

Healthy Lifespan Inequality (e-dagger)

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Attempt to calculate Healthy lifespan Inequality according to Permanyer et al. 2022: “On the measurement of healthy lifespan inequality”

My speculation about e-dagger (Vaupel, 1986)

$$HLI : He^{\dagger}(x, t) = \frac{1}{S(x, t)} \int_x^{\infty} hle(a, t) \cdot d'(a, t) da$$

where $d'(a, t)$ are the number of deaths and individuals ceasing to be in good health between ages x and $x + 1$, (see, Permanyer paragraph “Estimating health distributions”) multiplying the lx column of the life table (showing the number of survivors at age x) by $(1\pi_x)$ (the percent of population at age x not limited to carry out daily activities). The $hle(a, t)$ is the healthy life expectancy according to the Sullivan method.

```
hle.plus.edagg = function (rates, age=seq(start.age, open.age, 5), sex='f') {
  lengthvec <- length(rates)
  mx <- rates[1:(lengthvec / 2)]
  wx <- rates[(lengthvec / 2 + 1):lengthvec]

  n <- c(diff(age), 1)
  ax <- 0.5 * n

  #-----
  if (age[1] == 0) {
    if (sex == 'm') {
      ax[1] <- ifelse(mx[1] >= 0.08307, 0.29915,
                      ifelse(mx[1] < 0.023,
                              0.14929 - 1.99545 * mx[1],
                              0.02832 + 3.26021 * mx[1] ))}

    if (sex == 'f') {
      ax[1] <- ifelse(mx[1] >= 0.06891, 0.31411,
                      ifelse(mx[1] < 0.01724,
                              0.14903 - 2.05527 * mx[1],
                              0.04667 + 3.88089 * mx[1] ))} }

  qx <- (n * mx) / (1 + (n - ax) * mx)
  qx <- c(qx[-(length(qx))], 1)
  qx[qx > 1] <- 1
  px <- 1 - qx
  # survivors at age x (lx)
  lx <- c(100000, rep(0, (length(mx)-1)))
  for (i in 1:(length(mx) - 1)){
    lx[i+1] <- lx[i]*px[i] }
  # deaths between ages x and x+n (dx)
```

```

dx <- lx * qx
Lx <- rep(0,length(mx))
for (i in 1:length(mx) -1){
  Lx[i] <- lx[i+1]*n[i] + ax[i]*dx[i] }
Lx[length(mx)] <- lx[length(mx)]/mx[length(mx)]
Lx.health <- Lx*(1-wx)
ex.health <- sum(Lx.health)/lx[1]

#####
# e-dagger:
# see, Permanyer et al. Population Health Metrics (2022);
# paragraph Estimating health distributions.
# The author suggest - Multiplying the lx column of the life table,
# showing the number of survivors at age x,
# by 1 wx (the percent of population at age x not limited
# to carry out daily activities)
# we obtain lx' : the number of healthy survivors at age x .
# This is the so-called 'morbidity curve'.
# From the lx and lx' columns we derive the standard dx and dx' distributions
#####

lx <- c(100000,rep(0,(length(mx)-1)))
for (i in 1:(length(mx) -1)){
  lx[i+1] <- lx[i]*px[i] }
lx.health <- lx*(1-wx)
dx.health <- lx.health * qx

# Healty e-dagger at age x
ed.health <- sum(dx.health*ex.health)/lx[1]
return(c(ex.health,ed.health))
}

# Data from example A. A. van Raalte and M. R. Nepomuceno
# Defining the variables for the start of the first interval,
# the start of the open-aged interval, and the years

start.age = 65
open.age = 85
year1 = 1970; year2 = 1990

mx1 <- c(0.0204, 0.0325, 0.0533, 0.0867,
         0.1640)
mx2 <- c(0.0161, 0.0246, 0.0384, 0.0646,
         0.1410)

wx1 <- c(0.3000,0.3657,0.4552, 0.5285,
         0.6822)
wx2 <- c(0.3056,0.3831,0.4552, 0.5424,
         0.6441)

```

```
# Making a single vector of mx followed by wx.  
# we need these as input for either horiuchi or stepwise_replacement  
mxwx1 <- c(mx1,wx1)  
mxwx2 <- c(mx2,wx2)  
  
hle.plus.edagg(rates=mxwx1)  
  
## [1] 9.691891 4.564243  
hle.plus.edagg(rates=mxwx2)  
  
## [1] 10.597281 4.832563
```