Resource Summary Report

Generated by NIF on Apr 17, 2025

Q-Value Software

RRID:SCR_008538
Type: Tool

Proper Citation

Q-Value Software (RRID:SCR_008538)

Resource Information

URL: http://genomine.org/qvalue/

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Description: Features: * This software takes a list of p-values resulting from the simultaneous testing of many hypotheses and estimates their q-values. A point-and-click interface is now available! * The q-value of a test measures the proportion of false positives incurred (called the false discovery rate) when that particular test is called significant. * A short tutorial on q-values and false discovery rates is provided with the manual. * Various plots are automatically generated, allowing one to make sensible significance cut-offs. * Several mathematical results have recently been shown on the conservative accuracy of the estimated q-values from this software. * The software can be applied to problems in genomics, brain imaging, astrophysics, and data mining. This research was supported in part by a National Science Foundation graduate research fellowship.

Synonyms: Q-Value Software

Resource Type: software resource

Funding:

Resource Name: Q-Value Software

Resource ID: SCR_008538

Alternate IDs: nif-0000-31382

Record Creation Time: 20220129T080248+0000

Record Last Update: 20250410T065724+0000

Ratings and Alerts

No rating or validation information has been found for Q-Value Software.

No alerts have been found for Q-Value Software.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Filippou P, et al. (2021) Systems biology reveals key tissue-specific metabolic and transcriptional signatures involved in the response of Medicago truncatula plant genotypes to salt stress. Computational and structural biotechnology journal, 19, 2133.

Pellegrini M, et al. (2016) Protein complex prediction for large protein protein interaction networks with the Core&Peel method. BMC bioinformatics, 17(Suppl 12), 372.

Szoboszlay M, et al. (2016) The Effect of Root Exudate 7,4'-Dihydroxyflavone and Naringenin on Soil Bacterial Community Structure. PloS one, 11(1), e0146555.

Liu YZ, et al. (2009) Genome-wide association analyses identify SPOCK as a key novel gene underlying age at menarche. PLoS genetics, 5(3), e1000420.

Crawford NP, et al. (2005) Evaluation of SLC11A1 as an inflammatory bowel disease candidate gene. BMC medical genetics, 6, 10.