Package 'webbioc'

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Version 1.81.0

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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 devel

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Repository Bioconductor 3.22

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Contents

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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

Author(s)

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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 cor-
                respond 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="pairt"`, 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`.

Author(s)

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