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, BiocInstaller

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

NeedsCompilation no

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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

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

Value  A data frame with components

index  Vector of row indices, between 1 and \( \text{nrow}(X) \), 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 \text{teststat}[\text{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 \text{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 \text{plower} do not control the FWER. Comparison of \text{plower} and \text{adjp} gives an idea of the discreteness of the permutation distribution. Values in \text{plower} are ordered according to index.

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