

Three-strategy decision tree in R - HVE

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.

```
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("here", "dplyr", "devtools", "scales", "ellipse", "ggplot2", "lazyeval", "igraph", "truncnorm",
# load (install if required) packages from GitHub
# install_github("DARTH-git/dampack", force = TRUE) Uncomment if there is a newer version
#install_github("DARTH-git/dectree", force = TRUE) #Uncomment if there is a newer version
p_load_gh("DARTH-git/dampack", "DARTH-git/dectree")
```

02 Load functions

```
source(here('functions', 'Functions.R'))
```

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

# 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

# store the parameters into a list
l_params_all <- as.list(data.frame(p_HVE, p_HVE_comp, p_OVE_comp, p_HVE_comp_tx, p_OVE_comp_tx, p_biops,
c_VE, c_VE_comp, c_tx, c_biopsy,
```

```

                                q_VE, q_VE_comp, q_loss_biopsy))
# store the names of the parameters into a vector
v_names_params <- c('p_HVE', 'p_HVE_comp', 'p_OVE_comp', 'p_HVE_comp_tx', 'p_OVE_comp_tx', 'p_biopsy_dea
                    'c_VE', 'c_VE_comp', 'c_tx', 'c_biopsy', 'q_VE', 'q_VE_comp', 'q_loss_biopsy')

```

04 Create and run decision tree model

```

decision_tree_HVE_output <- with(as.list(l_params_all), {

  # 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)

return(df_output)
})

# model output
decision_tree_HVE_output

```

```
##      Strategy      Cost      Effect      NMB
## No Tx      No Tx  4117.20 19.62600 1958483
## Tx All     Tx All 12908.96 19.71680 1958771
## Biopsy     Biopsy 32599.41 19.69896 1937297
```

04.1 Plot the decision tree

```
branches <- read.csv(here('data','decision_tree_HVE_branches.csv'), stringsAsFactors = F, header = T)
tree      <- create_tree(branches)
#plot_tree(tree, font.size = 5)
#estimate_tree(tree, payoffs = "effect")
```

05 Cost-Effectiveness Analysis

```
# create the transition probability matrix for NO treatment
decision_tree_HVE_cea <- calculate_icers(cost      = decision_tree_HVE_output$Cost,
                                         effect     = decision_tree_HVE_output$Effect,
                                         strategies = decision_tree_HVE_output$Strategy)
decision_tree_HVE_cea
```

```
##   Strategy      Cost      Effect Inc_Cost Inc_Effect      ICER Status
## 1   No Tx  4117.20 19.62600      NA      NA      NA      ND
## 2   Tx All 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")
```

