

Simple 3-state Markov 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. *Med Decis Making*. Online First <https://doi.org/10.1177/0272989X19893973>

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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

## Loading required package: pacman
# load (install if required) packages from CRAN
p_load("diagram")

## Installing package into '/Users/evaenns/Library/R/3.6/library'
## (as 'lib' is unspecified)
## also installing the dependency 'shape'
##
## The downloaded binary packages are in
## /var/folders/sh/f45kz13d0js3_wxd5x9spk5h0000gn/T//RtmpMr7M7l/downloaded_packages
##
## diagram installed
## Warning: package 'diagram' was built under R version 3.6.2
## Warning: package 'shape' was built under R version 3.6.2
```

02 Load functions

```
# no functions required
```

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

p_HD <- 0.02 # probability to die when healthy
p_HS <- 0.05 # probability to become sick when healthy
p_SD <- 0.1 # probability to die when sick

# Costs and utilities
c_H <- 400 # cost of remaining one cycle healthy
```

```

c_S <- 1000                                # cost of remaining one cycle sick
c_D <- 0                                    # cost of remaining one cycle dead
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)

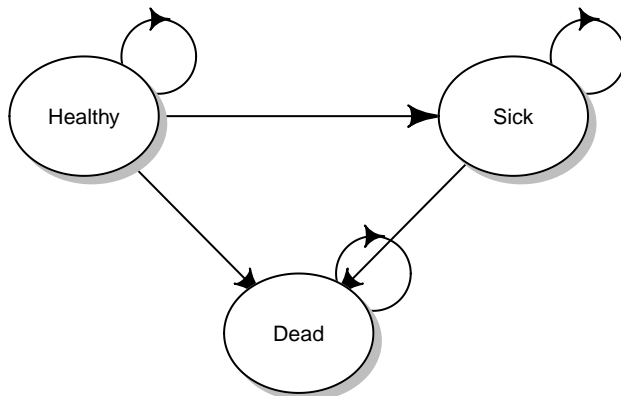
```

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, ] <- c(1, 0, 0)           # 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 - p_HS
m_P["Healthy", "Sick"]    <- 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
```

```
# check rows add up to 1
rowSums(m_P)
```

```
## Healthy    Sick    Dead
##          1      1      1
```

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

```
matplot(m_M, type = 'l',
        ylab = "Probability of state occupancy",
        xlab = "Cycle",
```

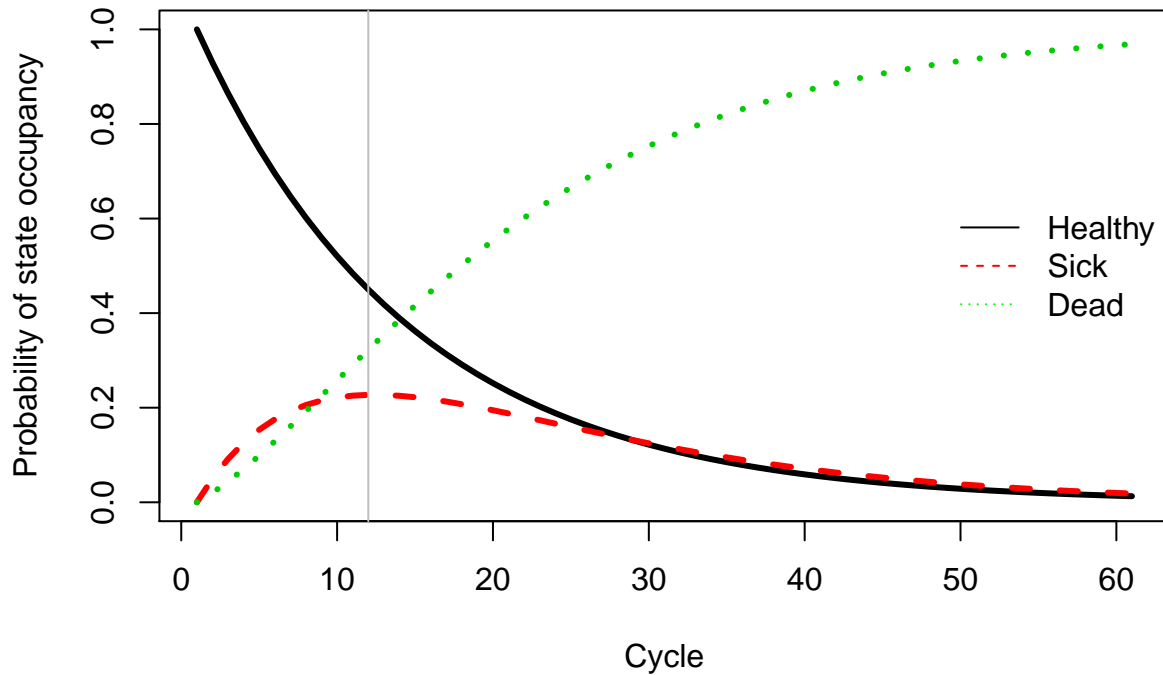
```

    main = "Cohort Trace", lwd = 3)                                # create a plot of the data
legend("right", v_n, col = c("black", "red", "green"),           # add a legend to the graph
      lty = 1:3, bty = "n")

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

```

Cohort Trace



06.2 Overall Survival (OS)

```

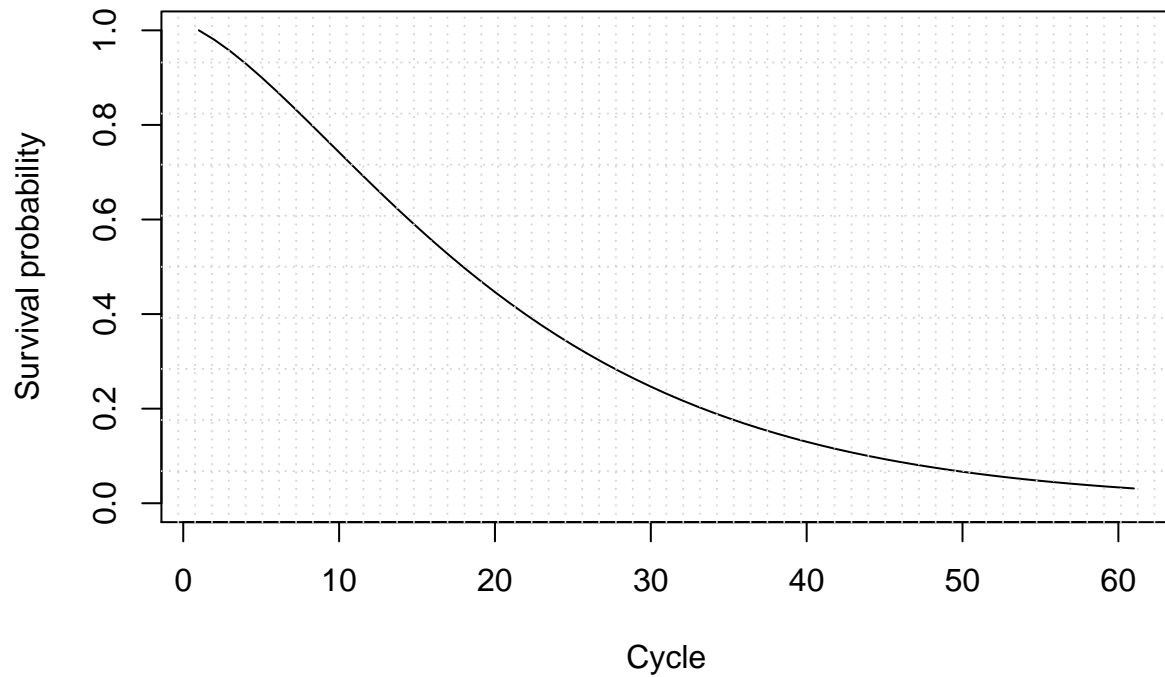
v_os <- 1 - m_M[, "Dead"]                                # calculate the overall survival (OS) probability
v_os <- rowSums(m_M[, 1:2])                             # alternative way of calculating the OS probability

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)

```

Overall Survival

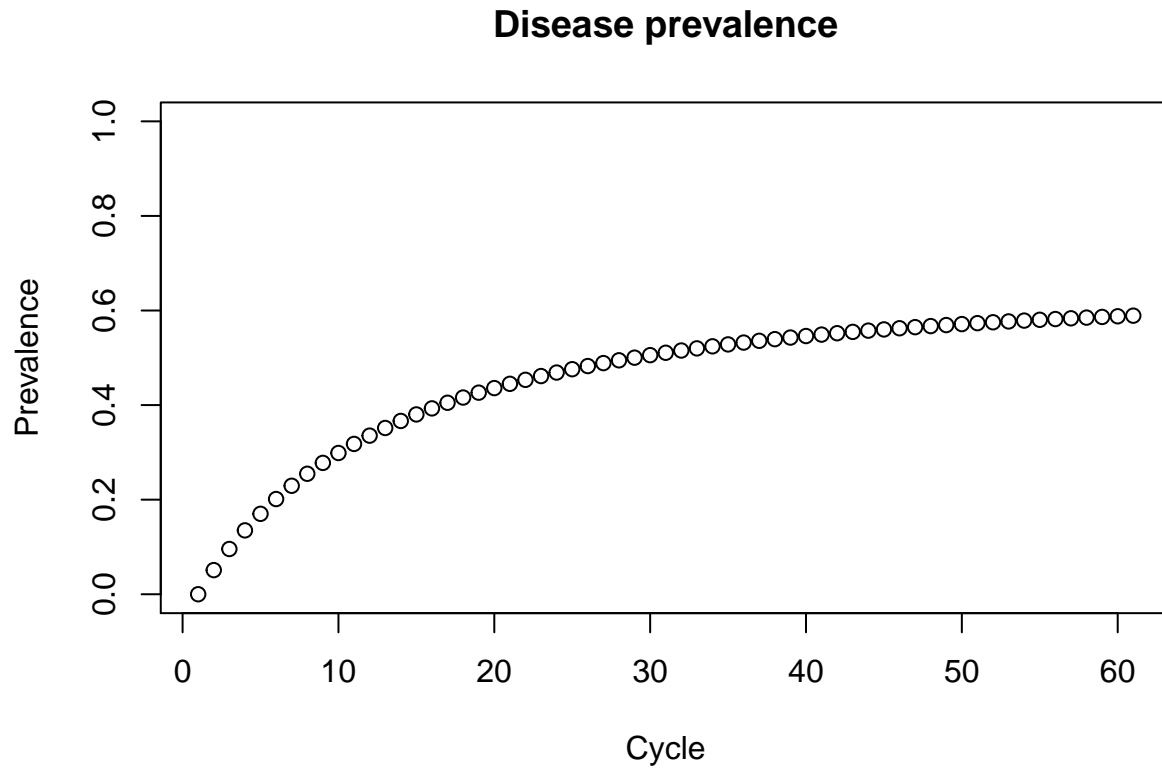


06.2.1 Life Expectancy (LE)

```
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_dw
# Discount QALYs by multiplying the QALYs vector with discount weights (v_dw)
v_te_d <- t(v_tu) %*% v_dwe
```

07.3 Results

```
results <- data.frame( "Total Discounted Cost" = v_tc_d,
                      "Life Expectancy" = v_le,
                      "Total Discounted QALYs" = v_te_d,
```

```
check.names = F)
results
```

##	Total Discounted Cost	Life Expectancy	Total Discounted QALYs
## 1	8043.131	21.00019	10.18939