Resource Summary Report

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GraphWeb

RRID:SCR_005746
Type: Tool

Proper Citation

GraphWeb (RRID:SCR_005746)

Resource Information

URL: http://biit.cs.ut.ee/graphweb/

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Description: GraphWeb allows the detection of modules from biological, heterogeneous and multi-species networks, and the interpretation of detected modules using Gene Ontology, cis-regulatory motifs and biological pathways. GraphWeb is a public web server for graph-based analysis of biological networks that: * analyses directed and undirected, weighted and unweighted heterogeneous networks of genes, proteins and microarray probesets for many eukaryotic genomes; * integrates multiple diverse datasets into global networks; * incorporates multispecies data using gene orthology mapping; * filters nodes and edges based on dataset support, edge weight and node annotation; * detects gene modules from networks using a collection of algorithms; * interprets discovered modules using Gene Ontology, pathways, and cis-regulatory motifs. Platform: Online tool

Abbreviations: GraphWeb

Resource Type: data analysis service, production service resource, analysis service resource, service resource

Defining Citation: PMID:18460544

Keywords: analysis, biological network, ontology or annotation visualization, protein interaction, gene id conversion, orthology mapping, network visualization, graph clustering, gene ontology, cis-regulatory motif, module, network, pathway, biological pathway, motif, visualization, protein interaction, orthology mapping, network visualization, graph clustering, analysis, statistical analysis, term enrichment

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Availability: Open unspecified license - Free for academic use

Resource Name: GraphWeb

Resource ID: SCR_005746

Alternate IDs: nlx_149205

Record Creation Time: 20220129T080232+0000

Record Last Update: 20250419T055021+0000

Ratings and Alerts

No rating or validation information has been found for GraphWeb.

No alerts have been found for GraphWeb.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Zhang X, et al. (2019) Inferring immune-associated signatures based on a co-expression network in Guillain-Barré syndrome. Cell proliferation, 52(4), e12634.

Guan L, et al. (2019) A prognostic prediction system for hepatocellular carcinoma based on gene co-expression network. Experimental and therapeutic medicine, 17(6), 4506.

Wang Y, et al. (2018) A 44-gene set constructed for predicting the prognosis of clear cell renal cell carcinoma. International journal of molecular medicine, 42(6), 3105.

Zhang Y, et al. (2018) A 63 signature genes prediction system is effective for glioblastoma prognosis. International journal of molecular medicine, 41(4), 2070.

Wang H, et al. (2018) Detection of dysregulated competing endogenous RNA modules associated with clear cell kidney carcinoma. Molecular medicine reports, 18(2), 1963.

Zheng B, et al. (2018) Construction of a prognostic prediction system for pancreatic ductal adenocarcinoma to investigate the key prognostic genes. Molecular medicine reports, 17(1), 216.

Jiang H, et al. (2018) A 65?gene signature for prognostic prediction in colon adenocarcinoma. International journal of molecular medicine, 41(4), 2021.

Li Y, et al. (2017) Immunoglobulin superfamily genes are novel prognostic biomarkers for breast cancer. Oncotarget, 8(2), 2444.

Zhao L, et al. (2017) Identification of potential prognostic ceRNA module biomarkers in patients with pancreatic adenocarcinoma. Oncotarget, 8(55), 94493.

Pavlopoulos GA, et al. (2015) Visualizing genome and systems biology: technologies, tools, implementation techniques and trends, past, present and future. GigaScience, 4, 38.

Jia X, et al. (2014) Cancer-risk module identification and module-based disease risk evaluation: a case study on lung cancer. PloS one, 9(3), e92395.

Qu X, et al. (2014) Identifying colon cancer risk modules with better classification performance based on human signaling network. Genomics, 104(4), 242.