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