Accounting for temporal variation in morbidity measurement and projections

Alyson van Raalte*1 and Tim Riffe1

¹Max Planck Institute for Demographic Research

September 25, 2015

Abstract

This is important stuff!

G is a bad health condition that varies as a function of time to death, y and not as a function of chronological age, a. However, there will still be an apparent age function, g'(a), given that g(y) is regular and mortality is sort of stable, but not really. g'(a), in this case, is an aggregate based on both mortality and the real underlying time-to-death process:

$$g'(a) = \frac{\int_0^\omega g(y)N(a,y) \, \mathrm{d}y}{N(a)} \tag{1}$$

$$= \frac{\int_0^\omega g(y)N(a)\mu(a+y)\frac{\ell(a+y)}{\ell(a)}\,\mathrm{d}y}{N(a)}$$
(2)

$$= \int_0^\omega g(y)f(y|a) \, \mathrm{d}y \tag{3}$$

a little exercise we still need to do: find the g'(a) that belongs to g(y) in our canned example. It will be different for males and females because they have different mortality schedules. In this case, we can make the healthy l;ife expectancy function be based on mortality and g'(a) and see what would be the prediction if g'(a) is held constant and we induce mortality improvement. The answer is that mortality improvement will appear to increase the proportion of remaining life expectancy that is unhealthy: also the absolute years spent unhealthy, but the change in sex gap is maybe ambiguous (gotta check, maybe not), depending on the changes induced.

brief interlude This is a simple case of g(y), but in reality morbidity often varies as a function of both chronological and than atological age, and we ought to have a function g(a, y).

^{*}vanraalte@demogr.mpg.de

1 temp section, out of sync, jsut for latex

Given the numbers from Figures X, there are various methods that one can use to calculate period and cohort lifetables. For the sake of reproducibility for our toy example, we describe steps as follows, first for periods, then for cohorts.

1.1 Period quantities

We use event exposure lifetables, though it would be possible to jump straight to death quotients from the given Lexis diagram. Exposures for age x in year t, E(x,t), are calculated, per the HMD Methods Protocol (cite) as:

$$E(x,t) = \frac{C(x,t) + C(x,t+1)}{2} + D_L(x,t) - D_U(x,t)6 \qquad , \tag{4}$$

where C(x,t) is the census population in age interval [x,x+1] on January 1 of year t, $D_L(x,t)$ are deaths in the lower Lexis triangle of age x in year t, i.e., belonging to the cohort born in the year interval [t-x,t-x+1). $D_U(x,t)$ are deaths in the upper Lexis triangle of age x in year t, i.e., belonging to the cohort born in the year interval [t-x-1,t-x). All standard period lifetable steps are followed from the HMD Methods Protocol, with the exception of the a(x) assumption. The HMD assumes period a(x) values of $\frac{1}{2}$. Instead, we apply the following formula:

$$a(x,t) = \frac{D_L(x,t)\frac{1}{3} + D_U(x,t)\frac{2}{3}}{D_L(x,t) + D_U(x,t)}$$
 (5)

We then proceed to calculate all columns through e(x).

The average value of the unhealthy condition G at age xin year t, g(x,t) is calculated as follows. We first convert counts unhealthy on birthdays to proportions, and then take the arithmetic average of the proportion unhealthy at age x and age x + 1. Expectancies are then calculated as follows:

$$e(0,t) = \sum_{0}^{2} L(x,t)$$
 (6)

$$e_U(0,t) = \sum_{0}^{2} L(x,t)g(x,t)$$
 (7)

$$e_H(0,t) = e(0,t) - e_U(0,t)$$
 , (8)

where e(0,t) is the life expectancy at birth in year t, $e_U(0,t)$ is unhealthy life expectancy, and $e_H(0,t)$ is healthy life expectancy.