## Exercise 1: Age-specific decomposition of a difference between life expectancies

The aim of this exercise is to apply the linear integral model proposed by Horiuchi et al (2008). The example is applied to life expectancy for Venezuelan males. The aim is to quantify the effect of age-specific mortality changes on life expectancy between 1996 and 2013.

The COD object contains lifetable and cause of death data for the years 1996 and 2013. Names 1:10 are ten exhaustive and exclusive, assummed to be independent, cause-of-death groups. The exercise consists on quantifying the age effect on the change in life expectancy.

First load the data

```
library(ggplot2)
#install.packages('DemoDecomp')
library(DemoDecomp)

#load the data
load('Decomp_Data_L4.RData')
```

Following the method, we require two vectors of rates: one for 2013 and one for 1996

```
# first we need to vectors of mortality rates
mx1 <- age.specific.mx[age.specific.mx$year == 1996,]$mx

mx2 <- age.specific.mx[age.specific.mx$year == 2013,]$mx</pre>
```

We will need a life expectancy function that can be calculated from a vector of covariates (age-cause specific rates in our case) and the algorithm for decomposition. Luckily for us Tim Riffe released a package in CRAN. But you can also check the algorith in the functions file

```
#load some functions and some info for graphs
source('Functions_4.R')
```

Let's take look to the life expectancy function

```
e0.frommx
```

```
## function (nmx = mx, sex = 1, age = c(0, 1, seq(5, 85, 5)), nax = NULL)
##
       n <- c(diff(age), 999)</pre>
        if (is.null(nax)) {
##
##
            nax <- 0.5 * n
            if (n[2] == 4) {
##
                if (sex == 1) {
##
                     if (nmx[1] >= 0.107) {
##
                       nax[1] < -0.33
##
##
                       nax[2] < -1.352
                     }
##
##
                     else {
##
                       nax[1] \leftarrow 0.045 + 2.684 * nmx[1]
##
                       nax[2] \leftarrow 1.651 - 2.816 * nmx[1]
##
##
##
                if (sex == 2) {
                     if (nmx[1] >= 0.107) {
##
```

```
##
                         nax[1] < -0.35
##
                        nax[2] <- 1.361
##
                      }
##
                      else {
##
                         nax[1] \leftarrow 0.053 + 2.8 * nmx[1]
                         nax[2] \leftarrow 1.522 - 1.518 * nmx[1]
##
##
                 }
##
##
             }
        }
##
##
        nqx <- (n * nmx)/(1 + (n - nax) * nmx)
##
        nqx \leftarrow c(nqx[-(length(nqx))], 1)
        nqx[nqx > 1] \leftarrow 1
##
        npx <- 1 - nqx
##
##
        lx <- cumprod(c(1, npx))</pre>
##
        ndx <- -diff(lx)
##
        lxpn \leftarrow lx[-1]
##
        nLxpn \leftarrow n * lxpn + ndx * nax
##
        nLx <- c(nLxpn[-length(nLxpn)], lxpn[length(lxpn) - 1]/nmx[length(nmx)])</pre>
##
        Tx <- rev(cumsum(rev(nLx)))</pre>
##
        lx <- lx[1:length(age)]</pre>
##
        ex <- Tx/lx
        e0 <- ex[1]
##
##
        return(e0)
## }
```

Let's take look to the algorithm

## Decomp

```
## function (func, rates1, rates2, N, ...)
## {
##
        y1 <- func(rates1, ...)</pre>
        y2 <- func(rates2, ...)
##
##
        d <- rates2 - rates1
##
        n <- length(rates1)</pre>
##
        delta <- d/N
        x \leftarrow rates1 + d * matrix(rep(0.5:(N - 0.5)/N, length(rates1)),
##
            byrow = TRUE, ncol = N)
##
        cc <- matrix(0, nrow = n, ncol = N)</pre>
##
        for (j in 1:N) {
##
##
            for (i in 1:n) {
##
                 z \leftarrow rep(0, n)
##
                 z[i] \leftarrow delta[i]/2
                 cc[i, j] \leftarrow func((x[, j] + z), ...) - func((x[, j] - z), ...))
##
                      z), ...)
##
             }
##
##
        }
##
        return(rowSums(cc))
## }
```

Now we can perform the decomposition following the arguments of the function. We'll get a vector with the age-specific contributions to the change in life expectancy. Use the function Horiuchi in the DemoDecomp package.

```
#Now we can perfom the decomposition Results <- horiuchi(func = e0.frommx, pars1 = mx1, pars2 = mx2,N = 100)
```

Check the results

Results

```
## [1] 0.548578198 0.238453633 0.055370532 0.036289114 -0.308392214

## [6] -0.511607774 -0.280022896 -0.173391001 -0.060898629 0.024443227

## [11] 0.047212050 0.006173258 0.090497818 0.181146595 0.376724271

## [16] 0.351641464 0.316616151 0.416496331 0.296039894
```

Check consitency with the original difference in life expectancy

```
#original
original <- e0.frommx(mx2) - e0.frommx(mx1)</pre>
```

with the once obtained with the decomposition

```
#with decomp
with.decomp <- sum(Results)</pre>
```

Just do the difference and you will get the error term

original

```
## [1] 1.651372
with.decomp
```

```
## [1] 1.65137
```

```
#error
with.decomp - original
```

```
## [1] -1.903336e-06
```

Finally, graph and interpret the results.

```
#now graph results
ggplot()+
   ggtitle(bquote(~'Change in '~ e[0] ~'1996-2013' ))+
   geom_bar(aes(x = age_names, y= Results), stat = "identity", position = "stack")
```

