

# Simple 3-state microsimulation model

Includes age and sex specific probability of dying when healthy

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

## 02 Load functions

```
# No functions needed
```

## 03 Input model parameters

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

# Model structure
v_n  <- c("healthy", "sick", "dead")      # vector with state names
n_t  <- 60                                # number of cycles
n_i  <- 10000                              # number of individuals
d_e <- d_c <- 0.03                         # equal discount of costs and QALYs by 3%

#### Deterministic analysis ####

# Transition probabilities
p_HS      <- 0.05      # probability healthy -> sick
p_HD_female <- 0.0382   # probability health -> dead when female
p_HD_male  <- 0.0463   # probability health -> dead when male
p_SD      <- 0.1       # probability sick -> dead

# Costs inputs
c_H <- 1500      # cost of one cycle in healthy state
c_S <- 5000      # cost of one cycle in sick state
c_D <- 0

# utility inputs
```

```

u_H <- 1          # utility when healthy
u_S <- 0.85       # utility when sick
u_D <- 0          # utility when dead

n_states <- length(v_n)          # number of states

# calculate discount weights for costs for each cycle based on discount rate d_c
v_dwc <- 1 / (1 + d_e) ^ (0:n_t)
# calculate discount weights for effectiveness for each cycle based on discount rate d_e
v_dwe <- 1 / (1 + d_c) ^ (0:n_t)

m_p_HD <- data.frame(Sex = c("Female", "Male"), p_HD = c(p_HD_female, p_HD_male))

```

## 04 Sample individual level characteristics

### 04.1 Static characteristics

```

# randomly sample the sex of an individual (50% female)
v_sex <- sample(x = c("Female", "Male"), prob = c(0.5, 0.5), size = n_i, replace = TRUE)
df_X <- data.frame(ID = 1:n_i, Sex = v_sex)

```

### 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("healthy", times = n_i)

```

## 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) {
  # Arguments:
  # M_t: health state occupied at cycle t (character variable)
  # df_X: data frame with individual characteristics data
  # 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, m_p_HD, by = c("Sex"))
p_HD      <- p_HD_all[M_t == "healthy", "p_HD"]

# update m_p_t with the appropriate probabilities
# transition probabilities when healthy
m_p_t[, M_t == "healthy"] <- rbind(1 - p_HD - p_HS, p_HS, p_HD)
# transition probabilities when sick
m_p_t[, M_t == "sick"]    <- rbind(0, 1 - p_SD, p_SD)
# transition probabilities when dead
m_p_t[, M_t == "dead"]    <- rbind(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) {
  # M_t: current health state
  c_t <- c()
  c_t[M_t == "dead"]    <- c_D      # costs at dead state
  c_t[M_t == "healthy"] <- c_H      # costs accrued by being healthy this cycle
  c_t[M_t == "sick"]    <- c_S      # costs accrued by being sick this cycle

  return(c_t) # return costs accrued this cycle
}

```

## 05.3 Health outcome function

The Effs function to update the utilities at every cycle.

```

Effs <- function (M_t) {
  # M_t: current health state
  q_t <- c()
  q_t[M_t == "dead"]    <- u_D      # QALYs at dead state
  q_t[M_t == "healthy"] <- u_H      # QALYs accrued by being healthy this cycle
  q_t[M_t == "sick"]    <- u_S      # QALYs accrued by being sick this cycle

  return(q_t) # return the QALYs accrued this cycle
}

```

## 06 Run Microsimulation

```

MicroSim <- function(n_i, df_X, seed = 1) {
  # Arguments:
  # n_i:      number of individuals
  # df_X:     data frame with individual data

```

```

# seed:      defaults is 1
# Returns
# a list with information about the individuals transitions, associated costs and
# effects and total costs and rewards

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

m_M[, 1] <- v_M_init           # initial health state
m_C[, 1] <- Costs(m_M[, 1])    # costs accrued during cycle 0
m_E[, 1] <- Effe(m_M[, 1])     # QALYs accrued during cycle 0

# 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)
  # sample the current health state and store that state in matrix m_M
  m_M[, t + 1] <- samplev(m_P)
  m_C[, t + 1] <- Costs(m_M[, t + 1]) # calculate costs
  m_E[, t + 1] <- Effe(m_M[, t + 1]) # calculate QALYs

  # 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

```

```

# Run the simulation model
outcomes <- MicroSim(n_i = n_i, df_X = df_X, seed = 1)

# Show results
results <- data.frame("Total Cost" = outcomes$tc_hat, "Total QALYs" = outcomes$te_hat)
results

```

## 07 Visualize results

```

options(scipen = 999)
plot(density(outcomes$tc), main = paste("Total cost per person"), xlab = "Cost ($)")
plot(density(outcomes$te), main = paste("Total QALYs per person"), xlab = "QALYs")
plot_m_TR(outcomes$m_M) # health state trace

```