

# Package ‘webbioc’

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**Version** 1.76.0

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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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**Repository** Bioconductor 3.19

**Date/Publication** 2024-05-01

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

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**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> |
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**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 <a href="#">read.table</a> .   |
| 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.<br>If test="t", the tests are based on two-sample Welch t-statistics (unequal variances).<br>If 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 $k = 2$ .<br>If test="wilcoxon", the tests are based on standardized rank sum Wilcoxon statistics.<br>If test="f", the tests are based on F-statistics.<br>If 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 $k = 2$ .<br>If test="blockf", the tests are based on F-statistics which adjust for block differences (cf. two-way analysis of variance). |
| rawpvalc   | 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.<br>If side="abs", two-tailed tests, the null hypothesis is rejected for large absolute values of the test statistic.<br>If side="upper", one-tailed tests, the null hypothesis is rejected for large values of the test statistic.<br>If side="lower", one-tailed tests, the null hypothesis is rejected for small values of the test statistic.  |
| ...        | Further arguments for mt.maxT, mt.minP, 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. |
|-------|--|

|                       |   |
|-----------------------|---|
| <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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