

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: analysis service resource, data analysis service, production 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: 20260905T133131+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 [PRECISE-TBI](#).

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.

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

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.