

Resource Summary Report

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Network Analysis, Visualization and Graphing TORonto

RRID:SCR_008373

Type: Tool

Proper Citation

Network Analysis, Visualization and Graphing TORonto (RRID:SCR_008373)

Resource Information

URL: <http://ophid.utoronto.ca/navigator/>

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Description: A software package for visualizing and analyzing protein-protein interaction networks. NAViGaTOR can query OPHID / I2D - online databases of interaction data - and display networks in 2D or 3D. To improve scalability and performance, NAViGaTOR combines Java with OpenGL to provide a 2D/3D visualization system on multiple hardware platforms. NAViGaTOR also provides analytical capabilities and supports standard import and export formats such as GO and the Proteomics Standards Initiative (PSI). NAViGaTOR can be installed and run on Microsoft Windows, Linux / UNIX, and Mac OS systems. NAViGaTOR is written in Java and uses JOGL (Java bindings for OpenGL) to support scalability, highlighting or suppressing of information, and other advanced graphic approaches.

Abbreviations: NAViGaTOR

Synonyms: NAViGaTOR - Network Analysis Visualization and Graphing TORonto, NAViGaTOR - Network Analysis Visualization & Graphing TORonto

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

Defining Citation: [PMID:19837718](#)

Keywords: fly, algorithm, capacity, graphical, graphing, human, interaction, interactome, intersection, mouse, network, node, protein, proteomic, rat, worm, yeast, graphing application, 2d visualization, 3d visualization, visualization, biological network, protein-protein interaction, gene, bio.tools

Funding: Genome Canada ;
Ontario Genomics Institute ;
Canada Research Chair Program ;
Ontario Research Fund Research Excellence ;
Canada Foundation for Innovation 12301;
Canada Foundation for Innovation 203383

Availability: Freely-downloadable for academic and not-for-profit institutions

Resource Name: Network Analysis, Visualization and Graphing TORonto

Resource ID: SCR_008373

Alternate IDs: nif-0000-25610, biotools:navigator

Alternate URLs: <https://bio.tools/navigator>

Record Creation Time: 20220129T080247+0000

Record Last Update: 20260801T042639+0000

Ratings and Alerts

No rating or validation information has been found for Network Analysis, Visualization and Graphing TORonto.

No alerts have been found for Network Analysis, Visualization and Graphing TORonto.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 52 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Mei H, et al. (2025) Network analysis of multivariate time series data in biological systems: methods and applications. Briefings in bioinformatics, 26(3).

Tavallae G, et al. (2022) Contribution of MicroRNA-27b-3p to Synovial Fibrotic Responses in Knee Osteoarthritis. Arthritis & rheumatology (Hoboken, N.J.), 74(12), 1928.

Cabral-Marques O, et al. (2022) Autoantibodies targeting GPCRs and RAS-related molecules associate with COVID-19 severity. Nature communications, 13(1), 1220.

Bhat M, et al. (2021) Estrogen Receptor 1 Inhibition of Wnt/?-Catenin Signaling Contributes to Sex Differences in Hepatocarcinogenesis. Frontiers in oncology, 11, 777834.

França TT, et al. (2021) CD40L modulates transcriptional signatures of neutrophils in the bone marrow associated with development and trafficking. *JCI insight*, 6(16).

Reiter A, et al. (2020) Interleukin-6 Gene Expression Changes after a 4-Week Intake of a Multispecies Probiotic in Major Depressive Disorder-Preliminary Results of the PROVIT Study. *Nutrients*, 12(9).

Boutin JA, et al. (2020) The five dimensions of receptor pharmacology exemplified by melatonin receptors: An opinion. *Pharmacology research & perspectives*, 8(1), e00556.

Felix TF, et al. (2019) MicroRNA modulated networks of adaptive and innate immune response in pancreatic ductal adenocarcinoma. *PloS one*, 14(5), e0217421.

Kotlyar M, et al. (2019) IID 2018 update: context-specific physical protein-protein interactions in human, model organisms and domesticated species. *Nucleic acids research*, 47(D1), D581.

Monette A, et al. (2019) Immune-enrichment of non-small cell lung cancer baseline biopsies for multiplex profiling define prognostic immune checkpoint combinations for patient stratification. *Journal for immunotherapy of cancer*, 7(1), 86.

Wong SWH, et al. (2018) Modeling tumor progression via the comparison of stage-specific graphs. *Methods (San Diego, Calif.)*, 132, 34.

Zhou G, et al. (2018) OmicsNet: a web-based tool for creation and visual analysis of biological networks in 3D space. *Nucleic acids research*, 46(W1), W514.

Pinheiro M, et al. (2017) HABP2 p.G534E variant in patients with family history of thyroid and breast cancer. *Oncotarget*, 8(25), 40896.

Lu CL, et al. (2017) Uncovering the relationship and mechanisms of Tartary buckwheat (*Fagopyrum tataricum*) and Type II diabetes, hypertension, and hyperlipidemia using a network pharmacology approach. *PeerJ*, 5, e4042.

Sokolina K, et al. (2017) Systematic protein-protein interaction mapping for clinically relevant human GPCRs. *Molecular systems biology*, 13(3), 918.

Mello JB, et al. (2017) Genomic profile in gestational and non-gestational choriocarcinomas. *Placenta*, 50, 8.

Posfai E, et al. (2017) Position- and Hippo signaling-dependent plasticity during lineage segregation in the early mouse embryo. *eLife*, 6.

Kuasne H, et al. (2017) Integrative miRNA and mRNA analysis in penile carcinomas reveals markers and pathways with potential clinical impact. *Oncotarget*, 8(9), 15294.

Bhat M, et al. (2017) Impact of Immunosuppression on the Metagenomic Composition of the Intestinal Microbiome: a Systems Biology Approach to Post-Transplant Diabetes. *Scientific reports*, 7(1), 10277.

Stojanova A, et al. (2016) MYC interaction with the tumor suppressive SWI/SNF complex member INI1 regulates transcription and cellular transformation. *Cell cycle (Georgetown, Tex.)*, 15(13), 1693.