

Introduction to Decision Trees in R

Case Study: Invasive meningococcal disease

Petros Pechlivanoglou

Wednesday, September 13, 2023

R software

The R Project for Statistical Computing: <https://www.r-project.org/>

Installing R

Install R

Download R version 4.3.1 from <https://cran.r-project.org/bin/windows/base/old/4.3.1/>

Download the file `R-4.3.1-win.exe` and follow the installation procedure.

Install RStudio

Download and install the free version of RStudio Desktop from: <https://posit.co/download/rstudio-desktop/#download>

Background

Invasive meningococcal disease (IMD):

- Acute and serious communicable disease caused by the bacterium *Neisseria meningitidis*,
- Clinical manifestations: meningitis, septicemia (meningococemia) or both.
- Case fatality ratio: 5-11%
- Sequelae in ~1/3 of survivors, including hearing loss, neurologic disabilities, and digit or limb amputations
- Most frequent serogroups associate with IMD: A, B, C, W-135 and Y

Serogroup B meningococcal (MenB) disease:

- Endemic in Ontario
- Most common cause of life-threatening IMD in children

Vaccines

- Most frequent serogroups associate with IMD: A, B, C, W-135 and Y
- Current vaccines:
 - Men C: 12 months of age
 - Men ACYW-135 vaccine: 7th grade
- MenB?
 - A novel MenB vaccine was submitted for regulatory approval in Europe, Australia and Canada (Spring 2011).

Decision Problem

You are a member of the National Advisory Committee on Immunization. At a recent meeting the committee was informed about a new MenB vaccine that is currently under development and appears to be safe and effective.

Anticipating that the vaccine may be approved for use in Canada within the next 2-3 years, the committee is interested in exploring the potential cost-effectiveness of the new vaccine in the Canadian context to support timely decision-making.

Building a Tree

This R Markdown document provides a foundation for constructing a decision tree model for CAD:

Target population: children

Time horizon: lifetime

The two strategies being compared are:

1. Vaccination
2. No vaccination

The outcomes being considered are:

- Costs
- Benefit from vaccination
- Risk of adverse events

Objective: To assess the cost-utility of meningococcal serogroup B vaccination in infants compared to no vaccination from the healthcare payer perspective in Canada.

imited options, though, for sensitivity analysis.

Building a Tree with Variables

Much greater flexibility is possible if numeric quantities in the tree are defined as variables or expressions.

Variables can be globally defined and live in the Global Environment in R and applied to the whole tree.

Steps for using variables:

1. Declare name — Based on its intended function in your model, decide on a clear name for the variable.
2. Use — Anywhere the corresponding value is used in the tree (e.g., payoffs or probabilities).

Simplest way to create a variable is to type it in a R chunk like below:

```
# Probabilities
p_AE      <- 0.002  # Probability of adverse event
p_IMD     <- 0.2    # Probability of invasive MenB disease
p_death   <- 0.05   # Probability of acute death
p_sequelae <- 0.05   # Probability of long-term sequelae given survival of acute disease (major)
e_Vacc    <- 0.58   # Vaccine effectiveness
e_NoVacc  <- 0      # No vaccine effectiveness

# Utilities
u_AE      <- 0.9996 # Utility, Adverse event
u_IMD     <- 0.87   # Utility, Invasive MenB disease
u_sequelae <- 0.78   # Utility, Long-term sequelae
u_well    <- 1      # Utility, Well
u_death   <- 0      # Utility, Death

# Costs
c_Vacc    <- 300    # Cost, Vaccination
c_AE      <- 673    # Cost, Adverse event
c_IMD     <- 16630  # Cost, Invasive MenB disease (acute)
c_sequelae <- 12256 # Cost, Long-term sequelae (per year)
```

Using Subtrees

In R you can create subtrees and assign them to functions with desired names. For example, the subtree describing outcomes for those experiencing IMD or not can be assigned into a function and we can call it `Effectiveness_Subtree`. The arguments of this function include probability of IMD, probability of acute death, probability of long-term sequelae, and costs and utilities.

```

# p_IMD:      Probability of invasive MenB disease
# p_death:    Probability of acute death
# p_sequelae: Probability of long-term sequelae
# e:          Effectiveness of strategy (Vaccine vs. No Vaccine)
# u_IMD:      Utility, Invasive MenB disease
# u_sequelae: Utility, Long-term sequelae
# u_well:     Utility, Well
# u_death:    Utility, Death
# c_IMD:      Cost, Invasive MenB disease (acute)
# c_sequelae: Cost, Long-term sequelae (per year)
Effectiveness_Subtree <- function(p_IMD, p_death, p_sequelae, e,
                                u_IMD, u_sequelae, u_well, u_death,
                                c_IMD, c_sequelae) {
  # Utility
  u <- p_IMD*(1 - e) *      p_death * (u_IMD * u_death) +
      p_IMD*(1 - e) * (1 - p_death) *      p_sequelae *
      (u_IMD * u_sequelae) +
      p_IMD*(1 - e) * (1 - p_death) * (1 - p_sequelae) *
      (u_IMD * u_well) +
      (1 - p_IMD*(1 - e)) * u_well

  # Cost
  c <- p_IMD*(1 - e) *      p_death * c_IMD +
      p_IMD*(1 - e) * (1 - p_death) *      p_sequelae *
      (c_IMD + c_sequelae) +
      p_IMD*(1 - e) * (1 - p_death) * (1 - p_sequelae) *
      c_IMD +
      (1 - p_IMD*(1 - e)) * 0

  return(list(u = u,
              c = c))
}

```

To use this subtree function, you just need to pass values to the arguments. Below we calculate QALY outcomes for both medicine and surgery while using subtree `Effectiveness_Subtree` for both strategies.

```

# Vaccine
subtree_Vacc <- Effectiveness_Subtree(p_IMD      = p_IMD,
                                     p_death     = p_death,
                                     p_sequelae   = p_sequelae,
                                     e            = e_Vacc,
                                     u_IMD       = u_IMD,
                                     u_sequelae   = u_sequelae,
                                     u_well      = u_well,
                                     u_death     = u_death,
                                     c_IMD       = c_IMD,
                                     c_sequelae   = c_sequelae)

## Vaccine, Adverse event
tu_Vacc_AE <- p_AE * u_AE * subtree_Vacc$u
tc_Vacc_AE <- p_AE * (c_AE + c_Vacc + subtree_Vacc$c)

## Vaccine, No Adverse event
tu_Vacc_noAE <- (1 - p_AE) * subtree_Vacc$u
tc_Vacc_noAE <- (1 - p_AE) * (c_Vacc + subtree_Vacc$c)

```

```

tu_Vacc <- tu_Vacc_AE + tu_Vacc_noAE
tc_Vacc <- tc_Vacc_AE + tc_Vacc_noAE

# No Vaccine
subtree_NoVacc <- Effectiveness_Subtree(p_IMD      = p_IMD,
                                         p_death    = p_death,
                                         p_sequelae  = p_sequelae,
                                         e          = e_NoVacc,
                                         u_IMD      = u_IMD,
                                         u_sequelae  = u_sequelae,
                                         u_well     = u_well,
                                         u_death    = u_death,
                                         c_IMD      = c_IMD,
                                         c_sequelae  = c_sequelae)

tu_NoVacc <- subtree_NoVacc$u
tc_NoVacc <- subtree_NoVacc$c

df_output <- data.frame(Strategy = c("Vaccine", "No Vaccine"),
                        Cost      = c(tc_Vacc, tc_NoVacc),
                        Effect    = c(tu_Vacc, tu_NoVacc))

df_output

```

```

##      Strategy      Cost      Effect
## 1    Vaccine 1747.167 0.9846615
## 2 No Vaccine 3442.432 0.9634817

```