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multtest

platforms	all	rank	42 / 2041	support	0 / 0	in Bioc	> 16.5 years
build	warnings	updated	before release	dependencies	15		

DOI: [10.18129/B9.bioc.multtest](https://doi.org/10.18129/B9.bioc.multtest) [f](#) [t](#)

Resampling-based multiple hypothesis testing

Bioconductor version: Release (3.13)

Non-parametric bootstrap and permutation resampling-based multiple testing procedures (including empirical Bayes methods) for controlling the family-wise error rate (FWER), generalized family-wise error rate (gFWER), tail probability of the proportion of false positives (TPFP), and false discovery rate (FDR). Several choices of bootstrap-based null distribution are implemented (centered, centered and scaled, quantile-transformed). Single-step and step-wise methods are available. Tests based on a variety of t- and F-statistics (including t-statistics based on regression parameters from linear and survival models as well as those based on correlation parameters) are included. When probing hypotheses with t-statistics, users may also select a potentially faster null distribution which is multivariate normal with mean zero and variance covariance matrix derived from the vector influence function. Results are reported in terms of adjusted p-values, confidence regions and test statistic cutoffs. The procedures are directly applicable to identifying differentially expressed genes in DNA microarray experiments.

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Citation (from within R, enter `citation("multtest")`):

Pollard KS, Dudoit S, van der Laan MJ (2005). *Multiple Testing Procedures: R multtest Package and Applications to Genomics, in Bioinformatics and Computational Biology Solutions Using R and Bioconductor*. Springer.

Installation

To install this package, start R (version "4.1") and enter:

```
if (!requireNamespace("BiocManager", quietly = TRUE))
  install.packages("BiocManager")
```

```
BiocManager::install("multtest")
```

For older versions of R, please refer to the appropriate [Bioconductor release](#).

Documentation

[PDF](#) Reference Manual

Details

biocViews	DifferentialExpression , Microarray , MultipleComparison , Software
Version	2.48.0
In Bioconductor since	BioC 1.6 (R-2.1) or earlier (> 16.5 years)
License	LGPL
Depends	R (>= 2.10), methods, BiocGenerics , Biobase
Imports	survival , MASS , stats4
LinkingTo	
Suggests	snow
SystemRequirements	
Enhances	
URL	
Depends On Me	aCGH , BicARE , iPAC , KCsmart , PREDA , rain , REDseq , SAGx , siggenes , webbioc
Imports Me	a4Base , ABarray , adSplit , ALDEx2 , anota , anota2seq , ChIPpeakAnno , IsoGeneGUI , mAPKL , metabomxtr , nethet , OCplus , phyloseq , RTopper , SingleCellSignalR , singleCellTK , synapter , webbioc
Suggests Me	annaffy , BiocCaseStudies , ecolitr , factDesign , GOstats , GSEAlm , maigesPack , pcot2 , ropls , topGO , xcms
Links To Me	Build Report

Package Archives

Follow [Installation](#) instructions to use this package in your R session.

Source Package	multtest_2.48.0.tar.gz
Windows Binary	multtest_2.48.0.zip
macOS 10.13 (High Sierra)	multtest_2.48.0.tgz
Source Repository	git clone https://git.bioconductor.org/packages/multtest
Source Repository (Developer Access)	git clone git@git.bioconductor.org:packages/multtest
Package Short Url	https://bioconductor.org/packages/multtest/
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