

Package ‘classComparison’

October 13, 2019

Title Class Comparison between Groups of Arrays

Version 0.3

Description An implementation of the Class Comparison tool in ArrayTools

Depends R (>= 3.5.0)

License Same as BRB-ArrayTools
(<https://brb.nci.nih.gov/BRB-ArrayTools/>)

Imports sendplot

Encoding UTF-8

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RoxygenNote 6.1.1

Suggests knitr, rmarkdown

VignetteBuilder knitr

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classComparison	<i>Class Comparison between Groups of Arrays</i>
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Description

This function is used for comparing two or more pre-defined classes. The classes to be compared are in a vector. The vector can be any set of numerical, character or character string data. If an entry for a particular sample is left blank in the vector, that sample will be omitted from the class comparison analysis.

Usage

```
classComparison(exprData, geneIds, ClassVariableName, ClassVariableValues,
  geneFilter, IsSingleChannel, isPaired = FALSE, HasBlock = FALSE,
  HasDuplic = FALSE, GroupVariable = NULL, BlockVariable = NULL,
  duplic = NULL, BlockVariableName = NULL,
  ProportionOp = "optUnivariateTest", UnivarSignifLevel = 0.001,
  MaxProportionFD = 0.1, ConfLevel = 80, SignifLFDR = 0.05,
  DoRandomVariance = TRUE, DoUnivariatePermTest = FALSE,
  NumPermUnivariate = 10000, GlobalTest = FALSE,
  NumPermMultivariate = 1000, DoFoldThresh = FALSE,
  NumFoldThreshold = 2, NumAlphaPairwise = 0.01,
  IngenuityRefClass = "Automatically create the combination output",
  projectPath, outputName = "ClassComparison", generateHTML = FALSE)
```

Arguments

exprData	matrix of gene expression data for samples. Rows are genes and columns are arrays. Its column names must be provided.
geneIds	matrix/data frame of gene identifiers, such as Gene Symbols, Unique Ids, Clone Ids, Entrez Ids.
ClassVariableName	character string of the sample class variable name.
ClassVariableValues	vector of sample classes.
geneFilter	vector of 1/0's of the same length as genes. 1 means to keep the gene while 0 means to exclude the gene.
IsSingleChannel	logical. If TRUE, the data are single channel data, such as Affymatrix data.
isPaired	logical. If TRUE, samples are paired.
HasBlock	logical. If TRUE, samples have block variables.
HasDuplic	logical. If TRUE, samples need to average over replicate variables.
GroupVariable	vector of pairing variables for samples.
BlockVariable	vector of block variables for samples.
duplic	vector of average over replicate variables for samples.
BlockVariableName	character string of the block variable name.
ProportionOp	character string of the method used to find gene lists. <ul style="list-style-type: none"> "optUnivariateTest": Univariate tests. "optProportion": Multivariate permutation tests. "optLocalFDR": Local False Discovery Rate tests.
UnivarSignifLevel	numeric for a significance level of univariate tests. Default is 0.001.
MaxProportionFD	numeric for maximum proportion of false discoveries. Default is 0.1.
ConfLevel	numeric for multivariate permutation tests, between 0 and 100 percent. Default is 80.

SignifLFDR	numeric for a significance level of local False discovery rate tests. Default is 0.05.
DoRandomVariance	logical. If TRUE, use the random variance model for univariate tests. Default is TRUE.
DoUnivariatePermTest	logical. If TRUE, perform univariate permutation tests. Default is FALSE.
NumPermUnivariate	numeric specifying the number of permutations for the univariate permutation tests. Default is 10000.
GlobalTest	logical. If TRUE, perform P-value for global tests. Default is FALSE.
NumPermMultivariate	numeric specifying the number of permutations for the multivariate tests. Default is 1000.
DoFoldThresh	logical. If TRUE, restrict gene list based on fold change threshold. Default is FALSE.
NumFoldThreshold	numeric specifying the fold change threshold. Default is 2.
NumAlphaPairwise	numeric specifying the P-value threshold for pairwise difference. Default is 0.01.
IngenuityRefClass	character string of the reference class name for Ingenuity output. Default is "Automatically create the combination output".
projectPath	character string specifying the full project path.
outputName	character string specifying the output file folder name. The folder is in the projectPath. Default is "ClassComparison".
generateHTML	logical. If TRUE, show an HTML file with detailed class comparison results in the system default browser.

Details

The Class Comparison between Groups of Arrays function computes a t-test or F-test separately for each gene using the normalized log-ratios for cDNA arrays and the normalized log-intensities for one color oligonucleotide arrays. The F-test is a generalization of the two-sample t-test for comparing values among groups. It has the option of using the random variance version of the t-test or F-test. They provide for sharing information among genes of the within-class variance in log-ratios or log signals. The class comparison function computes the number of genes that are differentially expressed among the classes at the statistical significance level selected in the F-test and creates a gene list containing information about the significant genes.

It implements the Class Comparison between Groups of Arrays tool in BRB-ArrayTools.

Please see the BRB-ArrayTools manual (<https://brb.nci.nih.gov/BRB-ArrayTools/Documentation.html>) for details.

Value

A list includes the following objects:

- classifierTable: a data frame with the performance of classifiers.
- workPath: the path for Fortran and other intermediate output files.
- outputPath: the path for final result output files.

Note

Following functions were disabled:

- Create the chromosome distribution plot.
- Perform GO Observed vs Expected analysis.

See Also

[test.classComparison](#)

Examples

```
dataset<-"Brca"
# Gene IDs
geneIds <- read.delim(system.file("extdata", paste0(dataset, "_GENEID.txt")
, package = "classComparison"), as.is = TRUE, colClasses = "character")
# Expression data, and here are log ratio.
x <- read.delim(system.file("extdata", paste0(dataset, "_LOGRAT.TXT")
, package = "classComparison"), header = FALSE)
# Gene filter information, 1 - pass the filter, 0 - filtered
geneFilter <- scan(system.file("extdata", paste0(dataset, "_FILTER.TXT")
, package = "classComparison"), quiet = TRUE)
# Class information
expDesign <- read.delim(system.file("extdata", paste0(dataset, "_EXPDESIGN.txt")
, package = "classComparison"), as.is = TRUE)
# Pick the first column as the array IDs.
arrayIds <- expDesign[, 1]
exprData <- x
colnames(exprData) <- expDesign[, 1]
# Pick the 3rd column as the class variable.
nColumn = 3
ClassVariableName = gsub("[.]", " ", colnames(expDesign)[nColumn])
ClassVariableValues <- expDesign[, nColumn]
projectPath <- tempdir()
outputName = "ClassComparison"
singleChannel <- ifelse(dataset == "Pomeroy", TRUE, FALSE)
generateHTML = TRUE
resList <- classComparison(exprData=exprData,
                           geneIds=geneIds,
                           ClassVariableName=ClassVariableName,
                           ClassVariableValues=ClassVariableValues,
                           geneFilter=geneFilter,
                           IsSingleChannel=singleChannel,
                           projectPath=projectPath,
                           outputName=outputName,
                           generateHTML=generateHTML)
```

test.classComparison *Test classComparison() function*

Description

This function will load a test dataset to run the `classComparison` function.

Usage

```
test.classComparison(dataset = c("Brca", "Perou", "Pomeroy"),  
  projectPath, outputName = "ClassComparison", generateHTML = FALSE)
```

Arguments

<code>dataset</code>	character string specifying one of "Brca", "Perou" or "Pomeroy" datasets.
<code>projectPath</code>	character string specifying the project path. Default is C:/Users/UserName/Documents/\$dataset.
<code>outputName</code>	character string for the output folder name.
<code>generateHTML</code>	logical. If TRUE, show an HTML file with detailed class comparison results in the system default browser.

Value

A list as returned by `classComparison`.

See Also

[classComparison](#)

Examples

```
test.classComparison("Brca")
```

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