



Nadezhda T. Doncheva

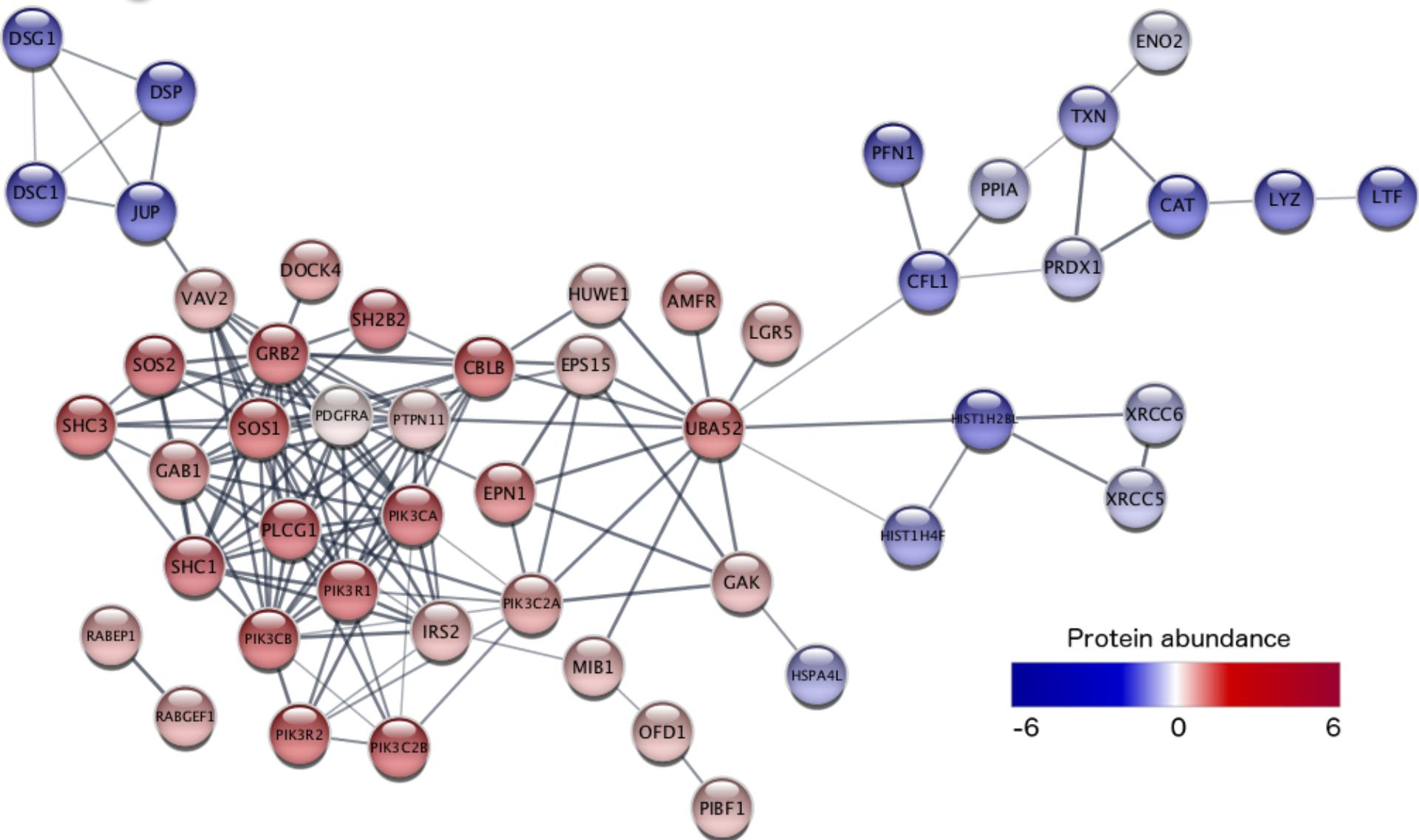
EMBO Course, NCBS campus, Bangalore  
December 3, 2019



# Motivation

	A	B	C	D	E	F	G	H	I	J
1	UniProt	Gene name	Peptides	Sequence coverage [%]	5 min ratio exp. 1	5 min ratio exp. 2	5 min log ratio	10 min ratio exp. 1	10 min ratio exp. 2	10 min log ratio
2	Q99880	HIST1H2BL	5	35.7	0.27	0.04	-2.66	0.24	0.08	-2.66
3	Q8TER5	ARHGEF40	34	28.3	3.65	4.09	1.95	2.64	3.24	1.56
4	Q8IZ07	ANKRD13A	12	19.2	2.22	1.99	1.07	1.99	2.25	1.08
5	P62805	HIST1H4A	11	57.3	0.36	0.05	-2.31	0.65	0.11	-1.39
6	Q08380	LGALS3BP	14	28.2	0.09	0.13	-3.16	0.12	0.14	-2.98
7	O00750	PIK3C2B	35	24.2	4.49	4.77	2.21	4.64	5.27	2.31
8	O00443	PIK3C2A	29	17.8	2.32	2.07	1.13	2.39	2.41	1.26
9	Q9UJ41	RABGEF1	6	6.5	1.67	1.50	0.67	1.86	2.36	1.08
10	Q8TC07	TBC1D15	12	19.1	1.27	1.44	0.43	1.78	2.39	1.06
11	Q9UN70	PCDHGC3	9	12.7	1.29	1.05	0.23	1.65	1.78	0.78
12	Q75VX8	GAREML	26	37.5	8.59	5.97	2.86	9.71	7.57	3.11
13	P42336	PIK3CA	21	22.8	4.43	4.95	2.23	6.09	5.92	2.59
14	P27986	PIK3R1	19	28.2	4.13	3.61	1.95	4.97	5.83	2.43
15	O00459	PIK3R2	21	40.2	3.88	3.77	1.94	4.59	4.89	2.24
16	P42338	PIK3CB	12	13.4	3.68	2.72	1.68	4.86	3.88	2.13
17	Q96S55	WRNIP1	16	29.8	1.42	1.59	0.59	1.86	2.44	1.10
18	Q15276	RABEP1	22	31.1	1.34	1.51	0.51	1.73	2.31	1.02
19	P16234	PDGFRA	24	24.3	1.52	1.75	0.71	1.10	1.36	0.30
20	Q06124	PTPN11	27	48.4	1.22	1.44	0.41	1.31	2.08	0.76
21	P36896	ACVR1B	4	10.1	1.09	0.87	-0.03	2.80	2.18	1.32
22	Q6ZNH5	ZNF497	2	3.8	0.44	0.69	-0.82	2.13	15.14	3.11
23	P06702	S100A9	9	74.6	0.17	0.05	-3.17	0.07	0.05	-4.12
24	Q13410	BTN1A1	3	9.3	0.27	0.10	-2.44	1.38	0.19	-0.34
25	O95757	HSPA4L	15	21.2	0.20	0.33	-1.93	0.30	0.63	-1.12
26	O14492	SH2B2	5	9.5	6.55	6.69	2.73	7.05	10.85	3.16
27	P19174	PLCG1	69	50	5.63	7.23	2.69	6.06	8.07	2.82
28	Q9H706	GAREM	17	23.9	4.72	4.61	2.22	4.14	5.78	2.31

# Motivation





# Goals

- Understand the major applications of network biology to the study of PPIs
- Find relevant networks and pathways
- Import your data into Cytoscape
- Master network layouts and data visualization
- Find relevant Cytoscape apps and tutorials

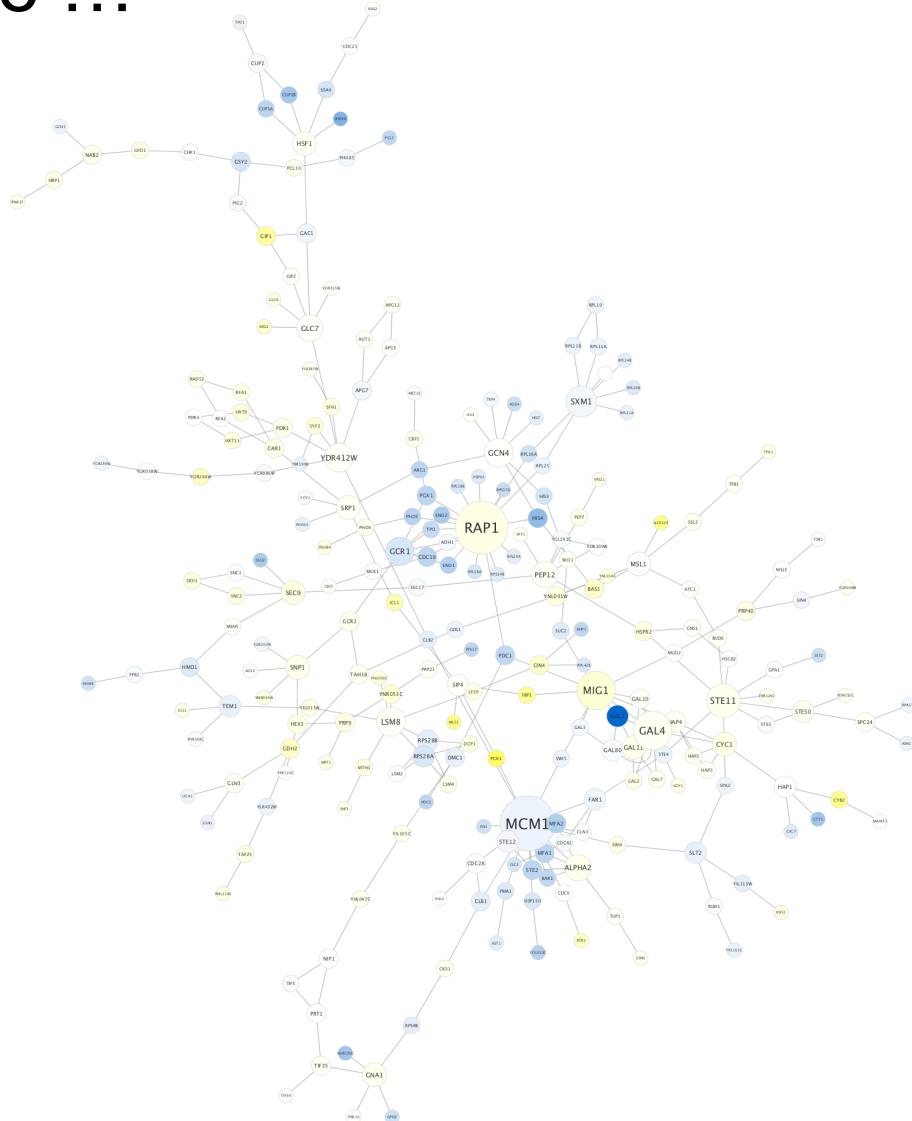


# Why do we use networks?



# Why Networks?

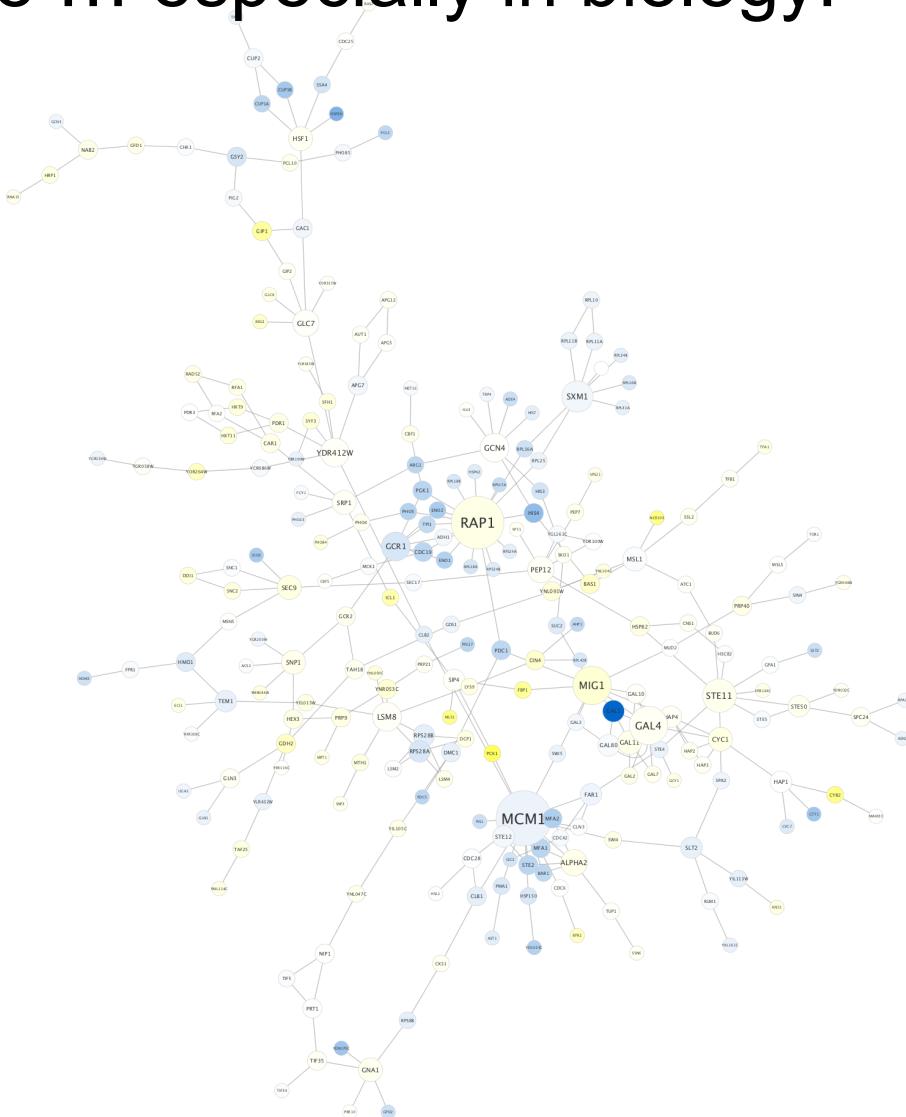
- Networks are everywhere ...
  - Molecular networks
  - Cell-cell communication
  - Nervous systems
  - Social networks





# Why Networks?

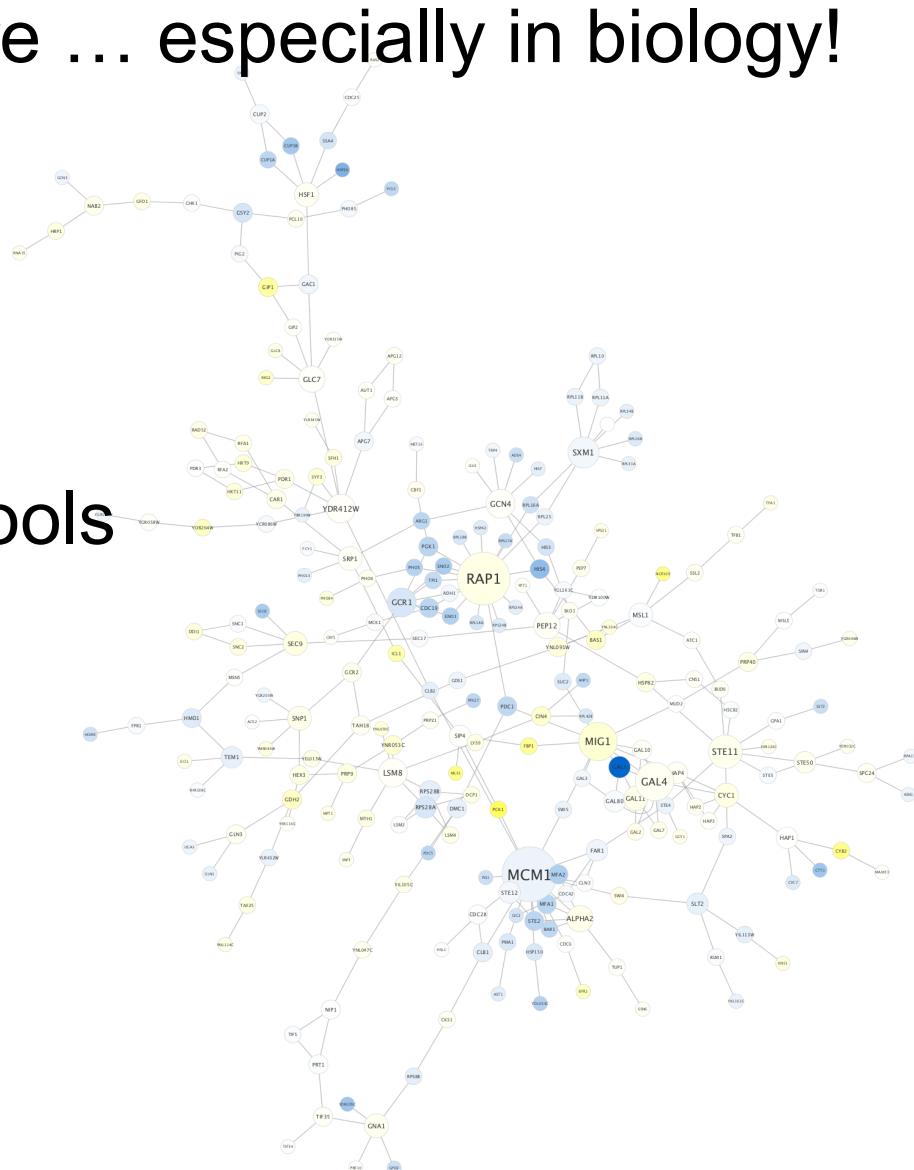
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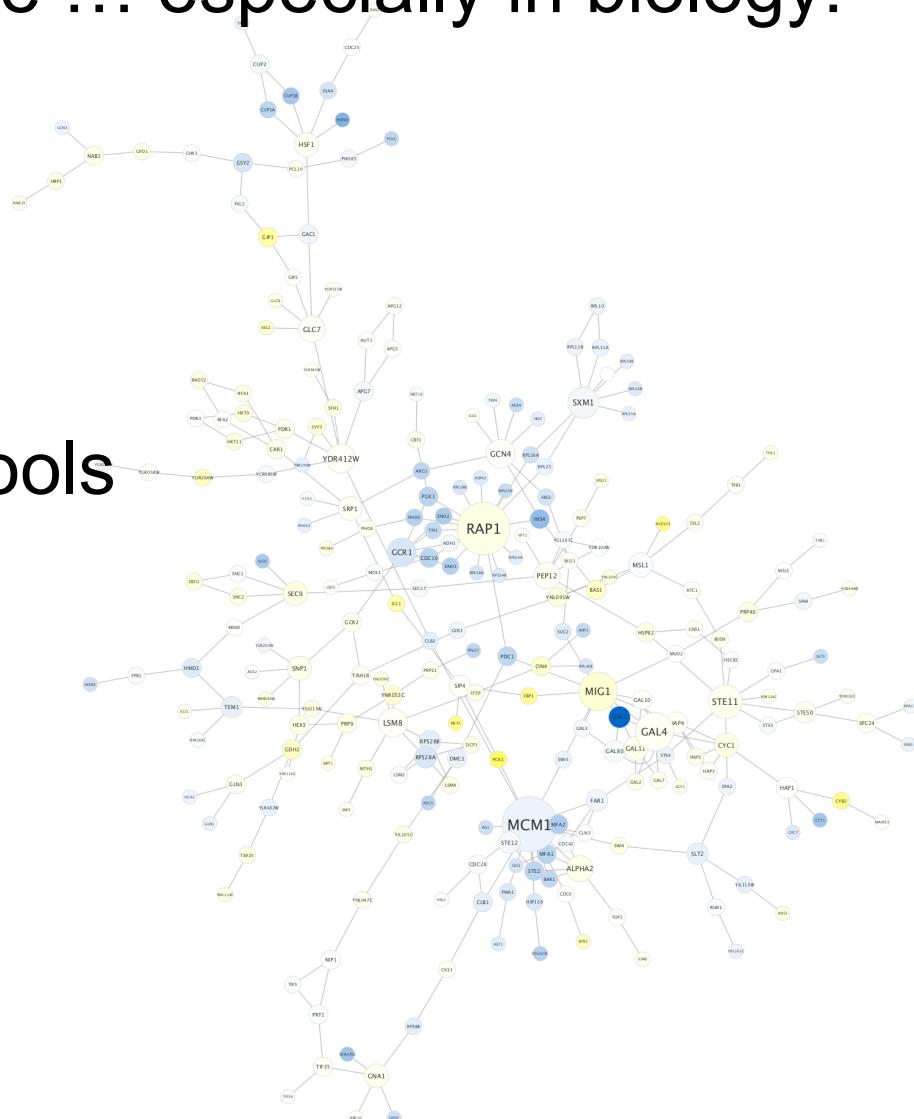
- Networks are everywhere ... especially in biology!
  - Molecular networks
  - Cell-cell communication
  - Nervous systems
  - Social networks
- Networks are powerful tools
  - ✓ Reduce complexity
  - ✓ More efficient than tables
  - ✓ Great for data integration
  - ✓ Intuitive visualization





# Why Networks?

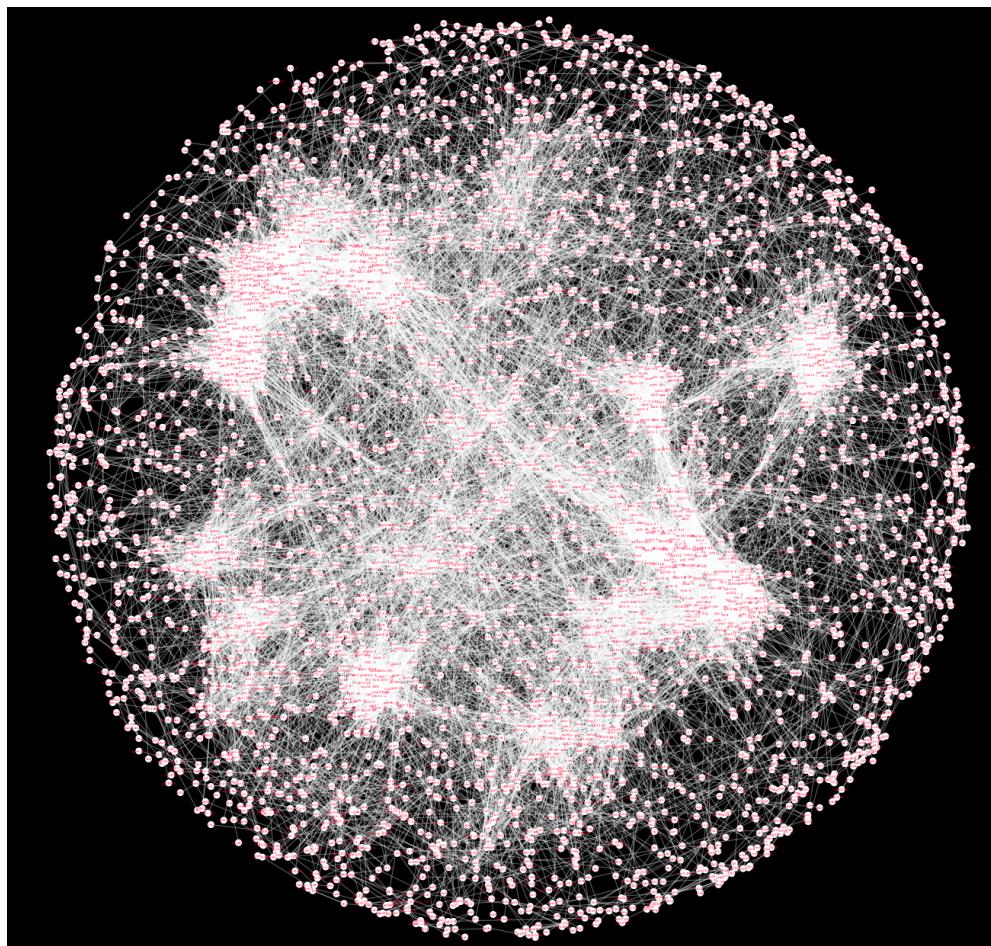
- Networks are everywhere ... especially in biology!
  - Molecular networks
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  - Nervous systems
  - Social networks
- Networks are powerful tools
  - ✓ Reduce complexity
  - ✓ More efficient than tables
  - ✓ Great for data integration
  - ✓ Intuitive visualization
- But also... Challenging!





# The Challenge

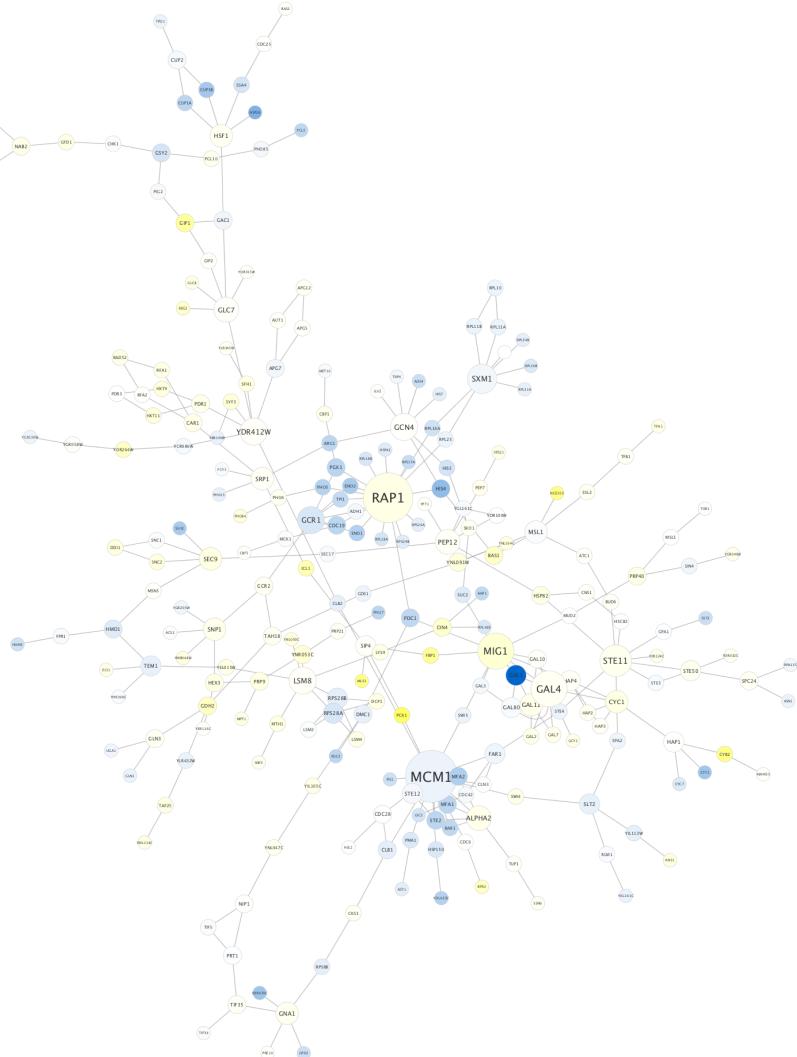
- Making sense out of biological networks....





# Networks as Tools

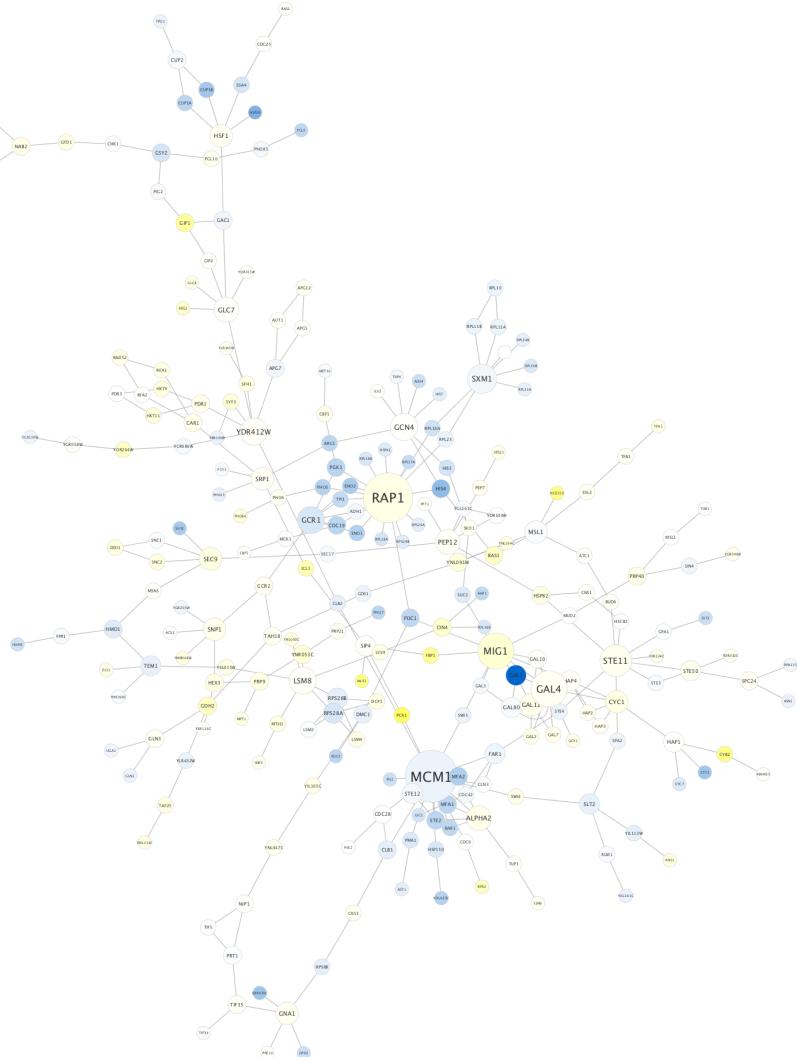
- Seldom tell us anything by themselves
- **Analysis**
- **Visualization**





# Networks as Tools

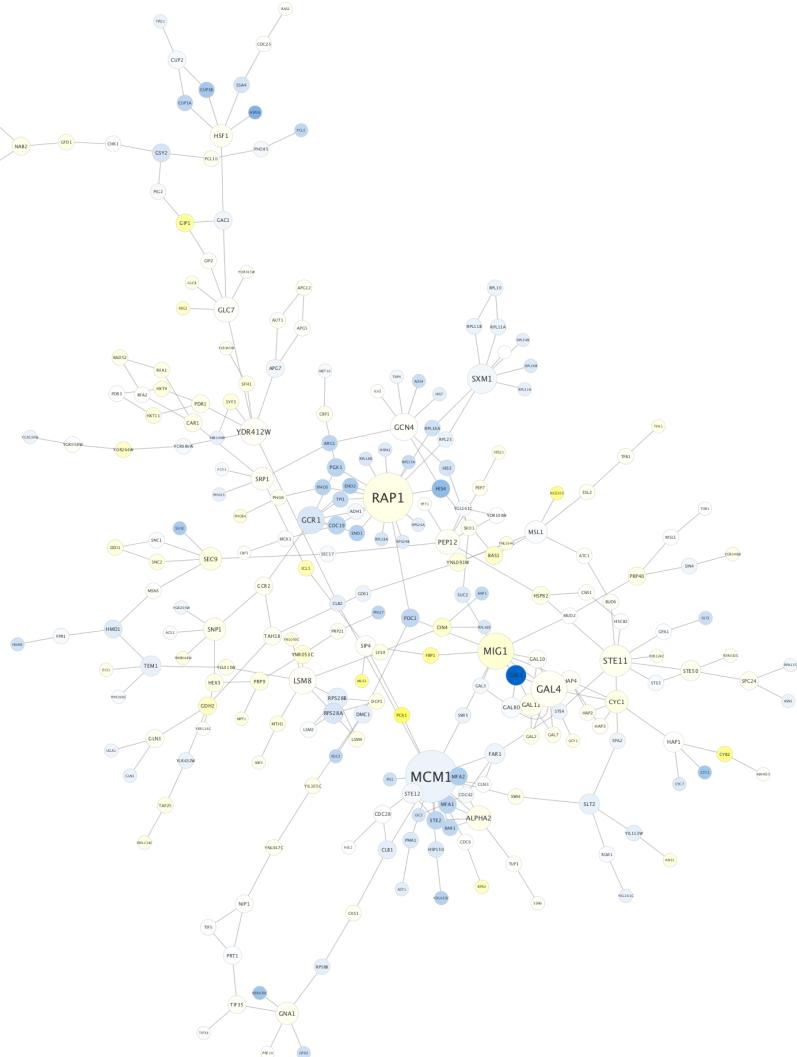
- Seldom tell us anything by themselves
- **Analysis** involves:
  - Topological properties
  - Hubs and subnetworks
  - Modularity
  - Data integration





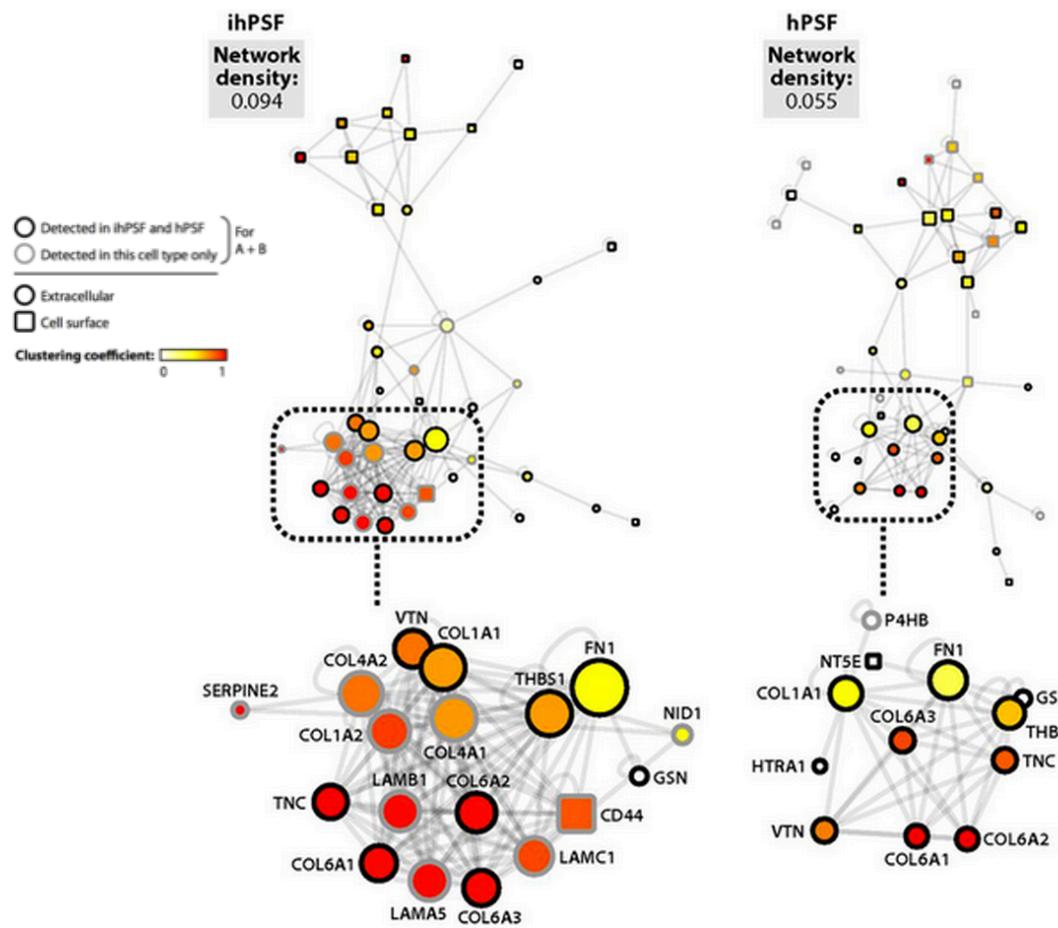
# Networks as Tools

- Seldom tell us anything by themselves
- **Analysis** involves:
  - Topological properties
  - Hubs and subnetworks
  - Modularity
  - Data integration
- **Visualization** involves:
  - Data overlays
  - Layouts and animation
  - Exploratory analysis
  - Context and interpretation





# Examples



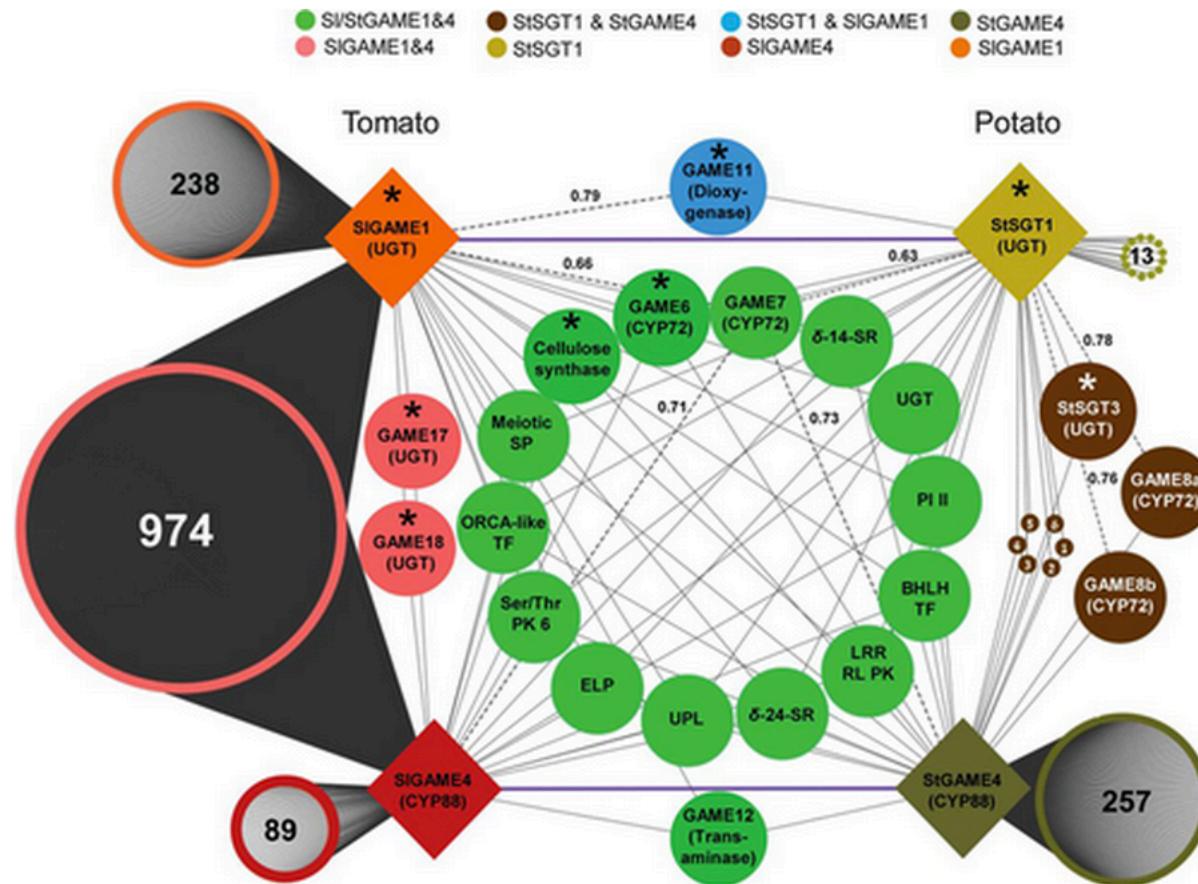
Comparative proteomic analysis of supportive and unsupportive extracellular matrix substrates for human embryonic stem cell maintenance.

Soteriou et al, J Biol Chem. 2013 Jun 28;288(26):18716-31.

<http://cytoscape-publications.tumblr.com/archive>



# Examples



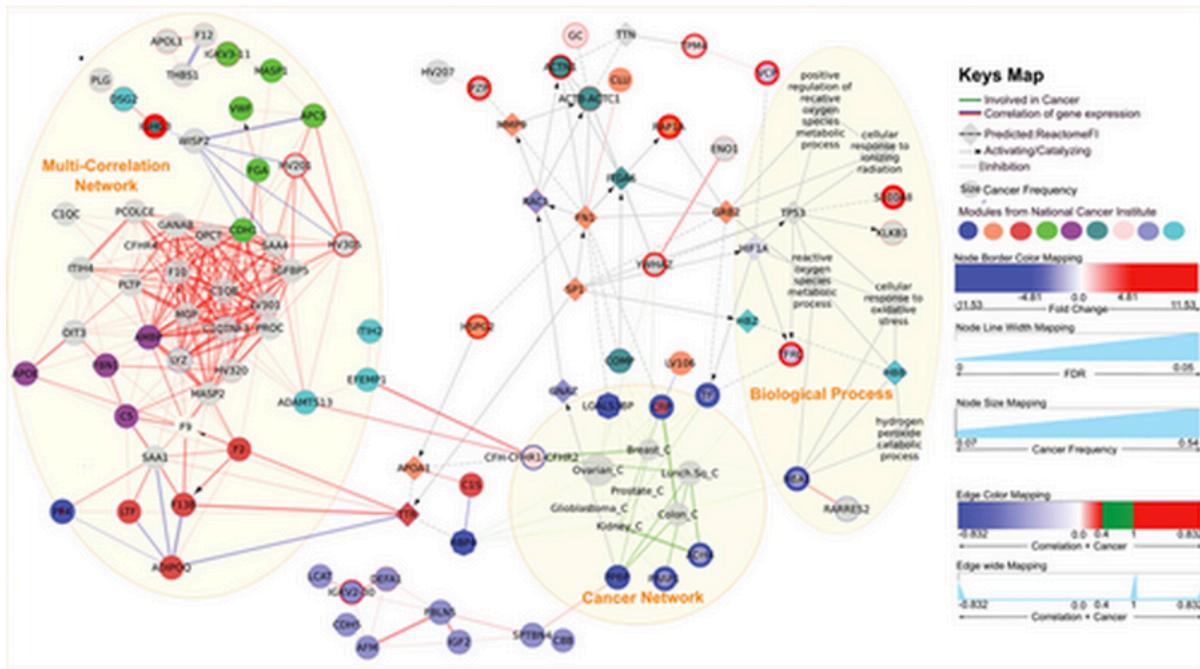
Biosynthesis of antinutritional alkaloids in solanaceous crops is mediated by clustered genes.

Itkin et al, Science. 2013 Jul 12;341(6142):175-9.

<http://cytoscape-publications.tumblr.com/archive>



# Examples



Graphical Identification of Cancer-Associated Gene Subnetworks Based on Small Proteomics Data Sets.

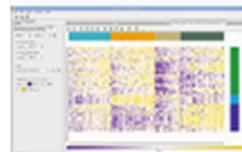
Mezhoud et al, OMICS. 2013 May 3.

<http://cytoscape-publications.tumblr.com/archive>

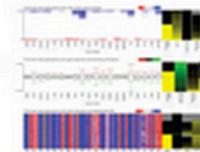


# Examples

Matrix heatmaps

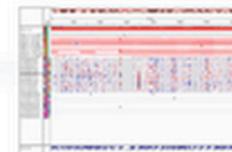


Gitoools



UCSC/ Cancer  
Genetics Browser

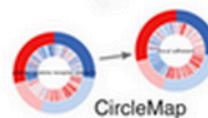
Genomic coordinates



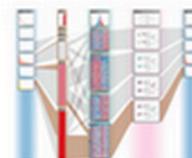
IGV



Savant



CircleMap



Caleydo / StratomeX



Regulome explorer



Cytoscape

Networks

Visualizing multidimensional cancer genomics data.  
Schroeder et al, *Genome Med.* 2013 Jan 31;5(1):9.

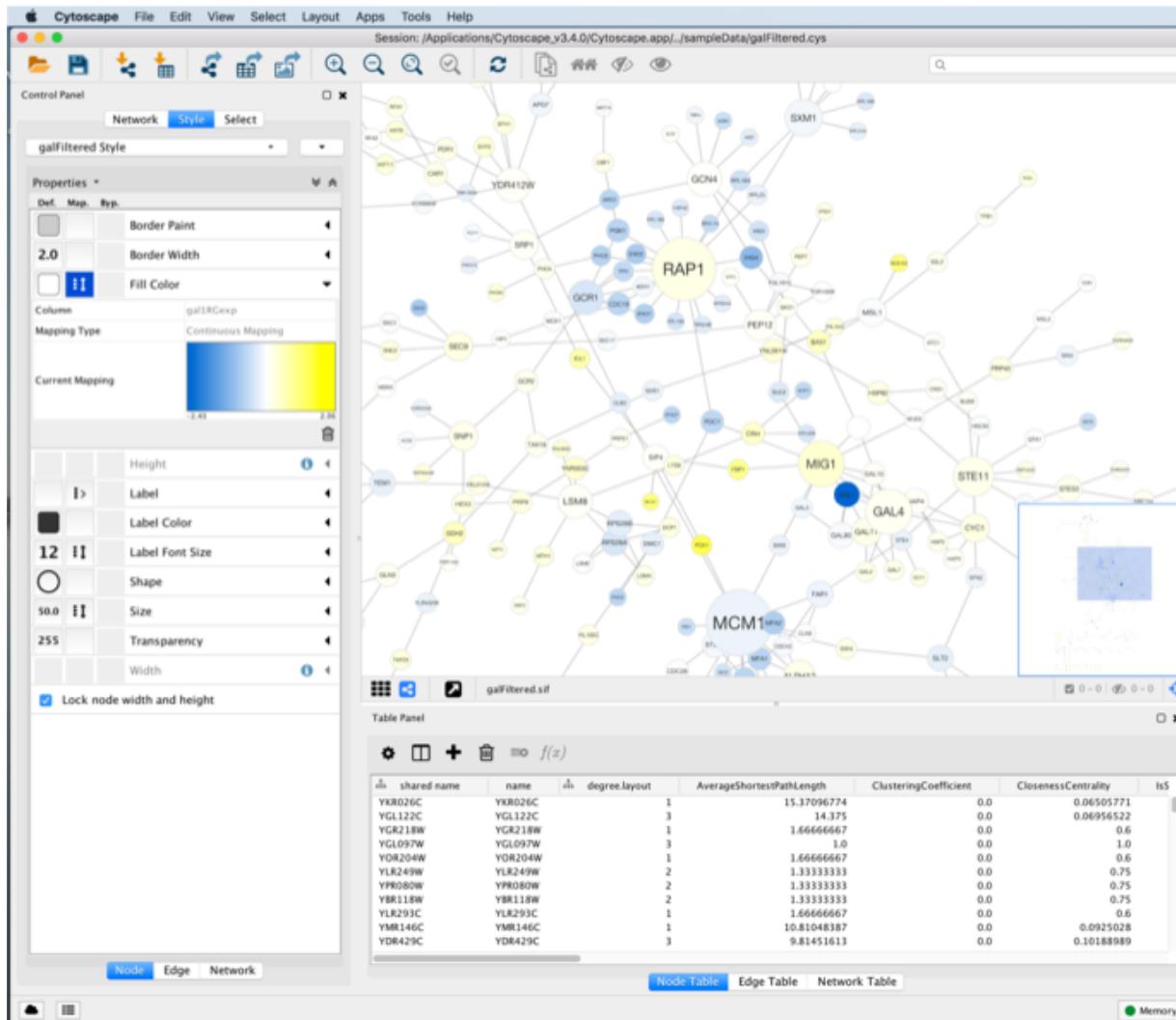
<http://cytoscape-publications.tumblr.com/archive>



# What is Cytoscape?



# Cytoscape



- Open source
- Cross platform
- Consortium
- Active community



Institute for Systems Biology



University of California at San Diego



Institut Pasteur



University of California at San Francisco



University of Toronto

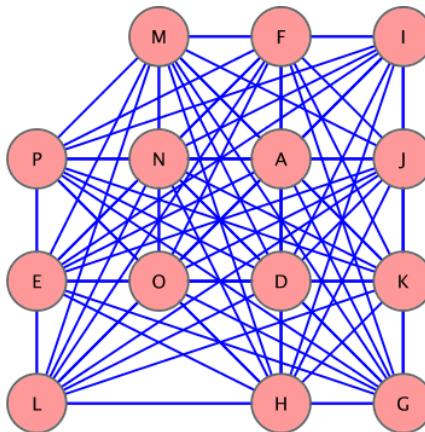
**GLADSTONE  
INSTITUTES**

**NRNB**



# Core Concepts

- Networks and Tables



	A	B	C	D	E	F	G	H	I	J
	GI_Number	Gene	HPRD_ID	REFSEQ	Entrez_ID	OMIM_ID	SWISSP	Gene_Description	Architecture	Arch
1	gi 19923959	SDSL	11542	NP_644411.1	113675		SDSL		SP	Motif
2	gi 191026	SEC23B	11543	NP_644781.1	10483		Q15423	Sec23B	CEL	Doma
3	gi 1602492	SCMH1	11540	AAH09752.1	22955		Q96GD1	SCMH1	SAM	Doma
4	gi 14625034	EXOC2	11544	NP_060773.3	55770		Q96KP1	SECS like 1	IPT	Doma
5	gi 21361625	SERPINB12	11548	NP_536722.1	89777		Q96P63	Serpin B12	SERPIN	Doma
6	gi 17998551		18447	NP_00101372	440275	609280		Similar to GCN2 eIF2alpha kinase	S_T_Y_Kinase	Doma
7	gi 5287717	EIF2AK4	4998	NP_003323.1	7305	604142	Q43914	DAP12	ITAM	Doma
8	gi 4507755	TYROB3	4995	NP_006841.1	11009	604136	Q13007	Interleukin 24	IL10	Doma
9	gi 5803086	IL24	4995	NP_006841.1	11009	604136	Q13007	ADAMTS13	TSP1	Doma
10	gi 21265034	ADAMTS13	4994	NP_620594.1	11093	604134				
11	gi 1743873	PIP5K1A	4470	AAC50911.1	8394	603275	Q99755	Phosphatidylinositol-4-phosphate	PIPKc	Doma
12	gi 14625034		4992	NP_060773.3	6000	604125	Q95425	Survivin	VBL	Doma
13	gi 63386	SULF2B1	4991	NP_014444.1	6820	604125				
14	gi 21040399	RBBP8	4990	AAH30590.1	5932	604124	Q99708	CTP	LZ	Motif
15	gi 4758378	FIGF	2102	NP_004460.1	2277	300091	Q43915	VEGF D	PDGF	Doma
16	gi 11321617	DPYSL4	7463	NP_006417.1	10570	608407	Q14531	Collapsin response mediator protein 3		
17	gi 8923202	TASP1	7460	NP_060184.1	55617	608270	Q9H6P5	Threonine aspartate 1		
18	gi 5454090	SSR4	2101	NP_006271.1	6748	300090	P51571	Signal sequence receptor delta	SP	Motif
19	gi 5730045	SLC16A2	2106	NP_06508.1	6567	300095	P36021	X linked PEST containing transport	TM	Doma
20	gi 1968027	FTS	7467	NP_071921.1	64400	608483	Q9HB70	FTS	UBC	Doma
21	gi 8255885	PRKCI	2105	NP_002731.3	5584	600539	P41743	Protein kinase C, iota type	S_T_kinase	Doma
22	gi 5914000	RPA4	6303	NP_060773.3	29925				TPA	
23	gi 3376812	PPP1R2P9	6593	NP_079486.1	80316				TRNA	
24	gi 1526862		6595	NP_206375.1	9006					
25	gi 7661844	CCDC22	6594	NP_054727.1	28952				CC	Motif
26	gi 6005794	PRAF2	6596	NP_009144.1	11230				CC	Motif

## Networks

e.g., PPIs or pathways

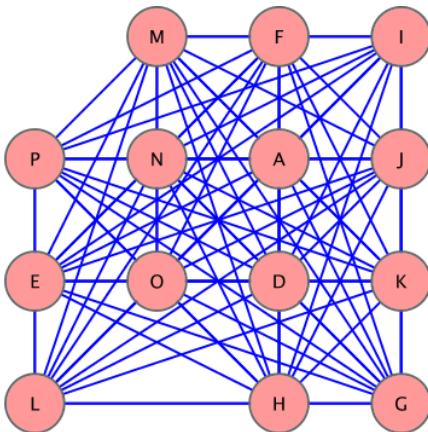
## Tables

e.g., data or annotations



# Core Concepts

- Networks and Tables



A screenshot of a Microsoft Excel spreadsheet titled "hprd.noa". The table contains 26 rows of data, each representing a gene entry. The columns are labeled: GI\_Number, Gene, HPRD\_ID, REFSEQ, Entrez\_ID, OMIM\_ID, SWISSP, Gene\_Description, Architecture, and ArchMotif. The data includes various gene identifiers, their descriptions, and associated biological motifs or domains.

	A	B	C	D	E	F	G	H	I	J
1	GI_Number	Gene	HPRD_ID	REFSEQ	Entrez_ID	OMIM_ID	SWISSP	Gene_Description	Architecture	ArchMotif
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4	gi 4602492	SCMH1	11540	AAH09752.1	22955		Q96GD1	SCMH1	SAM	Doma
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9	gi 5803086	IL24	4995	NP_006841.1	11009	604136	Q13007	Interleukin 24	IL10	Doma
10	gi 21265034	ADAMTS13	4994	NP_620594.1	11093	604134	ADAMTS13	TSP1	Doma	
11	gi 1743873	PIP5K1A	4470	AAC50911.1	8394	603275	Q99755	Phosphatidylinositol-4-phosphate	5_PIPKc	Doma
12	gi 1463382	PPM1A	4992	NP_00101371	6860	604125	059425	Survivillin	VIM	Doma
13	gi 563386	SULF2B1	4991	NP_014444.1	6820	604125		Sulfatransferase family 2b, member 1		
14	gi 21040399	RBBP8	4990	AAH30590.1	5932	604124	Q99708	CTP	LZ	Motif
15	gi 4758378	FIGF	2102	NP_004460.1	2277	300091	043915	VEGF D	PDGF	Doma
16	gi 11321617	DPYSL4	7463	NP_006417.1	10570	608407	Q14531	Collapsin response mediator protein 3		
17	gi 8923202	TASP1	7460	NP_060184.1	55617	608270	Q9H6P5	Threonine aspartate 1		
18	gi 5454090	SSR4	2101	NP_006271.1	6748	300090	P51571	Signal sequence receptor delta	SP	Motif
19	gi 5730045	SLC16A2	2106	NP_006508.1	6567	300095	P36021	X linked PEST containing transport	TM	Doma
20	gi 1968027	FTS	7467	NP_071921.1	64400	608483	Q9H8T0	FTS	UBC	Doma
21	gi 8255885	PRKC1	2105	NP_002731.3	5584	600539	P41743	Protein kinase C, iota type	S_T_kinase	Doma
22	gi 591026	PPAP4	6303	NP_00101370.1	29935		PPAP4		TRNAA	Doma
23	gi 3376812	PPP1R2P9	6593	NP_079486.1	80316					
24	gi 5026862		6595	NP_206375.1	90006			JM11 protein	CC	Motif
25	gi 7661844	CCDC22	6594	NP_054727.1	28952			JM1 protein	CC	Motif
26	gi 6005794	PRAF2	6596	NP_009144.1	11230			JM4 protein	TM	Doma

Networks

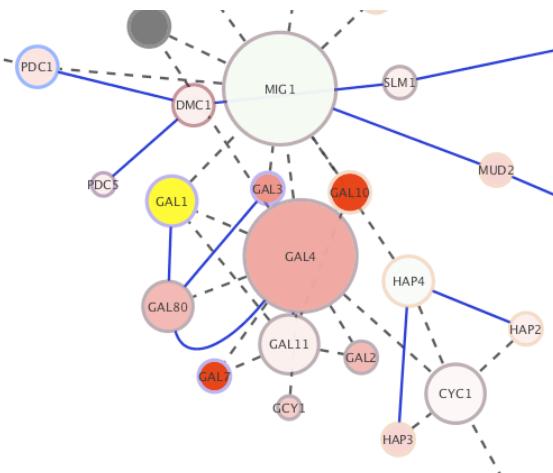
Tables

Visual Styles



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11	gi 1462054	RBBP8	4992	NP_614441.1	6820	604125	Q99708	Survivin	VHL	Doma
12	gi 63386	SUPT2B1	4991	NP_614444.1	6820	604125	Q99708	Sulfatetransferase family 2b, member 1	LZ	Motif
13	gi 21040399	RBBP8	4990	AAH30590.1	5932	604124	Q99708	Survivin	PDGF	Doma
14	gi 4758378	FIGF	2102	NP_004460.1	2277	300091	Q43915	VEGF D		
15	gi 11321617	DPYSL4	7463	NP_006417.1	10570	608407	Q14531	Collapsin response mediator protein 3		
16	gi 8923202	TASP1	7460	NP_060184.1	55617	608270	Q9H6P5	Threonine aspartate 1		
17	gi 5454090	SSR4	2101	NP_006271.1	6748	300090	P51571	Signal sequence receptor delta	SP	Motif
18	gi 5730045	SLC16A2	2106	NP_006508.1	6567	300095	P36021	X linked PEST containing transport	TM	Doma
19	gi 1968027	FTS	7467	NP_071921.1	64400	608483	Q9H6P70	FTS	UBC	Doma
20	gi 8255885	PRKC1	2105	NP_002731.3	5584	600539	P41743	Protein kinase C, iota type	S_T_kinase	Doma
21	gi 918442	RPA4	6303	NP_060921.1	29935		Q99708	RPA4	TRNAA	Doma
22	gi 3376812	PPP1R2P9	6593	NP_079486.1	80316			Triplex 1 protein phosphatase inhibitor		
23	gi 15026862		6595	NP_206375.1	90060			JM11 protein	CC	Motif
24	gi 7661844	CCDC22	6594	NP_054727.1	28952			JM1 protein	CC	Motif
25	gi 6005794	PRAF2	6596	NP_009144.1	11230			JM4 protein	TM	Doma

Networks

Tables

Visual Styles



# Cytoscape Apps

[apps.cytoscape.org](https://apps.cytoscape.org)

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- [data visualization](#)
- [network generation](#)
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- [network analysis](#)
- [online data import](#)
- [integrated analysis](#)
- [clustering](#)
- [systems biology](#)
- [utility](#)
- [data integration](#)
- [visualization](#)
- [enrichment analysis](#)
- [automation](#)
- [layout](#)
- [core app](#)
- [annotation](#)
- [pathway database](#)
- [ontology analysis](#)
- [network comparison](#)

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## Newest Releases

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3.0+

Performs a weighted k-shell decomposition

**Petri Net Implementation for Cytoscape**

3.0+

Implements Petri nets for Cytoscape, allowing creation,

**WordCloud**

3.0+

Summarizes functions of interacting clusters as logos,

**CyTargetLinker**

3.0+

Flexible network extension app

**AutoAnnotate**

3.0+

Finds clusters and visually annotates them with labels and

**PathInsight**

3.0+

An open-source application that models the effects of small binding

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## Top Downloaded Apps

**ClueGO**

3.0+

Creates and visualizes a functionally grouped network of

**BiNGO**

3.0+

Calculates overrepresented GO terms in the network and display

**CluePedia**

3.0+

CluePedia: A ClueGO plugin for pathway insights using integrated

**GeneMANIA**

3.0+

Imports interaction networks from public databases from a list of

**clusterMaker2**

3.0+

Multi-algorithm clustering app for Cytoscape

**MCODE**

3.0+

Clusters a given network based on topology to find densely



# stringApp

Import and augment Cytoscape networks from STRING



(16)

52104 downloads | helpdesk | citations | discussions



Details

Release History

Categories: annotation, automation, data visualization, disease, enrichment analysis, gene-disease association, gene function prediction, import, interaction database, network generation, online data import, PPI-network, visualization



*stringApp* imports protein-protein and protein-chemical interaction data from **STRING**, **Viruses.STRING**, **STITCH**, **DISEASES** and from PubMed text mining into Cytoscape. Users provide a list of one or more gene, protein, compound, disease, or PubMed queries, the species, and a confidence score and *stringApp* will query the database and return the matching network. Currently, four different queries are supported:

- STRING: protein query -- enter a list of protein names (e.g. gene symbols or UniProt identifiers/accession numbers) to obtain a STRING network for the proteins
- STRING: PubMed query -- enter a PubMed query and utilize text mining to get a STRING network for the top N proteins associated with the query
- STRING: disease query -- enter a disease name to retrieve a STRING network of the top N proteins associated with the specified disease
- STITCH: protein/compound query -- enter a list of protein or compound names to obtain a network for them from STITCH

CYTOSCAPE 3

Download

Version 1.5.0

Released 10 Sep 2019

Works with Cytoscape 3.7

Download Stats [Click here](#)

## RESOURCES

- Ask a question
- Search helpdesk
- Search BioStars

- Website
- Tutorial
- Cite this App
- Code Repository
- Automation Support
- E-mail

# Wall of Apps 339 total

## collections



## data visualization



## network generation



## graph analysis





# What can Cytoscape do?



# Load network data

- **Own data**
  - from files, e.g. Excel tables, Text files (TSV, CSV)
  - from R or Python via automation
- Data from **public databases**
  - STRING (via stringApp)
  - PSICQUIC (built-in)
  - KEGG (CytoKEGG app)
  - Reactome (via ReactomeFI app)
  - WikiPathways (via WikiPathways app)
  - And many others...



# Load network from file

Session: New Session

Control Panel

Network Style Select

Welcome to Cytoscape

Start New Session

- With Empty Network
- From Network File...**
- From Network Database...

Open Recent Session

- example\_network.cys
- test.cys
- example\_proteomics.cys
- test\_network.cys
- example.cys
- string\_db\_f800o.cys
- test\_network2.cys

Open Session File...

Latest News

Cytoscape 3.4.0 is up to date.

Sep 1: **Public network database service is up**

New Users: See:  
tutorials @ <http://bit.ly/1AbvA3n>  
slides @ <http://bit.ly/1Fpsf0A>

About Cytoscape Documentation Tutorials

Don't show again

Close

Node Table Edge Table Network Table

Memory



# Load network from file

Session: New Session

Control Panel

Network Style Select

Import Network From Table

Preview

Click on a column to edit it.

Source column	Source node name	Target column	Target node name	Interaction type	Interaction score
Node 1	A	Node 4	D	interacts with	0.7
Node 1	A	Node 3	C	interacts with	0.8
Node 1	A	Node 2	B	interacts with	0.8
Node 2	B	Node 4	D	interacts with	0.5
Node 2	B	Node 3	C	interacts with	0.8
Node 3	C	Node 4	D	interacts with	0.9
Node 4	D	Node 5	E	interacts with	0.8
Node 5	E	Node 8	H	interacts with	0.8
Node 5	E	Node 6	F	interacts with	0.5
Node 6	F	Node 7	G	interacts with	0.8
Node 7	G	Node 8	H	interacts with	0.8
Node 4	D	Node 9	I	activates	0.2
Node 4	D	Node 10	J	inhibits	0.5

Select All Select None

Advanced Options...

Cancel OK

Node Table Edge Table Network Table

Memory



# Load network from file

Session: New Session

Control Panel

Network Style Select

1 of 1 Network selected

Sheet1

Sheet1 10 13

Node 10  
Node 9  
Node 4  
Node 5  
Node 6  
Node 7  
Node 3  
Node 2  
Node 8  
Node 6  
Node 7  
Node 9  
Node 10

Node 1  
Node 4  
Node 3  
Node 2  
Node 5  
Node 8  
Node 6  
Node 7  
Node 9  
Node 10

Node 1  
Node 4  
Node 3  
Node 2  
Node 5  
Node 8  
Node 6  
Node 7  
Node 9  
Node 10

Node 1  
Node 4  
Node 3  
Node 2  
Node 5  
Node 8  
Node 6  
Node 7  
Node 9  
Node 10

Table Panel

$f(x)$

shared name	name	Source node name	Target node name
Node 1	Node 1	A	
Node 4	Node 4	D	D
Node 3	Node 3	C	C
Node 2	Node 2	B	B
Node 5	Node 5	E	E
Node 8	Node 8	H	
Node 6	Node 6	F	F
Node 7	Node 7	G	G
Node 9	Node 9	I	
Node 10	Node 10	J	

Node Table Edge Table Network Table

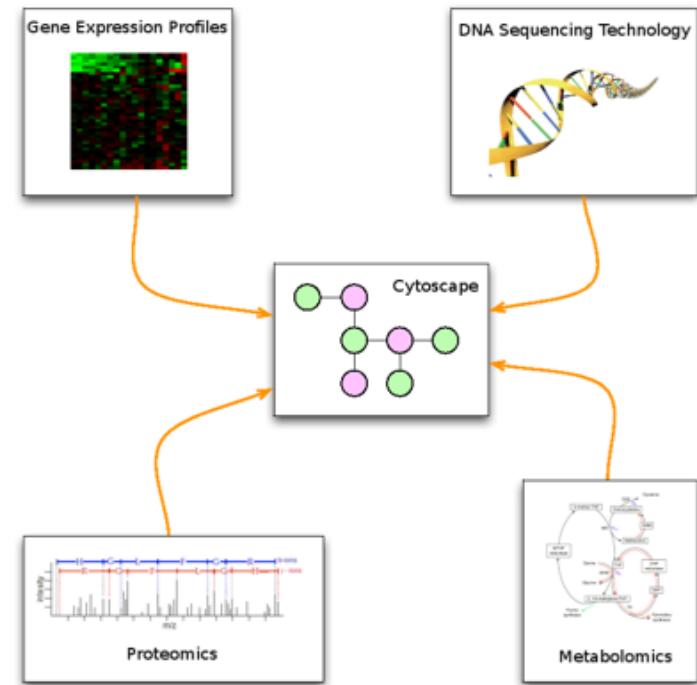
Cloud icon: Loading network from table

Memory icon: Memory



# Load attribute data

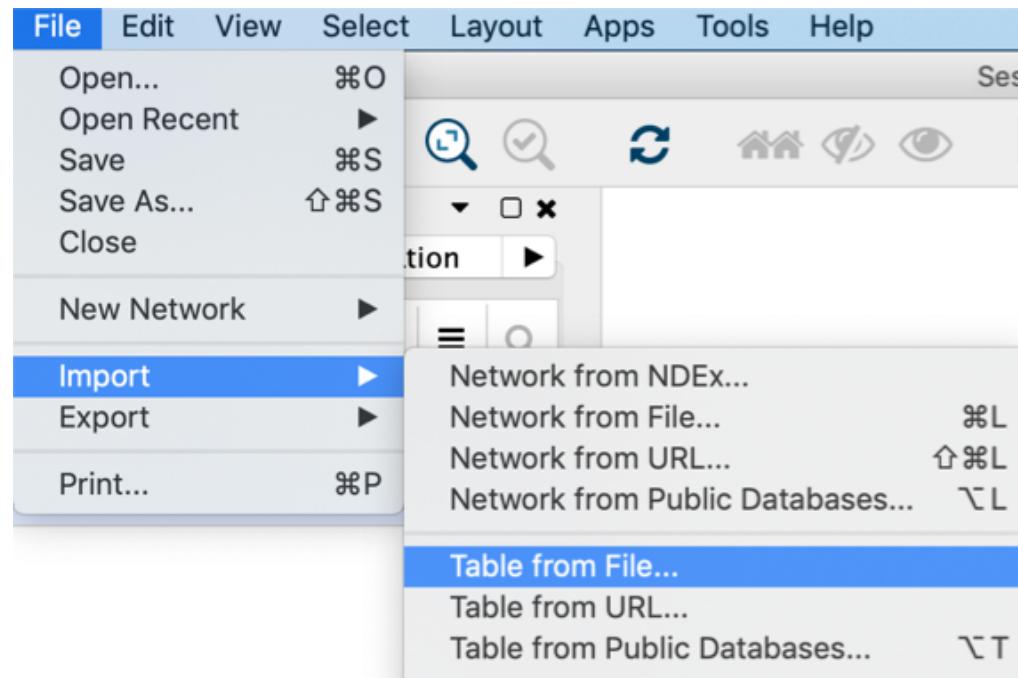
- **Nodes and edges can have data associated with them**
  - Gene expression data
  - Mass spectrometry data
- Load **own data from files**, e.g. Excel sheets, or via automation from R or Python
- Cytoscape supports multiple data types: Numbers, Text, Boolean, Lists...





# Load table from file

- Use import table from file
  - Excel file
  - Comma or tab delimited text





# Load table from file

Session: New Session

Control Panel

Network Style Select

1 of 1 Network selected

Sheet1 Sheet1

Import Columns From Table

Target Table Data

Where to Import Table Data: To a Network Collection

Select a Network Collection

Network Collection: Sheet1

Import Data as: Node Table Columns

Key Column for Network: shared name

Case Sensitive Key Values:

Preview

Click on a column to edit it.

Select All Select None

Node	Node name	Belongs to	Confidence
Node 1	A	complex 1	0.9
Node 2	B	complex 1	0.5
Node 3	C	complex 1	0.9
Node 4	D	complex 1	0.9
Node 5	E	complex 2	0.8
Node 6	F	complex 2	0.7
Node 7	G	complex 2	0.7
Node 8	H	complex 2	0.8

Advanced Options...

Cancel OK

Node Table Edge Table Network Table

Memory



# Load table from file

Session: New Session

Control Panel

Network Style Select

1 of 1 Network selected

Sheet1 Sheet1 10 13

Node 9  
Node 10  
Node 6  
Node 7  
Node 5  
Node 4  
Node 3  
Node 2

Node 1  
Node 4  
Node 3  
Node 2  
Node 5  
Node 8  
Node 6  
Node 7  
Node 9  
Node 10

Node 1 Node 4 Node 3 Node 2 Node 5 Node 8 Node 6 Node 7 Node 9 Node 10

Node name complex 1 complex 1 complex 1 complex 1 complex 2 complex 2 complex 2 complex 1 complex 1

Confidence 0.9 0.9 0.9 0.5 0.8 0.8 0.7 0.1 0.1

Table Panel

Sheet1

Node Table Edge Table Network Table

Memory

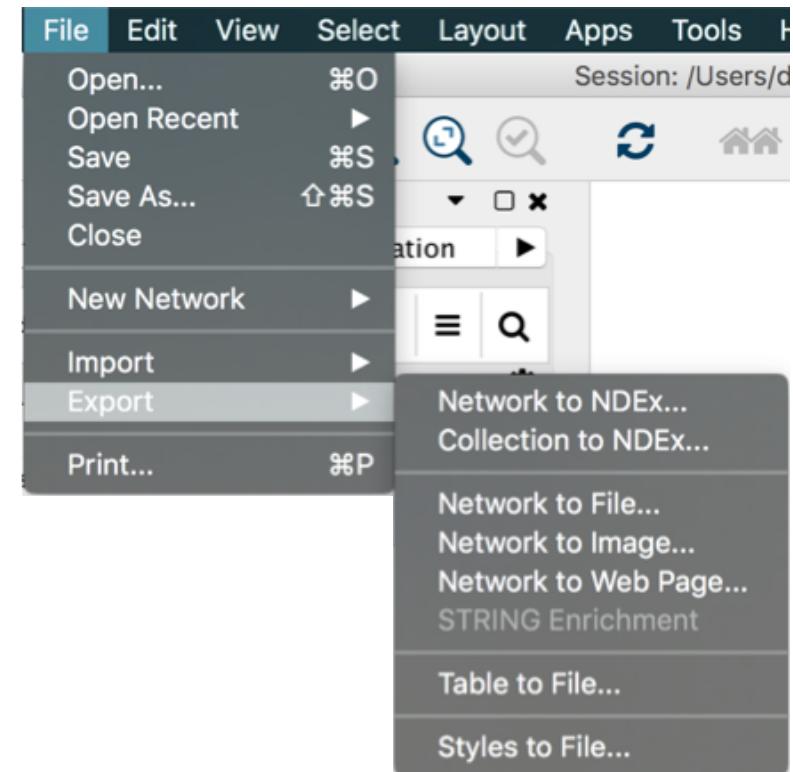
The screenshot shows the Gephi software interface. The main area displays a network graph with 10 nodes labeled Node 1 through Node 10. Node 4 is the central hub, connected to Nodes 2, 3, 5, 6, 7, and 10. Nodes 2, 3, and 5 are also interconnected. A small inset graph in the bottom right corner shows a zoomed-in view of a cluster of nodes. The Control Panel on the left indicates "1 of 1 Network selected" and lists "Sheet1" twice. The Table Panel at the bottom contains a table with columns: shared name, name, Node name, Belongs to, and Confidence. The data is as follows:

shared name	name	Node name	Belongs to	Confidence
Node 1	Node 1	A	complex 1	0.9
Node 4	Node 4	D	complex 1	0.9
Node 3	Node 3	C	complex 1	0.9
Node 2	Node 2	B	complex 1	0.5
Node 5	Node 5	E	complex 2	0.8
Node 8	Node 8	H	complex 2	0.8
Node 6	Node 6	F	complex 2	0.7
Node 7	Node 7	G	complex 2	0.7
Node 9	Node 9	I	complex 1	0.1
Node 10	Node 10	J	complex 1	0.1



# Save data

- Sessions save everything (.cys files)
- Export networks in different formats
- Export tables as CSV files
- Publication quality graphics in several formats





**Do you want to try it out  
yourself?**



# Installation

- How many have installed Cytoscape 3.7.2?
- If not installed yet, get it from here:  
<http://cytoscape.org/download.php>
- Do Tour of Cytoscape in CyBrowser:  
<https://cytoscape.github.io/cytoscape-tutorials/protocols/tour-of-cytoscape/>



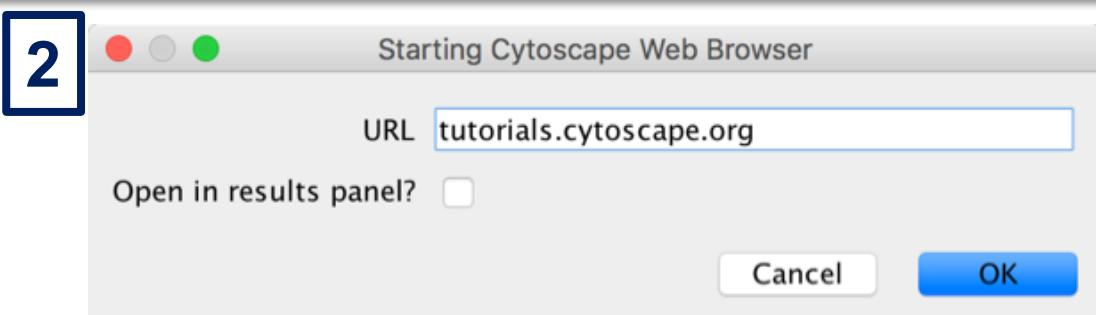
# Tour of Cytoscape

1

Tools Help

- Color Cast ▶
- NetworkAnalyzer ▶
- Cytoscape web browser
- Merge ▶
- Workflow ▶
- Job Status Monitor
- Command Line Dialog
- Execute Command File... ▶
- Diffuse ▶

2



3



This is a collection of protocols for Cytoscape and Cytoscape Apps, ranging from introductory training to advanced analysis.

Cytoscape is an open source bioinformatics software platform for visualizing molecular interaction networks and integrating these interactions with gene expression profiles and other state data. Many apps are available for network and molecular profiling analyses, new layouts, additional file format support, scripting, and connection with databases.

Our protocols are organized into categories below. For a complete list of protocols, presentations, modules and more, see the [complete list](#).

## Getting Started

Tour of Cytoscape

New to Cytoscape? Our "Tour of Cytoscape" tutorial gives you a high-level introduction to Cytoscape's capabilities and features, and directs you to detailed training content for each step.



<https://cytoscape.github.io/cytoscape-tutorials/protocols/tour-of-cytoscape/>



# Exercise: Intro to Cytoscape

## Basic data visualization

Presents a scenario of how expression data can be assessed in the context of networks to tell a biological story through data visualization.

<https://cytoscape.org/cytoscape-tutorials/protocols/basic-data-visualization/>