file: produceType\_avgFiles.R

function: typeAvgFiles()

#read the signature matrix file and put each cell type values in a separate file.

#Then, it calculaes the acerage value (between samples) for each cell type and return each in a separate file.

File: valculateAdjPval.R

Function: pvalCalculation()

#read the separated file for each cell type, number of probes x number of samples, and calculate the pairwise adjusted p-value between cell types and return the ones for each cell type in a separate file (PvalB, PvalG, ...)

File: calculateEffectSize.R

Function: effectSize()

#read the files with the average values for each cell types, and return the effect size matrixes for them

file: produceSigMat

function: makeSigMat

#read the Pvalue, effectSize and average value files.

#check the threshold for Pvalues and effect size apirwise between cell types for each probe

#every probe which passes both threshold will be save in signature matrix with its average (between samples) values (between samples)

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file: Merge\_Mix\_SigMat.R

# extract the signature matrix probes and their values from mixture Matrix (example: LM22, merge ExampleMixtures-GEPs ), to be used for modeling

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File: svr.R

# Read the signature matrix and the mixture data (for the probes from signature matrix), and build the model using e1071 package.

(scale = F, type = "nu-regression")

---------------------------------------------

File: nnlm.R

# Read the signature matrix and the mixture data (for the probes from signature matrix), and build the model using nnls package.

---------------------------------------------

File: comPlotType

# reads the observed data and the predicted data from a single file (format important) amd make the scatterplot of predicted versus observed for each cell type.