Simple 3-state Digitized Partitioned Survival model in R

The DARTH workgroup

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Please cite our publications when using this code:

- Jalal H, Pechlivanoglou P, Krijkamp E, Alarid-Escudero F, Enns E, Hunink MG. An Overview of R in Health Decision Sciences. Med Decis Making. 2017; 37(3): 735-746. https://journals.sagepub.com/doi/abs/10.1177/0272989X16686559
- Krijkamp EM, Alarid-Escudero F, Enns EA, Jalal HJ, Hunink MGM, Pechlivanoglou P. Microsimulation modeling for health decision sciences using R: A tutorial. Med Decis Making. 2018;38(3):400–22. https://journals.sagepub.com/doi/abs/10.1177/0272989X18754513
- Krijkamp EM, Alarid-Escudero F, Enns E, Pechlivanoglou P, Hunink MM, Jalal H. A Multidimensional Array Representation of State-Transition Model Dynamics. BioRxiv 670612 2019.https://www.biorxiv.org/content/10.1101/670612v1

Change `eval` to `TRUE` if you want to knit this document.

```
rm(list = ls())      # clear memory (removes all the variables from the workspace)
```

01 Load packages

```
if (!require('pacman')) install.packages('pacman'); library(pacman) # use this package to conveniently
# load (install if required) packages from CRAN
p_load("here", "dplyr", "devtools", "gems", "flexsurv", "survHE", "ggplot2", "msm", "igraph", "mstate",
       "reshape2", "knitr")
```

02 Load functions

```
source("functions.R")
```

03 Input model parameters

```
v_n       <- c("healthy", "sick", "dead")  # state names
n_s       <- length(v_n)                   # No of states
c_l       <- 1 / 12                        # cycle length (a month)
n_t       <- 20                            # number of years (20 years)
times     <- seq(0, n_t, c_l)              # the cycles in years
d_r       <- 0.03                          # discount rate
set.seed(2009)                             # set the seed

c_H       <- 200                           # cost of remaining one cycle healthy
c_S       <- 500                           # cost of remaining one cycle sick
c_D       <- 0                             # cost of remaining one cycle dead
v_c       <- c(c_H, c_S, c_D)              # store in a vector

u_H       <- 0.75                          # utility when healthy
u_S       <- 0.30                          # utility when sick
u_D       <- 0                             # utility when dead
v_u       <- c(u_H, u_S, u_D)              # store in a vector

v_dw      <- 1 / (1 + d_r) ^ (times)       # discount weight
```

04 Digitized Data

Use the function `digitise()` to translate the digitised OS and PFS data into patient level information.

```r
# Create IPD and KM data for the OS curves
digitise("OS_Examp.txt",
         "OS_Examp_AtRisk.txt",
         km_output  = "KMdata_OS.txt",
         ipd_output = "IPDdata_OS.txt")

# Create IPD and KM data for the PFS curves (there have been 99 events in the cohort)
digitise("PFS_Examp.txt",
         "PFS_Examp_AtRisk.txt",
         km_output  = "KMdata_PFS.txt",
         ipd_output = "IPDdata_PFS.txt")

# Link the IPD files across the two arms of the trial for OS and PFS
IPD_OS  <- make.ipd(ipd_files = c("IPDdata_OS.txt"), ctr = 1,
                    var.labs  = c("time","event","arm"))
IPD_PFS <- make.ipd(ipd_files = c("IPDdata_PFS.txt"), ctr = 1,
                    var.labs  = c("time","event","arm"))
```

05 Analysis

05.1 Partitioned Survival model

```r
# fit all parametric models to the data and extract the AIC/BIC
# Select the one with the most appropriate fit
# Repeat for PFS and OS
fit_PFS  <- fit.fun(time ="time", status = "event", data = IPD_PFS, times = times,
                    extrapolate = T)
fit_OS   <- fit.fun(time = "time", status = "event" , data = IPD_OS, times = times,
                    extrapolate = T)

best_PFS <- fit_PFS[["Weibull"]]
best_OS  <- fit_OS [["Weibull"]]

# construct a partitioned survival model out of the fitted models
m_M_PSM <- partsurv(best_PFS,best_OS, time = times)$trace
matplot(m_M_PSM, type="l")
legend("right",v_n, col= 1:3, lty=1:3, bty="n")
```

Calculate total cost and QALYs per cycle.

```r
v_c_t <- m_M_PSM   %*% v_c
v_u_t <- m_M_PSM   %*% v_u

tot_c <-  t(v_c_t) %*% v_dw
tot_u <-  t(v_u_t) %*% v_dw

# display results
results <- data.frame(Total_Cost = tot_c, Total_QALYs = tot_u)
results
```