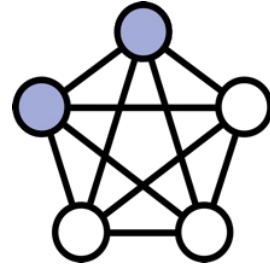




Cytoscape

stringApp



Introduction to Cytoscape and stringApp

Nadezhda T. Doncheva

nadezhda.doncheva@cpr.ku.dk

Statistical methods in bioinformatics, KU

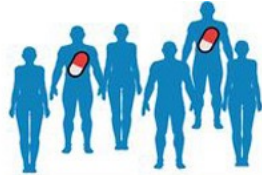
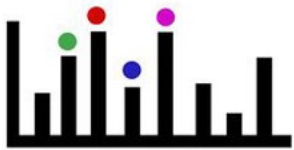
March 28th, 2023



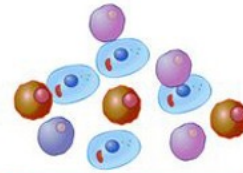
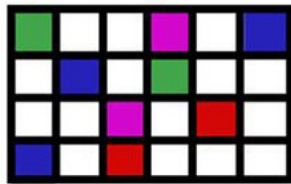
High-throughput technologies



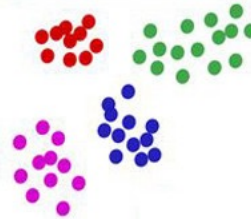
Proteomics



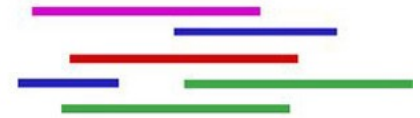
Microarray



scRNA-seq



RNA-seq



- Enable us to characterize genome- and proteome-wide expression changes
- Usually result in hundreds of regulated molecular players (genes, proteins, etc.)
- It is challenging to derive relevant biological insights from 'omics data



A typical data table

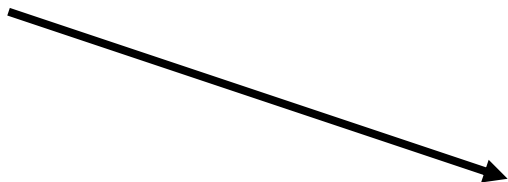
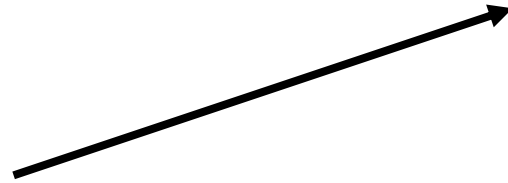
- Temporal analysis of the proteome of neuroblastoma cells in response to NGF (nerve growth factor) using mass spectrometry
- Identification of 78 proteins that interact with TrkA (tropomyosin-related kinase A) upon NGF stimulation

	A	B	C	D	G	J
1	UniProt	Gene name	Peptides	Sequence coverage [%]	5 min log ratio	10 min log ratio
2	Q99880	HIST1H2BL	5	35.7	-2.66	-2.66
3	Q8TER5	ARHGEF40	34	28.3	1.95	1.56
4	Q8IZ07	ANKRD13A	12	19.2	1.07	1.08
5	P62805	HIST1H4A	11	57.3	-2.31	-1.39
6	Q08380	LGALS3BP	14	28.2	-3.16	-2.98
7	O00750	PIK3C2B	35	24.2	2.21	2.31
8	O00443	PIK3C2A	29	17.8	1.13	1.26
9	Q9UJ41	RABGEF1	6	6.5	0.67	1.08
10	Q8TC07	TBC1D15	12	19.1	0.43	1.06



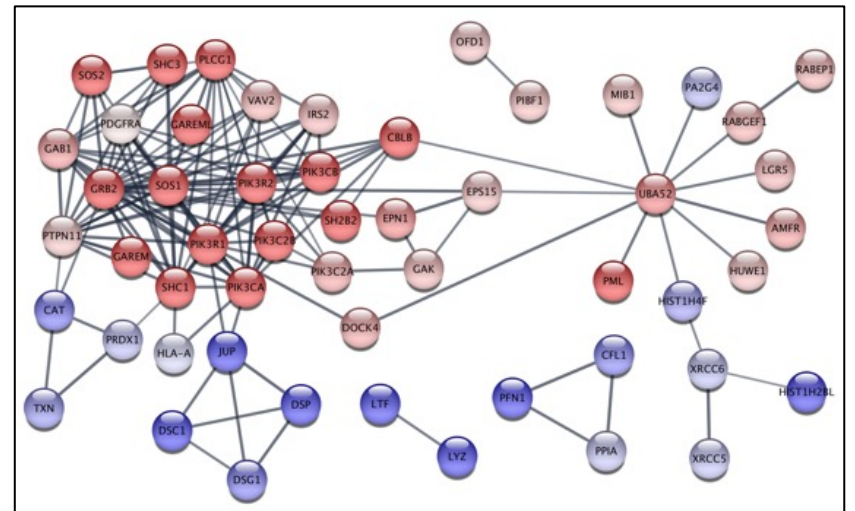
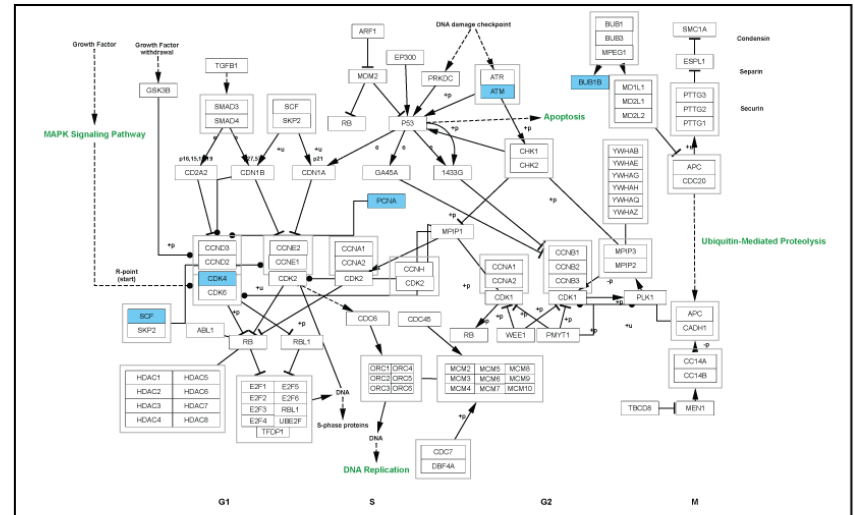
From gene lists to networks

Functional enrichment:
Identify relevant pathways & processes, e.g. KEGG & GO



Network analysis & visualization:
Identify target genes and their cellular context, e.g. STRING

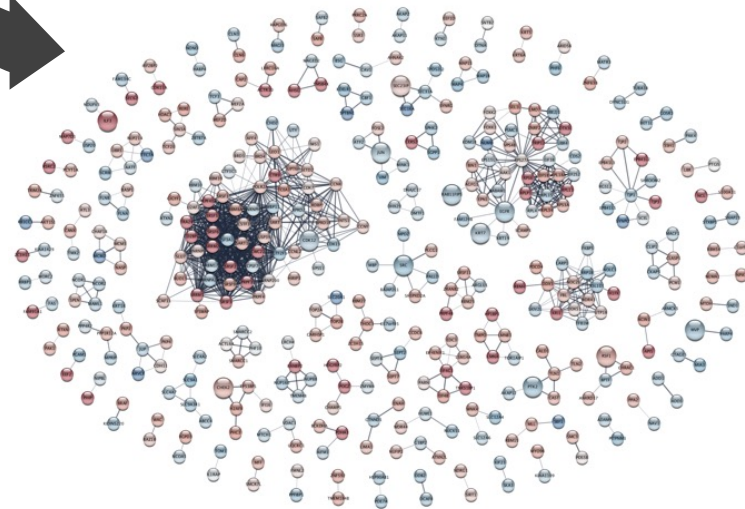
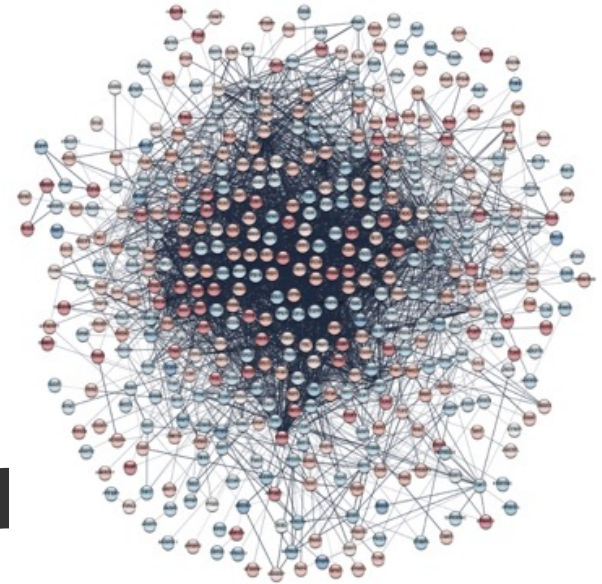
UniProt
Q99880
Q8TER5
Q8IZ07
P62805
Q08380
O00750
O00443
Q9UJ41
Q8TC07





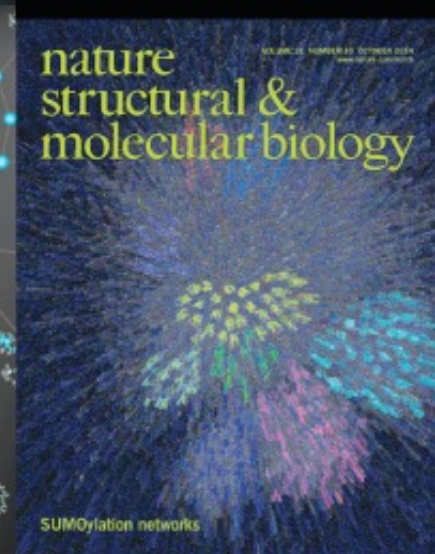
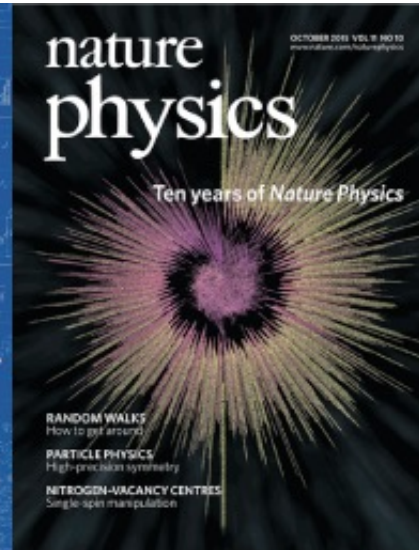
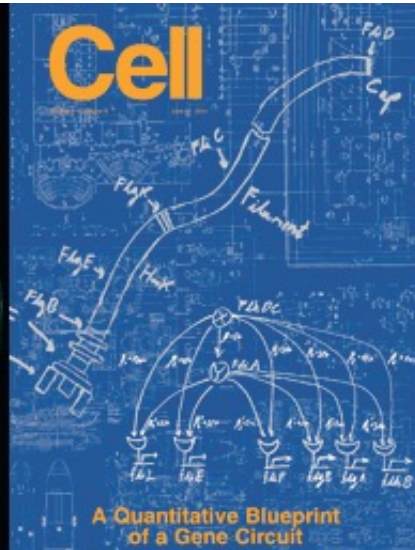
Why use (biological) networks?

- Networks are **powerful tools**
 - ✓ More efficient than tables
 - ✓ Reduce complexity
 - ✓ Great for data integration
 - ✓ Intuitive visualization
- But also... Challenging!
- Network **analysis and visualization techniques** enable us to make the best use of networks.





Applications in Research

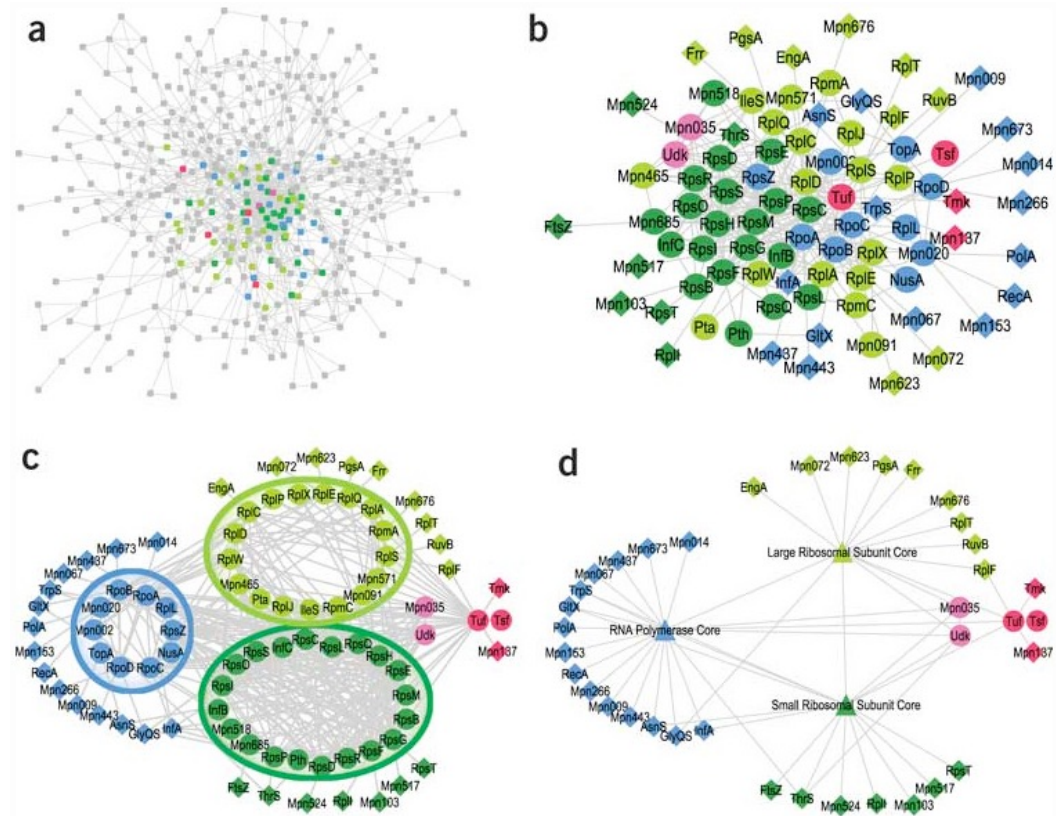




Omic data visualization

In 2010, a Nature Methods paper introduced major *themes* of network visualization:

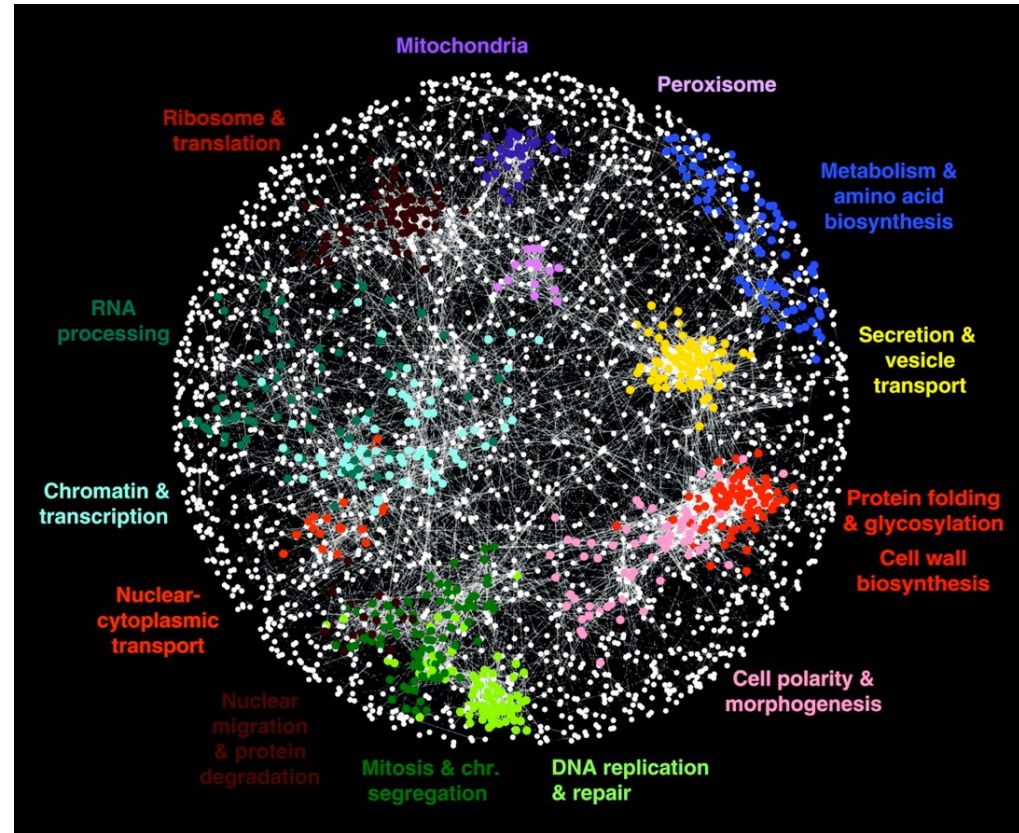
- Mass spec analysis: 400 PPI in pneumonia microbe
- Subnetwork with function annotations
- Layout with knowledge of complexes
- Collapsed meta-nodes to reduce complexity





Yeast genetic interactions

- Genetic interactions for the entire yeast genome
- Synthetic lethal screen of 1,712 genes resulting in 170,000 interactions
- Visualization of clustering within and between GO annotated functional groups
- Prediction of functions and identification of regulatory subnetworks

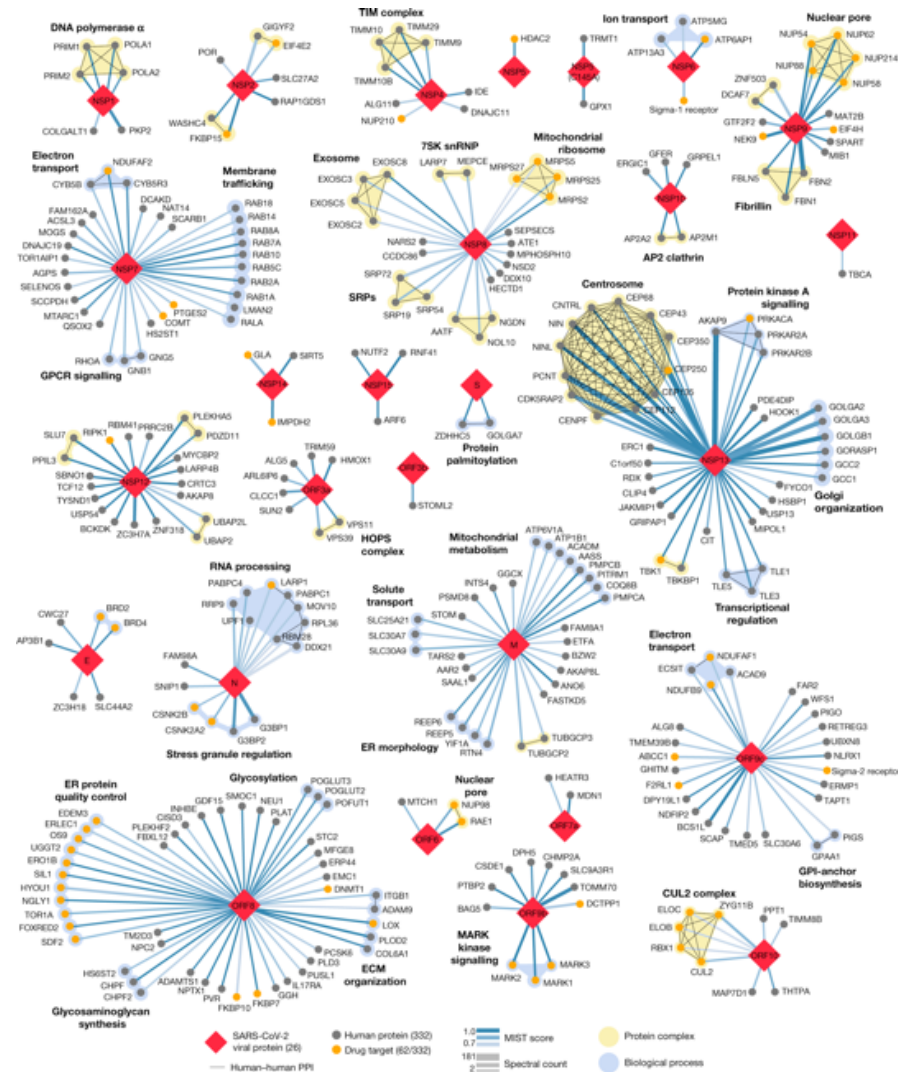


Costanzo *et al.* (2010) The genetic landscape of a cell. *Science*, 22, Fig. 1



SARS-CoV-2-human network

- AP-MS with 26 SARS-CoV-2 proteins reveals 332 interactions with human proteins
- Merged human-human physical protein interactions to identify complexes
- Used fill color to highlight known drug targets



Gordon *et al.* (2020): A SARS-CoV-2 protein interaction map reveals targets for drug repurposing. *Nature*, 583, Fig. 3

Do you already have some ideas, if and how you can use networks in your project(s)?



Welcome to STRING

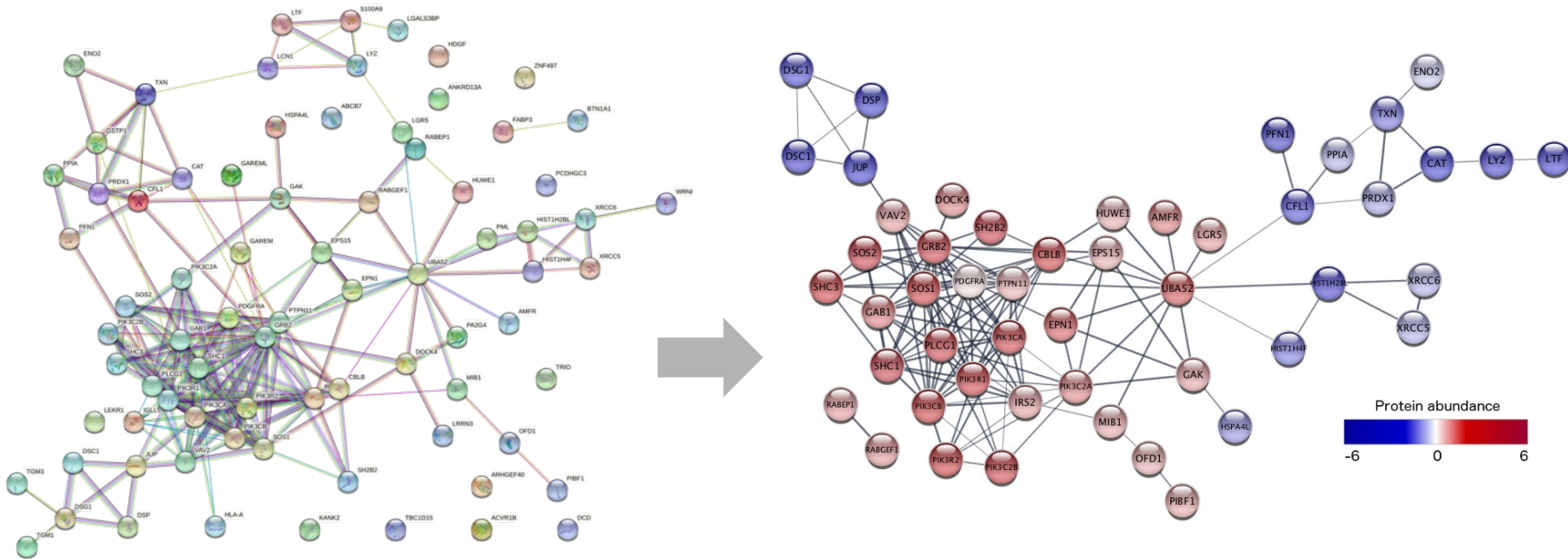
Protein-Protein Interaction Networks
Functional Enrichment Analysis

ORGANISMS		PROTEINS		INTERACTIONS
14094		67.6 mio		>20 bln

[SEARCH](#)



From STRING to Cytoscape

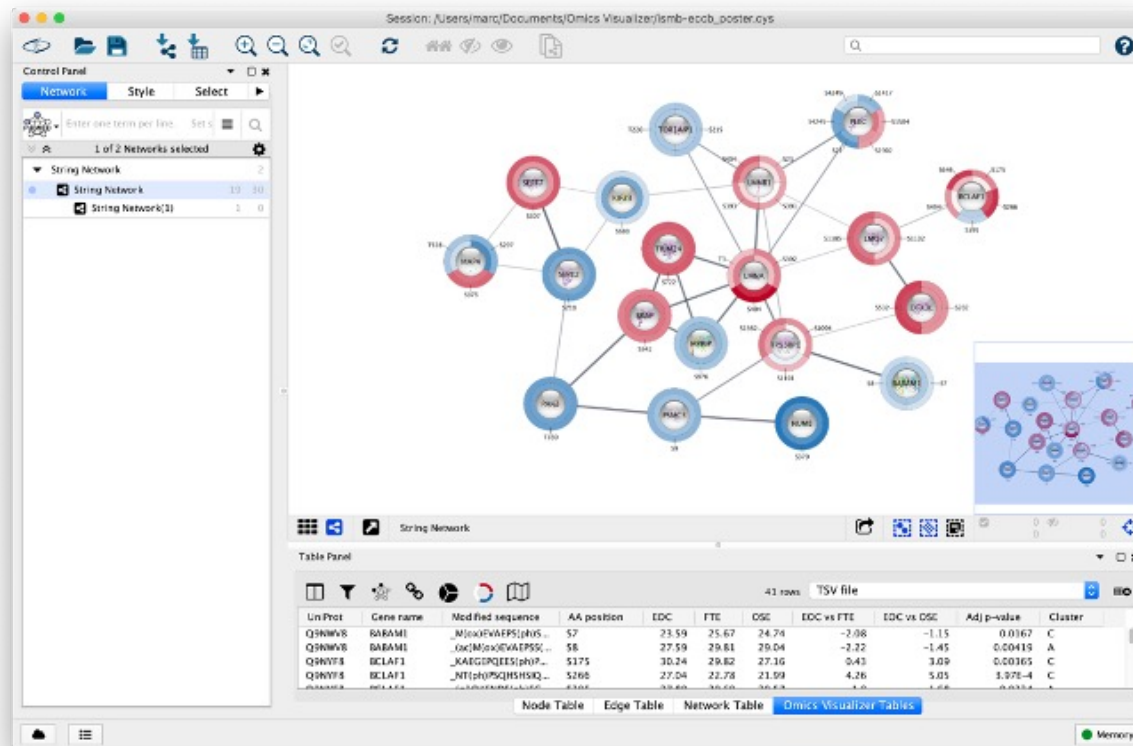


- Ideally, we want to be able to:
 - Integrate and easily show additional experimental data
 - Have more powerful analysis and visualization options
 - Create networks for large lists of genes



Cytoscape

- Open source tool for network analysis and visualization
 - Large, active community of developers & users
 - However, Cytoscape itself doesn't know any biology
- **Cytoscape apps:** apps.cytoscape.org



All Apps







Categories

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

more »







Newest Releases

Get Started with the App Store »

 <p>BNMatch2 3.0+</p> <p>BNMatch provides a reliable and optimized mapping between</p>	 <p>DKernel 3.0+</p> <p>DKernel uses Diffusion Kernel algorithm to propagate sub-</p>
 <p>BioGateway Cytoscape Plugin 3.0+</p> <p>An explorative network building plugin that works with the</p>	 <p>IntAct App 3.0+</p> <p>BETA: Build molecular interaction networks from IntAct database.</p>
 <p>CyCommunityDetection 3.0+</p> <p>Integrates multiscale community detection and functional</p>	 <p>dot-app 3.0+</p> <p>Import/export of Graphviz files in Cytoscape</p>

[more newest releases »](#)

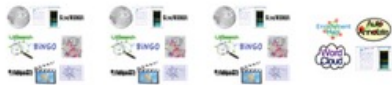
Top Downloaded Apps

 <p>ClueGO 3.0+</p> <p>Creates and visualizes a functionally grouped network of</p>	 <p>BiNGO 3.0+</p> <p>Calculates overrepresented GO terms in the network and display</p>
 <p>CluePedia 3.0+</p> <p>CluePedia: A ClueGO plugin for pathway insights using integrated</p>	 <p>GeneMANIA 3.0+</p> <p>Imports interaction networks from public databases from a list of</p>
 <p>stringApp 3.0+</p> <p>Import and augment Cytoscape networks from STRING</p>	 <p>MCODE 3.0+</p> <p>Clusters a given network based on topology to find densely</p>

[more top downloads »](#)

Wall of Apps 372 total

collections



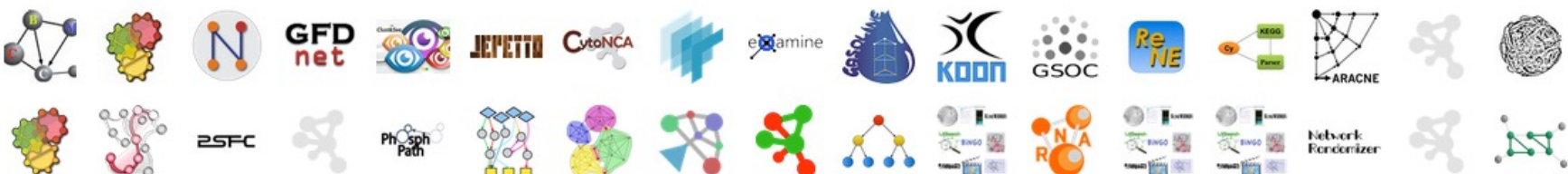
data visualization



network generation



network analysis





stringApp

Import and augment Cytoscape networks from STRING

★★★★★ (28)

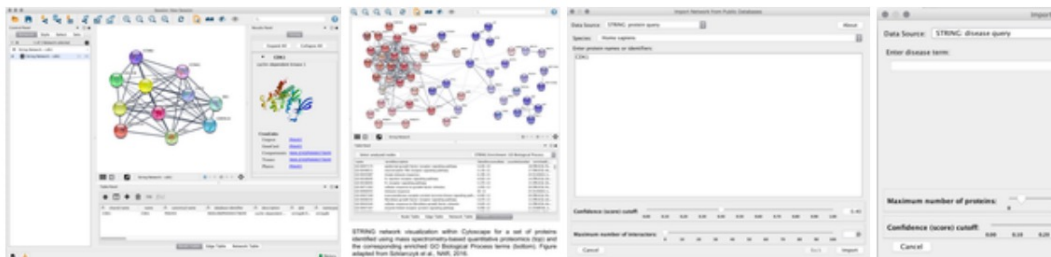
188212 downloads | [citations](#) | [discussions](#)



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 functional associations or physical interactions between protein-protein and protein-chemical pairs 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, the network type, and a confidence score and *stringApp* queries the database to return the matching network. Currently, five 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
- STRING: cross-species query -- choose two species to obtain a STRING network between and within the proteins of the interacting species

CYTOSCAPE 3

 **Download**

Version 2.0.1



Released 24 Jan 2023







Works with [Cytoscape 3.8](#)

Download Stats [Click here](#)

cytoscape not running

RESOURCES

-  [Ask a question](#)
-  [Search BioStars](#)

-  [Website](#)
-  [Tutorial](#)
-  [Cite this App](#)
-  [Code Repository](#)
-  [Automation Support](#)
-  [E-mail](#)



Cytoscape core concepts



Networks

e.g., protein-protein interaction networks

Node Table ▾

name	Degree	COMMON	gal1RGexp	gal1Rgsig
YDL194W	1	SNF3	0.139	0.018043
YDR277C	2	MTH1	0.243	2.186E-5
YBR043C	1	YBR043C	0.454	5.373E-8
YPR145W	1	ASN1	-0.195	3.174E-5
YER054C	2	GIP2	0.057	0.16958
YBR045C	3	GIP1	0.786	5.5911E-6
YBL079W	1	NUP170	-0.186	2.5668E-4
YLR345W	1	YLR345W	0.108	0.012373
YIL052C	1	RPL34B	-0.258	3.7855E-5

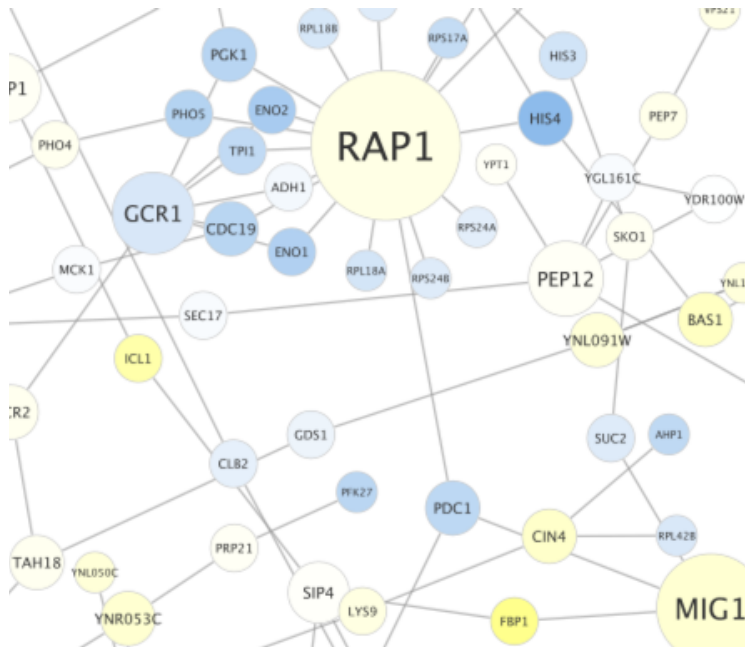
Tables

e.g., actual network data or annotations

Visual Styles



Cytoscape core concepts



Node Table ▾

name	Degree	COMMON	gal1RGexp	gal1RGsig
YDL194W	1	SNF3	0.139	0.018043
YDR277C	2	MTH1	0.243	2.186E-5
YBR043C	1	YBR043C	0.454	5.373E-8
YPR145W	1	ASN1	-0.195	3.174E-5
YER054C	2	GIP2	0.057	0.16958
YBR045C	3	GIP1	0.786	5.5911E-6
YBL079W	1	NUP170	-0.186	2.5668E-4
YLR345W	1	YLR345W	0.108	0.012373
YIL052C	1	RPL34B	-0.258	3.7855E-5

Networks

e.g., protein-protein interaction networks

Tables

e.g., actual network data or annotations

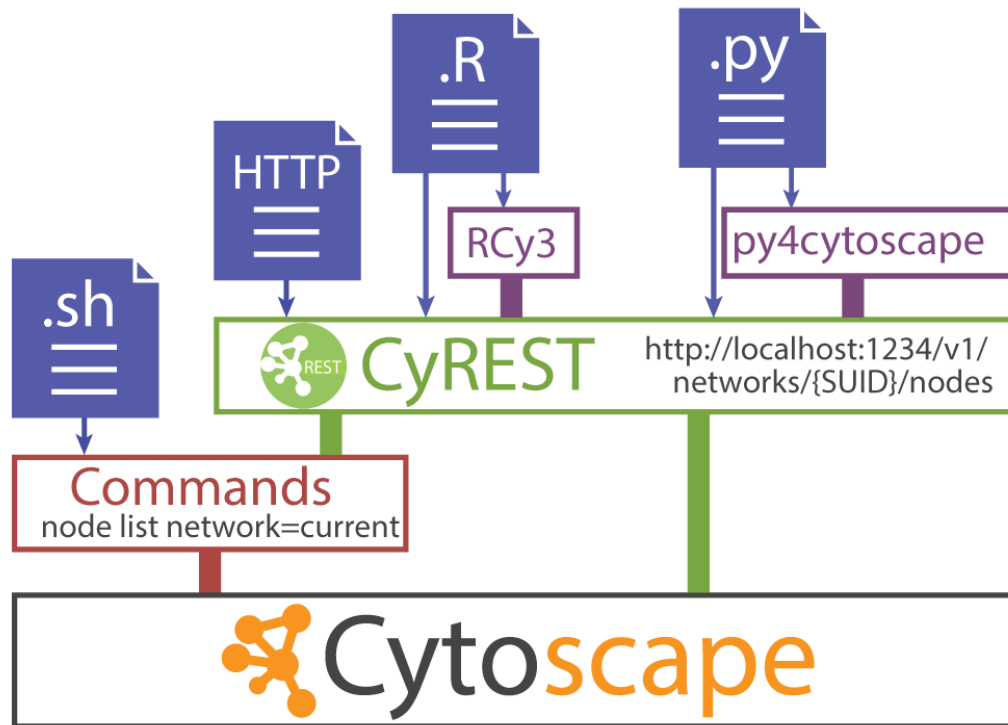


Visual Styles



Cytoscape automation

- Use commands from R, Python, or JavaScript to execute Cytoscape, stringApp, and other apps' functionality



<https://github.com/cytoscape/cytoscape-automation/wiki>



Let's try it out!

How many have installed Cytoscape **3.9.1**?

If not installed yet, get it from here:

<http://cytoscape.org/download.php>



Launch Cytoscape

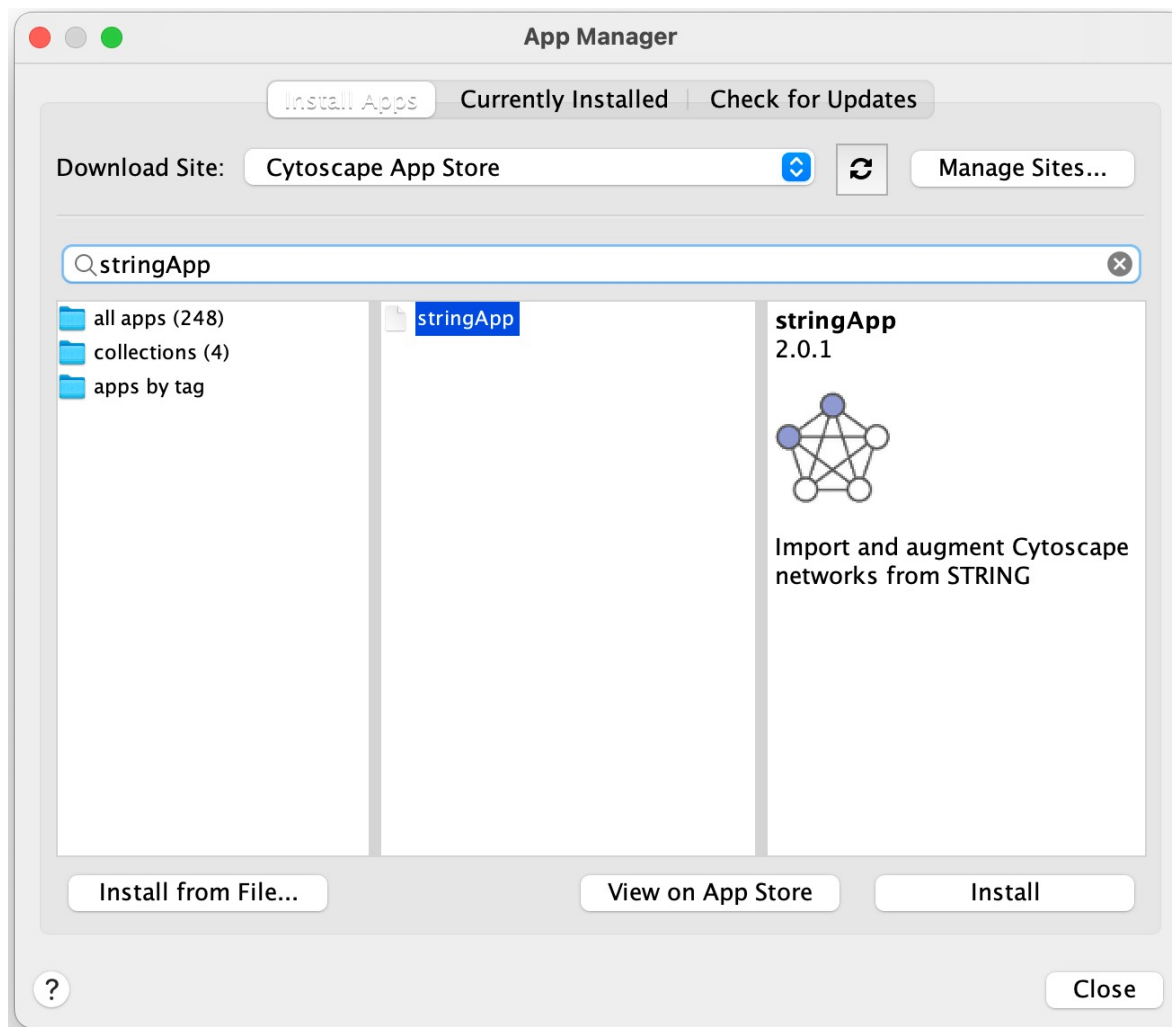
The screenshot shows the Cytoscape application window with the following components and callouts:

- Default layout:** A callout box pointing to the top toolbar containing icons for file operations, zooming, and layout.
- Zoom in/out:** A callout box pointing to the zoom icons in the toolbar.
- Control panel:** A large callout box on the left side of the interface, listing:
 - List of networks
 - Visual styles
 - Selection filters
 - Layout tools
- Network view:** A callout box pointing to the main central area where a network graph is displayed.
- Table panel:** A callout box pointing to the bottom panel, which includes:
 - Node Attributes Table
 - Edge Attributes Table

The interface also features a top menu bar (File, Edit, View, Select, Layout, Apps, Tools, Help), a search bar, and a status bar at the bottom with a 'Load Preset Styles' button.



Install stringApp v2





stringApp exercise 1

In this exercise, we will perform some simple queries to retrieve molecular networks in Cytoscape using the stringApp

1.1 Protein queries

Go to **File** → **Import** → **Network from Public Databases**. In the import dialog, choose **STRING: protein query** as **Data Source** and type your favorite protein into the **Enter protein names or identifiers** field (e.g. SORCS2).

***Question 1:** How many nodes and edges are in the resulting network? What types of information does the **Node Table** provide?*

1.2 Disease queries

Go to **File** → **Import** → **Network from Public Databases**. In the import dialog, choose **STRING: disease query** as **Data Source** and type a disease of interest into the **Enter disease term** field (e.g. Alzheimer's disease). The next dialog selects the first of all the matches that the stringApp finds for your disease query. Select the intended disease and press **Import** to continue.

***Question 2:** Which additional attribute column do you get in the **Node Table** for a disease query compared to a protein query? Hint: check the last column.*

Questions?

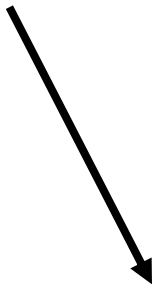
Lunch break!



From tables to styled networks

	A	B	C	D	G	J
1	UniProt	Gene name	Peptides	Sequence coverage [%]	5 min log ratio	10 min log ratio
2	Q99880	HIST1H2BL	5	35.7	-2.66	-2.66
3	Q8TER5	ARHGEF40	34	28.3	1.95	1.56
4	Q8IZ07	ANKRD13A	12	19.2	1.07	1.08
5	P62805	HIST1H4A	11	57.3	-2.31	-1.39
6	Q08380	LGALS3BP	14	28.2	-3.16	-2.98
7	O00750	PIK3C2B	35	24.2	2.21	2.31
8	O00443	PIK3C2A	29	17.8	1.13	1.26
9	Q9UJ41	RABGEF1	6	6.5	0.67	1.08
10	Q8TC07	TBC1D15	12	19.1	0.43	1.06

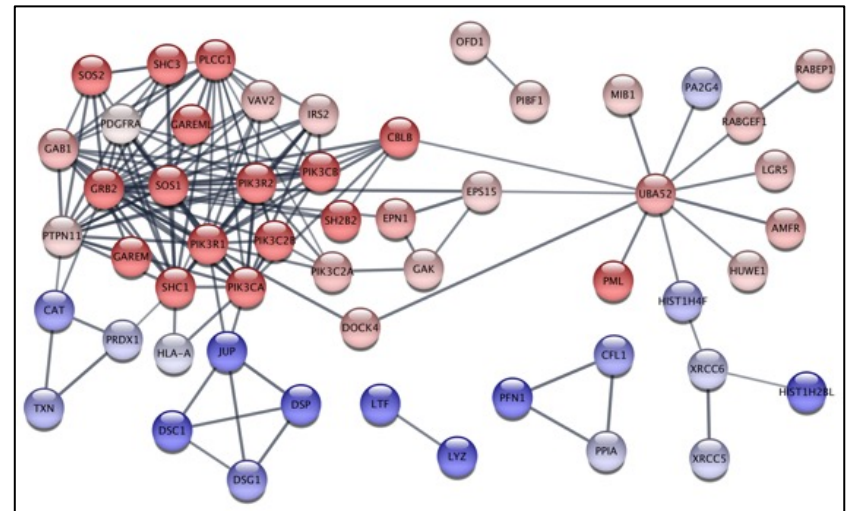
Emdal *et al.*, *Science Signaling*, 2015



UniProt
Q99880
Q8TER5
Q8IZ07
P62805
Q08380
O00750
O00443
Q9UJ41
Q8TC07



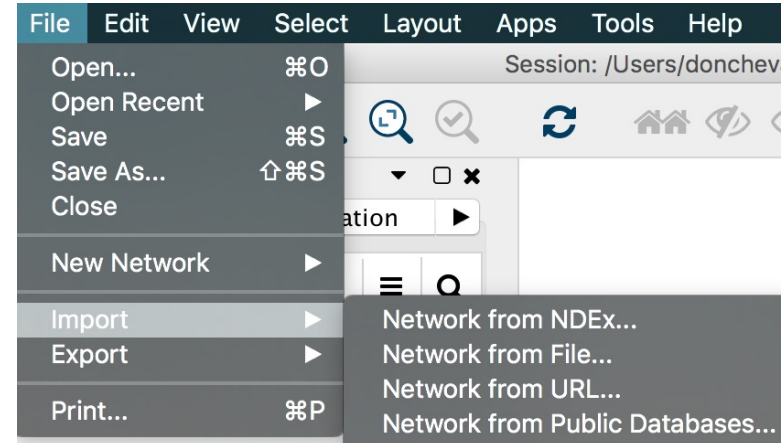
stringApp





Import networks in Cytoscape

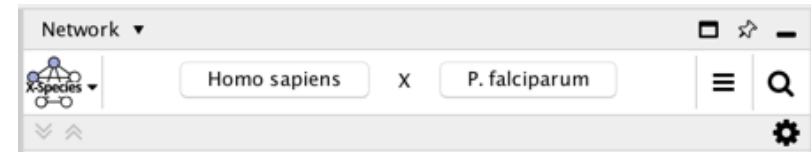
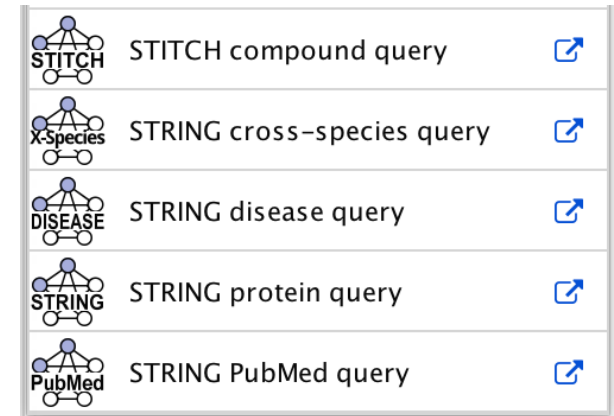
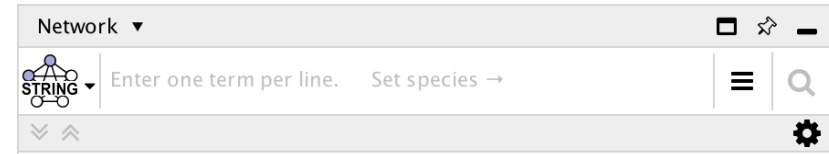
- **Starting with a list of genes and no network data**
 - stringApp
 - IntAct app
- **Starting with a pathway of interest**
 - KEGGscape app
 - ReactomeFI app
 - WikiPathways app
- **Starting with your own network data**
 - from files, e.g. Excel tables or text files
 - from R or Python via automation





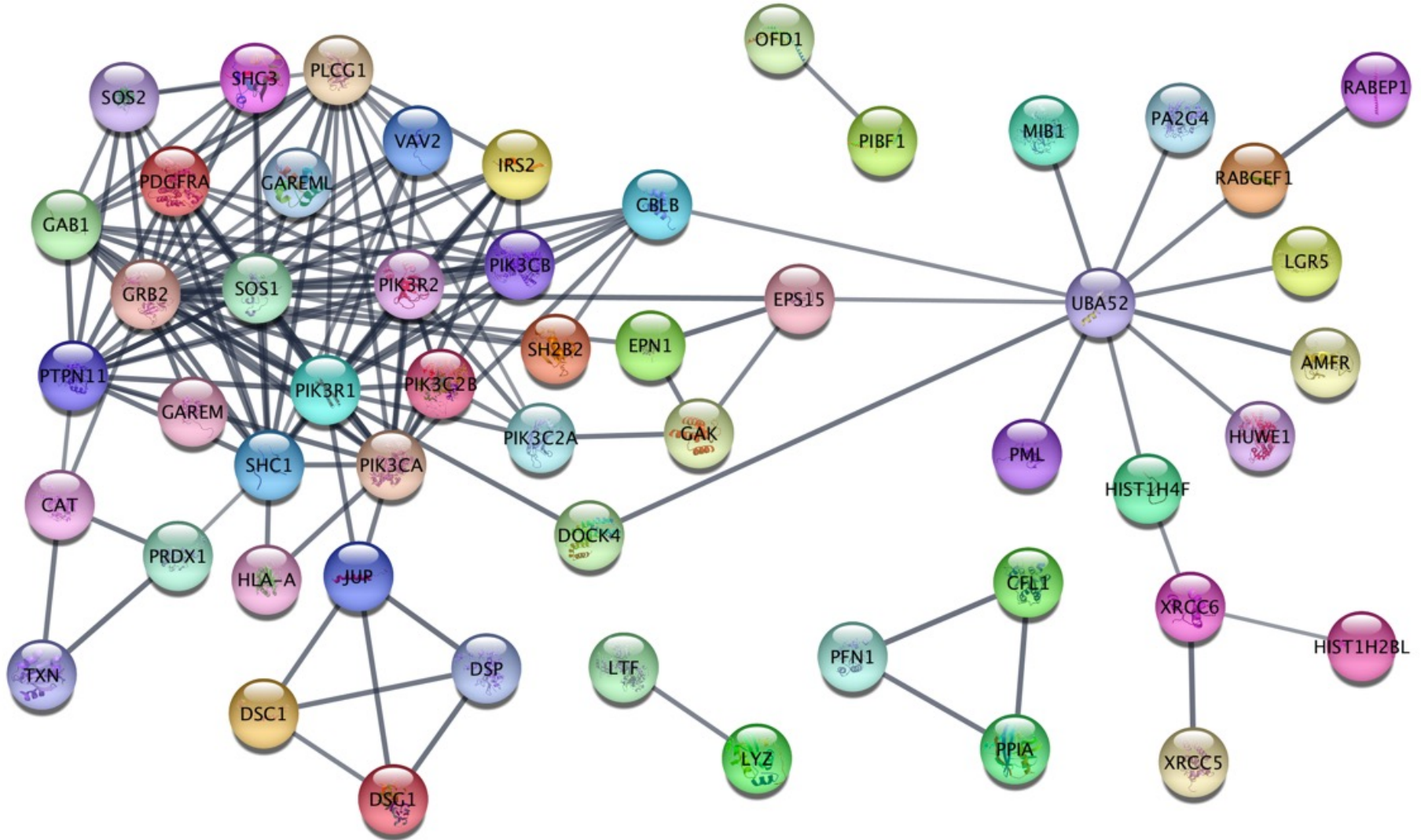
stringApp

- **STRING protein query**
 - Queries for STRING interactions for **one** protein or for a **list** of identifiers
- **STRING compound query**
 - Queries for protein-compound interactions
- **STRING disease query**
 - Queries for disease-associated proteins from DISEASES and for STRING interactions between them
- **STRING PubMed query**
 - Retrieves STRING interactions for proteins co-occurring with the query term in PubMed
- **STRING cross-species query**
 - retrieves STRING interactions between and within the proteins of two interacting species





STRING network in Cytoscape





Node table (attributes)

Nodes (and edges) can have data associated with them, here protein information from STRING database

Table Panel

⚙️ 📄 + 🗑️ 📊 $f(x)$ ↻

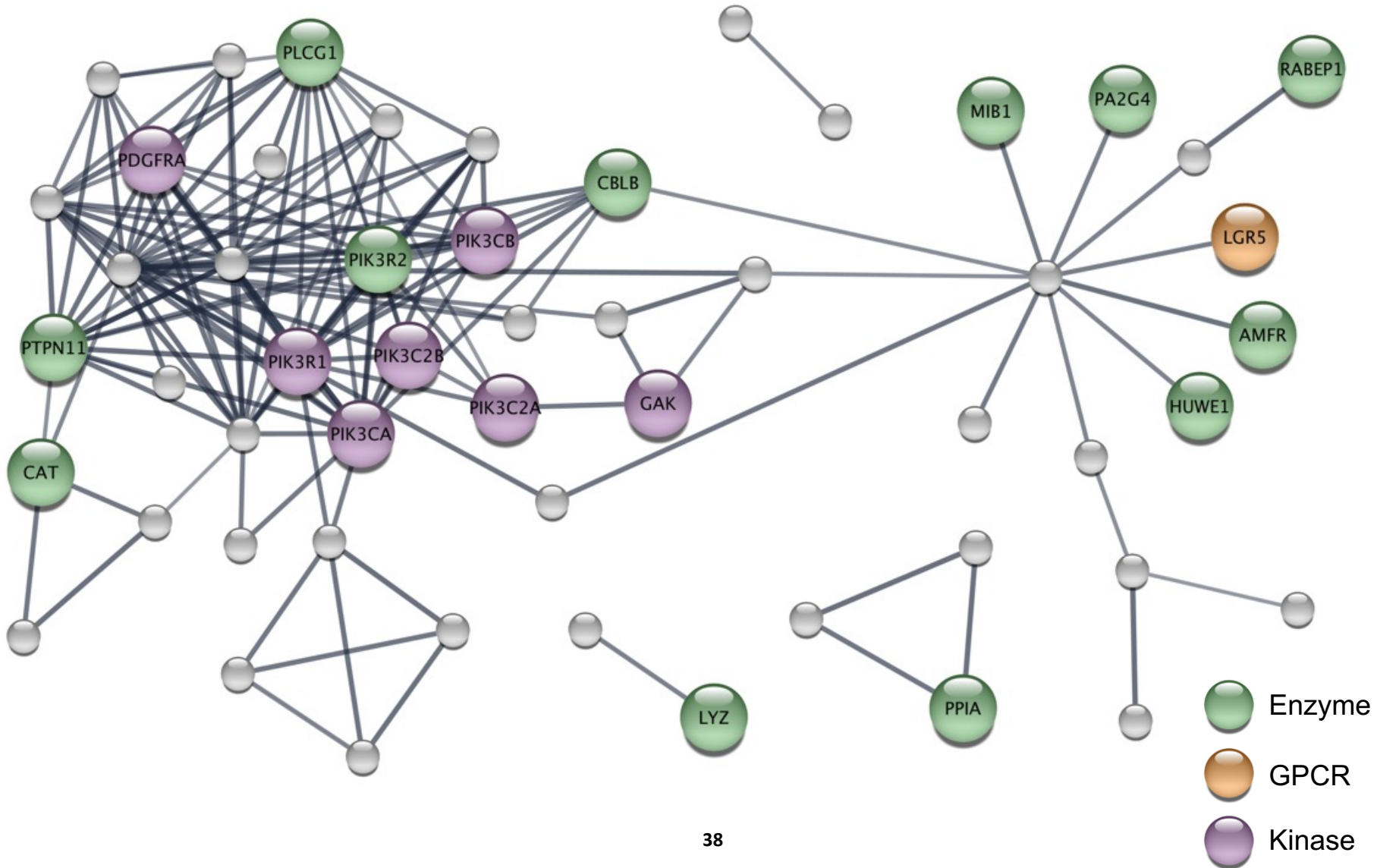
👤 display name	📄 stringdb canonical name	📄 stringdb description	📄 stringdb sequence	📄 stringdb species	🟢 compartment cytoskeleton	🟢 compartment cytosol	🟠 tissue blood
PHF1	O43189	Polycomb-like prot...	MAQPPRLSRSGAS...	Homo sapiens	5.0	0.326524	0.766667
EDAR	Q9UNE0	Tumor necrosis fac...	MAHVGDTCTPW...	Homo sapiens		0.328125	0.750488
IL6	P05231	B-cell stimulatory f...	MNSFSTSAFGPVA...	Homo sapiens	2.617751	2.977923	4.0
CREB1	P16220	Cyclic AMP-respon...	MTMESGAENQQS...	Homo sapiens	1.709787	1.861972	3.449199
MS4A5	Q9H3V2	Membrane-spanni...	MDSSTAHSVFLV...	Homo sapiens			
YWHAQ	P27348	Tyrosine 3-monoo...	MEKTELIQKAKLA...	Homo sapiens	2.200642	4.573817	4.794277
AKT1	P31749	V-akt murine thym...	MSDVAIVKEGWLH...	Homo sapiens	4.742235	5.0	3.61311
ADAM10	O14672	Disintegrin and me...	MVLLRLVLLLLSWA...	Homo sapiens	0.905751	0.670166	4.566774
BIN1	O75514	Box-dependent my...	MAEMGSKGVTAG...	Homo sapiens	4.193255	4.589923	4.468784
NCSTN	Q92542	Nicastrin; Essential ...	MATAGGGSGADP...	Homo sapiens	2.584858	0.28125	1.411382
NRGN	Q92686	Neurogranin (prote...	MDCCTENACSKP...	Homo sapiens	1.019197	4.181165	2.951829
GIG25	Q6NSC9	Serpin peptidase in...	MERMLPLLALGLL...	Homo sapiens	2.315754	1.121397	3.634819
SYP	P08247	Major synaptic vesi...	MLLLADMVNVNQ...	Homo sapiens	3.11418	1.395096	1.911957

Node Table | Edge Table | Network Table

- Subcellular localization scores (<https://compartments.jensenlab.org/>)
- TISSUES expression scores (<https://tissues.jensenlab.org/>)
- Drug target information (<https://pharos.nih.gov/>)



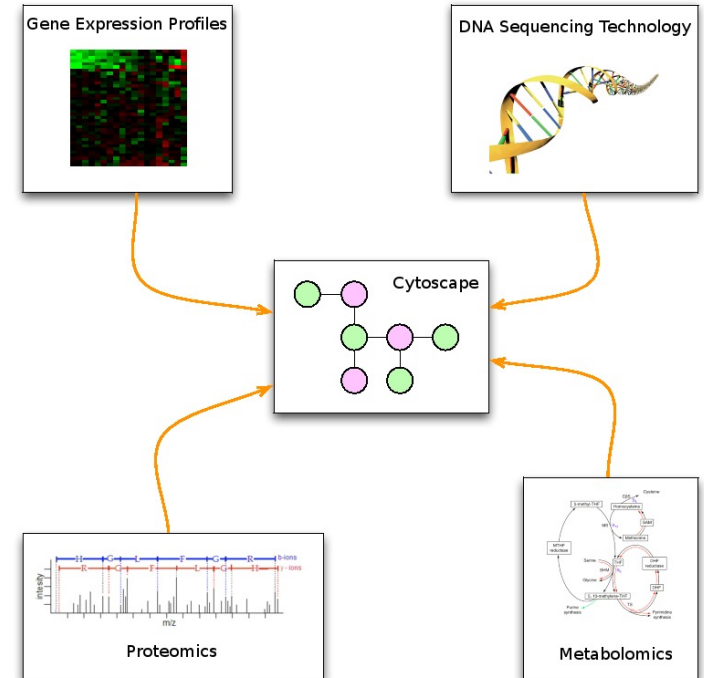
Pharos drug target information





Import attribute (table) data

- **Import own data from files**, e.g. Excel sheets, TSV, CSV
- Import data from public repositories, e.g. BioMart
- Import complex omics data via apps like Omics Visualizer
- Import data via automation from R or Python
- **Identifiers have to match!**





Know your identifiers

	A	B	C	D	G	J
1	UniProt	Gene name	Peptides	Sequence coverage [%]	5 min log ratio	10 min log ratio
2	Q99880	HIST1H2BL	5	35.7	-2.66	-2.66
3	Q8TER5	ARHGEF40	34	28.3	1.95	1.56
4	Q8IZ07	ANKRD13A	12	19.2	1.07	1.08
5	P62805	HIST1H4A	11	57.3	-2.31	-1.39
6	Q08380	LGALS3BP	14	28.2	-3.16	-2.98
7	O00750	PIK3C2B	35	24.2	2.21	2.31
8	O00443	PIK3C2A	29	17.8	1.13	1.26
9	Q9UJ41	RABGEF1	6	6.5	0.67	1.08
10	Q8TC07	TBC1D15	12	19.1	0.43	1.06

Table Panel

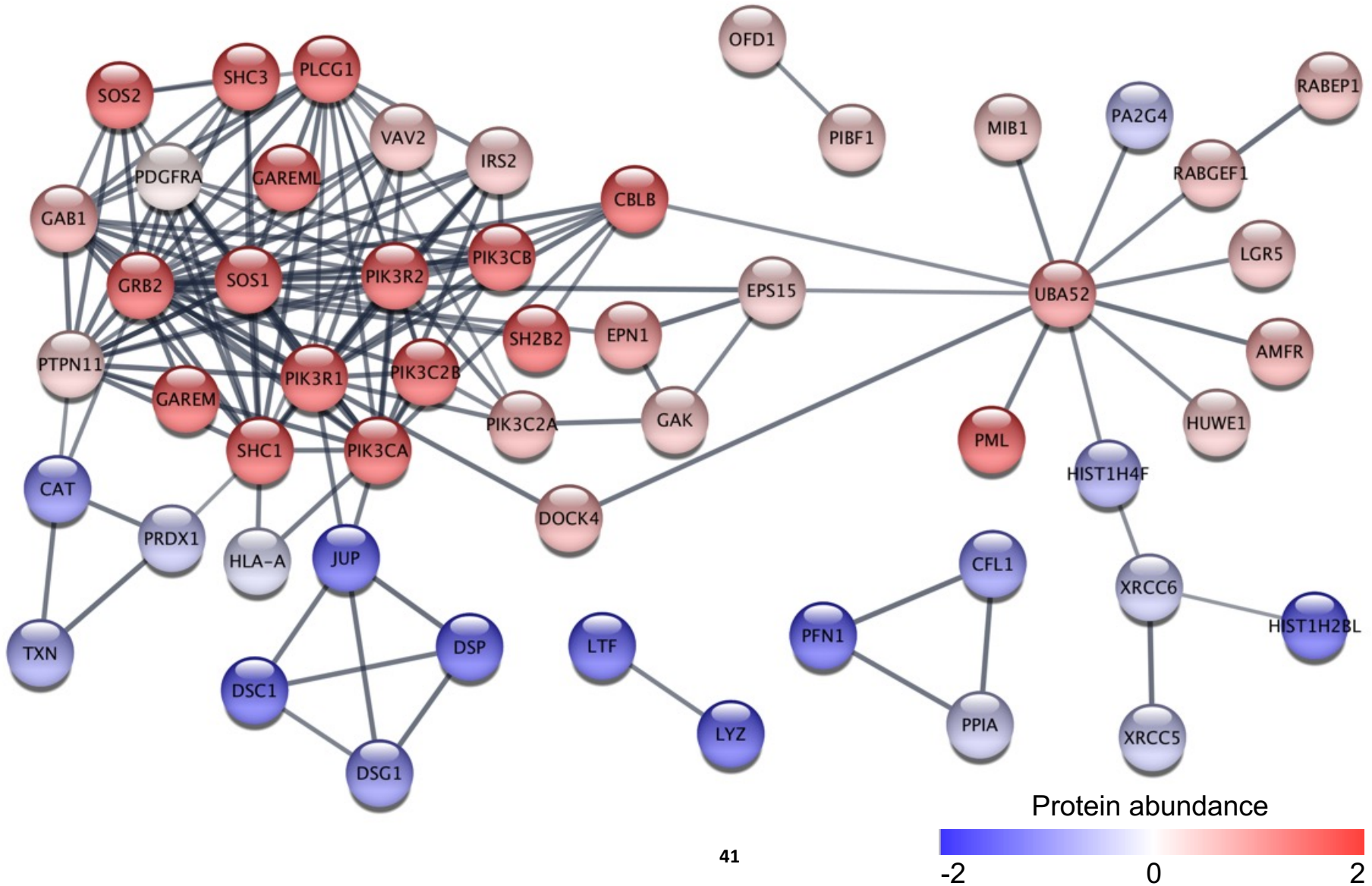
⚙️ 📄 + 🗑️ $f(x)$

🔍 query term	name ^	🔍 description	🔍 target family	🔍 tissue nervous system	🔍 5 min log ratio	🔍 10 min log ratio
O14976	GAK	cyclin G associated kinase	Kinase	5	0.38	0.94
P62993	GRB2	growth factor receptor-bound ...		5	2.39	2.52
Q99880	HIST1H2BL	histone cluster 1, H2bl		2	-2.66	-2.66
P62805	HIST1H4F	histone cluster 1, H4f		5	-2.31	-1.39
O95757	HSPA4L	heat shock 70kDa protein 4-like		3	-1.93	-1.12
Q7Z6Z7	HUWE1	HECT, UBA and WWE domain co...		5	0.1	0.82
Q9Y4H2	IRS2	insulin receptor substrate 2		4	0.28	0.97
P14923	JUP	junction plakoglobin		4	-2.59	-2.18
O75473	LGR5	leucine-rich repeat containing ...	GPCR	3	0.61	1.0
P02788	LTF	lactotransferrin		4	-3.26	-2.39
P61626	LYZ	lysozyme		3	-3.96	-2.88
Q86YT6	MIB1	mindbomb E3 ubiquitin protei...		5	-0.43	0.88
O75665	OFD1	oral-facial-digital syndrome 1		4	-0.52	0.85
P16234	PDGFRA	platelet-derived growth factor ...	Kinase	5	0.71	0.3

Node Table | Edge Table | Network Table



Expression data as node colors





Visualize data using styles

- Visual attributes
 - **Nodes:** fill color, border color, border width, size, shape, opacity, label, etc.
 - **Edges:** line style, line color, line width, line opacity, ending type, ending color, etc.
- Mapping types
 - **Continuous (numeric values)**
 - Expression values, edge interaction scores
 - **Discrete (categories)**
 - Type of interaction, protein family
 - **Pass-through (labels)**
- Pre-defined visual styles



Styles: User interface

Styles tab

Available styles

Default fill color: grey

Fill color mapping:
rainbow colors

Bypass mapping

Node tab

Edge tab

STRING style v1.5

Def.	Map.	Byp.	Property
			Border Paint
0.0			Border Width
			Fill Color
			Height
			Image/Chart 1
			Image/Chart 2
			Label
			Label Color
12			Label Font Size
			Shape
30.0			Size
255			Transparency
			Width

Lock node width and height

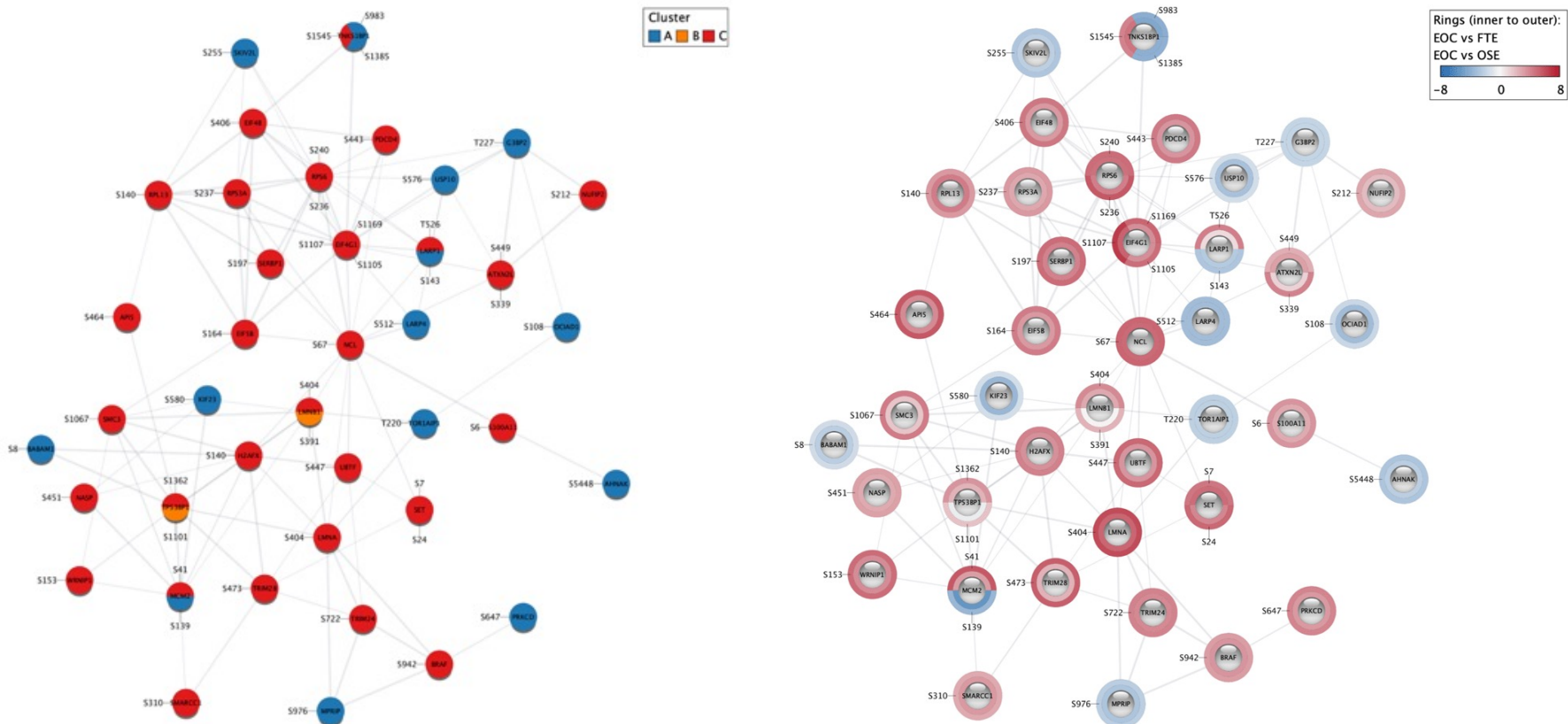
Node Edge Network



Omics Visualizer app

How to visualize multi-omics data, time series, or phospho-proteomics data, i.e. tables with multiple rows for each protein?

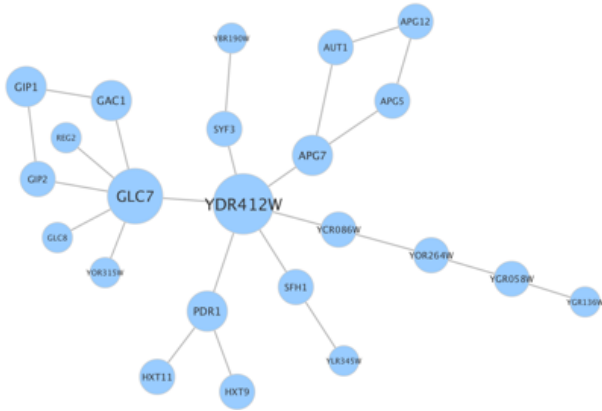
→ OV creates pies inside or donuts around the nodes.



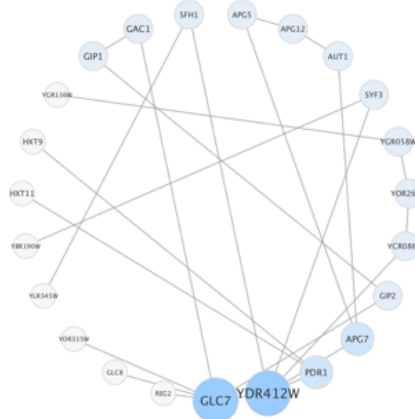


Layouts

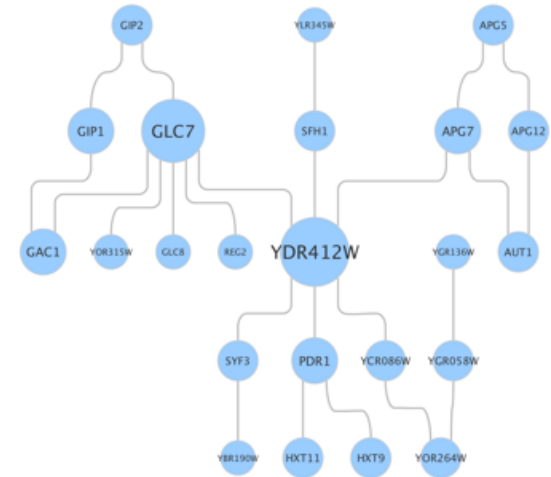
- Layouts determine the location of nodes and (sometimes) the paths of edges
- Use them to convey the relationships between nodes
- Recommended apps: yFiles Layouts, layoutSaver



Force-directed



Circular





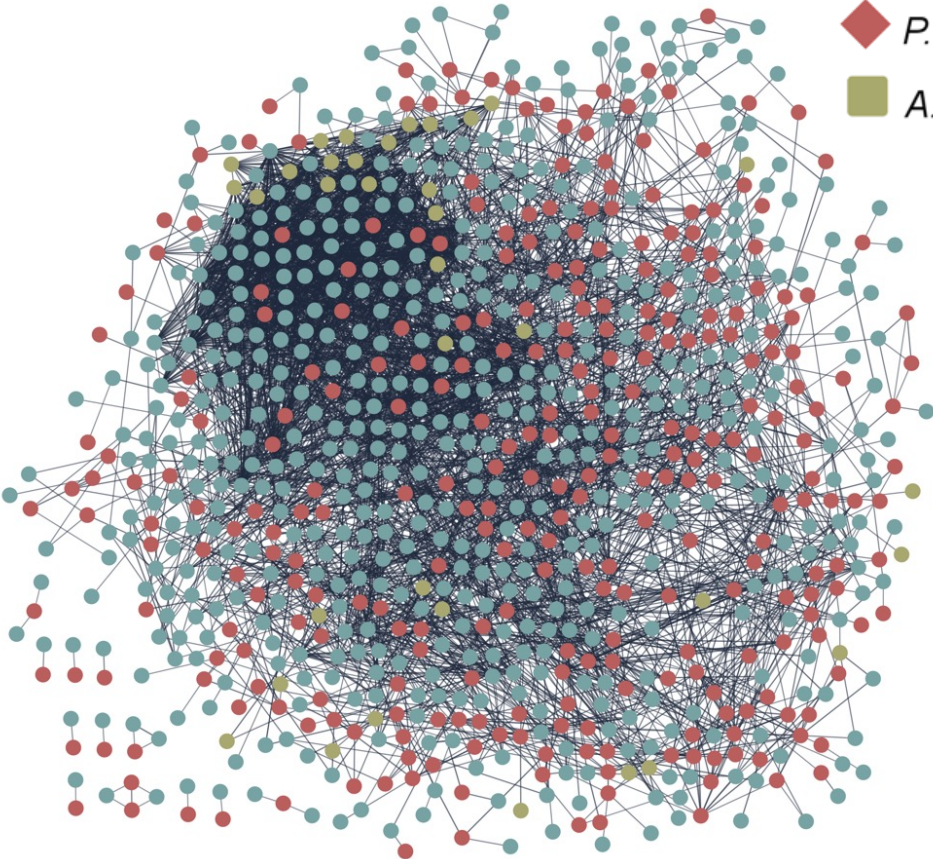
Hierarchical

- There is not one *correct* layout → Try different things!

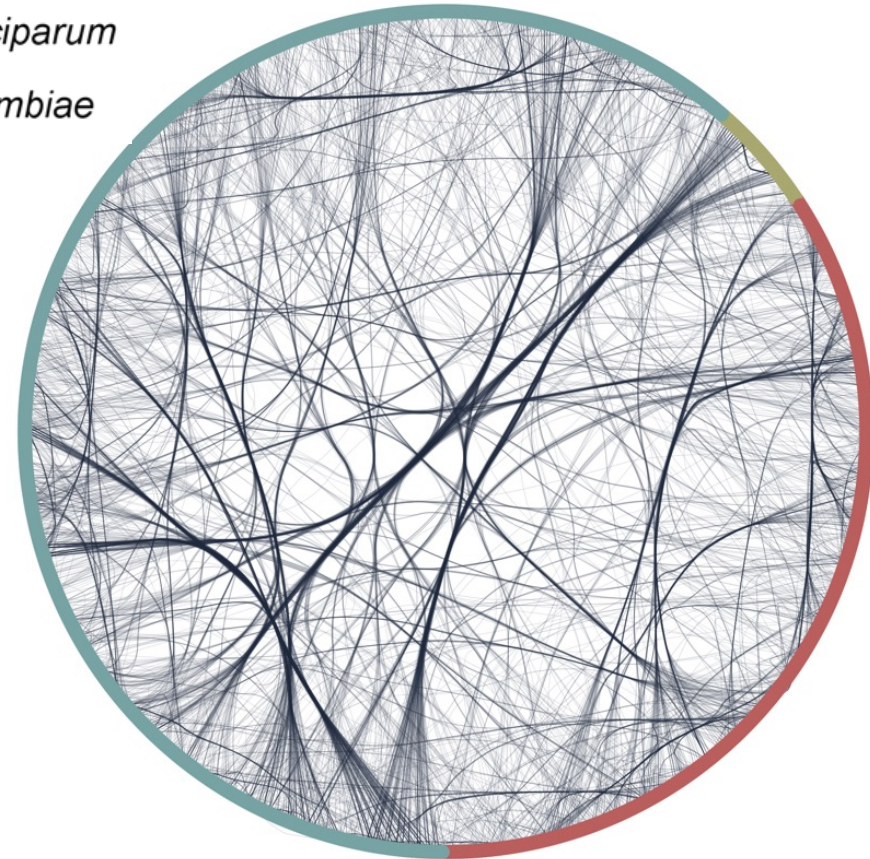


Layout examples

-  *H. sapiens*
-  *P. falciparum*
-  *A. gambiae*



Force-directed

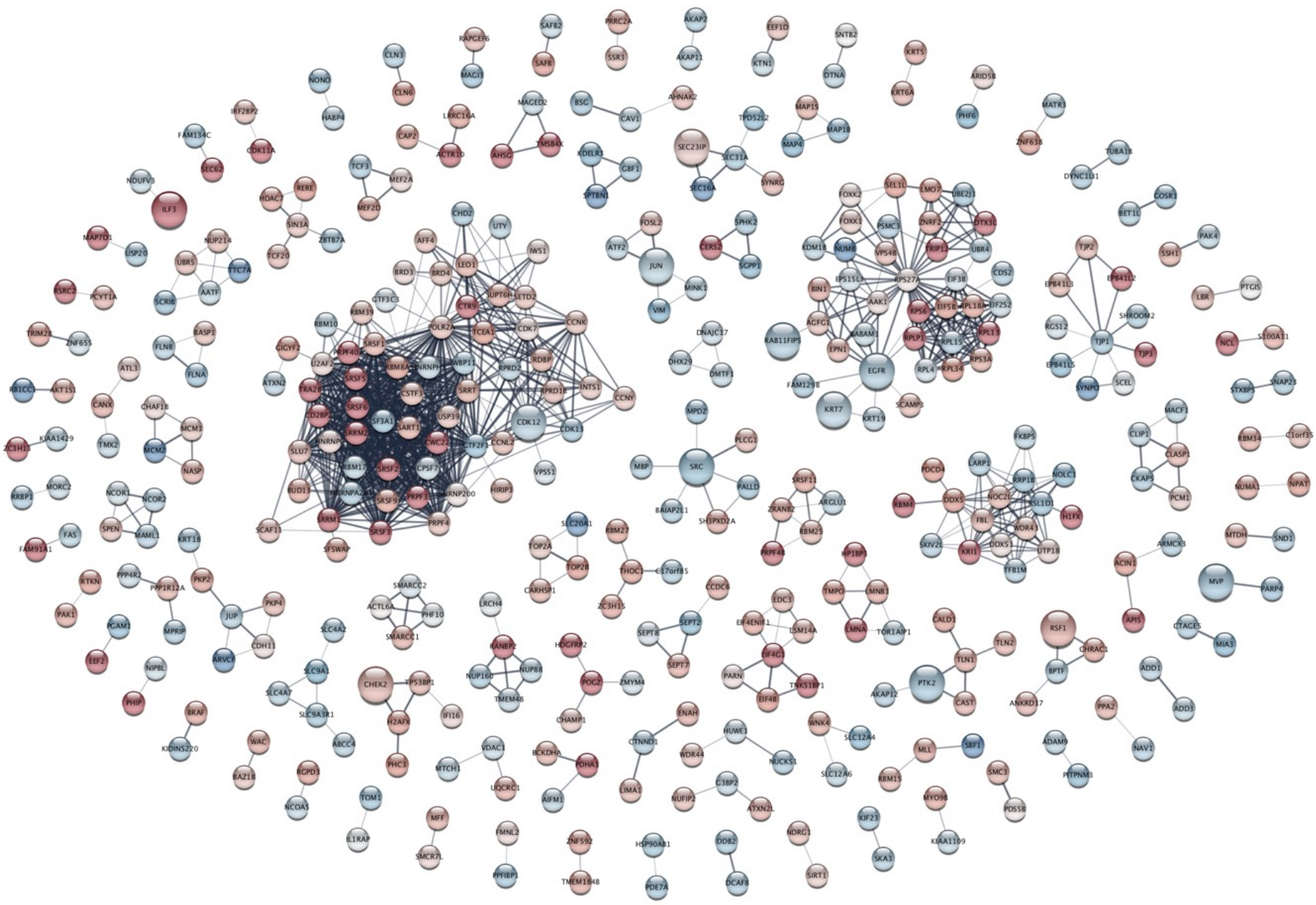


Circular



Network clustering

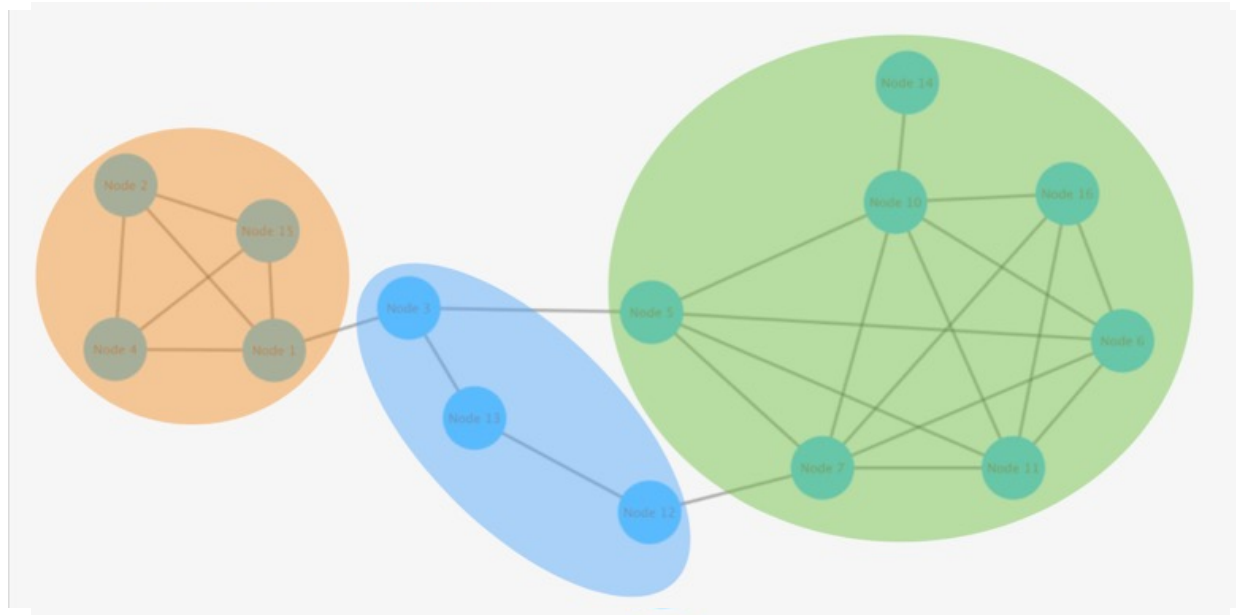
- Capture the structure of the network by identifying dense subgraphs, e.g.
 - Protein complexes in protein-protein interaction networks
 - Functional modules in functional association networks
 - Protein families in protein similarity networks
- Advantages for visualization → it can guide the layout of the network and be used for network simplification, e.g.
 - Represent each cluster as one node
 - Show only edges within clusters





Network clustering example

- Group nodes together based on a measure of similarity between the nodes, e.g. edges or edge weights
- MCL (Markov CLustering)
 - Fast algorithm
 - No need to specify number of clusters





Clustering in Cytoscape



clusterMaker2

Multi-algorithm clustering app for Cytoscape

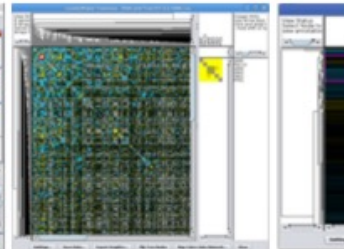
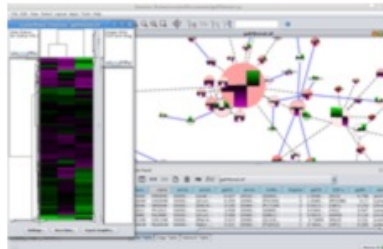
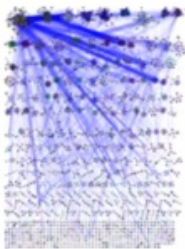
★★★★☆ (23) 89244 downloads | citations | discussions



Details

Release History

Categories: automation, clustering, data visualization, gene expression, grouping, heat map visualization, visualization



clusterMaker2 is the Cytoscape 3 version of the clusterMaker plugin. clusterMaker2 provides several clustering algorithms for clustering data within columns as well as clustering nodes within a network. This version also provides support for two new algorithms: Fuzzy C-Means and a new "Fuzzifier". In addition to providing clustering algorithms, clusterMaker2 provides heatmap visualization of both node data and edge data as well as the ability to create new networks based on the results of a clustering algorithm.

Current node attribute algorithms:

- Hierarchical
- K-Means
- K-Medoid

CYTOSCAPE 3

 Download

Version 1.3.1

Released 30 Oct 2018

Works with Cytoscape 3.6

Download Stats [Click here](#)


RESOURCES

 [Ask a question](#)

 [Search BioStars](#)

 [Website](#)

 [Tutorial](#)

 [Cite this App](#)

 [Code Repository](#)

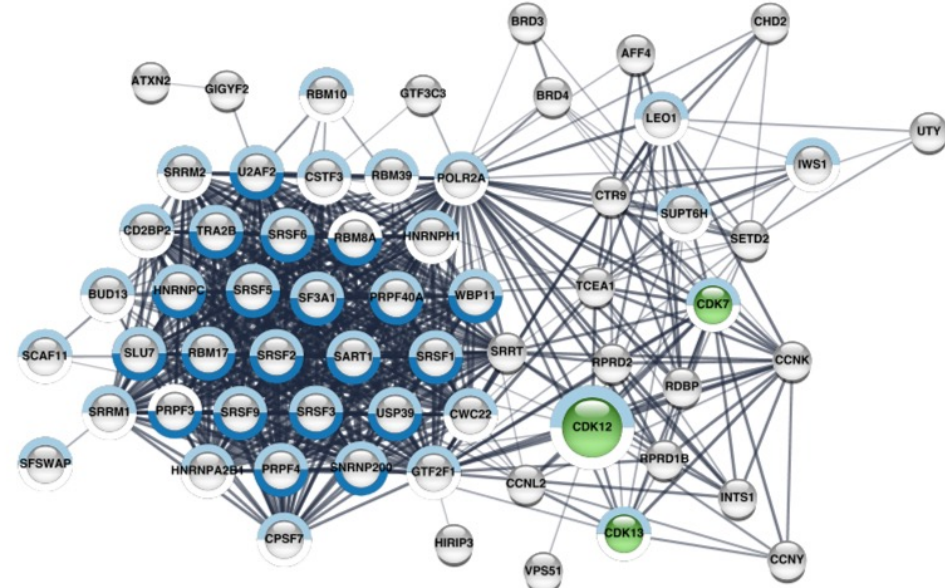
 [Automation Support](#)

 [E-mail](#)



stringApp functional enrichment

- Can be very **useful for visualization**
- Filter terms by category, remove redundant terms
- Visualize significant terms
- Many categories: Gene Ontology terms, Pathways, Diseases & phenotypes, Tissues & subcellular localization, Protein domains, Publications



Merged Network cluster 1

Table Panel

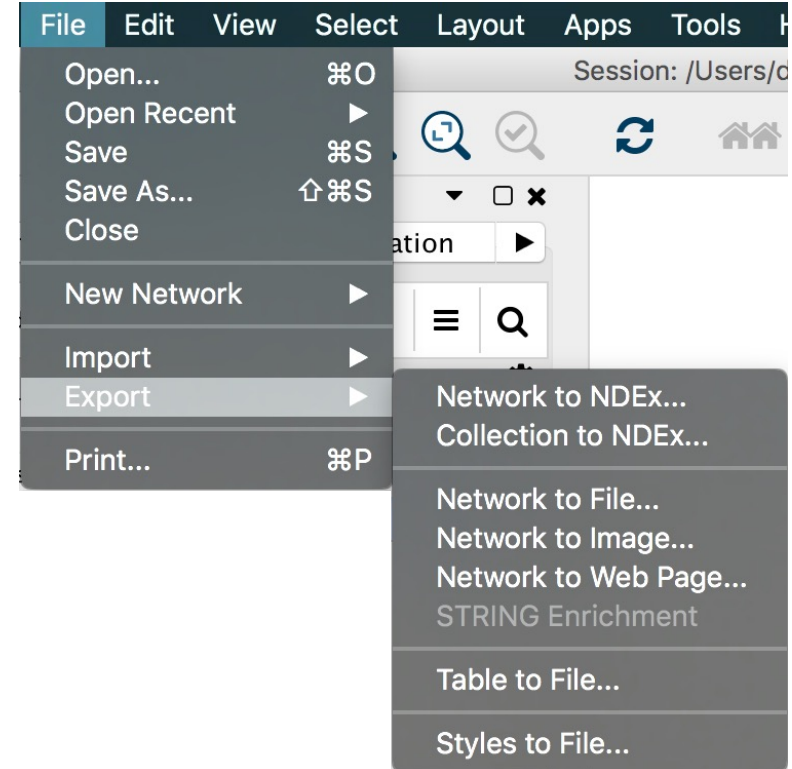
category	chart color	term name	description	FDR value	# genes	# background ...	genes
GO Process		GO.0006397	mRNA processing	2.33E-16	42	74	[CDK13, SF3A...
Reactome Pathw...		HSA-73857	RNA Polymerase ...	1.47E-8	29	66	[CDK13, SRSF9...
KEGG Pathways		map03040	Spliceosome	3.37E-8	20	29	[SF3A1, SRSF9...
UniProt Keywords		KW-0747	Spliceosome	2.62E-7	18	25	[SF3A1, SRSF1...
GO Component		GO.1902494	catalytic complex	2.17E-6	26	70	[CDK13, SF3A...
GO Process		GO.0006368	transcription elo...	3.41E-6	14	15	[CDK13, CDK7...
GO Process		GO.0043484	regulation of RN...	3.86E-6	18	30	[SF3A1, SRSF9...
GO Process		GO.0031123	RNA 3'-end proc...	3.35E-5	14	20	[SRSF9, SRSF6...
GO Process		GO.1903311	regulation of mR...	3.35E-5	20	46	[SF3A1, SRSF9...

Node Table | Edge Table | Network Table | STRING Enrichment



Save data

- **Cytoscape sessions** save everything (.cys files)
- Export networks in different formats
- Export node & edge tables as text files
- Publication quality graphics in several formats





Supporting lectures

The STRING database



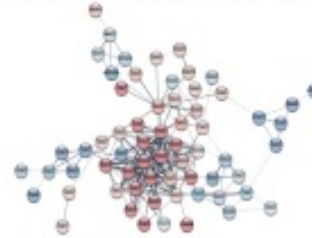
The Cytoscape platform



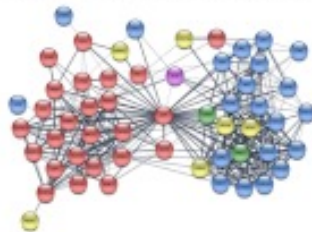
Cytoscape stringApp



Basic stringApp tutorial



The DISEASES database



Enrichment analysis





Tutorials & getting help

- STRING & stringApp:
 - YouTube videos: <https://www.youtube.com/c/LarsJuhlJensen>
 - Tutorials & exercises: <https://jensenlab.org/training/>
 - Automation repository:
https://github.com/scaramonche/EuBIC2020_Cytoscape
- Cytoscape
 - Tutorials: <https://github.com/cytoscape/cytoscape-tutorials/wiki>
 - YouTube videos:
<https://www.youtube.com/channel/UCv6auk9FK4NgXiXiqrDLccw>
 - Helpdesk mailing list: cytoscape-helpdesk@googlegroups.com
 - Publications using Cytoscape:
<https://cytoscape-publications.tumblr.com/>
 - Automation: <https://github.com/cytoscape/cytoscape-automation/wiki>

Questions?



Hands-on exercises

- Continue with stringApp exercises
 - Exercises 2 to 5: <https://jensenlab.org/training/stringapp/>
- Work with your own data
 - Follow stringApp exercises but adapt them to your own data
- Try out one of the Cytoscape tutorials
 - Basic data visualization
 - RNA-seq data analysis
 - Differentially Expressed Genes
 - Using WikiPathways App
 - And many more...

<https://github.com/cytoscape/cytoscape-tutorials/wiki>



stringApp exercise 2

In this exercise, we will work with the list of proteins associated with epithelial ovarian cancer (EOC) in the study by [Francavilla et al.](#) to perform typical network import and visualization tasks.

2.1 Protein network retrieval & layout

Question 1: *How many nodes and edges are there in the resulting network? Do the proteins all form a connected network? Why?*

Question 2: *Does any of the suggested layouts make patterns in the network easy to recognize? (Recommended: install the app **yFiles Layout Algorithms**)*

2.2 Discrete color mapping

Question 3&4: *How many of the proteins in the network are ion channels (IC) or GPCRs? How many kinases are in the network?*

2.3 Data import

Question 5: *Do you see the columns from the Excel table in the Node Table?*

2.4 Continuous color mapping

Question 6: *Are the up-regulated nodes grouped together?*



stringApp exercise 3

In this exercise, we will work with the list of differentially abundant proteins from the study by [Francavilla *et al.*](#) and perform typical network analysis tasks.

Prerequisites: *install the app* **ClusterMaker2**

3.1 Network clustering

Question 1: *How many clusters have at least 10 nodes?*

3.2 Subnetworks

Question 2: *How many nodes and edges are there in this cluster?*

Question 3: *How many edges does the resulting network contain and why are there now fewer edges?*

3.3 Functional enrichment

Question 4: *How many statistically significant terms are in the table? Which is the most significant term for each of the categories GO Biological Process, Reactome and KEGG Pathways?*

3.4 Functional enrichment extras

Question 5: *What is the title of the most recent publication?*