

SA: Simple 3-state Markov model in R

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 Feb;40(2):242-248. <https://journals.sagepub.com/doi/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("dplyr", "devtools", "scales", "ellipse", "ggplot2", "lazyeval", "igraph", "ggraph", "reshape2")
# 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

```
# all functions are in the darthtools package
```

03 Input model parameters

```
# Strategy names
v_names_str <- c("Standard of Care", "Treatment")

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

v_init <- c("Healthy" = 1,
            "Sick"    = 0,
            "Dead"    = 0)          # initial cohort distribution (everyone allocated to the
                                   # "healthy" state)

# Transition probabilities
p_HD <- 0.02                       # probability of dying when healthy
p_HS <- 0.05                       # probability of becoming sick when healthy, under standard of care
p_HS_trt <- 0.03                   # probability of becoming sick when healthy, under treatment
p_SD <- 0.1                        # probability of dying when sick

# 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
c_trt <- 800                       # cost of treatment (per cycle)
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          # discount rate per cycle equal discount of costs and QALYs by 3%

n_str     <- length(v_names_str)  # Number of strategies
n_states  <- length(v_n)          # number of states

# Discount weights for costs and effects
v_dwc     <- 1 / (1 + d_c) ^ (0:n_t)
v_dwe     <- 1 / (1 + d_e) ^ (0:n_t)

```

Draw the state-transition cohort model

```

m_P_diag <- matrix(0, nrow = n_states, ncol = n_states, dimnames = list(v_n, v_n))
m_P_diag["Healthy", "Sick" ]      = ""
m_P_diag["Healthy", "Dead" ]      = ""
m_P_diag["Healthy", "Healthy" ]   = ""
m_P_diag["Sick" , "Dead" ]        = ""
m_P_diag["Sick" , "Sick" ]        = ""
m_P_diag["Dead" , "Dead" ]        = ""
layout.fig <- c(2, 1)
plotmat(t(m_P_diag), t(layout.fig), self.cex = 0.5, curve = 0, arr.pos = 0.8,
        latex = T, arr.type = "curved", relsize = 0.85, box.prop = 0.8,
        cex = 0.8, box.cex = 0.7, lwd = 1)

```

04 Define and initialize matrices and vectors

04.1 Cohort trace

```

# create the cohort trace
m_M_SoC <- m_M_trt <- matrix(NA,
                             nrow = n_t + 1, # create Markov trace (n_t + 1 because R doesn't
                                                # understand Cycle 0)
                             ncol = n_states,
                             dimnames = list(0:n_t, v_n))

m_M_SoC[1, ] <- m_M_trt[1, ] <- v_init      # initialize first cycle of Markov trace

```

04.2 Transition probability matrix

```

# create the transition probability matrices
m_P_SoC <- m_P_trt <- matrix(0,
                             nrow = n_states, ncol = n_states,
                             dimnames = list(v_n, v_n)) # name the columns and rows of the matrix

# print the probability matrices
m_P_SoC # for standard of care
m_P_trt # treatment

```

Fill in the transition probability matrix:

```
# For Standard of Care
# from Healthy
m_P_SoC["Healthy", "Healthy"] <- (1 - p_HD) * (1 - p_HS)
m_P_SoC["Healthy", "Sick"]    <- (1 - p_HD) * p_HS
m_P_SoC["Healthy", "Dead"]    <- p_HD

# from Sick
m_P_SoC["Sick", "Sick"] <- 1 - p_SD
m_P_SoC["Sick", "Dead"] <- p_SD

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

# Under treatment
m_P_trt <- m_P_SoC # Assign the matrix for standard of care to the transition probability matrix for t
# replace values that are different under treatment
m_P_trt["Healthy", "Healthy"] <- (1 - p_HD) * (1 - p_HS_trt)
m_P_trt["Healthy", "Sick"]    <- (1 - p_HD) * p_HS_trt
```

04.3 Check if transition probability structure and probabilities are valid

```
# Check that transition probabilities are in [0, 1]
check_transition_probability(m_P_SoC, verbose = TRUE)
check_transition_probability(m_P_trt, verbose = TRUE)
# Check that all rows sum to 1
check_sum_of_transition_array(m_P_SoC, n_states = n_states, n_cycles = n_t, verbose = TRUE)
check_sum_of_transition_array(m_P_trt, n_states = n_states, n_cycles = n_t, verbose = TRUE)
```

05 Run Markov model

```
for (t in 1:n_t){ # loop through the number of cycles
  m_M_SoC[t + 1, ] <- m_M_SoC[t, ] %*% m_P_SoC # estimate the state vector for the next cycle (t + 1)
  m_M_trt[t + 1, ] <- m_M_trt[t, ] %*% m_P_trt # for treatment
}
```

06 Compute and Plot Epidemiological Outcomes

06.1 Cohort trace

Standard of Care:

```
matplot(m_M_SoC, type = 'l',
        ylab = "Probability of state occupancy",
        xlab = "Cycle",
        main = "Cohort Trace - standard of care", lwd = 3) # create a plot of the data
```

```

legend("right", v_n, col = c("black", "red", "green"),
      lty = 1:3, bty = "n")          # add a legend to the graph

abline(v = which.max(m_M_SoC[, "Sick"]), col = "gray")      # plot a vertical line that helps identify

```

Treatment:

```

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

abline(v = which.max(m_M_trt[, "Sick"]), col = "gray")      # plot a vertical line that helps identify

```

06.2 Overall Survival (OS)

Standard of Care:

```

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

plot(v_os_SoC, type = 'l',
     ylim = c(0, 1),
     ylab = "Survival probability",
     xlab = "Cycle",
     main = "Overall Survival - Standard of Care")          # create a simple plot showing the OS

# add grid
grid(nx = n_t, ny = 10, col = "lightgray", lty = "dotted", lwd = par("lwd"),
     equilog = TRUE)

```

Treatment:

```

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

plot(v_os_trt, type = 'l',
     ylim = c(0, 1),
     ylab = "Survival probability",
     xlab = "Cycle",
     main = "Overall Survival - Treatment")                  # create a simple plot showing the OS

# 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_SoC <- sum(v_os_SoC) # summing probability of OS over time (i.e. life expectancy)
v_le_trt <- sum(v_os_trt) # summing probability of OS over time (i.e. life expectancy), treatment
```

06.3 Disease prevalence

Standard of Care:

```
v_prev_SoC <- m_M_SoC[, "Sick"]/v_os_SoC
plot(v_prev_SoC,
     ylim = c(0, 1),
     ylab = "Prevalence",
     xlab = "Cycle",
     main = "Disease prevalence - Standard of care")
```

Treatment:

```
v_prev_trt <- m_M_trt[, "Sick"]/v_os_trt
plot(v_prev_trt,
     ylim = c(0, 1),
     ylab = "Prevalence",
     xlab = "Cycle",
     main = "Disease prevalence - Treatment")
```

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_SoC <- m_M_SoC %*% c(c_H, c_S, c_D) # Standard of Care
v_tc_trt <- m_M_trt %*% c(c_H, c_S + c_trt, c_D) # Treatment
# calculate expected QALYs by multiplying m_M with the utilities for the different
# health states
v_tu_SoC <- m_M_SoC %*% c(u_H, u_S, u_D) # Standard of Care
v_tu_trt <- m_M_trt %*% c(u_H, u_S, u_D) # Treatment
```

07.2 Discounted Mean Costs and QALYs

```
# Discount costs by multiplying the cost vector with discount weights
tc_d_SoC <- t(v_tc_SoC) %*% v_dwc # Standard of Care
tc_d_trt <- t(v_tc_trt) %*% v_dwc # Treatment
# Discount QALYs by multiplying the QALYs vector with discount weights
tu_d_SoC <- t(v_tu_SoC) %*% v_dwe # Standard of Care
```

```

tu_d_trt <- t(v_tu_trt) %*% v_dwe # Treatment

# store them into a vector
v_tc_d <- c(tc_d_SoC, tc_d_trt)
v_tu_d <- c(tu_d_SoC, tu_d_trt)

# Dataframe with discounted costs and effectiveness
df_ce <- data.frame(Strategy = v_names_str,
                    Cost      = v_tc_d,
                    Effect    = v_tu_d)

df_ce

```

07.3 Compute ICERs of the Markov model

```

df_cea <- calculate_icers(cost      = df_ce$Cost,
                          effect    = df_ce$Effect,
                          strategies = df_ce$Strategy)

df_cea

```

07.4 Plot frontier of the Markov model

```

plot(df_cea, effect_units = "QALYs", xlim = c(10, 12))

# note: you need to adjust the xlim values to values that are covering the range of effect values in your data

```

08 Deterministic Sensitivity Analysis

08.1 List of input parameters

Create list `l_params_all` with all input probabilities, cost and utilities.

```

l_params_all <- as.list(data.frame(
  p_HD = 0.02, # probability of dying when healthy
  p_HS = 0.05, # probability of becoming sick when healthy, conditioned on not dying
  p_HS_trt = 0.03, # probability of becoming sick when healthy, conditioned on not dying
  p_SD = 0.1, # probability of dying when sick
  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
  c_trt = 800, # cost of treatment (per cycle)
  u_H = 0.8, # utility when healthy
  u_S = 0.5, # utility when sick
  u_D = 0, # utility when dead
  d_e = 0.03, # discount factor for effectiveness
  d_c = 0.03 # discount factor for costs
))

```

```
# store the parameter names into a vector
v_names_params <- names(l_params_all)
```

08.2 Load Sick-Sicker Markov model function

```
source("Functions_markov_3state.R")
# Test if the functions works
calculate_ce_out(l_params_all)

# NOTE: the function calculate_ce_out makes use of the functions decision_model.
```

08.3 One-way sensitivity analysis (OWSA)

```
options(scipen = 999) # disabling scientific notation in R
# dataframe containing all parameters, their base case values, and the min and
# max values of the parameters of interest
df_params_owsa <- data.frame(pars = c("c_trt", "c_S", "u_H"),
                             min = c(300, 500, 0.7), # min parameter values
                             max = c(1200, 2000, 0.9) # max parameter values
                             )

owsa_nmb <- run_owsa_det(params_range = df_params_owsa, # dataframe with parameters for OWSA
                        params_basecase = l_params_all, # list with all parameters
                        nsamp = 100, # number of parameter values
                        FUN = calculate_ce_out, # function to compute outputs
                        outcomes = c("NMB"), # output to do the OWSA on
                        strategies = v_names_str, # names of the strategies
                        n_wtp = 2000) # extra argument to pass to FUN

#Note: the function calculate_ce_out creates the outputs Cost, Effect and NMB. Those can be selected for
# You and also run the function for all 3 outcomes useind c("Cost", "Effect", "NMB"). Each outcome is s
```

08.3.1 Plot OWSA

```
plot(owsa_nmb, txtsize = 10, n_x_ticks = 4,
     facet_scales = "free") +
  theme(legend.position = "bottom")
```

08.3.2 Optimal strategy with OWSA

Only useful if we have more than one strategie to compare.

```
owsa_opt_strat(owsa = owsa_nmb, txtsize = 10)
```


08.3.3 Tornado plot

```
owsa_tornado(owsa = owsa_nmb, txtsize = 11)
```

08.4 Two-way sensitivity analysis (TWSA)

```
# dataframe containing all parameters, their basecase values, and the min and  
# max values of the parameters of interest  
df_params_twsa <- data.frame(pars = c("c_trt", "u_H"),  
                             min = c(300, 0.7), # min parameter values  
                             max = c(1200, 0.9) # max parameter values  
                             )  
  
twsa_nmb <- run_twsa_det(params_range = df_params_twsa, # dataframe with parameters for TWSA  
                       params_basecase = l_params_all, # list with all parameters  
                       nsamp = 40, # number of parameter values  
                       FUN = calculate_ce_out, # function to compute outputs  
                       outcomes = c("NMB"), # output to do the TWSA on  
                       strategies = v_names_str, # names of the strategies  
                       n_wtp = 2000) # extra argument to pass to FUN
```

08.4.1 Plot TWSA

Only useful if we have more than one strategies to compare.

```
plot(twsa_nmb)
```

09 Probabilistic Sensitivity Analysis (PSA)

```
# Function to generate PSA input dataset  
gen_psa <- function(n_sim = 1000, seed = 071818){  
  set.seed(seed) # set a seed to be able to reproduce the same results  
  df_psa <- data.frame(  
    # Transition probabilities (per cycle)  
    # probability to become sick when healthy  
    p_HS = rbeta(n_sim, shape1 = 24, shape2 = 450),  
    p_HS_trt = rbeta(n_sim, shape1 = 9, shape2 = 281), # under treatment  
    # probability of dying when healthy  
    p_HD = rbeta(n_sim, shape1 = 16, shape2 = 767),  
    # probability of dying when sick  
    p_SD = rbeta(n_sim, shape1 = 22.4, shape2 = 201.6),  
  
    # Cost vectors with length n_sim  
    # cost of remaining one cycle in state H  
    c_H = rgamma(n_sim, shape = 16, scale = 25),  
    # cost of remaining one cycle in state S1  
    c_S = rgamma(n_sim, shape = 100, scale = 10),  
  )  
}
```

```

# cost of being in the death state
c_D      = 0,
# cost of treatment (per cycle)
c_trt    = rgamma(n_sim, shape = 64, scale = 12.5),

# Utility vectors with length n_sim
# utility when healthy
u_H      = rbeta(n_sim, shape1 = 50.4, shape2 = 12.6),
# utility when sick
u_S      = rbeta(n_sim, shape1 = 49.5, shape2 = 49.5),
# utility when dead
u_D      = 0
)
return(df_psa)
}
# Try it
gen_psa(10)

# Number of simulations
n_sim <- 1000

# Generate PSA input dataset
df_psa_input <- gen_psa(n_sim = n_sim)
# First six observations
head(df_psa_input)

# Histogram of parameters
ggplot(melt(df_psa_input, variable.name = "Parameter"), aes(x = value)) +
  facet_wrap(~Parameter, scales = "free") +
  geom_histogram(aes(y = ..density..)) +
  theme_bw(base_size = 16) +
  theme(axis.text = element_text(size=8))

# Initialize dataframes with PSA output
# Dataframe of costs
df_c <- as.data.frame(matrix(0,
                             nrow = n_sim,
                             ncol = n_str))
colnames(df_c) <- v_names_str
# Dataframe of effectiveness
df_e <- as.data.frame(matrix(0,
                             nrow = n_sim,
                             ncol = n_str))
colnames(df_e) <- v_names_str

```

09.1 Conduct probabilistic sensitivity analysis

```

# Run Markov model on each parameter set of PSA input dataset
for(i in 1:n_sim){
  l_out_temp <- calculate_ce_out(df_psa_input[i, ])
  df_c[i, ] <- l_out_temp$Cost
  df_e[i, ] <- l_out_temp$Effect
}

```

```

# Display simulation progress
if(i/(n_sim/10) == round(i/(n_sim/10), 0)) { # display progress every 10%
  cat('\r', paste(i/n_sim * 100, "% done", sep = " "))
}
}

```

09.2 Create PSA object for dampack

```

l_psa <- make_psa_obj(cost      = df_c,
                     effectiveness = df_e,
                     parameters  = df_psa_input,
                     strategies  = v_names_str)

```

09.2.1 Save PSA objects

```

save(df_psa_input, df_c, df_e, v_names_str, n_str, l_psa,
     file = "markov_3state_PSA_dataset.RData")

```

Vector with willingness-to-pay (WTP) thresholds.

```

v_wtp <- seq(0, 5000, by = 1000)

```

09.3.1 Cost-Effectiveness Scatter plot

```

plot(l_psa)

```

09.4 Conduct CEA with probabilistic output

```

# Compute expected costs and effects for each strategy from the PSA
df_out_ce_psa <- summary(l_psa)

# Calculate incremental cost-effectiveness ratios (ICERs)
df_cea_psa <- calculate_icers(cost      = df_out_ce_psa$meanCost,
                             effect    = df_out_ce_psa$meanEffect,
                             strategies = df_out_ce_psa$Strategy)

df_cea_psa

# Save CEA table with ICERs
# As .RData
save(df_cea_psa,
     file = "markov_3state_probabilistic_CEA_results.RData")
# As .csv
write.csv(df_cea_psa,
          file = "markov_3state_probabilistic_CEA_results.csv")

```

09.4.1 Plot cost-effectiveness frontier

```
plot(df_cea_psa)
```

09.4.2 Cost-effectiveness acceptability curves (CEACs) and frontier (CEAF)

```
ceac_obj <- ceac(wtp = v_wtp, psa = l_psa)
# Regions of highest probability of cost-effectiveness for each strategy
summary(ceac_obj)
# CEAC & CEAF plot
plot(ceac_obj)
```

09.4.3 Expected Loss Curves (ELCs)

The expected loss is the quantification of the foregone benefits when choosing a suboptimal strategy given current evidence.

```
elc_obj <- calc_exp_loss(wtp = v_wtp, psa = l_psa)
elc_obj
# ELC plot
plot(elc_obj, log_y = FALSE)
```

09.4.4 Expected value of perfect information (EVPI)

```
evpi <- calc_evpi(wtp = v_wtp, psa = l_psa)
# EVPI plot
plot(evpi, effect_units = "QALY")
```