

Three-strategy decision tree in R - HVE

with “OpenTree”

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("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

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 = "HVEsolution2", dir_name = getwd())
```

```
## [1] "E25A33BB"
```

Extract probability weights and outcomes of the decision tree.

```
# extract the probability weights and outcomes
df_tree <- evaluate_model("HVEsolution2", 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
```

```
##      Strategy      Cost      Effect      NMB
## 1 Do not treat  4117.20  19.62600 1958483
## 2      Treat 12908.96  19.71680 1958771
## 3     Biopsy 32599.41  19.69901 1937302
```

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	19.69901	NA	NA	NA	D

05.1 Plot frontier of Decision Tree

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

