

Simple 3-state Markov model in R

The DARTH workgroup

Developed by the Decision Analysis in R for Technologies in Health (DARTH) workgroup:

Fernando Alarid-Escudero, PhD (1) Eva A. Enns, MS, PhD (2)
M.G. Myriam Hunink, MD, PhD (3,4) Hawre J. Jalal, MD, PhD (5) Eline M. Krijkamp, MSc (3)
Petros Pechlivanoglou, PhD (6,7) Alan Yang, MSc (7)

In collaboration of:

1. Division of Public Administration, Center for Research and Teaching in Economics (CIDE), Aguascalientes, Mexico
2. University of Minnesota School of Public Health, Minneapolis, MN, USA
3. Erasmus MC, Rotterdam, The Netherlands
4. Harvard T.H. Chan School of Public Health, Boston, USA
5. University of Pittsburgh Graduate School of Public Health, Pittsburgh, PA, USA
6. University of Toronto, Toronto ON, Canada
7. The Hospital for Sick Children, Toronto ON, Canada

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>
- 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*. 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

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

03 Input model parameters

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

# 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_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
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)

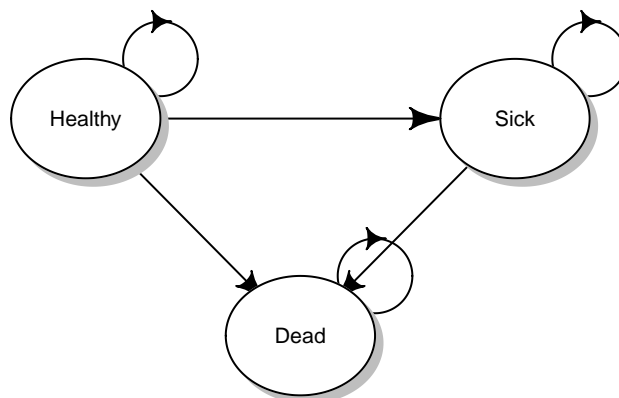
```

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

04.2 Transition probability matrix

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

m_P
```

```
##           Healthy Sick Dead
## Healthy      0      0      0
## Sick         0      0      0
## Dead         0      0      0
```

Fill in the transition probability matrix:

```
# from Healthy
m_P["Healthy", "Healthy"] <- (1 - p_HD) * (1 - p_HS)
m_P["Healthy", "Sick"]    <- (1 - p_HD) * p_HS
m_P["Healthy", "Dead"]    <- p_HD

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

# from Dead
m_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(m_P, verbose = TRUE)
# Check that all rows sum to 1
check_sum_of_transition_array(m_P, n_states = n_states, n_cycles = n_t, verbose = TRUE)
```

05 Run Markov model

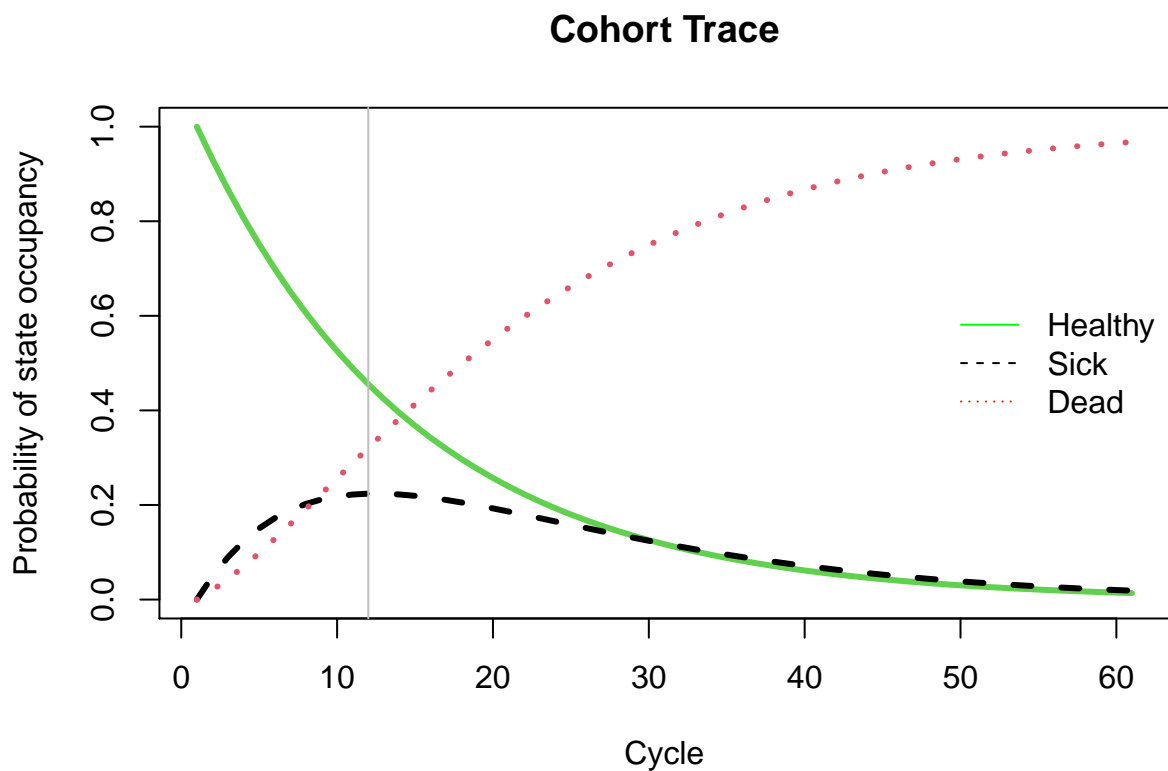
```
for (t in 1:n_t){                                # loop through the number of cycles
  m_M[t + 1, ] <- m_M[t, ] %*% m_P             # estimate the state vector for the next cycle (t + 1)
}
```

06 Compute and Plot Epidemiological Outcomes

06.1 Cohort trace

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

abline(v = which.max(m_M[, "Sick"]), col = "gray") # plot a vertical line that helps identifying at whi
```

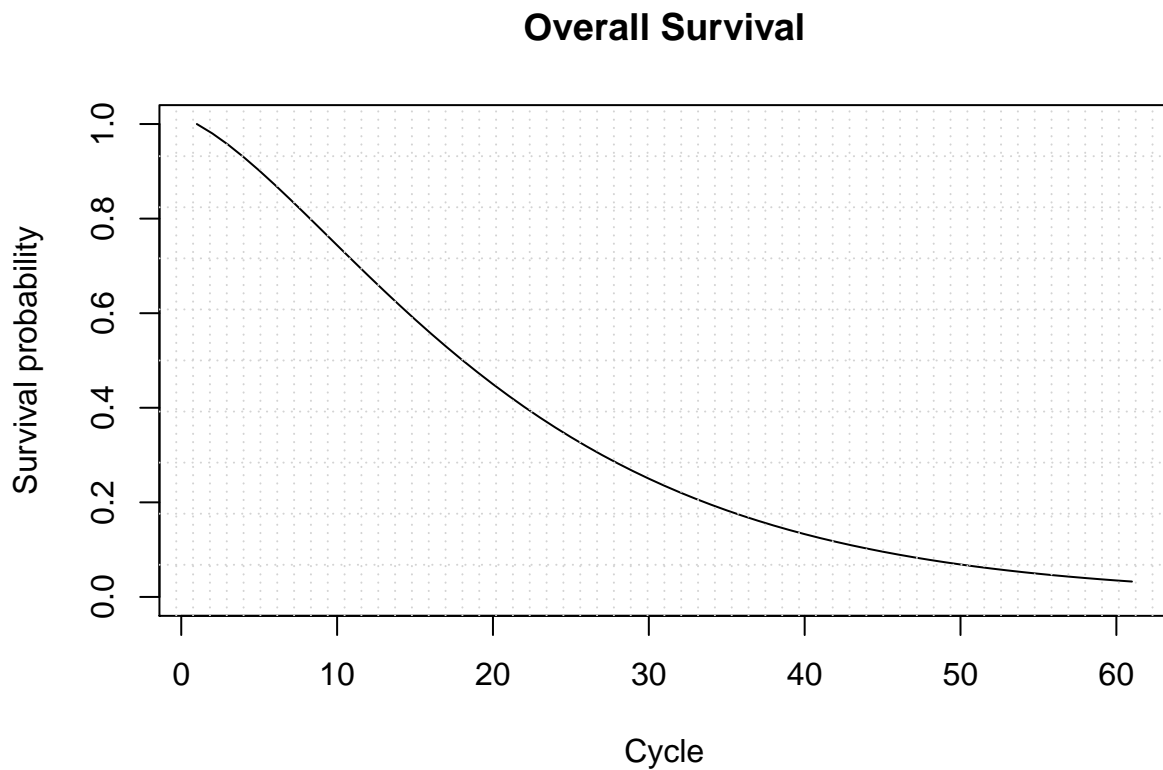


06.2 Overall Survival (OS)

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

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

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

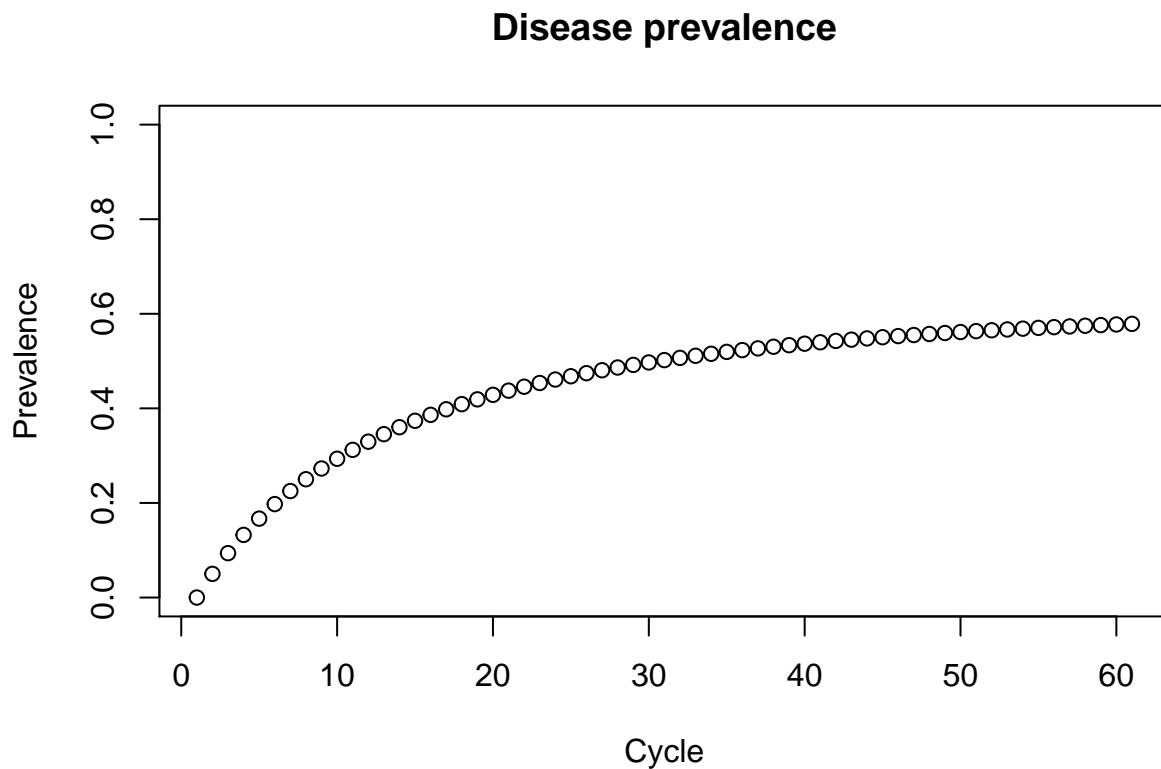


06.2.1 Life Expectancy (LE)

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

06.3 Disease prevalence

```
v_prev <- m_M[, "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 %*% 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 %*% 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_dwc
# 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
```

```
##      Total Discounted Cost Life Expectancy Total Discounted QALYs
## 1                8043.139         21.14245          10.25087
```