

A decomposition of longevity inequality by deprivation quantiles

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Abstract

Within-variance is way bigger than between variance we suppose. Let's see. And also see how it changes over age and time.

1 Data and methods

1.1 Variance decomposition

We have a set of lifetables for subareas of Scotland that can be assigned to deprivation quantiles. The index k refers to subpopulations. Given $p_x = 1 - q_x$ for a subpopulation, calculate:

$$\mathbf{U}_k = \begin{bmatrix} 0 & \dots & \dots & \dots & 0 \\ p_1 & & & & \vdots \\ 0 & \ddots & & & \vdots \\ \vdots & & \ddots & & 0 \\ 0 & \dots & 0 & p_{\omega-1} & p_{\omega} \end{bmatrix} \quad (1)$$

Then calculate the conditional remaining survivorship as

$$\mathbf{N}_k = (\mathbf{I} - \mathbf{U}_k)^{-1} \quad (2)$$

\mathbf{N}_k ends up being 0s in the upper triangle, and conditional remaining survivorship in columns descending from the subdiagonal. The first moment is the same as remaining life expectancy, and can be calculated as:

$$\eta_1^{(k)} = (1^T \mathbf{N}_k)^T \quad (3)$$

The second moment is defined as:

$$\eta_2^{(k)} = [1^T \mathbf{N}_k (2\mathbf{N}_k - \mathbf{I})]^T \quad (4)$$

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These can be used together to calculate the variance of remaining lifespan:

$$V(\eta^{(k)}) = \eta_2^{(k)} - \left[\eta_1^{(k)} \circ \eta_1^{(k)} \right] \quad (5)$$

Thus far everything has been denoted with respect to the k^{th} subpopulation. These may aggregate to a total lifetable according to some mixing distribution, π . The most natural mixture is to give age-specific weights according to observed relative population counts in each subpopulation, $\pi(a, k)$. Other mixtures may be based on an age-pattern to π based on the stationary population produced by each subpopulation's lifetable. By this method, lower mortality lifetables result in greater relative weight in older ages. In this case, weight is assigned only to the lifetable radix. Good choice might be assigning weight relative to the total population size of each area, or simply giving uniform weights. Since in our case subpopulations are aggregated into deprivation quantiles, they end up being of approximately equal size and the uniform radix mixing distribution is not very bad.

Given $\pi(a, k)$ we can decompose the variance of the total aggregation of subpopulations due to (5) into variance due to stochasticity within subpopulations and variance due to differences between populations in the lifespan distribution. These two variance components sum to (5) when the same age vector $\pi^{(k)}$, is used to blend lifetables for (5) and in the following equations:

$$V_{within} = \mathbb{E}_{\pi} \left(V(\eta_1^{(k)}) \right) \quad (6)$$

$$= \sum_{k=1}^N \pi_k V(\eta_1^{(k)}) \quad (7)$$

and

$$V_{between} = V_{\pi} \left(V(\eta_1^{(k)}) \right) \quad (8)$$

$$= \sum_{k=1}^N \pi_k \circ \eta_1^{(k)} \circ \eta_1^{(k)} - \left[\sum_{k=1}^N \pi_k \circ \eta_1^{(k)} \right] \circ \left[\sum_{k=1}^N \pi_k \circ \eta_1^{(k)} \right] \quad (9)$$

2 Results

First some descriptives.

Now some graphs:

Figure 1: Standard deviation of remaining lifespan by age, census years 1981 until 2011.

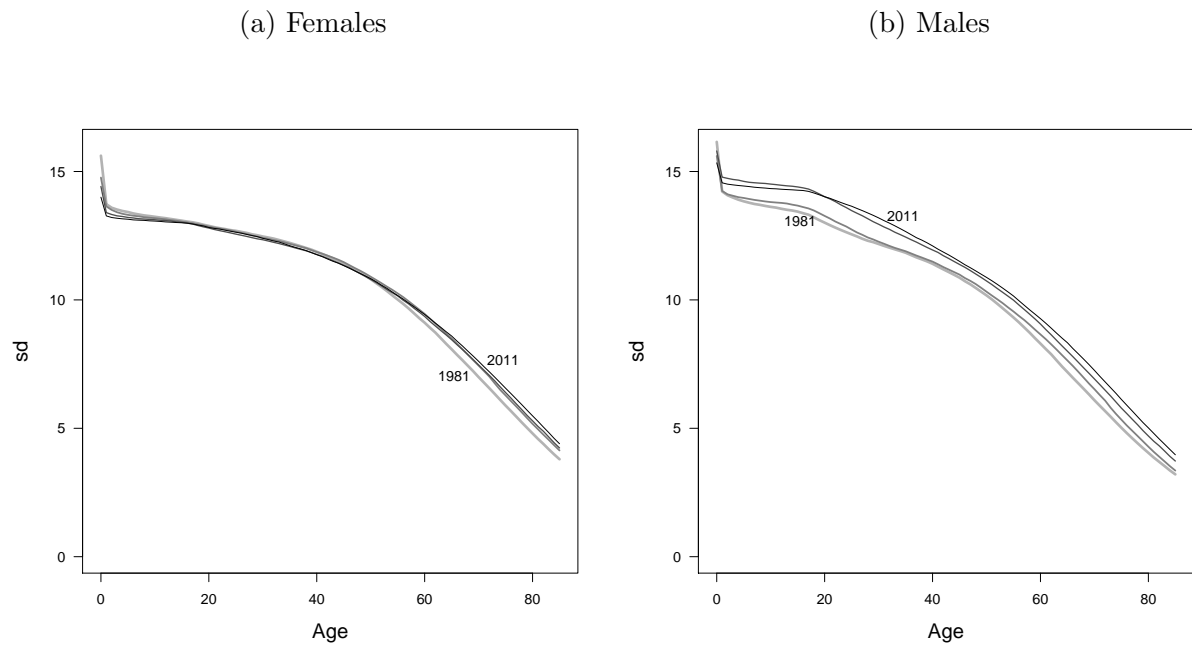


Figure 2: Proportion of variance due to differences between deprivation quintiles by age, census years 1981 until 2011.

