Resource Summary Report

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FunNet - Transcriptional Networks Analysis

RRID:SCR_006968
Type: Tool

Proper Citation

FunNet - Transcriptional Networks Analysis (RRID:SCR_006968)

Resource Information

URL: http://www.funnet.info/

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Description: Functional Analysis of Transcriptional Networks (FunNet) is designed as an integrative tool for analyzing gene co-expression networks built from microarray expression data. The analytical model implemented in this tool involves two abstraction layers: transcriptional (i.e. gene expression profiles) and functional (i.e. biological themes indicating the roles of the analyzed transcripts). A functional analysis technique, which relies on Gene Ontology and KEGG annotations, is applied to extract a list of relevant biological themes from microarray gene expression data. Afterwards multiple-instance representations are built to relate relevant biological themes to their annotated transcripts. An original non-linear dynamical model is used to quantify the contextual proximity of relevant genomic themes based on their patterns of propagation in the gene co-expression network (i.e. capturing the similarity of the expression profiles of the transcriptional instances of annotating themes). In the end an unsupervised multiple-instance spectral clustering procedure is used to explore the modular architecture of the co-expression network by grouping together biological themes demonstrating a significant relationship in the co-expression network. Functional and transcriptional representations of the co-expression network are provided, together with detailed information on the contextual centrality of related transcripts and genomic themes. FunNet is provided both as a web-based tool and as a standalone R package. The standalone R implementation can be run on any operating system for which an R environment implementation is available (Windows, Mac OS, various flavors of Linux and Unix) and can be downloaded from the FunNet website, or from the worldwide mirrors of CRAN. Both implementations of the FunNet tool are provided freely under the GNU General Public License 2.0. Platform: Online tool, Windows compatible, Mac OS X compatible, Linux compatible, Unix compatible

Abbreviations: FunNet

Synonyms: Functional Analysis of Transcriptional Networks, Functional Analysis of Transcriptional Networks (FunNet)

Resource Type: analysis service resource, data analysis service, production service resource, software application, service resource, data processing software, software resource

Defining Citation: PMID:18208606

Keywords: genome, transcriptional interaction, microarray, gene expression, statistical analysis

Funding:

Availability: Free for academic use, GNU General Public License, v2

Resource Name: FunNet - Transcriptional Networks Analysis

Resource ID: SCR_006968

Alternate IDs: nlx_149243

Record Creation Time: 20220129T080239+0000

Record Last Update: 20250407T215624+0000

Ratings and Alerts

No rating or validation information has been found for FunNet - Transcriptional Networks Analysis.

No alerts have been found for FunNet - Transcriptional Networks Analysis.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 16 mentions in open access literature.

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

Zuo Q, et al. (2017) Dynamic expression and regulatory mechanism of TGF-? signaling in

chicken embryonic stem cells differentiating into spermatogonial stem cells. Bioscience reports, 37(4).

Zuo Q, et al. (2015) Study on the regulatory mechanism of the lipid metabolism pathways during chicken male germ cell differentiation based on RNA-seq. PloS one, 10(2), e0109469.

Fang Z, et al. (2015) UNC50 prompts G1/S transition and proliferation in HCC by regulation of epidermal growth factor receptor trafficking. PloS one, 10(3), e0119338.

Naillat F, et al. (2015) Identification of the genes regulated by Wnt-4, a critical signal for commitment of the ovary. Experimental cell research, 332(2), 163.

Gravez B, et al. (2015) Aldosterone promotes cardiac endothelial cell proliferation in vivo. Journal of the American Heart Association, 4(1), e001266.

Sidler C, et al. (2014) SUV39H1 downregulation induces deheterochromatinization of satellite regions and senescence after exposure to ionizing radiation. Frontiers in genetics, 5, 411.

Sidler C, et al. (2014) A role for SUV39H1-mediated H3K9 trimethylation in the control of genome stability and senescence in WI38 human diploid lung fibroblasts. Aging, 6(7), 545.

Sidler C, et al. (2014) WI-38 senescence is associated with global and site-specific hypomethylation. Aging, 6(7), 564.

Sidler C, et al. (2013) Immunosenescence is associated with altered gene expression and epigenetic regulation in primary and secondary immune organs. Frontiers in genetics, 4, 211.

Wang L, et al. (2013) Histone H3K9 methyltransferase G9a represses PPAR? expression and adipogenesis. The EMBO journal, 32(1), 45.

Mi D, et al. (2013) Pax6 exerts regional control of cortical progenitor proliferation via direct repression of Cdk6 and hypophosphorylation of pRb. Neuron, 78(2), 269.

Kim MJ, et al. (2012) Inflammatory pathway genes belong to major targets of persistent organic pollutants in adipose cells. Environmental health perspectives, 120(4), 508.

Correa-Costa M, et al. (2012) Transcriptome analysis of renal ischemia/reperfusion injury and its modulation by ischemic pre-conditioning or hemin treatment. PloS one, 7(11), e49569.

Murphy D, et al. (2012) The hypothalamic-neurohypophyseal system: from genome to physiology. Journal of neuroendocrinology, 24(4), 539.

Marques F, et al. (2011) Transcriptome signature of the adult mouse choroid plexus. Fluids and barriers of the CNS, 8(1), 10.

Bando SY, et al. (2011) Hippocampal CA3 transcriptome signature correlates with initial precipitating injury in refractory mesial temporal lobe epilepsy. PloS one, 6(10), e26268.