Appendix

A1. Adjustments to accommodate discrete data

We presented our method and examples in continuous time, but demographic data is usually collected on a discrete-time basis, forming 'life tables'. Lifetable functions can be defined either *within* an age interval, such as age-specific mortality, probability of surviving or dying during an age class, or *up to* exact age x, such as survivorship up to age x. In our fertility scenario, the *within* and *up to* types of function are respectively represented by age-specific fertility $m(x)$, which happens during the age interval x to $x + n$, where n denotes the length of an age class, and by cumulative reproduction $B(x)$, which happens up to exact age x. This implies for both mortality and fertility that we need k age classes, but $k + 1$ exact ages in order to define an age-range that is closed at both ends.

In lifetables, the initial age group starts from zero, and initial survivorship is defined as 100% at exact age zero. The last age group is also defined by its lower bound, but is left open to the top. The remaining death counts within that open interval are included in the cumulative death counts by assuming an average remaining lifetime common to those individuals.

For fertility, we require for cumulative reproduction that $B(\alpha) = 0$, and $B = B(\beta)$. Since reproduction happens within age classes, first age-specific reproduction $m(\alpha)$ happens within the initial adult age class α to $\alpha + n$, and last reproduction $m(\beta - n)$ happens within the age-interval $\beta - n$ to β. Therefore

$$B(x) = \begin{cases} 0 & \text{if } x = \alpha \\ \sum_{t=\alpha}^{x-n} m(t) & \text{otherwise.} \end{cases} \tag{1}$$

For $x = \beta$, the sum includes all reproduction until age $\beta - n$. In the data it has to be ensured then that indeed $m(\beta - n)$ corresponds to the final age class where reproduction exceeds zero.

This note of caution is important because, typically, data end at the age of last non-zero reproduction, as most species do not have a postreproductive lifespan. Here problems arise because the age range includes only k instead of $k + 1$ age groups. Then a pseudo age-group has to be added to properly define β as the age when all reproduction has been completed. Otherwise, reproduction in the last age class is not counted.

Again, analogous to closing the lifetable for the final survivors that die within the last open-

28 ended age-interval, we must make assumptions about how to close the cumulative birth function

29 for offspring experiencing the event of birth during the final age interval.

30 If passed any $m(x)$ data with a final value other than NA, our R functions thus assume that

31 (for k age classes) the age of reproductive cessation equals the age at last reproduction plus the

32 difference between the final two reproductive ages, $\beta = x(k) + x(k) - x(k-1)$.

33 Once we have defined β and calculated $B(x)$, we find for shape that

$$S = \frac{1}{\tau B} \left(\sum_{x=\alpha}^{\beta} B(x) - \frac{\tau B}{2} \right). \tag{2}$$

34 and for pace that

$$P = \tau (0.5 - S). \tag{3}$$

35 As an example, given an age vector of $x = [1,2,3,4,5]$ and an associated age-specific reproduc-

36 tion schedule of $m(x)$ $[0,1,3,4,2]$, we define age of maturity $\alpha = 2$ and consequently $B(2) = 0$,

37 $B(3) = 1$, ..., $B(5) = 8$. $B(5) \neq B$, as $m(5) > 0$. : the last two offspring are born at age

38 $5 < x < \beta$. We may assume that the life table has not been fully completed and that $\beta = 6$, or

39 we may know that is the case. Then, x becomes $[1,2,3,4,5,6]$ and $m(x)$ becomes $[0,1,3,4,2,NA]$.

40 Thus we can complete $B(x)$: $[0,0,1,4,8,10]$.

41 **A2. Extension of the method to mortality trajectories**

42 Let $\mu(x)$ denote the age-specific mortality function that captures the average hazard of death of

43 an individual at age x. Function $H(x)$ defines the cumulative hazard up to age x as

$$H(x) = \int_{\alpha}^{x} \mu(t)dt. \tag{4}$$

44 In line with the framework presented in this paper, we consider the hazard over reproductive

45 ages, that is beginning at age α. Note that $H(x)$ corresponds to the logarithmic transformation of

46 the survivorship function, i.e. $H(x) = -\ln l(x)$, where $l(x)$ captures the fraction of individuals

47 that survive from initial age (here defined as α) up to age x

48 Constant age-specific mortality represents the benchmark case and corresponds to a linearly

49 increasing cumulative hazard function $H(x)$. Analogous to fertility, it forms a triangular shape

50 in the x-Hx-space with an area calculated as the halfened product of its edges: adult lifespan

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51 ($\tau \equiv \omega - \alpha$) times maximum cumulative hazard at the final age, $H \equiv H(\omega)$, divided by two,

52 which gives $\tau H/2$. Here, ω denotes maximum age, which can be defined as the age until which

53 less than a small fraction (e.g. 1%) of adults will survive.

54   Analog to the fertility case, the difference of the area under the $H(x)$ curve to the benchmark

55 area $\tau H/2$ indicates, whether the actual mortality pattern follows a predominantly increasing

56 or decreasing pattern over age. Standardising for adult lifespan, the *shape of mortality* is given

57 by an equivalent expression as

$$S = \frac{1}{\tau}\left(\frac{\tau H}{2} - \int_{\alpha}^{\omega} H(x)dx\right). \tag{5}$$

58 Compared to the shape of fertility, we reversed the order of terms in the shape expression for

59 mortality to remain consistent with the logic of positive/negative senescence being associated

60 with positive/negative shape values: positive senescence is associated with worsening and corre-

61 sponds to a decrease in fertility, but an increase in mortality; negative senescence is associated

62 with improvement and corresponds to an increase in fertility, but a decrease in mortality.

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        S>0   Positive (mortality) senescence,

        S=0   Nil (mortality) senescence,

        S<0   Negative (mortality) senescence.

64   As for fertility, shape values of mortality here range within the interval $-0.5 < S < 0.5$.

65 **A3. Comparison to the Gini coefficient**

66 How different is this new shape measure of mortality to the Gini coefficient, a main candidate

67 for measuring survival shape? Even though the logic of a diagonal benchmark reminds of the

68 Gini coefficient, the shape measure suggested here differs in important aspects. First, the Gini

69 coefficient for survival is calculated based on a population that is rank-ordered by increasing

70 lifespan (Shkolnikov, Andreev, Begun, 2003), similar to the original Gini coefficient being cal-

71 culated based on a rank-ordered population of increasing income (Gini, 1921). Consequently,

72 the cumulative lifespan/income curves of the Gini coefficient always fall below the benchmark,

73 which in economics is known as the Lorentz curve (Lorenz, 1905). In contrast, our measures

74 depict cumulative curves of reproduction (or mortality) over age, and age-specific cumulative

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curves may cross the benchmark at any point. This allows for an intuitive understanding of positive and negative areas of senescence balancing each other over the life cycle. Second, Gini is calculated based on a ratio of the difference between the benchmark and the cumulative curve to the total area of the triangle. Our measure simply calculates the difference between the benchmark and the cumulative curve. Still, our measure will be closely linked to Gini as well as other measures of mortality shape.

The main advantage of suggesting this new shape measure of mortality here is its direct comparability to the shape measure of fertility, which allows measuring the processes of birth and death with similar tools.

References

Gini, C. (1921). Measurement of inequality of incomes. The Economic Journal, 31(121), 124-126.

Lorenz, M. O. (1905). Methods of measuring the concentration of wealth. Publications of the American Statistical Association, 9(70), 209-219.

Shkolnikov, V. M., Andreev, E. E. & Begun, A. Z. (2003) Gini coefficient as a life table function: computation from discrete data, decomposition of differences and empirical examples. Demographic Research, 8, 305-358.