

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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```
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_death',
                    '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
    (1-p_biopsy_death) * p_HVE * p_HVE_comp_tx , # no biopsy death., HVE w/tx, complications
    (1-p_biopsy_death) * p_HVE * (1-p_HVE_comp_tx) , # no biopsy death., HVE w/tx, no complications
    (1-p_biopsy_death) * p_OVE_comp , # 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")
```

