A decomposition of longevity inquality by deprivation quantiles

Rosie Seaman[*1], Hal Caswell[2], and Tim Riffe[1]

[1]Max Planck Institute for Demographic Research, Rostock, Germany
[2]University of Amsterdam

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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   Hal's notes

Suppose we have 1000+ lifetables at four time points 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 subpopualtion, calculate:

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

Then calculate the conditional remaining survivorship as

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

$\mathbf{N}_k$ 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:

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

The second moment is defined as:

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

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[*]seaman@demogr.mpg.de

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

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

Thus far everything has been denoted with respect to the kth subpopulation. These may aggregate to a total lifetable according to some mixing distribution, π. The most natural mixture is to 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 $\pi(a, k)$ is used to blend lifetables for (5) and in the following equations:

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

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

and

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

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

2   Results

Here are some descriptives.

Table 1: Descriptive statistics, males

	1981		1991		2001		2011	
N	481000		494000		494000		519000	
e_0 (e_{35})	71.6	(38.4)	74.5	(40.9)	77.6	(43.7)	80.2	(46.3)
sd_0 (sd_{35})	14.7	(10.6)	13.5	(10.2)	12.4	(9.8)	11.9	(9.2)
N	484000		470000		491000		513000	
e_0 (e_{35})	69.9	(37.1)	72.9	(39.5)	75.3	(41.9)	78.5	(44.7)
sd_0 (sd_{35})	15.6	(11.0)	14.2	(10.7)	14.0	(10.5)	13.0	(10.2)
N		481000		480000		485000	513000	
e_0 (e_{35})	69.1	(36.4)	72.1	(38.8)	73.9	(40.5)	77.0	(43.4)
sd_0 (sd_{35})	15.7	(11.2)	14.6	(10.9)	14.3	(11.0)	13.6	(10.7)
N		493000		474000		485000	512000	
e_0 (e_{35})	68.2	(35.5)	70.4	37.6	72.2	39.1	75.3	41.7
sd_0 (sd_{35})	15.9	(11.3)	15.5	11.2	15.2	11.4	14.3	11.4
N		488000		473000		479000	510000	
e_0 (e_{35})	66.4	33.8	68.3	35.8	69.0	36.6	72.4	39.2
sd_0 (sd_{35})	16.1	11.7	16.0	11.7	16.4	12.3	15.3	12.3
N		2426000		2392000		2432000	2567000	
Total 17	69.0	36.2	71.6	38.5	73.5	40.3	76.7	43.1
18	15.7	11.2	14.9	11.0	14.8	11.2	13.9	10.9