Package ‘webbioc’

April 26, 2017

Version  1.48.0
Date     2009-02-05
Title    Bioconductor Web Interface
Author   Colin A. Smith <colin@colinsmith.org>
Maintainer Colin A. Smith <colin@colinsmith.org>
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

R topics documented:

installReps ................................................................. 2
mt.wrapper ................................................................. 2
Index 4
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 do download

**Author(s)**

Colin A. Smith <webbioc@colinsmith.org>

---

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 `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 \( \text{nrow}(X) \), 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 \texttt{index}. To get the test statistics in the original data order, use \texttt{teststat[order(index)]}.

rawp
Vector of raw (unadjusted) \( p \)-values, ordered according to \texttt{index}.

adjp
Vector of adjusted \( p \)-values, ordered according to \texttt{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 \texttt{index}.

Author(s)
Colin A. Smith <webbioc@colinsmith.org>
Index

*Topic file
  installReps, 2
  mt.wrapper, 2

installReps, 2

mt.minP, 3
mt.wrapper, 2

read.table, 2