

Resource Summary Report

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multtest

RRID:SCR_001255

Type: Tool

Proper Citation

multtest (RRID:SCR_001255)

Resource Information

URL: <http://www.bioconductor.org/packages/release/bioc/html/multtest.html>

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Description: Software package for 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.

Abbreviations: multtest

Synonyms: multtest - Resampling-based multiple hypothesis testing

Resource Type: software resource

Keywords: differential expression, microarray, multiple comparison, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: multtest

Resource ID: SCR_001255

Alternate IDs: biotools:multtest, OMICS_02085

Alternate URLs: <https://bio.tools/multtest>

License: GNU Lesser General Public License

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Ratings and Alerts

No rating or validation information has been found for multtest.

No alerts have been found for multtest.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 35 mentions in open access literature.

Listed below are recent publications. The full list is available at [ASWG](#) .

Roig-Villanova I, et al. (2025) Plant proximity reduces seed yield in Arabidopsis plants by decreasing the number of ovule primordia. *Physiologia plantarum*, 177(2), e70220.

Wang W, et al. (2025) Mac-1 regulates disease stage-specific immunosuppression via the nitric oxide pathway in autoimmune disease. *Science advances*, 11(19), eads3728.

Baer JL, et al. (2025) Microbiome spatial scaling varies among members, hosts, and environments across model island ecosystems. *The ISME journal*, 19(1).

Xiong J, et al. (2025) A Meta-Analysis of the Effects of Chronic Stress on the Prefrontal Transcriptome in Animal Models and Convergence with Existing Human Data. *bioRxiv* : the preprint server for biology.

Ullrich LE, et al. (2024) A Retrospective Analysis of Career Outcomes in Neuroscience. *eNeuro*, 11(5).

Allen O, et al. (2024) Differential Serum Levels of CACNA1C, Circadian Rhythm and Stress Response Molecules in Subjects with Bipolar Disorder: Associations with Genetic and Clinical Factors. *medRxiv* : the preprint server for health sciences.

Preston NJ, et al. (2023) Feasibility testing of a standardised virtual clinic for follow-up of patients after hip and knee arthroplasty. *Annals of the Royal College of Surgeons of England*, 105(3), 252.

- Cho S, et al. (2023) Phenylpropionic acid produced by gut microbiota alleviates acetaminophen-induced hepatotoxicity. *Gut microbes*, 15(1), 2231590.
- Majed SO, et al. (2023) The profiles of miR-4510 expression level in breast cancer. *Scientific reports*, 13(1), 2262.
- Chen L, et al. (2022) Short- and long-read metagenomics expand individualized structural variations in gut microbiomes. *Nature communications*, 13(1), 3175.
- Luo H, et al. (2021) Single-cell Long Non-coding RNA Landscape of T Cells in Human Cancer Immunity. *Genomics, proteomics & bioinformatics*, 19(3), 377.
- Wang L, et al. (2021) Long non-coding RNAs ENST00000429730.1 and MSTRG.93125.4 are associated with metabolic activity in tuberculosis lesions of sputum-negative tuberculosis patients. *Aging*, 13(6), 8228.
- Arbet J, et al. (2021) Comparing Statistical Tests for Differential Network Analysis of Gene Modules. *Frontiers in genetics*, 12, 630215.
- Ullrich LE, et al. (2021) Factors That Influence Career Choice among Different Populations of Neuroscience Trainees. *eNeuro*, 8(3).
- Birt IA, et al. (2021) Genetic Liability for Internalizing Versus Externalizing Behavior Manifests in the Developing and Adult Hippocampus: Insight From a Meta-analysis of Transcriptional Profiling Studies in a Selectively Bred Rat Model. *Biological psychiatry*, 89(4), 339.
- Ferrando-Bernal M, et al. (2020) Mapping co-ancestry connections between the genome of a Medieval individual and modern Europeans. *Scientific reports*, 10(1), 6843.
- Champigny MJ, et al. (2020) Learning from methylomes: epigenomic correlates of *Populus balsamifera* traits based on deep learning models of natural DNA methylation. *Plant biotechnology journal*, 18(6), 1361.
- Herrmann M, et al. (2020) Lumenal calcification and microvasculopathy in fetuin-A-deficient mice lead to multiple organ morbidity. *PLoS one*, 15(2), e0228503.
- Kiel C, et al. (2020) A Circulating MicroRNA Profile in a Laser-Induced Mouse Model of Choroidal Neovascularization. *International journal of molecular sciences*, 21(8).
- Fujiwara K, et al. (2020) Interrogating the immune-modulating roles of radiation therapy for a rational combination with immune-checkpoint inhibitors in treating pancreatic cancer. *Journal for immunotherapy of cancer*, 8(2).