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

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

```r
# 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 complicati

# 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
```

```r
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

For the cost-effectiveness we make use uf the `calculate_icers` function from the **dampack** package. You can find more information about this package by typing `??calculate_icers` in your Console.

```r
# 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")
```