Resource Summary Report

Generated by NIF on May 21, 2025

JEPETTO

RRID:SCR_005909
Type: Tool

Proper Citation

JEPETTO (RRID:SCR_005909)

Resource Information

URL: http://apps.cytoscape.org/apps/jepetto

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Description: A Cytoscape plugin that performs integrated gene set analysis using information from interaction, pathways and processes databases. The plugin integrates information from three separate web servers specializing in enrichment analysis, pathways expansion and topological matching. It uses the TopoGSA server to identify topological analogies between the user selected gene set and the known pathways and processes. TopoGSA finds the most similar biological mechanism using the topological features of the interaction network of a user selected gene set. It is also able to suggest genes related to the query gene set using two pathway analysis servers EnrichNet and PathExpand. Both these servers are using a different topological matching algorithms that extends the query gene set with genes from the pathway databases. This integration substantially simplifies the analysis of user gene sets and the interpretation of the results.

Abbreviations: JEPETTO

Synonyms: Java Enrichment of Pathways Extended To Topology

Resource Type: software resource

Defining Citation: PMID:24363376

Keywords: gene set enrichment analysis, topological analysis, interaction network, java, enrichment analysis, functional analysis, gene prioritization, integrated analysis, network analysis, interaction, pathway, process, topology, gene

Funding:

Availability: GNU General Public License

Resource Name: JEPETTO

Resource ID: SCR_005909

Alternate IDs: OMICS_02247

Record Creation Time: 20220129T080233+0000

Record Last Update: 20250519T203423+0000

Ratings and Alerts

No rating or validation information has been found for JEPETTO.

No alerts have been found for JEPETTO.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Tribondeau A, et al. (2024) Overlapping action of T3 and T4 during Xenopus laevis development. Frontiers in endocrinology, 15, 1360188.

Buddham R, et al. (2022) Reconstruction and Exploratory Analysis of mTORC1 Signaling Pathway and Its Applications to Various Diseases Using Network-Based Approach. Journal of microbiology and biotechnology, 32(3), 365.

Hammouz RY, et al. (2020) Differential expression of lung adenocarcinoma transcriptome with signature of tobacco exposure. Journal of applied genetics, 61(3), 421.

Kerdivel G, et al. (2019) Opposite T3 Response of ACTG1-FOS Subnetwork Differentiate Tailfin Fate in Xenopus Tadpole and Post-hatching Axolotl. Frontiers in endocrinology, 10, 194.

Zheng JJ, et al. (2018) Low expression of aging-related NRXN3 is associated with Alzheimer disease: A systematic review and meta-analysis. Medicine, 97(28), e11343.

Miryala SK, et al. (2018) Discerning molecular interactions: A comprehensive review on

biomolecular interaction databases and network analysis tools. Gene, 642, 84.

Wang X, et al. (2018) Identification of Steroidogenic Components Derived From Gardenia jasminoides Ellis Potentially Useful for Treating Postmenopausal Syndrome. Frontiers in pharmacology, 9, 390.

Capaia M, et al. (2018) A hnRNP K?AR-Related Signature Reflects Progression toward Castration-Resistant Prostate Cancer. International journal of molecular sciences, 19(7).

Huang J, et al. (2017) Identification of the active compounds and significant pathways of yinchenhao decoction based on network pharmacology. Molecular medicine reports, 16(4), 4583.

Zhou XJ, et al. (2016) Novel identified associations of RGS1 and RASGRP1 variants in IgA Nephropathy. Scientific reports, 6, 35781.

Halabi NM, et al. (2016) Preferential Allele Expression Analysis Identifies Shared Germline and Somatic Driver Genes in Advanced Ovarian Cancer. PLoS genetics, 12(1), e1005755.

Kawase R, et al. (2016) EP300 Protects from Light-Induced Retinopathy in Zebrafish. Frontiers in pharmacology, 7, 126.

Sui S, et al. (2015) Gene set enrichment and topological analyses based on interaction networks in pediatric acute lymphoblastic leukemia. Oncology letters, 10(6), 3354.

Wang S, et al. (2015) Network pharmacological identification of active compounds and potential actions of Erxian decoction in alleviating menopause-related symptoms. Chinese medicine, 10, 19.

Monti C, et al. (2015) Systems biology analysis of the proteomic alterations induced by MPP(+), a Parkinson's disease-related mitochondrial toxin. Frontiers in cellular neuroscience, 9, 14.