Decision Analysis in R for Technologies in Health

Exercises

## Build Microsimulation in R Workshop at the 39th SMDM

**January 2017**

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Acknowledgements and attribution.

Please cite the following papers when using any of the material:

[Jalal H, et al. An Overview of R in Health Decision Sciences. *Med. Dec. Mak*. 2017; 37(3): 735-746.](https://www.ncbi.nlm.nih.gov/pubmed/?term=overview+of+R+jalal)

[Krijkamp E, et al. Microsimulation Modeling for Health Decision Sciences Using R: A Tutorial. *Med.* *Dec. Mak.* 2018; 38(3): 400-422.](http://journals.sagepub.com/doi/abs/10.1177/0272989X18754513)

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# Header 1

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1. domain:
2. diagnosis:
3. reference:

# Header 1 – titel of the assignment

## Header 2

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**1. Questions text**

*italic text for extra instructions*

**2. Questions text**

*italic text for extra instructions*

*extra paragraphe of italic text for extra instructions*

*Please give the variables the following names:*

* bullit points with R code
* P(Event | CVD+, Treat+): p.Event\_CVD\_Rx
* P(Event | CVD+, Treat-): p.Event\_CVD\_noRx
* P(Event | CVD-, Treat+): p.Event\_noCVD\_Rx
* P(Event | CVD-, Treat-): p.Event\_noCVD\_noRx

*Tip: Also make a variable called* p.AdverseEvent *and use this variable in your calculations. You will need this during the rest of the assignments.*

**3. Using the decision tree calculate algebraically the no treat - treat threshold of the prior (pre-test) probability of CAD.**

*Tip: use the examples in the lecture where they algebraically show how to calculate the no treat-treat threshold. You need to use your algebra skills here.*

Define the two function

f <- function(p){add the formula of the left side of the equation}   
g <- function(p){add the formula of the right side of the equation}   
  
# Make a range for the probability values p  
p <- seq(0, 1, 0.01)  
  
# Calculate the threshold. This is where the two functions are equal  
# the difference between the two graphs f(x) - g(x) should be 0   
NoTreat\_Treat\_Threshold <- optimize(function(p) abs(f(p) - g(p)), c(0,1))$minimum  
  
# Print your threshold using the "round()" command and round up to 3 decimals.   
round(No\_Treat\_Treat\_Threshold, 3)

To make use of this package your variables need to be saved in a data frame. If you correctly used the variable names as described in the assignments above, you can run the syntax below to create a data frame from your variables. Information about how to make a data frame can be found at the following website: [Data Frame from R Tutorial - An R introduction to Statistics.](http://www.r-tutor.com/r-introduction/data-frame)

### Header 3

You can calculate the expected number of individuals with (n.D) and without the disease (n.noD) using the theoretical cohort of 10000 individuals and the prior probability of disease (p.prior\_Disease)

At this point you can difine all the other variables in the 2x2 table by combining the variables n.D and n.noD with the variables sens and spec.

* Some tekst with bullit points 1
* An extra line of code

Save as) and go on using it as a Script editor to document your research steps. Once you have typed your command in the Script Editor, there are multiple ways of executing this command in the R Console. Perhaps the most laborious is copy-pasting each command from the Script Editor to the Console. Instead of typing in the script editor, copying the function typed and pasting it in the R Console you can execute a command written in the Script Editor in (at least) three time-saving ways: Select the piece of script that you want to run and

1. Click the button 'Run' on the top of the Script Editor
2. Press 'Ctrl+R' or 'Ctrl + Enter' if using Windows OS, or 'Cmnd + Enter' if using MAC OS
3. Drop down the menu 'Code' and select 'Run line(s)'

R and RStudio each have very comprehensive and useful 'Help' menus. By clicking on the R Help button in the Help menu a table of contents shows up at the bottom right of the RStudio interface. Except from a number of FAQs, the section in the help menu named 'Manuals' includes documents that offer a detailed introduction to R and its basic applications. RStudio has its own documentation (Help -> RStudio Docs) and Support (Help -> RStudio Support).

to an answer for your question, depending on the type of the question and how common it is:

* *Google*: The first place to search when you know what statistical approach you want to follow but do not know how it is done in R. Just type the method and the letter "R" next to it. Chances are that you will already find your answer this way.
* *RSeek*: A search engine for R FAQ functions and troubleshooting. RSeek uses Google to trace links that refer to the search terms provided. Together with Google, it is the best way to find which package/function you should use when you only have a hint about what you need to do.
* RSiteSearch(): Accessible directly through R, by typing RSiteSearch("foo") where foo should be replaced with the key term (e.g. RSiteSearch("mean")). This help function searches within forums, web discussions and mailing lists archived in CRAN for the keywords listed between the round brackets (in quotes). It is handy since it is accessed through the R Console but the key terms have to be rather well defined to reach to a topic related discussion.
* help.search(): Another function that is directly accessible from within the R Console. It performs a search within the help functions of the downloaded and installed packages for the provided key terms. Even less handy than RSiteSearch.
* ? or help(): Running a command with the name of a function and a question mark behind yields the help file for the function of interest. Very useful when you try to figure out how an exact function works. If you need information on a specific package rather than a function, the argument package = "the name of the package" should be included within the round brackets of the help() function (e.g., `help(package = "survival")
* User manuals and vignettes: If you need a proper example or you lack statistical background in the theoretical part of a function, reading the user manual of the package or even better the vignette is a very good idea. You can access the vignette using the function vignette("the name of the package"). Note however that not every R package comes with a vignette.

## Citing R

Using R in your work will possibly require you to reference R in your manuscript. To find out the appropriate reference for R just type citation() in the R Console and type Enter. Depending on the version of R you are using this will result to a citation similar to this: