Resource Summary Report

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GoBean - a Java application for Gene Ontology enrichment analysis

RRID:SCR_005808
Type: Tool

Proper Citation

GoBean - a Java application for Gene Ontology enrichment analysis (RRID:SCR_005808)

Resource Information

URL:
http://ftp://ftp.geneontology.org/pub/go/www/GO.tools_by_type.term_enrichment.shtml#gobean

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Description: GoBean is a Java application for gene ontology enrichment analysis. It utilizes the NetBeans platform framework. Features * Graphical comparison of multiple enrichment analysis results * Versatile filter facility for focused analysis of enrichment results * Effective exploitation of the graphical/hierarchical structure of GO * Evidence code based association filtering * Supports local data files such as the ontology obo file and gene association files * Supports late enrichment methods and multiple testing corrections * Built-in ID conversion for common species using Ensembl biomart service Platform: Windows compatible, Mac OS X compatible, Linux compatible

Abbreviations: GoBean

Resource Type: data processing software, software application, software resource

Defining Citation: PMID:22360891

Keywords: java, gene ontology, ontology, gene association, analysis, enrichment, term enrichment

Availability: Free for academic use

Resource Name: GoBean - a Java application for Gene Ontology enrichment analysis

Resource ID: SCR_005808

Alternate IDs: nlx_149296

Old URLs: http://neon.gachon.ac.kr/GoBean/

Record Creation Time: 20220129T080232+0000

Record Last Update: 20240626T053425+0000

Ratings and Alerts

No rating or validation information has been found for GoBean - a Java application for Gene Ontology enrichment analysis.

No alerts have been found for GoBean - a Java application for Gene Ontology enrichment analysis.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 21 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Deutsch EW, et al. (2023) The ProteomeXchange consortium at 10 years: 2023 update. Nucleic acids research, 51(D1), D1539.

Meng Y, et al. (2022) Novel factors contributing to fungal pathogenicity at early stages of Setosphaeria turcica infection. Molecular plant pathology, 23(1), 32.

Jadhao S, et al. (2022) RBCeq: A robust and scalable algorithm for accurate genetic blood typing. EBioMedicine, 76, 103759.

Chen H, et al. (2022) Two novel AMHR2 gene variants in monozygotic twins with persistent Müllerian duct syndrome: A case report and functional study. Molecular genetics & genomic medicine, 10(8), e1999.

Ji X, et al. (2022) Pituitary-Gland-Based Genes Participates in Intrauterine Growth Restriction in Piglets. Genes, 13(11).

Salifou K, et al. (2021) Chromatin-associated MRN complex protects highly transcribing genes from genomic instability. Science advances, 7(21).

Liu X, et al. (2020) Predicting Cancer Tissue-of-Origin by a Machine Learning Method Using DNA Somatic Mutation Data. Frontiers in genetics, 11, 674.

Wise MJ, et al. (2016) dCITE: Measuring Necessary Cladistic Information Can Help You Reduce Polytomy Artefacts in Trees. PloS one, 11(11), e0166991.

Fusar-Poli P, et al. (2016) Towards a Standard Psychometric Diagnostic Interview for Subjects at Ultra High Risk of Psychosis: CAARMS versus SIPS. Psychiatry journal, 2016, 7146341.

Hanrahan SJ, et al. (2016) Long-Term Task- and Dopamine-Dependent Dynamics of Subthalamic Local Field Potentials in Parkinson's Disease. Brain sciences, 6(4).

Reiss DJ, et al. (2015) cMonkey2: Automated, systematic, integrated detection of co-regulated gene modules for any organism. Nucleic acids research, 43(13), e87.

Pereira-Leal JB, et al. (2014) A comprehensive assessment of the transcriptome of cork oak (Quercus suber) through EST sequencing. BMC genomics, 15(1), 371.

Teo BG, et al. (2013) A deformable generic 3D model of haptoral anchor of Monogenean. PloS one, 8(10), e77650.

Wise MJ, et al. (2013) Mean protein evolutionary distance: a method for comparative protein evolution and its application. PloS one, 8(4), e61276.

Vlachos I, et al. (2013) Neural system prediction and identification challenge. Frontiers in neuroinformatics, 7, 43.

Villanueva-Cañas JL, et al. (2013) Improving genome-wide scans of positive selection by using protein isoforms of similar length. Genome biology and evolution, 5(2), 457.

Rubinstein WS, et al. (2013) The NIH genetic testing registry: a new, centralized database of genetic tests to enable access to comprehensive information and improve transparency. Nucleic acids research, 41(Database issue), D925.

Zycinski G, et al. (2013) Knowledge Driven Variable Selection (KDVS) - a new approach to enrichment analysis of gene signatures obtained from high-throughput data. Source code for biology and medicine, 8(1), 2.

Richmond P, et al. (2011) Democratic population decisions result in robust policy-gradient learning: a parametric study with GPU simulations. PloS one, 6(5), e18539.

Reardon W, et al. (2010) Expression profiling and cross-species RNA interference (RNAi) of desiccation-induced transcripts in the anhydrobiotic nematode Aphelenchus avenae. BMC molecular biology, 11, 6.