

Markov Sick-Sicker 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>

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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", "truncnorm",
       "reshape2", "knitr")
# 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

```
# no functions needed
```

03 Input model parameters

```
# Strategy names
v_names_str <- c("No Treatment", "Treatment")

# Number of strategies
n_str <- length(v_names_str)

# Markov model parameters
age      <- 25                # age at baseline
max_age  <- 55                # maximum age of follow up
n_t      <- max_age - age     # time horizon, number of cycles
v_n      <- c("H", "S1", "S2", "D") # the 4 states of the model: Healthy (H), Sick (S1),
                                   # Sicker (S2), Dead (D)
n_states <- length(v_n)      # number of health states

# Transition probabilities (per cycle)
p_HD      <- 0.005            # probability to die when healthy
p_HS1     <- 0.15             # probability to become sick when healthy
p_S1H     <- 0.5              # probability to become healthy when sick
p_S1S2    <- 0.105            # probability to become sicker when sick
hr_S1     <- 3                # hazard ratio of death in sick vs healthy
hr_S2     <- 10               # hazard ratio of death in sicker vs healthy
r_HD      # <- your turn      # rate of death in healthy
r_S1D     # <- your turn      # rate of death in sick
r_S2D     # <- your turn      # rate of death in sicker
p_S1D     # <- your turn      # probability to die in sick
p_S2D     # <- your turn      # probability to die in sicker

# Cost and utility inputs
c_H       <- 2000             # cost of remaining one cycle in the healthy state
c_S1      <- 4000             # cost of remaining one cycle in the sick state
c_S2      <- 15000            # cost of remaining one cycle in the sicker state
c_trt     <- 12000            # cost of treatment(per cycle)
```

```

c_D      <- 0                # cost of being in the death state
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 being treated

# Discounting factor
d_r      <- 0.03              # equal discount of costs and QALYs by 3%
# calculate discount weights for costs for each cycle based on discount rate d_c
v_dwc    <- 1 / (1 + d_r) ^ (0:n_t)
# calculate discount weights for effectiveness for each cycle based on discount rate d_e
v_dwe    <- 1 / (1 + d_r) ^ (0:n_t)

```

04 Define and initialize matrices and vectors

04.1 Cohort trace

```

# create the markov trace matrix M capturing the proportion of the cohort in each state
# at each cycle
m_M_notrt <- m_M_trt <- matrix(NA,
                                nrow      = n_t + 1, ncol = n_states,
                                dimnames = list(paste("cycle", 0:n_t, sep = " "), v_n))

head(m_M_notrt) # show first 6 rows of the matrix

# The cohort starts as healthy
m_M_notrt[1, ] <- m_M_trt[1, ] <- c(1, 0, 0, 0) # initiate first cycle of cohort trace

```

04.2 Transition probability matrix

```

# create the transition probability matrix for NO treatment
m_P_notrt <- matrix(0,
                    nrow = n_states,
                    ncol = n_states,
                    dimnames = list(v_n, v_n)) # name the columns and rows of the matrix

m_P_notrt

```

Fill in the transition probability matrix:

```

# from Healthy

# from Sick

# from Sicker

# from Dead

# create transition probability matrix for treatment same as no treatment
m_P_trt <- m_P_notrt

```

05 Run Markov model

your turn

06 Compute and Plot Epidemiological Outcomes

06.1 Cohort trace

your turn

06.2 Overall Survival (OS)

your turn

06.2.1 Life Expectancy (LE)

your turn

06.3 Disease prevalence

your turn

06.4 ratio of sick(S1) vs sicker(S2)

your turn

07 Compute Cost-Effectiveness Outcomes

07.1 Mean Costs and QALYs for Treatment and NO Treatment

your turn

07.2 Discounted Mean Costs and QALYs

your turn

07.3 Compute ICERs of the Markov model

your turn

07.4 Plot frontier of the Markov model

your turn