webbioc
April 19, 2009

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).

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
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, mt.minP, qvalue}.

Value

A data frame with components

index
Vector of row indices, between 1 and \( \texttt{nrow(X)} \), 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}. 

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)

Colin A. Smith (webbioc@colinsmith.org)
Index

*Topic file*
  installReps, 1
  mt.wrapper, 1

installReps, 1

mt.minP, 3
mt.wrapper, 1

read.table, 2