Resource Summary Report

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Network Ontology Analysis

RRID:SCR_005667
Type: Tool

Proper Citation

Network Ontology Analysis (RRID:SCR_005667)

Resource Information

URL: http://app.aporc.org/NOA/

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Description: Network Ontology Analysis (NOA) (abbreviated to NOA) is a freely available collection of Gene Ontology tools aiming to analyze functions of gene network instead of gene list. Network rewiring facilitates the function changes between conditions even with the same gene list. Therefore, it is necessary to annotate the specific function of networks by considering the fundamental roles of interactions from the viewpoint of systems biology. NOA is such a novel functional enrichment analysis method capable to handle both dynamic and static networks. The application of NOA in biological networks shows that NOA can not only capture changing functions in rewiring networks but also find more relevant and specific functions in traditional static networks. Platform: Online tool

Abbreviations: NOA

Synonyms: Network Ontology Analysis (NOA)

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

Defining Citation: PMID:21543451

Keywords: gene, ontology, ontology or annotation browser, statistical analysis, term enrichment, browser

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Knowledge Innovation Program of CAS KSCX2-EW-R-01;
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NSFC 10801131;
NSFC 60970091;
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Availability: Open unspecified license - Free for academic use

Resource Name: Network Ontology Analysis

Resource ID: SCR_005667

Alternate IDs: nlx_149105

Record Creation Time: 20220129T080231+0000

Record Last Update: 20250407T215531+0000

Ratings and Alerts

No rating or validation information has been found for Network Ontology Analysis.

No alerts have been found for Network Ontology Analysis.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Wang L, et al. (2019) Detecting Diagnostic Biomarkers of Alzheimer's Disease by Integrating Gene Expression Data in Six Brain Regions. Frontiers in genetics, 10, 157.

Dong X, et al. (2016) LEGO: a novel method for gene set over-representation analysis by incorporating network-based gene weights. Scientific reports, 6, 18871.

Wang M, et al. (2015) Identification of pLG72-Induced Oxidative Stress Using Systemic Approaches. BioMed research international, 2015, 429253.

Kim BY, et al. (2015) Helveticoside is a biologically active component of the seed extract of Descurainia sophia and induces reciprocal gene regulation in A549 human lung cancer cells. BMC genomics, 16(1), 713.

Liu YS, et al. (2012) Chemoattraction of macrophages by secretory molecules derived from

cells expressing the signal peptide of eosinophil cationic protein. BMC systems biology, 6, 105.

Liu R, et al. (2012) Identifying critical transitions and their leading biomolecular networks in complex diseases. Scientific reports, 2, 813.

Sandhu KS, et al. (2012) Large-scale functional organization of long-range chromatin interaction networks. Cell reports, 2(5), 1207.