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 install other packages  
# load (install if required) packages from CRAN  
p\_load( "dplyr", "devtools", "scales", "ellipse", "ggplot2", "lazyeval", "igraph" , "ggraph", "reshape2", "knitr", "stringr", "rstudioapi", "dampack")   
# 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

# 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  
  
# 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

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 <- your turn  
   
# v\_w\_biopsy <- your turn  
   
# 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 <- your turn  
   
# v\_qaly\_biopsy <- your turn  
   
   
# 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 <- your turn  
   
# v\_cost\_biopsy <- your turn

### alternatively using OpenTree  
# draw the tree using OpenTree  
  
  
open\_tree(file\_name = "HVEtemplate", dir\_name = getwd())  
  
# extract the probability weights and outcomes   
df\_tree <- evaluate\_model("HVEtemplate", n\_payoffs = 2)  
  
 total\_qaly\_no\_tx <- df\_tree[['Do not treat']]$prob %\*% df\_tree[['Do not treat']]$payoff1   
 total\_cost\_no\_tx <- df\_tree[['Do not treat']]$prob %\*% df\_tree[['Do not treat']]$payoff2

# 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  
   
v\_total\_qaly <- c(total\_qaly\_no\_tx, total\_qaly\_tx, total\_qaly\_biopsy) # vector of total QALYs  
v\_total\_cost <- c(total\_cost\_no\_tx, total\_cost\_tx, total\_cost\_biopsy) # vector of total costs  
v\_nmb <- v\_total\_qaly \* wtp - v\_total\_cost # calculate vector of nmb  
   
# 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  
  
# model output  
   
df\_output <- data.frame(Strategy = v\_names\_str,  
 Cost = v\_total\_cost,  
 Effect = v\_total\_qaly,  
 NMB = v\_nmb)

## 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")