

Simple 3-state Markov model in R

with dependency for time-since model start AND with state-residency dependency

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>
- Alarid-Escudero F, Krijkamp EM, Enns EA, Yang A, Hunink MGM, Pechlivanoglou P, Jalal H. Cohort State-Transition Models in R: A Tutorial. *arXiv:200107824v2*. 2020:1-48. <http://arxiv.org/abs/2001.07824>
- 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("diagram")
# 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

```
# Strategy names
v_names_str <- c("Base Case")

# Number of strategies
n_str <- length(v_names_str)

# Markov model parameters
v_n <- c("Healthy", "Sick", "Dead")      # state names
n_states <- length(v_n)                  # number of states
n_t <- 60                                # number of cycles

# Tunnels
n_tunnel_size <- n_t
# Sick state
v_Sick_tunnels <- paste("Sick_", seq(1, n_tunnel_size), "Yr", sep = "")
# Create variables for time-dependent model
v_n_tunnels <- c("Healthy", v_Sick_tunnels, "Dead") # state names
n_states_tunnels <- length(v_n_tunnels)             # number of states

p_HD <- seq(0.003, 0.01, length.out = n_t) # probability of dying when sick (age-dependent) - this is
p_HS <- 0.05                                # probability of becoming sick when healthy, conditioned on
p_SD <- 0.1                                # probability of dying when sick

# Weibull parameters
l <- 0.08
g <- 1.1
p_SD <- l*g*(1:n_tunnel_size)^(g-1)         # probability of dying when sick (time-in-state dependent)
```

```

# Costs and utilities
c_H <- 400                                # cost of one cycle in healthy state
c_S <- 1000                              # cost of one cycle in sick state
c_D <- 0                                  # cost of one cycle in dead state
u_H <- 0.8                                # utility when healthy
u_S <- 0.5                                # utility when sick
u_D <- 0                                  # utility when dead
d_e <- d_c <- 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_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)

```

04 Define and initialize matrices and vectors

04.1 Cohort trace

```

m_M <- matrix(NA,
              nrow = n_t + 1, # create Markov trace (n_t + 1) because R doesn't understand
                             # Cycle 0)
              ncol = n_states_tunnels,
              dimnames = list(0:n_t, v_n_tunnels))

# The cohort starts as healthy
# initialize first cycle of Markov trace accounting for the tunnels
m_M[1, ] <- c(1, rep(0, n_tunnel_size), 0)

```

04.2 Transition probability array

```

# create the transition probability array
a_P <- array(0,                                # Create 3-D array
             dim = c(n_states_tunnels, n_states_tunnels, n_t),
             dimnames = list(v_n_tunnels, v_n_tunnels, 0:(n_t-1)))

```

Fill in the transition probability array:

```

# from Healthy
a_P["Healthy", "Healthy", ] <- (1 - p_HD) * (1 - p_HS)
a_P["Healthy", "Sick_1Yr", ] <- (1 - p_HD) * p_HS
a_P["Healthy", "Dead", ] <- p_HD

# from Sick
for(i in 1:(n_tunnel_size - 1)){
  a_P[v_Sick_tunnels[i], v_Sick_tunnels[i + 1], ] <- 1 - p_SD[i]
  a_P[v_Sick_tunnels[i], "Dead", ] <- p_SD[i]
}

```

```

a_P[v_Sick_tunnels[n_tunnel_size], v_Sick_tunnels[n_tunnel_size], ] <- 1 - p_SD[n_tunnel_size]
a_P[v_Sick_tunnels[n_tunnel_size], "Dead", ] <- p_SD[n_tunnel_size]

# from Dead
a_P["Dead", "Dead", ] <- 1

```

04.3 Check if transition array and probabilities are valid

```

# Check that transition probabilities are in [0, 1]
check_transition_probability(a_P, verbose = TRUE)
# Check that all rows sum to 1
check_sum_of_transition_array(a_P, n_states = n_states_tunnels, n_cycle = n_t, verbose = TRUE)

```

05 Run Markov model

```

for (t in 1:n_t) {
  m_M[t + 1, ] <- m_M[t, ] %*% a_P[, , t]
}
head(m_M)

```

loop through the number of cycles
estimate the Markov trace for cycle t + 1
using the t-th matrix from the
probability array

Create aggregated trace.

```

m_M_tunnels <- cbind(Healthy = m_M[, "Healthy"],
  Sick = rowSums(m_M[, 2:(n_tunnel_size + 1)]),
  Dead = m_M[, "Dead"])
head(m_M_tunnels)

```

show the first rows of the aggregated Markov trace

06 Compute and Plot Epidemiological Outcomes

06.1 Cohort trace

```

# create a plot of the data
matplot(m_M_tunnels, type = 'l',
  ylab = "Probability of state occupancy",
  xlab = "Cycle",
  main = "Cohort Trace", lwd = 2)
# add a legend to the graph
legend("right", v_n, col = c("black", "red", "green"), lty = 1:3, bty = "n")

```

06.2 Overall Survival (OS)

```

v_os <- 1 - m_M_tunnels[, "Dead"]      # calculate the overall survival (OS) probability
v_os <- rowSums(m_M_tunnels[, 1:2])    # alternative way of calculating the OS probability

# create a simple plot showing the OS
plot(v_os, type = 'l',
     ylim = c(0, 1),
     ylab = "Survival probability",
     xlab = "Cycle",
     main = "Overall Survival")
# add grid
grid(nx = n_t, ny = 10, col = "lightgray", lty = "dotted", lwd = par("lwd"), equilog = TRUE)

```

06.2.1 Life Expectancy (LE)

```

v_le <- sum(v_os) # summing probability of OS over time (i.e. life expectancy)

```

06.3 Disease prevalence

```

v_prev <- m_M_tunnels[, "Sick"]/v_os
plot(v_prev,
     ylim = c(0, 1),
     ylab = "Prevalence",
     xlab = "Cycle",
     main = "Disease prevalence")

```

07 Compute Cost-Effectiveness Outcomes

07.1 Mean Costs and QALYs

```

# per cycle
# calculate expected costs by multiplying m_M with the cost vector for the different
# health states
v_tc <- m_M_tunnels %*% c(c_H, c_S, c_D)
# calculate expected QALYs by multiplying m_M with the utilities for the different
# health states
v_tu <- m_M_tunnels %*% c(u_H, u_S, u_D)

```

07.2 Discounted Mean Costs and QALYs

```

# Discount costs by multiplying the cost vector with discount weights (v_dw)
v_tc_d <- t(v_tc) %*% v_dw
# Discount QALYs by multiplying the QALYs vector with discount weights (v_dw)
v_te_d <- t(v_tu) %*% v_dwe

```

07.3 Store Results

```
df_ce <- data.frame("Total Discounted Cost" = v_tc_d,  
                    "Life Expectancy"      = v_le,  
                    "Total Discounted QALYs" = v_te_d,  
                    check.names = F)  
df_ce
```