

# Three-strategy decision tree in R - HVE

with “OpenTree”

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*. 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("devtools", "scales", "ellipse", "lazyeval", "igraph", "ggraph", "reshape2", "knitr", "stringr")
# 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("Do not treat", "Treat", "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 death 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 (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

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

```

```

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

# 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 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_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,
                        NMB       = v_nmb)

# model output
df_output

```

```

##           Strategy      Cost   Effect   NMB
## Do not treat Do not treat 4117.20 19.62600 1958483
## Treat       Treat 12908.96 19.71680 1958771
## Biopsy      Biopsy 32599.41 19.69896 1937297

```

## 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

```

```

##           Strategy      Cost   Effect Inc_Cost Inc_Effect   ICER Status

```

## 1	Do not treat	4117.20	19.62600	NA	NA	NA	ND
## 2	Treat	12908.96	19.71680	8791.76	0.0908	96825.55	ND
## 3	Biopsy	32599.41	19.69896	NA	NA	NA	D

## 05.1 Plot frontier of Decision Tree

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

