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

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("dplyr", "devtools", "scales", "ellipse", "ggplot2", "lazyeval", "igraph",  "ggraph", "reshape2"
# 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("No Tx", "Tx All", "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 dying 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



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(c_death_biopsy    ,   # 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
```

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")
```