Introduction to Cytoscape

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www.cranfield.ac.uk

Why networks?

- Complex systems are better described as networks of interacting components
- The topology of a network characterises the underlying complex system (global topology parameters) and its individual components (local topology parameters)
- Network topology parameters are easily compared
- Useful for discovering patterns in large data sets
- Allow the integration of multiple data types

Networks in biology

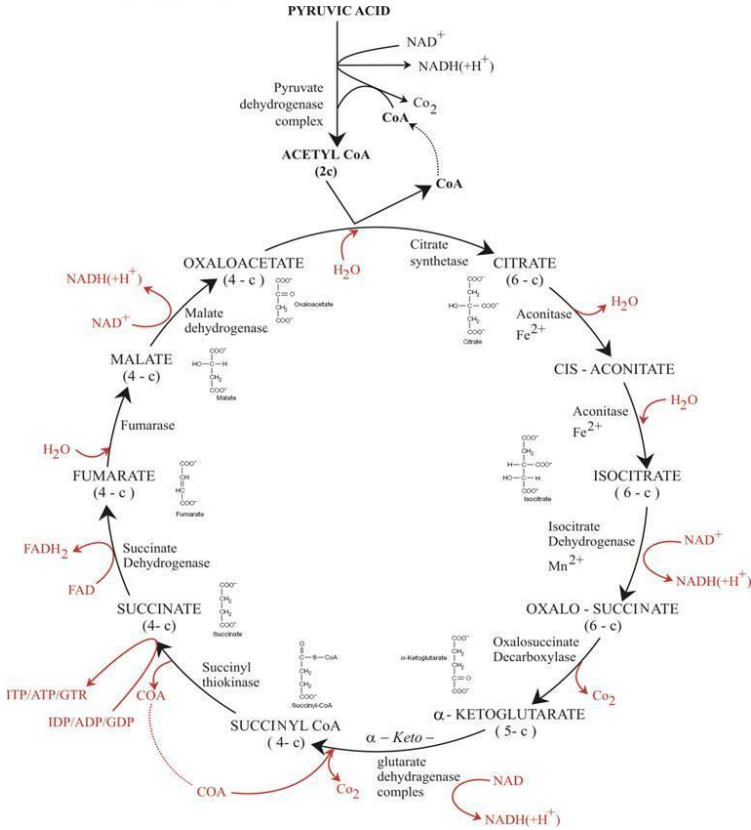
Two main types of networks in biology:

- Interaction networks (protein-protein - PPI, protein-ligand, protein-transcript…) - molecular interactions between proteins, or between proteins and chemicals e.g. MINT, Intact

- Pathways (regulatory, signaling, metabolic…) - Sequence of enzymatic or other reactions by which one biological material is converted to another e.g. Biocarta, Reactome, Biopax

Also:

- Association networks – genes and proteins often associated in the literature or in expression studies
- Author networks – who works with whom!



Networks as graphs

Formal **graph definition**: A graph G is a pair of two sets V (nodes) and E (edges): G = (V, E)

Neighbors are two nodes n_1 and n_2 connected by an edge

Neighborhood is the set of all neighbors of node n

Connectivity k_n is the size of the neighborhood of n

Degree k is the number of edges incident on n

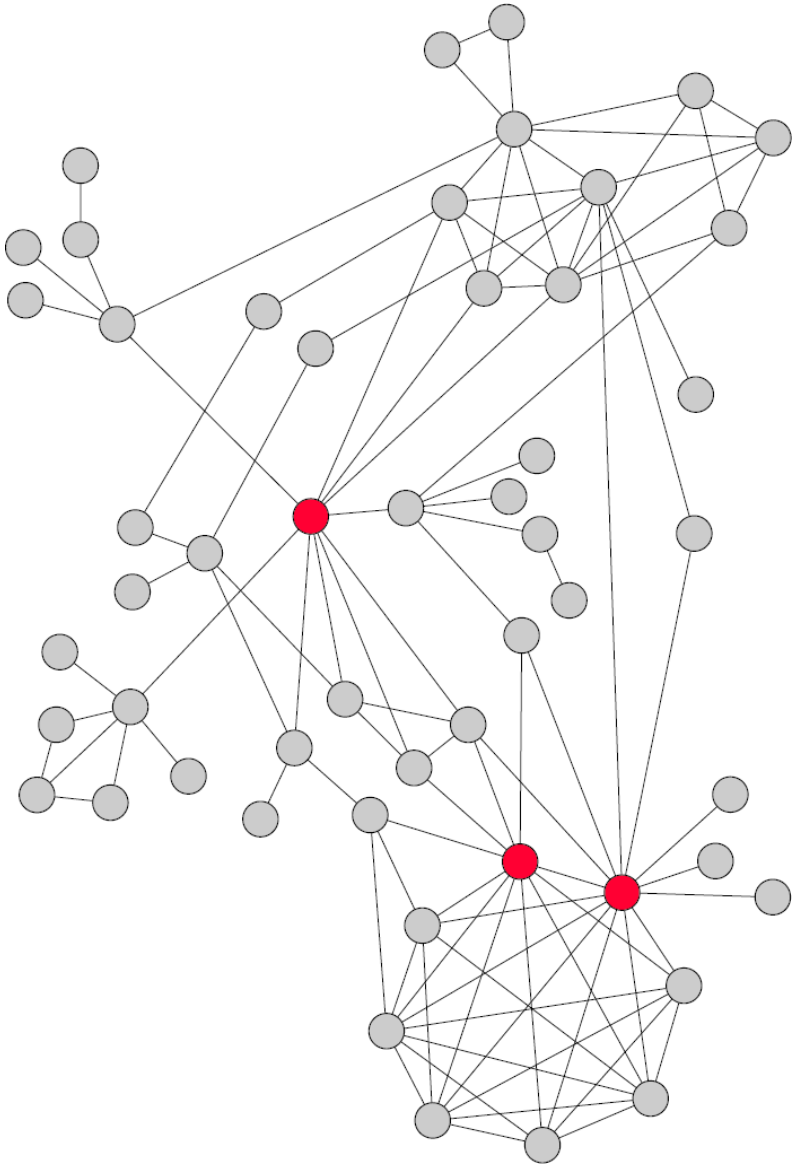
Node degree and shortest path

A **hub** is a node with an exceptionally high degree, larger than the average node degree (see red nodes).

A **shortest path** between the nodes n and m is a path between n and m of minimal length.

The shortest path length, or **distance**, between n and m is the length of a shortest path between n and m.

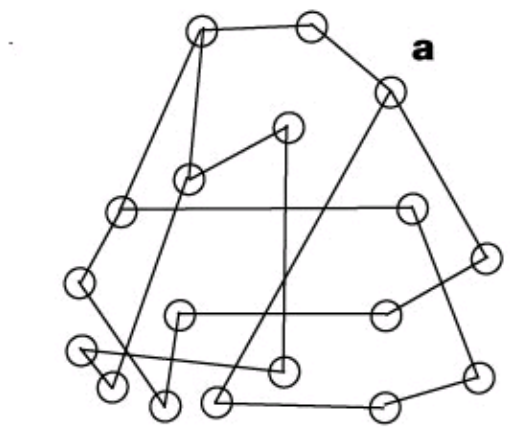
The **characteristic path length** is the average shortest path length, the expected distance between two connected nodes.

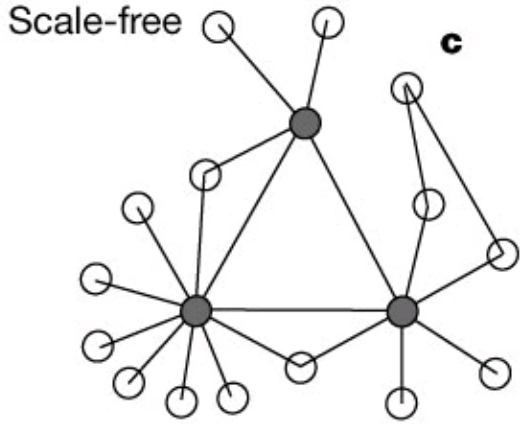


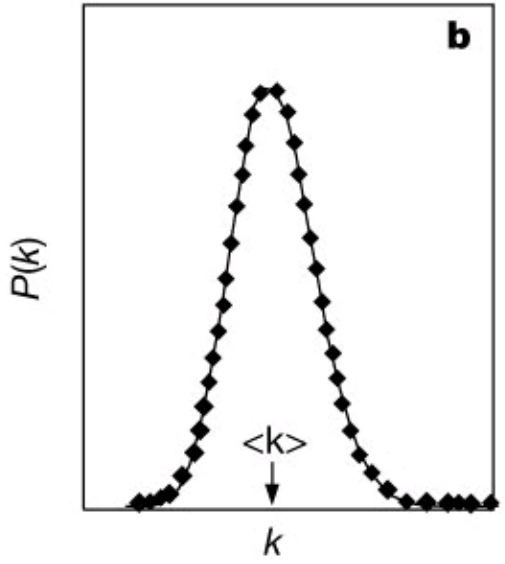
Random networks vs. scale-free networks

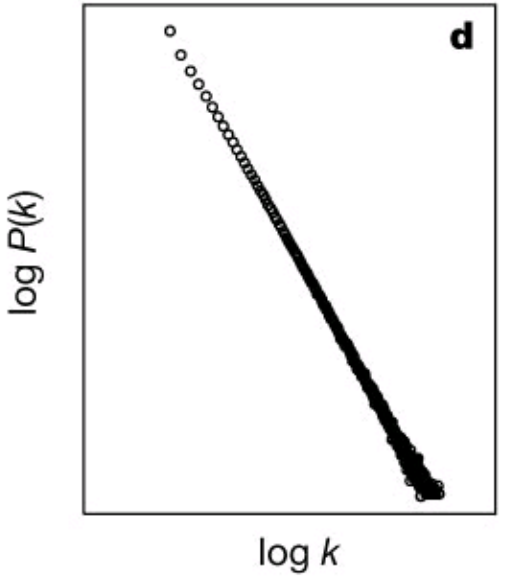
Random networks are homogeneous, most nodes have the same number of links:
- not robust to arbitrary node failure

Scale-free networks have a number of highly connected nodes:
- robust to random failure
- very sensitive to hub failures







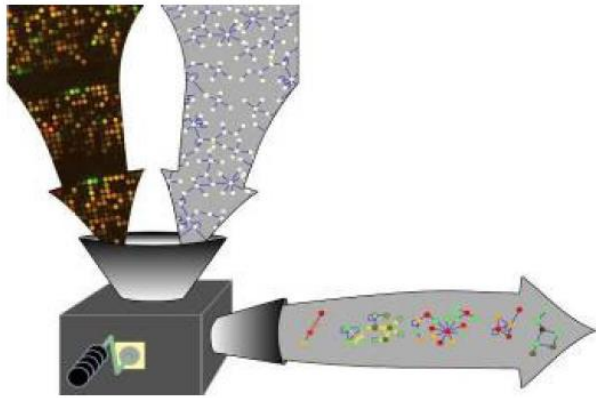


Cytoscape

Open source software for visualising, integrating, and analysing biological data.

Main interface:

- Data importing and visualisation
- Advanced parsing allowing the association of data from many different formats
- Complex layout customisation and automation options



Ideker and Lauffenburger, *Trends in Biotech.* (2003) -
Cited from UCSD presentation 18th January

More advanced: Apps

- Clustering
- Enrichment analysis
- Gene expression analysis
- Gene function prediction
- Network evolution
- …

Consortium

- Institute for Systems Biology
- University of California at San Diego
- Memorial Sloan-Kettering Cancer Center
- Institut Pasteur
- Agilent Technologies
- University of California at San Francisco
- University of Toronto
- University of Michigan
- Unilever

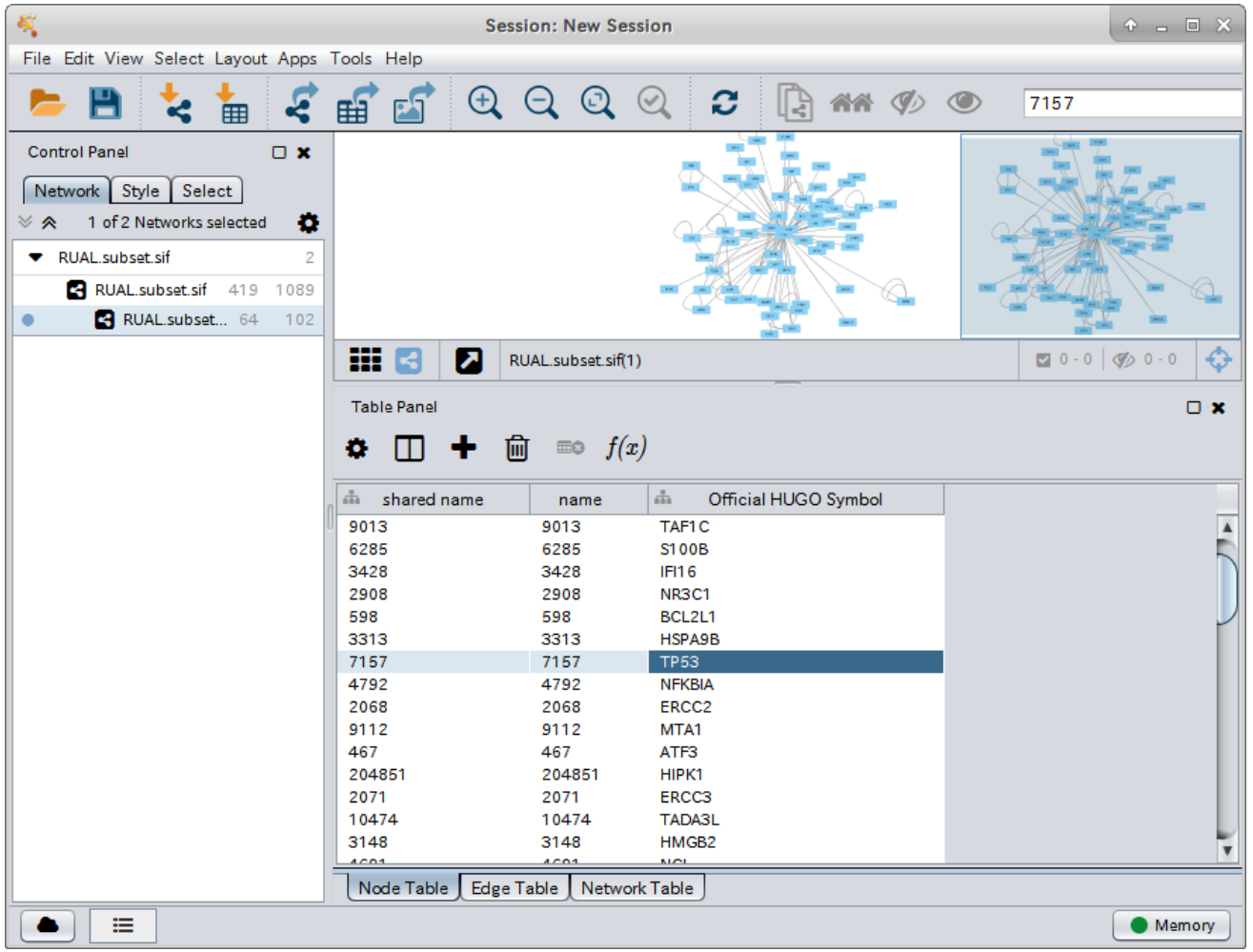
Data tables

Nodes and edges can have additional data associated with them and stored in tables.

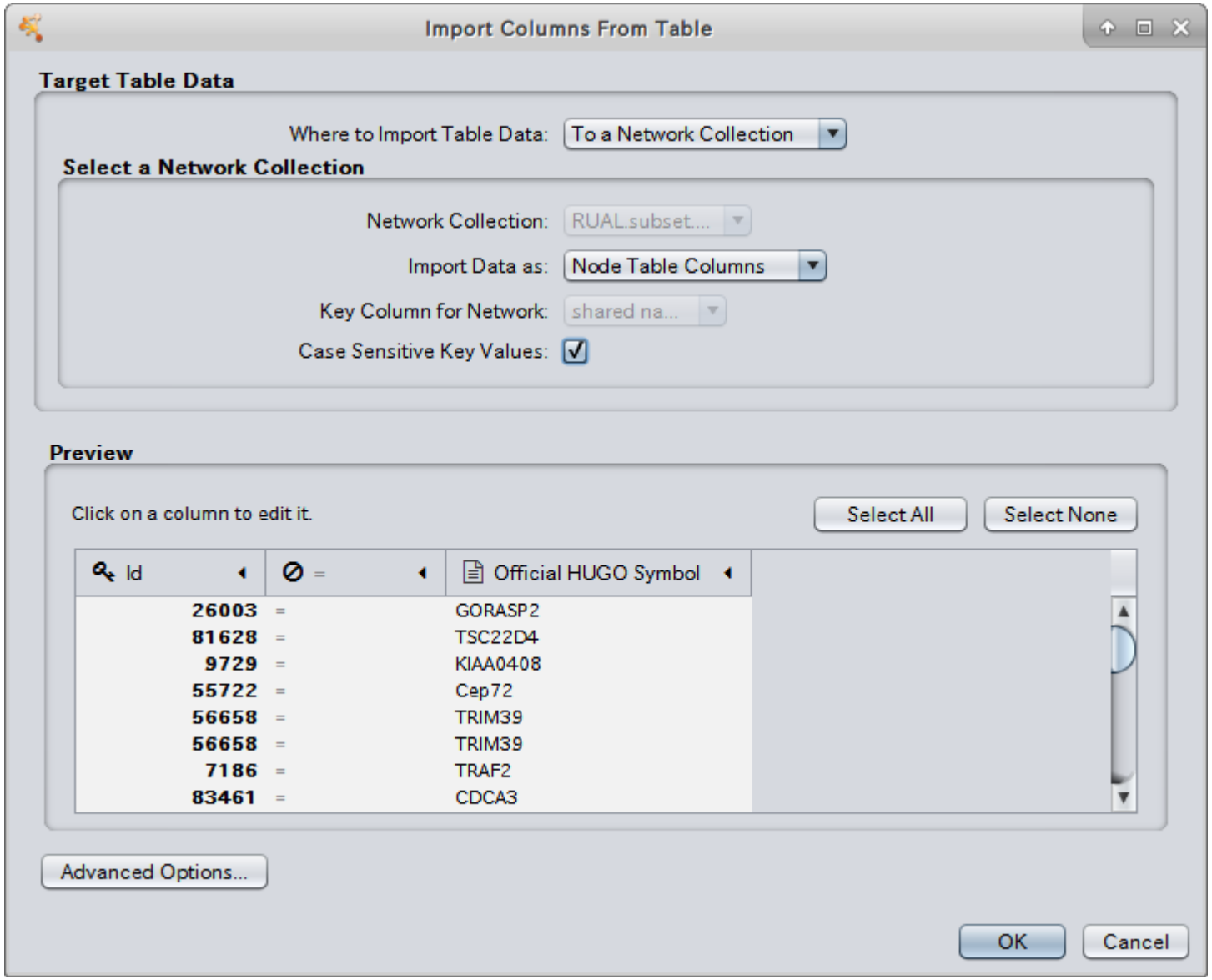
- Annotation
- Gene ontology
- Mass spectrometry data
- Gene expression data
- Identifiers from different databases

Filters allow you to search for nodes or edges based on that data.

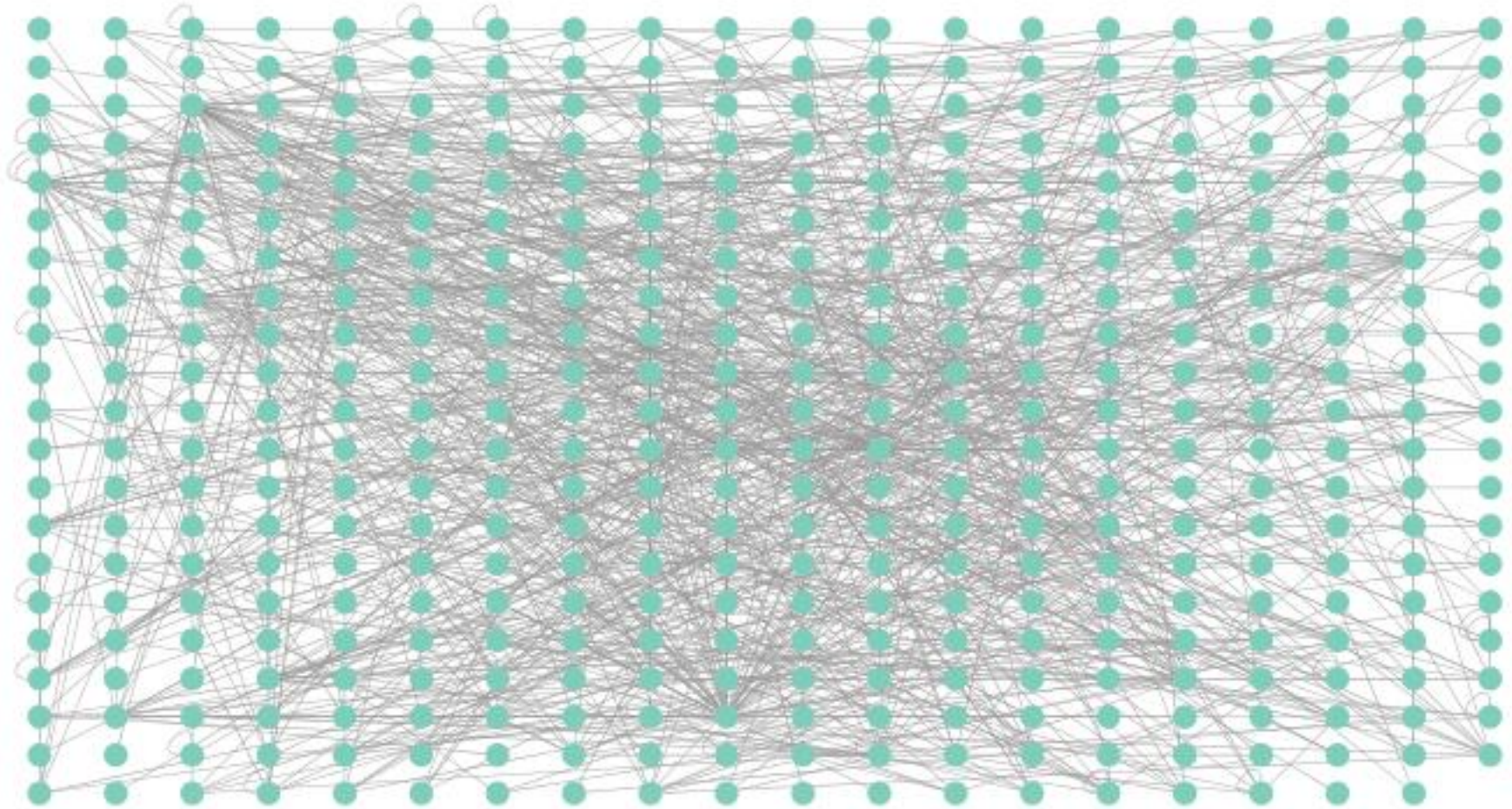
It is also available to analysis apps.



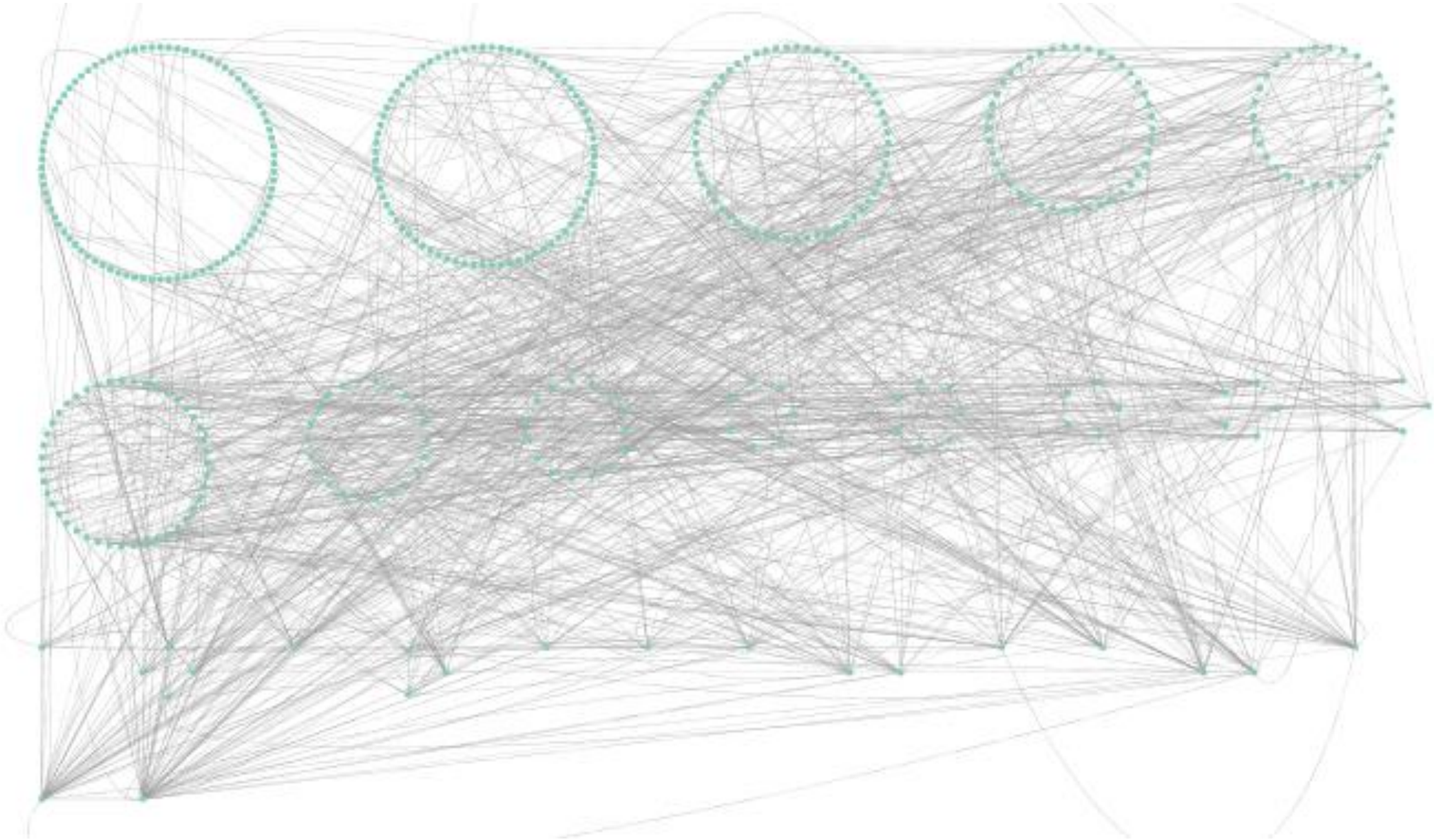
Data import


Import Columns From Table
Target Table Data
Where to Import Table Data:
To a Network Collection
Select a Network Collection
Network Collection:
RUAL.subset....
Import Data as:
Node Table Columns
Key Column for Network:
shared na...
Case Sensitive Key Values:
Preview
Click on a column to edit it.
Select All
Select None
Id
=
Official HUGO Symbol
26003 = GORASP2
81628 = TSC22D4
9729 = KIAA0408
55722 = Cep72
56658 = TRIM39
56658 = TRIM39
7186 = TRAF2
83461 = CDCA3
Advanced Options...
OK
Cancel

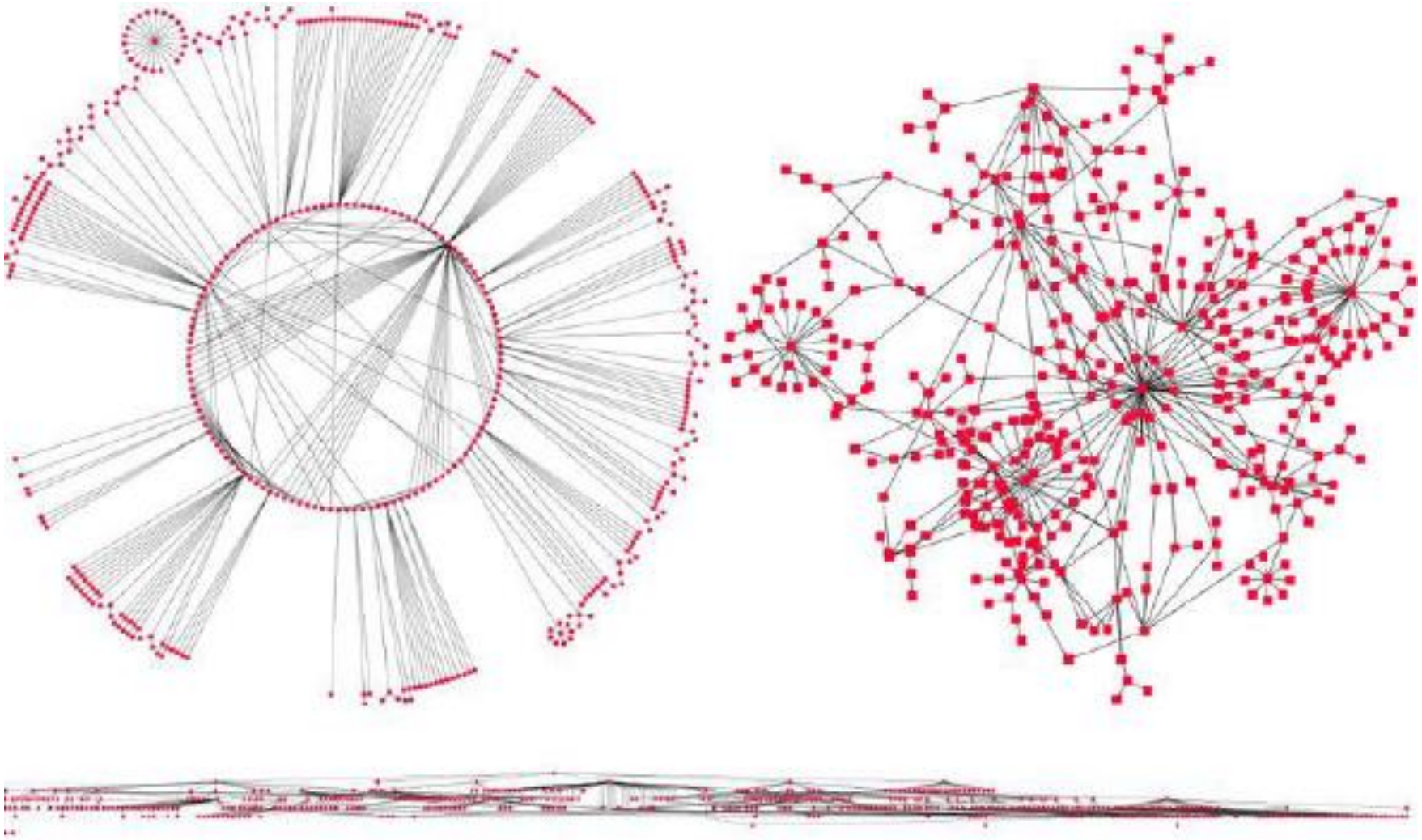
Layouts



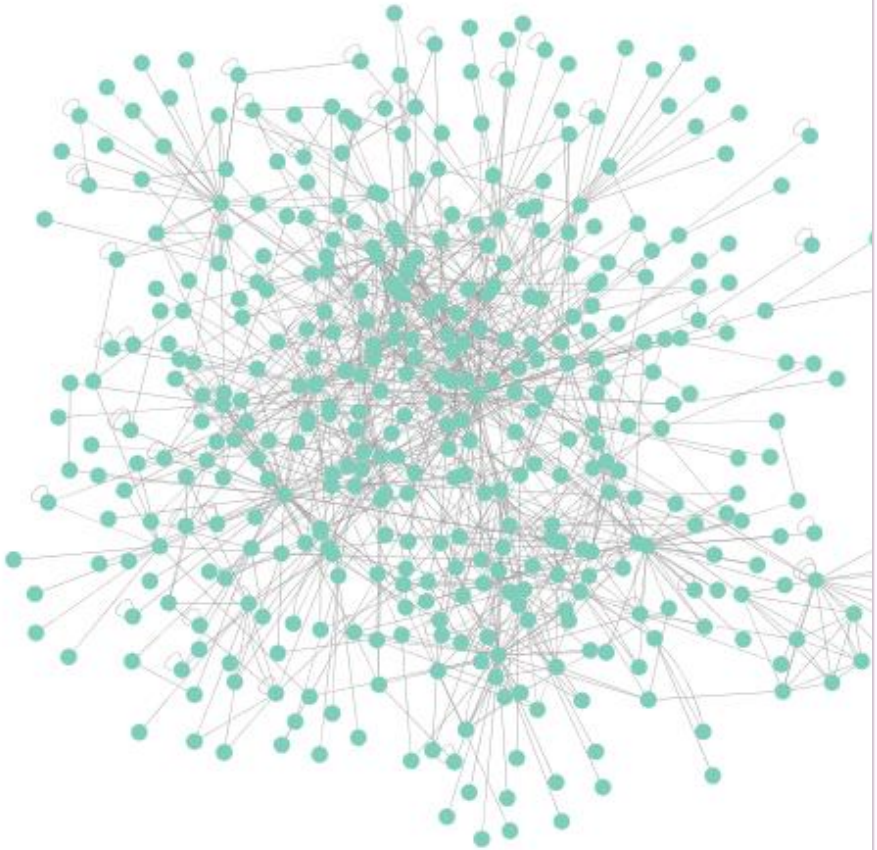
Layouts

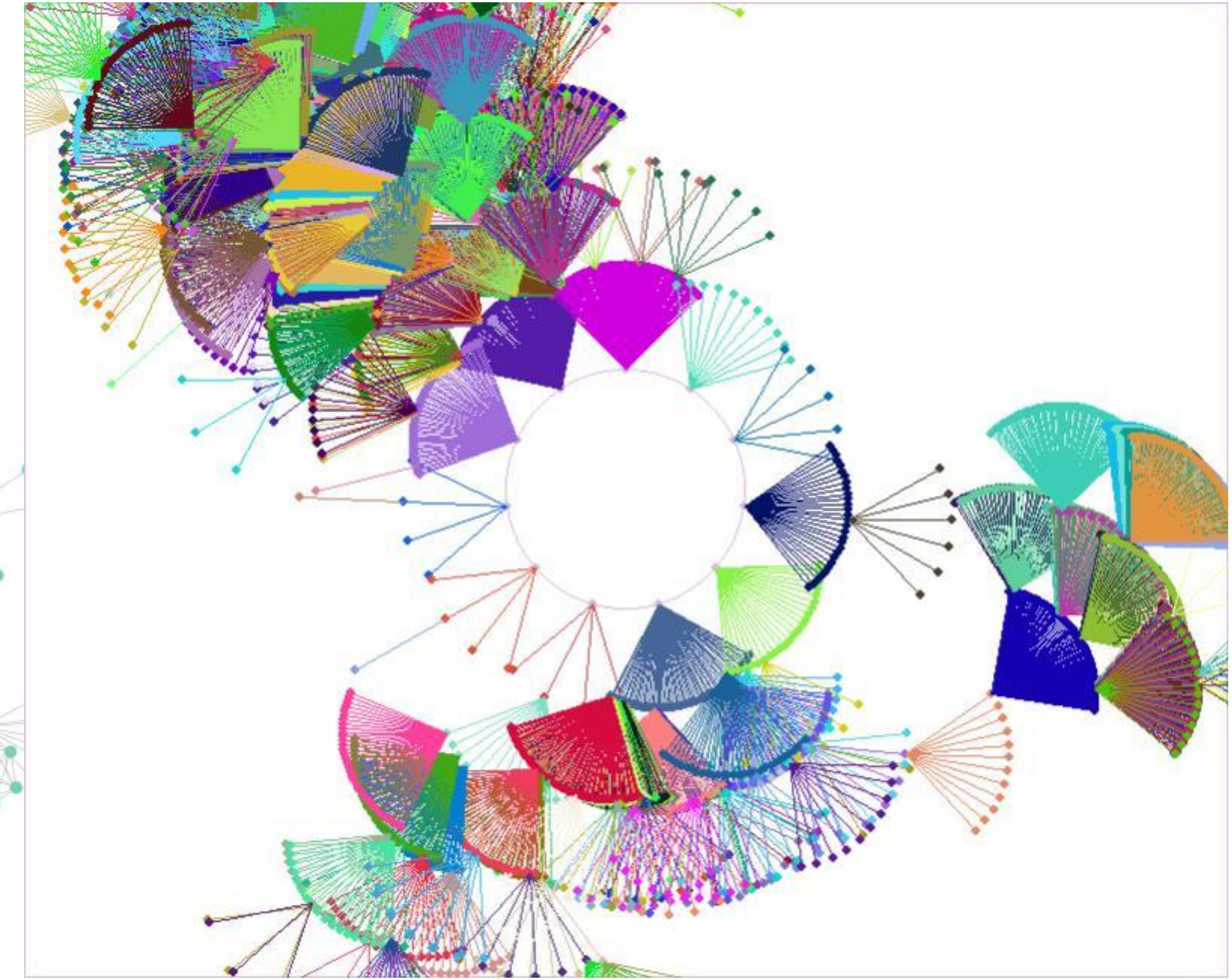


Layouts



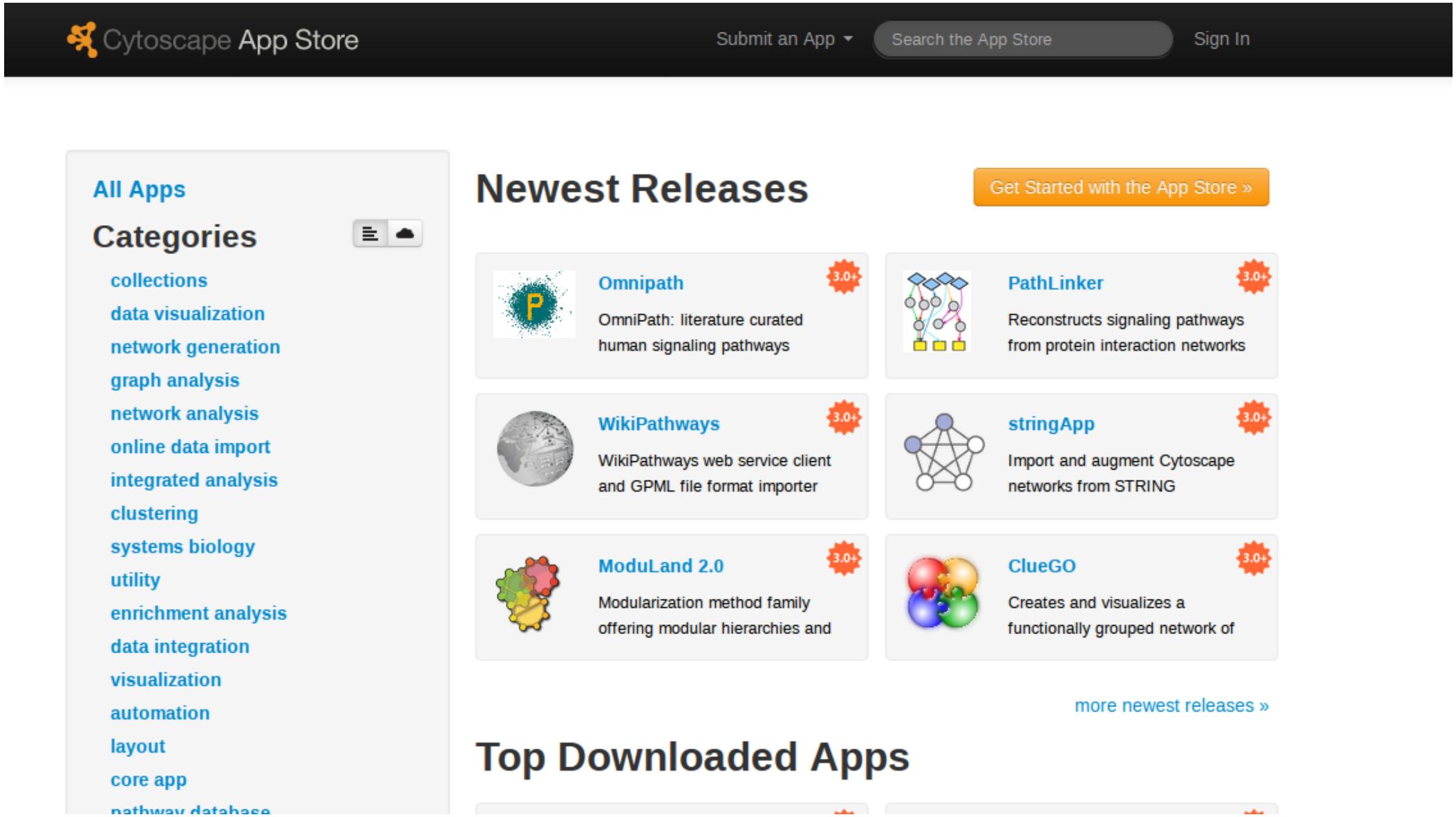
Layouts



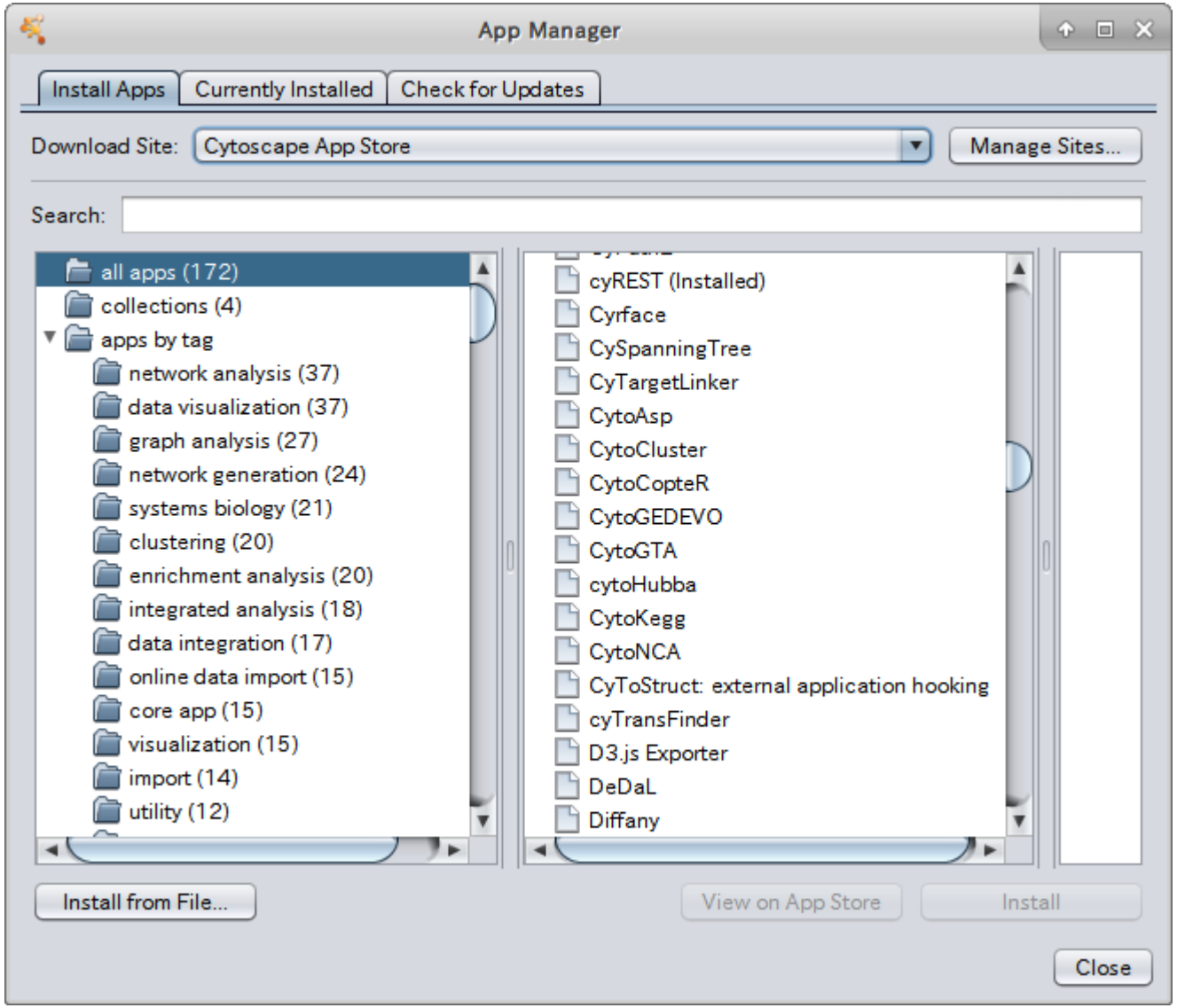


Apps

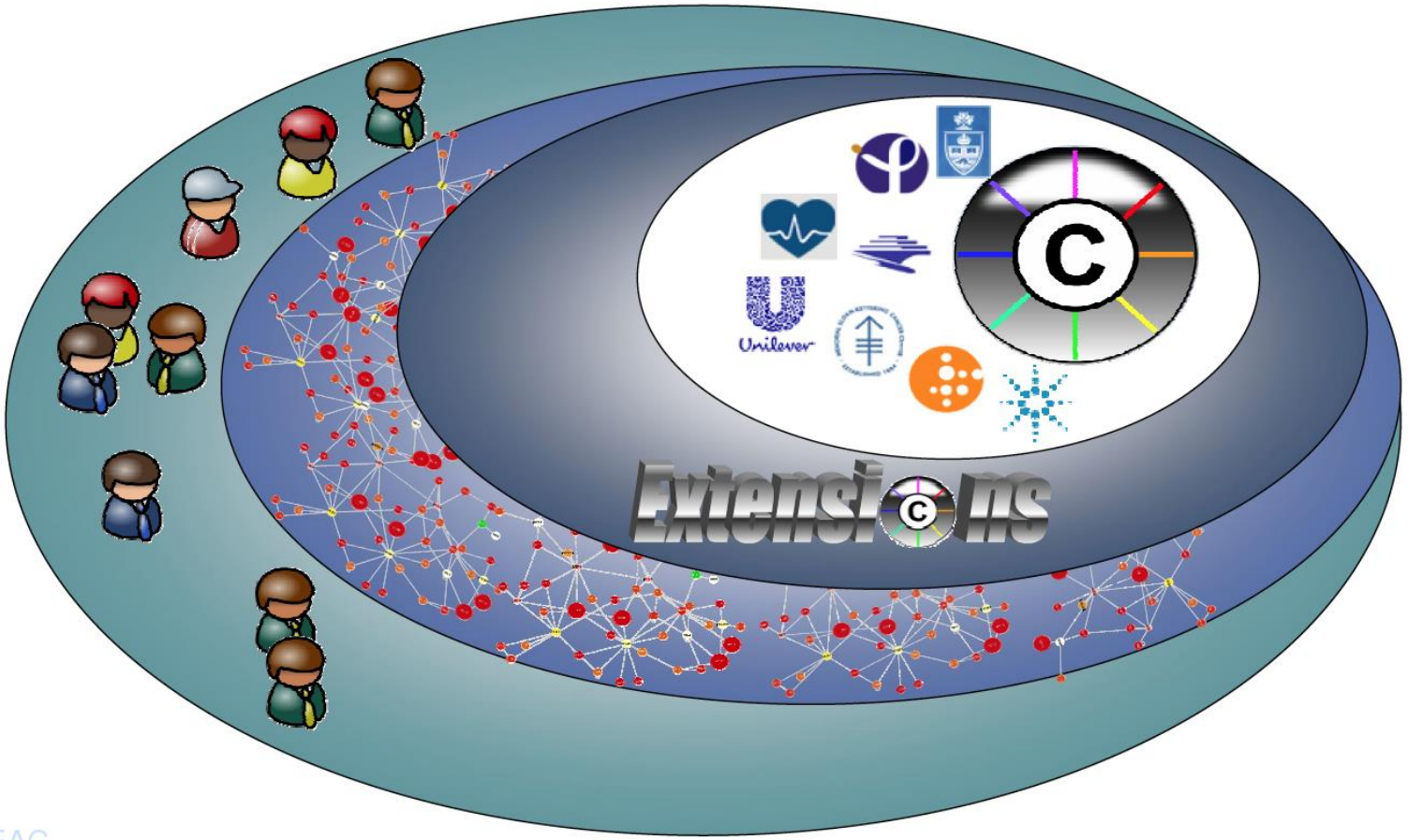
https://apps.cytoscape.org



Apps

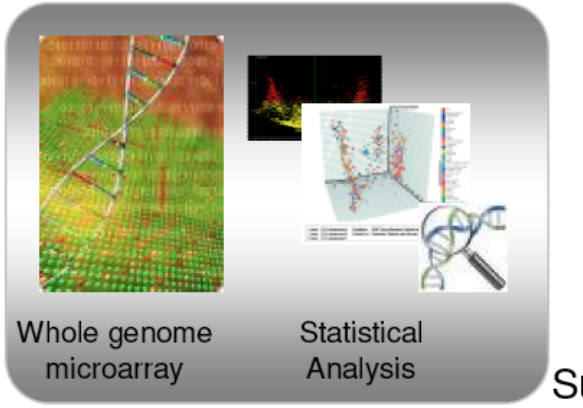

App Manager
Install Apps
Currently Installed
Check for Updates
Download Site:
Cytoscape App Store
Manage Sites...
Search:
all apps (172)
collections (4)
apps by tag
network analysis (37)
data visualization (37)
graph analysis (27)
network generation (24)
systems biology (21)
clustering (20)
enrichment analysis (20)
integrated analysis (18)
data integration (17)
online data import (15)
core app (15)
visualization (15)
import (14)
utility (12)
cyREST (Installed)
Cyrface
CySpanningTree
CyTargetLinker
CytoAsp
CytoCluster
CytoCopteR
CytoGEDEVO
CytoGTA
cytoHubba
CytoKegg
CytoNCA
CyToStruct: external application hooking
cyTransFinder
D3.js Exporter
DeDaL
Diffany
Install from File...
View on App Store
Install
Close

Cytoscape community



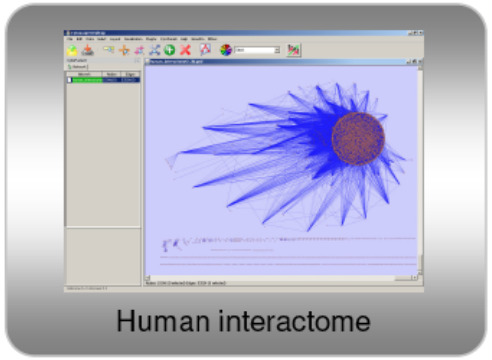
SEAC

Identify important subnetworks



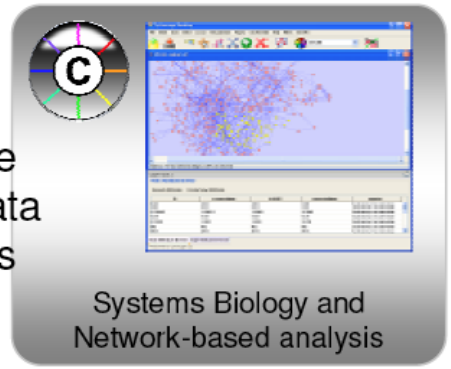
Whole genome microarray

Statistical Analysis

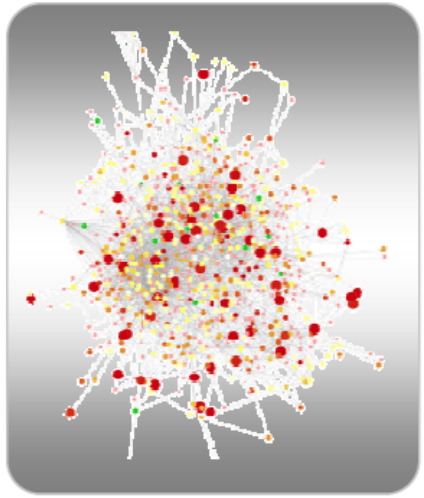


Human interactome

Superimpose expression data and P-values



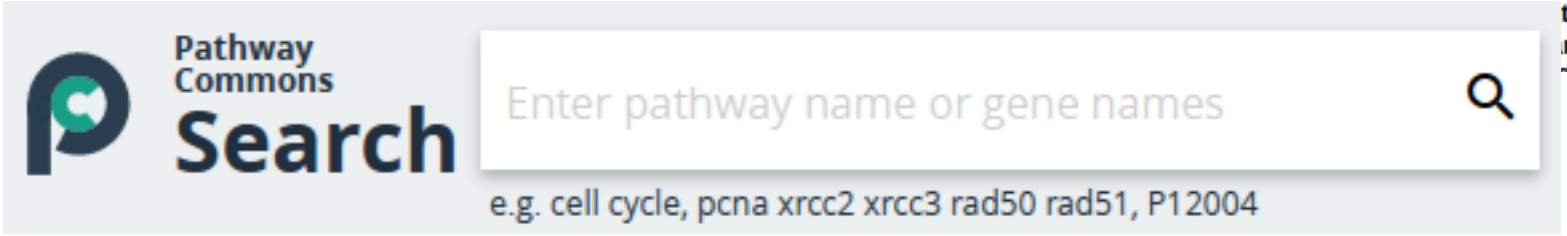
Systems Biology and Network-based analysis



Apply network analysis tools to identify significant sub-networks associated with condition if interest

Molecular Interaction and Network Resources for Cytoscape

- Import from web-services (NDEx, Pathway Commons)
- Sources:Mint, Reactome, IntAct, HPRD, Biogrid, SBCNY, MSKCC, BioGRID
- Pathway or Molecular interactions.
- Upload a network file (tab delimited, MITAB, SIF, CX).
- Build your own network!



Nature **437**, 1173-1178 (20 October 2005) | doi:10.1038/nature04209; Received 21 July 2005; Accepted 8 September 2005; Published online 28 September 2005

Towards a proteome-scale map of the human protein–protein interaction network

Jean-François Rual[1,8], Kavitha Venkatesan[1,8], Tong Hao[1], Tomoko Hirozane-Kishikawa[1], Amélie Dricot[1], Ning Li[1], Gabriel F. Berriz[2], Francis D. Gibbons[2], Matija Dreze[1,3], Nono Ayivi-Guedehoussou[1], Niels Klitgord[1], Christophe Simon[1], Mike Boxem[1], Stuart Milstein[1], Jennifer Rosenberg[1], Debra S. Goldberg[2], Lan V. Zhang[2], Sharyl L. Wong[2], Giovanni Franklin[2], Siming Li[1,7], Joanna S. Albala[1,7], Janghoo Lim[4], Carlene Fraughton[1], Estelle Llamosas[1], Sebiha Cevik[1], Camille Bex[1], Philippe Lamesch[1,3], Robert S. Sikorski[5], Jean Vandenhaute[3], Huda Y. Zoghbi[4], Alex Smolyar[1], Stephanie Bosak[6], Reynaldo Sequerra[6], Lynn Doucette-Stamm[6], Michael E. Cusick[1], David E. Hill[1], Frederick P. Roth[2] & Marc Vidal[1]

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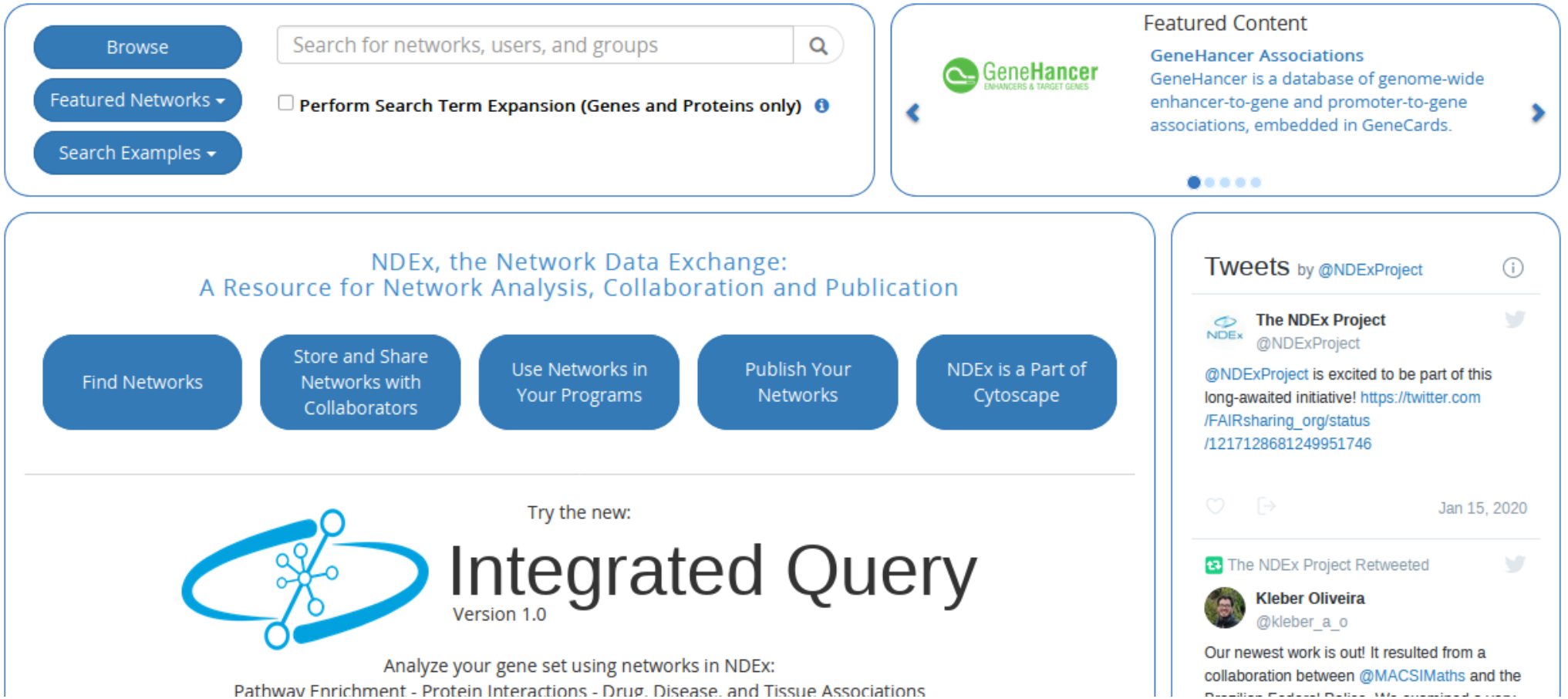
3. Unité de Recherche en Biologie Moléculaire, Facultés Notre-Dame de la Paix, 61 Rue de Bruxelles, 5000 Namur, Belgium
4. Howard Hughes Medical Institute, and Departments of Pediatrics, Neurology, Neuroscience, and Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, Texas 77030, USA
5. Arcbay, Inc., 6 Whittier Place, Suite 7J, Boston, Massachusetts 01915, USA
6. Agencourt Bioscience Corporation, 500 Cummings Center, Suite 2450, Beverly, Massachusetts 01915, USA
7. †Present addresses: ArQule, Inc., 19 Presidential Way, Woburn, Massachusetts 01081, USA (S.L.); Departments of Cancer Biology, and Otolaryngology, Head and Neck Surgery, University of California Davis, 2521 Stockton Blvd, Suite 7200, Sacramento, California 95817, USA (J.S.A.)
8. *These authors contributed equally to this work

Correspondence to: David E. Hill[1]Frederick P. Roth[2]Marc Vidal[1] Correspondence and requests for materials should be addressed to M.V. (Email: marc_vidal@dfci.harvard.edu), F.P.R. (Email: fritz_roth@hms.harvard.edu) or D.E.H. (Email: david_hill@dfci.harvard.edu).

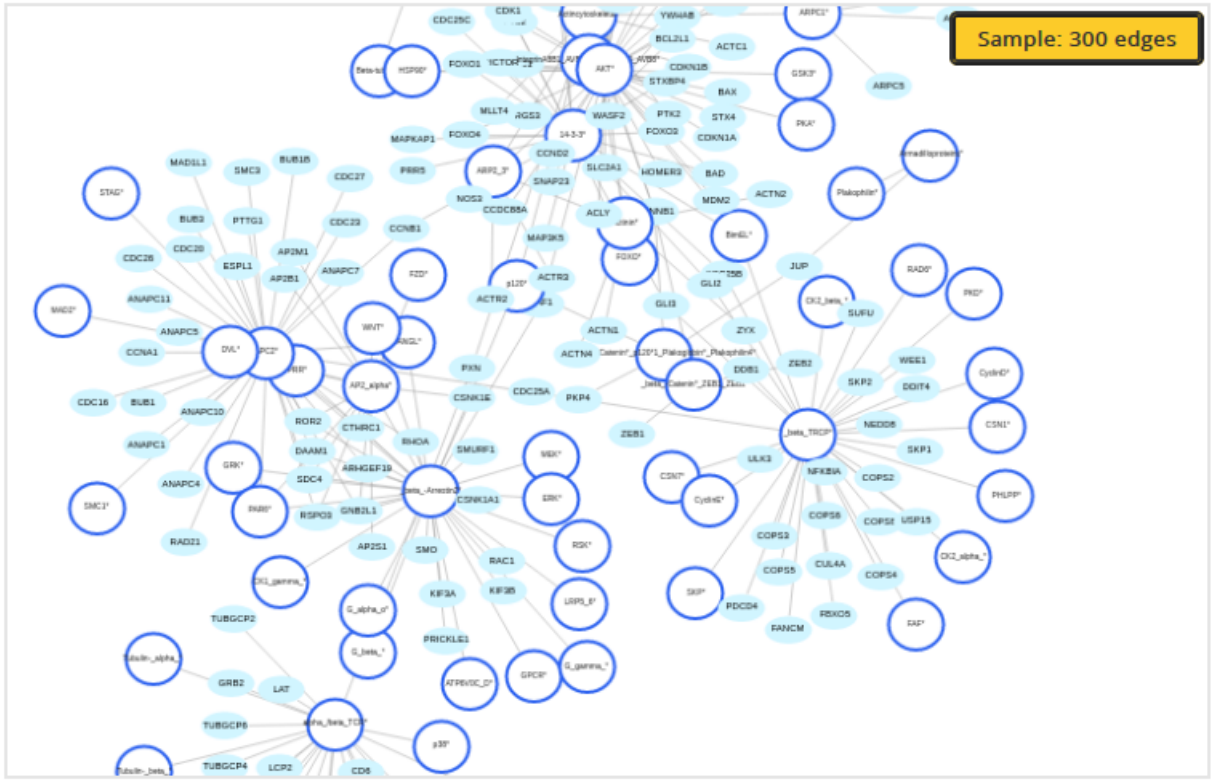
Systematic mapping of protein–protein interactions, or 'interactome' mapping, was ted in model organisms, starting with defined biological processes[1, 2] and then nding to the scale of the proteome[3, 4, 5, 6, 7]. Although far from complete, such

https://www.pathwaycommons.org/pc2/datasources

NDEx


Browse
Featured Networks
Search Examples
Search for networks, users, and groups
Perform Search Term Expansion (Genes and Proteins only)
Featured Content
GeneHancer
GeneHancer Associations
GeneHancer is a database of genome-wide enhancer-to-gene and promoter-to-gene associations, embedded in GeneCards.
NDEx, the Network Data Exchange:
A Resource for Network Analysis, Collaboration and Publication
Find Networks
Store and Share Networks with Collaborators
Use Networks in Your Programs
Publish Your Networks
NDEx is a Part of Cytoscape
Try the new:
Integrated Query
Version 1.0
Analyze your gene set using networks in NDEx:
Pathway Enrichment - Protein Interactions - Drug, Disease, and Tissue Associations
Tweets by @NDExProject
The NDEx Project
@NDExProject
@NDExProject is excited to be part of this long-awaited initiative! https://twitter.com/FAIRsharing_org/status/1217128681249951746
Jan 15, 2020
The NDEx Project Retweeted
Kleber Oliveira
@kleber_a_o
Our newest work is out! It resulted from a collaboration between @MACSIMaths and the

NDEx



Network Info | Nodes/Edges

ACSN 2.0 Master - Protein-Protein Interactions

Nodes: 2540 **Edges:** 14090
PUBLIC Read Only Copy URL
@context: view namespaces

Owner: Atlas of Cancer Signalling Network
Created: May 17, 2019 12:28:18 AM
Last Modified: Aug 12, 2019 11:27:51 PM
UUID: 49488c61-7832-11e9-848d-0ac135e8bacf
Format: Unknown

Description:

The Atlas of Cancer Signalling Networks (ACSN) is a web-based multi-scale resource of biological maps depicting molecular processes in cancer cell and tumor microenvironment.

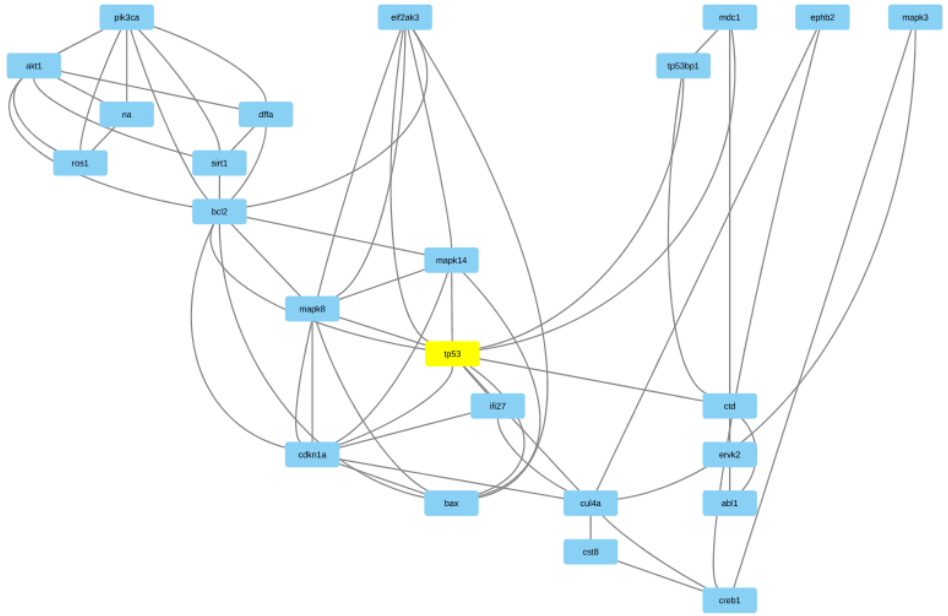
This is the Master Map containg all protein-protein interactions available in ACSN 2.0.

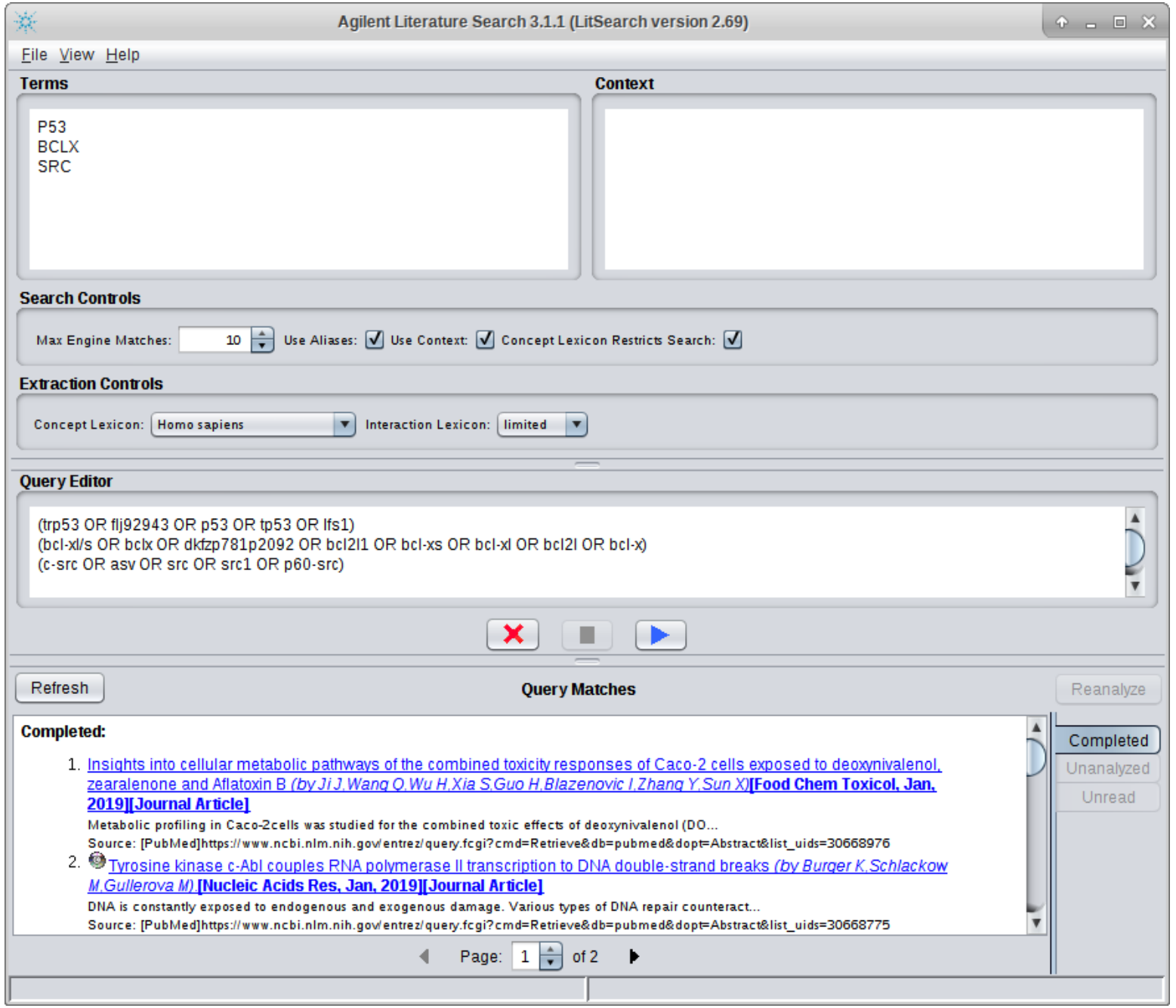
Rights Holder: Institut Curie

Query Terms (i.e., AKT1 or WNT*) **Type:** 1-step neighborhood Run Query

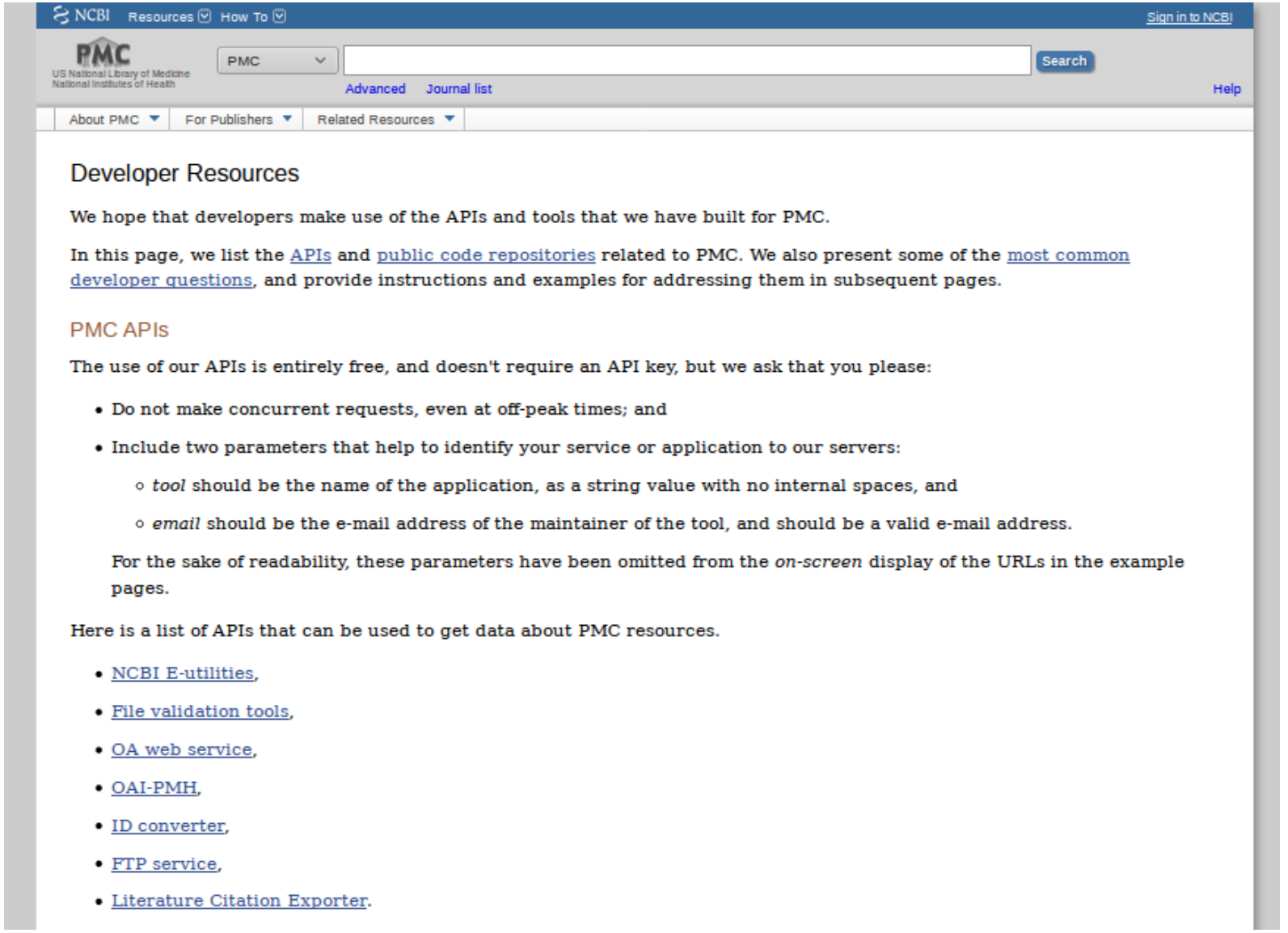
Open in Cytoscape Table Log in

Literature mining





NCBI / PubMed API



NCBI Resources How To Sign in to NCBI

PMC US National Library of Medicine National Institutes of Health

PMC Search

Advanced Journal list Help

About PMC For Publishers Related Resources

Developer Resources

We hope that developers make use of the APIs and tools that we have built for PMC.

In this page, we list the APIs and public code repositories related to PMC. We also present some of the most common developer questions, and provide instructions and examples for addressing them in subsequent pages.

PMC APIs

The use of our APIs is entirely free, and doesn't require an API key, but we ask that you please:

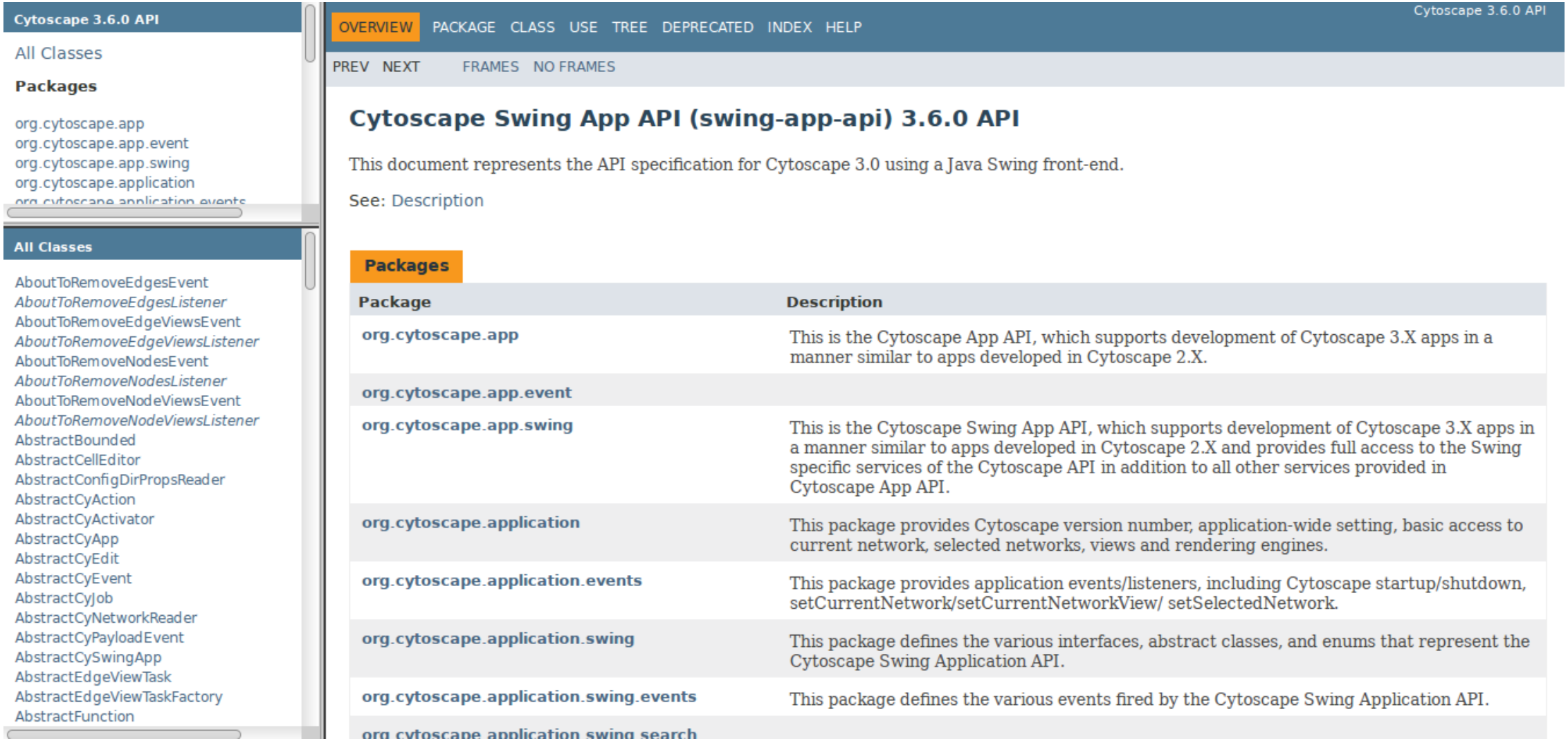
- Do not make concurrent requests, even at off-peak times; and
- Include two parameters that help to identify your service or application to our servers:
  - *tool* should be the name of the application, as a string value with no internal spaces, and
  - *email* should be the e-mail address of the maintainer of the tool, and should be a valid e-mail address.

  For the sake of readability, these parameters have been omitted from the *on-screen* display of the URLs in the example pages.

Here is a list of APIs that can be used to get data about PMC resources.

- NCBI E-utilities,
- File validation tools,
- OA web service,
- OAI-PMH,
- ID converter,
- FTP service,
- Literature Citation Exporter.

Cytoscape API



Cytoscape 3.6.0 API

All Classes

Packages

org.cytoscape.app
org.cytoscape.app.event
org.cytoscape.app.swing
org.cytoscape.application
org.cytoscape.application.events

All Classes

AboutToRemoveEdgesEvent
AboutToRemoveEdgesListener
AboutToRemoveEdgeViewsEvent
AboutToRemoveEdgeViewsListener
AboutToRemoveNodesEvent
AboutToRemoveNodesListener
AboutToRemoveNodeViewsEvent
AboutToRemoveNodeViewsListener
AbstractBounded
AbstractCellEditor
AbstractConfigDirPropsReader
AbstractCyAction
AbstractCyActivator
AbstractCyApp
AbstractCyEdit
AbstractCyEvent
AbstractCyJob
AbstractCyNetworkReader
AbstractCyPayloadEvent
AbstractCySwingApp
AbstractEdgeViewTask
AbstractEdgeViewTaskFactory
AbstractFunction

OVERVIEW PACKAGE CLASS USE TREE DEPRECATED INDEX HELP

Cytoscape 3.6.0 API

PREV NEXT FRAMES NO FRAMES

Cytoscape Swing App API (swing-app-api) 3.6.0 API

This document represents the API specification for Cytoscape 3.0 using a Java Swing front-end.

See: Description

Packages

Package	Description
org.cytoscape.app	This is the Cytoscape App API, which supports development of Cytoscape 3.X apps in a manner similar to apps developed in Cytoscape 2.X.
org.cytoscape.app.event	
org.cytoscape.app.swing	This is the Cytoscape Swing App API, which supports development of Cytoscape 3.X apps in a manner similar to apps developed in Cytoscape 2.X and provides full access to the Swing specific services of the Cytoscape API in addition to all other services provided in Cytoscape App API.
org.cytoscape.application	This package provides Cytoscape version number, application-wide setting, basic access to current network, selected networks, views and rendering engines.
org.cytoscape.application.events	This package provides application events/listeners, including Cytoscape startup/shutdown, setCurrentNetwork/setCurrentNetworkView/ setSelectedNetwork.
org.cytoscape.application.swing	This package defines the various interfaces, abstract classes, and enums that represent the Cytoscape Swing Application API.
org.cytoscape.application.swing.events	This package defines the various events fired by the Cytoscape Swing Application API.
org.cytoscape.application.swing.search	

Cytoscape.js

Cytoscape.js: a graph theory library for visualisation and analysis

Max Franz; Christian T. Lopes; Gerardo Huck; Yue Dong; Onur Sumer; Gary D. Bader

Bioinformatics (2015) 32 (2): 309-311.
DOI: https://doi.org/10.1093/bioinformatics/btv557
Published: 28 September 2015 **Article history**

Views PDF Cite Share Tools

Abstract

Summary: Cytoscape.js is an open-source JavaScript-based graph library. Its most common use case is as a visualization software component, so it can be used to render interactive graphs in a web browser. It also can be used in a headless manner, useful for graph operations on a server, such as Node.js.

Availability and implementation: Cytoscape.js is implemented in

JavaScript library for network visualization. Extendable with *Extensions* (not compatible with *Apps*).

Long-term goal of closer integration between Cytoscape and Cytoscape.js.

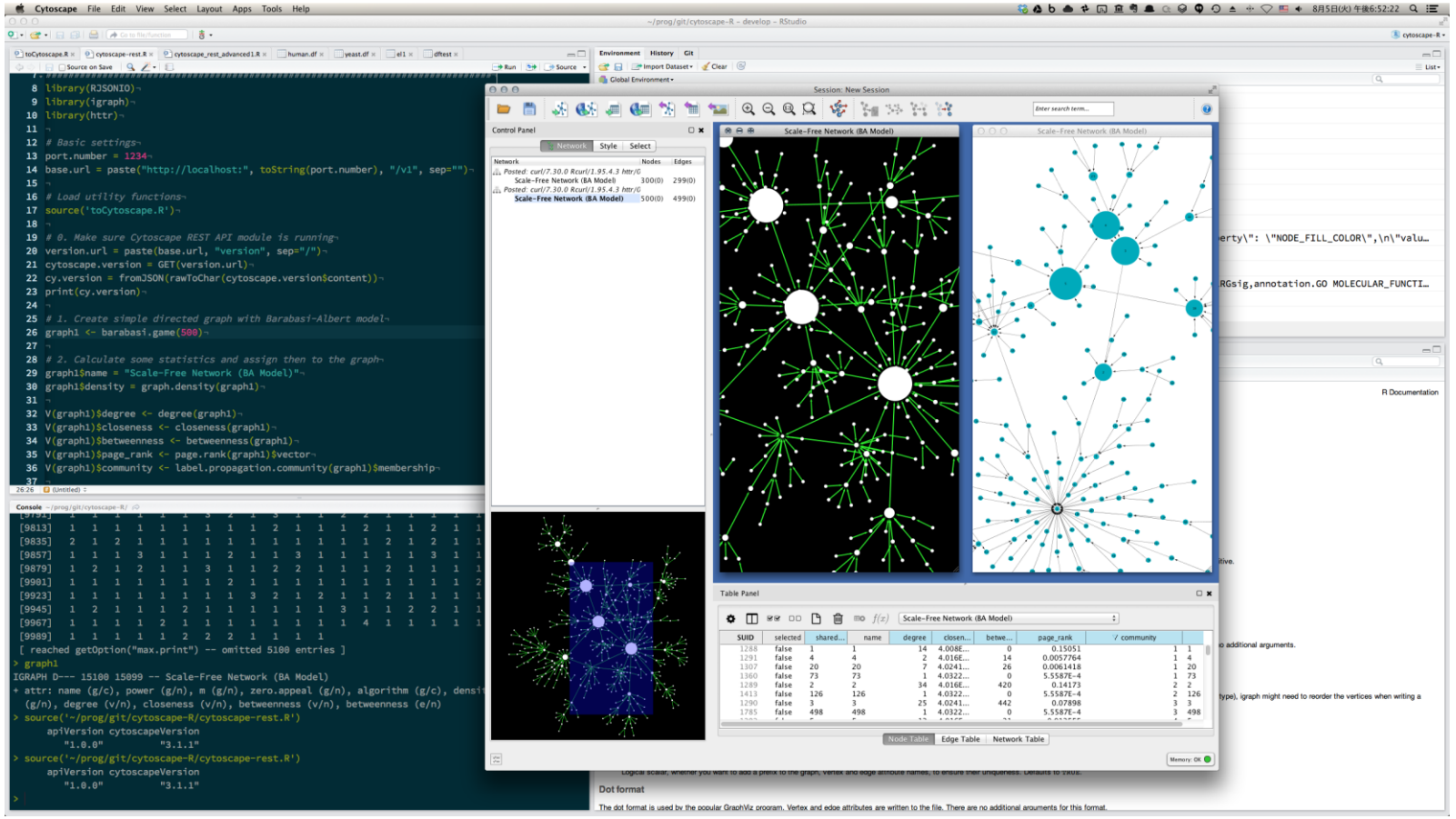
You can export Cytoscape networks into Cytoscape.js and vice-versa.

http://js.cytoscape.org/

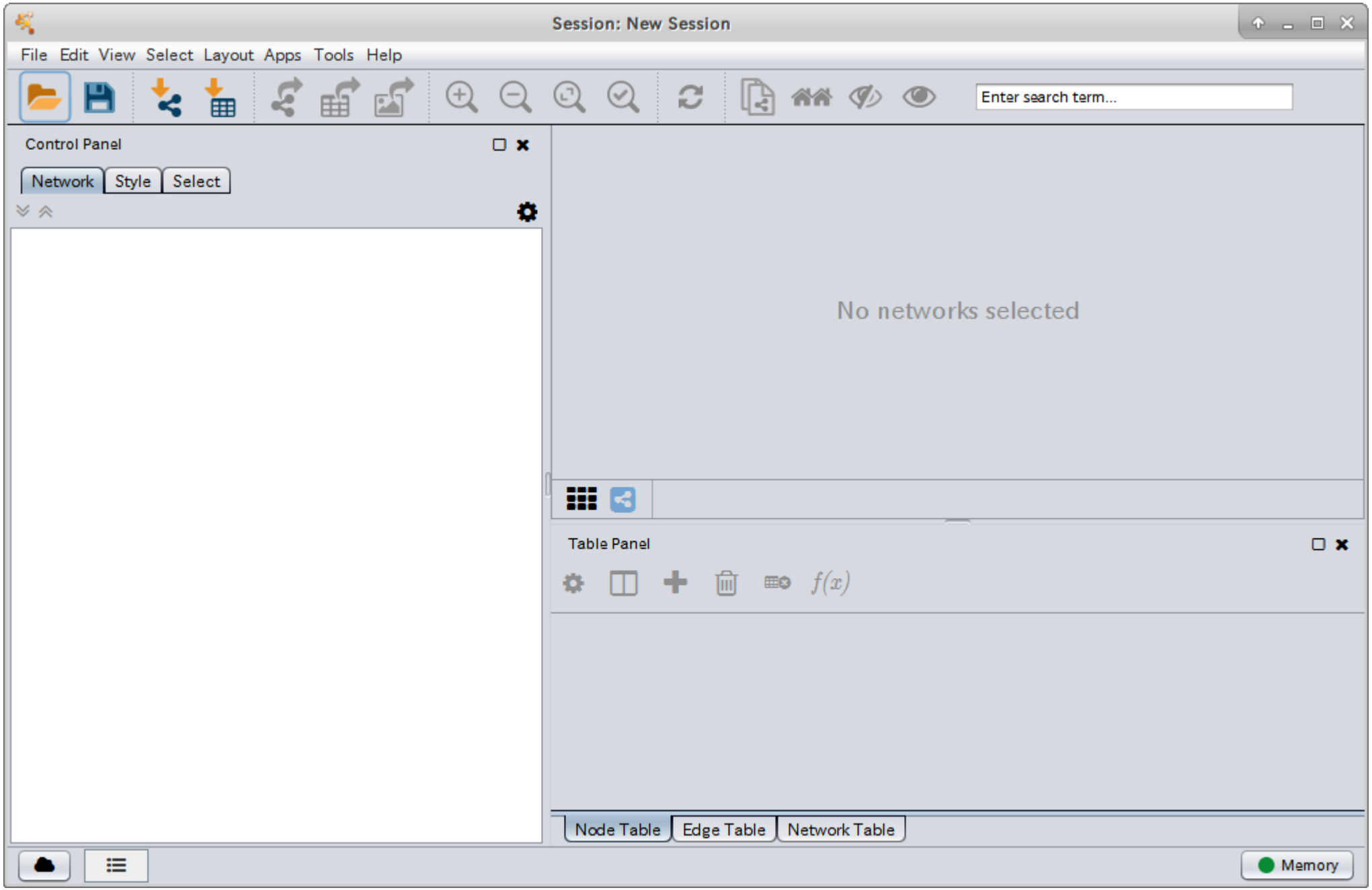
cyREST

Originally an app, now fully integrated with core Cytoscape (running on localhost port 1234).

You can use the desktop Cytoscape app through a REST API, from R, Python, Jupyter notebooks, and other languages (it is a REST API after all...)



Ono, Keiichiro, et al. "CyREST: Turbocharging Cytoscape Access for External Tools via a RESTful API." F1000Research 4 (2015).


Session: New Session
File Edit View Select Layout Apps Tools Help
Enter search term...
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Network
Style
Select
No networks selected
Table Panel
f(x)
Node Table
Edge Table
Network Table
Memory