

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_19

git_last_commit 0dc07a7

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| | |
|-------------|--|
| installReps | <i>Install all repository packages</i> |
|-------------|--|

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 | <i>Multiple Testing Wrapper Function</i> |
|------------|--|

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

| | |
|-------------------------|---|
| <code>proc</code> | 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". |
| <code>X</code> | 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 . |
| <code>classlabel</code> | 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 $k - 1$. |
| <code>test</code> | 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 <code>test="t"</code> , the tests are based on two-sample Welch t-statistics (unequal variances). If <code>test="t.equalvar"</code> , 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 <code>test="wilcoxon"</code> , the tests are based on standardized rank sum Wilcoxon statistics. If <code>test="f"</code> , the tests are based on F-statistics. If <code>test="pairt"</code> , 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 <code>test="blockf"</code> , the tests are based on F-statistics which adjust for block differences (cf. two-way analysis of variance). |
| <code>rawpcalc</code> | A character string specifying how to calculate nominal/raw p-values. The possible choices are "Parametric" or "Permutation". |
| <code>side</code> | A character string specifying the type of rejection region. If <code>side="abs"</code> , two-tailed tests, the null hypothesis is rejected for large absolute values of the test statistic. If <code>side="upper"</code> , one-tailed tests, the null hypothesis is rejected for large values of the test statistic. If <code>side="lower"</code> , one-tailed tests, the null hypothesis is rejected for small values of the test statistic. |
| <code>...</code> | Further arguments for <code>mt.maxT</code> , <code>mt.minP</code> , <code>qvalue</code> . |

Value

A data frame with components

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

| | |
|-----------------------|---|
| <code>teststat</code> | Vector of test statistics, ordered according to <code>index</code> . To get the test statistics in the original data order, use <code>teststat[order(index)]</code> . |
| <code>rawp</code> | Vector of raw (unadjusted) p -values, ordered according to <code>index</code> . |
| <code>adjp</code> | Vector of adjusted p -values, ordered according to <code>index</code> . |
| <code>plower</code> | For <code>mt.minP</code> 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 <code>plower</code> do not control the FWER. Comparison of <code>plower</code> and <code>adjp</code> gives an idea of the discreteness of the permutation distribution. Values in <code>plower</code> are ordered according to <code>index</code> . |

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