setwd("/.../") # to load the dataset in the environment
library(hgu133acdf) # to load the Affymetrix CDF in the environment
library(gcrma) # to load the GCRMA package in the environment
library(pegase) # to load the Pegase package in the environment
library(hgu133atranscriptccds)
data(hgu133atranscriptccds) # this couple of commands allows to load the AffyProbeMiner’s CDF
hgu133atranscriptccdsdim<-hgu133adim # to replace the Affymetrix CDF by the AffyProbeMiner’s CDF
a<-justGCRMA(cdfname="hgu133atranscriptccds") # to use the AffyProbeMiner’s CDF and to pre-process the data into an expression set
b<-exprs(a) # to convert the expression set into a matrix
d<-b[,1:X]
e<-b[,X+1:Y] # these two commands allow to separate the matrix between the two conditions of the experiment
f<-pegase(A=d,B=e,steps=c("prepare","run"),methods=c("win.welch")) # to process the data, the two first arguments specify the matrix of each condition, the third argument specifies the steps of the processing, the last argument specifies the method used, here the Window Welch t test. The p values are stored in f$pvals
g<-sort(f$pvals) # to rank the probe sets in ascending order of their p values
h<-g[(1:50)] # to select the 50 most significant probe sets