Package 'webbioc'

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Title Bioconductor Web Interface

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Depends R (>= 1.8.0), Biobase, affy, multtest, annaffy, vsn, gcrma, qvalue

Imports multtest, qvalue, stats, utils, BiocManager

SystemRequirements Unix, Perl (>= 5.6.0), Netpbm

Description An integrated web interface for doing microarray analysis using several of the Bioconductor packages. It is intended to be deployed as a centralized bioinformatics resource for use by many users. (Currently only Affymetrix oligonucleotide analysis is supported.)

License GPL (>= 2)

URL http://www.bioconductor.org/

LazyLoad yes

biocViews Infrastructure, Microarray, OneChannel, DifferentialExpression

git_url https://git.bioconductor.org/packages/webbioc

git_branch RELEASE_3_21

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Repository Bioconductor 3.21

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Contents

`installReps` *Install all repository packages*

Description

Using reposTools, install/update all packages from given repositories.

Usage

```
installReps(repNames = "aData", lib = .libPaths()[1],
            type = getOption("pkgType"))
```

Arguments

`repNames`	A character vector containing repository names. A listing of known repository names can be found with the getReposOption() function.
`lib`	A path to install/update the packages. If this directory does not exist, it will be created (if possible).
`type`	type of package do download

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`mt.wrapper` *Multiple Testing Wrapper Function*

Description

A wrapper for some of the functionality for the `multtest` package. It also includes hooks to calculate q-values with John D. Storey's '`q-value.R`' code.

Usage

```
mt.wrapper(proc, X, classlabel, test="t", rawpcalc="Parametric", side="abs", ...)
```

Arguments

proc	A character string containing the name of the multiple testing procedure for which adjusted p-values are to be computed. This vector should include any of the following: "Bonferroni", "Holm", "Hochberg", "SidakSS", "SidakSD", "BH", "BY", "maxT", "minP", "q".
X	A data frame or matrix, with m rows corresponding to variables (hypotheses) and n columns to 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.
classlabel	A vector of integers corresponding to observation (column) class labels. For k classes, the labels must be integers between 0 and $k-1$. For the blockf test option, observations may be divided into n/k blocks of k observations each. The observations are ordered by block, and within each block, they are labeled using the integers 0 to $k-1$.
test	A character string specifying the statistic to be used to test the null hypothesis of no association between the variables and the class labels. If test="t", the tests are based on two-sample Welch t-statistics (unequal variances). If test="t.equalvar", the tests are based on two-sample t-statistics with equal variance for the two samples. The square of the t-statistic is equal to an F-statistic for $k=2$. If test="wilcoxon", the tests are based on standardized rank sum Wilcoxon statistics. If test="f", the tests are based on F-statistics. If test="pair", the tests are based on paired t-statistics. The square of the paired t-statistic is equal to a block F-statistic for $k=2$. If test="blockf", the tests are based on F-statistics which adjust for block differences (cf. two-way analysis of variance).
rawpcalc	A character string specifying how to calculate nominal/raw p-values. The possible choices are "Parametric" or "Permutation".
side	A character string specifying the type of rejection region. If side="abs", two-tailed tests, the null hypothesis is rejected for large absolute values of the test statistic. If side="upper", one-tailed tests, the null hypothesis is rejected for large values of the test statistic. If side="lower", one-tailed tests, the null hypothesis is rejected for small values of the test statistic.
...	Further arguments for mt.maxT, mt.minP, qvalue.

Value

A data frame with components

index	Vector of row indices, between 1 and nrow(X), where rows are sorted first according to their adjusted p-values, next their unadjusted p-values, and finally their test statistics.

teststat	Vector of test statistics, ordered according to index. To get the test statistics in the original data order, use teststat[order(index)].
rawp	Vector of raw (unadjusted) p-values, ordered according to index.
adjp	Vector of adjusted p-values, ordered according to index.
plower	For mt.minP function only, vector of "adjusted p-values", where ties in the permutation distribution of the successive minima of raw p-values with the observed p-values are counted only once. Note that procedures based on plower do not control the FWER. Comparison of plower and adjp gives an idea of the discreteness of the permutation distribution. Values in plower are ordered according to index.

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