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RESEARCH

Calculating 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. 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.

Results: We visualize a multistate death distribution as a 2-D contour plot over years spent in good and poor health. We show this distribution to consist of three different marginal lifetime distributions, representing years lived in good health, poor health, and the overall lifetime distribution.

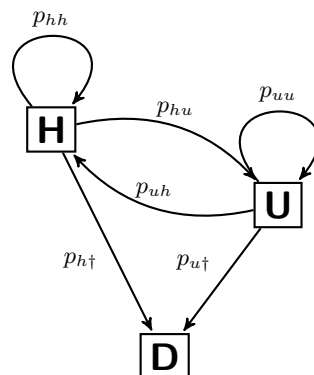
Conclusions: Multivariate state distributions and summary indices derived from them give a holistic representation of population health inequality. We offer selected summary indices of the multivariate distribution with different demographic interpretations from the measures derived from univariate distributions. 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: multistate; discrete time Markov; health; mortality; inequality

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

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



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 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 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 (\dagger), 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.

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

^[1]These expectancies can be more refined or precise by making functional approximations of $\ell(x)$ 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.

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.

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 $h \leq x$. 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 $\ell^H(x, h)$ equals to $p_{hh}(x)$), 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 equation 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 and healthy at age x ($\ell(x, h)$) are also healthy and 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 lives accumulated is then:

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

If a limit to the lifespan is set at $x = \omega$, i.e. $p_{h\uparrow}(\omega) = p_{u\uparrow}(\omega) = 1$, 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 (averages) 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 operationalize 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) ?

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

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

Empirical Illustration

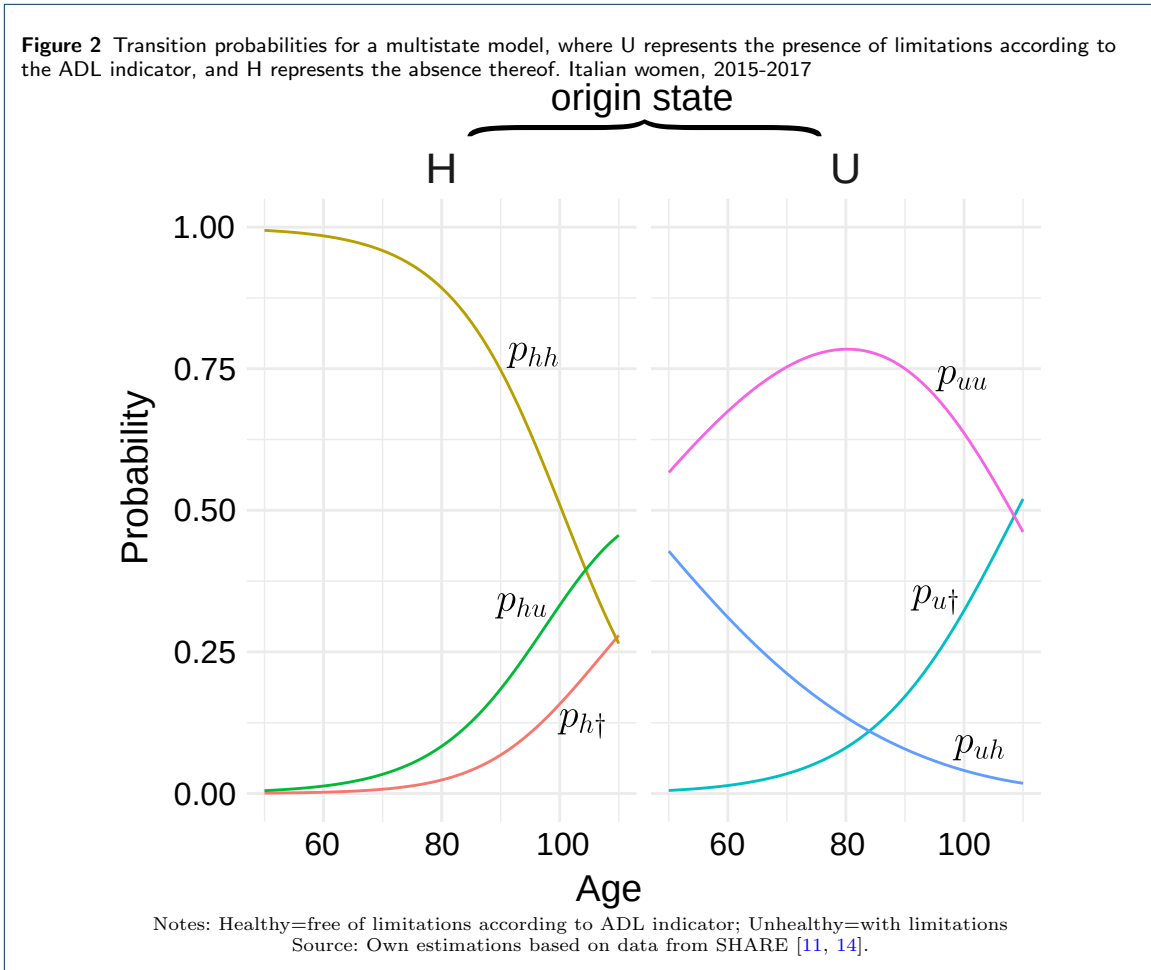
Our empirical application is based on waves 6 and 7 of the Survey of Health, Ageing and Retirement in Europe (SHARE) [11, 14] for Italian women in 2015-2017. Health states are operationalized using information on limitations in activities of daily living using the ADL indicator, which asks respondents 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 zero (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 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, Lièvre, 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. 2.

Code for preparing data and executing the transition estimation using IMaCh is available at https://github.com/mmuszynskasp/health_transitions_imach

Fig. 3 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.

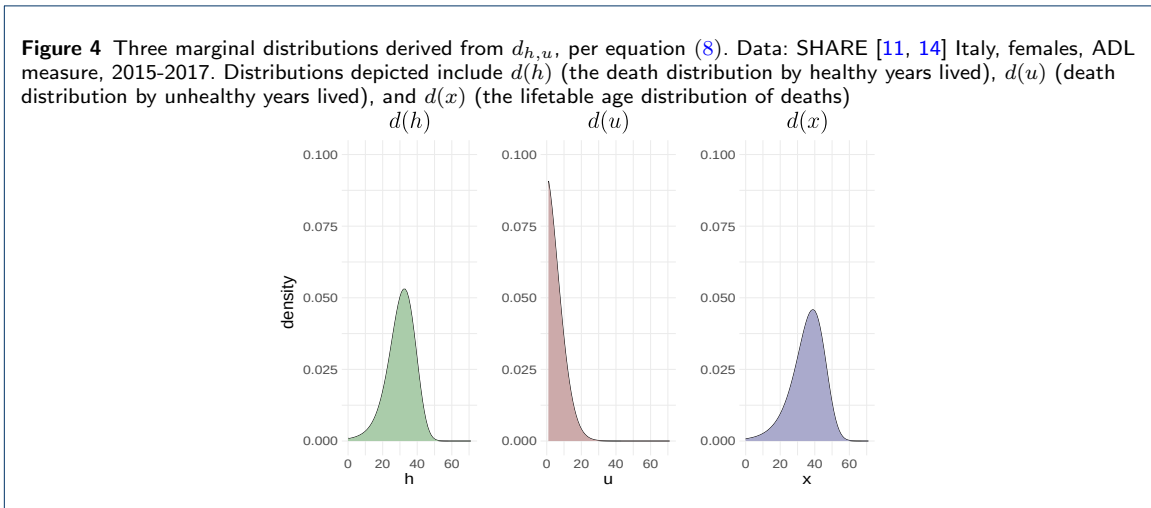
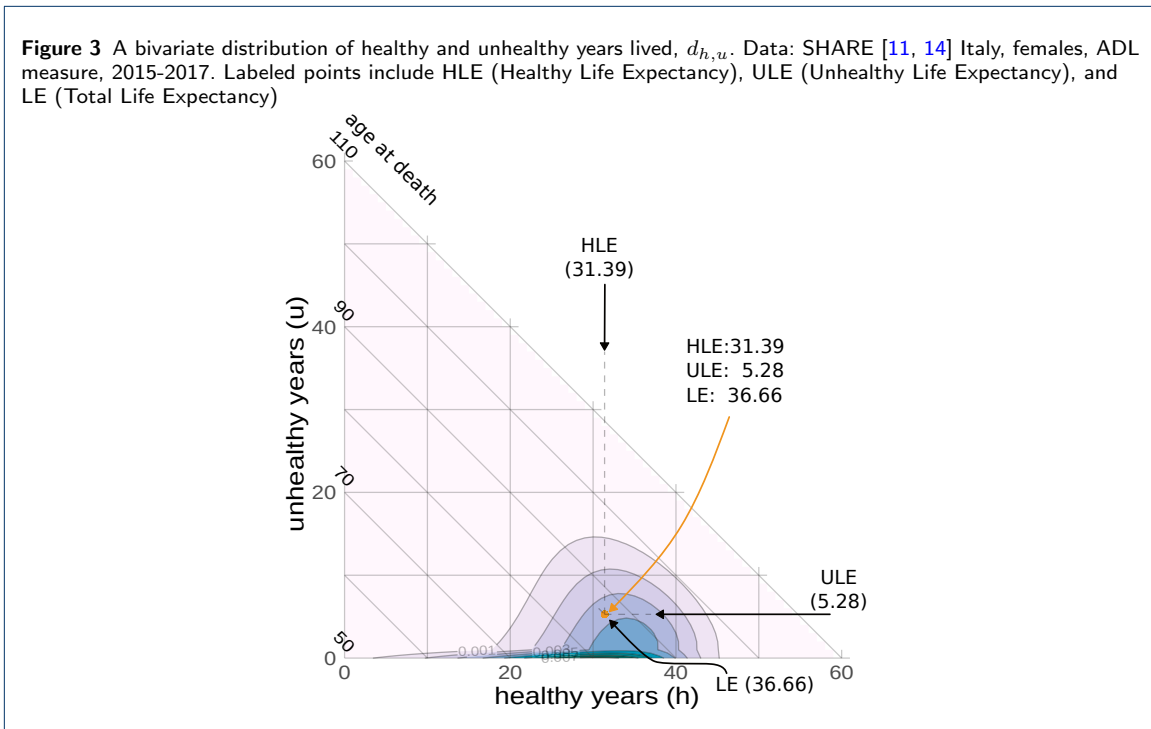
For this health definition, the density is highest along the boundary $0 < u \leq 1$, due to the very high mortality among those with functional limitations and hence low probability to accumulate many unhealthy years prior to death.

Fig. 4 shows the marginal distributions $d(h)$, $d(u)$, and $d(x)$, following equation (8). The age distribution $d(x)$ is, in our case, the *diagonal* margin of Fig. 3. 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.

	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

Table 1 Means, variances and standard deviations corresponding to the three densities shown in Fig. 4. 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].



Noting that the covariance between years lived healthy and unhealthy for this variable is 0.12, equation (10) can be verified.

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

Euclidean	Chebyshev	Manhattan
8.25	7.55	10.40

Table 2 Holistic inequality indices of health and mortality, based on the joint distribution $d(h, u)$ per Eq. (12). Euclidean distance is *as the crow flies*, Chebyshev is the *Queen* distance, and Manhattan is the *Rook* distance.

All other R code to reproduce these results is available at: https://github.com/timriffe/ms_dist

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, we use SHARE data from Italy. We calculate the multistate death distribution (Fig. ??), and its marginal distributions (Fig. 4). From these, we calculate the marginal distributions of years in good and poor health.

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 Equation (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. 3. 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.

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. 4). A compressed distribution of unhealthy years $d(u)$ is consistent with end-of-life (*thanatological*) conditions previously identified by [17], 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 [18], 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 [18]. 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.

We define three synthetic inequality indices intended to summarize the rich information in the multistate death distribution (Equation (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 we expect these indices to correlate with one another, and to generally map to a holistic summary of health inequality over the life course, none of the indices offer any particular demographic appeal.

Specifically, we should prefer a distance measure that is consistent with possible transition trajectories. Just as an individual life course on a standard Lexis surface snaps to a cohort diagonal and

can only increment age and time upward, an individual life course in our multistate coordinate space (refer to Fig. 3) can only move rightward (increment h) or upward (increment u) in a given time step. These are possible *Pac-Man* (or a *rook*) moves, with the restriction that in a given move either h or u must increment. 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. 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. A multistate redux of the lifespan inequality metric e^\dagger (the average years of life lost due to death)[19–22] would give a more intuitive demographic interpretation in this setting, but this is left for future work.

Limitations

The transition probabilities we use in equation (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 ([23–25]), 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* [26–31]. 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.

Competing interests

The authors declare that they have no competing interests.

Author's contributions

Tim Riffe Conceptualization, Investigation, Methodology, Software, Validation, Formal analysis, Writing - Original draft preparation, reviewing & editing, Visualization. **Iñaki Permanyer** Writing - reviewing & editing. **Rustam Tursun-zade** Software, Validation, Formal analysis, Writing - reviewing & editing. **Muszynska-Spielauer** Methodology, Formal analysis, Writing - Original draft preparation, reviewing & editing, Software.

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References

- Sullivan, D.F.: A single index of mortality and morbidity. *HSMHA Health Reports* **86**(4), 347 (1971). doi:[10.2307/4594169](https://doi.org/10.2307/4594169)
- Barendregt, J.J., Bonneux, L., Van Der Maas, P.J.: How good is sullivan's method for monitoring changes in population health expectancies? *Journal of Epidemiology and Community Health* **51**(5), 578 (1997). doi:[10.1136/jech.51.1.80](https://doi.org/10.1136/jech.51.1.80)
- Barendregt, J.J., Bonneux, L., Van der Maas, P.J.: Health expectancy: an indicator for change? technology assessment methods project team. *Journal of Epidemiology & Community Health* **48**(5), 482–487 (1994). doi:[10.1136/jech.49.3.330](https://doi.org/10.1136/jech.49.3.330)
- Laditka, S.B., Hayward, M.D.: The Evolution of Demographic Methods to Calculate Health Expectancies, pp. 221–234. John Wiley & Sons, Ltd, ??? (2002). Chap. 11. doi:[10.1002/0470858885.ch11](https://doi.org/10.1002/0470858885.ch11)
- Rogers, A., Rogers, R.G., Belanger, A.: Longer life but worse health? Measurement and dynamics. *The Gerontologist* **30**(5), 640–649 (1990). doi:[10.1093/geront/30.5.640](https://doi.org/10.1093/geront/30.5.640)
- Muszynska-Spielauer, M., Riffe, T., Spielauer, M.: Healthy lifespan statistics derived from cross-sectional prevalence data using the sullivan method are informative summary measures of population health. *Comparative Population Studies* **49**, 55–80 (2024). doi:[10.12765/CPoS-2024-03](https://doi.org/10.12765/CPoS-2024-03)
- Lievre, A., Brouard, N., Heathcote, C.: The estimation of health expectancies from cross-longitudinal surveys. *Mathematical Population Studies* **10**(4), 211–248 (2003). doi:[10.1080/713644739](https://doi.org/10.1080/713644739)
- Caswell, H., van Daalen, S.: Healthy longevity from incidence-based models. *Demographic Research* **45**, 397–452 (2021). doi:[10.4054/DemRes.2021.45.13](https://doi.org/10.4054/DemRes.2021.45.13)
- Dudel, C.: Expanding the markov chain toolbox: Distributions of occupation times and waiting times. *Sociological Methods & Research* **50**(1), 401–428 (2021). doi:[10.1177/0049124118782541](https://doi.org/10.1177/0049124118782541)
- Laditka, S.B., Wolf, D.A.: New methods for analyzing active life expectancy. *Journal of Aging and Health* **10**(2), 214–241 (1998). doi:[10.1177/089826439801000206](https://doi.org/10.1177/089826439801000206)
- Börsch-Supan, A.: Survey of Health, Ageing and Retirement in Europe (SHARE) waves 1-7. release version: 7.1.0. SHARE-ERIC. data set (2020). doi:[10.6103/SHARE.w7.710](https://doi.org/10.6103/SHARE.w7.710)
- Preston, S.H., Heuveline, P., Guillot, M.: *Demography: Measuring and Modeling Population Processes*. Blackwell, Malden, MA, USA (2001)
- Aburto, J.M., Basellini, U., Baudisch, A., Villavicencio, F.: Drenowski's index to measure lifespan variation: Revisiting the gini coefficient of the life table. *Theoretical population biology* **148**, 1–10 (2022). doi:[10.1016/j.tpb.2022.08.003](https://doi.org/10.1016/j.tpb.2022.08.003)
- Börsch-Supan, A., Brandt, M., Hunkler, C., Kneip, T., Korbmacher, J., Malter, F., Schaan, B., Stuck, S., Zuber, S.: Data resource profile: the Survey of Health, Ageing and Retirement in Europe (SHARE). *International Journal of Epidemiology* **42**(4), 992–1001 (2013). doi:[10.1093/ije/dyt088](https://doi.org/10.1093/ije/dyt088)
- De Luca, G., Rosetti, C.: Weights and imputations. In: Bergmann, M., Scherpenzeel, A., Börsch-Supan, A. (eds.) *SHARE WAVE 7 METHODOLOGY: Panel Innovations and Life Histories*, pp. 167–189. Munich: MEA, Max Planck Institute for Social Law and Social Policy, Munich, DE (2019)
- Dudel, C., Schneider, D.C.: How bad could it be? worst-case bounds on bias in multistate models due to unobserved transitions. *Sociological Methods & Research* **52**(4), 1816–1837 (2023). doi:[10.1177/0049124121995540](https://doi.org/10.1177/0049124121995540)
- Riffe, T., Chung, P.H., Spijker, J., MacInnes, J.: Time-to-death patterns in markers of age and dependency. *Vienna Yearbook of Population Research* **14**, 229–254 (2016). doi:[10.1553/populationyearbook2016s229](https://doi.org/10.1553/populationyearbook2016s229)
- Permanyer, I., Bramajo, O.: The race between mortality and morbidity: Implications for the global distribution of health. *Population and Development Review* **49**(4), 909–937 (2023). doi:[10.1111/padr.12582](https://doi.org/10.1111/padr.12582)
- Mitra, S.: A short note on the taeuber paradox. *Demography* **15**(4), 621–623 (1978). doi:[10.2307/2061211](https://doi.org/10.2307/2061211)
- Vaupel, J.W.: How change in age-specific mortality affects life expectancy. *Population studies* **40**(1), 147–157 (1986). doi:[10.1080/0032472031000141896](https://doi.org/10.1080/0032472031000141896)
- Goldman, N., Lord, G.: A new look at entropy and the life table. *Demography* **23**(2), 275–282 (1986). doi:[10.2307/2061621](https://doi.org/10.2307/2061621)
- Vaupel, J.W., Romo, V.C.: Decomposing change in life expectancy: A bouquet of formulas in honor of nathan keyfitz's 90th birthday. *Demography* **40**, 201–216 (2003). doi:[10.1353/dem.2003.0018](https://doi.org/10.1353/dem.2003.0018)
- Dudel, C., Schneider, D., Lorenti, A., Li, P.L., Myrskylä, M.: Discrete-time multistate models: estimation, inference, properties. *European Population Conference* (2024). <https://epc2024.eaps.nl/abstracts/240060>
- Shen, T., O'Donnell, J.: Incorporating Duration Dependency in Healthy Life Expectancy: How serious is the bias? *European Population Conference* (2024). <https://epc2024.eaps.nl/abstracts/240418>
- Batyrbekova, N., Bower, H., Dickman, P.W., Szulkin, R., Lambert, P.C., Andersson, T.M.-L.: Potential bias introduced by not including multiple time-scales in survival analysis: a simulation study. *Communications in Statistics-Simulation and Computation* **53**(2), 993–1006 (2024). doi:[10.1080/03610918.2022.2038626](https://doi.org/10.1080/03610918.2022.2038626)
- Wolf, D.A.: The multistate life table with duration-dependence. *Mathematical Population Studies* **1**(3), 217–245 (1988). doi:[10.1080/0889848809525276](https://doi.org/10.1080/0889848809525276)

27. Carollo, A., Eilers, P.H.C., Putter, H., Gampe, J.: Smooth hazards with multiple time scales. *arXiv* (2023). doi:[10.48550/arXiv.2305.09342](https://doi.org/10.48550/arXiv.2305.09342). [2305.09342](https://arxiv.org/abs/2305.09342)
28. Carollo, A., Putter, H., Eilers, P.H., Gampe, J.: Event history analysis with two time scales. an application to transitions out of cohabitation (2023). doi:[10.31235/osf.io/4ewv3](https://doi.org/10.31235/osf.io/4ewv3)
29. Batyrbekova, N., Bower, H., Dickman, P.W., Ravn Landtblom, A., Hultcrantz, M., Szulkin, R., Lambert, P.C., Andersson, T.M.: Modelling multiple time-scales with flexible parametric survival models. *BMC Medical Research Methodology* **22**(1), 290 (2022). doi:[10.1186/s12874-022-01773-9](https://doi.org/10.1186/s12874-022-01773-9)
30. Bower, H., Andersson, T.M.-L., Crowther, M.J., Lambert, P.C.: Flexible parametric survival analysis with multiple timescales: Estimation and implementation using `stms`. *The Stata Journal* **22**(3), 679–701 (2022). doi:[10.1177/1536867X22112455](https://doi.org/10.1177/1536867X22112455)
31. Tassistro, E., Bernasconi, D.P., Rebora, P., Valsecchi, M.G., Antolini, L.: Modeling the hazard of transition into the absorbing state in the illness-death model. *Biometrical Journal* **62**(3), 836–851 (2020). doi:[10.1002/bimj.201800267](https://doi.org/10.1002/bimj.201800267)