Differential expression analysis: DESeq2

Realized in R studio V 4.1.3

Packages needed ------

# BiocManager::install('EnhancedVolcano')

# devtools::install\_github('kevinblighe/EnhancedVolcano')

# BiocManager::install("airway")

# BiocManager::install("DESeq2")

# BiocManager::install("org.Hs.eg.db")

## Load Libraries ------

library(tidyverse)

library(EnhancedVolcano)

library(airway)

library(DESeq2)

library(org.Hs.eg.db)

library(magrittr)

library(readxl)

####################### DATA GENES PRACTICAL TRUE DATA ##########################

## Define The working directory

setwd("")

## load the data matrix (countData)

mcountData <- as.matrix(read\_excel("Data\_genes.xlsx", sheet = 1, col\_types = c("text", rep("numeric", 1082)), col\_names = TRUE))

## prepare the data for the differential equation

rownames(mcountData) <- mcountData[, 1] ## Set index rowname

mcountData <- mcountData[-1, -1] ## remove the 1st column and line

storage.mode(mcountData) <- "integer" ## Change from characters to numbers

## Prepare the data coldata (colData)

colData <- data.frame(condition=ifelse(grepl("Col0C", colnames(mcountData)), "control", "triggered")) ## define analysis condition

rownames(colData) <- colnames(mcountData) ## Attribute categories

colData$condition <- factor(colData$condition) ## Change to factor

## Run the function (part 1) ----

dds <- DESeqDataSetFromMatrix(mcountData, colData, formula(~ condition))

## Conduct differential expression using DESeq2 in order to create 2 sets of results: -----

dds2 <- DESeq(dds, betaPrior = FALSE)

res <- results(dds2, contrast = c('condition','control','triggered'))

res2 <- lfcShrink(dds2, contrast = c('condition','control','triggered'), res = res, type = 'normal')

normCounts <- counts(dds2, normalized = T)

## Plot basic volcano plot ------

EnhancedVolcano(res2,

lab = rownames(res2),

x = 'log2FoldChange',

y = 'pvalue',

title = 'Bleue versus Rouge',

pCutoff = 10e-8, ## can be set to : 10e-30, 10e-10

FCcutoff = 0.4, ## can be set to : 0.5, 0.3

pointSize = 3.0,

labSize = 6.0)