Riffe *et al. Population Health Metrics (2024) 22:33*
https://doi.org/10.1186/s12963-024-00354-w

Population Health Metrics

RESEARCH

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The joint distribution of years lived in good and poor health

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Abstract

Background Incidence-based multistate models of population health are commonly applied to calculate state expectancies, such as a healthy life expectancy (HLE), or unhealthy life expectancy (UHE). These models also allow the computation of other summary indices, such as the distributions of healthy or unhealthy lifespans.

Objective We aim to show how a multistate health model implies a multistate death distribution, giving joint information on years lived in good and poor health. We also propose three aggregate indices of joint health and mortality inequality.

Methods We propose a double-accounting approach to increment-decrement life table methods to intuitively derive a multistate health distribution over age and cumulative duration spent in each state. We then define a variety of summary lifespan inequality indices based on different distance metrics, namely Euclidean, Chebyshev, and Manhattan distances.

Results We apply the method to multistate transition probabilities between health states based on the activities of daily living index for Italian women from the Survey of Health, Ageing and Retirement in Europe in 2015-2017. We demonstrate the added value of accounting for joint years lived in health states in multistate models for our understanding of the period health and mortality conditions from the perspective of health-specific lifespans of individuals.

Conclusions Multivariate state distributions and summary indices derived from them give a holistic representation of population health inequality. We offer selected summary indices of the multivariate distribution with different demographic interpretations from the measures derived from univariate distributions. Although more theoretical and methodological work is required to motivate a single comprehensive population health inequality index, this direction is a promising path for a better understanding of population health dynamics and relationships between univariate statistics.

Keywords Population health, Health inequality, Mortality, Multistate

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Background

Healthy life expectancy (HLE) summarises the average life years lived in good health in a synthetic life-table cohort, and it is used as an indicator of population health. HLE is most commonly calculated using the Sullivan method [1], which is based on cross-sectional health prevalence and life table data. Although the strong assumptions of the Sullivan method are well understood [2–5], it is still widely applied due to its minimal data requirements and computational simplicity. HLE should be understood as the mean of a distribution of healthy life years. For the Sullivan method, whereas HLE can be estimated for any health dimension, a healthy-years distribution can only be directly inferred for the case of health dimensions where recovery is not possible [6].

HLE and the healthy years distribution can be readily derived using multistate methods. Such methods (microsimulation, Markov chains with rewards, or increment-decrement life tables) require detailed information on transitions between health states. These methods derive summary measures from transitions representing the health and mortality dynamics strictly within a study period, whereas the Sullivan method uses the prevalence of health states, which depend on the past experience of cohorts observed in the study period [7]. Moreover, multistate models are an attractive alternative to the Sullivan method because they are based on transitions between health states and they accommodate different mortality patterns and levels depending on underlying health status.

Formulas to calculate a greater variety of synthetic health indicators, including distribution statistics based on statistical moments, were given by [8]. These included the variance, standard deviation, and skewness of state occupancy times. These methods were further developed by [9] to derive distribution statistics, such as quantiles, and other synthetic measures, such as the mean waiting time before the first transition or final exit from a state.

We offer a new calculation approach to generate the state occupancy distribution time for multistate life tables. The method is a direct and efficient way to calculate the inter-individual distribution of time spent in a health state as a univariate duration distribution and a multistate death distribution. A multistate death distribution has as many time dimensions as there are health states. As far as we know, this is a new statistical concept for multistate models, although previously proposed matrix algebra methods [8] and microsimulation methods [4, 10] enable its calculation. We show other properties of the multidimensional death distribution, including a relationship to the stationary lifetable population, and how the variance of life lived in each health state relates to the variance of the total death distribution.

We give a worked example based on a small multistate model of limitations in activities of daily living (ADL), and we show a data application based on transition probabilities estimated from the Survey of Health, Ageing and Retirement in Europe (SHARE) [11] for Italian women in 2015-2017.

Methods

Notation

In our setting, the state space consists of two transient states $\{H,U\}$ and an absorbing state of death (†), as shown in Fig. 1. Our transition probabilities $p_{ij}(x) = P(Z_{x+1} = j|Z_x = i)$ define a discrete-time multistate health model, where Z_x denotes the random variable of a health state at exact age x, and Z_{x+1} at exact age $x+1$. Hence $i \in \{H, U\}$ and $j \in \{H, U, \dagger\}$. We presume single-age data and omit the notation for the subsequent age $x+1$. For example, $p_{hu}(x)$ denotes the probability of moving from the state of good health (H) to poor health (U) between ages x and $x+1$, $p_{hh}(x)$ denotes the probability of remaining healthy, $p_{h\dagger}(x)$ denotes the probability of dying in the age interval given good health at the initial age x, and so on. Transitions between health states occur only once in an age interval, and we assume that they happen at the beginning of each age step.

As we work with an initial population (radix) of 1, we denote the radix fraction healthy (unhealthy) as $\ell^H(0)$ ($\ell^U(0)$), such that $1 = \ell^H(0) + \ell^U(0)$. In the following formulas, the radix age of zero is the starting age of observation, which may be different from the chronological age of zero.

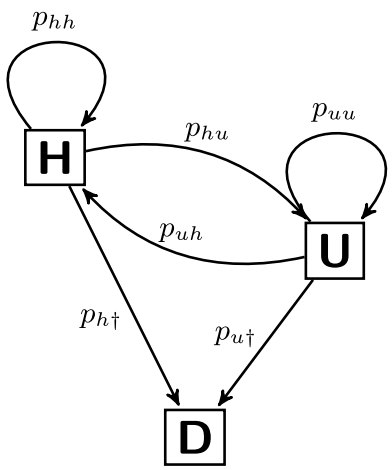

Fig. 1 State space diagram for the discrete-time health model considered

The multistate survival function

Using this notation, the probability of being alive and healthy $\ell^H(x+1)$ (unhealthy $\ell^U(x+1)$) at age $x+1$ can be calculated as:

$$\begin{aligned}\ell^H(x+1) &= \ell^H(x)\cdot p_{hh}(x) + \ell^U(x)\cdot p_{uh}(x)\\ \ell^U(x+1) &= \ell^U(x)\cdot p_{uu}(x) + \ell^H(x)\cdot p_{hu}(x) \quad .\end{aligned} \tag{1}$$

These stocks can also be interpreted as the probability that a randomly selected person in the stationary population resulting from the model will be $x+1$ years old and in good (poor) health at that age, independent of their health state trajectory in previous ages. The survivors in good and poor health of a certain age add up to the total survivors of that age (that is: $\ell^H(x)+\ell^U(x)=\ell(x)$). In addition, summing the respective health stocks over age also gives a point estimate of healthy (unhealthy) life expectancy, (HLE, ULE)[1]:

$$\begin{aligned}HLE &= \sum_x \ell^H(x)\\ ULE &= \sum_x \ell^U(x)\\ LE &= HLE + ULE \quad .\end{aligned} \tag{2}$$

So far, we have defined the proportion of individuals who survived up to age x (i.e., $\ell(x)$), and among those, what proportion live in healthy or unhealthy states *at that age* (i.e., $\ell^H(x)$,$\ell^U(x)$). We now define the proportion of those individuals who have accumulated a certain number of years in good health. For that purpose, we need further notation. Let lowercase h and u denote the accumulated duration spent in the respective states H and U out of the $x=h+u$ life-years. We index the accumulated years by duration healthy (h) and duration alive ($x=h+u$), and omit the notation for duration unhealthy. In other words, we are currently indexing x and h, but there is a redundant third index u that we omit to keep the notation manageable, although it is always available. For example, $\ell^H(10,5)=\ell^H(x=10,h=5)$ reads as the stock of *radix* + 10-year-olds who are currently healthy and have been healthy for a total of five accumulated years (either continuously or discontinuously). $\ell^U(10,5)$ are those ten years older than the radix age, with five accumulated healthy years (either continuously or discontinuously), but that are currently unhealthy. Again, we index age starting at the radix with $x=0$ and we set all cumulative healthy (unhealthy) years to zero at the initial radix age.

[1] These expectancies can be more refined or precise by making functional approximations of $l(x)$ for the interval between x and $x+1$, e.g. as a linear approximation of exposure, similar to what we do for lifetable exposure $L(x)$ in lifetable calculations.

According to this notation, the proportions of healthy and unhealthy in the radix are:

$$\begin{aligned}\ell^H(0,0) &= \ell^H(0)\\ \ell^U(0,0) &= \ell^U(0) = 1-\ell^H(0) \quad .\end{aligned} \tag{3}$$

To calculate the remaining stocks, we iterate conditionally up age and duration within age per (4), noting that $h \le x$. This means that, in an age step, x always increments, but health duration h only increments if the destination state at the next age step is good health. Notice that the notation here assumes that transitions are structured by age rather than by age and duration. If double-indexed transition probabilities (age and duration) were available, one needs to be careful to either ensure duration-dependence is estimated over accumulated time, or else modify formulas to allow for spell-specific age-duration dependence.

$$\begin{aligned}\ell^H(x+1,h+1) &= \ell^H(x,h)\cdot p_{hh}(x) + \ell^U(x,h)\cdot p_{uh}(x)\\ \ell^U(x+1,h) &= \ell^H(x,h)\cdot p_{hu}(x) + \ell^U(x,h)\cdot p_{uu}(x) \quad .\end{aligned} \tag{4}$$

In words, $\ell^H(x+1,h+1)$ is the health stock at age $x+1$ and health duration $h+1$. It consists of those healthy at exact age x that have h accumulated years healthy ($\ell^H(x,h)$) and that stay healthy (in the stationary population share of those out of $\ell^H(x,h)$ is $p_{hh}(x)$), plus those having accumulated the same amount of healthy years by age x (h) but that are unhealthy at age x ($\ell^U(x,h)$) and then move to good health ($p_{uh}(x)$).

In the second Eq. of (4) we have survivors in each health state with the same age x and accumulated healthy years h, who advance to poor health in the next age. In this case, we increment age, but h stays the same.

The following relationships hold:

$$\begin{aligned}\ell(x,h) &= \ell^H(x,h) + \ell^U(x,h)\\ \ell(x) &= \sum_{h=0}^{x} \ell(x,h)\\ HLE &= \sum_{x=0}^{\omega}\sum_{h=0}^{x} \ell^H(x,h) = \sum_{x=0}^{\omega} \ell^H(x)\\ ULE &= \sum_{x=0}^{\omega}\sum_{h=0}^{x} \ell^U(x,h) = \sum_{x=0}^{\omega} \ell^U(x)\\ LE &= \sum_{x=0}^{\omega} \ell(x) = HLE + ULE \quad .\end{aligned} \tag{5}$$

In words, the overall stock of individuals aged x with h accumulated years healthy ($\ell(x,h)$) is the sum of those with matching age and healthy years indexes irrespective of the current health status. Aggregating $\ell(x,h)$ over

accumulated years healthy gives the stock $\ell(x)$, which is the overall survivor function. Finally, HLE is the sum over age and duration of the stock of those with current-status healthy ($\ell^H(x,h)$). This means that those who are alive with h years healthy at age x ($\ell(x,h)$) are also alive in the whole age interval $[x, x+1)$. In a life-table notation, this means that $L(x,h) = \ell(x,h)$ and $L(x,u) = \ell(x,u)$. This shows HLE, ULE, and by extension life expectancy, to be a sum of healthy and unhealthy years accumulated over the lifespan by age, state, and total duration.

Other life table quantities

As in the stationary population derived based on this model $L(x,h) = \ell(x,h)$, the proportion of the stationary population that is healthy and aged $[x, x+1)$ is

$$C(x,h) = \frac{\ell(x,h)}{LE} \quad . \tag{6}$$

The quantity $C(x,\ h)$ gives the stationary age-duration distribution i.e., the probability that a randomly selected individual from the stationary population is of a particular age x and has accumulated h years in good health. That is, it gives the hypothetical census distribution of accumulated years lived in good health, a 2-D version of the more well-known life-table stationary population [12].

The probability that an individual from the radix population dies at age x with h years of healthy life accumulated is then:

$$d(x,h) = \ell^H(x,h) \cdot p_{h\dagger} + \quad \ell^U(x,h) \cdot p_{u\dagger} \quad . \tag{7}$$

If a limit to the lifespan is set at $x = \omega$, i.e. $p_h\dagger(\omega) = p_u\dagger(\omega) = 1$, then $\sum\sum d(x,h) = 1$, and $d(x,\ h)$ is the probability distribution of a two-dimensional random variable of distribution of years lived ($\mathcal{X}$) and healthy years accumulated ($\mathcal{H}$), implying a third random index variable $\mathcal{U} = \mathcal{X} - \mathcal{H}$.

Let us denote the joint probability distribution (or two-dimensional death distribution) as $d(h,u) = P(\mathcal{H} = h, \mathcal{U} = u)$. It is an arbitrary choice which two variables out of $\{\mathcal{X}, \mathcal{H}, \mathcal{U}\}$ we decide to call dimensions. We denote the marginal probability distribution $d(x) = P(\mathcal{X} = h + u)$ for the total number of years lived, $d(h) = P(\mathcal{H} = h)$ for healthy years, and $d(u) = P(\mathcal{U} = u)$ for unhealthy years. The following formulas define the marginal distributions:

$$\begin{aligned} d(x) &= \sum_h d(x,h) \\ d(h) &= \sum_x d(x,h) = \sum_u d(h,u) \\ d(u) &= \sum_h d(h,u) = \sum_x d(x,u) \quad . \end{aligned} \tag{8}$$

The first moments (means) of these marginal distributions return the state-specific and overall life expectancies:

$$\begin{aligned} LE &= \sum x \cdot d(x) \\ HLE &= \sum h \cdot d(h) \\ ULE &= \sum u \cdot d(u) \quad . \end{aligned} \tag{9}$$

Lifespan inequality measures

One may calculate other moments of these marginal distributions as [8], or flexibly derive inequality measures analogous to standard lifetable inequality measures, such as variance, Theil, or Drewnowski indices [13], and further decompose them to quantities of interest. For example, the total variance in the number of years lived can be decomposed as:

$$Var(x) = Var(h) + Var(u) + 2 \cdot Cov(h,u) \quad . \tag{10}$$

where

$$\begin{aligned} Var(x) &= \sum (x - LE)^2 \cdot d(x) \\ Var(h) &= \sum (h - HLE)^2 \cdot d(h) \\ Var(u) &= \sum (u - ULE)^2 \cdot d(u) \\ Cov(h,u) &= \sum\sum (h - HLE) \cdot (u - ULE) \cdot d(h,u) \quad . \end{aligned} \tag{11}$$

Rather than list the various possible one-dimensional lifetable inequality indices that one could calculate on the three marginal distributions, we propose a few simple indices that might be used to summarize variability (or inter-individual inequality) in the two-dimensional distribution. That is, given a distribution on a simplex over (h, u, x), how might one reduce this information to a single index using some notion of distance from the simplex mean point (*HLE*, *ULE*, *LE*)?

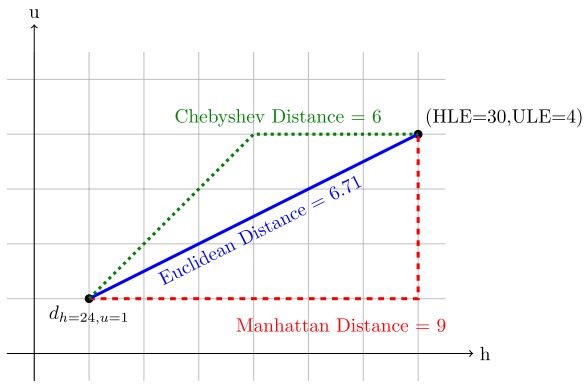

Fig. 2 Diagram of three distance measures considered in Eq. (12). Notes: The 45° diagonal displacements for Chebyshev are exactly 1 step each, such that the hypotenuse is not accurately depicted, similar to cohort time steps on a standard Lexis diagram. The *paths* drawn for Manhattan and Chebyshev distances are illustrative examples, as different paths are possible, each with the same respective total length

$$\begin{aligned} Ineq^{Euclidean}(h,u) &= \sum\sum d_{h,u} \cdot \sqrt{(h-HLE)^2 + (u-ULE)^2)} \\ Ineq^{Chebyshev}(h,u) &= \sum\sum d_{h,u} \cdot argmax(|h-HLE|, |u-ULE|) \\ Ineq^{Manhattan}(h,u) &= \sum\sum d_{h,u} \cdot (|h-HLE| + |u-ULE|) \quad . \end{aligned} \tag{12}$$

The different notions of distance used in Eq. 12 are explained visually in Fig. 2.

We consider the interpretations and shortcomings of such indices in the Discussion section.

Empirical illustration

The aim of the empirical illustration is to demonstrate the added value of accounting for joint years lived in health states in multistate models for our understanding of period health and mortality conditions.

Data and methods to derive transitions between health states

Our empirical application is based on waves 6 and 7 of the Survey of Health, Ageing and Retirement in Europe (SHARE) [11, 14] for Italian women in 2015-2017. Health states are operationalized using information on limitations in activities of daily living using the ADL indicator, which asks respondents if they have difficulty with the following activities: 1. Dressing, including putting on shoes and socks; 2. Walking across a room; 3. Bathing or showering; 4. Eating, such as cutting up food; 5. Getting in or out of bed; 6. Using the toilet, including getting up or down. We use a binary summary of these responses, which categorizes responses into those with no difficulty (H, in our state space) versus difficulty with at least one activity (U). We apply individual cross-sectional weights for wave 6, as the longitudinal weights do not include weighting scores for deaths [15]. The sample consists of 2766 individual observations.

Transition probabilities between health states are estimated with a discrete-time Markov-chain model. We estimate yearly transition probabilities between the functional states, with death as an absorbing state, using a multinomial logistic regression model and assuming an embedded Markov chain (EMC), which follows the approach originally proposed by Laditka [10]. In the EMC model, the probability of an observed sequence of functional status transitions at the interview is expressed as a product of possible single-period (e.g. monthly, half-yearly) transition probabilities. Next, the single-period transition probabilities are estimated using maximum likelihood methods. The idea behind the model is that we only observe a snapshot of health status at the time of the interview, although transitions between health states might occur more often than the interview waves, which creates bias by limiting our observation of short-duration spells [16]. We assume that in the long run, the prevalence of health states resulting from the disablement-recovery processes converge to a stable distribution of a given functional form and that the observations are snapshots from this distribution. We use the `IMaCh` (interpolated Markov chain approach) computer program developed by Brouard, Liévre, and others [7], based on the EMC assumption, to estimate transition probabilities between the functional states. The transition probabilities are estimated using multinomial logit functions, assuming log-linear age dependence. Transitions between health states are estimated for ages 50-90 years and then projected to older age groups (up to age 110) based on the estimated transition models.

The resulting transition probabilities are as seen in Fig. 3.

Results

Figure 4 shows the multistate death distribution on the simplex plane of healthy years, unhealthy years, and age at death. A given point on this plane represents a lifetime total accumulation of healthy and unhealthy years. Color levels and contours represent the 2-D death density. We label the respective state expectancies and remaining life expectancy at age 50. These expectancies match those calculated in the standard way, and they converge on the same point.

For this health definition, the density is highest along the boundary $0 < u <= 1$, due to the very high mortality among those with functional limitations and hence low probability to accumulate many unhealthy years prior to death.

Figure 5 shows the marginal distributions $d(h)$, $d(u)$, and $d(x)$, following Eq. (8). The age distribution $d(x)$ is,

in our case, the *diagonal* margin of Fig. 4. For the present case, inequality in unhealthy appears far lower than inequality in healthy years (see Table 1). Indeed, since most of life is spent disability-free, inequality in healthy years accounts for most inequality within the death distribution.

Holistic inequality based on each of the distance measures in Eq. (12) are given in Table 2

We expect the indices of Table 2 to correlate with one another, and to generally map to a holistic summary of health inequality over the life course, but only the Manhattan distance offers a demographic interpretation. Specifically, we might prefer a distance measure that is consistent with possible transition trajectories. Unlike movements on a Lexis diagram, where an individual life course snaps to a cohort diagonal to increment age and time upward, an individual life course in our multistate coordinate space (refer to Fig. 4 and Fig. 2) can only move rightward (increment h) *or* upward (increment u) in a single time step. These are possible *Pac-Man* (or *rook*) moves, with the restriction that in a given move either h or u must increment. To derive an inequality statistic, we estimate an average of distances traversed for a synthetic cohort. Of the indices we present, only the Manhattan-based index is consistent with these restrictions. Specifically, the Manhattan distance tells us the minimum number of transition swaps required to move from a given point (h, u) to the mean (HLE, ULE). This metric does not consider the effort or costs that it would take to swap a transition. Put differently, the Manhattan inequality index treats increments in h or u in equivalent (year) units, with no weights.

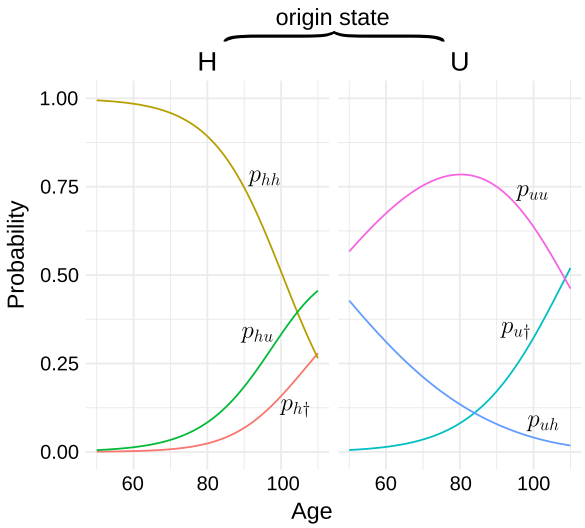

Fig. 3 Transition probabilities for a multistate model, where U represents the presence of limitations according to the ADL indicator, and H represents the absence thereof. Italian women, 2015-2017. Notes: Healthy=free of limitations according to ADL indicator; Unhealthy=with limitations Source: Own estimations based on data from SHARE [11, 14]

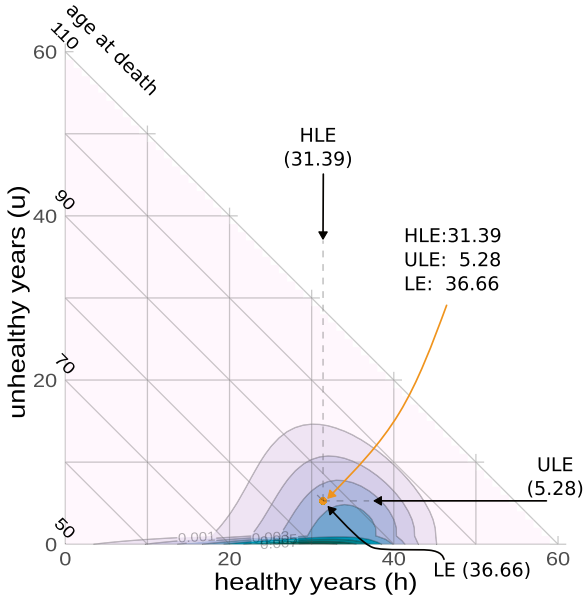

Fig. 4 A bivariate distribution of healthy and unhealthy years lived, $d_{h,u}$. Data: SHARE [11, 14] Italy, females, ADL measure, 2015-2017. Labeled points include HLE (Healthy Life Expectancy), ULE (Unhealthy Life Expectancy), and LE (Total Life Expectancy)

Two of these inequality measures have lifetable analogs. The 2d Manhattan distance is exactly equal to the mean absolute deviation (MAD) of the overall multistate lifetable (i.e. MAD calculated using $d(x)$ of Eq. (8)) although the multistate MAD is decomposable into healthy and unhealthy parts. The 2d Euclidean inequality index is analogous to, but always smaller than, the lifetable standard deviation [17]. The 2d Chebyshev index has no lifetable analog yet.

Discussion

We propose a new multistate method to calculate the components of within-population health inequality based on life table calculations over two simultaneous timescales: years lived in good health (h) and years lived in poor health (u). These calculations yield a multistate survival distribution and a multistate death distribution, each obtained from health and mortality transition probabilities, as often used for multistate expectancies. These new multistate constructs have the potential to better reflect within-population health disparities over the synthetic life course. Visualizing the multistate death distribution in and of itself reveals disparities in healthy and unhealthy life years and it might enable valuable insights into morbidity compression. To illustrate these concepts,

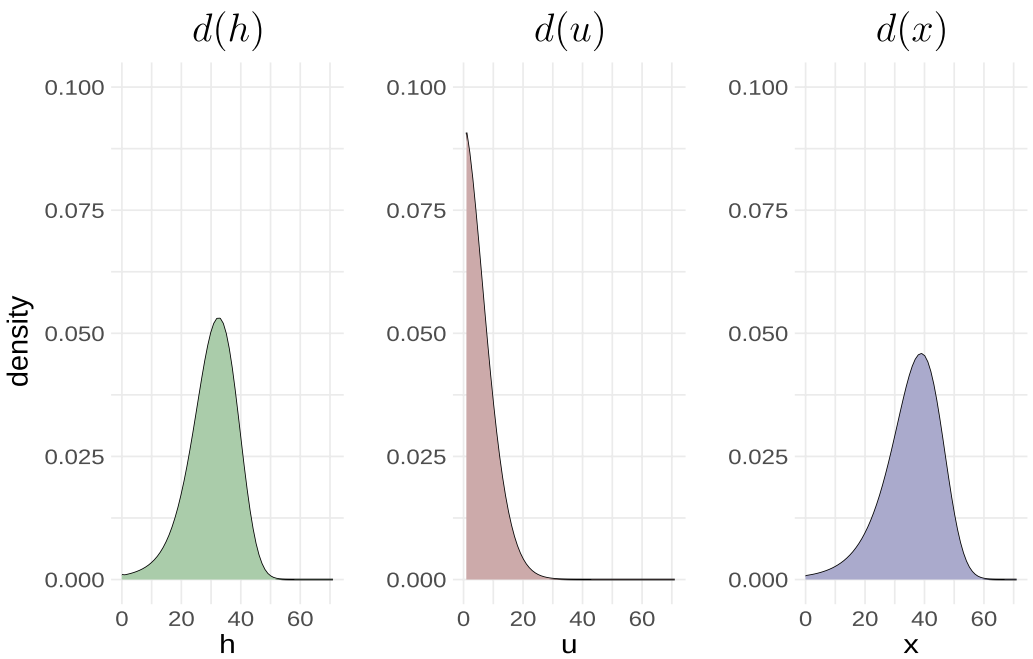

Fig. 5 Three marginal distributions derived from $d_{h,u}$, per Eq.(8). Data: SHARE [11, 14] Italy, females, ADL measure, 2015-2017. Distributions depicted include $d(h)$ (the death distribution by healthy years lived), $d(u)$ (death distribution by unhealthy years lived), and $d(x)$ (the lifetable age distribution of deaths)

Table 1 Means, variances and standard deviations corresponding to the three densities shown in Fig. 5. Source: Own estimations based on data from SHARE [11, 14]

	Expectancy (sd)	var	sd
HLE	30.90	65.07	8.07
ULE	5.77	26.13	5.11
LE	36.16	91.45	9.56

Healthy=free of limitations according to ADL indicator; Unhealthy=with limitations

Italian women, 2015-2017. Noting that the covariance is 0.12, Equation (10) can be verified

Table 2 Holistic inequality indices of health and mortality, based on the joint distribution $d(h, u)$ per Eq. (12)

Euclidean	Chebyshev	Manhattan
8.25	7.55	10.40

Euclidean distance is *as the crow flies*, Chebyshev is the *Queen* distance, and Manhattan is the *Rook* distance

we use SHARE data from Italy. We calculate the multistate death distribution (Fig. 4), and its marginal distributions (Fig. 5).

From the state-specific marginal death distributions, one can calculate well-known 1d inequality statistics, such as the standard deviation or variance of years lived in a state. State variances relate to the total variance of age at death plus a covariance term (see Eq. (10)). This well-known but satisfying relationship relates the multistate death distribution to the standard life table death distribution $d(x)$, which is the diagonal margin of the simplex displayed in Fig. 4. The relationship allows a demographic explanation: If, on average, those with a longer healthy lifespan are also among those with a shorter unhealthy lifespan (i.e., if we observe a negative covariance), then lifespan inequality is lower than the sum of inequality in healthy and unhealthy years. This relationship has important implications for research on inter-individual health inequalities in populations, as it demonstrates that individual-level conclusions concerning the relationship between the quantity and quality of years lived cannot be drawn based on the aggregated data results. For example, in a society where long-lived individuals also have exceptionally long healthy lives compared to short-lived individuals, the resulting inter-individual inequalities in quality-adjusted lifespans are together much greater than what the marginal lifespan inequality would tell us.

Also, the correlation, based on the covariance, between individual healthy and unhealthy life years is an important measure of population health. The ability to calculate the covariance, and hence the correlation, between health state occupancy times depends on the joint death distribution calculations of Eq. (7). As life expectancy increases, changes in the correlation between health state

occupancy times can answer the question of whether observed increases in length of life are associated with more healthy years and, hence, a smaller proportion of unhealthy years. This result would be indicated by a stronger negative correlation between individual healthy and unhealthy years of life. From our limited testing of transitions derived from other health conditions and datasets, the covariance can, in practice, turn out to be either positive or negative. We infer that conditions with high lethality penalties and low recovery will likely lead to negative covariance, although this relationship remains to be formalized. The key point is that a given set of marginal distributions of healthy and unhealthy life years is compatible with many joint distributions. Information on the covariance between healthy and unhealthy years should complement our assessments around the process of morbidity compression and that statistics belonging to the marginal distributions (HLE, ULE) are necessary but insufficient metrics.

We speculate that the elements of Eq. (10), or some transformation of them, might serve as useful input parameters (among others) for models that aim to transform Sullivan parameters (a lifetable and the prevalence of some condition) [1] into incidence parameters [c.f. [18, 19]]. This undertaking is left for future research.

In our example, the margin $d(h)$ accounts for most of the variance in $d(x)$, whereas the distribution of years lived in poor health $d(u)$ is relatively compressed (See Fig. 5). A compressed distribution of unhealthy years $d(u)$ is consistent with end-of-life (*thanatological*) conditions previously identified by [20], which arise when large mortality differences are observed between states, especially when recovery rates are also low. Although on a different scale and different metric, this relationship indirectly coheres with the between-country analysis of [21], where most between-country variability in life expectancy was accounted for by variation in HLE, whereas between-country variability in ULE was far lower. We might consider the schematic relationship between $d(h)$ and $d(u)$ to be the within-population analog of the findings in [21]. The finding that variation in $d(h)$ is greater than $d(u)$ in our application is for absolute measures, but it might not hold for relative measures.

Also coherent with our findings, Luy [22] proposed the CroHaM (cross-sectional association between health and mortality) hypothesis, suggesting that LE positively correlates with spending less time in health states with high mortality penalties and more time in states characterized by chronic conditions with lower mortality penalties. Nielsen et al. [23] demonstrated that the time spent in non-frail states (states with low mortality penalties) has increased over the past decade, while frail life expectancy remained unchanged. Solé-Auró and Gumà [24] and Carreras et al. [25] studied age, geography, and education strata using multistate modeling. Their findings show that mortality varies less across these strata than other transitions, such as disease onset. Boissonneault and Rios [26] found that working life expectancy with manageable chronic conditions like hypertension or arthritis increased over 14 OECD countries. This highlights the potential role of ULE (with low mortality penalties) in explaining longevity growth in low-mortality countries and the corresponding inequality in LE across populations. These findings should condition our observation that inequality in healthy life years within populations explains the majority of overall lifespan inequality: The statement should hold more strongly for health conditions with high mortality penalties, such as the ADLs in our data application.

We define three synthetic inequality indices intended to summarize the rich information in the multistate death distribution (Eq. (12)). These indices differ in their treatment of distance between a given pair $((h, u))$ on the multistate death distribution and the distribution mean (where HLE, ULE, and LE meet). While these indices may be useful in practice, we think these and alternatives should be further investigated.

Limitations

The transition probabilities we use in Eq. (4) in our empirical application rely on the Markov assumption. This simplifies our analysis but does not fully capture the complexity of health trajectories. Although the mean point of the multistate death distribution (*HLE*, *ULE*) is well-identified, even if the generating process is not strictly Markovian ([27–29]), the shape of the distribution (and its resulting inequality statistics) may be biased, for instance, if transition probabilities vary according to a second unrecognized duration timescale. Equation (4) could directly account for duration dependence, for instance, by simply adding a duration index to the transitions. In this case, one must be careful about how duration is defined. In our formulas, duration means cumulative lifetime duration, whereas most work on estimating transitions with multiple timescales refers to the duration *within episode* [30–35]. These two definitions of duration are the same only if health transitions are irreversible. Most data sources do not allow the direct estimation of transitions by both age and cumulative lifetime duration spent in different states for models with reversible health transitions. This would require a very long panel or register data series with sufficient detail to capture recoveries. For transition probabilities, a within-episode duration clock is likely to better articulate risk profiles than cumulative lifetime duration. Equation (4)

would need further modification to use double-indexed transitions using a within-episode definition of duration.

Conclusions

In a multistate health model, a death distribution can be calculated as a joint distribution of total life lived in each state. Previous matrix algebra derivations of the marginal healthy years distribution [8] did not point out the multidimensional death distribution as such, nor how these relate to the lifetable death distribution. We propose a demographically intuitive derivation of these quantities using lifetable logic.

A concise variance-covariance relationship relates the marginal distribution to the overall lifetable death distribution. Other inequality indices could be calculated on the joint health distribution; these mostly lack demographic appeal, although an inequality measure based on Manhattan distance from the joint mean point has a clear interpretation as a minimum number of transition swaps to reach the mean. We suggest visualizing a multistate death distribution as a good way to explore and understand morbidity compression.

Acknowledgements

We'd like to thank several people whose comments helped to improve this work, including James Oeppen, Jutta Gampe, Alyson van Raalte, Ugofillipo Basellini, Jose Manuel Aburto, Hill Kulu, and Angelo Lorenti. This paper uses data from SHARE Waves 6 and 7 (DOIs: 10.6103/SHARE.w6.900, 10.6103/SHARE.w7.900) The SHARE data collection has been funded by the European Commission, DG RTD through FP5 (QLK6-CT-2001-00360), FP6 (SHARE-I3: RII-CT-2006-062193, COMPARE: CIT5-CT-2005-028857, SHARELIFE: CIT4-CT-2006-028812), FP7 (SHARE-PREP: GA No 211909, SHARE-LEAP: GA No 227822, SHARE M4: GA No 261982, DASISH: GA No 283646) and Horizon 2020 (SHARE-DEV3: GA No 676536, SHARE-COHESION: GA No 870628, SERISS: GA No 654221, SSHOC: GA No 823782, SHARE-COVID19: GA No 101015924) and by DG Employment, Social Affairs & Inclusion through VS 2015/0195, VS 2016/0135, VS 2018/0285, VS 2019/0332, VS 2020/0313 and SHARE-EUCOV: GA No 101052589 and EUCOVII: GA No 101102412. Additional funding from the German Ministry of Education and Research, the Max Planck Society for the Advancement of Science, the U.S. National Institute on Aging (U01_AG09740-13S2, P01_AG005842, P01_AG08291, P30_AG12815, R21_AG025169, Y1-AG-4553-01, IAG_BSR06-11, OGHA_04-064, BSR12-04, R01_AG052527-02, HHSN271201300071C, RAG052527A) and from various national funding sources is gratefully acknowledged (see www.share-eric.eu).

Author Contributions

T.R. Conceptualization, Investigation, Methodology, Software, Validation, Formal analysis, Writing - Original draft preparation, reviewing & editing, Visualization. I.P. Writing - reviewing & editing. R.T.Z. Software, Validation, Formal analysis, Writing - reviewing & editing. M.M.S. Methodology, Formal analysis, Writing - Original draft preparation, reviewing & editing, Software.

Funding

T.R. was supported by the Spanish Ministry of Science and Innovation (grant PID2022-142762OA-I00) and from the "la Caixa" Foundation Social Research programme (grant SR22-00502). I.P. was supported by the European Research Council under the European Union's Horizon 2020 research and innovation programme (grant 2019-CoG-864616) and the Spanish Ministry of Science and Innovation R+D LONGHEALTH project (grant PID2021-128892OB-I00). M.M.S. was supported by the European Research Council within the Horizon 2020 research and innovation programme (grant 2017-CoG-725187). The funders had no role in the data application, data analysis, preparation of manuscript, or decision to write and submit this paper. The responsibility for all conclusions drawn from the data lies entirely with the authors.

Availability of data and materials

The original SHARE survey data that support the findings of this study are free to use (https://share-eric.eu/data/) but restrictions apply to access these data, which were used under license for the current study, and so are not publicly available. Data are however available from the authors upon reasonable request and with permission of SHARE. The R code used to process SHARE data is available in an open repository (https://github.com/mmuszynskasp/health_transitions_imach), and a dataset of annualized transition probabilities, and all R code to reproduce all our results is available in an open repository (https://github.com/timriffe/ms_dist)

Declarations

Ethics approval and consent to participate

This paper is based on data from the Survey on Health and Retirement (SHARE), which is anonymized microdata. Thus, ethics approval is not necessary.

Consent for publication

Not applicable

Competing interest

The authors declare that they have no Conflict of interest.

Received: 1 July 2024 Accepted: 6 November 2024
Published: 23 November 2024

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