

# Simple 3-state Markov model in R

with age dependency

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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. *Med Decis Making*. 2020 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

```
# no packages required
```

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

```
# 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 array

```
# create the transition probability array
a_P <- array(0, # Create 3-D array
            dim = c(n_states, n_states, n_t),
            dimnames = list(v_n, v_n, 0:(n_t - 1))) # name the dimensions of the array
```

Fill in the transition probability array:

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

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

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

### 04.3 Check if transition array and probabilities are valid

```
verbose <- TRUE
# Check if transition probabilities are valid (i.e., in [0, 1])
m_indices_notvalid <- arrayInd(which(a_P < 0 | a_P > 1),
                               dim(a_P))

try(
  if(dim(m_indices_notvalid)[1] != 0){
    v_rows_notval <- rownames(a_P)[m_indices_notvalid[, 1]]
    v_cols_notval <- colnames(a_P)[m_indices_notvalid[, 2]]
    v_cycles_notval <- dimnames(a_P)[[3]][m_indices_notvalid[, 3]]

    df_notvalid <- data.frame(`Transition probabilities not valid:` =
                             matrix(paste0(paste(v_rows_notval, v_cols_notval,
                                                  sep = "->"),
                                           "; at cycle ",
                                           v_cycles_notval), ncol = 1),
```

```

                                check.names = FALSE)
  if(verbose){
    message("Not valid transition probabilities")
    stop(print(df_notvalid), call. = FALSE)
  }
}
)

# Check if transition probability array is valid
valid <- apply(a_P, 3, function(x) all.equal(sum(rowSums(x)), n_states))
if (!isTRUE(all.equal(as.numeric(sum(valid)), as.numeric(n_t)))) {
  if(verbose){
    stop("This is not a valid transition Matrix")
  }
}
}

```

## 05 Run Markov model

```

for (t in 1:n_t){ # t<-1                # loop through the number of cycles
  m_M[t + 1, ] <- m_M[t, ] %*% a_P[, , t] # estimate the Markov trace for cycle t + 1
                                           # using the t-th matrix from the
                                           # probability array
}
head(m_M) # print the first lines of the matrix

```

```

##      Healthy      Sick      Dead
## 0 1.0000000 0.0000000 0.0000000
## 1 0.9471500 0.0498500 0.0030000
## 2 0.8969864 0.0920748 0.0109388
## 3 0.8493784 0.1275714 0.0230501
## 4 0.8042016 0.1571407 0.0386577
## 5 0.7613370 0.1814970 0.0571660

```

## 06 Compute and Plot Epidemiological Outcomes

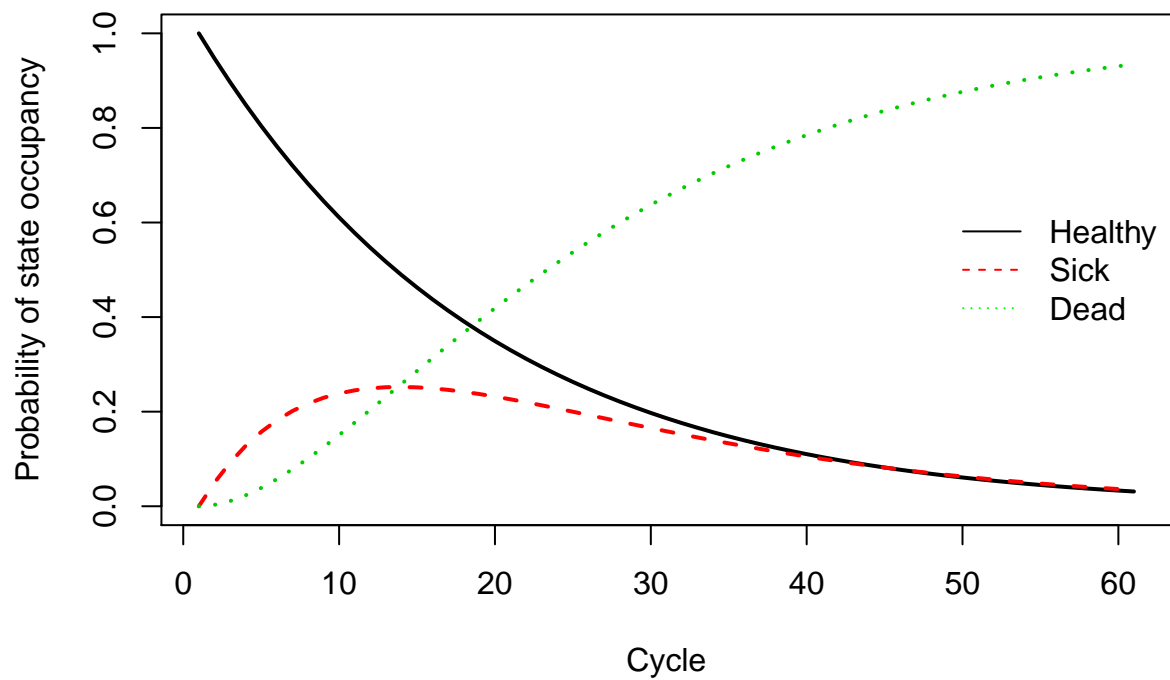
### 06.1 Cohort trace

```

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

```

## Cohort Trace



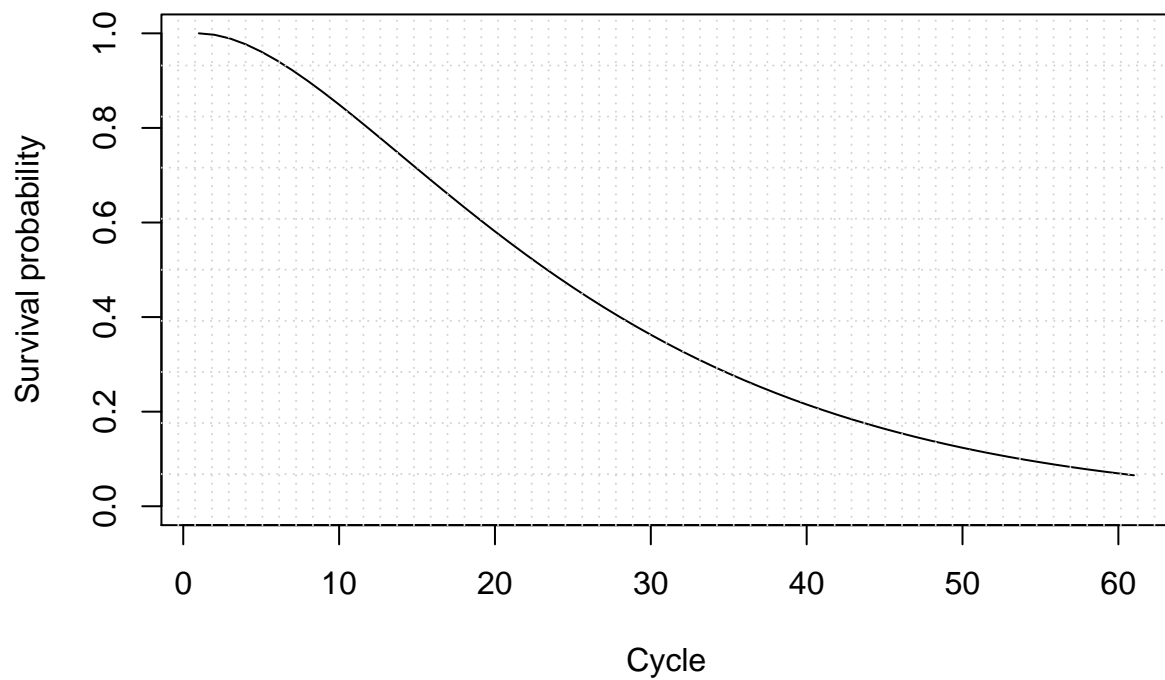
### 06.2 Overall Survival (OS)

```
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

# 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"),
     equilogs = TRUE)
```

## Overall Survival



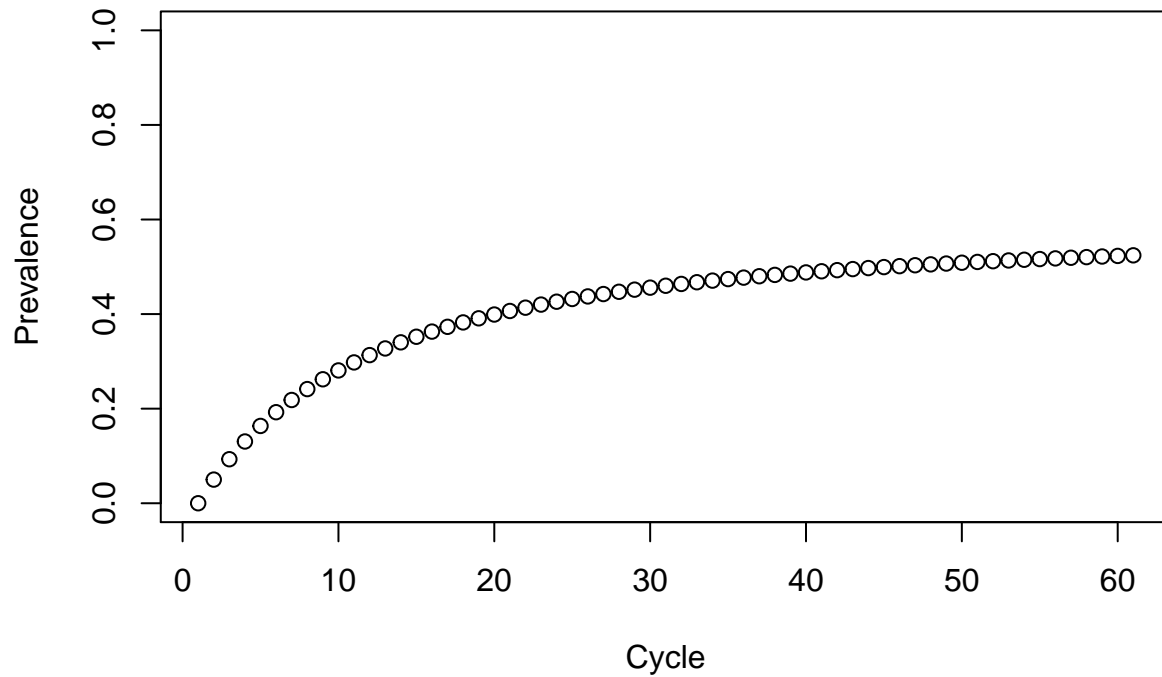
### 06.2.1 Life Expectancy (LE)

```
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")
```

## 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	9504.301	26.32364	12.06788