Supplementary information for

Healthy lifespan inequality: morbidity compression from a global perspective

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Table of contents

Appendix 1. Regional and country classification

We used the same regional and country classification as the Global Burden of Disease (GBD) Study 2019.¹ This comprises 204 countries and territories, 19 regions, and seven super-regions. Estimates at the global/world level are also provided.

The classification can be visualized at [https://www.iapb.org/learn/vision-atlas/about/definitions-and](https://www.iapb.org/learn/vision-atlas/about/definitions-and-regions/)[regions/](https://www.iapb.org/learn/vision-atlas/about/definitions-and-regions/) (accessed on May 2, 2022) and is summarized in the tables below. These tables have the following variables/columns:

- ISO3: Three-letter country codes (only for countries/territories)
- location_id: Location number assigned by GBD
- location_name: Name of the super-region, region, and country/territory
- Type: Whether the location is a super-region or a region
- Super-region: Super-region at which a country/territory belongs
- Region: Region at which a country/territory belongs

Table S1. Regional classification

location_id	location_name	Type
1	Global/World	
$\overline{4}$	Southeast Asia, east Asia and Oceania	Super-region
5	East Asia	Region
9	Southeast Asia	Region
21	Oceania	Region
31	Central Europe, eastern Europe and central Asia	Super-region
32	Central Asia	Region
42	Central Europe	Region
56	Eastern Europe	Region
64	High-income countries	Super-region
65	High-income Asia Pacific	Region
70	Australasia	Region
73	Western Europe	Region
96	Southern Latin America	Region
100	High-income North America	Region
103	Latin America and Caribbean	Super-region
104	Caribbean	Region
120	Andean Latin America	Region
124	Central Latin America	Region
134	Tropical Latin America	Region
137	North Africa and Middle East	Super-region/Region
158	South Asia	Super-region/Region
166	Sub-Saharan Africa	Super-region
167	Central sub-Saharan Africa	Region
174	Eastern sub-Saharan Africa	Region
192	Southern sub-Saharan Africa	Region
199	Western sub-Saharan Africa	Region

Table S2. Country classification

Appendix 2. Reconstruction of mortality and morbidity curves

All the concepts and definitions relating to life tables presented in the following have already been introduced and widely discussed in the literature. For additional details, the reader is referred to two useful handbooks by Chiang 2 and Preston et al. 3

2.1 Mortality curves

The Global Burden of Disease (GBD) Study 2019 publishes life table data for all countries and a great diversity of regions from 1950 to 2019.⁴ Specifically, it reports data on age-specific probabilities of dying and age-specific remaining life expectancy that can be used to reconstruct life tables for all regionand country-years.

GBD reports estimates in 5-year age groups, except for the first two groups of length 1 and 4, respectively. Let $A = \{0, 1, 5, 10, \dots, 105, 110\}$ be the set of starting ages of all the age groups reported by GBD. Let $_{n}q_{x}$ denote the unconditional probability of dying between ages x and $x + n$, where $x \in$ A and $n = 5$, except for the first two age groups in which $n = 1$ and $n = 4$, respectively. Then, the survival probability from birth to exact age x is

$$
\ell_x = \prod_{y \in A, y < x} (1 - nq_y) \tag{A1}
$$

with the convention that the probability of surviving from birth to age 0 is $\ell_0 = 1$ (also known as the radix of the life table). The survival curve defined in [\(A1\)](#page-6-3) is what we refer to as 'mortality curve' and can be used to calculate life expectancy (figure 1 panel A in the main manuscript). From [\(A1\),](#page-6-3) we can derive the distribution of ages at death, given by

$$
{}_{n}d_{x} = \ell_{x} - \ell_{x+n} \tag{A2}
$$

for all $x \in A \setminus \{110\}$. For the last age group 110+, $d_x = \ell_x$ to close the life table. Note that $d_x d_x$ denotes the proportion of deaths between ages x and $x + n$, and that $\sum_{x \in A} n dx = 1$. The distribution of ages at death defined in [\(A2\)](#page-6-4) can be used to measure the variability in ages at death and calculate lifespan inequality (LI) indicators (figure 1 panel C in the main manuscript).

2.2 Morbidity curves

In recent years, GBD has been publishing estimates of age- and sex-specific health-adjusted life expectancy (HALE) for all countries from 1990 to 2019.^{1,5} These estimates are obtained using models that incorporate data of years lived with disability, life tables, and standard demographic methods,¹ but the underlying 'life tables in good health' remain unknown. However, if one has age-specific mortality data from a given population and makes mild assumptions of the average person-years lived in each age interval by individuals dying in that interval (the $_n a_x$ values),³ it is possible to reconstruct the full life table. To estimate the $n a_x$ values we use the following result.

Proposition. Let e_x and e_{x+n} be the remaining life expectancies at ages x and $x + n$, respectively. Let $p_{n}q_{x}$ be the unconditional probability of dying between ages x and $x + n$. Then, the average person*years lived between ages* x *and* $x + n$ *by individuals dying in that age interval is given by*

$$
{}_{n}a_{x} = \frac{e_{x} - (e_{x+n} + n) (1 - nq_{x})}{nq_{x}}
$$
 (A3)

If $_{n}q_{x} = 0$ *, then* $_{n}a_{x} = 0$ *.*

Proof. Equation [\(A3\)](#page-7-0) is an immediate result of the properties and relationships of the different columns of the life table. Following [\(A1\),](#page-6-3) the probability of surviving from birth to age $x + n$ can be estimated as

$$
\ell_{x+n} = \left(1 - {}_{n}q_{x}\right) \ell_{x} \tag{A4}
$$

provided that $(1 - _nq_x)$ is the probability of surviving from x to $x + n$.

Let T_x and T_{x+n} be the person-years lived above ages x and $x + n$, respectively. By definition, the remaining life expectancies at ages x and $x + n$ are

$$
e_x = \frac{T_x}{\ell_x} \qquad \qquad \text{and} \qquad \qquad e_{x+n} = \frac{T_{x+n}}{\ell_{x+n}}
$$

Hence, the person-years lived between x and $x + n$ can be expressed in terms of the life expectancy and the survivorship as

$$
{}_{n}L_{x} = T_{x} - T_{x+n} = e_{x} \ell_{x} - e_{x+n} \ell_{x+n}
$$
(A5)

On the other hand, let $n \cdot \ell_{x+n}$ be the person-years lived between ages x and $x + n$ by those who survived the age interval, and $_n a_x (\ell_x - \ell_{x+n})$ the person-years lived by those who died. The $_n L_x$ values are commonly computed as the sum of these two, say

$$
{}_{n}L_{x} = n \cdot \ell_{x+n} + {}_{n}a_{x} (\ell_{x} - \ell_{x+n}) = (n - {}_{n}a_{x}) \ell_{x+n} - {}_{n}a_{x} \ell_{x}
$$
(A6)

Combining [\(A4\),](#page-7-1) [\(A5\)](#page-7-2) and [\(A6\)](#page-7-3) yields

$$
e_{x} \ell_{x} - e_{x+n} (1 - nq_{x}) \ell_{x} = (n - nq_{x})(1 - nq_{x}) \ell_{x} + nq_{x} \ell_{x}
$$

\n
$$
e_{x} - e_{x+n} (1 - nq_{x}) = n (1 - nq_{x}) + nq_{x} nq_{x}
$$

\n
$$
nq_{x} = \frac{e_{x} - (e_{x+n} + n)(1 - nq_{x})}{nq_{x}}
$$

which proves [\(A3\).](#page-7-0) If $_{n}q_{x} = 0$, then $_{n}a_{x} = 0$ by definition, since there are no deaths between x and $x + n$. $x + n$.

Corollary. Let e_x and e_{x+n} be the remaining life expectancies at ages x and $x + n$, respectively. Let $h_n a_x$ be the average person-years lived between ages x and $x + n$ by individuals dying in that age *interval. Then, re-arranging terms in* [\(A](#page-7-0)*3*)*, the age-specific unconditional probability of death can be estimated as*

$$
{}_{n}q_{x} = \frac{e_{x+n} + n - e_{x}}{e_{x+n} + n - {}_{n}a_{x}} \tag{A7}
$$

Equation (A7) is the key relationship that enables building a full life table using data on age-specific remainin[g life](#page-7-4) expectancy only, assuming data are available for all ages and that the $n a_x$ values are provided or can be reasonably estimated.

Using data on age-specific probabilities of dying ($_nq_x$) and age-specific remaining life expectancy (e_x) from GBD,⁴ for each country/region, sex, and year we calculated the $_n a_x$ values by applying [\(A3\).](#page-7-0) Next, we used the corresponding $n \alpha_x$ values from each life table, in combination with the age-specific HALE estimates,⁵ to reconstruct morbidity curves and the age-at-morbidity onset distributions.

Formally, let e_x^* denote the remaining health-adjusted life expectancy (HALE) at age x, and A^* $\{0, 1, 5, 10, \ldots, 90, 95\}$ the set of starting ages of all the age groups for which GBD reports HALE data.⁵ In the following we add an asterisk as superscript to denote all the terms that relate to morbidity instead of mortality. Using [\(A7\),](#page-7-4) the age-specific probabilities of health loss can be estimated as

$$
{}_{n}q_{x}^{*} = \frac{e_{x+n}^{*} + n - e_{x}^{*}}{e_{x+n}^{*} + n - {}_{n}a_{x}}
$$
 (A8)

for all $x \in A^*\backslash\{95\}$. For the last age group $95+$ we assume $nq_x^* = 1$. Once these probabilities are estimated, applying analogous formulas to [\(A1\)](#page-6-3) and [\(A2\),](#page-6-4) we reconstructed the survival curves in good health or morbidity curves (figure 1 panel B in the main manuscript),

$$
\ell_x^* = \prod_{y \in A^*, y < x} (1 - n q_y^*) \tag{A9}
$$

and the age-at-morbidity onset distributions

$$
{}_{n}d_{x}^{*} = \ell_{x}^{*} - \ell_{x+n}^{*} \tag{A10}
$$

As previously, $\ell_0^* = 1$ and for the last age group 95+ $_n d_x^* = \ell_x^*$. The $_n d_x^*$ values denote the proportion of individuals ceasing to be in good health between ages x and $x + n$, and can be used to measure the variability of ages-at-morbidity onset and calculate healthy lifespan inequality (HLI) indicators (figure 1 panel D in the main manuscript).

2.3 Adjustments of the $_{n}a_{x}$ values

Equation [\(A8\)](#page-8-1) combines the age-specific HALE estimates from GBD (e_x^*) ,⁵ and the average personyears lived in each age interval by individuals dying in that interval ($_n a_x$) obtained by applyin[g \(A3\)](#page-7-0) to GBD mortality data.⁴ This equation works as long as two conditions are met for all $x \in A^* \setminus \{95\}$:

- 1. $e_{x+n}^* + n > e_x^*$ and $e_{x+n}^* + n > n_a$, so that the probabilities are positive; and
- 2. $e_x^* > n a_x$ to ensure that the denominator is larger and $n a_x^* \in (0,1)$.

Condition 1 is always met, but condition 2 is not, particularly at older ages. This is, in part, because GBD mortality estimates go up to age 110+, whereas HALE estimates end at 95+. In 5-year age groups, $n_{\alpha}a_x$ values hover around 2.5 and start decreasing, approximately, at ages above 75 years. However, it may happen that at ages 75 to 95 years the remaining health-adjusted life expectancy is considerably lower than 2.5, therefore $e_x^* \leq n a_x$ and condition 2 is not met. See, for instance, the case of Chinese males in 1990: at age 90, applying [\(A3\)](#page-7-0) we get $_5a_{90} = 1.68$, but GBD reports $e_{90}^* = 1.62$. In these situations, the $_n a_x$ values needed to be adjusted before applying [\(A8\)](#page-8-1) to avoid $_n a_x^* > 1$.

From the 20,790 morbidity life tables (204 countries and territories, 19 regions, 7 super-regions, global level, 3 sex groups, and 30 years) reconstructed, in 18,038 (86.8%) of them $e_x^* > n a_x$ for all age groups and condition 2 was always met. Inconsistencies were detected in 2,752 (13.2%) of the cases, among which

1) In 2,050 (9.9%) of the cases the issue was solved by imputing

$$
5a{90}=\frac{5a_{85}+e_{95}^*}{2}
$$

that is, in the 90−95 age group $5a_{90}$ was calculated as the average between the values in the thirdlast and last age groups. Note that, by definition, in the last age group $e_{95}^* = \frac{1}{5}a_{95}$.

- 2) In the remaining 702 (3.4%) life tables usually not only the second-last age group (90−95) required an adjustment. In these cases, we proceeded as follows:
	- a) Using all the mortality data from GBD,⁴ we calculated the average ratio $n a_x/e_x$ for the age groups 90−95, 95−100, 100−105, and 105−110 (from the fifth-last to the second-last):

b) Next, we applied these ratios to calculate $_n a_x$ from e_x^* whenever inconsistencies were detected and ensure that $e_x^* > \frac{a_x}{n}$. The estimated ratio of the 105−110 age group was applied to the second-last group (90−95) of the morbidity life tables, and so on.

Appendix 3. Inequality measures and uncertainty

3.1 The standard deviation as a measure of inequality

Using life table notation, the standard deviation of an age-at-death distribution beginning at age x is defined as

$$
SD_x = \sqrt{\frac{1}{\ell_x} \sum_{y \in A, y \ge x} n d_y (y + n d_y - x - e_x)^2}
$$
 (A11)

where x is the age at which the age-at-death distribution starts (in this paper we only report for $x = 0$ and $x = 65$), ℓ_x is the initial life table population at age x, e_x is the remaining life expectancy at age x, and $_n d_y$ and $_n a_y$ are, respectively, the proportion of deaths and the average-person years lived in the interval by those dying in the interval (or average age at death in the interval) between y and $y + n$. This is a very popular and basic indicator that measures the variability in the ages at death around the mean of the distribution, and that we adopt as a lifespan inequality (LI) indicator.

The same formula can be applied to an age-at-morbidity onset distribution (whose derivation is explained in Appendix 2) to calculate the corresponding level of healthy lifespan inequality (HLI). Thus, the standard deviation of the age-at-morbidity onset distribution beginning at age x is calculated as

$$
SD_x^* = \sqrt{\frac{1}{\ell_x^*} \sum_{y \in A^*, y \ge x} n d_y^* (y + n a_y - x - e_x^*)^2}
$$
 (A12)

where ℓ^*_x is the initial life table population in good health, e^*_x is the health-adjusted remaining life expectancy (HALE) at age x, and $_n d_y^*$ is the proportion of individuals ceasing to be in good health between ages y and $y + n$. The HLI indicator SD_x^* measures the variability in individuals' healthy lifespans.

3.2 Other inequality measures

We compared our lifespan inequality (LI) and healthy lifespan inequality (HLI) measures based on the standard deviation with those derived from using the coefficient of variation (CoV) and the Gini coefficient (G) as inequality measures by applying the following formulas:

$$
CoV_x = \frac{SD_x}{e_x + x}
$$

\n
$$
GoV_x^* = \frac{SD_x^*}{e_x^* + x}
$$

\n
$$
GoV_x^* = \frac{SD_x^*}{e_x^* + x}
$$

\n
$$
GoV_x^* = \frac{SD_x^*}{e_x^* + x}
$$

$$
G_x^* = \frac{1}{2(\ell_x^*)^2} \sum_{y \in A^*, y \ge x} \sum_{z \in A^*, z \ge x} n d_y^* n d_z^* |(y + n a_y) - (z + n a_z)|
$$

The coefficient of variation is simply the relative version of the standard deviation, while the Gini coefficient is a very popular index of inequality that measures the expected difference between two randomly chosen observations.

As shown in Figs. S1 and S2, all measures of HLI are highly correlated $(r > 0.91)$, both for females and males.

Figure S1. Relationship between healthy lifespan inequality measured with the standard deviation and healthy lifespan inequality measured with the coefficient of variation by sex between 1990 and 2019. For each region, the lightest colour corresponds to 1990 and darkness increases over time up to 2019; r denotes the correlation coefficient between these measures across all countries. The outlier dots representing Rwanda 1994 are not shown. Source: Authors' elaboration based on GBD data. $4,5$

Figure S2. Relationship between healthy lifespan inequality measured with the standard deviation and healthy lifespan inequality measured with the Gini index by sex between 1990 and 2019. For each region, the lightest colour corresponds to 1990 and darkness increases over years up to 2019; *denotes the correlation between these measures across countries. The outlier dots representing* Rwanda 1994 are not shown. Source: Authors' elaboration based on GBD data.^{4,5}

3.3 Uncertainty estimation

We assessed the uncertainty of the LI and HLI estimates based on the uncertainty of the input data from GBD. Uncertainty was obtained by sampling from the corresponding 95% uncertainty intervals of life expectancy (e_x) , death probabilities $({}_nq_x)$, and HALE (e_x^*) reported by GBD on Monte Carlo simulations, applying a similar approach than used elsewhere.⁶

We assumed GBD data are normally distributed with mean values equal to the point estimates. For each country/region, sex, and year we proceeded as follows:

- 1) For each age-specific estimate $(e_x, nq_x,$ and e_x^* , we approximated the standard deviation by dividing the range of the corresponding 95% uncertainty interval by 3.92.
- 2) We randomly drew 10,000 samples of age-specific e_x , $_nq_x$, and e_x^* from a truncated normal distribution with means equal to the point estimates and corresponding standard deviations:
	- a) For e_x and e_x^* we set a lower bound of 0 to only have positive values, with no upper limit.
	- b) For $t_n q_x$ the distribution was truncated between 0 and 1.
- 3) For each draw of age-specific e_x and $_nq_x$, we applied [\(A1\)](#page-6-3) an [\(A2\)](#page-6-4) to calculate 10,000 sets of survival curves (ℓ_x) and age-at-death distributions ($_n d_x$).
- 4) From the sets of $_n d_x$, we applied [\(A11\)](#page-10-3) to obtain 10,000 estimates of SD_x at ages $x = 0$ and $x =$ 65, from which we calculated the corresponding 80% uncertainty intervals of the LI levels reported in the paper.
- 5) Besides, for each draw of age-specific e_x^* , we applied [\(A8\)](#page-8-1) to calculate 10,000 sets of age-specific probabilities of health loss (nq_x^*).
	- a) We did not incorporate any uncertainty on the $n a_x$ values, as this generated too much noise. We used the point estimates of $n \alpha_x$ calculated as described in Appendices 2.2 and 2.3.
	- b) When applying [\(A8\)](#page-8-1) to random draws of e_x^* we faced a new challenge: Condition 1 in Appendix 2.3 was not always met. Due to randomness, it may happen that $e_{x+n}^* + n < e_x^*$ or $e_{x+n}^* + n < a_x$. As a result, $_n q_x^*$ could take any values and were not only restricted to the interval (0,1).
	- c) To address this issue, we re-sampled $_nq_x^*$ from a log-normal distribution.
		- i) For each sample of age-specific $_n q_x^*$ obtained by applying [\(A8\)](#page-8-1) we calculated its mean m and its standard deviation s.
		- ii) We then used standard formulae to obtain the usual log-normal parameters mean μ and variance σ^2 , given by

$$
\mu = \log\left(\frac{m^2}{\sqrt{s^2 + m^2}}\right)
$$
 and $\sigma^2 = \log\left(1 + \frac{s^2}{m^2}\right)$

- iii) By drawing random values from a truncated log-normal distribution with upper bound set at 1 and these μ and σ^2 parameters we ensured $_n q_x^* \in (0,1)$.
- 6) Next, we applied [\(A9\)](#page-8-2) and [\(A10\)](#page-8-3) to calculate 10,000 sets of morbidity curves (ℓ^*_x) and age-atmorbidity onset distributions ($_n d_x^*$).
- 7) From the sets of $_n d_x^*$, we applied [\(A12\)](#page-10-4) to obtain 10,000 estimates of SD_x^* at ages $x = 0$ and $x =$ 65, from which we calculated the corresponding 80% uncertainty intervals of the HLI levels reported in the paper.

3.4 Transparency and replicability

We carried out our analyses using the open-source statistical software R (version 4.1.1).⁷ The source code to replicate the analyses, input data, and results are publicly available for research purposes on the GitHub repository [https://github.com/panchoVG/HLI.](https://github.com/panchoVG/HLI)

Appendix 4. The GATHER checklist

Appendix 5. Lifespan inequality and healthy lifespan inequality estimates

Global, regional, and national estimates of lifespan inequality (LI) and healthy lifespan inequality (HLI) for the period 1990−2019, and the corresponding 80% uncertainty intervals, are available on the GitHub repository [https://github.com/panchoVG/HLI.](https://github.com/panchoVG/HLI)

The file 'EstimatesHLI-LI-1990-2019.csv' containing all the estimates has the following variables/columns:

- location_id: Location number assigned by GBD
- location name: Name of the location
- ISO3: Three-letter country codes (only for countries/territories)
- Type: Whether the location is a super-region, super-region/region, region, or country/territory
- SuperRegion: Super-region at which a region or country/territory belong
- Region: Region at which a country/territory belongs
- Year: 1990−2019
- Sex: Female, male, or both sexes combined
- Age: 0 for estimates that refer to all ages, and 65 for estimates that refer to ages above 65 years
- Measure: 'Mortality' for estimates of lifespan inequality, and 'Morbidity' for estimates of healthy lifespan inequality
- ex: Corresponding values of life expectancy or HALE reported by GBD
- SD: Estimated level of lifespan inequality/healthy lifespan inequality, measured as standard deviation of the corresponding age-at-death/age-at-morbidity onset distribution
- SDlow10: Lower bound (10% percentile) of the estimated standard deviation of the corresponding age-at-death/age-at-morbidity onset distribution
- SDup90: Upper bound (90% percentile) of the estimated standard deviation of the corresponding age-at-death/age-at-morbidity onset distribution

Appendix 6. Global and regional HLI/LI ratios

Global, regional, and national estimates of the ratio between healthy lifespan inequality and lifespan inequality (HLI/LI) for the period 1990−2019, and the corresponding 80% uncertainty intervals, are available on the GitHub repository<https://github.com/panchoVG/HLI> (file 'RatiosHLI-LI-1990-2019.csv').

Figure S3. Global and regional trends in the ratio between healthy lifespan inequality (HLI) and lifespan inequality (LI) by sex, 1990−2019. Shadowed areas represent 80% uncertainty intervals. Source: Authors' elaboration based on GBD data.^{4,5}

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