

# Three-strategy decision tree in R - HVE

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. *Med Decis Making*. 2020 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("dplyr", "devtools", "scales", "ellipse", "ggplot2", "lazyeval", "igraph", "ggraph", "reshape2")
# load (install if required) packages from GitHub
p_load_gh("DARTH-git/darthtools")
```

## 02 Load functions

```
# all functions are in the darthtools package so no need for additional functions
```

## 03 Define parameter input values

```
v_names_str    <- c("No Tx", "Tx All", "Biopsy")  # names of strategies
n_str          <- length(v_names_str)            # number of strategies
wtp            <- 100000                          # willingness to pay threshold

# Probabilities
p_HVE          <- 0.52    # prevalence of HVE
p_HVE_comp     <- 0.71    # complications with untreated HVE
p_OVE_comp     <- 0.01    # complications with untreated OVE
p_HVE_comp_tx  <- 0.36    # complications with treated HVE
p_OVE_comp_tx  <- 0.20    # complications with treated OVE
p_biopsy_death <- 0.005   # probability of death due to biopsy

# Costs
c_VE           <- 1200    # cost of viral encephalitis care without complications
c_VE_comp      <- 9000    # cost of viral encephalitis care with complications
c_tx           <- 9500    # cost of treatment
c_biopsy       <- 25000   # cost of brain biopsy
c_death_biopsy <- 0       # cost of dying from brain biopsy

# QALYs
q_VE           <- 20      # remaining QALYs for those without VE-related complications
q_VE_comp      <- 19      # remaining QALYs for those with VE-related complications
q_loss_biopsy  <- 0.01    # one-time QALY loss due to brain biopsy
q_death_biopsy <- 0       # remaining QALYs for those who died during biopsy
```

## 04 Create and run decision tree model

```

# Create vector of weights for each strategy

v_w_no_tx <- c(
  p_HVE * p_HVE_comp, # HVE, complications
  p_HVE * (1 - p_HVE_comp), # HVE, no complications
  (1 - p_HVE) * p_OVE_comp, # OVE, complications
  (1 - p_HVE) * (1 - p_OVE_comp)) # OVE, no complications

v_w_tx <- c(
  p_HVE * p_HVE_comp_tx, # HVE w/tx, complications
  p_HVE * (1 - p_HVE_comp_tx), # HVE w/tx, no complications
  (1 - p_HVE) * p_OVE_comp_tx, # OVE w/tx, complications
  (1 - p_HVE) * (1 - p_OVE_comp_tx)) # OVE w/tx, no complications

v_w_biopsy <- c(
  p_biopsy_death, # biopsy death
  # no biopsy death., HVE w/tx, complications
  (1 - p_biopsy_death) * p_HVE * p_HVE_comp_tx,
  # no biopsy death., HVE w/tx, no complications
  (1 - p_biopsy_death) * p_HVE * (1 - p_HVE_comp_tx),
  # no biopsy death., OVE, complications
  (1 - p_biopsy_death) * (1 - p_HVE) * p_OVE_comp,
  # no biopsy death., OVE, no complications
  (1 - p_biopsy_death) * (1 - p_HVE) * (1 - p_OVE_comp))

# Create vector of outcomes being complications for each strategy
v_comp_no_tx <- c(1, # HVE, complications
  0, # HVE, no complications
  1, # OVE, complications
  0) # OVE, no complications

v_comp_tx <- c(1, # HVE, complications
  0, # HVE, no complications
  1, # OVE, complications
  0) # OVE, no complications

v_comp_biopsy <- c(1, # biopsy complications
  1, # no biopsy comp., HVE w/tx, complications
  0, # no biopsy comp., HVE w/tx, no complications
  1, # no biopsy comp., OVE, complications
  0) # no biopsy comp., OVE, no complications

# Create vector of outcomes (QALYs) for each strategy
v_qaly_no_tx <- c(q_VE_comp, # HVE, complications
  q_VE, # HVE, no complications
  q_VE_comp, # OVE, complications
  q_VE) # OVE, no complications

v_qaly_tx <- c(q_VE_comp, # HVE, complications
  q_VE, # HVE, no complications
  q_VE_comp, # OVE, complications
  q_VE) # OVE, no complications

```

```

v_qaly_biopsy <- -q_loss_biopsy      + # loss due to biopsy
                  c(q_death_biopsy , # biopsy complications
                    q_VE_comp       , # no biopsy comp., HVE w/tx, complications
                    q_VE            , # no biopsy comp., HVE w/tx, no complications
                    q_VE_comp       , # no biopsy comp., OVE, complications
                    q_VE)           , # no biopsy comp., OVE, no complications

# Create vector of costs for each strategy
v_cost_no_tx  <- c(c_VE_comp ,      # HVE, complications
                  c_VE       ,      # HVE, no complications
                  c_VE_comp ,      # OVE, complications
                  c_VE)          , # OVE, no complications

v_cost_tx     <- c_tx +             # cost of treatment
                  c(c_VE_comp ,      # HVE, complications
                    c_VE       ,      # HVE, no complications
                    c_VE_comp ,      # OVE, complications
                    c_VE)          , # OVE, no complications

v_cost_biopsy <- c_biopsy           + # cost of biopsy procedure
                  c(c_death_biopsy , # cost of death (zero)
                    c_VE_comp + c_tx , # no biopsy comp., HVE w/tx, complications
                    c_VE       + c_tx , # no biopsy comp., HVE w/tx, no complications
                    c_VE_comp ,      # no biopsy comp., OVE, complications
                    c_VE)           , # no biopsy comp., OVE, no complications

# Calculate expected complications for each strategy
total_comp_no_tx <- v_w_no_tx %*% v_comp_no_tx
total_comp_tx   <- v_w_tx %*% v_comp_tx
total_comp_biopsy <- v_w_biopsy %*% v_comp_biopsy

# Calculate total utilities for each strategy
total_qaly_no_tx <- v_w_no_tx %*% v_qaly_no_tx
total_qaly_tx   <- v_w_tx %*% v_qaly_tx
total_qaly_biopsy <- v_w_biopsy %*% v_qaly_biopsy

# Calculate total costs for each strategy
total_cost_no_tx <- v_w_no_tx %*% v_cost_no_tx
total_cost_tx   <- v_w_tx %*% v_cost_tx
total_cost_biopsy <- v_w_biopsy %*% v_cost_biopsy

# vector of expected complications
v_total_comp <- c(total_comp_no_tx, total_comp_tx, total_comp_biopsy)
# vector of total QALYs
v_total_qaly <- c(total_qaly_no_tx, total_qaly_tx, total_qaly_biopsy)
# vector of total costs
v_total_cost <- c(total_cost_no_tx, total_cost_tx, total_cost_biopsy)
# calculate vector of nmb
v_nmb       <- v_total_qaly * wtp - v_total_cost

```

```

# Name outcomes
names(v_total_comp) <- v_names_str # names for the elements of the total comp vector
names(v_total_qaly) <- v_names_str # names for the elements of the total QALYs vector
names(v_total_cost) <- v_names_str # names for the elements of the total cost vector
names(v_nmb) <- v_names_str # names for the elements of the nmb vector

df_output <- data.frame(Strategy = v_names_str,
                        Cost      = v_total_cost,
                        Effect     = v_total_qaly,
                        Complications = v_total_comp,
                        NMB        = v_nmb)

# model output
df_output

```

## 05 Cost-Effectiveness Analysis

```

# create the transition probability matrix for NO treatment
decision_tree_HVE_cea <- calculate_icers(cost      = df_output$Cost,
                                         effect    = df_output$Effect,
                                         strategies = df_output$Strategy)

decision_tree_HVE_cea

```

### 05.1 Plot frontier of Decision Tree

```

plot(decision_tree_HVE_cea, effect_units = "QALYs", label="all")

```