



Advanced Topic: Automation

ISMB - Prague

21 July 2017



Goals and Motivations

By the end of this workshop you should be able to:

- Know when and how to use Cytoscape
- Identify relevant types and sources of networks
- Command programmatic control over Cytoscape
- Integrate Cytoscape into your bioinformatics pipelines
- Publish, share and export networks online

Introductions and Concepts

Finding Network Data

Network Visualization

Network Analysis

Automation via CyREST

Introductions

John "Scooter" Morris, UCSF

- Adjunct Assistant Prof, Pharmaceutical Chemistry
- Executive Director RBVI
- Cytoscape team since 2006
- Author of over a dozen Cytoscape apps

Alex Pico, Gladstone Inst.

- Associate Director, Bioinformatics
- Executive Director NRNB
- Cytoscape team since 2006
- Author of half a dozen Cytoscape apps

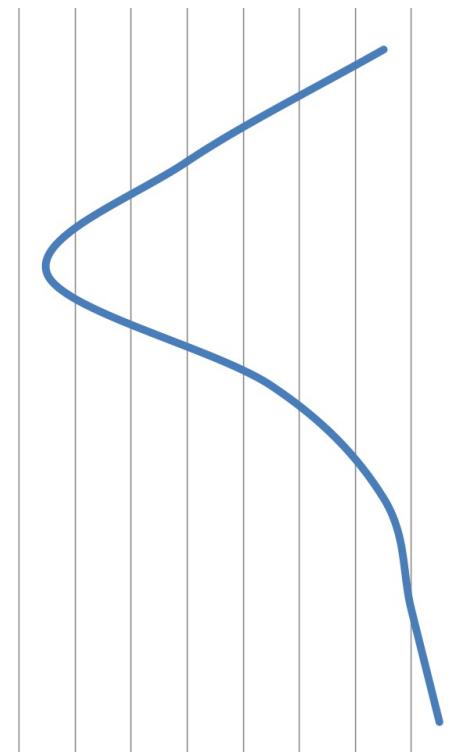
Introductions

Barry Demchak, UCSD

- Project Manager, Ideker lab
- Chief Architect for Cytoscape
- Cytoscape team since 2012
- Author of Cytoscape apps and CyREST

Introductions

What about you?



- Clinicians
- Bench Biologists
- Bioinformaticians
- Computer Scientists
- Chemists
- Mathematicians
- Other

Introduction to Network Biology

Why Networks?

Networks are everywhere...
especially in biology!

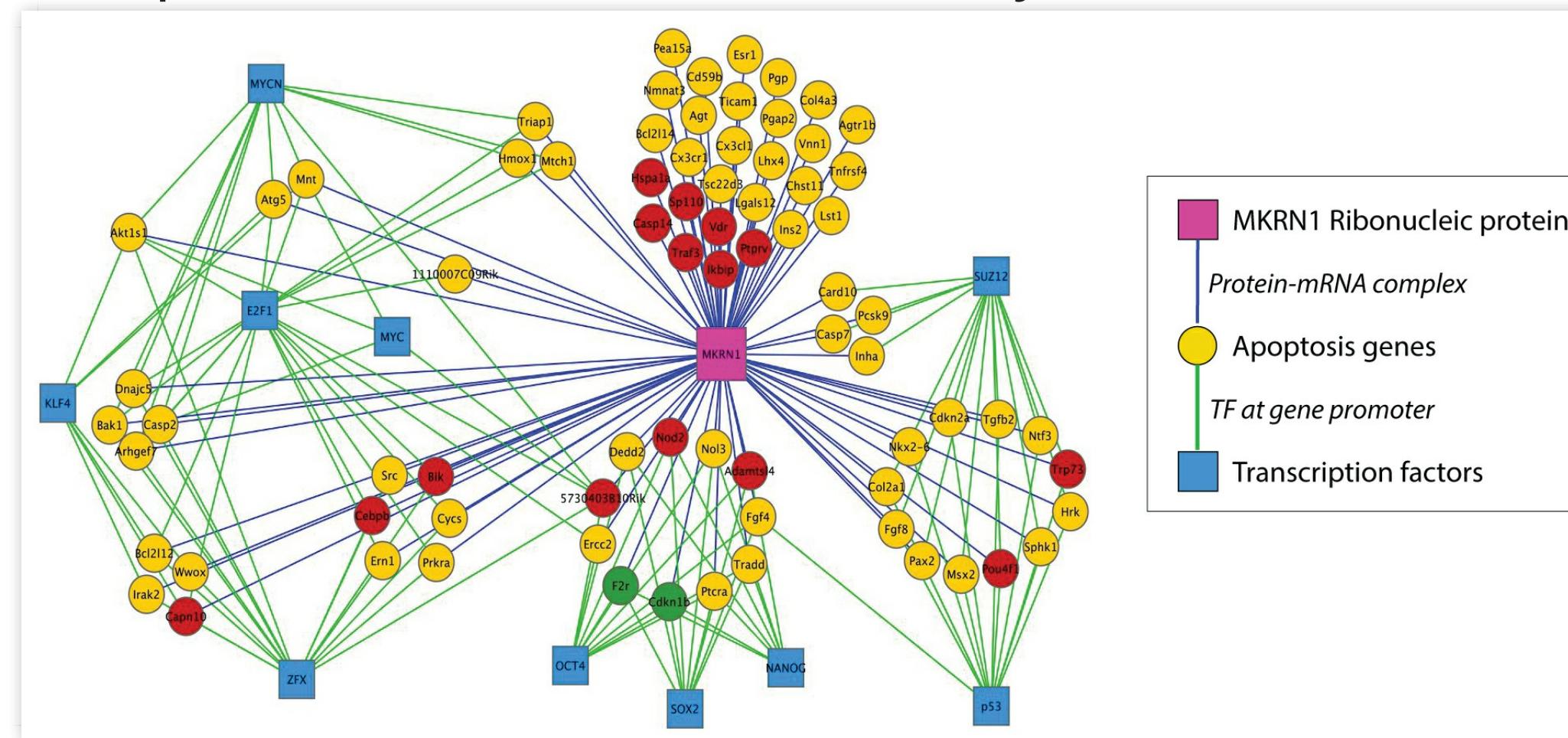
- Molecular networks
- Cell-cell communication
- Nervous systems
- Social networks

Networks are powerful tools...
especially in biology!

- Reduce complexity
- More efficient than tables
- Great for data integration
- Intuitive visualization

Networks as Tools

Transcription factors targeting apoptosis genes that bind MKRN1 in protein-mRNA network in embryonic stem cells.



One network figure conveys results from multiple technologies.



Cassar, *EMBO Reports* 2015, Fig.8

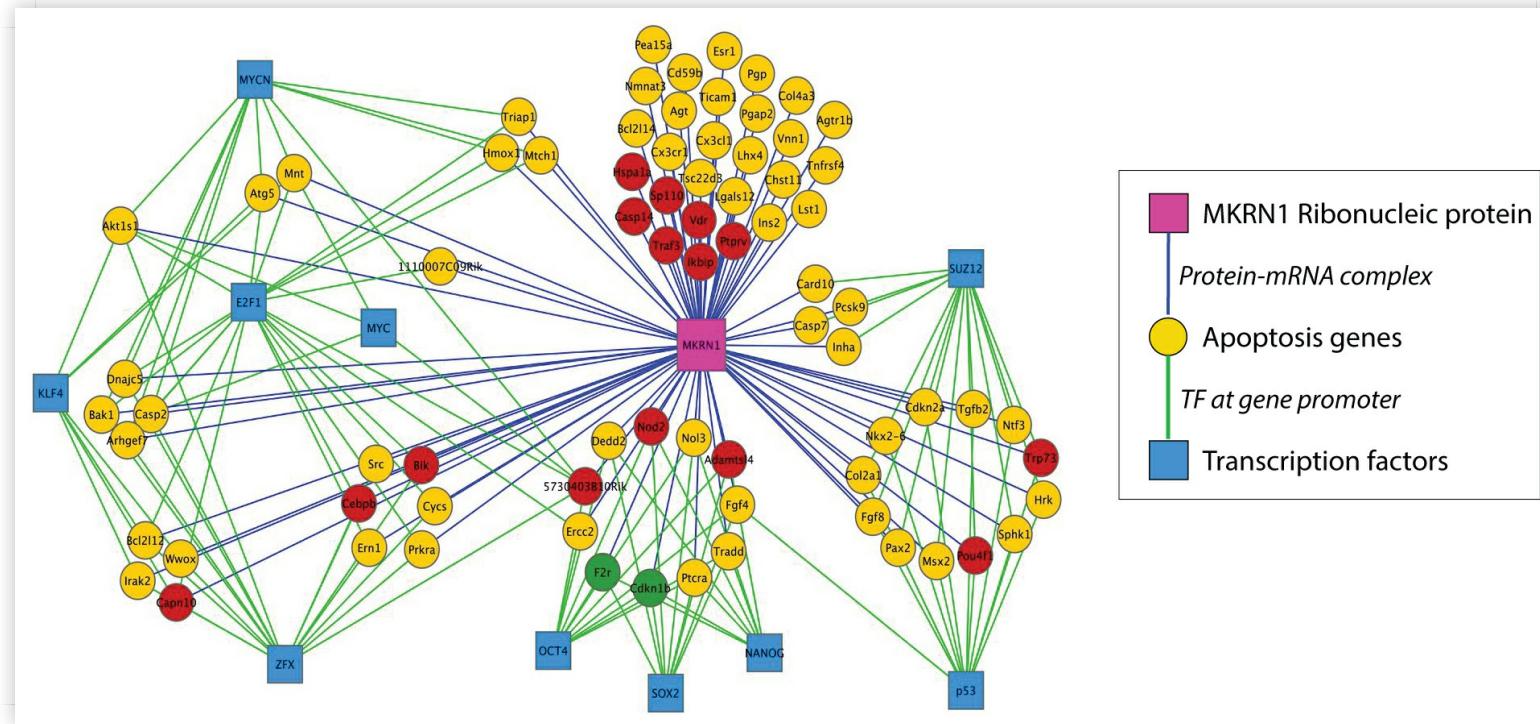
Networks as Tools

Analysis

- Topological properties
 - Hubs and subnetworks
 - Classify, cluster and diffuse
 - Data integration

Visualization

- Data overlays
 - Layouts and animation
 - Exploratory analysis
 - Context and interpretation



 Cytoscape 3.6.0

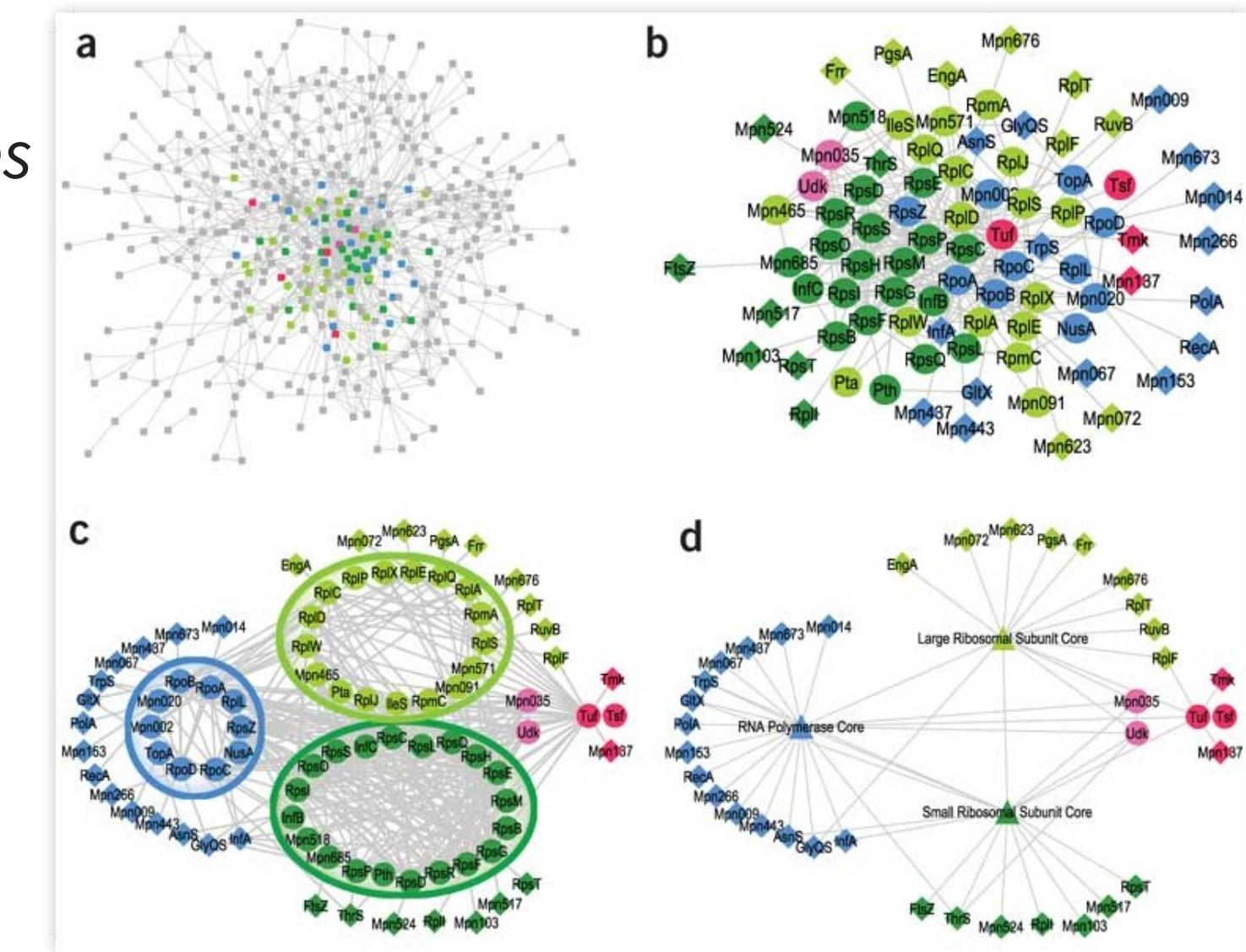
Cassar, EMBO Reports 2015, Fig.8

Applications in Research



Applications in Research

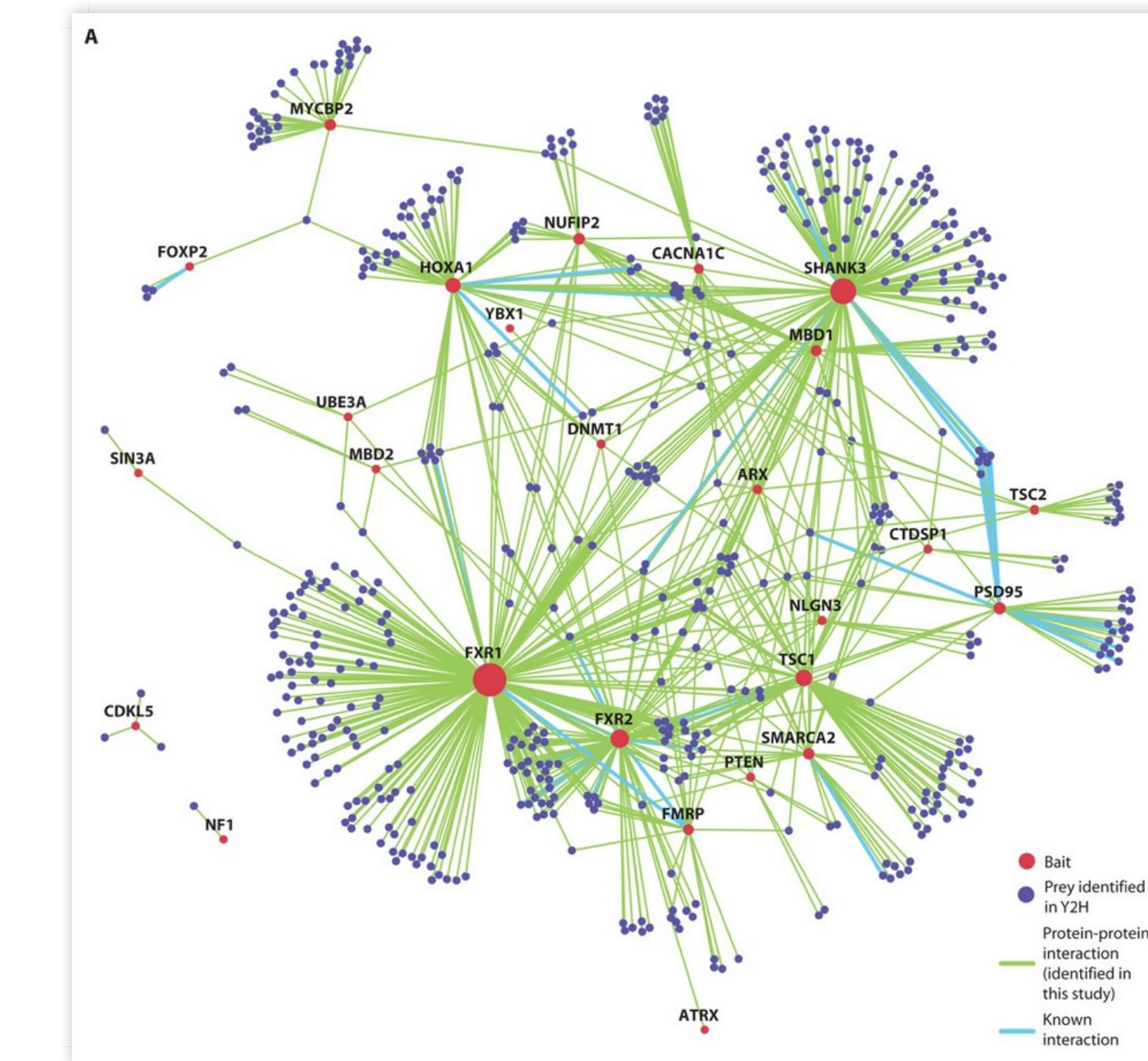
- In 2010, a Nature Methods paper introduced major *themes* of network visualization.
- (a) Mass spec analysis: 400 PPI in pneumonia microbe.
- (b) Subnetwork with function annotations.
- (c) Layout with knowledge of complexes.
- (d) Collapsed metanodes to reduce complexity.



Cytoscape 3.6 Gehlenborg (2010) Visualization of omics data for systems biology. *Nature Methods*, 7, Fig. 1

Applications in Research

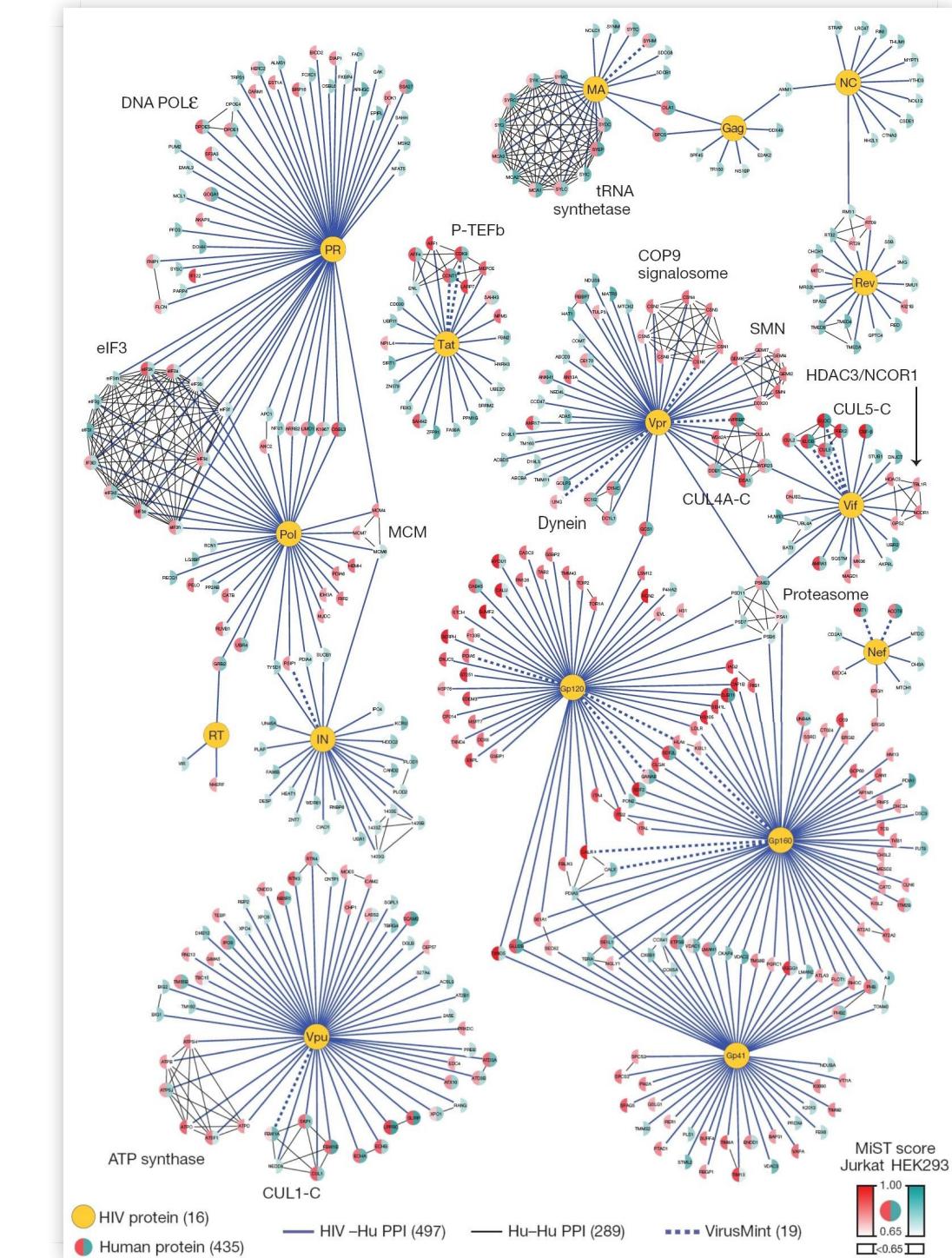
- Study of interactions with ASD-associated proteins.
- Y2H with human protein fragments of 26 ASD proteins: 848 interactions with 539 proteins.
- Merged with known interactions from public datasets.



Cytoscape 3.6.0 (2011) Protein Interactome Reveals Converging Molecular Pathways Among Autism Disorders.
Science Trans. Med., 3(86), Fig. 1

Applications in Research

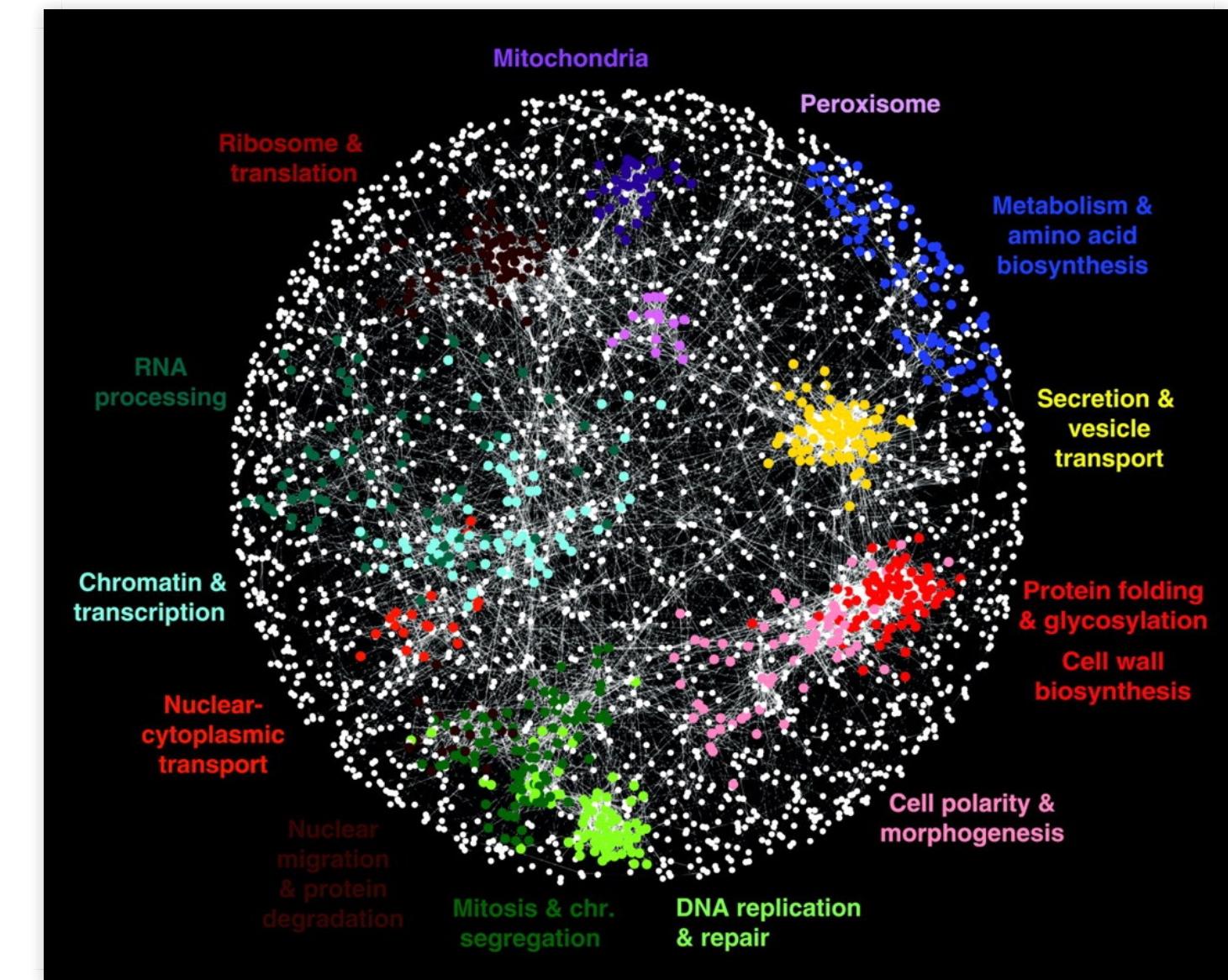
- HIV-human interactions.
- AP-MS with 16 HIV proteins: 497 interactions with 435 human proteins.
- Merged human-human PPI datasets to identify complexes.
- Used split gradient fills to show MiST scores for two cell lines.



Jager (2011) Global landscape of HIV-human protein complexes. *Nature*, 481(7381), Fig. 3

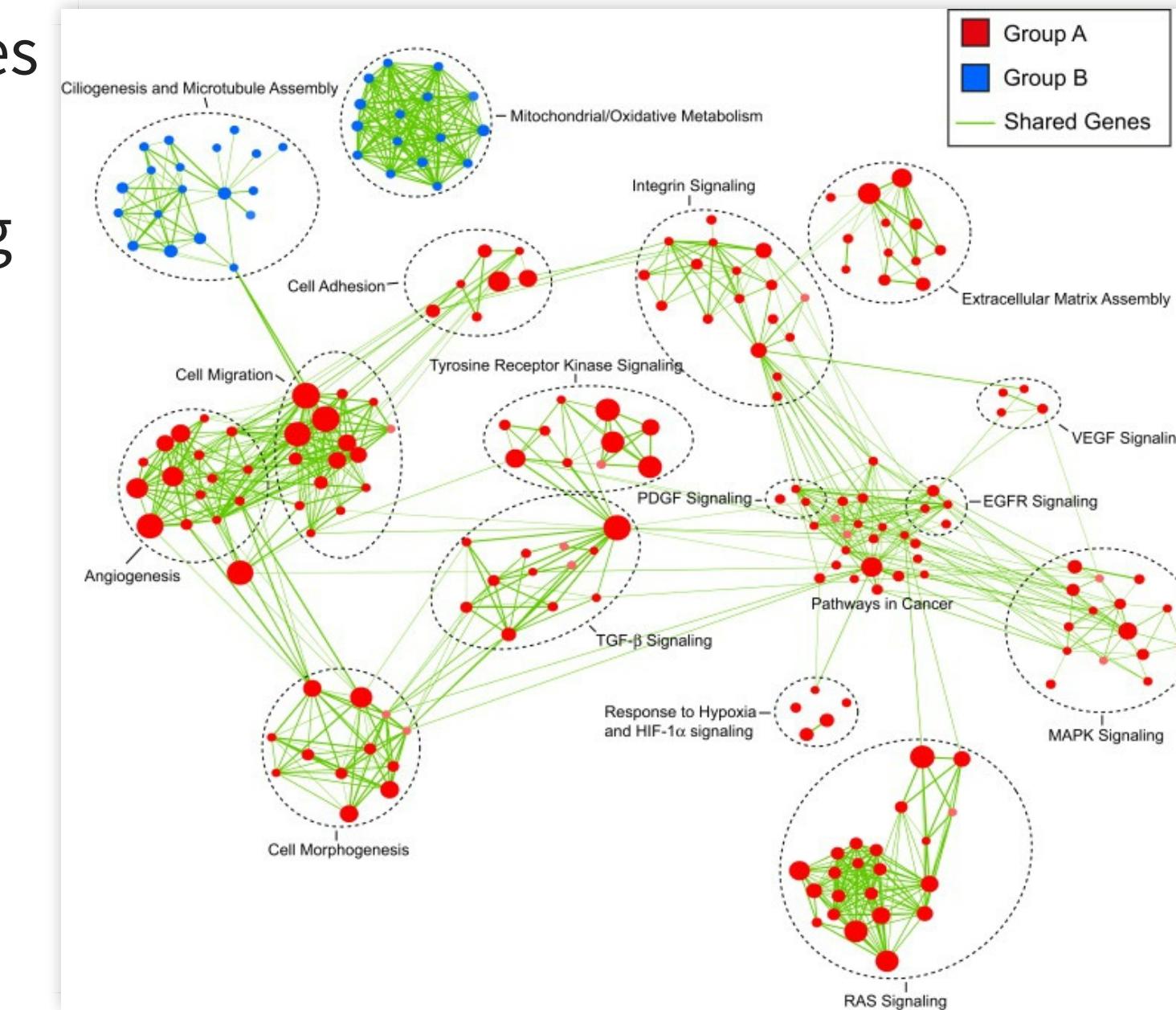
Applications in Research

- Genetic interactions for the entire yeast genome.
- Synthetic lethal screen of 1712 genes: 170,000 interactions.
- Visualization of clustering within and between functional groups annotated by GO.
- Predict functions and identify regulatory subnetworks.



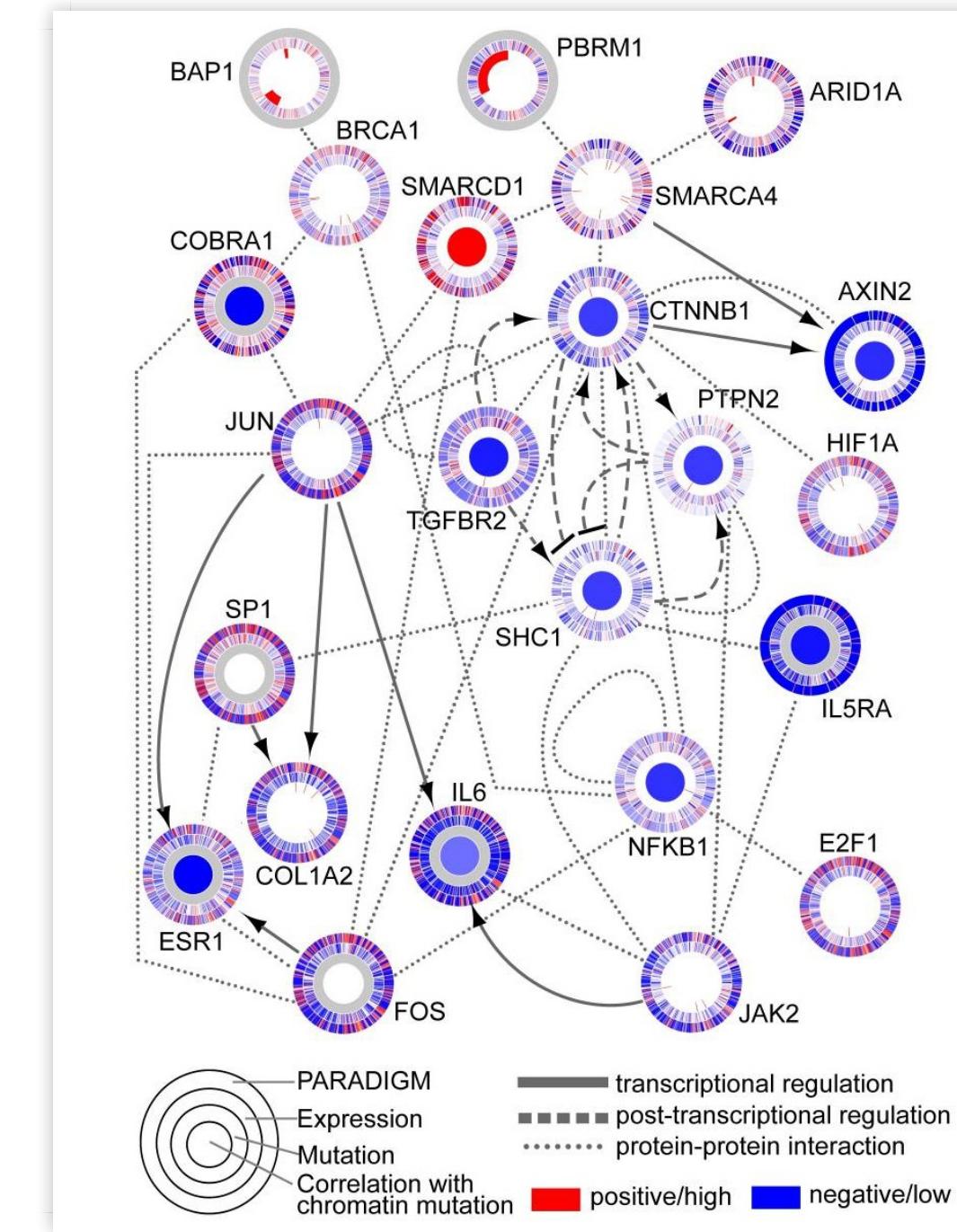
Applications in Research

- Molecular profiling of two types of brain tumors.
- GSEA to identify distinguishing gene sets (nodes).
- Functional annotation of a network of gene sets.



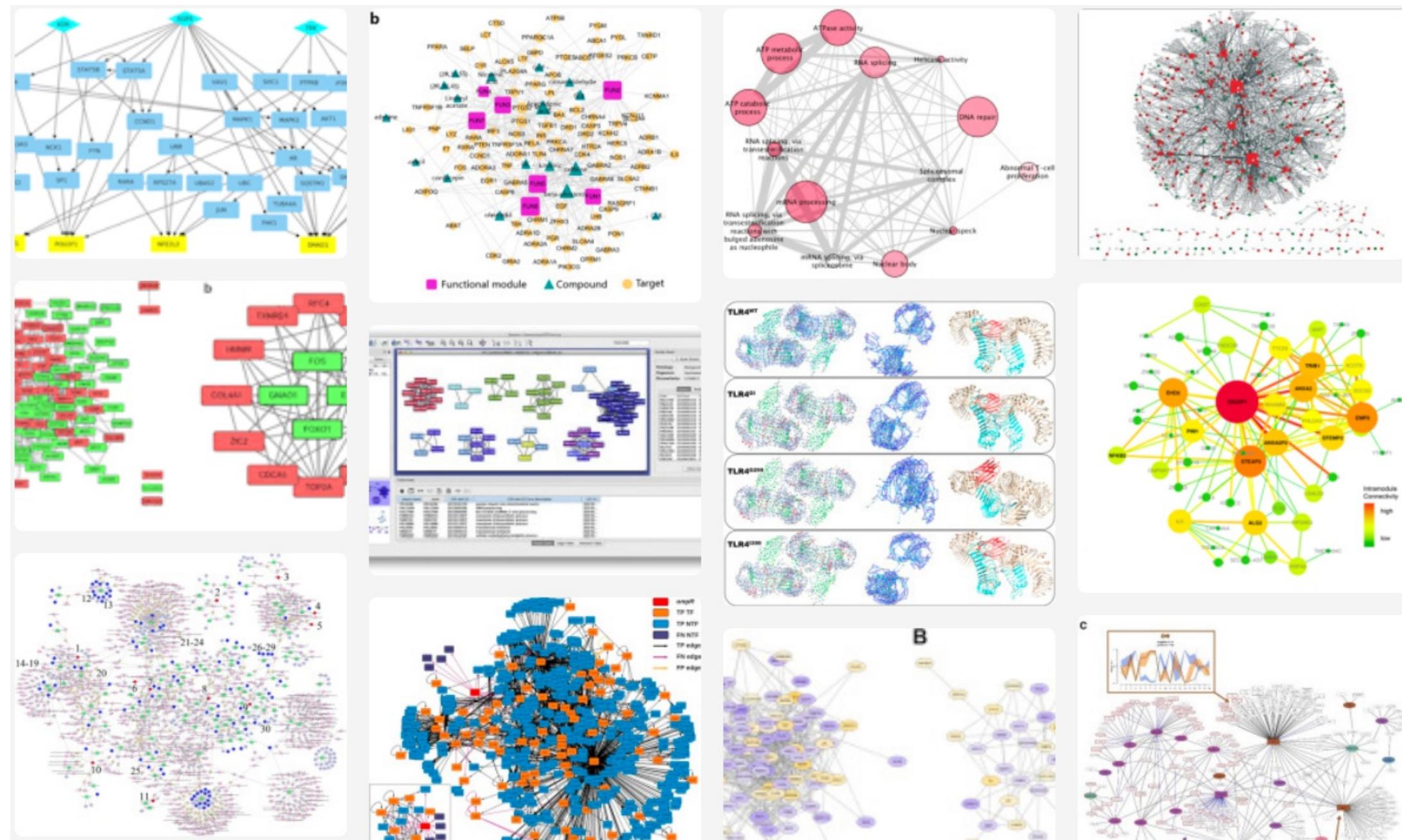
Applications in Research

- TCGA's series of molecular cancer profiles.
- Clinical, genomic, methylation, RNA and proteomic signatures.
- Multiple data types integrated onto signaling network.
- Includes patient sample-level data.



TCGA (2013) Comprehensive molecular characterization of clear cell renal cell carcinoma. *Nature*, 499, Fig. 4

Applications in Research

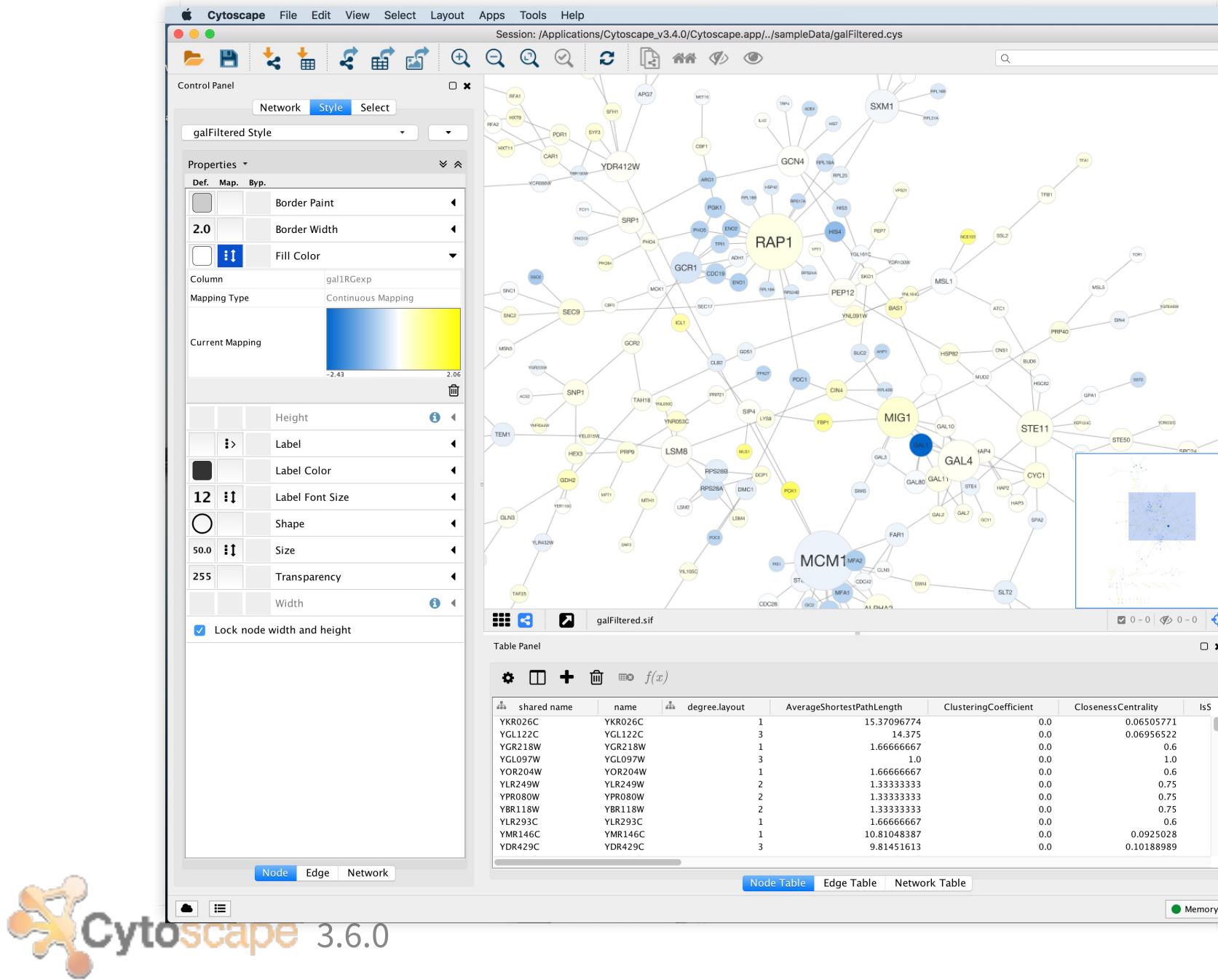


Introduction to Cytoscape

- Overview
- Core Concepts
 - Networks and Tables
 - Visual Properties
 - Cytoscape Apps
- Working with Data
 - Loading network from files and online databases
 - Loading data tables from CSV or Excel files
 - The Table Panel



Cytoscape

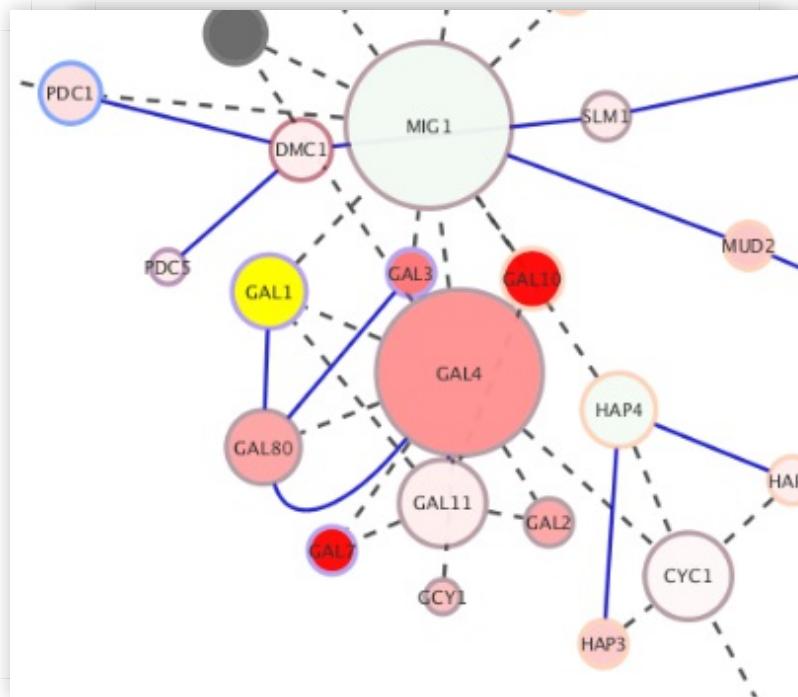


- Open source
- Cross platform
- Consortium



Core Concepts

Networks and Tables



Networks

A	B	C	D	E	F	G	H	I
GI_Number	Gene	HPRD_ID	REFSEQ	Entrez_ID	OMIM_ID	SWISSP_Gene_Description	Architecture	Arch
2	gi19923959	SDSL	11542	NP_612441.1	113675	SDSL	SP	Motif
3	gi14591926	SEC23B	11543	NP_116781.1	10483	Q15437 Protein transport protein SEC23B	GEL	Domain
4	gi14602492	SCMH1	11540	AAH09752.1	22955	Q96GD3 SCMH1	SAM	Domain
5	gi21361625	EXOC2	11544	NP_060773.3	55770	Q96KP1 SEC5 like 1	IPT	Domain
6	gi17998551	SERPINB12	11548	NP_536722.1	89777	Q96P63 Serpin B12	SERPIN	Domain
7	gi65287717	EIF2AK4	18447	NP_00101372	440275	609280 Similar to GCN2 eIF2alpha kinase	S_T_Y_Kinase	Domain
8	gi4507755	TYROBP	4996	NP_00323.1	7305	604142 DAP12	ITAM	Domain
9	gi5803086	IL24	4995	NP_006841.1	11009	604136 Q13007 Interleukin 24	IL10	Domain
10	gi21265034	ADAMTS13	4994	NP_620594.1	11093	604134 ADAMTS 13	TSP1	Domain
11	gi1743873	PIP5K1A	4470	AAC50911.1	8394	603275 Q99755 Phosphatidylinositol-4-phosphate 5	PIPk	Domain
12	gi11496982	SVIL	4992	NP_068506.1	6840	604126 095425 Survivin	VHP	Domain
13	gi31563386	SULT2B1	4991	NP_814444.1	6820	604125 Sulfotransferase family 2B, member 1		
14	gi21040399	RBBP8	4990	AAH30590.1	5932	604124 Q99708 CTIP	LZ	Motif
15	gi4758378	FIGF	2102	NP_004460.1	2277	300091 043915 VEGF D	PDGF	Domain
16	gi11321617	DPYSL4	7463	NP_006417.1	10570	608407 O14531 Collapsin response mediator protein 3		
17	gi8923202	TASP1	7460	NP_060184.1	55617	608270 Q9H6P5 Threonine aspartase 1		
18	gi5454090	SSR4	2101	NP_006271.1	6748	300090 P51571 Signal sequence receptor delta	SP	Motif
19	gi5730045	SLC16A2	2106	NP_006508.1	6567	300095 P36021 X linked PEST containing transporte	TM	Domain
20	gi11968027	FTS	7467	NP_071921.1	64400	608483 Q9H8T0 FTS	UBC	Domain
21	gi48255885	PRKCI	2105	NP_002731.3	5584	600539 P41743 Protein kinase C, iota type	S_T_kinase	Domain
22	gi9558731	RPA4	6591	NP_037479.1	29935		RPA4	TRNA
23	gi13376812	PPP1R2P9	6593	NP_079486.1	80316			
24	gi15826862		6595	NP_296375.1	90060		JM11 protein	CC
25	gi7661844	CCDC22	6594	NP_054727.1	28952		JM1 protein	CC
26	gi6005794	PRAF2	6596	NP_009144.1	11230		JM4 protein	TM

Tables



Visual Styles



apps.cyto... psicquic Tech News

Cytoscape App Store Submit an App Search the App Store Sign In

Wall of Apps 295 total

collections

data visualization

network generation

online data import

graph analysis

network analysis

integrated analysis

clustering

utility

enrichment analysis

systems biology

data integration

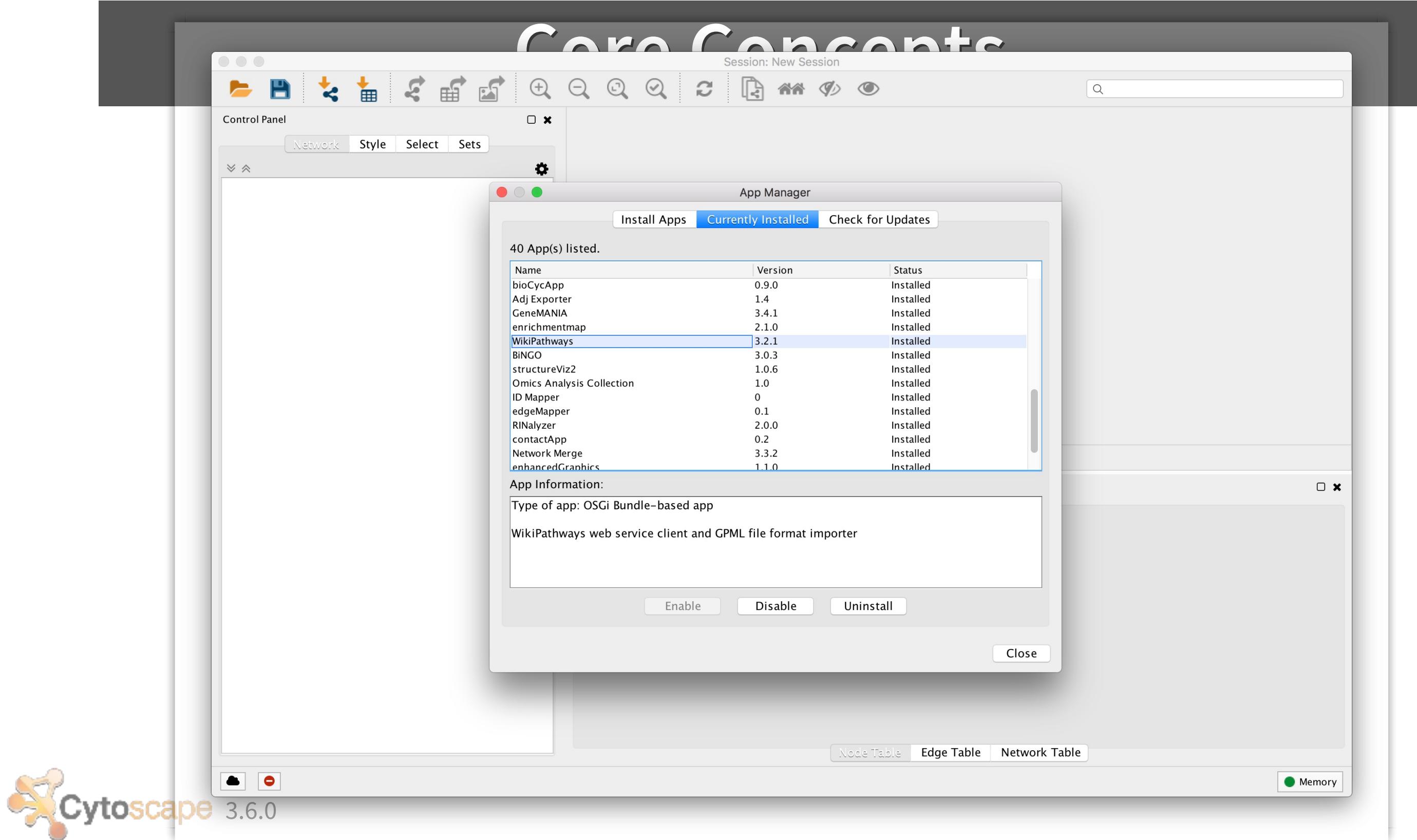
layout

ontology analysis

295 Apps!

apps.cyto... vitaligraphicalization

The image shows a screenshot of the Cytoscape App Store interface. The main title "Wall of Apps" is displayed above a grid of 295 app icons. The apps are categorized into rows: collections, data visualization, network generation, online data import, graph analysis, network analysis, integrated analysis, clustering, utility, enrichment analysis, systems biology, data integration, and layout. A large, bold text "295 Apps!" is overlaid in the center of the grid. At the bottom left, there is a watermark for "Cytoscape 3.6.0".



Loading Data

- Cytoscape can import network data from:
 - Files (or URLs)
 - Excel, TSV, CSV
 - **eXtensible Graph Markup and Modelling Language: XGMML**
 - **Systems Biology Markup Language (SBML)**
 - **BioPAX**
 - **PSI-MI**
 - Simple Interaction Format: SIF
 - Graph Markup Language: GML
 - ... and others depending on loaded Apps

* **Bold:** loads table data also



Loading Data

- Cytoscape can import network data from:
 - Public repositories:
 - **EBI/PSICQUIC**
 - **STRING** (via the stringApp)
 - **Reactome** (via the ReactomeFI App)
 - **Wikipathways** (via the Wikipathways App)
 - **Pathway Commons** (via the CyPath2 App)

* **Bold:** loads table data also

Loading Data

- Cytoscape can load tables from:
 - Files (or URLs)
 - Excel, TSV, CSV

Loading Data

- Sessions save everything as **.cys** files:
Networks, Tables, Styles, Screen sizes, etc.
- Export networks in different formats:
SIF, GML, XGMML, BioPAX, PSI-MI 1 & 2.5
- Export tables as CSV files
- Publication quality graphics in several formats:
PDF, SVG, PNG, and JPEG

Finding Network Data

Where do I find *the network*?

There is no such thing!

550 different interaction databases



in 2013!

It depends on your biological question and your analysis plan,

But know what you are getting.....

Importing Network Data

Cytoscape can import network data from:

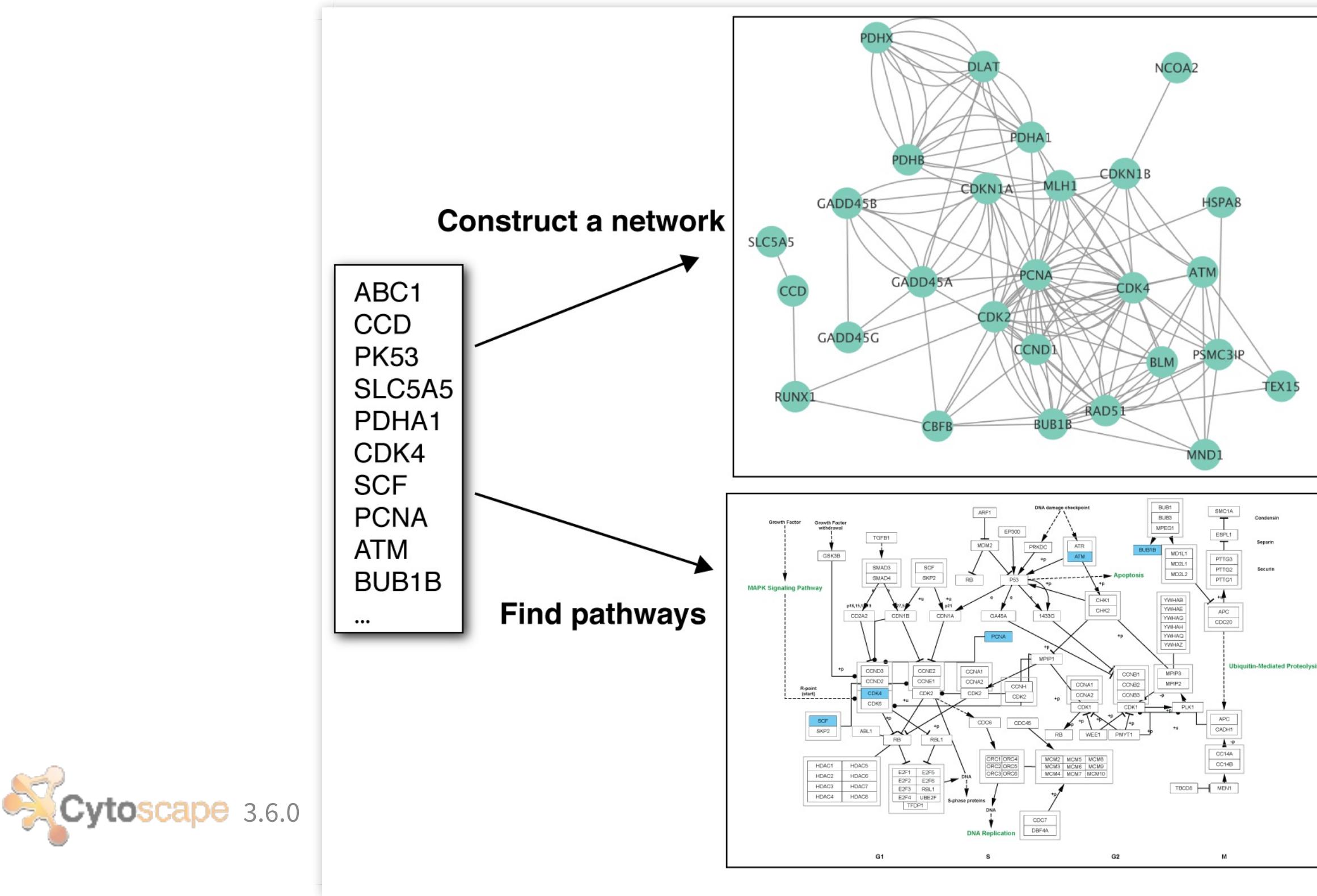
- Public repositories:
 - **EBI/PSICQUIC**
 - **STRING** (via the stringApp)
 - **Reactome** (via the ReactomeFI App)
 - **Wikipathways** (via the Wikipathways App)
 - **Pathway Commons** (via the CyPath2 App)

Cytoscape Apps for Finding Network Data

The screenshot shows the Cytoscape App Store interface. At the top, there is a navigation bar with the Cytoscape logo, "Cytoscape App Store", "Submit an App", a search bar containing "Search the App Store", and a "Sign In" button. On the left, a sidebar titled "All Apps" lists various categories: collections, data visualization, network generation, graph analysis, online data import, network analysis, integrated analysis, clustering, utility, systems biology, enrichment analysis, data integration, visualization, layout, ontology analysis, and pathway database. Below the sidebar, the main content area is titled "Interaction database". It features two links: "Search for posts about interaction database →" and "Ask a question about interaction database →". A sorting menu "Sort by" allows users to sort by name (selected), downloads, votes, or newest release. The main content displays six app cards:

- Bisogenet** (3.0+ stars): Retrieves interactions associated with input IDs. Sophisticated UI.
- CHAT** (3.0+ stars): Identify contextually relevant hubs in biological networks.
- CyPath2** (3.0+ stars): Pathway Commons (BioPAX L3 database) web service GUI client.
- ncINetView** (3.0+ stars): A network visualization tool.
- ReactomeFIPPlugin** (3.0+ stars): Explore Reactome pathways and search for diseases related.
- stringApp** (3.0+ stars): Import and augment Cytoscape network from String-db.

Starting with a gene list.....



Networks

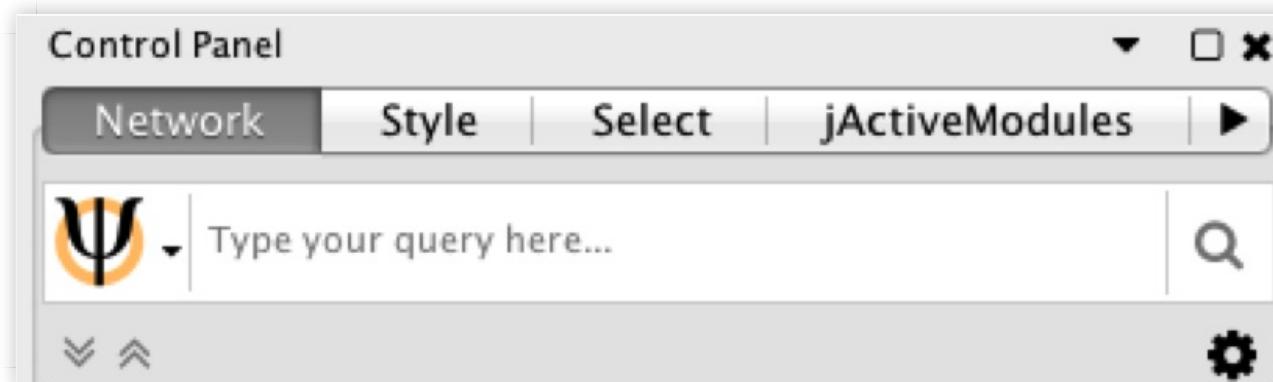
Broad coverage / Low resolution

- PSICQUIC
- STRING (stringApp)
- GeneMANIA (Web)
- NDEx (CyNDEx App)

PSICQUIC

PSI common query interface

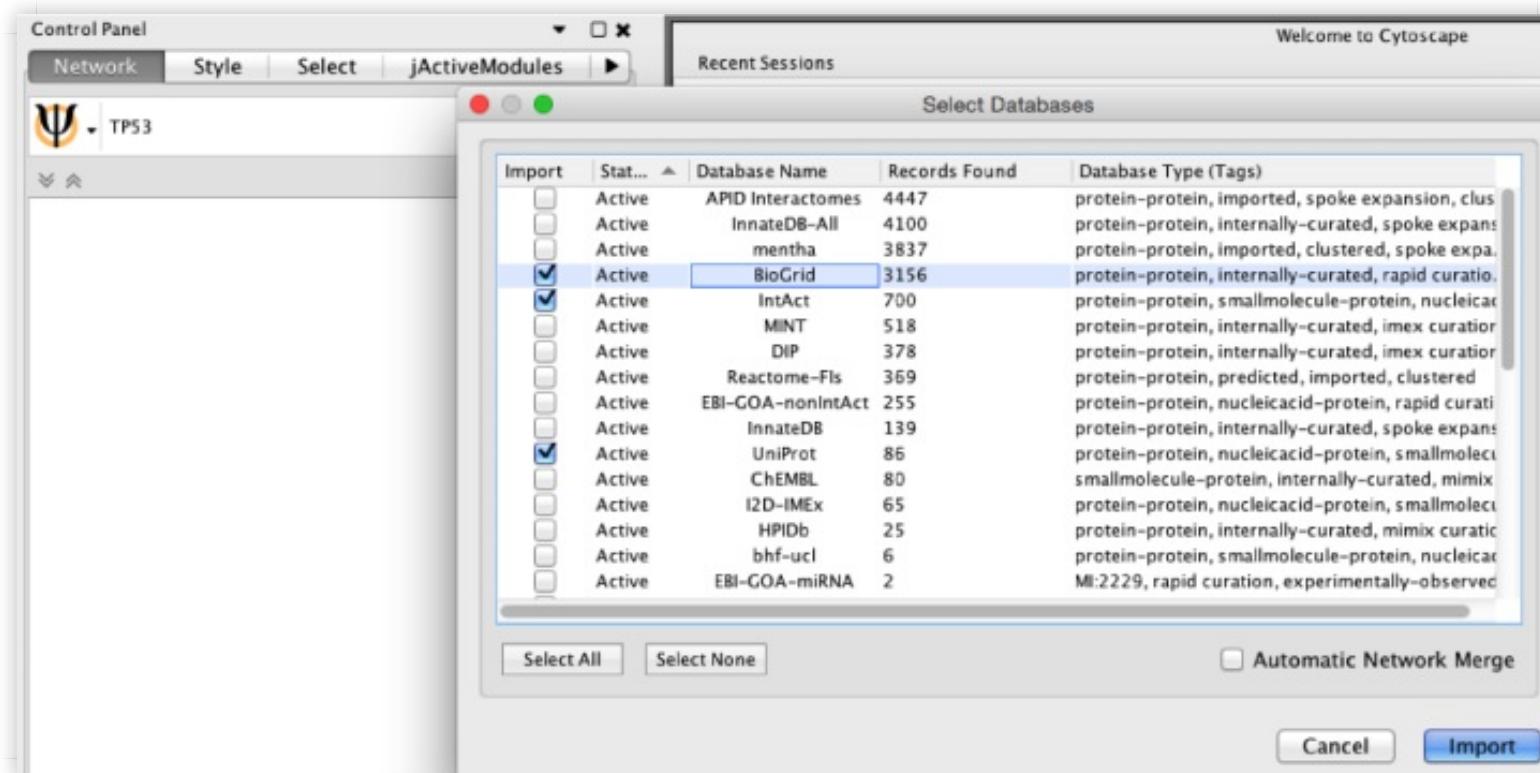
Cytoscape network search tool uses PSICQUIC app by default:



Data from multiple sources and types:

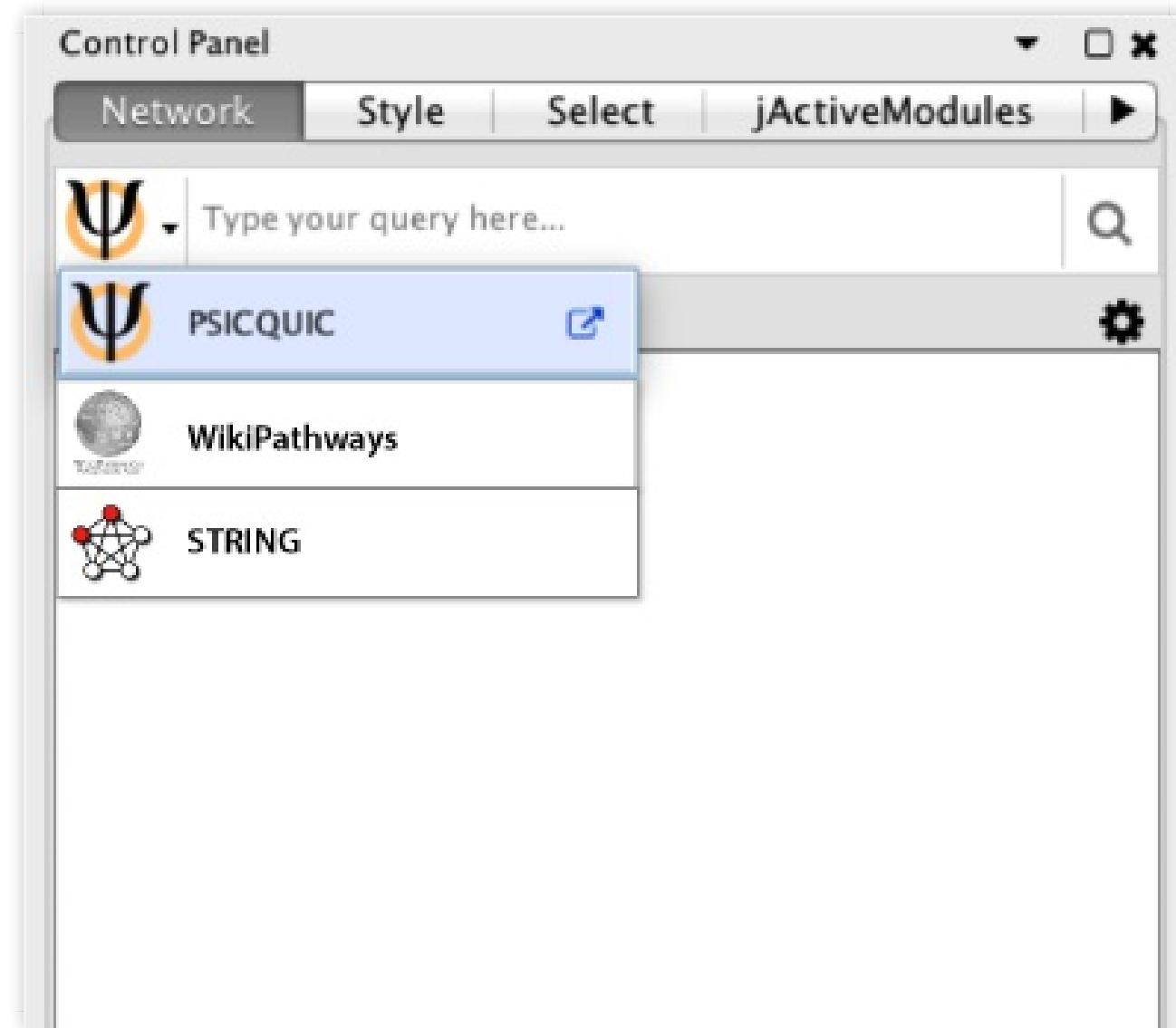
- Internally curated
- Experimentally observed
- Predicted

PSICQUIC search results



- Select results from multiple sources
- Interaction type is included

Network search tool pull-down shows resources based on installed apps:



STRING

stringApp

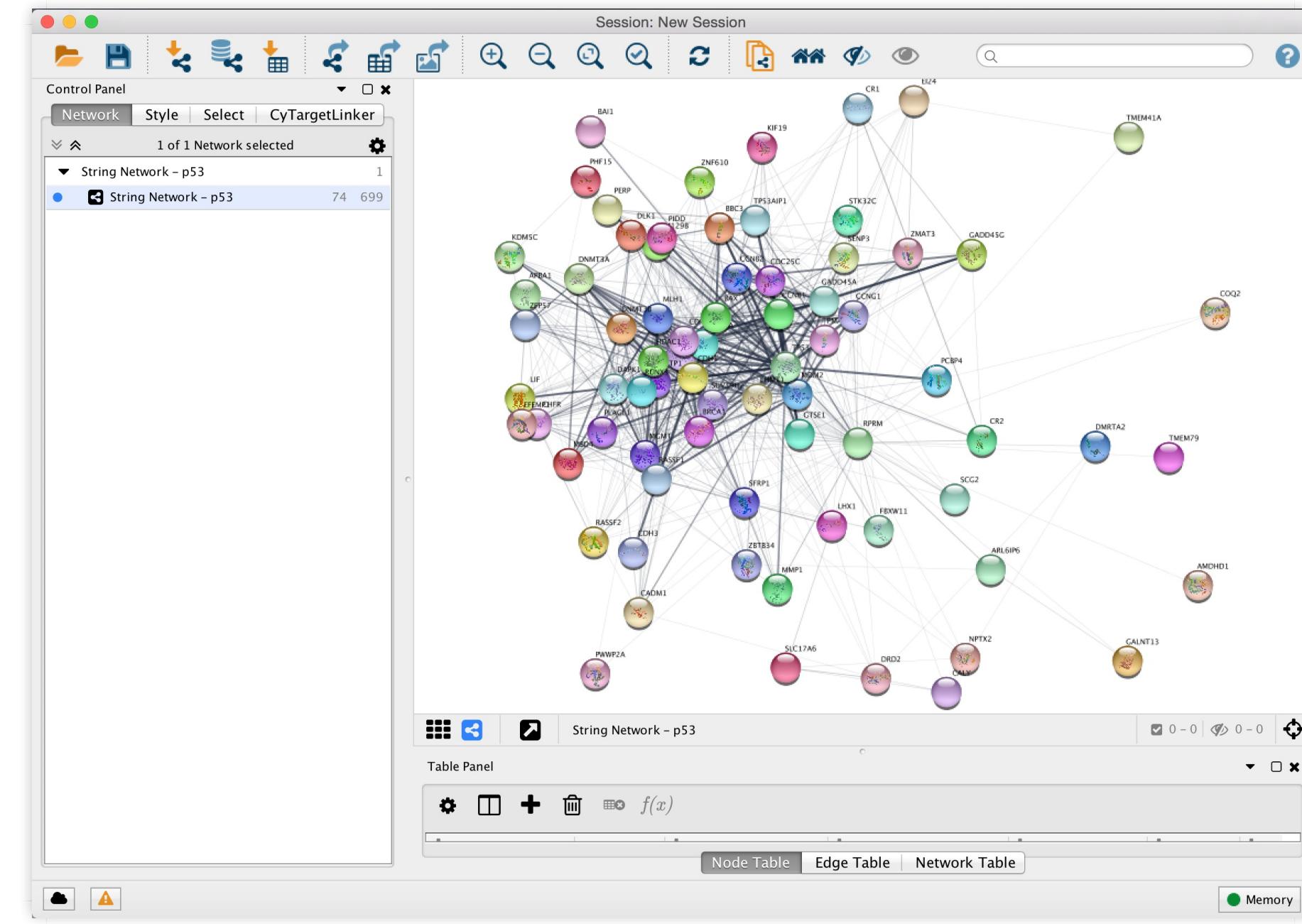
Data types:

- Genomic Context Predictions
- High-throughput Lab Experiments
- (Conserved) Co-Expression
- Automated Textmining
- Previous Knowledge in Databases

STRING Input

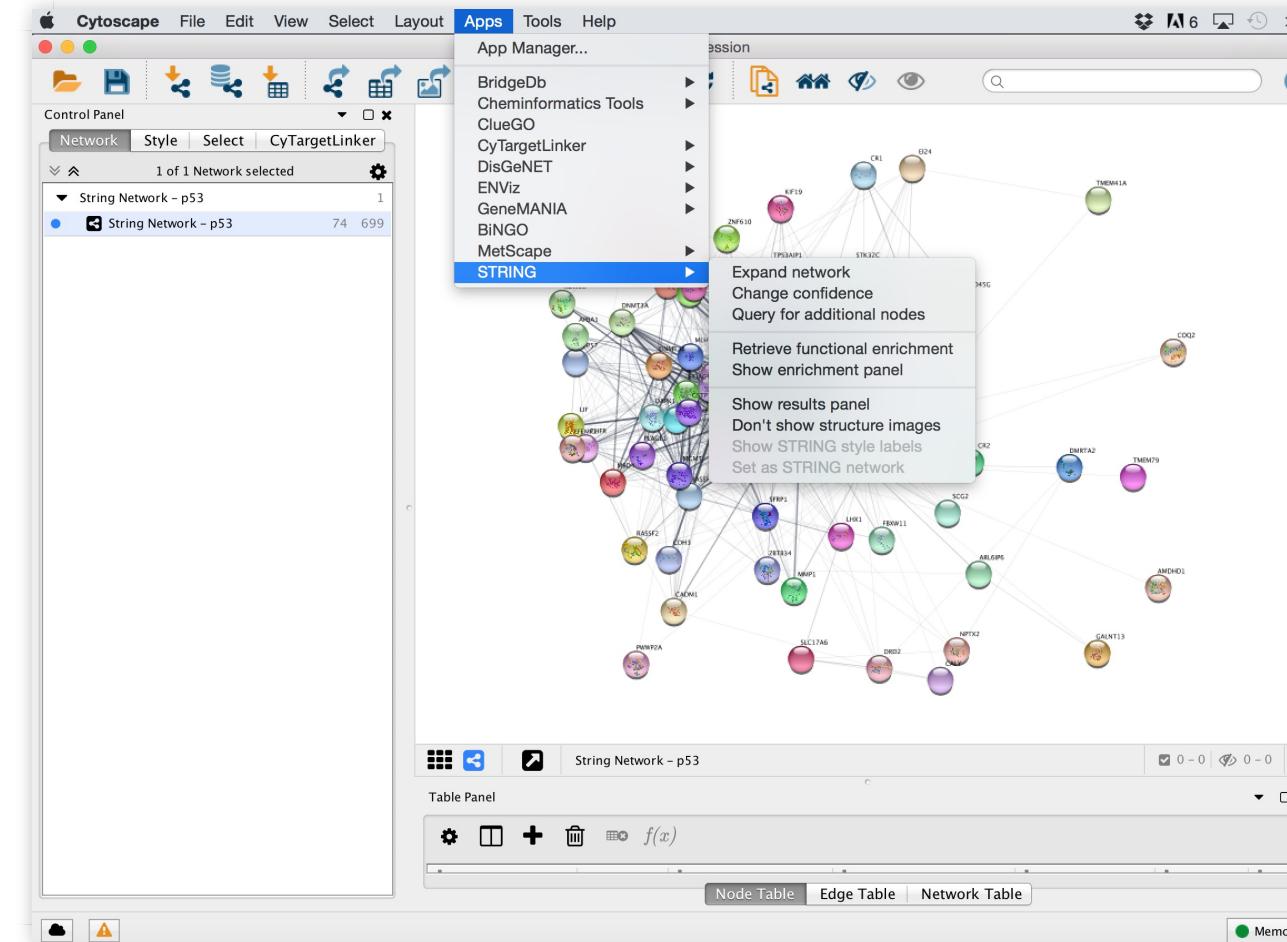


STRING Results



 Cytoscape 3.6.0

STRING Results



The STRING App has options to:

- Change confidence level of interactions
- Expand network
- Functional Enrichment

GeneMANIA

<http://genemania.org>

Data types:

- Co-expression
- Genetic interactions
- Predicted interactions
- Co-localization
- Pathway co-occurrence
- Shared protein domains



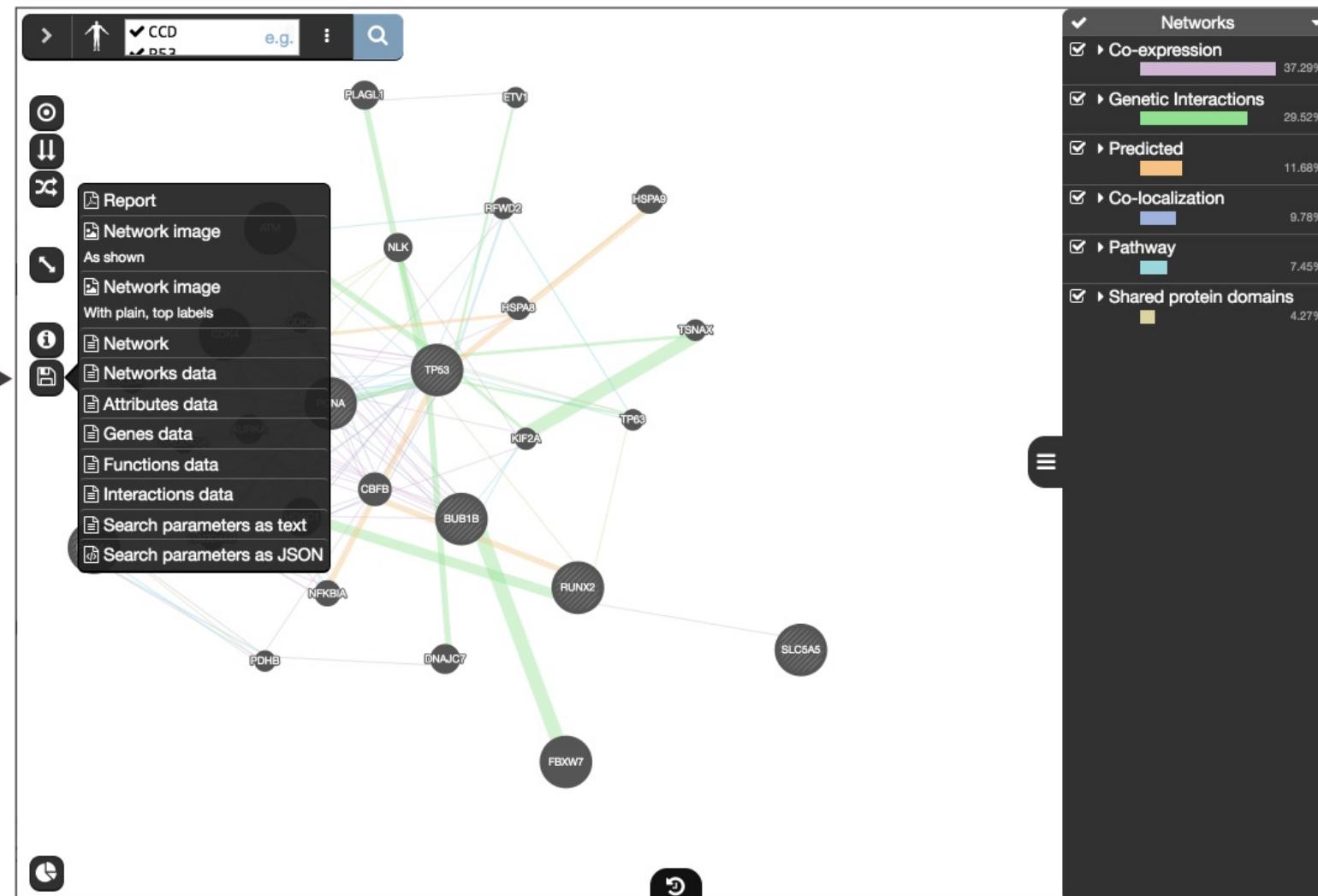
GeneMANIA Input

The screenshot shows the GeneMANIA input page. At the top left is a navigation bar with back, forward, and refresh buttons, followed by the URL "genemania.org". To the right are a star icon and a three-dot menu icon. Below the navigation is a search bar with a magnifying glass icon. To the left of the search bar is a sidebar containing a list of genes with checked checkboxes: CCD, P53, SLC5A5, PDHA1, CDK4, SCF, PCNA, ATM, and BUB1B. Below this list is a button with the text "Enter one gene per line". The main title "GENEMANIA" is prominently displayed in large, bold, dark letters. Below the title are links to "Cytoscape app", "Help", "Contact", "Cite", and "© UToronto". A descriptive text block states: "GeneMANIA helps you predict the function of your favourite genes and gene sets. Indexing 2,277 association networks containing 597,392,998 interactions mapped to 163,599 genes from 9 organisms." At the bottom left is the Cytoscape logo, which consists of a stylized orange and brown molecular structure icon next to the word "Cytoscape".

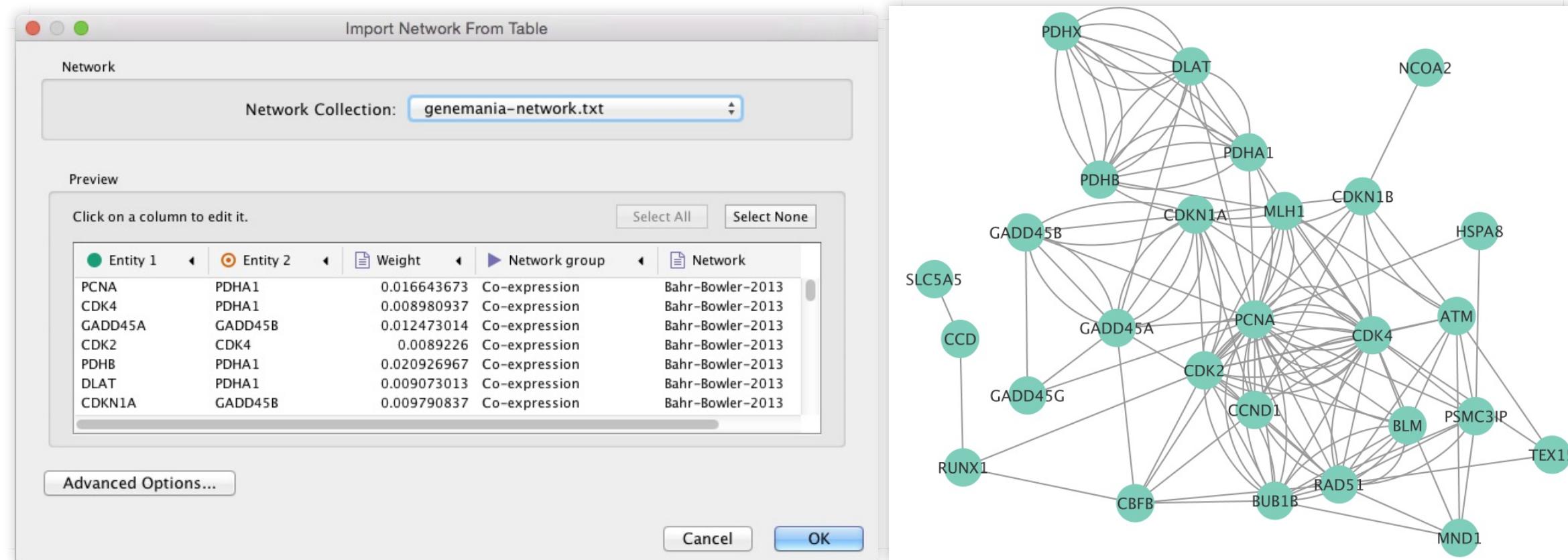
GeneMANIA Results

Export network
for import to →
Cytoscape

← Filter interactions
based on type



Import GeneMANIA Network to Cytoscape



NDEx

CyNDEx App

NDEx data:

- Repository for biological network knowledge
- Organisations and individual scientists can deposit
- Use CyNDEx App to import/export networks
- Featured collections include:
 - Pathway Interaction Database (NCI-PID)
 - Cancer Cell Maps Initiative (CCMI)
 - The NDEx Butler
 - NetPath

NDEx Input

Find Networks

Current Source: PUBLIC (<http://public.ndexbio.org/v2>)

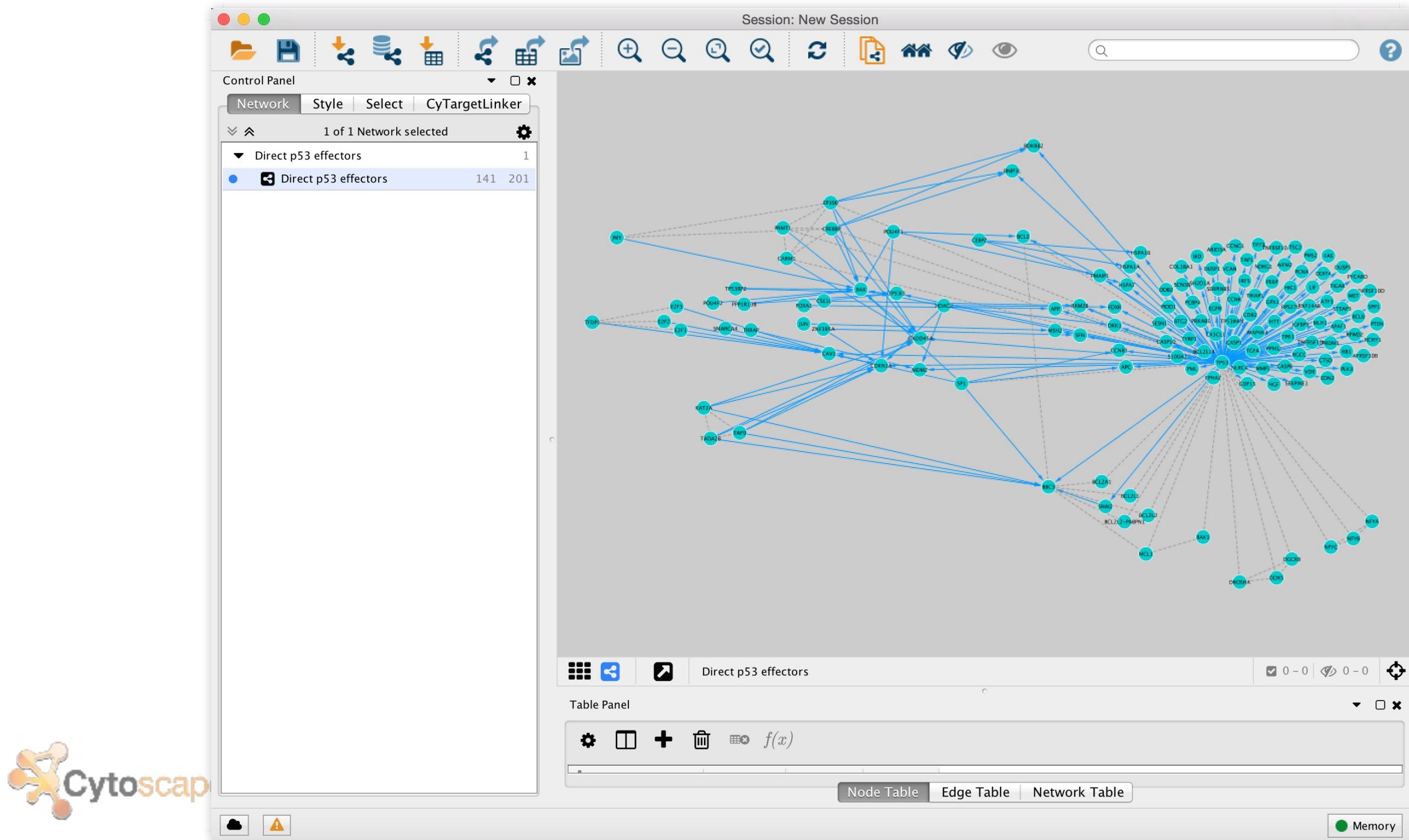
Authenticated As: Not Authenticated

Results

Network Title	Format	Number of Nodes	Number of Edges	Owned By	Last Modified
indra_assembled		134	180	bgyori	2016-04-08 19:36:43.446
rasmachine		232	292	bgyori	2016-04-11 14:21:11.592
p53 pathway		57	90	nci-pid	2016-12-20 16:59:01.317
nci_pid_preview		212	492	aarongary	2017-04-07 15:12:39.947
!!! NEW !!! PID MAP !!! NEW !!!		212	492	nci-pid	2017-04-10 14:17:36.517
net_of_nets_uuids.txt		214	21722	decarlin	2016-04-27 16:12:01.362
Direct p53 effectors		141	201	nci-pid	2016-12-20 16:58:50.229
Pathways Affected by Melanoma G...		489	1833	mgdb	2017-06-02 09:53:31.94
Apoptosis	SIF	148	2511	reactome	2015-09-28 21:00:46.884
TRAF6 Mediated Induction of pro... SIF		190	7816	reactome	2015-09-28 21:00:49.846
Pathways Affected by Melanoma G...		826	2953	mgdb	2017-06-02 09:53:52.847
TTD - Target-Disease Association...		1585	1652	ndexbutler	2016-04-28 15:55:05.421
DNA Repair	SIF	285	12174	reactome	2015-09-28 21:00:47.869
BindingDB - High Affinity Compou...		1038	2119	bindingdb	2016-05-05 14:04:35.229
Drugs Targeting Melanoma Genes		1102	1236	mgdb	2017-06-02 09:44:28.152
Cellular responses to stress	SIF	357	14673	reactome	2015-09-28 21:00:47.392



NDEx Results



Pathways

High resolution / Limited coverage (~40% of genes)

- WikiPathways (WikiPathways App)
- Reactome (ReactomeFI App)
- Pathway Commons (CyPath2 App)
- KEGG and others

WikiPathways

WikiPathways App

WikiPathways data:

- Manually curated content
- Collaborative wiki platform
- Over 2,400 pathways
- 25 species-specific collections



WikiPathways Search

The image shows two side-by-side windows of the 'Import Network from Public Databases' tool in Cytoscape, version 3.6.0. Both windows have 'WikiPathways' selected as the Data Source. The left window has a search term of 'Anopheles gambiae' and displays a table of pathways for this species. The right window has a search term of 'Statin' and displays a table of pathways related to statins across various species.

Left Window (Search: Anopheles gambiae):

Pathway	Species	ID
Statin Pathway	Rattus norvegicus	WP145
Statin Pathway	Canis familiaris	WP1157
Statin Pathway	Mus musculus	WP1
Statin Pathway PharmGKB	Pan troglodytes	WP921
Statin Pathway	Homo sapiens	WP430
Statin Pathway	Bos taurus	WP1041
Statin induced myopathy	Homo sapiens	WP3983
Demo	Homo sapiens	WP3590
WikiPathways Tutorial: demo_step3	Homo sapiens	WP3539
Demo_complete	Homo sapiens	WP3418

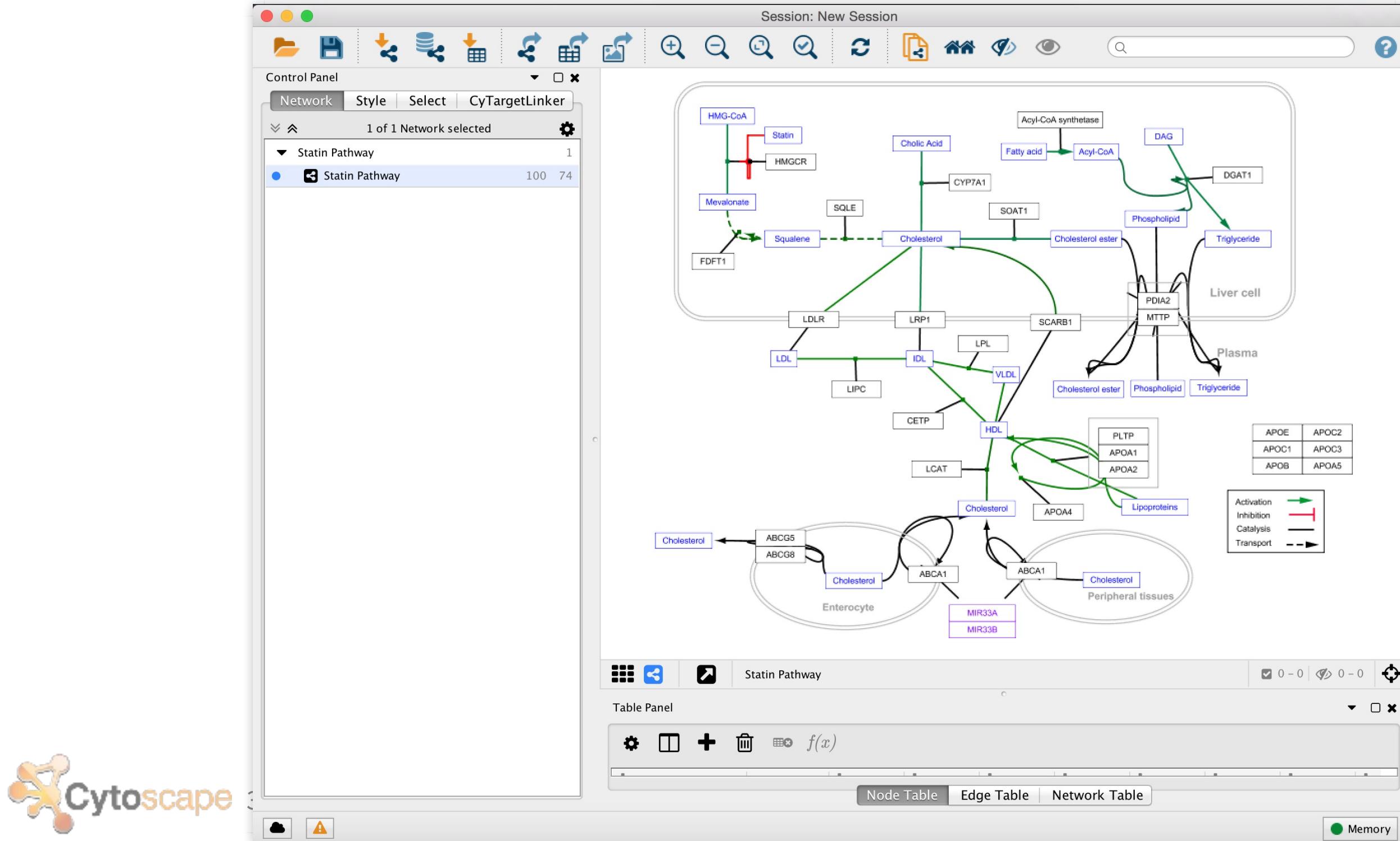
Right Window (Search: Statin):

Pathway	Species	ID
Statin Pathway	Rattus norvegicus	WP145
Statin Pathway	Canis familiaris	WP1157
Statin Pathway	Mus musculus	WP1
Statin Pathway PharmGKB	Pan troglodytes	WP921
Statin Pathway	Homo sapiens	WP430
Statin Pathway	Bos taurus	WP1041
Statin induced myopathy	Homo sapiens	WP3983
Demo	Homo sapiens	WP3590
WikiPathways Tutorial: demo_step3	Homo sapiens	WP3539
Demo_complete	Homo sapiens	WP3418

Both windows include buttons at the bottom: 'Import as Pathway', 'Import as Network', 'Open in Web Browser', and 'Preview →'. The 'Import as Network' button in the right window is circled in red.



WikiPathways Results



Reactome

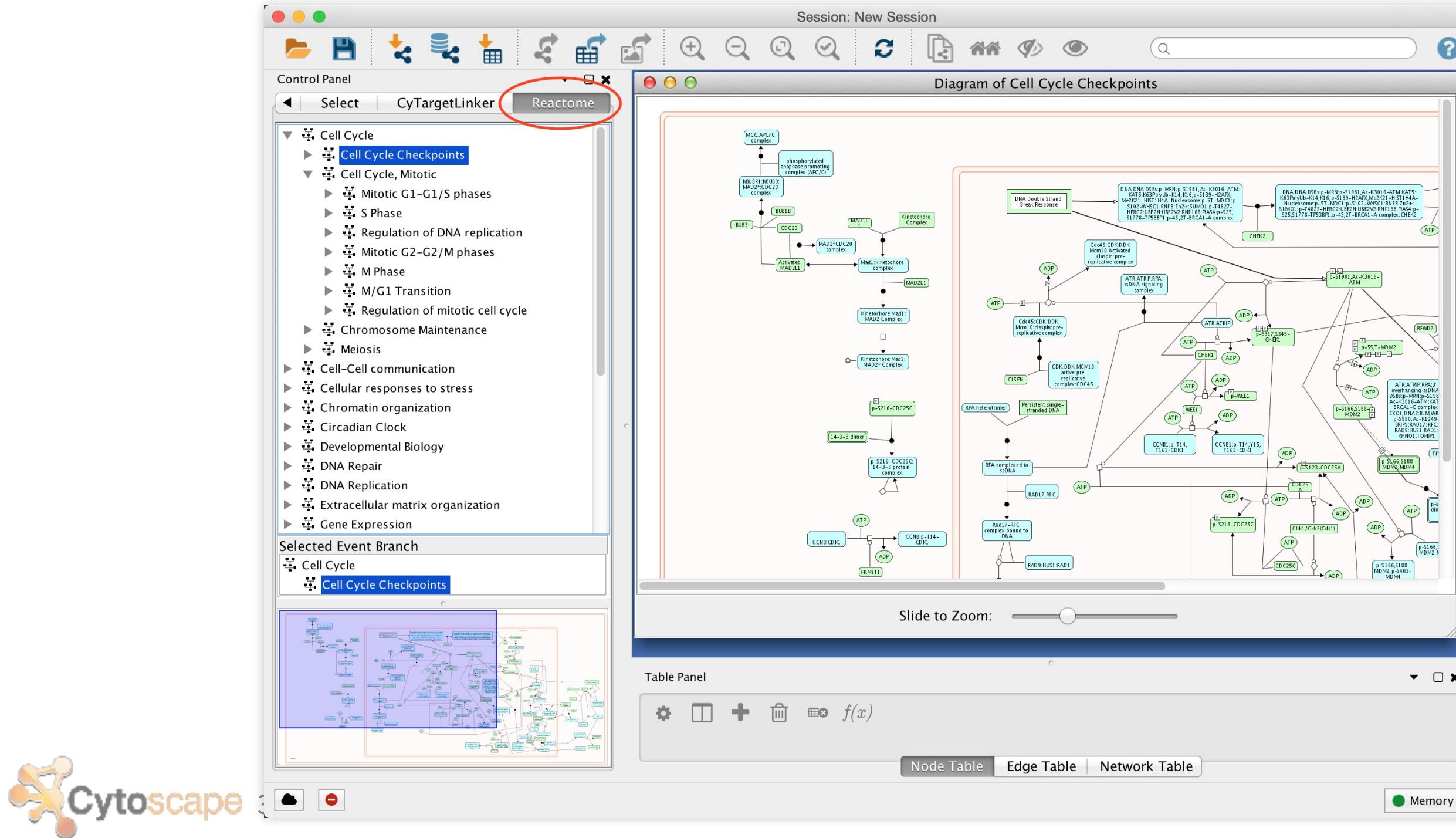
ReactomeFIPlugin

Reactome data:

- Manually curated and peer-reviewed content
- Content curated in human and inferred to other species
- Over 21,000 pathways
- 19 species covered



Reactome



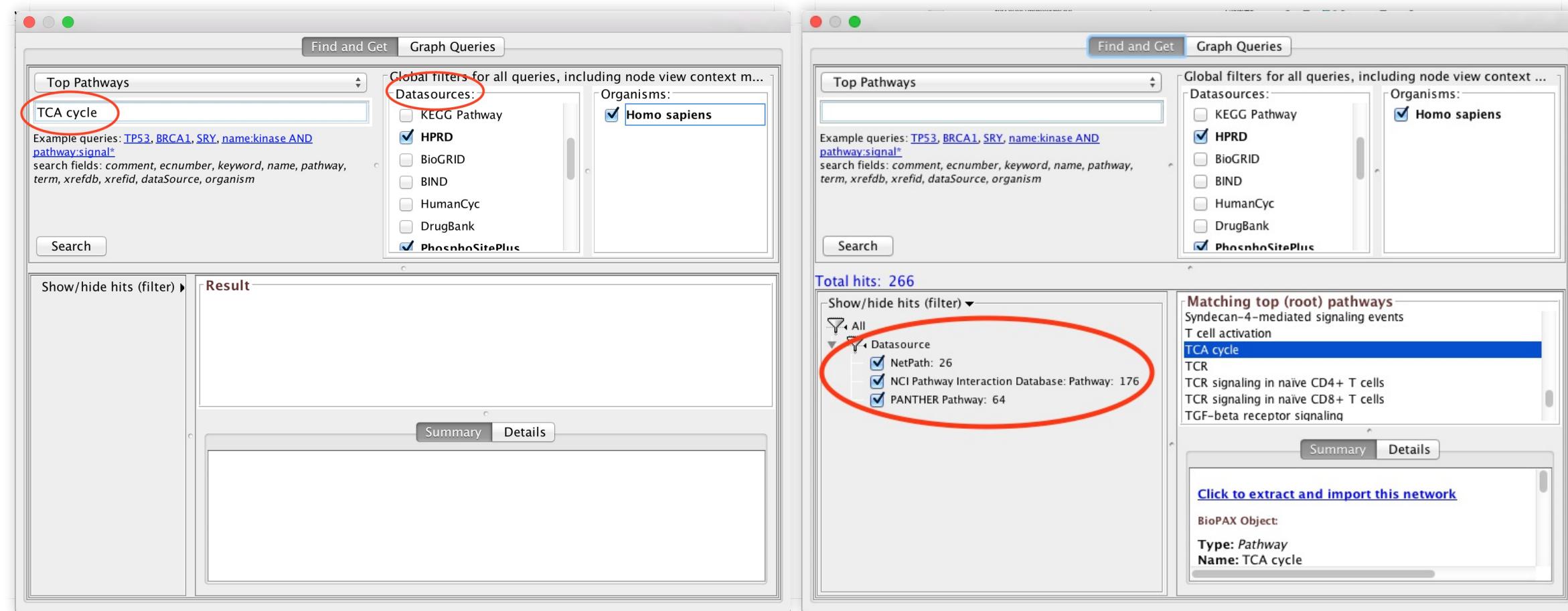
Pathway Commons

CyPath2 App

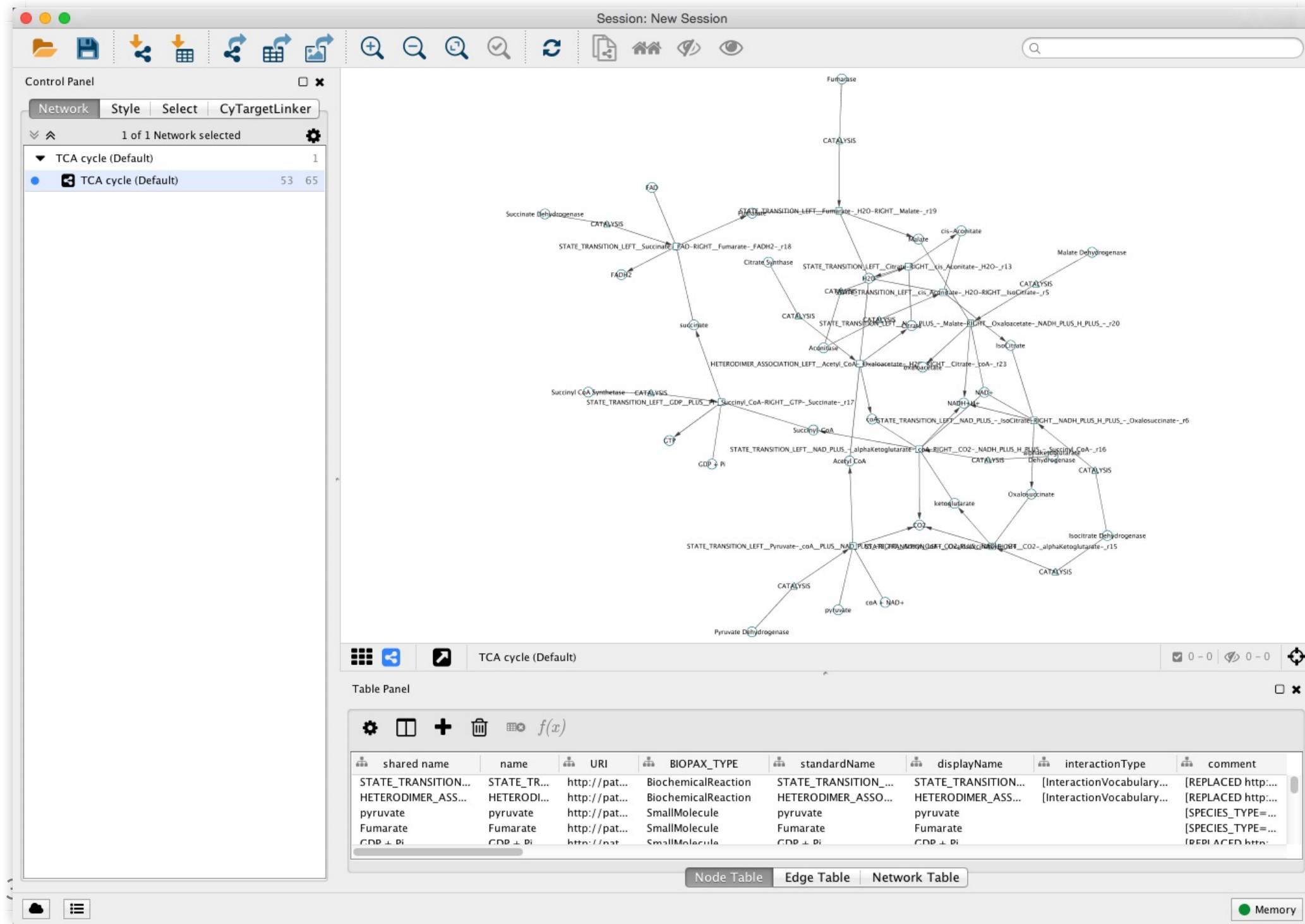
Pathway Commons data:

- Consolidated data from 22 public pathway databases
- Over 42,000 pathways
- Data sources include:
 - Reactome
 - PhosphoSitePlus
 - NCI
 - HumanCyc

CyPath2 App



CyPath2 App Results



KEGG

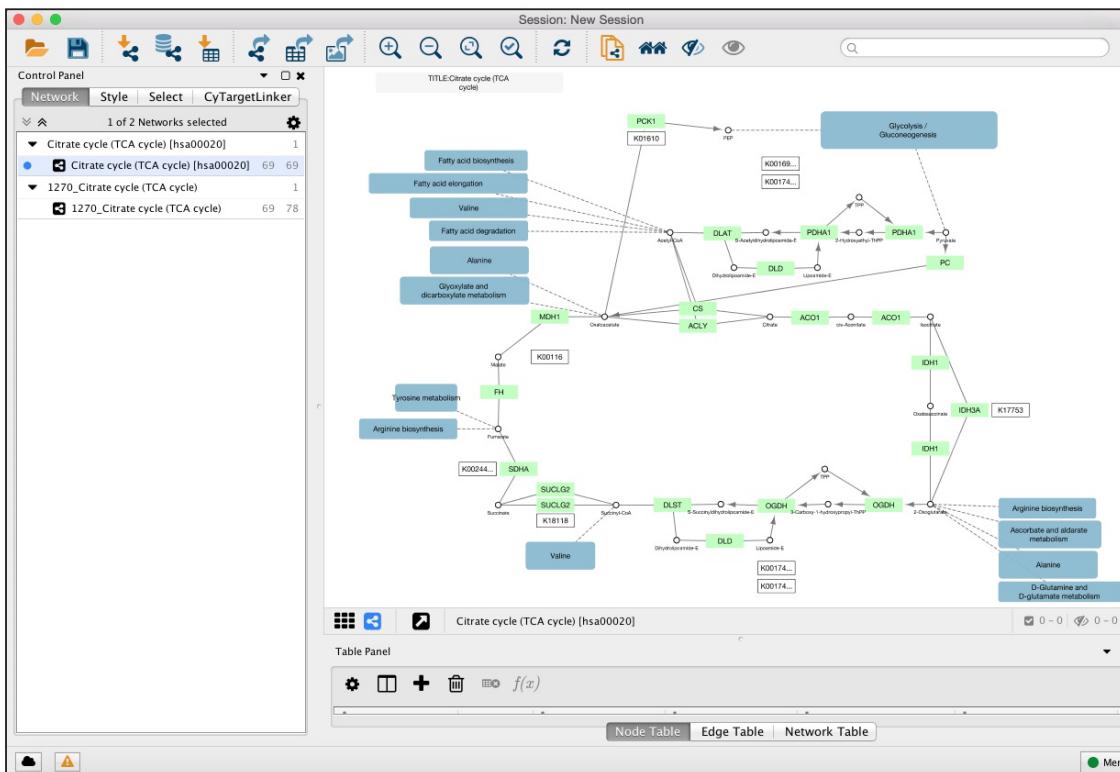
KEGGscape | CyKEGGParser

KEGG PATHWAY data:

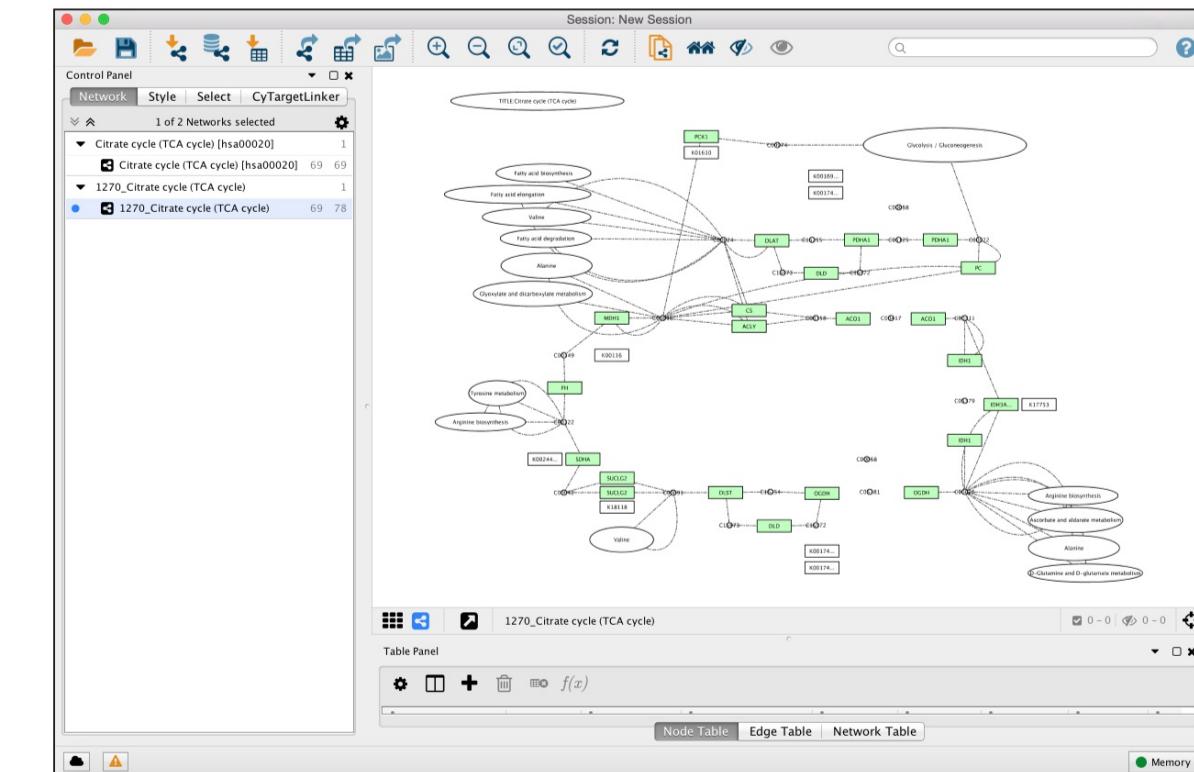
- Expert curated
- 500+ pathways
- Supports multiple species through inference



KEGG Apps



KEGGscape



CyKEGGParser



Introductions and Concepts

Finding Network Data

Network Visualization

Network Analysis

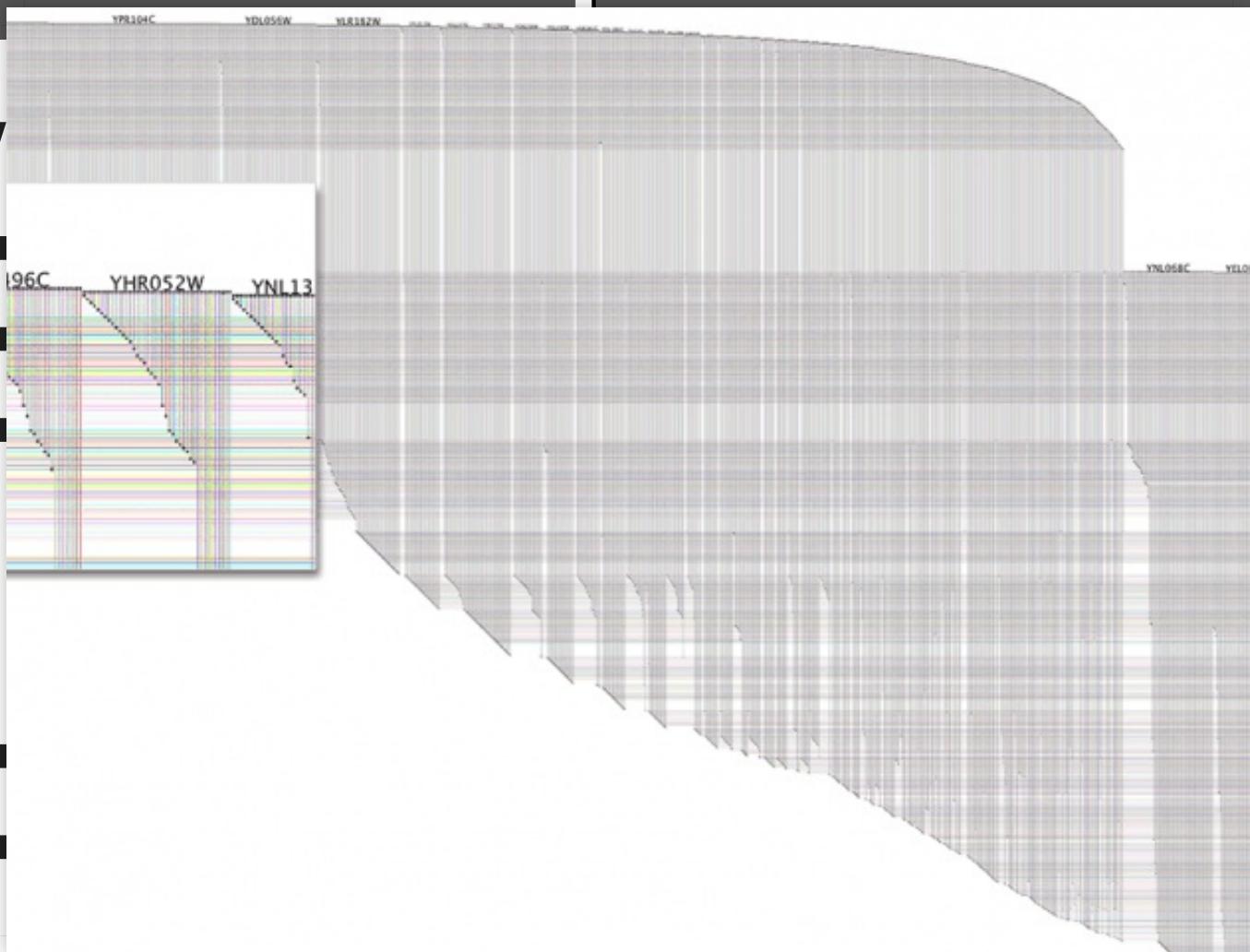
Automation via CyREST

Network Visualization

- Data Mapping
- Layouts
- Animation

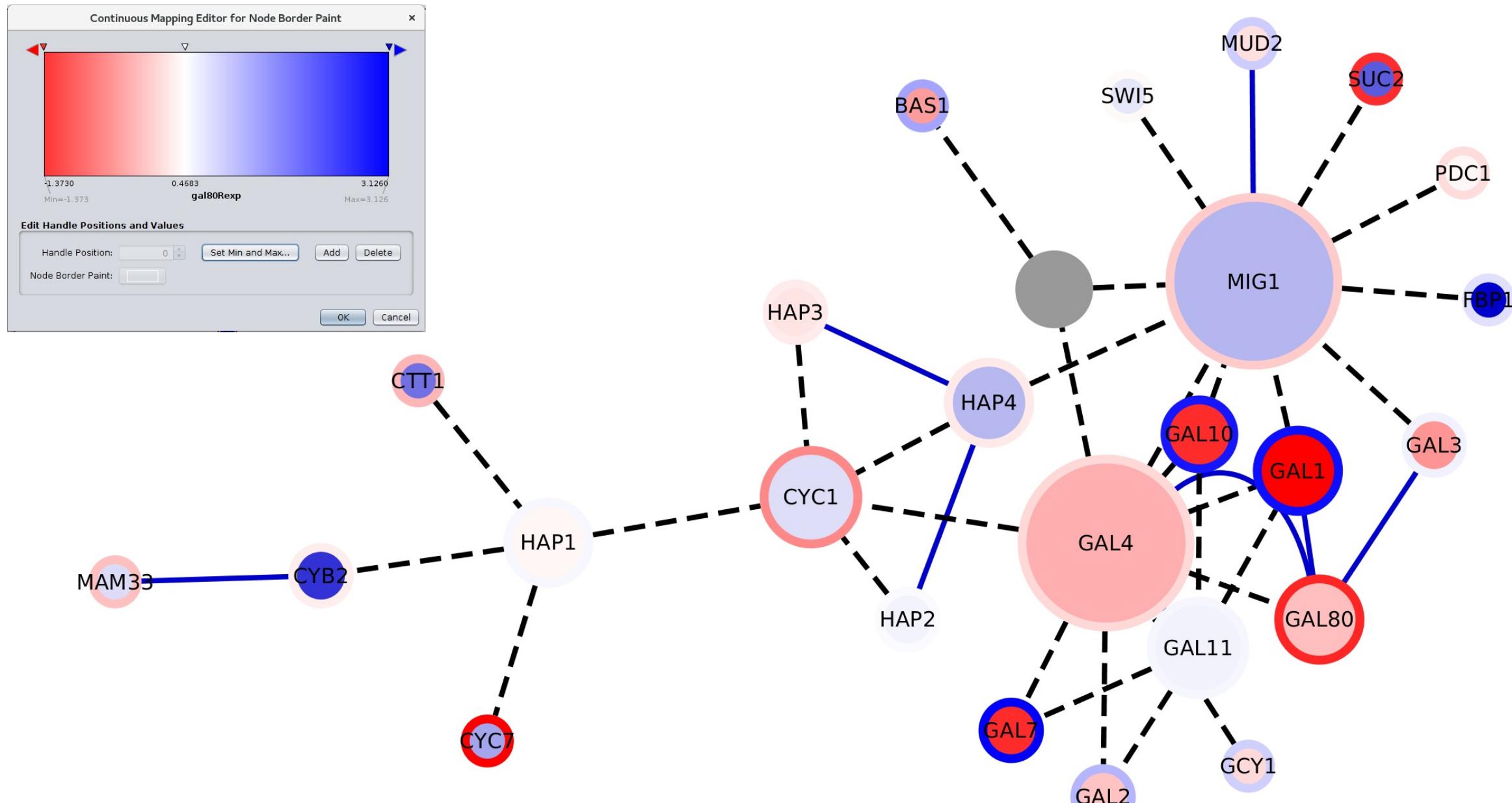
Depiction

- Visual works:
 - matrix
 - edges



Data Mapping

- Mapping of data values associated with graph elements onto graph visuals
- Visual attributes
 - Node fill color, border color, border width, size, shape, opacity, label
 - Edge type, color, width, ending type, ending size, ending color
- Mapping types
 - Passthrough (labels)
 - Continuous (numeric values)
 - Discrete (categories)



Data Mapping

- Avoid cluttering your visualization with too much data
 - Highlight meaningful differences
 - Avoid confusing the viewer
 - Consider creating multiple network images

Layouts

- Layouts determine the location of nodes and (sometimes) the paths of edges
 - Types:
 - Simple
 - Grid
 - Hierarchical
 - layout data as a tree or hierarchy
 - Works best when there are no loops
 - Circular (Radial)
 - arrange nodes around a circle
 - could use node attributes to govern position
 - e.g. degree sorted
 - Partitions

Layouts

- Types:
 - Force-Directed
 - simulate edges as springs
 - may be weighted or unweighted
 - Combining layouts
 - Use a general layout (force directed) for the entire graph, but use hierarchical or radial to focus on a particular portion
 - Multi-layer layouts
 - Partition graph, layout each partition then layout partitions
 - Many, many others

Layouts

- Use layouts to convey the relationships between the nodes.
- Layout algorithms may need to be “tuned” to fit your network.
- There is not one correct layout. Try different things.

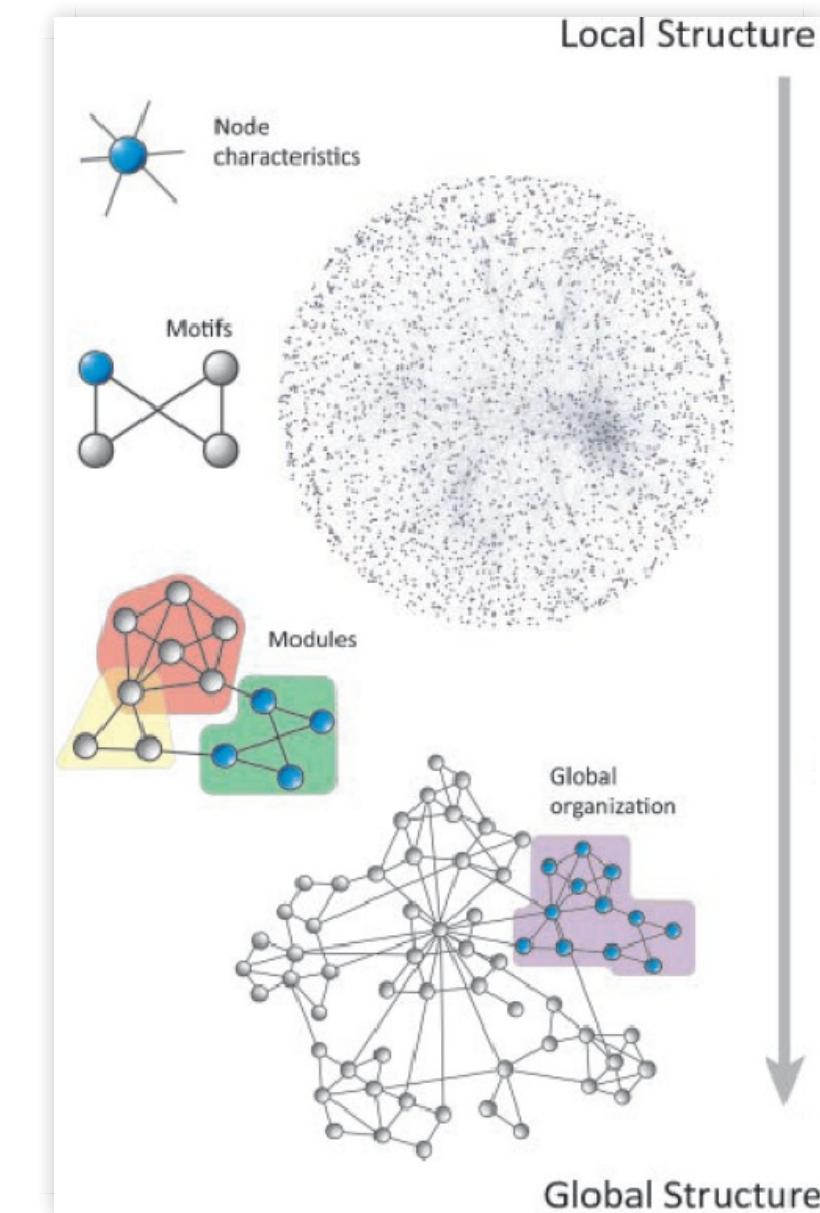
Animation

- Animation is useful to show changes in a network:
 - Over a time series
 - Over different conditions
 - Between species

Analytical Approaches

The levels of organization of complex networks:

- Node degree provides information about single nodes
- Three or more nodes represent a motif
- Larger groups of nodes are called modules or communities
- Hierarchy describes how the various structural elements are combined



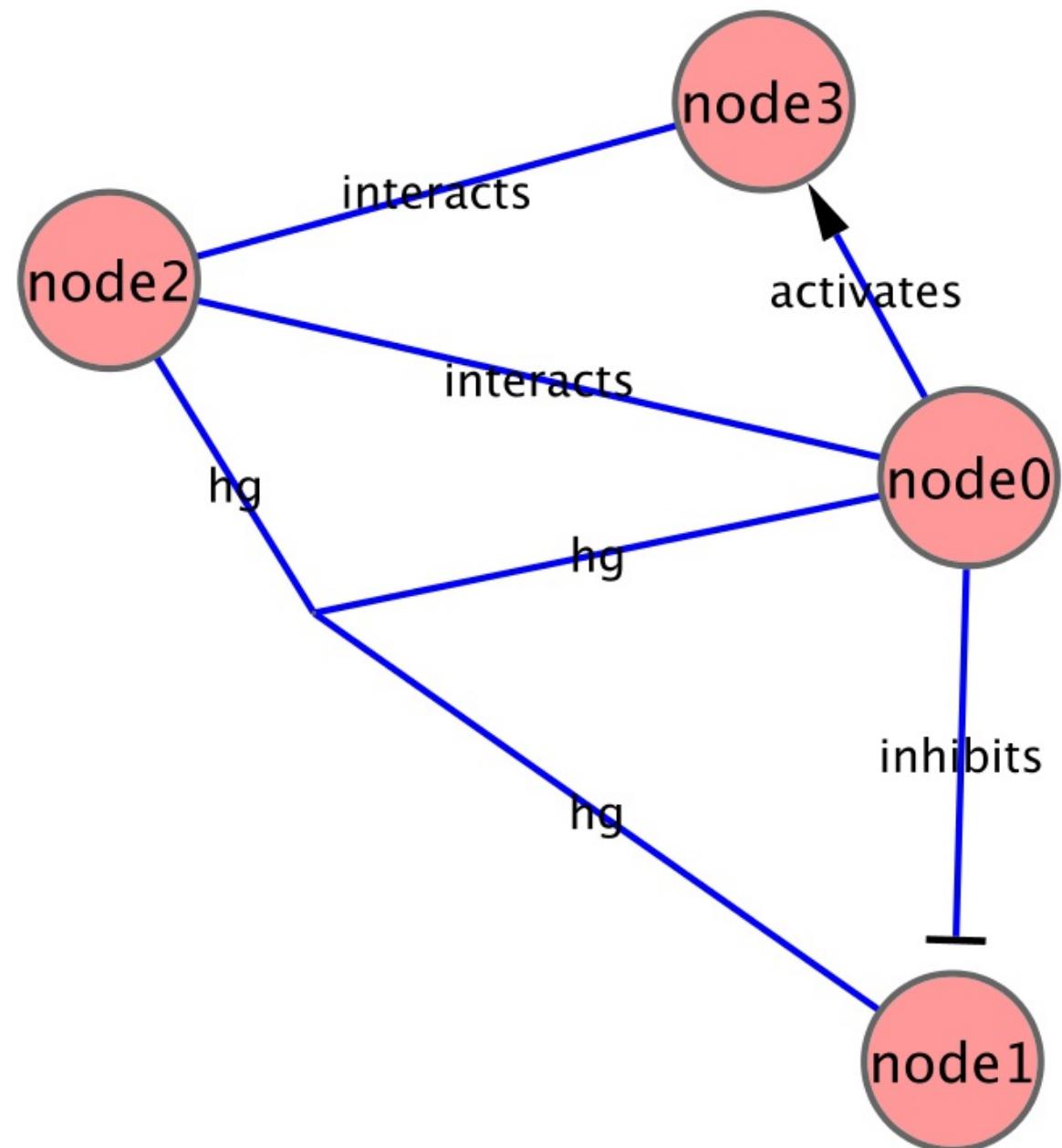
Analytical Approaches

Network topology statistics such as node degree, degree distribution, centralitiy, clustering coefficient, shortest paths, and robustness of the network to the random removal of single nodes are important network characteristics.

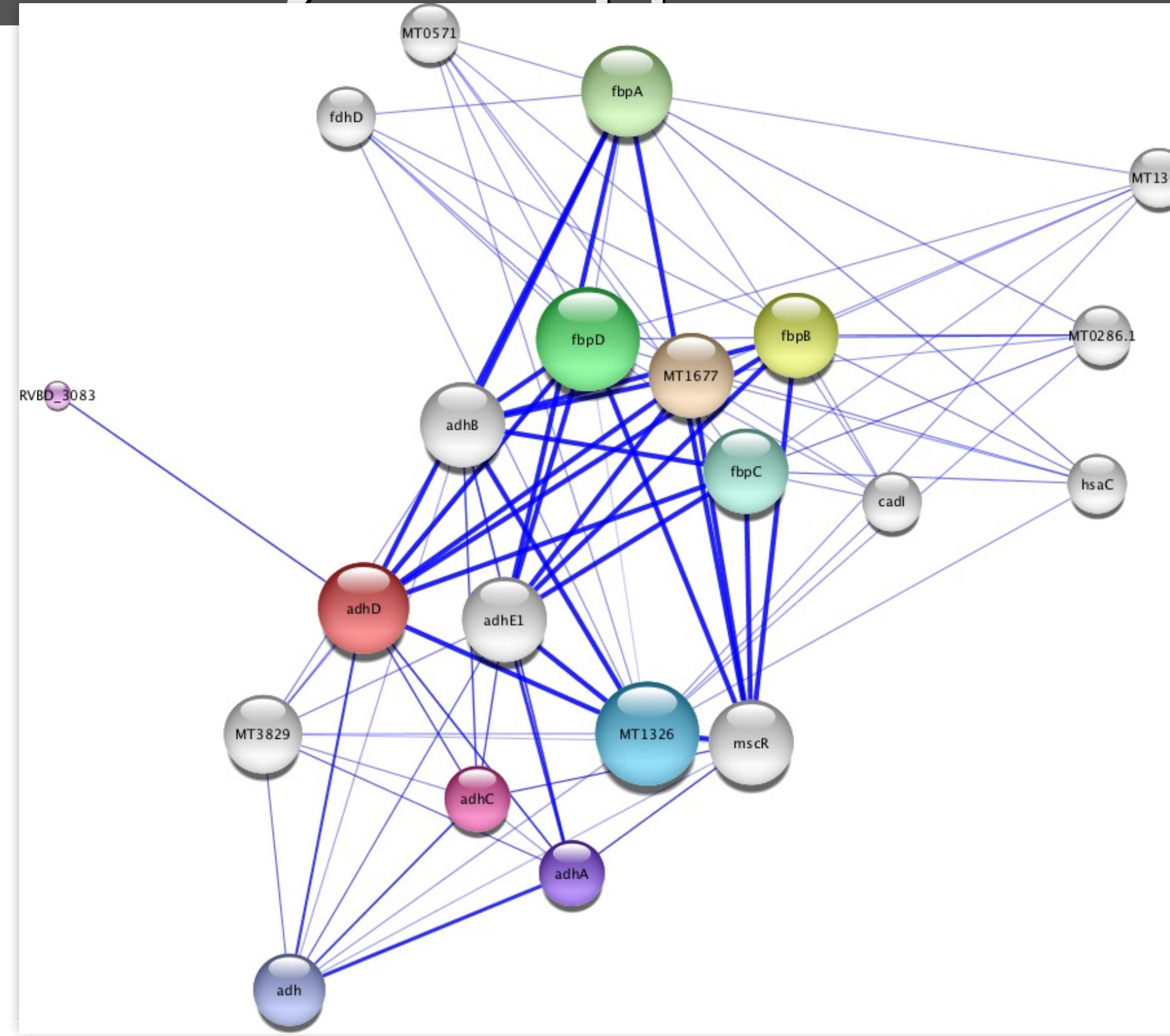
Modularity refers to the identification of sub-networks of interconnected nodes that might represent molecules physically or functionally linked that work coordinately to achieve a specific function.

Motif analysis is the identification of small network patterns that are over-represented when compared with a randomized version of the same network. Regulatory elements are often composed of such motifs.

Network alignment and comparison tools can identify similarities between networks and have been used to study evolutionary relationships between protein networks of organisms.



Analytical Approaches



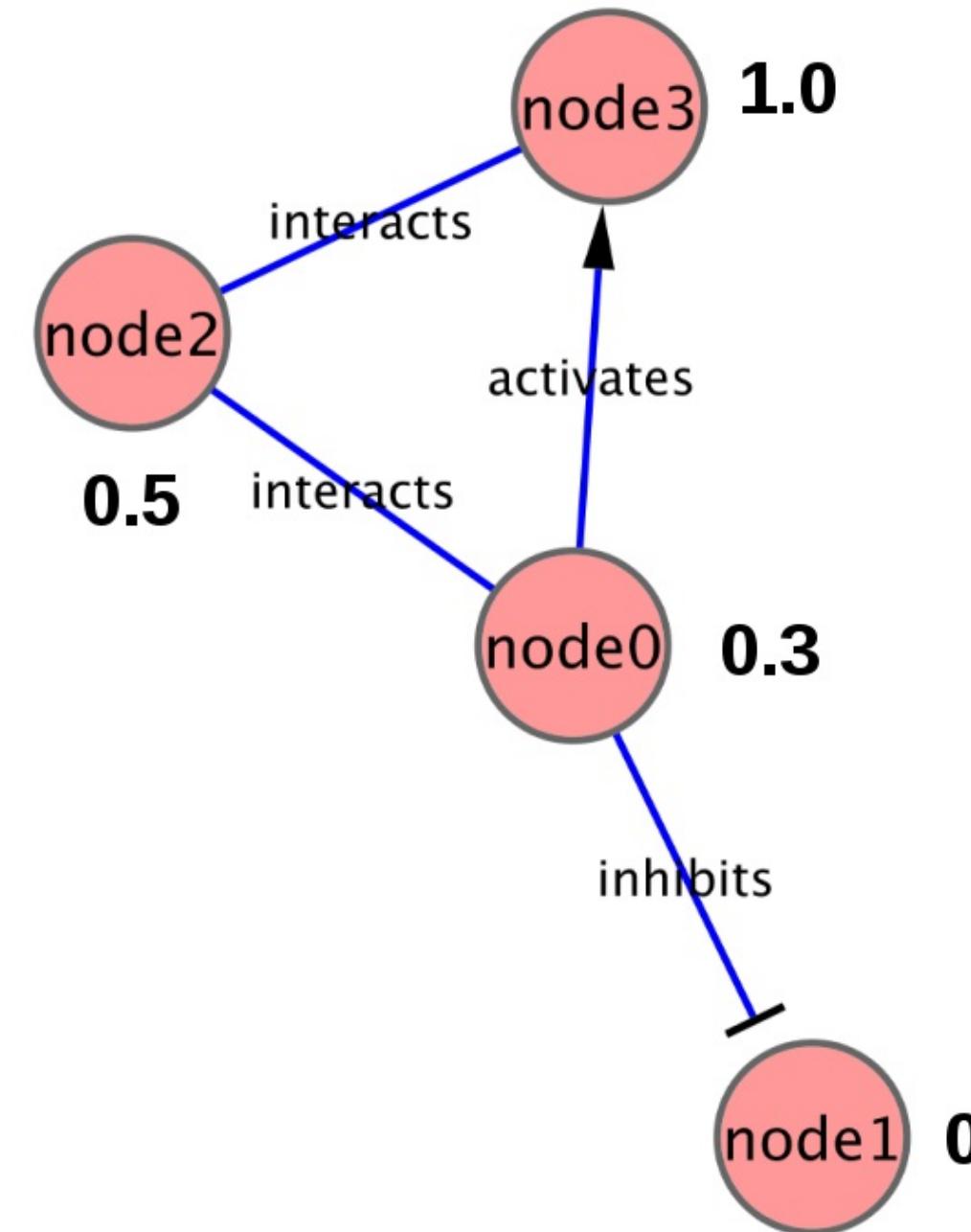
 Cytoscape 3.6.0

Analytical Approaches

- Network measures
 - **Diameter:** the largest distance between two nodes
 - **Radius:** the minimum of the maximum path between any two nodes
 - **Characteristic path length:** average shortest path length
 - **Density:** extent to which a network is fully connected
 - **Heterogeneity:** tendency of the network to contain hub nodes
 - **Connected components:** number of disconnected groups of nodes

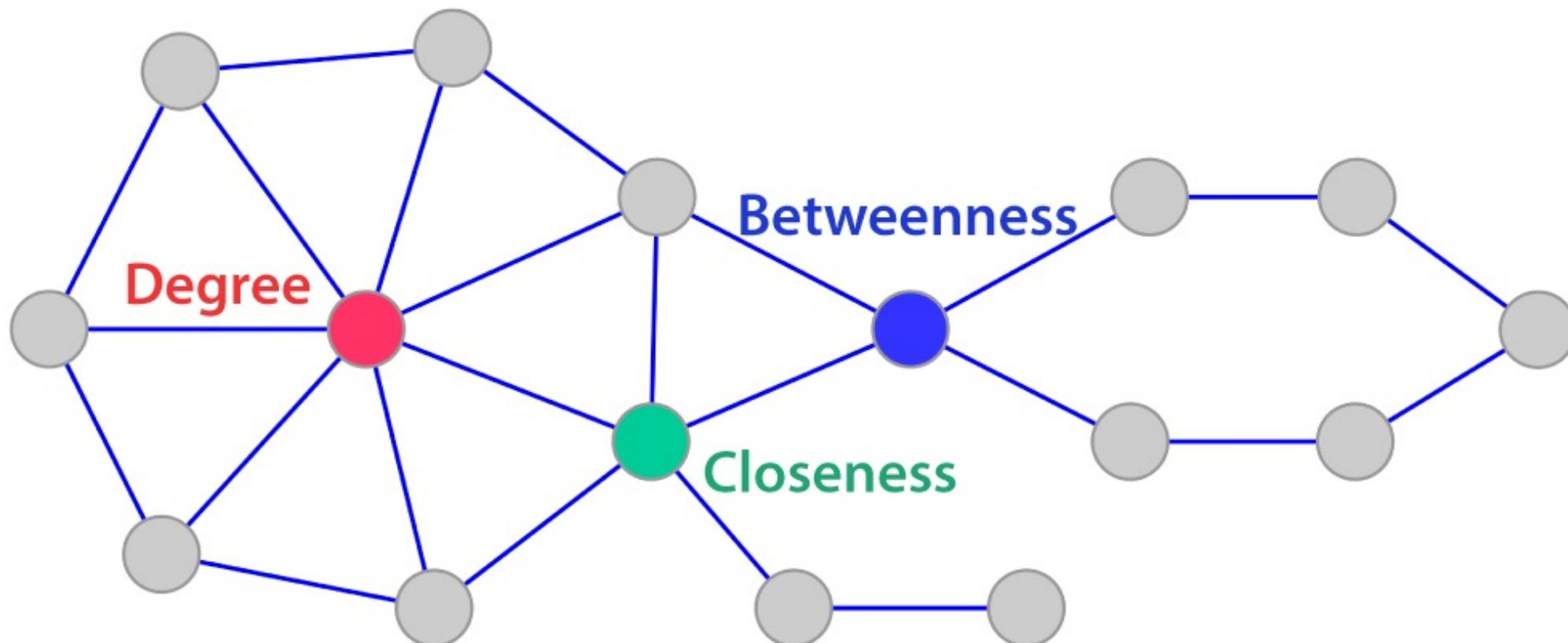
Analytical Approaches

- Network
▪ Clusters
 - Measure
 - Centrality
- Degree



Analytical Approaches

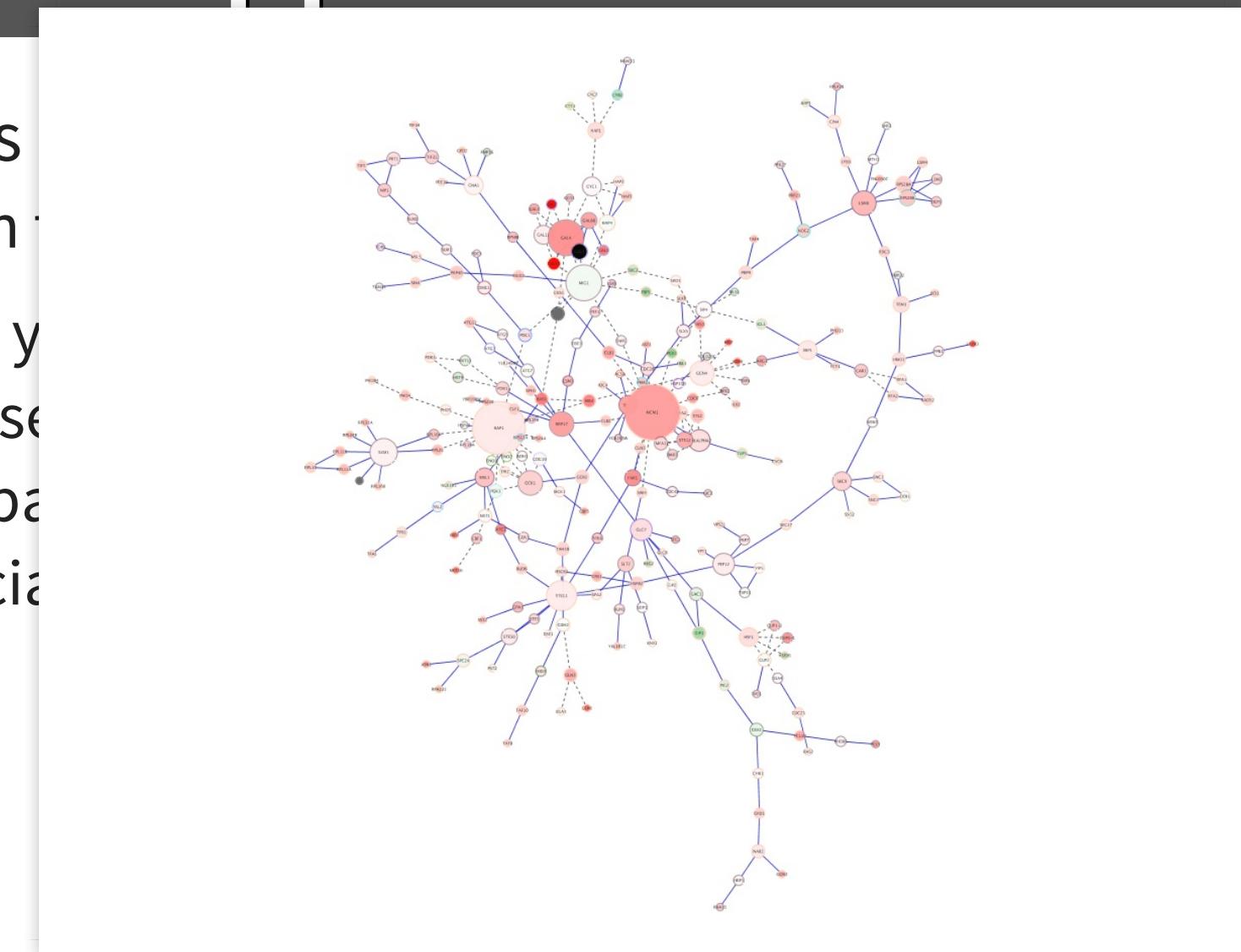
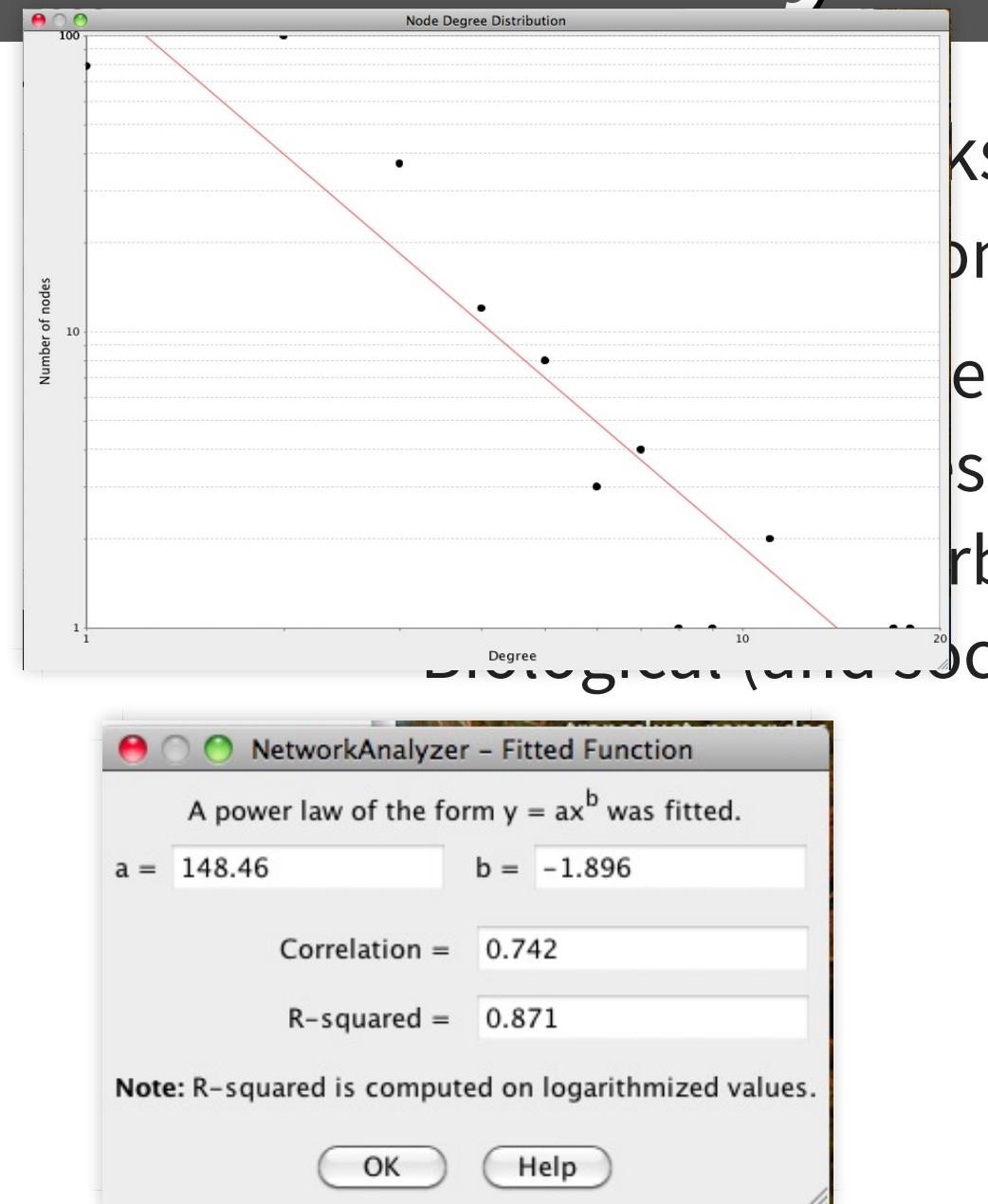
- Central
- Degree
 - CD
- Betweenness
 - CE
- Closest
 - C (



through
other

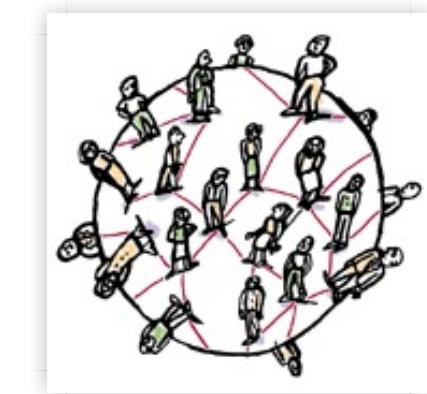
no	Degree	ClosenessCentrality	BetweennessCentrality
	7	0.45454545	0.29047619
	5	0.51724138	0.42380952
	4	0.48387097	0.4952381

Analytical Approaches



Analytical Approaches

- Small-world networks
 - any two arbitrary nodes are connected by a small number of intermediate edges
 - the network has an average shortest path length much smaller than the number of nodes in the network (Watts, Nature, 1998).
 - Interaction networks have been shown to be small-world networks (Barabási, Nature Reviews in Genetics, 2004)



Analytical Approaches

- Other techniques
 - Guilt-by association
 - Combine weak signals to get a stronger one
 - Over-representation analysis
 - Also called enrichment analysis
 - Statistical technique to determine if a set of terms are over-represented (enriched) in a network (or subnetwork)
 - Clustering
 - Also called unsupervised classification
 - Variety of techniques for group nodes based on attributes or connectivity

Analytical Approaches

- Other techniques
 - Motif finding
 - Finding subnetworks of interest

Automation Use Case

Biological Question

- What molecular changes occur in breast and ovarian tumors?
- Do they interact with each other and with other cancer genes?
- Are there key subnetworks affected in these cancers?

Dataset

- Gene expression and mutation data from TCGA

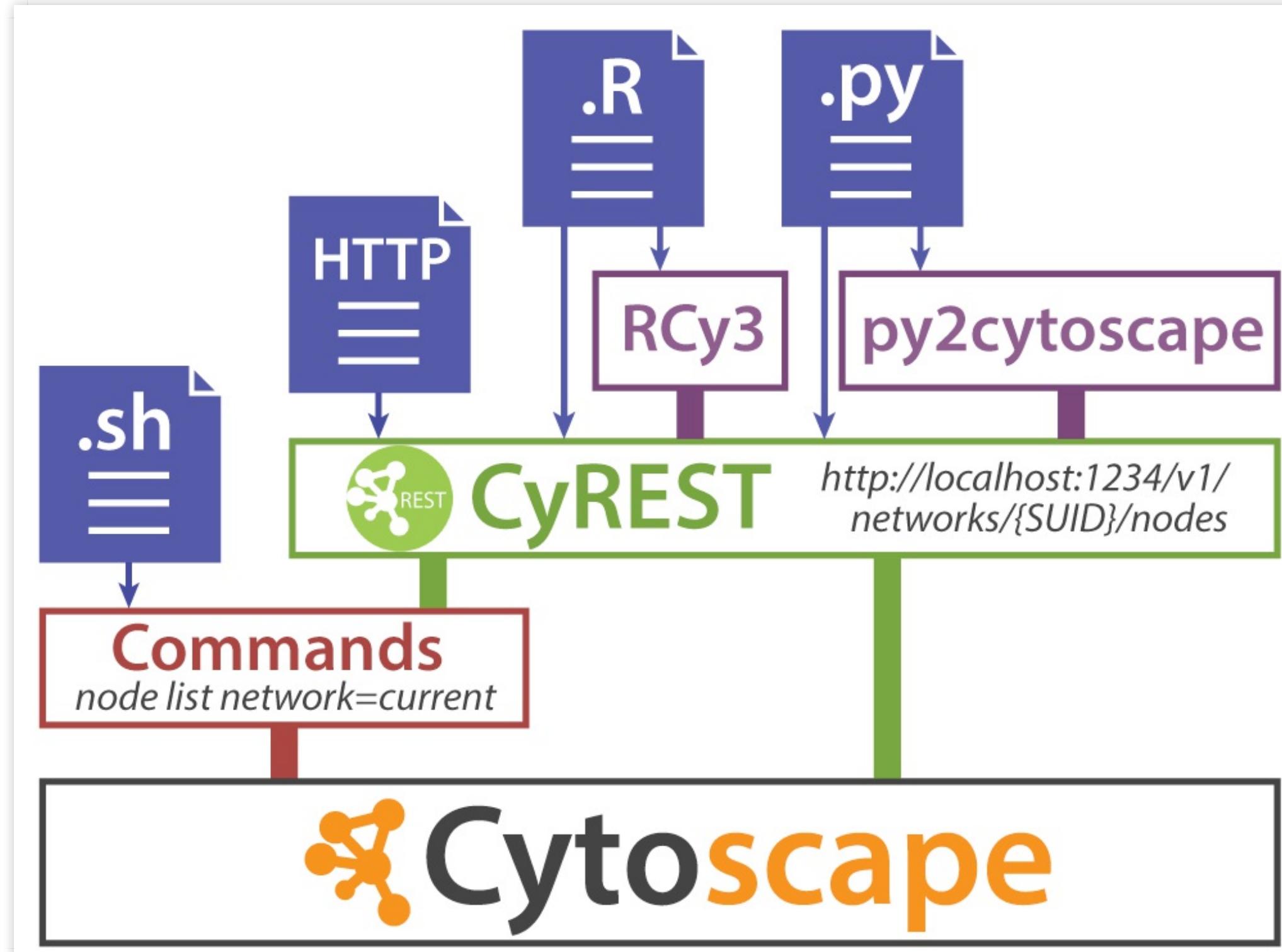
Approach

- Starting in R, connect to Cytoscape using CyREST
- Construct disease networks in Cytoscape from R
- Integrate TCGA data in R with networks
- Perform data overlays and network analysis
- Export images and sessions for sharing and publication



TCGA (2011) *Nature*. & TCGA (2012) *Nature*.

Brief History of Cytoscape Automation



When to Automate

Why run a script when I could just use Cytoscape directly?

- For things you want to do multiple times, e.g., loops
- For things you want to repeat in the future
- For things you want to share with colleagues or publish
- For things you are already working on in R or Python, etc

Tutorial Materials

github.com/cytoscape/cytoscape-automation

- OPTION 1: If you are familiar with git, then clone our repo:

```
git clone git@github.com:cytoscape/cytoscape-automation.git
```

- OPTION 2: Or you can download this file and unzip it:

github.com/cytoscape/cytoscape-automation/archive/master.zip

Next, open RStudio and start a new project (**File>New Project...**). Choose **Existing Directory** and navigate to *cytoscape-automation/for-scripters/R*.



Introductions and Concepts

Finding Network Data

Network Visualization

Network Analysis

Automation via CyREST

Thank You!

Here are additional resources you may find useful:

- manual.cytoscape.org
- tutorials.cytoscape.org
- apps.cytoscape.org
- cytoscape-publications.tumblr.com/
- cytoscape-helpdesk@googlegroups.com
- cytoscape-app-dev@googlegroups.com
- nrnb.org/training.html
- surveymonkey.com/r/cytoscape