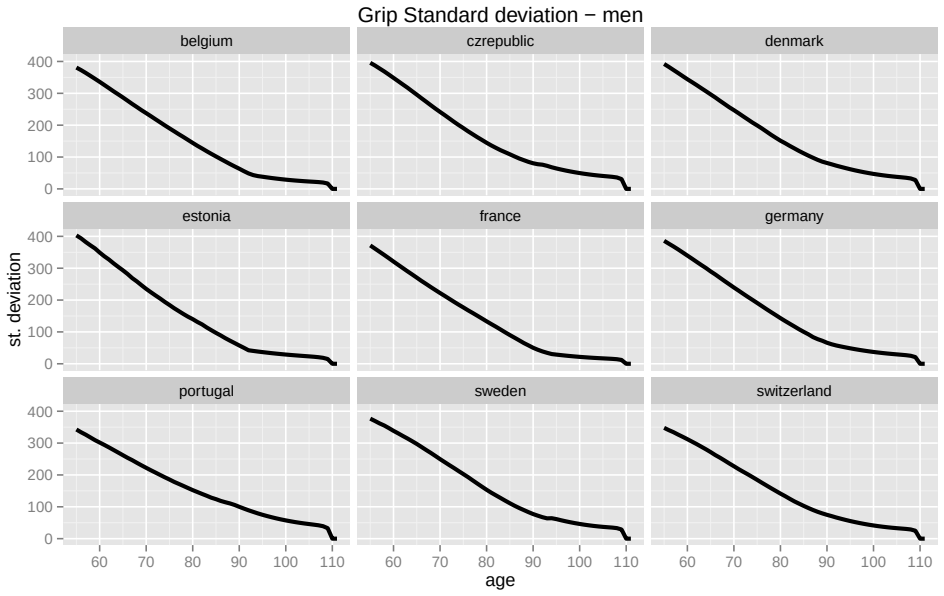

Figure 12: Standard deviation of healthy life, where health status is coded by grip strength, for men in nine countries, based on grip strength data from the SHARE study (see Methods).

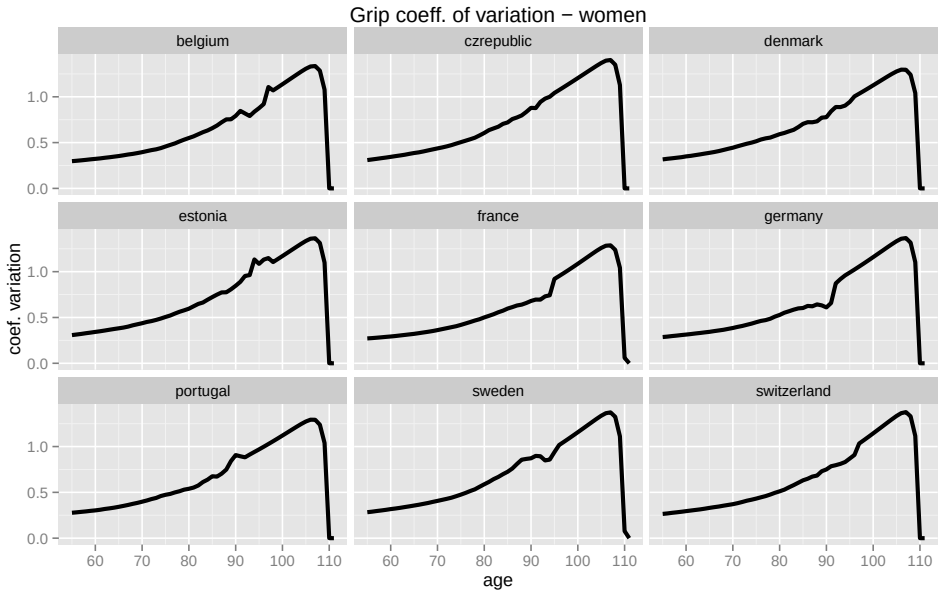

Figure 13: Coefficient of variation (CV) of healthy life, where health status is coded by grip strength, for women in nine countries, based on grip strength data from the SHARE study (see Methods).

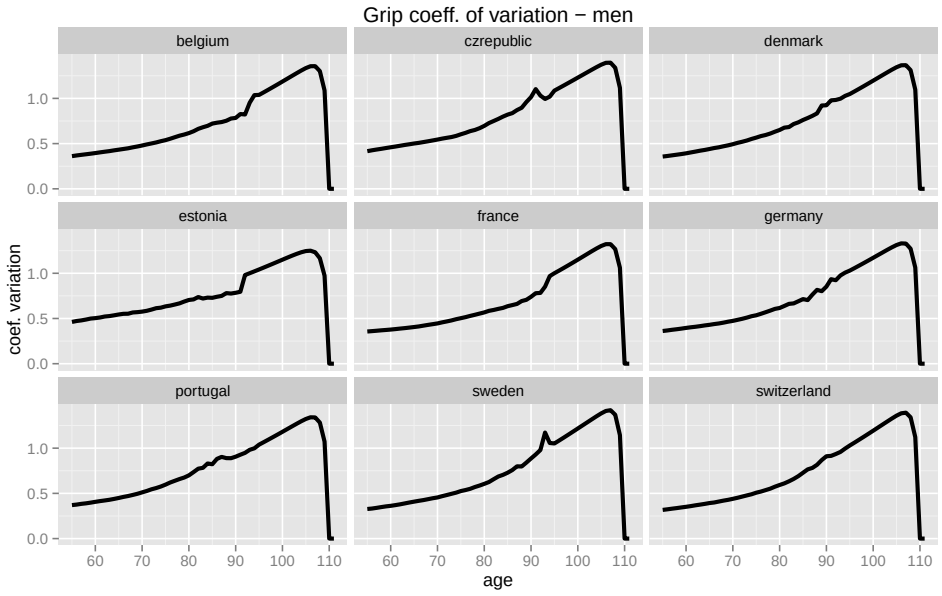

Figure 14: Coefficient of variation (CV) of healthy life, where health status is coded by grip strength, for men in nine countries, based on grip strength data from the SHARE study (see Methods).

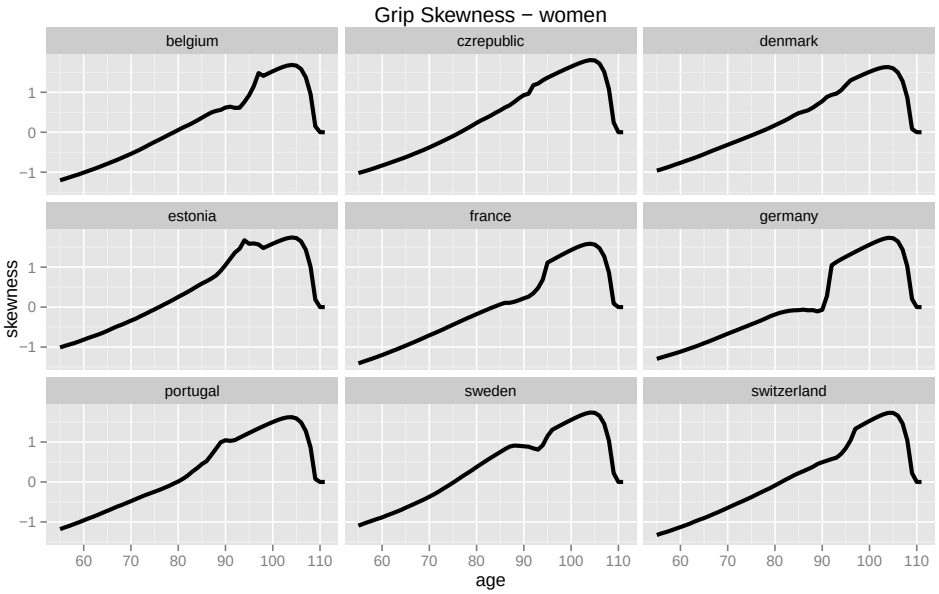

Figure 15: Skewness of healthy life, where health status is coded by grip strength, for women in nine countries, based on grip strength data from the SHARE study (see Methods).

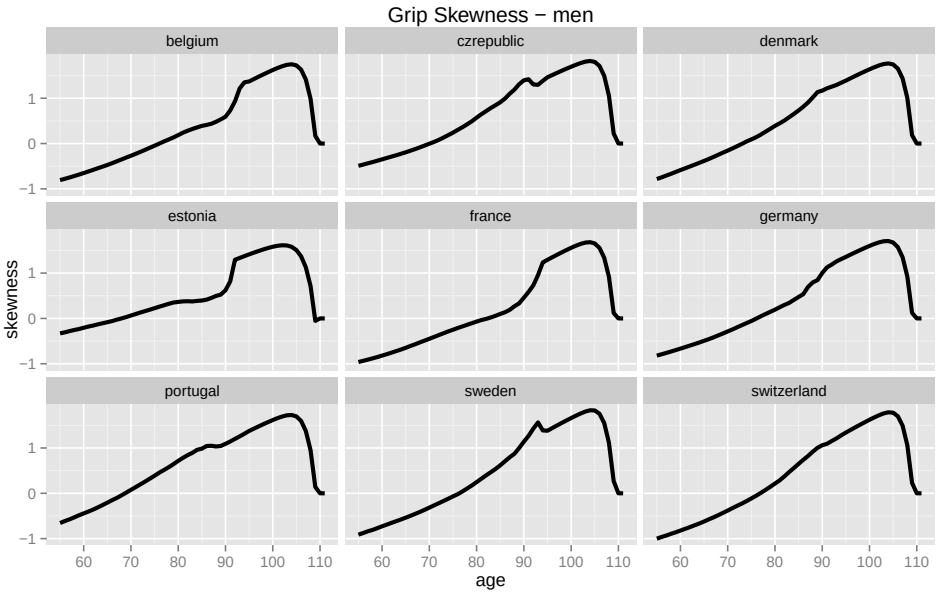

Figure 16: Skewness of healthy life, where health status is coded by grip strength, for men in nine countries, based on grip strength data from the SHARE study (see Methods).

8.3 DALY calculations

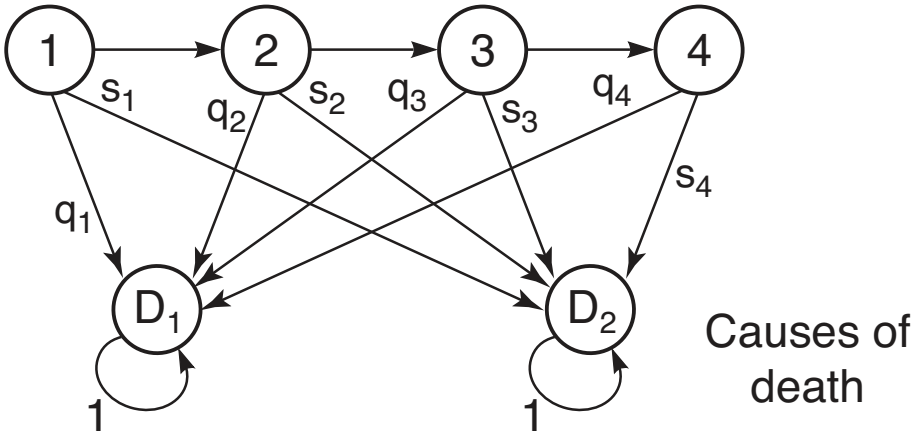

Figure 17: Partial life cycle graph for an age-classified life cycle with two causes of death