Package ‘fdrame’

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Title FDR adjustments of Microarray Experiments (FDR-AME)

Version 1.46.0

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Description This package contains two main functions. The first is fdr.ma which takes normalized expression data array, experimental design and computes adjusted p-values. It returns the fdr adjusted p-values and plots, according to the methods described in (Reiner, Yekutieli and Benjamini 2002). The second, is fdr.gui() which creates a simple graphic user interface to access fdr.ma

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Imports tcltk, graphics, grDevices, stats, utils

biocViews Microarray, DifferentialExpression, MultipleComparison

NeedsCompilation yes

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Description

A vector of integers specifying for each column(sample) to which group number it belongs.

Usage
data(design)
exp.arr

Format
The format is: num [1:16] 0 0 0 0 0 0 0 1 1 1 1 1 1 1 1

Details
In the example above there are two groups. Each group contains 8 samples

Examples
data(design)

data(exp.arr)  Normalized Expression Array

Description
The source of this Data is a lipid metabolism study described and analyzed in Dudoit,S., Yang,Y.H, Callow,M.J. and Speed,T.P. (2002) Statistical Methods for Identifying Differentially Expressed Genes in Replicated cDNA Microarray Experiments. Stat Sinica, 12, 111-139.

Usage
data(exp.arr)

Format
The format is: num [1:6384, 1:16] -0.2500 0.0329 -0.2065 -0.2240 -0.8542 ... - attr(*, "dim-names")=List of 2 Each row represents a gene: chr [1:6384] "1" "2" "3" "4" ... Each column represents a sample : chr [1:16] "X1" "X2" "X3" "X4" ...

Details
The data is normalized.

Source
http://www.stat.berkeley.edu/users/terry/zarray/Html/matt.html

References

Examples
data(exp.arr)
fdr.gui

Description
This function runs the fdrame Graphic User Interface.

Usage
fdr.gui()

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References

Examples
fdr.gui()

fdr.ma

Description
This function takes normalized expression data array, experimental design and computes adjusted p-values. It returns the fdr adjusted p-values and plots, according to the methods described in (Reiner, Yekutieli and Benjamini 2002)

Usage
fdr.ma(exp.arr,design,p.method="resampling",fdr.adj="BH-LSU",equal.var=TRUE,plot=c("pvlVSrank","adjVSstat"),perms.num=100)

Arguments
exp.arr A data frame or matrix, with m rows corresponding to the gene expression level of an observation and n columns to the observations. In the case of gene expression data, rows correspond to genes and columns to mRNA samples. The data can be read using 'read.table'. The matrix is as the X matrix in multtest package.
design A vector of charachters corresponding to observation (column) class labels. For k classes, the labels must be k different charachters. The vector is similar to classlabel vector in multtest package.
p.method A character string specifying whether resampling method may be used. If `p.method="resampling"`, resampling method is used. If `p.method="theoretic"`, statistic is computed without resampling.

fdr.adj A character string specifying which type of p-value adjustment method may be used. If `fdr.adj="BH-LSU"`, Benjamini-Hochberg Linear Step Up procedure is used. If `fdr.adj="point.est"`, point estimation procedure is used. (p.method value must be "resampling") If `fdr.adj="upper.est"`, upper estimation procedure is used. (p.method value must be "resampling") If `fdr.adj="adaptive"`, two-stage adaptive procedure is used.

equal.var A boolean variable specifying whether equal variance assumption may be taken. If TRUE, an equal group variances is assumed. If FALSE, welch approximation is used, for the unequal group variances

plot A vector of character strings specifying the plots that may be drawn. If the vector contains "pvlVSrank", a plot of p-values vs rank is drawn. If the vector contains "adjVSrank", a plot of adjusted p-values vs rank is drawn. If the vector contains "adjVSstat", a plot of adjusted p-values vs computed statistic (f or t, depends depends on the number of groups on the design) is drawn.

perms.num An integer specifying the number of permutations that would be used.

Value
A data frame with components

adj adjusted p-values.

dif When there are only two groups dif contains the differences between the means of the two groups. when there are more than two groups dif contains the multiple R-Squared values.

res.pvalues resampling p-values. (in case resampling was requested)

Author(s)
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References

Examples
```r
data(exp.arr,design)
output<-fdr.ma(exp.arr,design,p.method="theoretic",fdr.adj="BH-LSU",equal.var=TRUE,plot=c("pvlVSrank","adjVSrank","adjVSstat"))
```
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