

Day 3, exercise 1: Age-specific decomposition of a difference between life expectancies and lifespan variations

2022-05-07

The aim of this exercise is to apply the linear integral method proposed by Horiuchi et al (2008) as well as the stepwise replacement method proposed by Andreev et al (2002). The example is applied to life expectancy and lifespan variation for Mexican males. The aim is to quantify the contribution of age-specific mortality changes to differences in both these measures between 2005 and 2015.

The dataset contains lifetable and cause of death data for Mexican men over age 15 for the years 2005 and 2015. Columns 1:9 contain data for ten exhaustive and exclusive, assumed to be independent, cause-of-death groups. However, in this exercise we will focus on all-cause mortality. The data and analyses come from Aburto and Beltrán-Sánchez (2019).

First load the data and the necessary packages. We also load a separate script, which contains some functions and information we will need later on.

```
load('AburtoBeltranSanchez.RData')

library(DemoDecomp)
library(tidyverse)

source("Functions_D3.R")
```

Following the method, we require two vectors of rates: one for 2005 and one for 2015.

```
# first we need the vectors of mortality rates
mx1 <- data %>%
  filter(year==2005, age>15) %>%
  pull(mx)
mx2 <- data %>%
  filter(year==2015, age>15) %>%
  pull(mx)
```

Luckily for us Tim Riffe released a package in CRAN (DemoDecomp), which contains a number of useful decomposition functions. You can check the algorithm for the continuous change method by calling the right function. When looking at a function, always consider carefully the default settings, they might not be appropriate for you.

```
# horiuchi
decomp_cont

## function (func, pars1, pars2, N, ...)
## {
##   y1 <- rG.frommx(pars1, age = unique(data$age))
##   y2 <- rG.frommx(pars2, age = unique(data$age))
##   d <- pars2 - pars1
##   n <- length(pars1)
##   delta <- d/N
##   x <- pars1 + d * matrix(rep(0.5:(N - 0.5)/N, n), byrow = TRUE,
```



```
##      nLxpn <- n * lxpn + ndx * nax
##      nLx <- c(nLxpn[-length(nLxpn)], lxpn[length(lxpn) - 1]/nmx[length(nmx)])
##      Tx <- rev(cumsum(rev(nLx)))
##      lx <- lx[1:length(age)]
##      ex <- Tx/lx
##      e0 <- ex[start.age]
##      return(e0)
## }
```

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.

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

Let's have a look at the results.

```
results

## [1] 1.198434e-03 1.080514e-03 9.569737e-04 3.244721e-04 1.105501e-03
## [6] 1.455085e-03 1.708074e-03 2.194065e-03 2.236456e-03 2.760845e-03
## [11] 2.195083e-03 2.618506e-03 2.719373e-03 3.588402e-03 3.164393e-03
## [16] 4.215794e-03 4.284196e-03 4.826602e-03 5.068240e-03 5.870266e-03
## [21] 6.595605e-03 6.425887e-03 7.463080e-03 7.694838e-03 8.537161e-03
## [26] 9.337188e-03 1.016239e-02 1.125144e-02 1.203325e-02 1.262266e-02
## [31] 1.320610e-02 1.364143e-02 1.362174e-02 1.388062e-02 1.414974e-02
## [36] 1.400647e-02 1.394208e-02 1.430703e-02 1.430783e-02 1.467613e-02
## [41] 1.514574e-02 1.477909e-02 1.477408e-02 1.445811e-02 1.403288e-02
## [46] 1.365480e-02 1.300880e-02 1.255246e-02 1.181598e-02 1.108344e-02
## [51] 1.009441e-02 9.608552e-03 8.627848e-03 8.122388e-03 7.182437e-03
## [56] 5.857698e-03 5.385979e-03 5.073094e-03 4.763988e-03 4.857903e-03
## [61] 5.579635e-03 5.193740e-03 4.786113e-03 4.606401e-03 4.638417e-03
## [66] 5.149155e-03 4.153624e-03 3.104129e-03 2.366086e-03 2.344904e-03
## [71] 2.057427e-03 1.857535e-03 1.885238e-03 1.864765e-03 1.557502e-03
## [76] 1.098618e-03 1.306923e-03 8.679445e-04 7.258661e-04 5.860968e-04
## [81] 4.660079e-04 3.646099e-04 2.805289e-04 2.121049e-04 1.574960e-04
## [86] 1.147825e-04 8.206201e-05 5.752941e-05 3.953817e-05 2.664041e-05
## [91] 1.760677e-05 1.142807e-05 7.302920e-06 1.267375e-05
```

Check consistency with the original difference in life expectancy.

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

```
## [1] 0.547894
```

```
#with decomp
(with.decomp <- sum(results))
```

```
## [1] 0.547894
```

Just do the difference and you will get the error term.

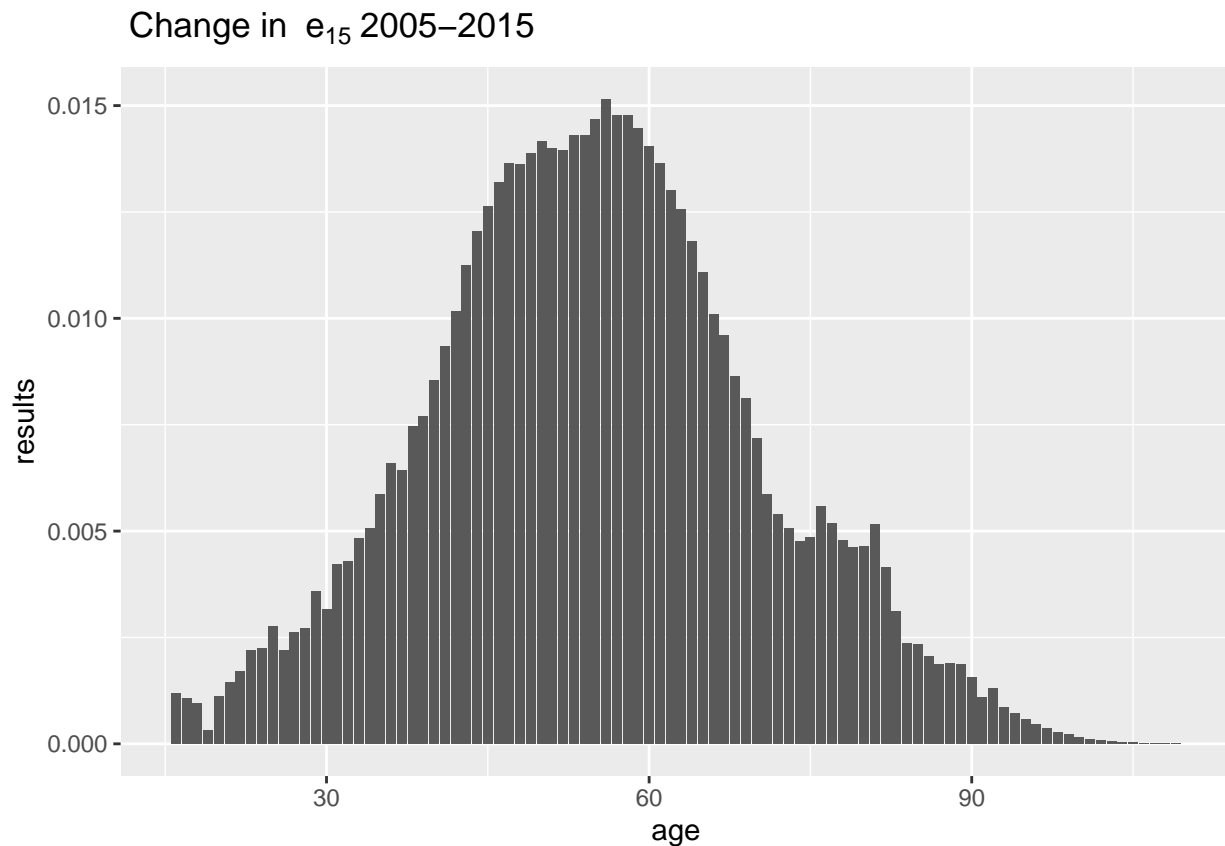
```
#error
with.decomp - original
```

```
## [1] -1.93009e-09
```

Finally, graph and interpret the results.

```
#now graph results
age <- data %>%
  filter(year==2005, age>15) %>%
  pull(age)

ggplot() +
  ggtitle(bquote(~'Change in ' ~ e[15] ~'2005-2015' )) +
  geom_bar(aes(x = age, y= results), stat = "identity", position = "stack")
```



Let's do the same with lifespan disparity

```
edagger.frommx

## function (mx, sex = 1, start.age = 1)
## {
##   i.openage <- length(mx)
##   OPENAGE <- i.openage - 1
##   RADIX <- 1
##   if (mx[i.openage] < 0.5 | is.na(mx[i.openage]))
##     mx[i.openage] = mx[i.openage - 1] * 1.1
##   ax <- mx * 0 + 0.5
##   ax[i.openage] <- if (mx[i.openage] == 0)
##     0.5
##   else 1/mx[i.openage]
##   qx <- mx/(1 + (1 - ax) * mx)
##   qx[i.openage] <- ifelse(is.na(qx[i.openage]), NA, 1)
##   px <- 1 - qx
```

```

##      px[is.nan(px)] <- 0
##      lx <- c(RADIX, RADIX * cumprod(px[1:OPENAGE]))
##      dx <- lx * qx
##      Lx <- lx - (1 - ax) * dx
##      Lx[i.openage] <- dx[i.openage] * ax[i.openage]
##      Lx[is.na(Lx)] <- 0
##      Tx <- c(rev(cumsum(rev(Lx[1:OPENAGE]))), 0) + Lx[i.openage]
##      ex <- Tx/lx
##      ex[is.na(ex)] <- 0
##      ex[i.openage] <- if (ex[OPENAGE] == 0)
##          0
##      else ax[i.openage]
##      v <- (ax * c(ex[-1L], 0) + (1 - ax) * ex)
##      v[length(ex)] <- ex[length(ex)]
##      v <- dx * v
##      e.dagger <- rev(cumsum(rev(v)))/lx
##      e.dagger[start.age]
## }

```

there are also other functions

sd.frommx

```

## function (mx, sex = 1, age, start.age = 1)
## {
##     i.openage <- length(mx)
##     OPENAGE <- i.openage - 1
##     RADIX <- 1
##     if (mx[i.openage] < 0.5 | is.na(mx[i.openage]))
##         mx[i.openage] = mx[i.openage - 1] * 1.1
##     ax <- mx * 0 + 0.5
##     ax[i.openage] <- if (mx[i.openage] == 0)
##         0.5
##     else 1/mx[i.openage]
##     qx <- mx/(1 + (1 - ax) * mx)
##     qx[i.openage] <- ifelse(is.na(qx[i.openage]), NA, 1)
##     px <- 1 - qx
##     px[is.nan(px)] <- 0
##     lx <- c(RADIX, RADIX * cumprod(px[1:OPENAGE]))
##     dx <- lx * qx
##     Lx <- lx - (1 - ax) * dx
##     Lx[i.openage] <- dx[i.openage] * ax[i.openage]
##     Lx[is.na(Lx)] <- 0
##     Tx <- c(rev(cumsum(rev(Lx[1:OPENAGE]))), 0) + Lx[i.openage]
##     ex <- Tx/lx
##     ex[is.na(ex)] <- 0
##     ex[i.openage] <- if (ex[OPENAGE] == 0)
##         0
##     else ax[i.openage]
##     sd <- sqrt(sum(dx/lx[1] * (age + ax - ex[1])^2))
##     return(sd)
## }

```

rG.frommx

```

## function (mx = pars1, sex = 1, age, start.age = 1)
## {

```

```
## i.openage <- length(mx)
## OPENAGE <- i.openage - 1
## RADIX <- 1
## if (mx[i.openage] < 0.5 | is.na(mx[i.openage]))
##   mx[i.openage] = mx[i.openage - 1] * 1.1
## ax <- mx * 0 + 0.5
## ax[i.openage] <- if (mx[i.openage] == 0)
##   0.5
## else 1/mx[i.openage]
## qx <- mx/(1 + (1 - ax) * mx)
## qx[i.openage] <- ifelse(is.na(qx[i.openage]), NA, 1)
## px <- 1 - qx
## px[is.nan(px)] <- 0
## lx <- c(RADIX, RADIX * cumprod(px[1:OPENAGE]))
## dx <- lx * qx
## Lx <- lx - (1 - ax) * dx
## Lx[i.openage] <- dx[i.openage] * ax[i.openage]
## Lx[is.na(Lx)] <- 0
## Tx <- c(rev(cumsum(rev(Lx[1:OPENAGE]))), 0) + Lx[i.openage]
## ex <- Tx/lx
## ex[is.na(ex)] <- 0
## ex[i.openage] <- if (ex[OPENAGE] == 0)
##   0
## else ax[i.openage]
## rG <- Gini.fun(x = age, nax = ax, ndx = dx/1e+05, ex = ex)
## return(rG[start.age])
## }
```

#Now we can perform the decomposition

```
results_edag <- horiuchi(func = edagger.frommx, pars1 = mx1, pars2 = mx2, N = 100)
```

NB: if you use another function, remember to define the additional arguments

Let's have a look at the results.

```
results_edag
```

```
## [1] -9.119879e-04 -8.176788e-04 -7.200223e-04 -2.426773e-04 -8.217229e-04
## [6] -1.074664e-03 -1.253165e-03 -1.598682e-03 -1.617974e-03 -1.982591e-03
## [11] -1.564214e-03 -1.851055e-03 -1.906397e-03 -2.493866e-03 -2.179359e-03
## [16] -2.876153e-03 -2.894088e-03 -3.226980e-03 -3.352064e-03 -3.838714e-03
## [21] -4.261970e-03 -4.100648e-03 -4.700194e-03 -4.779329e-03 -5.225359e-03
## [26] -5.627180e-03 -6.024865e-03 -6.555485e-03 -6.882608e-03 -7.079079e-03
## [31] -7.252480e-03 -7.325365e-03 -7.141067e-03 -7.091323e-03 -7.030587e-03
## [36] -6.753518e-03 -6.507274e-03 -6.445547e-03 -6.201854e-03 -6.098049e-03
## [41] -6.006851e-03 -5.566994e-03 -5.254678e-03 -4.821683e-03 -4.351228e-03
## [46] -3.896034e-03 -3.371220e-03 -2.905293e-03 -2.388324e-03 -1.895936e-03
## [51] -1.394369e-03 -9.917396e-04 -5.708630e-04 -2.179844e-04 1.072212e-04
## [56] 3.473910e-04 5.735011e-04 7.947173e-04 1.000594e-03 1.296271e-03
## [61] 1.826209e-03 2.034221e-03 2.202626e-03 2.456208e-03 2.834011e-03
## [66] 3.572734e-03 3.248846e-03 2.720370e-03 2.311467e-03 2.542571e-03
## [71] 2.466867e-03 2.454868e-03 2.738366e-03 2.969546e-03 2.713016e-03
## [76] 2.089001e-03 2.707600e-03 1.955678e-03 1.775865e-03 1.554504e-03
## [81] 1.338028e-03 1.131780e-03 9.401763e-04 7.665347e-04 6.129957e-04
## [86] 4.805305e-04 3.690374e-04 2.775075e-04 2.042373e-04 1.470621e-04
## [91] 1.035845e-04 7.137623e-05 1.521927e-04 0.000000e+00
```

Check consistency with the original difference in life expectancy.

```
#original  
(original <- edagger.frommx(mx2) - edagger.frommx(mx1))
```

```
## [1] -0.1440517
```

```
#with decomp  
(with.decomp <- sum(results_edag))
```

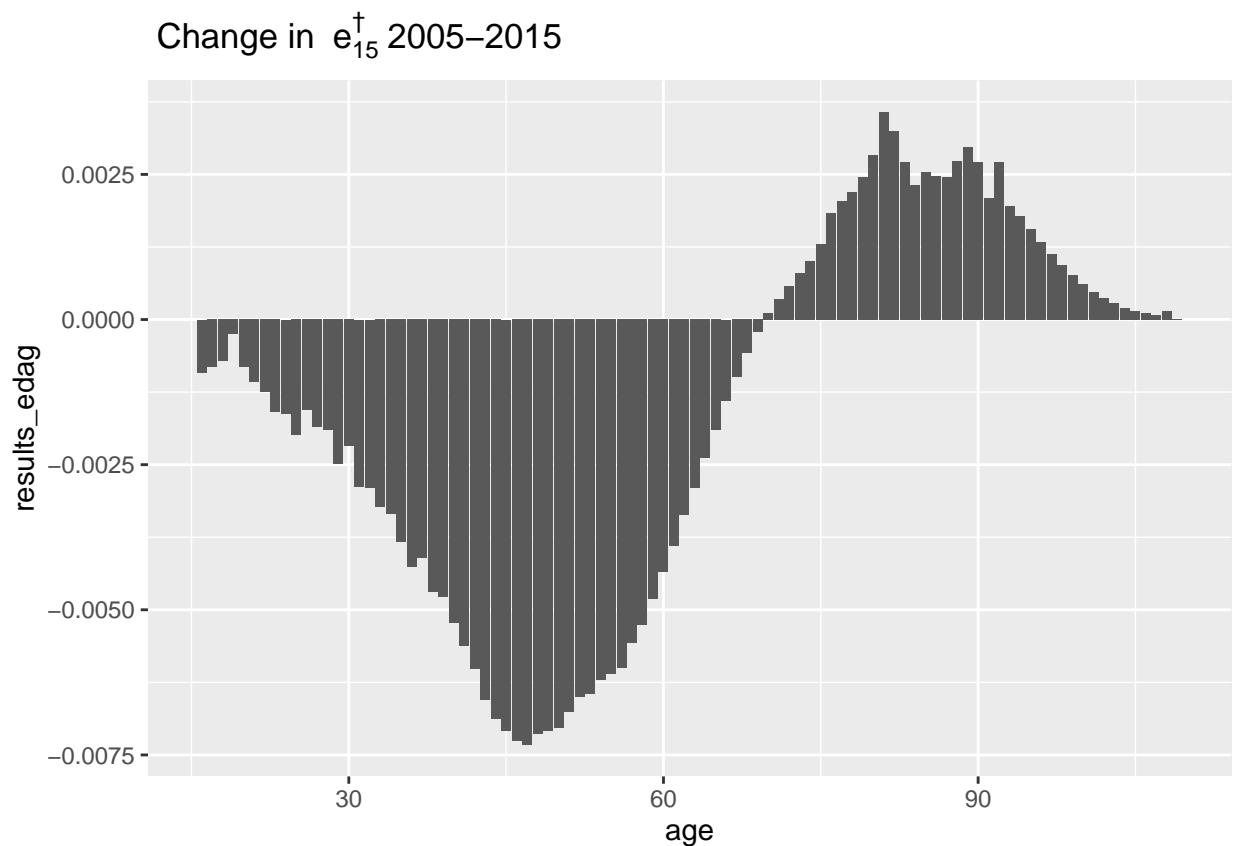
```
## [1] -0.1440517
```

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

```
## [1] 2.485777e-09
```

Finally, graph and interpret the results.

```
#now graph results  
ggplot()+  
ggtitle(bquote(~'Change in ' ~ e[15] ~ "\u2020" ~ '2005-2015' )) +  
geom_bar(aes(x = age, y= results_edag), stat = "identity", position = "stack")
```



The continuous change method is just one of those that exist. We can obtain very similar results with the stepwise replacement method, also included in the DemoDecomp package. Let's look at the algorithm.

```
#stepwise_replacement  
decomp_step
```

```
## function (func, pars1, pars2, symmetrical = TRUE, direction = "up",
```

```

## ... )
## {
##   direction <- tolower(direction)
##   stopifnot(direction %in% c("up", "down", "both"))
##   up <- direction %in% c("up", "both")
##   down <- direction %in% c("down", "both")
##   N <- length(pars1)
##   pars1Mat <- matrix(pars1, ncol = N + 1, nrow = N)
##   pars2Mat <- matrix(pars2, ncol = N + 1, nrow = N)
##   RM_1_2_up <- matrix(ncol = N + 1, nrow = N)
##   RM_1_2_down <- RM_1_2_up
##   RM_2_1_up <- RM_1_2_up
##   RM_2_1_down <- RM_1_2_up
##   r1ind <- lower.tri(pars1Mat, TRUE)
##   r2ind <- upper.tri(pars1Mat)
##   RM_1_2_up[r1ind] <- pars1Mat[r1ind]
##   RM_1_2_up[r2ind] <- pars2Mat[r2ind]
##   RM_1_2_down[r1ind[N:1, ]] <- pars1Mat[r1ind[N:1, ]]
##   RM_1_2_down[r2ind[N:1, ]] <- pars2Mat[r2ind[N:1, ]]
##   RM_2_1_up[r1ind] <- pars2Mat[r1ind]
##   RM_2_1_up[r2ind] <- pars1Mat[r2ind]
##   RM_2_1_down[r1ind[N:1, ]] <- pars2Mat[r1ind[N:1, ]]
##   RM_2_1_down[r2ind[N:1, ]] <- pars1Mat[r2ind[N:1, ]]
##   dec <- matrix(NA, nrow = N, ncol = 4)
##   if (up) {
##     dec[, 1] <- diff(apply(RM_1_2_up, 2, func, ...))
##   }
##   if (down) {
##     dec[, 2] <- diff(apply(RM_1_2_down, 2, func, ...))
##   }
##   if (symmetrical) {
##     if (up) {
##       dec[, 3] <- -diff(apply(RM_2_1_up, 2, func, ...))
##     }
##     if (down) {
##       dec[, 4] <- -diff(apply(RM_2_1_down, 2, func, ...))
##     }
##   }
##   dec_avg <- rowMeans(dec, na.rm = TRUE)
##   dec_avg
## }

```

Now let's get the results. We can use the same life expectancy and lifespan disparity functions as before.

```

# Life expectancy
results_step <- stepwise_replacement(e0.frommx, pars1 = mx1, pars2 = mx2)

#original
(original <- e0.frommx(mx2) - e0.frommx(mx1))

## [1] 0.547894

#with decomp
(with.decomp_step <- sum(results_step))

## [1] 0.547894

```



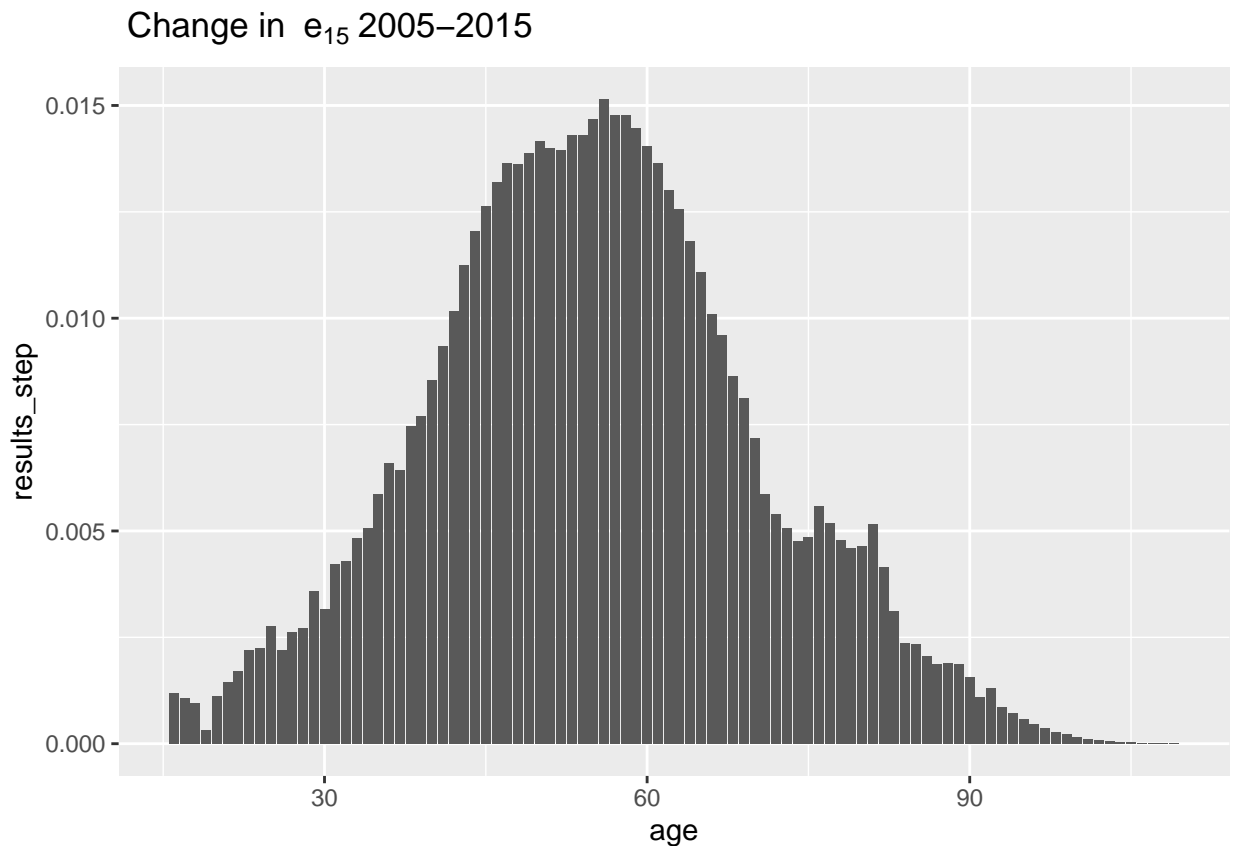
```

#error
with.decomp_step - original

## [1] 0

#now graph results
ggplot()+
  ggtitle(bquote(~'Change in ' ~ e[15] ~'2005-2015' ))+
  geom_bar(aes(x = age, y = results_step), stat = "identity", position = "stack")

```



How different are these results from the ones we obtained with the continuous change method?

```

results - results_step

## [1] -2.372842e-08 -2.166886e-08 -1.945230e-08 -6.697931e-09 -2.317218e-08
## [6] -3.089745e-08 -3.669780e-08 -4.761945e-08 -4.897748e-08 -6.092551e-08
## [11] -4.882190e-08 -5.872264e-08 -6.140788e-08 -8.137388e-08 -7.196597e-08
## [16] -9.595846e-08 -9.724317e-08 -1.089907e-07 -1.135018e-07 -1.298109e-07
## [21] -1.430821e-07 -1.362628e-07 -1.538681e-07 -1.530627e-07 -1.625239e-07
## [26] -1.680680e-07 -1.704774e-07 -1.725383e-07 -1.646424e-07 -1.497708e-07
## [31] -1.308234e-07 -1.067658e-07 -7.745063e-08 -4.864986e-08 -1.796140e-08
## [36] 1.369971e-08 4.468338e-08 7.776366e-08 1.094923e-07 1.442438e-07
## [41] 1.808901e-07 2.056640e-07 2.318257e-07 2.491815e-07 2.597368e-07
## [46] 2.661053e-07 2.622207e-07 2.573876e-07 2.426008e-07 2.247054e-07
## [51] 1.999619e-07 1.839441e-07 1.581811e-07 1.416788e-07 1.188770e-07
## [56] 9.436485e-08 8.705182e-08 8.328406e-08 8.032666e-08 8.390568e-08
## [61] 9.350233e-08 7.966790e-08 6.612822e-08 5.510545e-08 4.175268e-08
## [66] 1.556674e-08 -2.049937e-08 -3.423873e-08 -3.351897e-08 -3.868829e-08

```

```
## [71] -3.991013e-08 -4.092685e-08 -5.002892e-08 -6.657936e-08 -7.499110e-08
## [76] -6.351226e-08 -9.483680e-08 -8.060768e-08 -7.970094e-08 -7.575560e-08
## [81] -7.029344e-08 -6.368656e-08 -5.633866e-08 -4.865407e-08 -4.100846e-08
## [86] -3.372298e-08 -2.704734e-08 -2.115087e-08 -1.612241e-08 -1.197869e-08
## [91] -8.677826e-09 -6.136094e-09 -4.245113e-09 -8.990447e-09
```

Let's do the same for lifespan disparity

```
results_step_edag <- stepwise_replacement(edagger.frommx, pars1 = mx1, pars2 = mx2)
```

```
#original
```

```
(original <- edagger.frommx(mx2) - edagger.frommx(mx1))
```

```
## [1] -0.1440517
```

```
#with decomp
```

```
(with.decomp_step <- sum(results_step_edag))
```

```
## [1] -0.1440517
```

```
#error
```

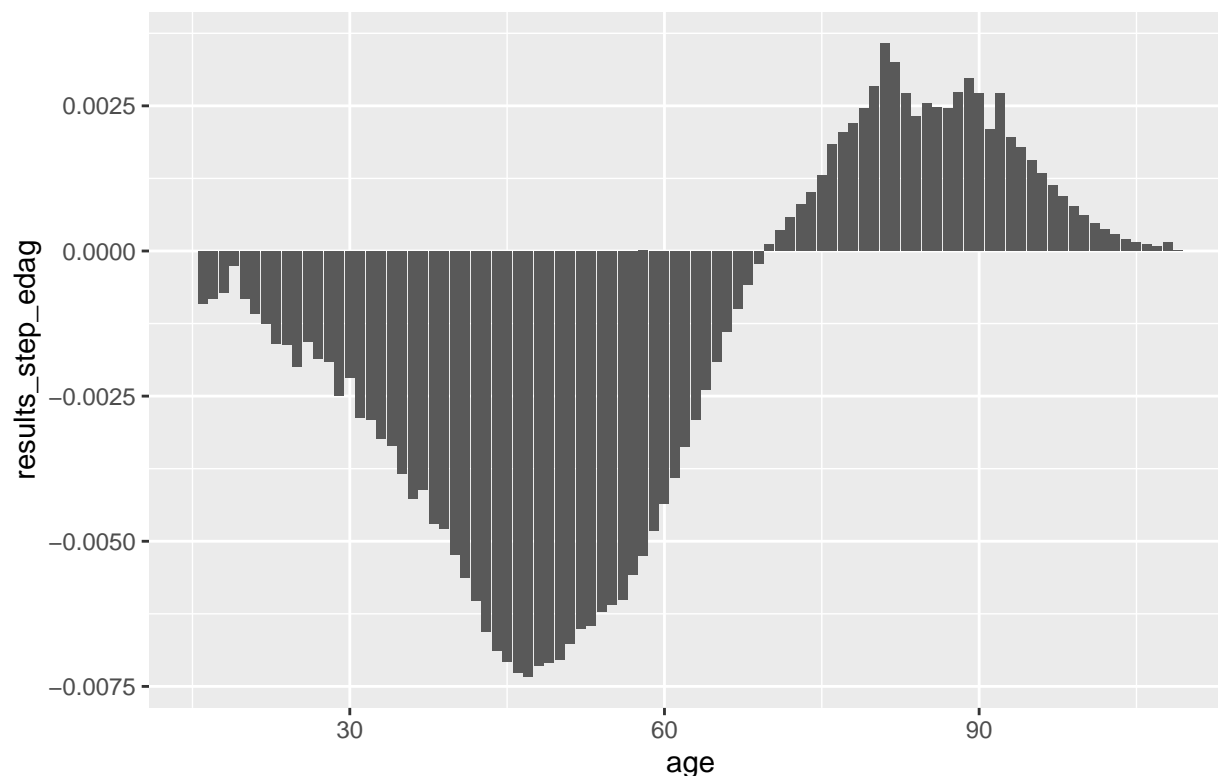
```
with.decomp_step - original
```

```
## [1] 0
```

```
#now graph results
```

```
ggplot()+
  ggtitle(bquote(~'Change in '~ e[15]~"\u2020" ~'2005-2015' ))+
  geom_bar(aes(x = age, y= results_step_edag), stat = "identity", position = "stack")
```

Change in e_{15}^+ 2005–2015



Difference between continuous change and stepwise replacement

results_edag - results_step_edag

```
## [1] 4.267199e-08 3.891918e-08 3.489808e-08 1.200750e-08 4.150631e-08
## [6] 5.525891e-08 6.550536e-08 8.479179e-08 8.696013e-08 1.078141e-07
## [11] 8.610156e-08 1.032083e-07 1.075046e-07 1.417727e-07 1.247096e-07
## [16] 1.652662e-07 1.662376e-07 1.847564e-07 1.905417e-07 2.154283e-07
## [21] 2.341144e-07 2.193871e-07 2.430723e-07 2.362632e-07 2.438854e-07
## [26] 2.432496e-07 2.353354e-07 2.231988e-07 1.939243e-07 1.528081e-07
## [31] 1.039388e-07 4.732968e-08 -1.316343e-08 -7.473250e-08 -1.385522e-07
## [36] -1.974585e-07 -2.542061e-07 -3.178212e-07 -3.717798e-07 -4.323544e-07
## [41] -4.928657e-07 -5.184458e-07 -5.462629e-07 -5.513732e-07 -5.404983e-07
## [46] -5.197701e-07 -4.784634e-07 -4.350039e-07 -3.747601e-07 -3.114315e-07
## [51] -2.425477e-07 -1.874332e-07 -1.266420e-07 -7.878404e-08 -3.411953e-08
## [56] -5.347570e-09 9.745611e-09 2.131942e-08 3.014959e-08 4.230027e-08
## [61] 7.365065e-08 1.015724e-07 1.243808e-07 1.513545e-07 1.920250e-07
## [66] 2.801419e-07 2.887591e-07 2.504894e-07 2.057193e-07 2.146436e-07
## [71] 1.977351e-07 1.847572e-07 1.944049e-07 2.013176e-07 1.731957e-07
## [76] 1.197789e-07 1.343560e-07 7.846022e-08 5.072964e-08 2.324565e-08
## [81] -1.134421e-09 -2.147579e-08 -3.718347e-08 -4.803820e-08 -5.419097e-08
## [86] -5.611650e-08 -5.453397e-08 -5.030742e-08 -4.434098e-08 -3.748427e-08
## [91] -3.045986e-08 -2.381915e-08 -7.121172e-08 0.000000e+00
```