

Microsimulation Sick-Sicker model

Includes individual characteristics: age, age dependent mortality probabilities, individual treatment effect modifier

The DARTH workgroup

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- 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. *Med Decis Making*. 2020 Online first. <https://doi.org/10.1177/0272989X19893973>

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```
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", "scales", "ellipse", "ggplot2", "lazyeval", "igraph", "ggraph", "r
# load (install if required) packages from GitHub
# install_github("DARTH-git/dampack", force = TRUE) Uncomment if there is a newer version
p_load_gh("DARTH-git/dampack")
```

02 Load functions

```
source(here("functions", "Functions.R"))
```

03 Input model parameters

```
set.seed(1) # set the seed

# Model structure
n_t   <- 30                # time horizon, 30 cycles
n_i   <- 100000            # number of simulated individuals
v_n   <- c("H", "S1", "S2", "D") # the model states names
n_states <- length(v_n)    # the number of health states
d_r   <- 0.03              # discount rate of 3% per cycle
v_dwe <- v_dwc <- 1 / ((1 + d_r) ^ (0:n_t)) # discount weight
v_names_str <- c("no treatment", "treatment") # strategy names
n_str <- length(v_names_str) # number of strategies

### Event probabilities (per cycle)
# Annual transition probabilities
p_HS1 <- 0.15              # probability of becoming sick when healthy
p_S1H <- 0.5               # probability of recovering to healthy when sick
p_S1S2 <- 0.105            # probability of becoming sicker when sick

# Annual probabilities of death
# load age dependent probability
p_mort <- read.csv(here("data", "mortProb_age.csv"))
# load age distribution
dist_Age <- read.csv(here("data", "MyPopulation-AgeDistribution.csv"))

p_S1D <- 0.0149            # probability to die in S1 by cycle
p_S2D <- 0.048             # probability to die in S2

# Cost inputs
```

```

c_H      <- 2000          # cost of one cycle in the healthy state
c_S1     <- 4000          # cost of one cycle in the sick state
c_S2     <- 15000         # cost of one cycle in the sicker state
c_D      <- 0             # cost of one cycle in the dead state
c_Trt    <- 12000         # cost of treatment (per cycle)

# Utility inputs
u_H      <- 1             # utility when healthy
u_S1     <- 0.75          # utility when sick
u_S2     <- 0.5           # utility when sicker
u_D      <- 0             # utility when dead
u_Trt    <- 0.95          # utility when sick(er) and being treated

```

04 Sample individual level characteristics

04.1 Static characteristics

```

v_x      <- runif(n_i, min = 0.95, max = 1.05) # treatment effect modifier at baseline
# sample from age distribution an initial age for every individual
v_age0   <- sample(x = dist_Age$age, prob = dist_Age$prop, size = n_i, replace = TRUE)
df_X     <- data.frame(ID = 1:n_i, x = v_x, Age = v_age0)

```

04.2 Dynamic characteristics

```

# Specify the initial health state of the individuals
# everyone begins in the healthy state (in this example)
v_M_init <- rep("H", n_i) # a vector with the initial health state for all individuals

```

05 Define Simulation Functions

05.1 Probability function

The function that updates the transition probabilities of every cycle is shown below.

```

Probs <- function(M_t, df_X, t) {
  # Arguments:
  # M_t: health state occupied by individual i at cycle t (character variable)
  # df_X: data frame with individual characteristics data
  # t: current cycle
  # Returns:
  # transition probabilities for that cycle

  # create matrix of state transition probabilities
  m_p_t <- matrix(0, nrow = n_states, ncol = n_i)
  rownames(m_p_t) <- v_n # give the state names to the rows

```

```

# lookup baseline probability and rate of dying based on individual characteristics
p_HD_all <- inner_join(df_X, p_mort, by = c("Age"))
p_HD      <- p_HD_all[M_t == "H", "p_HD"]

# update the m_p with the appropriate probabilities
# transition probabilities when healthy
m_p_t[, M_t == "H"] <- rbind(1 - p_HS1 - p_HD, p_HS1, 0, p_HD)
# transition probabilities when sick
m_p_t[, M_t == "S1"] <- rbind(p_S1H, 1 - p_S1H - p_S1S2 - p_S1D, p_S1S2, p_S1D)
# transition probabilities when sicker
m_p_t[, M_t == "S2"] <- rbind(0, 0, 1 - p_S2D, p_S2D)
# transition probabilities when dead
m_p_t[, M_t == "D"] <- rbind(0, 0, 0, 1)

return(t(m_p_t))
}

```

05.2 Cost function

The Costs function estimates the costs at every cycle.

```

Costs <- function (M_t, Trt = FALSE) {
  # M_t: health state occupied by individual i at cycle t (character variable)
  # Trt: is the individual being treated? (default is FALSE)

  c_t <- 0 # by default the cost for everyone is zero
  c_t[M_t == "H"] <- c_H # update the cost if healthy
  c_t[M_t == "S1"] <- c_S1 + c_Trtr * Trt # update the cost if sick conditional on treatment
  c_t[M_t == "S2"] <- c_S2 + c_Trtr * Trt # update the cost if sicker conditional on treatment
  c_t[M_t == "D"] <- c_D # update the cost if dead

  return(c_t) # return the costs
}

```

05.3 Health outcome function

The Effs function to update the utilities at every cycle.

```

Effs <- function (M_t, df_X, Trt = FALSE, cl = 1) {
  # M_t: health state occupied by individual i at cycle t (character variable)
  # df_X: data frame with individual characteristics data
  # Trt: is the individual treated? (default is FALSE)
  # cl: cycle length (default is 1)

  u_t <- 0 # by default the utility for everyone is zero
  u_t[M_t == "H"] <- u_H # update the utility if healthy
  u_t[M_t == "S1" & Trt == FALSE] <- u_S1 # update the utility if sick
  # update the utility if sick but on treatment (adjust for individual effect modifier)
  u_t[M_t == "S1" & Trt == TRUE] <- u_Trtr * df_X$x[M_t == "S1"]
  u_t[M_t == "S2"] <- u_S2 # update the utility if sicker
  u_t[M_t == "D"] <- u_D # update the utility if dead
}

```

```

QALYs <- u_t * c1 # calculate the QALYs during cycle t
return(QALYs)     # return the QALYs
}

```

06 Run Microsimulation

```

MicroSim <- function(n_i, df_X , Trt = FALSE, seed = 1) {
# Arguments:
# n_i:      number of individuals
# df_X      data frame with individual characteristics data
# Trt:      is this the individual receiving treatment? (default is FALSE)
# seed:     default is 1

set.seed(seed) # set the seed

# create three matrices called m_M, m_C and m_E
# number of rows is equal to the n_i, the number of columns is equal to n_t
# (the initial state and all the n_t cycles)
# m_M is used to store the health state information over time for every individual
# m_C is used to store the costs information over time for every individual
# m_E is used to store the effects information over time for every individual

m_M <- m_C <- m_E <- m_Ts <- matrix(nrow = n_i, ncol = n_t + 1,
                                   dimnames = list(paste("ind" , 1:n_i, sep = " "),
                                                    paste("cycle", 0:n_t, sep = " ")))

# initial health state at cycle 0 for individual i
m_M[, 1] <- v_M_init
# calculate costs per individual during cycle 0
m_C[, 1] <- Costs(m_M[, 1], Trt)
# calculate QALYs per individual during cycle 0
m_E[, 1] <- Effe(m_M[, 1], df_X, Trt)

# open a loop for time running cycles 1 to n_t
for (t in 1:n_t) {
  # calculate the transition probabilities for the cycle based on health state t
  m_P <- Probs(m_M[, t], df_X, t)
  # sample the current health state and store that state in matrix m_M
  m_M[, t + 1] <- samplev(m_P, 1)
  # calculate costs per individual during cycle t + 1
  m_C[, t + 1] <- Costs(m_M[, t + 1], Trt)
  # calculate QALYs per individual during cycle t + 1
  m_E[, t + 1] <- Effe(m_M[, t + 1], df_X, Trt)

  # update the age of individuals that are alive
  df_X$Age[m_M[, t + 1] != "D"] <- df_X$Age[m_M[, t + 1] != "D"] + 1

  # Display simulation progress
  if(t/(n_t/10) == round(t/(n_t/10), 0)) { # display progress every 10%

```

```

      cat('\r', paste(t/n_t * 100, "% done", sep = " "))
    }

  } # close the loop for the time points

  # calculate
  tc <- m_C %*% v_dwc      # total (discounted) cost per individual
  te <- m_E %*% v_dwe      # total (discounted) QALYs per individual
  tc_hat <- mean(tc)       # average (discounted) cost
  te_hat <- mean(te)       # average (discounted) QALYs

  # store the results from the simulation in a list
  results <- list(m_M = m_M, m_C = m_C, m_E = m_E, tc = tc , te = te, tc_hat = tc_hat,
                 te_hat = te_hat)

  return(results) # return the results
} # end of the MicroSim function

# By specifying all the arguments in the `MicroSim()` the simulation can be started
# In this example the outcomes of the simulation are stored in the variables `outcomes_no_tr` and `

# Run the simulation for both no treatment and treatment options
outcomes_no_trt <- MicroSim(n_i, df_X, Trt = FALSE, seed = 1)

```

```

##
10 % done
20 % done
30 % done
40 % done
50 % done
60 % done
70 % done
80 % done
90 % done
100 % done

```

```

outcomes_trt <- MicroSim(n_i, df_X, Trt = TRUE, seed = 1)

```

```

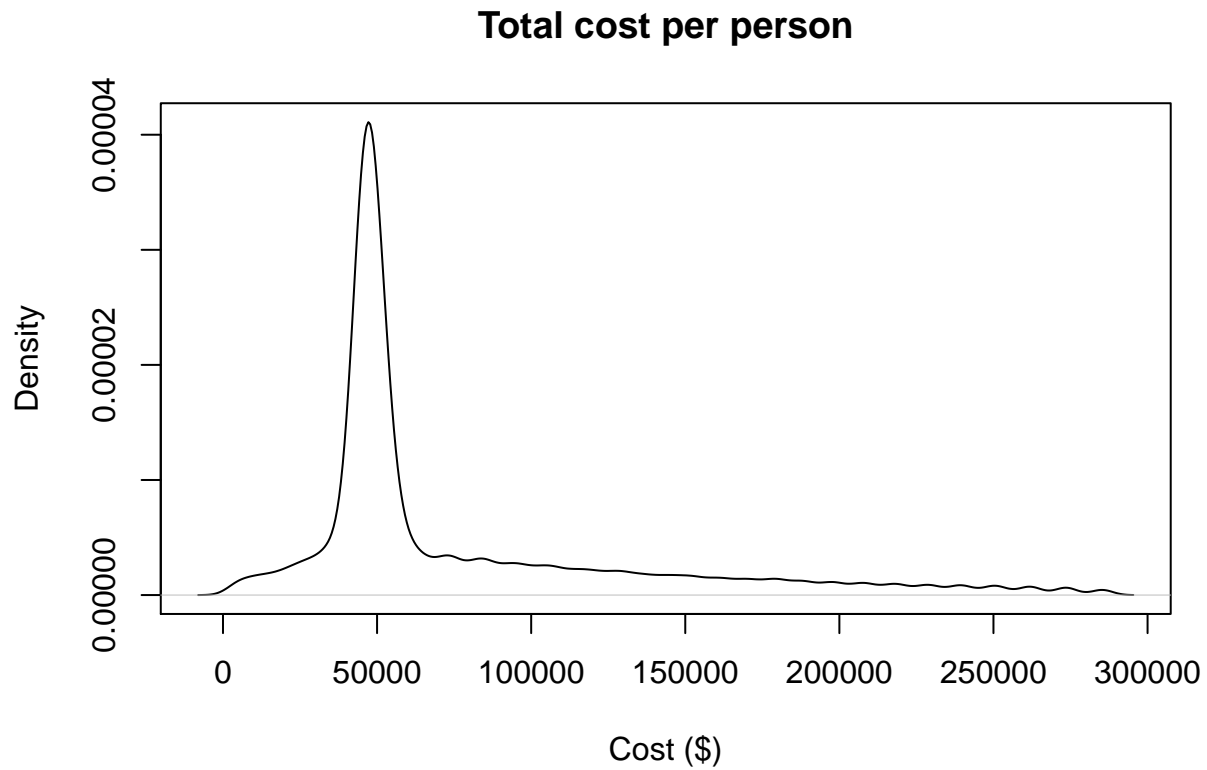
##
10 % done
20 % done
30 % done
40 % done
50 % done
60 % done
70 % done
80 % done
90 % done
100 % done

```

07 Visualize results

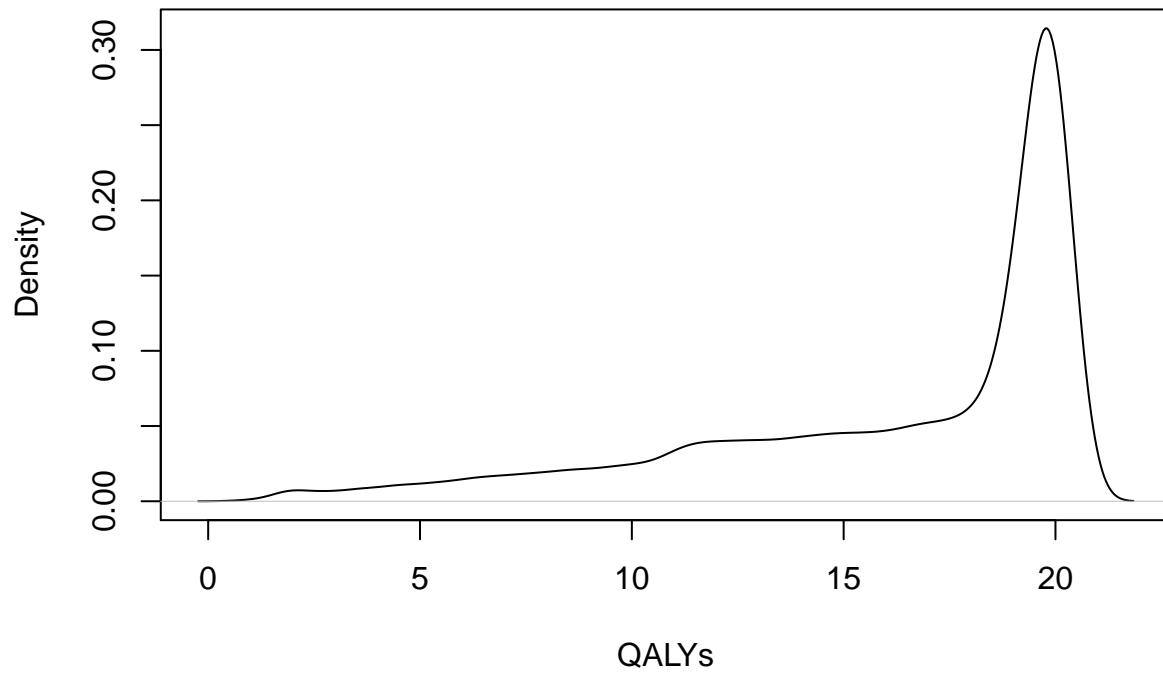
```
options(scipen = 999)

# No treatment
plot(density(outcomes_no_trt$tc), main = paste("Total cost per person"), xlab = "Cost ($)")
```



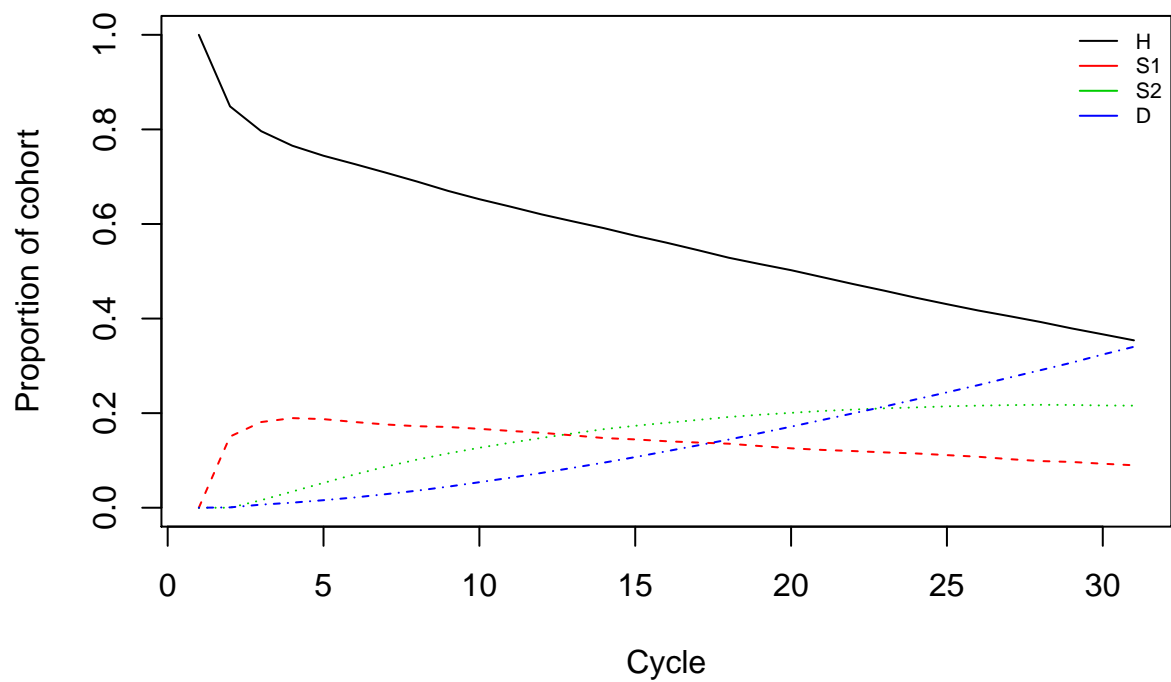
```
plot(density(outcomes_no_trt$te), main = paste("Total QALYs per person"), xlab = "QALYs")
```

Total QALYs per person



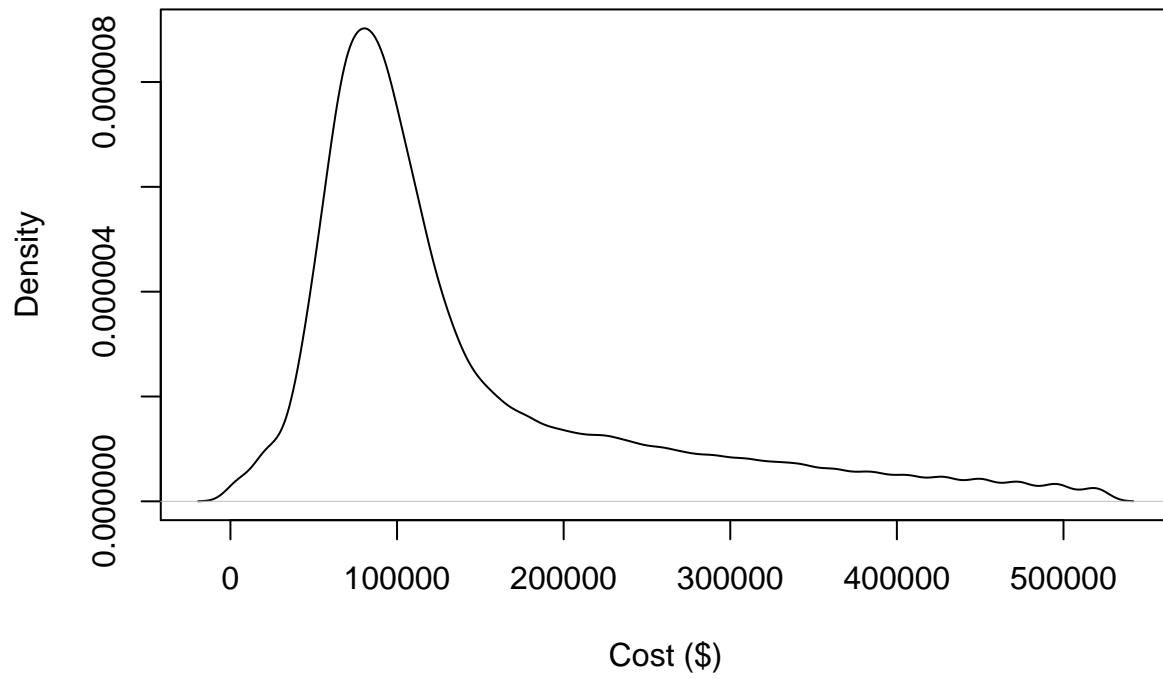
```
plot_m_TR(outcomes_no_trt$m_M) # health state trace
```

Health state trace



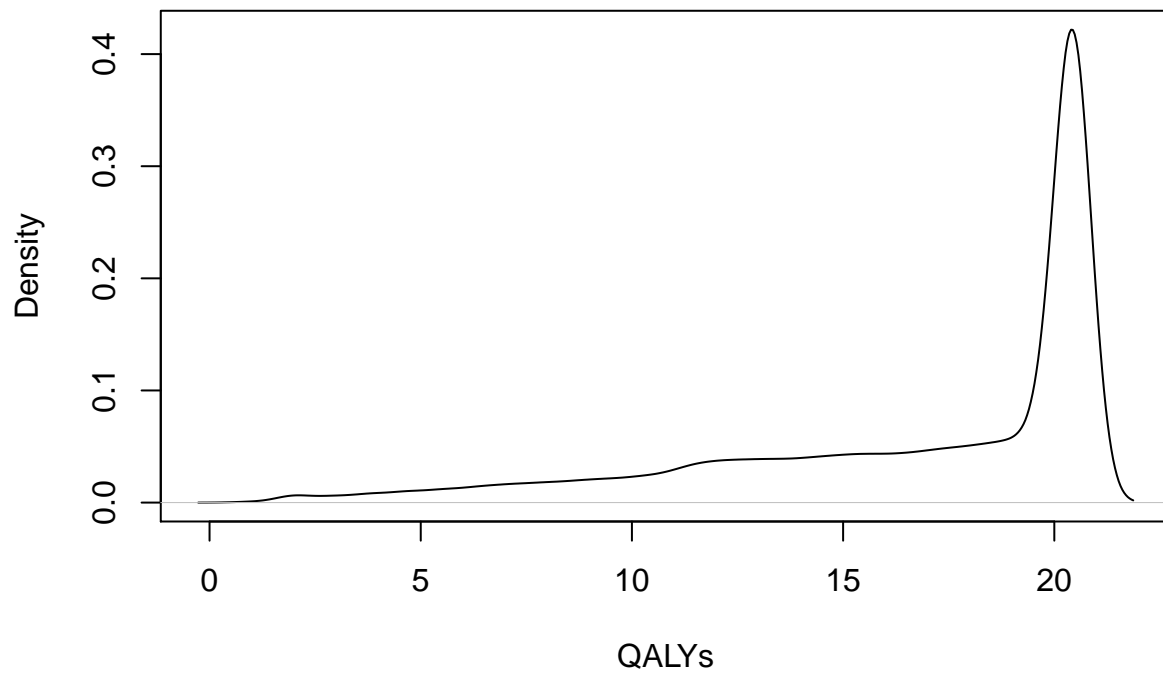
```
# Treatment
plot(density(outcomes_trt$tc), main = paste("Total cost per person"), xlab = "Cost ($)")
```


Total cost per person



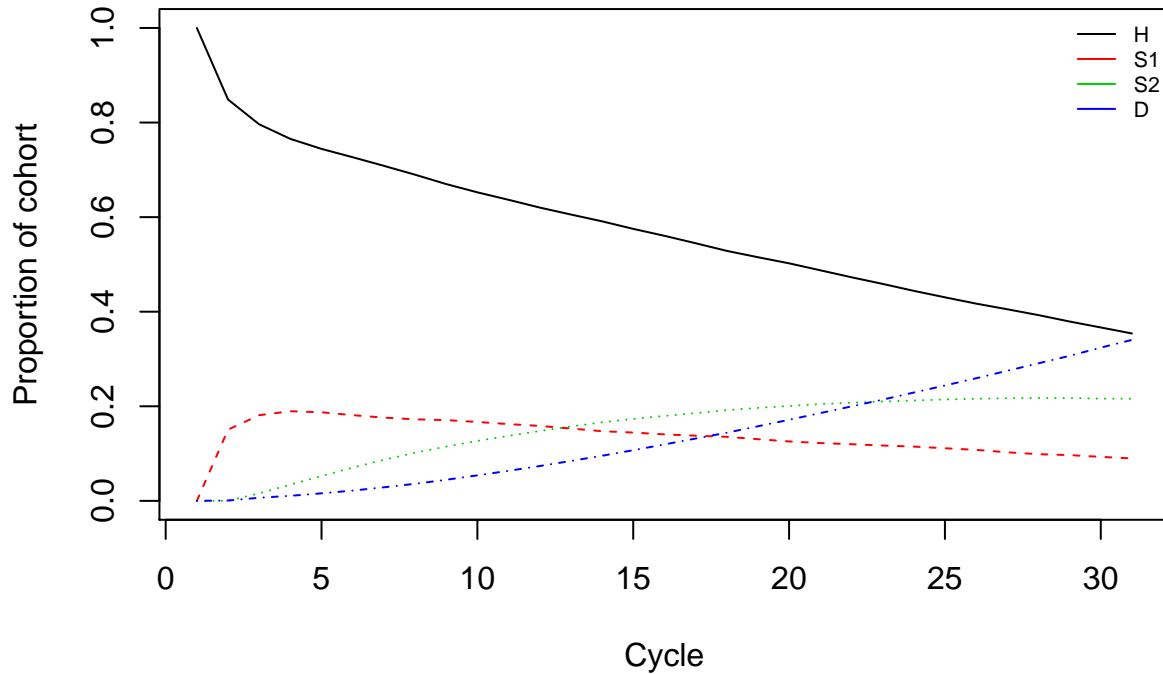
```
plot(density(outcomes_trt$te), main = paste("Total QALYs per person"), xlab = "QALYs")
```

Total QALYs per person



```
plot_m_TR(outcomes_trt$m_M) # health state trace
```

Health state trace



08 Cost Effectiveness Analysis

```
# store the mean costs of each strategy in a new variable C (vector of costs)
v_C <- c(outcomes_no_trt$tc_hat, outcomes_trt$tc_hat)
# store the mean QALYs of each strategy in a new variable E (vector of effects)
v_E <- c(outcomes_no_trt$te_hat, outcomes_trt$te_hat)

# use dampack to calculate the ICER
calculate_icers(cost      = v_C,
               effect     = v_E,
               strategies = v_names_str)
```

```
##      Strategy      Cost      Effect Inc_Cost Inc_Effect      ICER Status
## 1 no treatment  78123.37  16.24541      NA      NA      NA      ND
## 2 treatment  145589.23  16.82525  67465.86  0.5798416 116352.2      ND
```