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

- 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

```r
rm(list = ls())        # clear memory (removes all the variables from the workspace)
```

01 Load packages

```r
# no packages required
```

02 Load functions

```r
# no functions required
```

03 Input model parameters

```r
# 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_s  <- 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)
```

04 Define and initialize matrices and vectors

04.1 Cohort trace

```r
# 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_s,
              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

```r
# create the transition probability matrix
m_P  <- matrix(0,
               nrow = n_s,
               ncol = n_s,
               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:

```r
# 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

```r
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

```r
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"),
       lty = 1:3, bty = "n")                           # add a legend to the graph

abline(v=which.max(m_M[, "Sick"]), col = "gray")
```
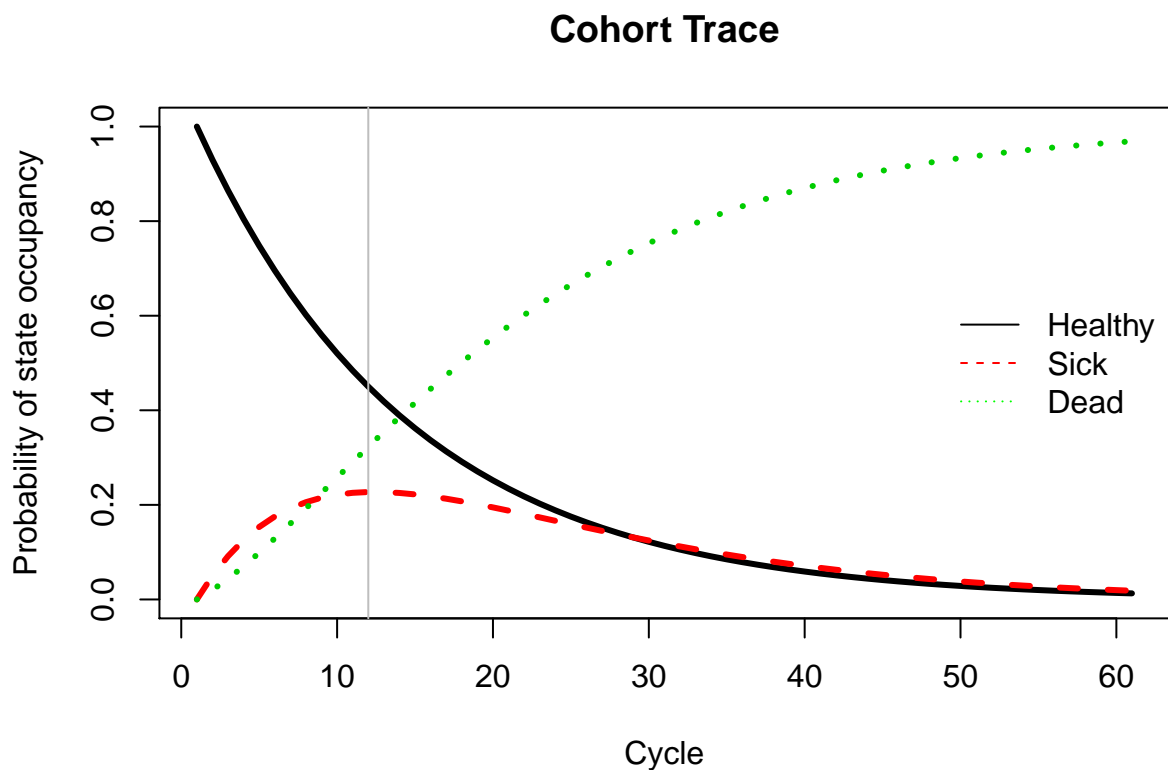

06.2 Overall Survival (OS)
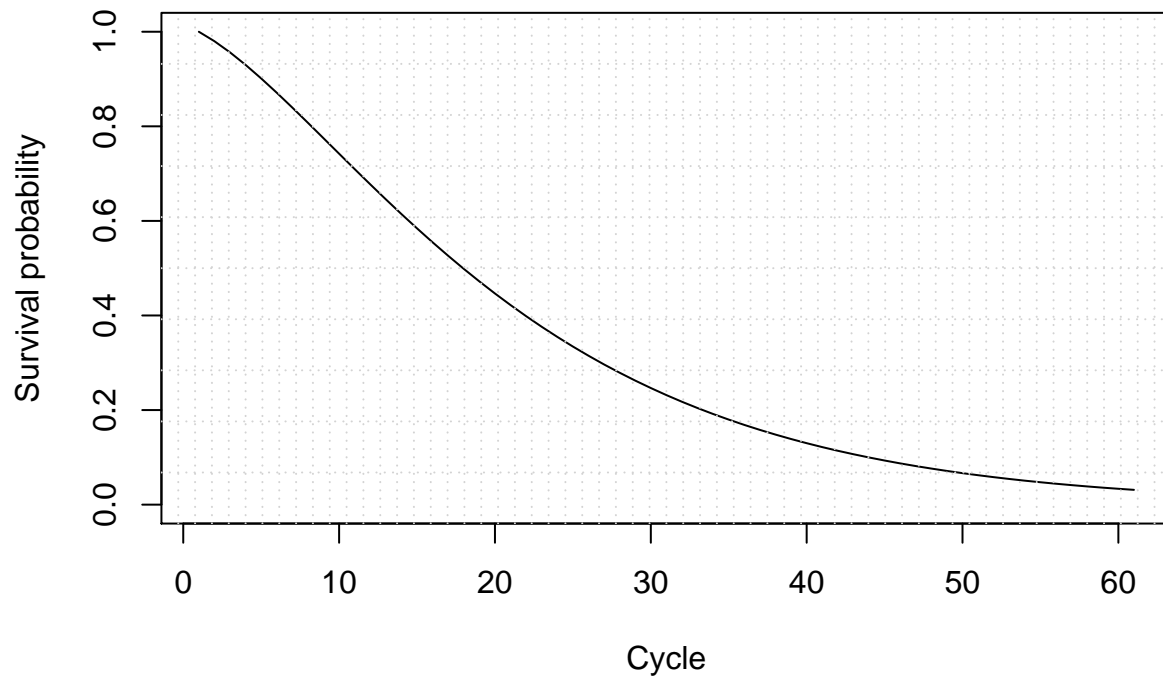
```
v_os <- 1 - m_M[, "Dead"]              # calculate the overall survival (OS) probability
v_os <- rowSums(m_M[, 1:2])            # alternative way of calculating the OS probability

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 probablity of OS over time   (i.e. life expectancy)
```
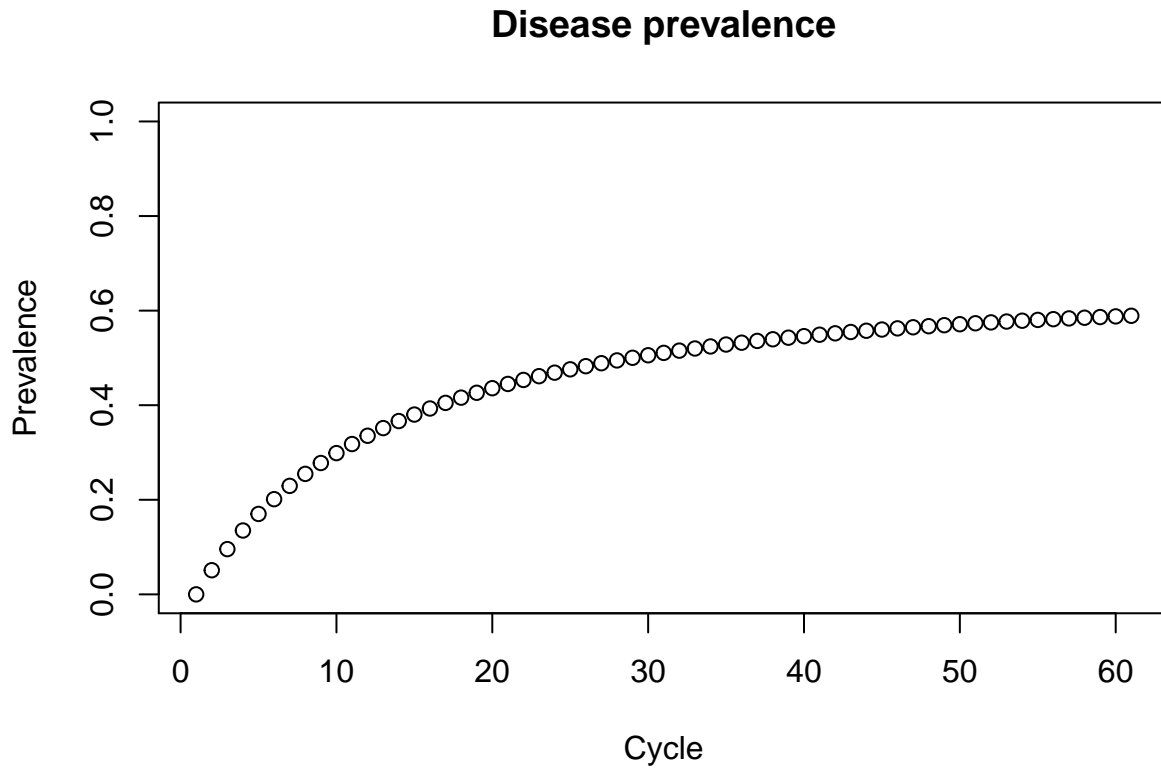
06.3 Disease prevalence

```
v_prev <- m_M[, "Sick"]/v_os
plot(v_prev,
    ylim = c(0, 1),
    ylab = "Prevalence",
```

```
      xlab = "Cycle",
      main = "Disease prevalence")
```

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 Results

```r
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
```