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 (TPPFP), 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

Funding:

Availability: GNU Lesser General Public License

Resource Name: multtest

Resource ID: SCR_001255

Alternate IDs: biotools:multtest, OMICS_02085

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

Record Creation Time: 20220129T080206+0000

Record Last Update: 20250420T014024+0000

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 31 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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.

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).

Herrmann M, et al. (2020) Lumenal calcification and microvasculopathy in fetuin-A-deficient mice lead to multiple organ morbidity. PloS one, 15(2), e0228503.

Sofer T, et al. (2020) Low oxygen saturation during sleep reduces CD1D and RAB20 expressions that are reversed by CPAP therapy. EBioMedicine, 56, 102803.

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).

Fernández R, et al. (2020) Selection following Gene Duplication Shapes Recent Genome Evolution in the Pea Aphid Acyrthosiphon pisum. Molecular biology and evolution, 37(9), 2601.

Shu T, et al. (2020) Plasma Proteomics Identify Biomarkers and Pathogenesis of COVID-19. Immunity, 53(5), 1108.

Kiel C, et al. (2020) Pleiotropic Locus 15q24.1 Reveals a Gender-Specific Association with Neovascular but Not Atrophic Age-Related Macular Degeneration (AMD). Cells, 9(10).