

Three-strategy decision tree in R - HVE

with “OpenTree”

The DARTH workgroup

Developed by the Decision Analysis in R for Technologies in Health (DARTH) workgroup:

Fernando Alarid-Escudero, PhD (1)

Eva A. Enns, MS, PhD (2)

M.G. Myriam Hunink, MD, PhD (3,4)

Hawre J. Jalal, MD, PhD (5)

Eline M. Krijkamp, MSc (3)

Petros Pechlivanoglou, PhD (6,7)

Alan Yang, MSc (7)

In collaboration of:

1. Drug Policy Program, Center for Research and Teaching in Economics (CIDE) - CONACyT, Aguascalientes, Mexico
2. University of Minnesota School of Public Health, Minneapolis, MN, USA
3. Erasmus MC, Rotterdam, The Netherlands
4. Harvard T.H. Chan School of Public Health, Boston, USA
5. University of Pittsburgh Graduate School of Public Health, Pittsburgh, PA, USA
6. University of Toronto, Toronto ON, Canada
7. The Hospital for Sick Children, Toronto ON, Canada

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>

Copyright 2017, THE HOSPITAL FOR SICK CHILDREN AND THE COLLABORATING INSTITUTIONS. All rights reserved in Canada, the United States and worldwide. Copyright, trademarks, trade names and any and all associated intellectual property are exclusively owned by THE HOSPITAL FOR SICK CHILDREN and the collaborating institutions. These materials may be used, reproduced, modified, distributed and adapted with proper attribution.

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", "DARTH-git/OpenTree")
```

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

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(0              ,      # 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 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

```

04.1 Use OpenTree to create and run decision tree model

Create or open decision tree.

The function `create_tree()` creates a blank tree and the function `open_tree()` opens an existing decision tree.

IMPORTANT: since `create_tree()` always creates blank new tree, do not use it to access or modify an existing tree, or else the tree will get erased. Always use `open_tree()` to open and modify existing trees.

Any changes made to the tree in OpenTree are automatically saved as a `.json` file to the working directory. If you are running it in an R script, the `.json` file will be saved to the path on your machine specified in `dir_name`. If you are running it in an R markdown document, the `.json` file will be saved to the path where the R markdown document is located.

```
#create_tree(file_name = "Helloworld", dir_name = getwd())
open_tree(file_name = "HVEsolution", dir_name = getwd())
```

Extract probability weights and outcomes of the decision tree.

```
# extract the probability weights and outcomes
df_tree <- evaluate_model("HVEsolution", n_payoffs = 2)
```

Compute total cost and QALYs.

```
# vector of total cost and QALYs
v_total_qaly <- v_total_cost <- vector(mode = "numeric", length = n_str)

# Calculate total costs and QALYs for each strategy
for (i in 1:n_str) {
  v_total_qaly[i] <- df_tree[[i]]$prob %*% df_tree[[i]]$payoff1
  v_total_cost[i] <- df_tree[[i]]$prob %*% df_tree[[i]]$payoff2
}

# calculate vector of nmb
v_nmb <- v_total_qaly * wtp - v_total_cost

df_output <- data.frame(Strategy = v_names_str,
                        Cost      = v_total_cost,
                        Effect     = v_total_qaly,
                        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")
```