

PSA: 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>
- Alarid-Escudero, F., Krijkamp, E. M., Enns, E. A., Hunink, M. G. M., Pechlivanoglou, P., & Jalal, H. (2020). Cohort state-transition models in R: From conceptualization to implementation. *arXiv:2001.07824v1*, 1–31. <http://arxiv.org/abs/2001.07824>
- Alarid-Escudero, F., Enns, E. A., Kuntz, K. M., Michaud, T. L., & Jalal, H. (2019). “Time Traveling Is Just Too Dangerous” But Some Methods Are Worth Revisiting: The Advantages of Expected Loss Curves Over Cost-Effectiveness Acceptability Curves and Frontier. *Value in Health*, 22(5), 611–618. <https://doi.org/10.1016/j.jval.2019.02.008>

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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("here", "dplyr", "devtools", "scales", "ellipse", "ggplot2", "lazyeval",  
       "igraph", "truncnorm", "ggraph", "reshape2", "knitr", "stringr", "reshape2")  
# 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  
# install_github("annaheath/EVSI", force = TRUE) #Uncomment if there is a newer version  
p_load_gh("DARTH-git/dampack", "DARTH-git/dectree")  
p_load_gh("annaheath/EVSI")
```

02 Load functions

```
source("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_comp <- 0.05 # probability of complications 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

# store the parameters into a list
l_params_all <- list(p_HVE, p_HVE_comp, p_OVE_comp, p_HVE_comp_tx,
                    p_OVE_comp_tx, p_biopsy_comp,
                    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_comp',
                    'c_VE', 'c_VE_comp', 'c_tx', 'c_biopsy',
                    'q_VE', 'q_VE_comp', 'q_loss_biopsy')

names(l_params_all) <- v_names_params

```

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( 1 , # On treatment
              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(1 , # Undergo biopsy
                 p_biopsy_comp , # biopsy complications
                 # no biopsy comp., HVE w/tx, complications
                 (1-p_biopsy_comp) * p_HVE * p_HVE_comp_tx ,
                 # no biopsy comp., HVE w/tx, no complications
                 (1-p_biopsy_comp) * p_HVE * (1-p_HVE_comp_tx),
                 # no biopsy comp., OVE, complications
                 (1-p_biopsy_comp) * (1-p_HVE) * p_OVE_comp ,
                 # no biopsy comp., OVE, no complications
                 (1-p_biopsy_comp) * (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(0          , # treatment does not directly add any QALYs
                   q_VE_comp , # HVE, complications
                   q_VE      , # HVE, no complications
                   q_VE_comp , # OVE, complications
                   q_VE)      # OVE, no complications

v_qaly_biopsy <- c(q_loss_biopsy, # loss due to biopsy
                   q_VE_comp , # 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(c_tx      , # cost of treatment
                   c_VE_comp , # HVE, complications
                   c_VE      , # HVE, no complications
                   c_VE_comp , # OVE, complications
                   c_VE)      # OVE, no complications

v_cost_biopsy <- c(c_biopsy   , # cost of biopsy procedure
                   c_VE_comp , # biopsy complications
                   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

```

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)

```

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

```

05.1 Plot frontier of Decision Tree

```

plot(decision_tree_HVE_cea, effect_units = "QALYs")

```

06 Deterministic Sensitivity Analysis

06.1 List of input parameters

```

l_params_all

```

06.2 Load decision tree model function

```
#### We wrapped the decision tree in a function which we called calculate_ce_out
# This function is stored in "Functions_decision_tree_HVE.R" and needs the list of parameters
source("Functions_decision_tree_HVE.R")
# Test function to see if it gives the CE results
calculate_ce_out(l_params_all)
```

06.3 One-way sensitivity analysis (OWSA)

```
options(scipen = 999) # disabling scientific notation in R
# dataframe containing all parameters, their basecase values, and the min and
# max values of the parameters of interest
df_params_owsa <- data.frame(pars = c("p_HVE", "p_biopsy_comp", "c_tx", "c_biopsy"),
                             min = c(0.01, 0.01, 1000, 5000), # min parameter values
                             max = c(0.99, 0.50, 15000, 40000) # max parameter values
                             )

owsa_nmb <- run_owsa_det(params_range = df_params_owsa, # dataframe with parameters for owsa
                        params_basecase = l_params_all, # list with all parameters
                        nsamp = 100, # number of parameter values
                        FUN = calculate_ce_out, # function to compute outputs
                        outcomes = c("NMB"), # output to do the OWSA on
                        strategies = v_names_str, # names of the strategies
                        n_wtp = 450000) # extra argument to pass to FUN
```

06.3.1 Plot OWSA

```
plot(owsa_nmb, txtsize = 16, n_x_ticks = 5, n_y_ticks = 3,
     facet_scales = "free") +
  theme(legend.position = "bottom",
        axis.text.x = element_text(angle = 45, vjust = 0.5))
```

06.3.2 Optimal strategy with OWSA

```
owsa_opt_strat(owsa = owsa_nmb)
```

06.3.3 Tornado plot

```
owsa_tornado(owsa = owsa_nmb) +
  theme(axis.text.x = element_text(angle = 45, vjust = 0.5))
```

06.4 Two-way sensitivity analysis (TWSA)

```

# dataframe containing all parameters, their basecase values, and the min and
# max values of the parameters of interest
df_params_twsa <- data.frame(pars = c("p_HVE", "c_biopsy"),
                             min  = c(0.01, 2000), # min parameter values
                             max  = c(0.99, 40000) # max parameter values
                             )

twsa_nmb <- run_twsa_det(params_range = df_params_twsa, # dataframe with parameters for twsa
                       params_basecase = l_params_all, # list with all parameters
                       nsamp          = 40,           # number of parameter values
                       FUN             = calculate_ce_out, # function to compute outputs
                       outcomes       = c("NMB"),      # output to do the twsa on
                       strategies     = v_names_str,   # names of the strategies
                       n_wtp          = 200000)        # extra argument to pass to FUN

```

06.4.1 Plot TWSA

```

plot(twsa_nmb) +
  ggtitle(label = "Two-way sensitivity analysis",
          subtitle = "Net monetary benefit") +
  theme(legend.position = "bottom")

```

07 Probabilistic Sensitivity Analysis (PSA)

```

# Function to generate PSA input dataset
generate_psa_params <- function(n_sim = 1000, seed = 071518){
  set.seed(seed)
  # Dataframe of input parameters
  df_psa_params <- data.frame(

    # Transition probabilities (per cycle)
    p_HVE          = rbeta(n_sim, 52, 48), # prevalence of HVE
    p_HVE_comp     = rbeta(n_sim, 71, 29), # complications with untreated HVE
    p_OVE_comp     = rbeta(n_sim, 1, 99),  # complications with untreated OVE
    p_HVE_comp_tx  = rbeta(n_sim, 36, 64), # complications with treated HVE
    p_OVE_comp_tx  = rbeta(n_sim, 20, 80), # complications with treated OVE
    p_biopsy_comp  = rbeta(n_sim, 1, 19),  # probability of complications due to biopsy

    # Costs
    c_VE          = rgamma(n_sim, shape = 36.0, scale = 33.33), # cost of remaining one cycle in state H
    c_VE_comp     = rgamma(n_sim, shape = 81.0, scale = 111.1), # cost of remaining one cycle in state S1
    c_tx          = rgamma(n_sim, shape = 74.6, scale = 127.4), # cost of remaining one cycle in state S2
    c_biopsy      = rgamma(n_sim, shape = 25.0, scale = 1000),  # cost of treatment (per cycle)

    # Utilities
    q_VE          = rnorm(n_sim, mean = 20, sd = 1), # utility when healthy
    q_VE_comp     = rnorm(n_sim, mean = 19, sd = 2), # utility when sick
    q_loss_biopsy = -rbeta(n_sim, shape1 = 4, shape2 = 380)
  )
}

```



```

    )
    return(df_psa_params)
}
# Try it
generate_psa_params(10)

# Generate PSA dataset for CEA
# Number of simulations
n_sim <- 1000

# Generate PSA input dataset
df_psa_input <- generate_psa_params(n_sim = n_sim)
# First six observations
head(df_psa_input)

# Histogram of parameters
ggplot(reshape2::melt(df_psa_input, variable.name = "Parameter",
                      value.name = "Parameter value"),
       aes(x = `Parameter value`)) +
  facet_wrap(~Parameter, scales = "free") +
  geom_histogram(aes(y = ..density..), alpha = 0.8) +
  scale_x_continuous(breaks = number_ticks(3)) +
  ylab("") +
  theme_bw(base_size = 14) +
  theme(axis.text.y = element_blank())

# Initialize dataframes with PSA output
# Dataframe of costs
df_c <- as.data.frame(matrix(0,
                             nrow = n_sim,
                             ncol = n_str))
colnames(df_c) <- v_names_str

# Dataframe of effectiveness
df_e <- as.data.frame(matrix(0,
                             nrow = n_sim,
                             ncol = n_str))
colnames(df_e) <- v_names_str

```

07.1 Conduct probabilistic sensitivity analysis

```

# Run decision tree on each parameter set of PSA input dataset
for(i in 1:n_sim){
  l_psa_input <- update_param_list(l_params_all, df_psa_input[i, ])
  df_out_psa <- calculate_ce_out(l_psa_input)
  df_c[i, ] <- df_out_psa$Cost
  df_e[i, ] <- df_out_psa$Effect
  # Display simulation progress
  if(i/(n_sim/10) == round(i/(n_sim/10),0)) { # display progress every 10%
    cat('\r', paste(i/n_sim * 100, "% done", sep = " "))
  }
}

```

07.2 Create PSA object for dampack

```
l_psa <- make_psa_obj(cost      = df_c,  
                     effectiveness = df_e,  
                     parameters  = df_psa_input,  
                     strategies  = v_names_str)
```

07.2.1 Save PSA objects

```
save(df_psa_input, df_c, df_e, v_names_str, n_str,  
     l_psa,  
     file = "decision_tree_HVE_PSA_dataset.RData")
```

07.3 Create probabilistic analysis graphs

```
load(file = "decision_tree_HVE_PSA_dataset.RData")
```

Vector with willingness-to-pay (WTP) thresholds.

```
v_wtp <- seq(0, 600000, by = 10000)
```

07.3.1 Cost-Effectiveness Scatter plot

```
plot(l_psa)
```

07.4 Conduct CEA with probabilistic output

```
# Compute expected costs and effects for each strategy from the PSA  
df_out_ce_psa <- summary(l_psa)  
df_out_ce_psa  
  
# Calculate incremental cost-effectiveness ratios (ICERs)  
df_cea_psa <- calculate_icers(cost      = df_out_ce_psa$meanCost,  
                             effect     = df_out_ce_psa$meanEffect,  
                             strategies = df_out_ce_psa$Strategy)  
df_cea_psa  
  
# Save CEA table with ICERs  
# As .RData  
save(df_cea_psa,  
     file = "decision_tree_HVE_probabilistic_CEA_results.RData")
```

```
# As .csv
write.csv(df_cea_psa,
          file = "decision_tree_HVE_probabilistic_CEA_results.csv")
```

07.4.1 Plot cost-effectiveness frontier

```
plot(df_cea_psa)
```

07.4.2 Cost-effectiveness acceptability curves (CEACs) and frontier (CEAF)

```
ceac_obj <- ceac(wtp = v_wtp, psa = l_psa)
# Regions of highest probability of cost-effectiveness for each strategy
summary(ceac_obj)
# CEAC & CEAF plot
plot(ceac_obj)
```

07.4.3 Expected Loss Curves (ELCs)

```
elc_obj <- calc_exp_loss(wtp = v_wtp, psa = l_psa)

# ELC plot
plot(elc_obj, log_y = FALSE)
```

07.4.4 Expected value of perfect information (EVPI)

```
evpi <- calc_evpi(wtp = v_wtp, psa = l_psa)
# EVPI plot
plot(evpi, effect_units = "QALY")
```

07.4.5 Expected value of partial perfect information (EVPPPI)

```
evppi <- calc_evppi(psa = l_psa,
                   wtp = v_wtp,
                   params = c("q_VE_comp"),
                   outcome = c("nmb"),
                   type = c("gam", "poly"),
                   poly.order = 2,
                   k = -1,
                   pop = 1
)

dampack::plot.evppi(evppi)
```