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
git_last_commit_date 2024-04-30
Repository Bioconductor 3.19
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installReps

*Install all repository packages*

**Description**

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

**Usage**

```r
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 to 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**

```r
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 \texttt{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 \texttt{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 \texttt{test="t"}, the tests are based on two-sample Welch t-statistics (unequal variances). If \texttt{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 \texttt{test="wilcoxon"}, the tests are based on standardized rank sum Wilcoxon statistics. If \texttt{test="f"}, the tests are based on F-statistics. If \texttt{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 \texttt{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 \texttt{side="abs"}, two-tailed tests, the null hypothesis is rejected for large absolute values of the test statistic. If \texttt{side="upper"}, one-tailed tests, the null hypothesis is rejected for large values of the test statistic. If \texttt{side="lower"}, one-tailed tests, the null hypothesis is rejected for small values of the test statistic.

... Further arguments for \texttt{mt.maxT}, \texttt{mt.minP}, \texttt{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 \texttt{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 \texttt{plower} do not control the FWER. Comparison of \texttt{plower} and \texttt{adjp} gives an idea of the discreteness of the permutation distribution. Values in \texttt{plower} are ordered according to index.

Author(s)

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