

Microsimulation Sick-Sicker model with time dependency

Includes individual characteristics: age, age dependent mortality, individual treatment effect modifier, state-residency for the sick (S1) state, increasing change of death in the first 6 year of sickness

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 EA, et al. A Multidimensional Array Representation of State-Transition Model Dynamics. *Med Decis Mak*. <https://doi.org/10.1177/0272989X19893973>

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)
# load (install if required) packages from CRAN
p_load("here", "devtools", "dplyr", "scales", "ellipse", "ggplot2", "lazyeval", "igraph", "truncnorm",
# load (install if required) packages from GitHub
# install_github("DARTH-git/darthtools", force = TRUE) # Uncomment if there is a newer version
p_load_gh("DARTH-git/darthtools")
```

02 Load functions

```
# No functions needed
```

03 Input model parameters

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

# Strategy names
v_names_str <- c("no treatment", "treatment") # strategy names
n_str      <- length(v_names_str)             # number of strategies

# Model structure
v_names_states <- c("H", "S1", "S2", "D") # the model states names
n_states <- length(v_names_states)        # the number of health states

# Model parameters
n_t      <- 30                # time horizon, 30 cycles
n_i      <- 100000            # number of simulated individuals
d_r      <- 0.03              # discount rate of 3% per cycle
v_dwe    <- v_dwc <- 1 / ((1 + d_r) ^ (0:n_t)) # discount weight

# Event probabilities (per cycle)
# Annual transition probabilities
# (all non-probabilities are conditional on survival)
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
# NOTE: if you don't have a data folder but the files in the same folder as your markdown you need
```

```

# read.csv("mortProb_age.csv") and
# read.csv("MyPopulation-AgeDistribution.csv")
p_mort    <- read.csv("mortProb_age.csv")
# load age distribution
dist_Age  <- read.csv("MyPopulation-AgeDistribution.csv")

# probability to die in S1 by cycle (is increasing)
p_S1D     <- c(0.0149, 0.018, 0.021, 0.026, 0.031, rep(0.037, n_t - 5))
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 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
# your turn

```

04.2 Dynamic characteristics

```

# Specify the initial health state of the individuals
# everyone begins in the healthy state (in this example)

# your turn

```

04.3 Create a dataframe with the individual characteristics

```

# your turn
# HINT: df_X <- # data.frame(# ADD ALL CHARACTERISTICS)

```

05 Define Simulation Functions

HINT: There is no need to make two functions for each strategy. We recommend to make one `Probs()`, one `Costs()` and one `Effs()` function and have a function argument `Trt` which you “switch” on and off (i.e. TRUE/FALSE - or 0/1) for the strategy of interest.

05.1 Probability function

The function that updates the transition probabilities. Please make sure you incorporate the time dependency

```
# your turn  
# HINT: In this function you have to incorporate age specific mortality  
# and incorporate the change in probability of the years spend in the sick state
```

05.2 Cost function

The `Costs` function estimates the costs at every cycle.

```
# your turn  
# Make sure you incorporate the cost of the treatment in the treatment strategy for both sick and sickle
```

05.3 Health outcome function

The `Effs` function to update the utilities at every cycle.

```
# your turn  
# HINT: Make sure you incorporate the treatment effect modifier  
# HINT: Remember treatment improves the quality of life for those in the Sick (S1) state but not for th
```

05.4 The Microsimulation function

You need to develop the main function `MicroSim()` that runs the microsimulation.

```
# your turn  
# HINT: Build your own `MicroSim` function here that calls the Probs(), Effs() and Costs() functions a
```

06 Run Microsimulation

You have to run the `Microsim()` function twice. Once for the treatment strategy and once of the no-treatment strategy, as follows:

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

07 Visualize results

```
# your turn  
# HINT: use functions from the example code
```

08 Cost Effectiveness Analysis

```
# store the mean costs of each strategy in a new variable v_C (vector of costs)  
# remove # below  
# v_C <- c(outcomes_no_trt$tc_hat, outcomes_trt$tc_hat)  
  
# store the mean QALYs of each strategy in a new variable v_E (vector of effects)  
# remove # below  
# v_E <- c(outcomes_no_trt$te_hat, outcomes_trt$te_hat)  
  
# remove # below  
# use dampack to calculate the ICER  
# calculate_icers(cost      = v_C,  
#                  effect   = v_E,  
#                  strategies = v_names_str)
```