

R code HSTM

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DISCLAIMER:

THIS CODE IS BASED ON THE TUTORIAL BY THE DARTH WORK GROUP:

Alarid-Escudero F, Krijkamp EM, Enns EA, Yang A, Hunink MGM, Pechlivanoglou P, Jalal H. Cohort state-transition models in R: A tutorial. arXiv:2001.07824, 2020.

LINK: <https://arxiv.org/abs/2001.07824>

Difference equation

```
rm(list = ls())
# Set up
v_names    <- c("PF", "PD", "D")      # state names
n_states   <- length(v_names)         # number of states
n_cycles   <- 30                      # number of cycles

# Define parameters
p_prog     <- 0.1 # probability to progress
p_death_pf <- 0.05 # probability to die from progression-free
p_death_pd <- 0.25 # probability to die from progressed

# Initialise matrix to store cohort simulation
m_hs <- matrix(NA, nrow = n_cycles + 1, ncol = n_states,
              dimnames = list(0:n_cycles, v_names)) # create Markov trace

m_hs[1, ] <- c(1000, 0, 0) # define starting position individuals

# Fill in cohort simulation
for (t in 1:n_cycles) {
  m_hs[t + 1, "PF"] <- m_hs[t, "PF"] * (1 - p_prog - p_death_pf) # calculate the prop of c
  m_hs[t + 1, "PD"] <- m_hs[t, "PF"] * p_prog + m_hs[t, "PD"] * (1 - p_death_pd) # calculate the prop
  m_hs[t + 1, "D"]  <- m_hs[t, "PF"] * p_death_pf + m_hs[t, "PD"] * p_death_pd + m_hs[t, "D"] # calc
}

# Visualise the results
kable(head(m_hs),
      caption = "Start cohort simulation")
```

Table 1: Start cohort simulation

	PF	PD	D
0	1000.0000	0.0000	0.0000
1	850.0000	100.0000	50.0000
2	722.5000	160.0000	117.5000
3	614.1250	192.2500	193.6250
4	522.0063	205.6000	272.3938
5	443.7053	206.4006	349.8941

Matrix multiplication

```
rm(list = ls())
# Set up
v_names    <- c("PF", "PD", "D")      # state names
n_states   <- length(v_names)         # number of states
n_cycles   <- 30                      # number of cycles

# Define parameters
p_prog     <- 0.1 # probability to progress
p_death_pf <- 0.05 # probability to die from progression-free
p_death_pd <- 0.25 # probability to die from progressed

# Define transition matrix
m_p <- matrix(0, nrow = n_states, ncol = n_states,
              dimnames = list(v_names, v_names))

m_p["PF", "PD"] <- p_prog
m_p["PF", "D"]  <- p_death_pf
m_p["PF", "PF"] <- 1 - p_prog - p_death_pf
m_p["PD", "D"]  <- p_death_pd
m_p["PD", "PD"] <- 1 - p_death_pd
m_p["D", "D"]   <- 1
rowSums(m_p)

## PF PD D
## 1 1 1

# Initialise matrix to store cohort simulation
m_hs <- matrix(NA, nrow = n_cycles + 1, ncol = n_states,
              dimnames = list(0:n_cycles, v_names)) # create Markov trace

m_hs[1, ] <- c(1000, 0, 0) # define starting position individuals

# Fill in cohort simulation
for (t in 1:n_cycles) {
  m_hs[t + 1, ] <- m_hs[t, ] %*% m_p
}

# Visualise the results
kable(head(m_hs),
      caption = "Start cohort simulation")
```

Table 2: Start cohort simulation

	PF	PD	D
0	1000.0000	0.0000	0.0000
1	850.0000	100.0000	50.0000
2	722.5000	160.0000	117.5000
3	614.1250	192.2500	193.6250
4	522.0063	205.6000	272.3938
5	443.7053	206.4006	349.8941

Array multiplication

```
rm(list = ls())
# Set up
v_names    <- c("PF", "PD", "D")      # state names
n_states   <- length(v_names)         # number of states
n_cycles   <- 30                      # number of cycles

# Define parameters
p_prog     <- 0.1 # probability to progress
v_r_death_pf <- seq(from = 0.01, to = 0.07, length.out = n_cycles) # death rate from progression-free
v_p_death_pf <- 1 - exp(-v_r_death_pf) # probability to die from progression-free
p_death_pd  <- 0.25 # probability to die from progressed

# Define transition matrix
a_p <- array(0,
             dim = c(n_states, n_states, n_cycles),
             dimnames = list(v_names,
                             v_names,
                             1:n_cycles))

a_p["PF", "PD", ] <- p_prog
a_p["PF", "D", ]   <- v_p_death_pf # use vector instead of "fixed" transition probability
a_p["PF", "PF", ]  <- 1 - p_prog - v_p_death_pf
a_p["PD", "D", ]    <- p_death_pd
a_p["PD", "PD", ]   <- 1 - p_death_pd
a_p["D", "D", ]     <- 1
rowSums(a_p[, , 10])

## PF PD D
## 1 1 1

# Initialise matrix to store cohort simulation
m_hs <- matrix(NA, nrow = n_cycles + 1, ncol = n_states,
              dimnames = list(0:n_cycles, v_names)) # create Markov trace

m_hs[1, ] <- c(1000, 0, 0) # define starting position individuals

# Fill in cohort simulation
for (t in 1:n_cycles) {
  m_hs[t + 1, ] <- m_hs[t, ] %*% a_p[, , t]
} # loop over both the cohort simulation and the different matrices of the array

# Visualise the results
kable(head(m_hs),
      caption = "Start cohort simulation")
```

Table 3: Start cohort simulation

	PF	PD	D
0	1000.0000	0.0000	0.000000
1	890.0498	100.0000	9.950166
2	790.3674	164.0050	45.627585
3	700.2351	202.0405	97.724372
4	618.9545	221.5539	159.491662
5	545.8498	228.0609	226.089317