

Computational & Systems Biology



**Yazdan Asgari
2020**



Cytoscape

Session: /Applications/Cytoscape_v3.0.0/sampleData/galFiltered.cys

Control Panel

Network Visual Styles Filters

Current Visual Style: Sample for galFiltered

Add Visual Properties

Def. Map. Byp.

Column: gal1RGexp Mapping Type: Continuous Mapping

Current Mapping: A color scale from blue (-2.43) to red (2.06)

Remove Visual Mapping

Height: 18

Pm Label

Label Color: 18

Label Font Size: 18

Shape: Circle

Size: Cm

Column: BetweennessCentrality Mapping Type: Continuous Mapping

Current Mapping: A color scale from blue (0.0) to red (200.0)

Node Edge Network

galFiltered.sif

Table Panel

galFiltered.sif

name	Average...	Degree	Between...	gal4R...	gal80R...	gal80R...	COMM...
YDL194W	13.1169...	1	0.0	0.333	0.011348	0.449	SNF3
YDR277C	12.1209...	2	0.00806...	0.192	5.727E-4	0.448	MTH1
YBR043C	1.5	1	0.0	0.023	0.999999	0.0	YBR043C
YPR145W	9.79838...	1	0.0	-0.614	0.00118...	-0.232	ASN1
YER054C	8.81854...	2	0.04427...	0.206	0.00436...	0.247	GIP2
YDR045C	0.00116...	1	0.0022	0.016200	0.016200	0.016200	GIP2

Node Table Edge Table Network Table

Read Session File

Memory: OK

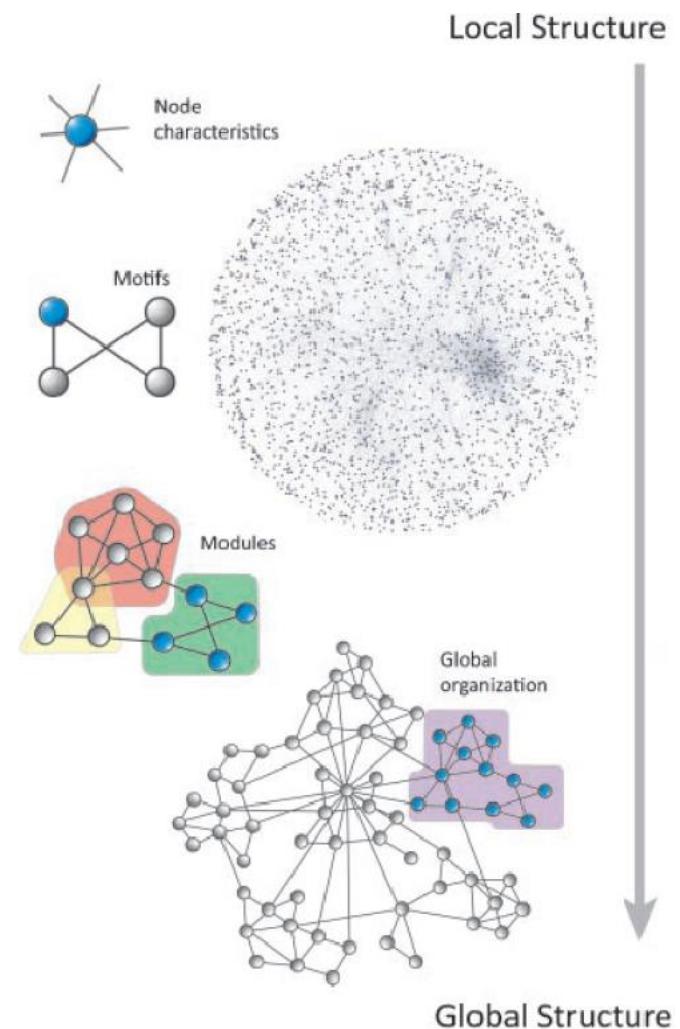
Open source
▪ Visualization
▪ Integration
▪ Analysis



Some Analysis with Cytoscape

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





Installation

- If you haven't already, please install Cytoscape 3.x
 - Core Apps
 - NetworkAnalyzer
 - Layouts
 - Apps:
 - Network Randomizer
 - cytoHubba
 - Bisogenet
 - GeneMANIA
 - CyKEGGParser
 - MetScape
 - ReactomeFIPPlugIn
 - WikiPathways
 - ClueGO
 - MCODE
 - clusterMaker2
 - Motif-Discovery



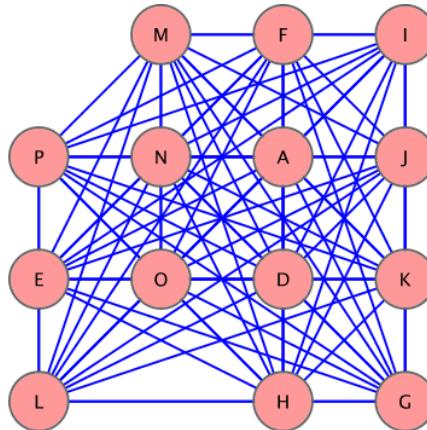
Introduction to Cytoscape

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



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	SWISS_Gene_Description		Architecture	Arch
1	gi 19923959	SDSL	11542	NP_644411.1	113675		SDSL		SP	Motif
2	gi 14602495	SEC23B	11543	NP_647914.1	103493	Q15437	Serine transport protein SEC23B	CEL	DDG	
3	gi 14602492	SCMH1	11540	AAH09752.1	22955	Q96CD1	SCMH1	SAM	Doma	
4	gi 14602492	EXOC2	11544	NP_060773.3	55770	Q96KP1	SECS like 1	IPT	Doma	
5	gi 1361625	SERPINB12	11548	NP_536722.1	89777	Q96PF3	Serpin B12	SERPIN	Doma	
6	gi 1798551	EIF2AK4	18447	NP_00101372	440275	609280	Similar to GCN2 eIF2alpha kinase	S_T_Y_Kinase	Doma	
7	gi 65287717	TYROB	4998	NP_003323.1	7305	604142	Q43914	DAP12	ITAM	Doma
8	gi 4507755	IL24	4995	NP_006841.1	11009	604136	Q13007	Interleukin 24	IL10	Doma
9	gi 5803086	ADAMTS13	4994	NP_620594.1	11093	604134	ADAMTS 13	TSP1	Doma	
10	gi 21265034	PIP5K1A	4470	AAC50911.1	8394	603275	Q99755	Phosphatidylinositol-4-phosphate 5	PIP5K	Doma
11	gi 1743873	SLC16A2	4992	NP_006508.1	6600	603275	Q99755	Surveillance	VAT	Doma
12	gi 1463386	RBBP8	4991	NP_144444.1	6820	604125	Surftransfere family 2B, member 1	LZ	Motif	
13	gi 1463386	SUJ1	4990	AAH30590.1	5932	604124	Q99708	CTP	PDGF	Doma
14	gi 21040399	DPYSL4	2102	NP_004460.1	2277	300091	Q43915	VEGF D		
15	gi 758378	TASP1	7463	NP_006417.1	10570	608407	Q14531	Collapsin response mediator protein 3		
16	gi 11321617	PRKC1	2105	NP_001731.3	55617	608270	Q9H6P5	Threonine aspartate 1	SP	Motif
17	gi 8923202	PRKCI	2105	NP_001731.3	55617	608270	Q9H6P5	Signal sequence receptor delta	ITAM	Doma
18	gi 5454090	PPP1R2P9	2101	NP_006271.1	6748	300090	P51571	X linked PEST containing transport	TM	Doma
19	gi 5730045	PRKCI	2106	NP_006508.1	6567	300095	P36021	Protein kinase C, iota type	UBC	Doma
20	gi 1968027	PRKCI	2106	NP_006508.1	64400	608483	Q9H8T0	Protein kinase C, iota type	S_T_kinase	Doma
21	gi 8255885	PRKCI	2105	NP_002731.3	5584	600539	P41743	Protein kinase C, iota type	RPAS	Doma
22	gi 5551612	PRKCI	6591	NP_002731.3	29925			TRNAA		
23	gi 176812	PRKCI	6593	NP_002731.3	80316					
24	gi 5026862	PRKCI	6595	NP_002735.1	90060					
25	gi 7661844	PRKCI	6594	NP_054727.1	28952					
26	gi 6005794	PRKCI	6596	NP_009144.1	11230					

Networks

e.g., PPIs or pathways

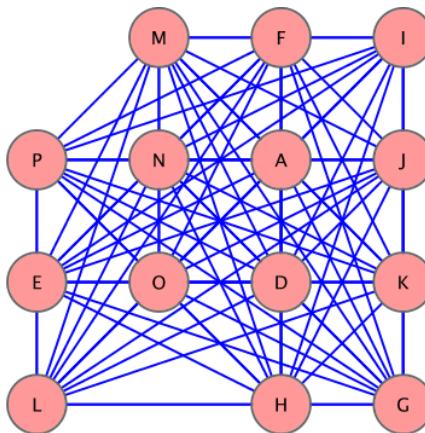
Tables

e.g., data or annotations



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	SWISS_Gene_Description		Architecture	Arch
1	gi 19923959	SDSL	11542	NP_604411.1	113675		SDSL		SP	Motif
2	gi 14602926	SEC23B	11543	NP_604791.1	103493	Q15437	Serine transport protein SEC23B	CEL	Dom	
3	gi 14602492	SCMH1	11540	AAH09752.1	22955	Q96CD1	SCMH1	SAM	Dom	
4	gi 14602492	EXOC2	11544	NP_060773.3	55770	Q96KP1	SECS like 1	IPT	Dom	
5	gi 1361625	SERPINB12	11548	NP_536722.1	89777	Q96P63	Serpin B12	SERPIN	Dom	
6	gi 1798551	EIF2AK4	18447	NP_00101372	440275	609280	Similar to GCN2 eIF2alpha kinase	S_T_Y_Kinase	Dom	
7	gi 65287717	TYROB3	4998	NP_003323.1	7305	604142	Q43914	DAP12	ITAM	Dom
8	gi 4507755	IL24	4995	NP_006841.1	11009	604136	Q13007	Interleukin 24	IL10	Dom
9	gi 5803086	ADAMTS13	4994	NP_620594.1	11093	604134	ADAMTS 13	TSP1	Dom	
10	gi 1265034	PIP5K1A	4470	AAC50911.1	8394	603275	Q99755	Phosphatidylinositol-4-phosphate 5 PIPKc	Dom	
11	gi 1743873	SLC16A2	4992	NP_00101372	60070	603275	Q99755	Slc16a2	VAT	Dom
12	gi 1463386	SUJ1T2B1	4991	NP_144444.1	6820	604125	Survivillin	SLC16A2	Dom	
13	gi 1463386	RBBP8	4990	AAH30590.1	5932	604124	Q99708	CTP	LZ	Motif
14	gi 21040399	FIGF	2102	NP_004460.1	2277	300091	Q43915	VEGF D	PDGF	Dom
15	gi 758378	DPYSL4	7463	NP_006417.1	10570	608407	Q14531	Collapsin response mediator protein 3		
16	gi 11321617	TASP1	7460	NP_060184.1	55617	608270	Q9H6P5	Threonine aspartate 1		
17	gi 8923202	SSR4	2101	NP_006271.1	6748	300090	P51571	Signal sequence receptor delta	SP	Motif
18	gi 5454090	SLC16A2	2106	NP_065083.1	6567	300095	P36021	X linked PEST containing transport	TM	Dom
19	gi 5730045	FTS	7467	NP_071921.1	64400	608483	Q9H8T0	FTS	UBC	Dom
20	gi 1968027	PRKC1	2105	NP_002731.3	5584	600539	P41743	Protein kinase C, iota type	S_T_Y_kinase	Dom
21	gi 8255885	PPP1R2P9	6591	NP_079482.1	29925			TPM 1 protein phosphatase inhibitor	RP48	
22	gi 55576812	PPA4	6593	NP_079486.1	80316			JM11 protein	CC	Motif
23	gi 1526862	CD22	6595	NP_206375.1	90060			JM1 protein	CC	Motif
24	gi 7661844	CCDC22	6594	NP_054727.1	28952			JM4 protein	TM	Dom
25	gi 6005794	PRAF2	6596	NP_009144.1	11230					

Networks

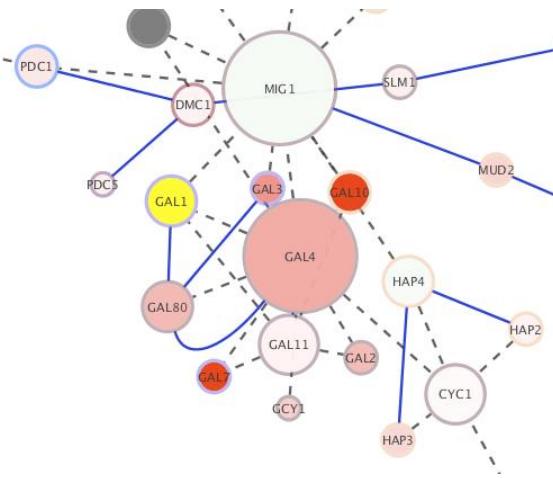
Tables

Visual Styles



Core Concepts

- Networks and Tables



	A	B	C	D	E	F	G	H	I	J	
	GI_Number	Gene	HPRD_ID	REFSeq_ID	Entrez_ID	OMIM_ID	SWISS_Gene_Description	Architecture	Arch	0	
1	gi 19923959	SDSL	11542	NP_614411.1	113675		SDSL	SP	Motif		
2	gi 14602926	SEC23B	11543	NP_614791.1	103493	Q15437	Serine transport protein SEC23B	CEL	Dom		
3	gi 14602492	SCMH1	11540	AAH09752.1	22955	Q96GDI	SCMH1	SAM	Dom		
4	gi 14602492	EXOC2	11544	NP_060773.3	55770	Q96KPI	SECS like 1	IPT	Dom		
5	gi 1361625	SERPINB12	11548	NP_536722.1	89777	Q96PF3	Serpin B12	SERPIN	Dom		
6	gi 17998551	EIF2AK4	18447	NP_00101372	440275	609280	Similar to GCN2 eIF2alpha kinase	S_T_Y_Kinase	Dom		
7	gi 65287717	TYROB3	4995	NP_00323.1	7305	604142	DAP12	ITAM	Dom		
8	gi 4507755	IL24	4995	NP_006841.1	11009	604136	Q13007	Interleukin 24	IL10	Dom	
9	gi 5803086	ADAMTS13	4994	NP_620594.1	11093	604134	ADAMTS 13	TSP1	Dom		
10	gi 21265034	PIP5K1A	4470	AAC50911.1	8394	603275	Q99755	Phosphatidylinositol-4-phosphate 5	PIP5K	Dom	
11	gi 1743873	SLC16A2	4992	NP_00101372	6090	600452	059425	Surveillance	VAT	Dom	
12	gi 1463386	RBBP8	4991	NP_144441.1	6820	604125	Subunit	LZ	Motif		
13	gi 1463386	SUJ1	4991	NP_144441.1	5932	604124	Q99708	CTP	PDGF	Dom	
14	gi 21040399	DPYSL4	4990	AAH30590.1	2277	300091	043915	VEGF D			
15	gi 4758378	TASP1	2102	NP_004460.1	10570	608407	Q14531	Collapsin response mediator protein 3			
16	gi 11321617	PRKC1	7463	NP_006417.1	55617	608270	Q9H6P5	Threonine aspartate 1			
17	gi 8923202	PRKA	7460	NP_060184.1	6748	300090	P51571	Signal sequence receptor delta	SP	Motif	
18	gi 5454090	PRKCI	2101	NP_006271.1	6567	300095	P36021	X linked PEST containing transport	TM	Dom	
19	gi 5730045	PRKACB	2106	NP_065083.1	64400	608483	Q9H8T0	FTS	UBC	Dom	
20	gi 1968027	PRKACB	7467	NP_071921.1	600539	600539	P41743	Protein kinase C, iota type	S_T_Y_kinase	Dom	
21	gi 8255885	PRKCI	2105	NP_002731.3	5584				TRNA	Dom	
22	gi 55576812	PPP1R2P9	6593	NP_079486.1	29935				TRNA	Dom	
23	gi 55576812	PRPA4	6593	NP_079486.1	80316				TRNA	Dom	
24	gi 15268682	JM1	6595	NP_206375.1	90060				TRNA	Dom	
25	gi 7661844	JM1	6594	NP_054727.1	28952				TRNA	Dom	
26	gi 6005794	JM4	6596	NP_009144.1	11230				TRNA	Dom	

Networks

Tables

Visual Styles



Core Concepts

 cytoscape app store

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network generation
online data import
data visualization
graph analysis
integrated analysis
utility
clustering
ontology analysis
enrichment analysis
scripting

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PSICQUICUniversalClient

PSICQUIC Web Service Client for importing interactions from public



ClueGO

Creates and visualizes a functionally grouped network of

BiNGO

BiNGO

Calculates overrepresented GO terms in the network and display



DynNetwork

Visualize dynamic networks in Cytoscape 3.0

Top Voted Apps



ClueGO

Creates and visualizes a functionally grouped network of



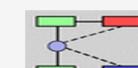
PathExplorer

Finds paths, filters them based on node and edge attributes and saves

GENEMANIA

GeneMANIA

Imports interaction networks from public databases from a list of



CytoKegg

Identify Kegg pathways associated to specific expression profiles.

Top Downloaded Apps



ClueGO

Creates and visualizes a functionally grouped network of



jActiveModules

Finds clusters where member nodes show significant changes in

GENEMANIA

GeneMANIA

Imports interaction networks from public databases from a list of



MCODE

Clusters a given network based on topology to find densely connected



Network
Randomizer

Network Randomizer

A tool for creating random networks and comparing them to the real ones

★★★★☆ (2) 4162 downloads | posts



Details Release History

Categories: centrality analysis, network analysis, network generation, network manipulation, randomization, random networks

Network Randomizer is a Cytoscape app for generating random networks, as well as randomizing the existing ones, by using multiple random network models. Further, it can process the statistical information gained from these networks in order to pinpoint their special, non-random characteristics.

It covers many popular random network models: Erdős–Rényi, Watts–Strogatz, Barabási–Albert, Community Affiliation Graph, edge shuffle, degree preserving edge shuffle, but it also features a new model which is based on the node multiplication.

The statistical module is based on the two-sample Kolmogorov-Smirnov test. It compares random and real networks finding the differences between them and thus providing insights into non-random processes upon which real networks are built.

Here you can find the Network Randomizer's manual: https://github.com/gabrielet/Network-Randomizer/blob/master/NetworkRandomizer_User_Manual.pdf

Network Randomizer's article available here: <https://f1000research.com/articles/5-2524/v3>

Authors:

- Gabriele Tosadori (Center for Biomedical Computing (CBMC), Verona University)
- Ivan Bestvina (Faculty of Electrical Engineering and Computing, University of Zagreb)

CYTOSCAPE 3

Upgrade

Version 1.1.3

Released 10 Nov 2017

Works with Cytoscape 3.2

Download Stats [Click here](#)

RESOURCES

Ask a question

Search posts

Code Repository



Wall of Apps 173 total

network
generation



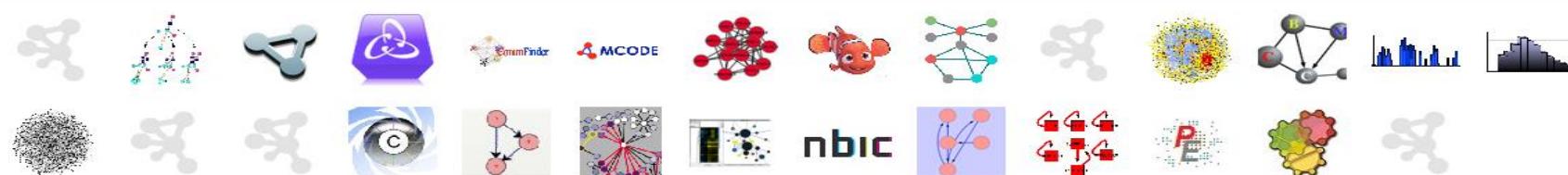
online data
import



data
visualization



graph
analysis





Loading Networks

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



Loading Networks

Cytoscape

File Edit View Select Layout Apps Tools Help

Recent Session
New
Open... ⌘O

Save ⌘S
Save As... ⌘⌘S

Import ► Network ► File... ⌘L
Export ► URL... ⌘⌘L
Load Data Table ► Public Databases... ⌘L
Merge Data Table...
Run...
Print Current Network... ⌘P

Session: New Session

Control Panel

Network

Table Panel

No Network

Node Table Edge Table Network Table

Read Session File

Memory: OK

This screenshot shows the Cytoscape application interface. The window title is 'Cytoscape'. The 'File' menu is open, with 'Import' selected. Under 'Import', there are several options: 'Network', 'File...', 'URL...', 'Public Databases...', 'Table', 'Vizmap File...', 'Ontology and Annotation...', and 'WikiPathways'. The 'Network' option is currently highlighted. Below the menu, a 'Table Panel' is visible, showing a message 'No Network'. At the bottom of the interface, there are status indicators: 'Read Session File' with a checkmark and 'Memory: OK'.



Loading Networks

Cytoscape Import Network From Table

Select a Network Collection

Network Collection Create new network collection

Mapping Column for New Network: shared name

Mapping Column for Existing Network: shared name

Interaction Definition

Source Interaction	Interaction Type	Target Interaction
Column 1	Column 3	Column 2

Columns in BLUE will be loaded as EDGE ATTRIBUTES.

Advanced

Show Text File Import Options

Preview

Excel™ Workbook Left Click: Enable/Disable Column, Right Click: Edit Column

Yeast Network Sheet 1

Column 1	Column 2	Column 3	Column 4	Column 5	Column 6
YKR026C	YGL122C	pp	false	abcd12345	1.2344543
YGR218W	YGL097W	pp	true	abcd12346	1.2344543
YGL097W	YOR204W	pp	true	abcd12347	1.2344543
YLR249W	YPR080W	pp	true	abcd12348	1.2344543
YLR249W	YBR118W	pp	true	abcd12349	1.2344543
YLR293C	YGL097W	pp	true	abcd12350	1.2344543
YMR146C	YDR429C	pp	true	abcd12351	1.2344543

OK Cancel

Read

OK



Loading Networks

Cytoscape File Edit View Select Layout Apps Tools Help

Session: New Session

Control Panel

Network

Network | No... | Ed...

Yeast Network Sheet 1
Yeast Network Sheet 33... 36...

Yeast Network Sheet 1

Table Panel

Yeast Network Sheet 1

shared...	name	isExclu...

Node Table Edge Table Network Table

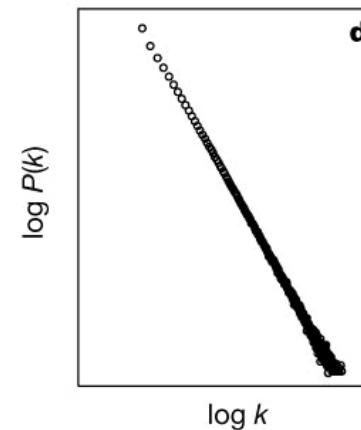
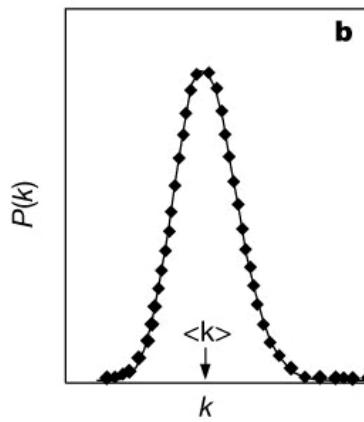
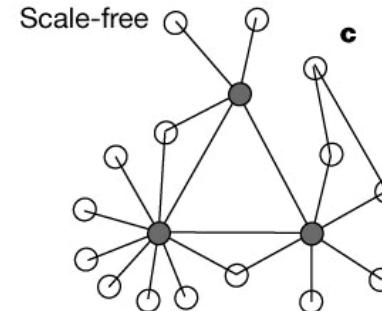
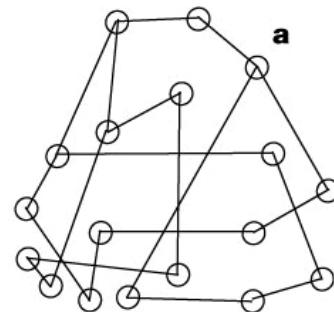
Memory: OK

✓ Loading network from table



Random networks

- Random networks
 - homogeneous, nodes have similar degrees, and not robust to arbitrary node failure





Some Analysis with Cytoscape

- Random networks
 - homogeneous, nodes have similar degrees, and not robust to arbitrary node failure
 - Algorithms exist to create random networks
 - Flat random network: Erdos-Renyi
 - Scale-free: Barabasi-Albert
 - Small-world (high clustering): Watts-Strogatz
 - Useful to compare your network vs. a random network



Visual Style Manager

- Click on Visual Styles tab



Visual Style Manager

Cytoscape File Edit View Select Layout Apps Tools Help

Session: /Applications/Cytoscape_v3.0.0/sampleData/galFiltered.cys

Control Panel

Network Visual Styles Filters

Current Visual Style
Sample for galFiltered

Add Visual Properties

Def. Map. Byp.

Border Paint
Border Width
Fill Color
Height
Label
Label Color
Label Font Size
Shape
Size
Transparency
Width

Node Edge Network

galFiltered.sif

Table Panel

galFiltered.sif

shared...	name	Average...	Cluster...	Closeness...	IsSingl...	Partne...	
YDL194W	YDL194W	13.1169...	0.0	0.07623...	false	0	0
YDR277C	YDR277C	12.1209...	0.0	0.08250...	false	0	0
YBR043C	YBR043C	1.5	0.0	0.66666...	false	0	0
YPR145W	YPR145W	9.79838...	0.0	0.10205...	false	0	0
YER054C	YER054C	8.81854...	0.0	0.11339...	false	0	0
YBR045C	YBR045C	9.64516...	0.0	0.10367...	false	0	0
YBL079W	YBL079W	2.0	0.0	0.5	false	0	0
YLR345W	YLR345W	9.11693...	0.0	0.10968...	false	0	0
YIL052C	YIL052C	0.14010...	0.0	0.10020...	false	0	0

Node Table Edge Table Network Table

Searching PSICQUIC Services Memory: OK



Visual Style Manager

Cytoscape File Edit View Select Layout Apps Tools Help

Session: /Applications/Cytoscape_v3.0.0/sampleData/galFiltered.cys

Control Panel

Network Visual Styles Filters

Current Visual Style
Sample for galFiltered

Add Visual Properties

Def. Map. Byp.

Border Paint

Border Width
2.0

Fill Color
Cm

Column gal1RGexp

Mapping Type Continuous Mapping

Current Mapping

-2.43 2.06

Remove Visual Mapping

Height

Pm Label

Label Color

Node Edge Network

galFiltered.sif

Table Panel

galFiltered.sif

shared...	name	Average...	Cluster...	Closeness...	IsSingl...	Partne...	...
YDL194W	YDL194W	13.1169...	0.0	0.07623...	false	0	0
YDR277C	YDR277C	12.1209...	0.0	0.08250...	false	0	0
YBR043C	YBR043C	1.5	0.0	0.66666...	false	0	0
YPR145W	YPR145W	9.79838...	0.0	0.10205...	false	0	0
YER054C	YER054C	8.81854...	0.0	0.11339...	false	0	0
YBR045C	YBR045C	9.64516...	0.0	0.10367...	false	0	0
YBL079W	YBL079W	2.0	0.0	0.5	false	0	0
YLR345W	YLR345W	9.11693...	0.0	0.10968...	false	0	0
YIL052C	YIL052C	0.14010	0.0	0.10020...	false	0	0

Node Table Edge Table Network Table

Searching PSICQUIC Services

Memory: OK



Visual Style Manager

Cytoscape File Edit View Select Layout Apps Tools Help

Session: /Applications/Cytoscape_v3.0.0/sampleData/galFiltered.cys

Control Panel

Network Visual Styles Filters

Current Visual Style
Sample for galFiltered

Add Visual Prop
Def. Map. Byp
2.0
Cm

Column
Mapping Type

Current Mapping
Label
Label Color

Node Edge Network

Continuous Mapping Editor for Node Fill Color

-2.4260 0.0060 2.0580
Min=-2.426 Max=2.058
gal1RGexp

Edit Handle Positions and Values
Selected Handle Position: 0 Min/Max Add Delete
Node Fill Color Change

Cancel OK

Node Table Edge Table Network Table

Searching PSICQUIC Services Memory: OK

galFiltered.sif

MUD2 SWI5 MFA2 BARI PDC1 STE12 ALPHA2 MCM1 MFA1 STE2 CLN3 PIS1 PMA1 TUF1 G1 SP150 CDP6

galFiltered.sif

Cluster...	Closeness...	IsSingl...	Partne...
	0.07623...	false	0
	0.08250...	false	0
	0.66666...	false	0
	0.10205...	false	0
	0.11339...	false	0
	0.10367...	false	0
	0.5	false	0
	0.10968...	false	0
	0.10020...	false	0



Visual Style Manager

Cytoscape File Edit View Select Layout Apps Tools Help

Session: /Applications/Cytoscape_v3.0.0/sampleData/galFiltered.cys

Control Panel

Network Visual Styles Filters

Current Visual Style

source Target	Sourced Target	Source → Target
Big Labels	default	Directed
Minimal	Nested Network Style	Ripple
Sample1	Sample for galFiltered	Solid
source Target		
Universe		

Node Edge Network

Node Table Edge Table Network Table

Memory: OK

galFiltered.sif

id...	name	Average...	Cluster...	Closeness...	IsSingl...	Partne...	...
W	YDL194W	13.1169...	0.0	0.07623...	false	0	0
C	YDR277C	12.1209...	0.0	0.08250...	false	0	0
YBR043C	YBR043C	1.5	0.0	0.66666...	false	0	0
YPR145W	YPR145W	9.79838...	0.0	0.10205...	false	0	0
YER054C	YER054C	8.81854...	0.0	0.11339...	false	0	0
YBR045C	YBR045C	9.64516...	0.0	0.10367...	false	0	0
YBL079W	YBL079W	2.0	0.0	0.5	false	0	0
YLR345W	YLR345W	9.11693...	0.0	0.10968...	false	0	0
YIL052C	YIL052C	0.1010...	0.0	0.10020...	false	0	0



Saving and Exporting

- Sessions save pretty much everything:
Networks, Properties, Visual styles, Screen sizes
- Export networks in different formats: SIF, GML,
XGMML, BioPAX, PSI-MI 1 & 2.5
- Publication quality graphics in several formats:
PDF, EPS, SVG, PNG, JPEG, and BMP



Some layouts in Cytoscape

- Use layouts to convey the relationships between the nodes
- Layout algorithms may need to be “tuned” to fit your network
 - Layouts→Settings... menu
- Lots of parameters to change layout algorithm behavior
- Can also consider laying out portions of your network

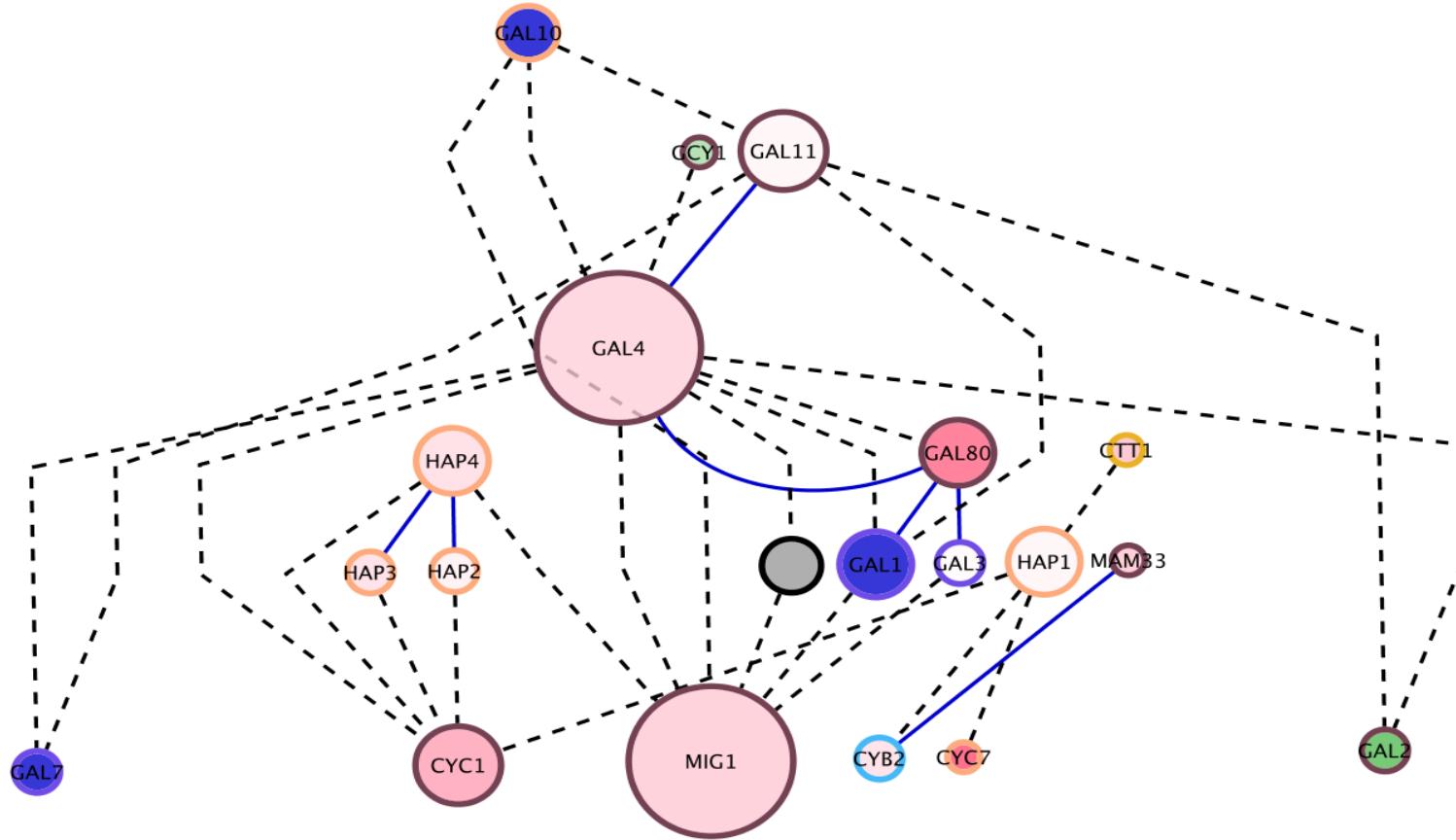


Some layouts in Cytoscape

- Layouts determine the location of nodes and (sometimes) the paths of edges
- Types:
 - Simple
 - Grid
 - Partitions
 - 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

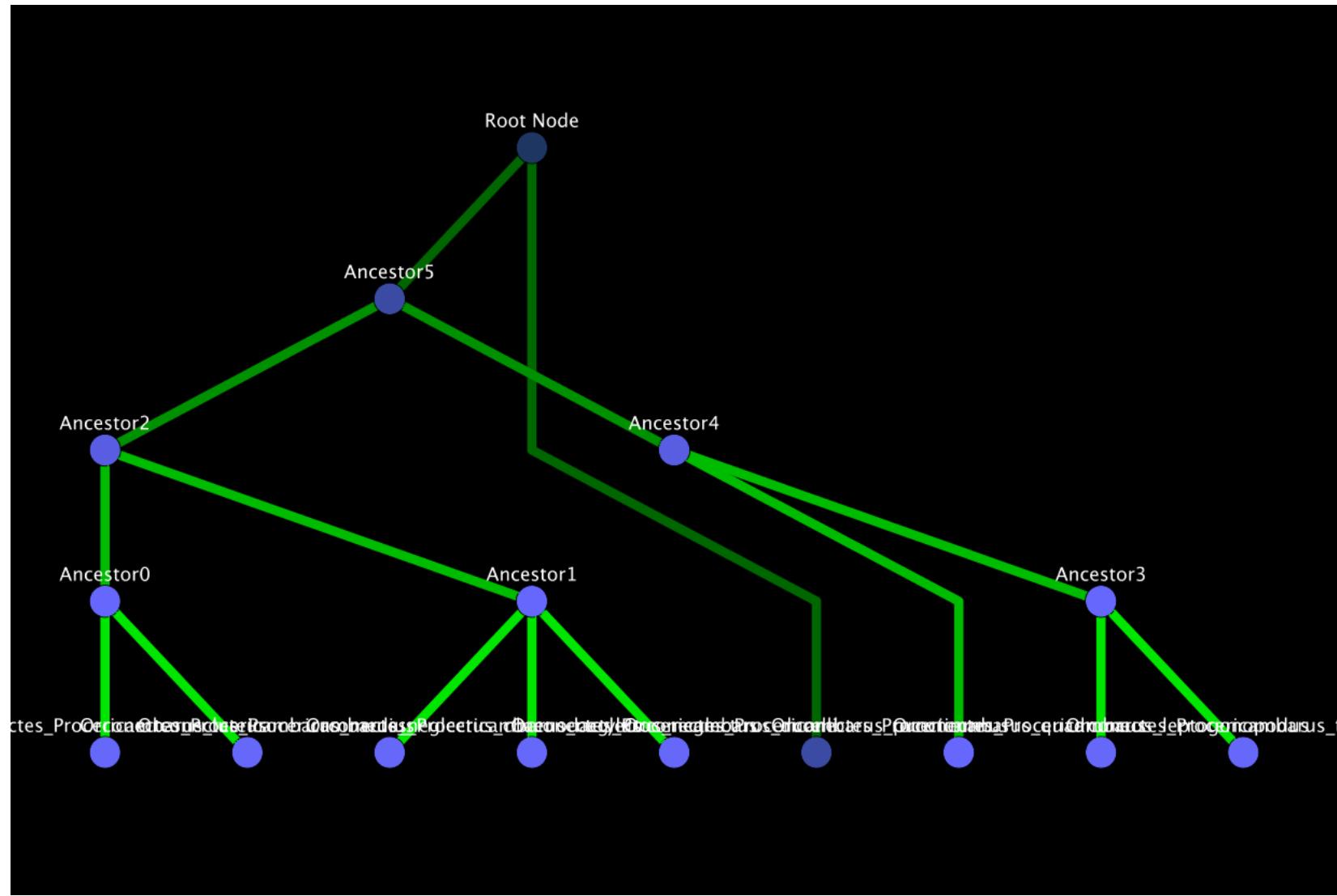


Some layouts in Cytoscape





Some layouts in Cytoscape



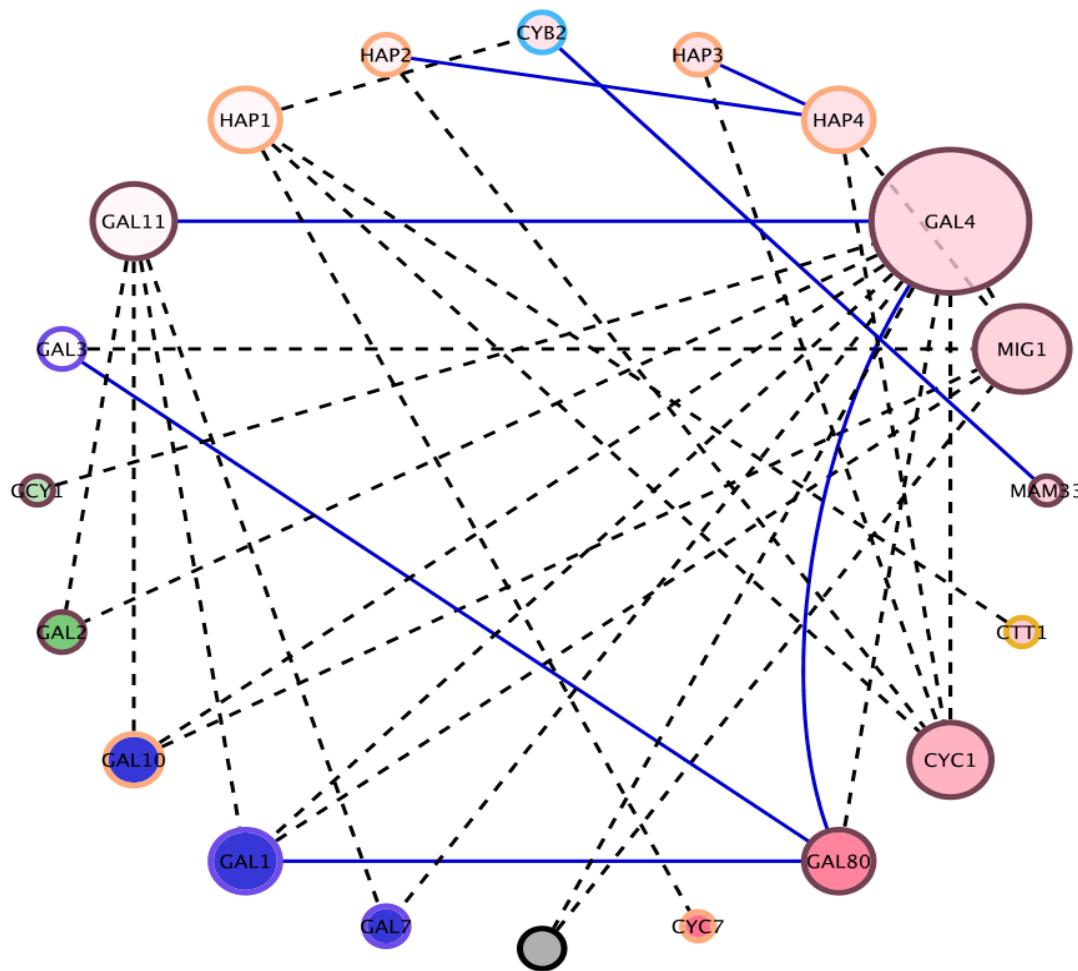


Some layouts in Cytoscape

- Layouts determine the location of nodes and (sometimes) the paths of edges
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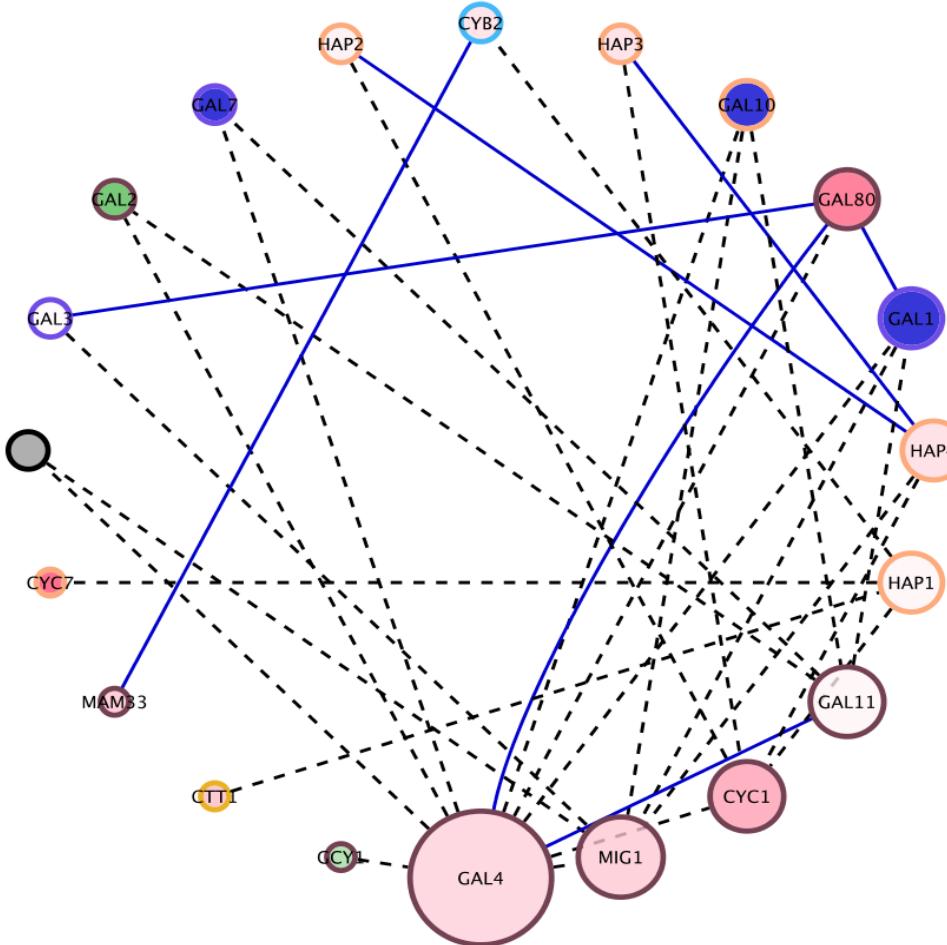


Some layouts in Cytoscape





Some layouts in Cytoscape



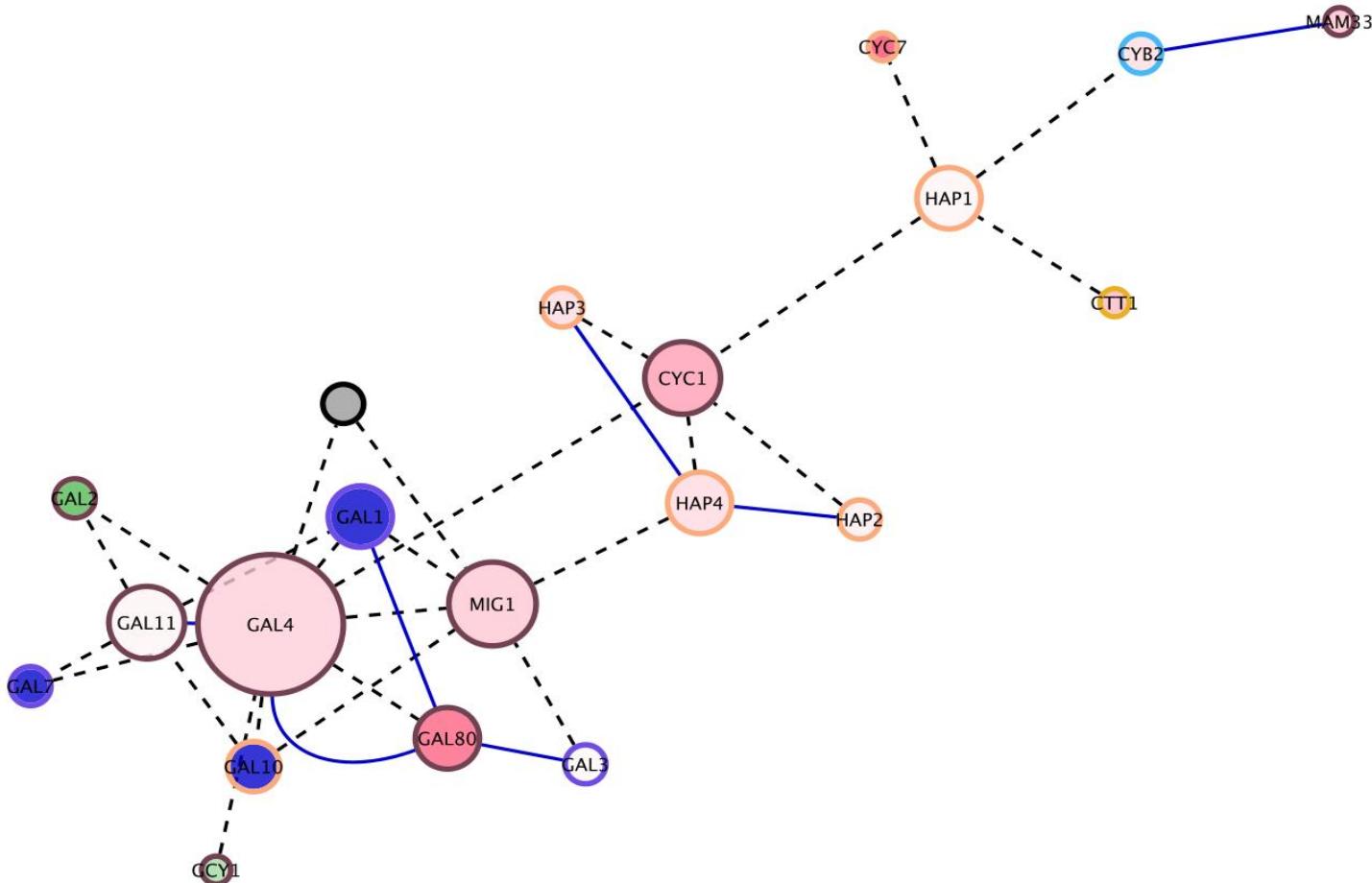


Some layouts in Cytoscape

- Types:
 - Force-Directed
 - simulate edges as springs
 - may be weighted or unweighted



Some layouts in Cytoscape



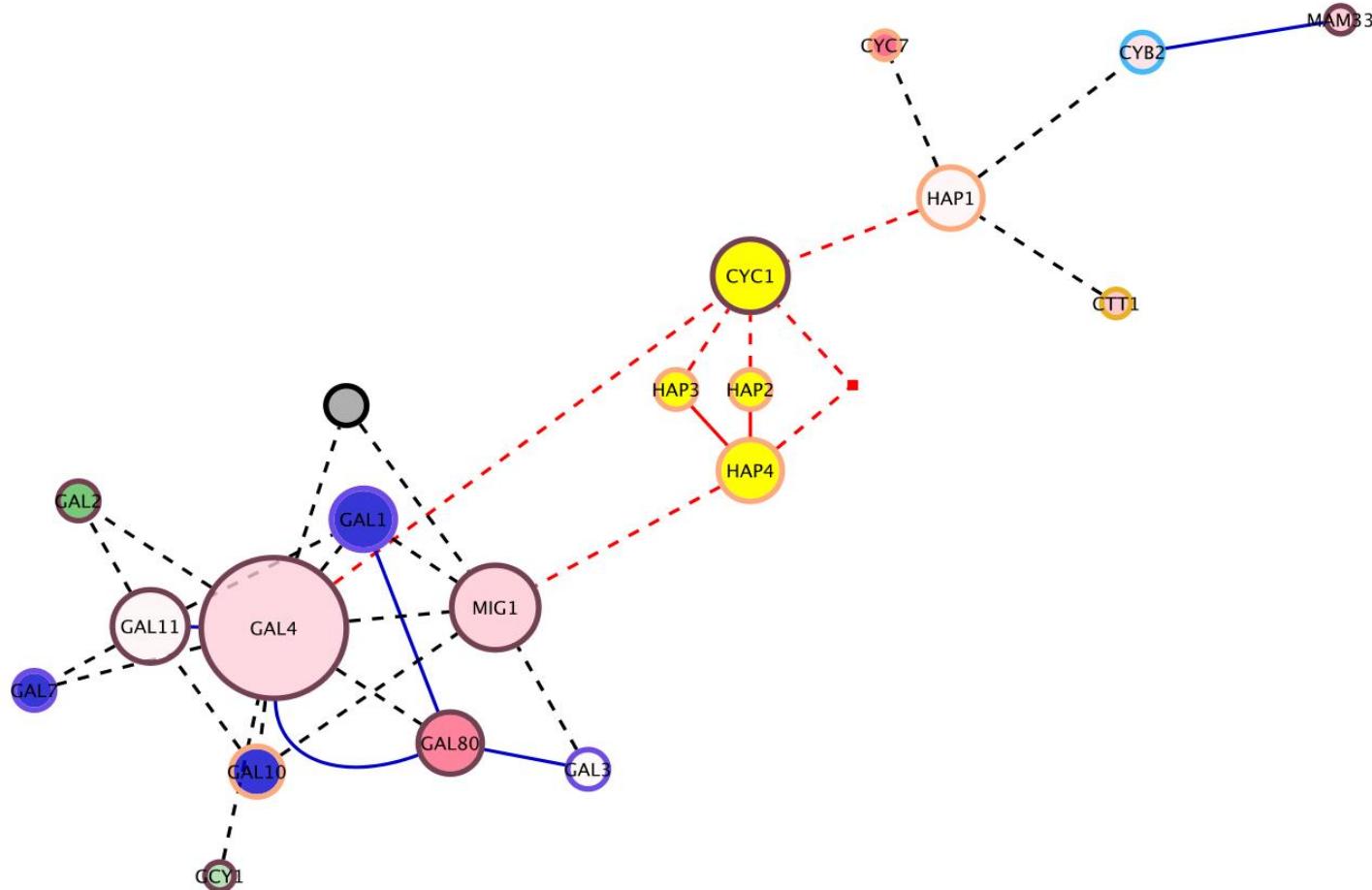


Some layouts in Cytoscape

- 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



Some layouts in Cytoscape



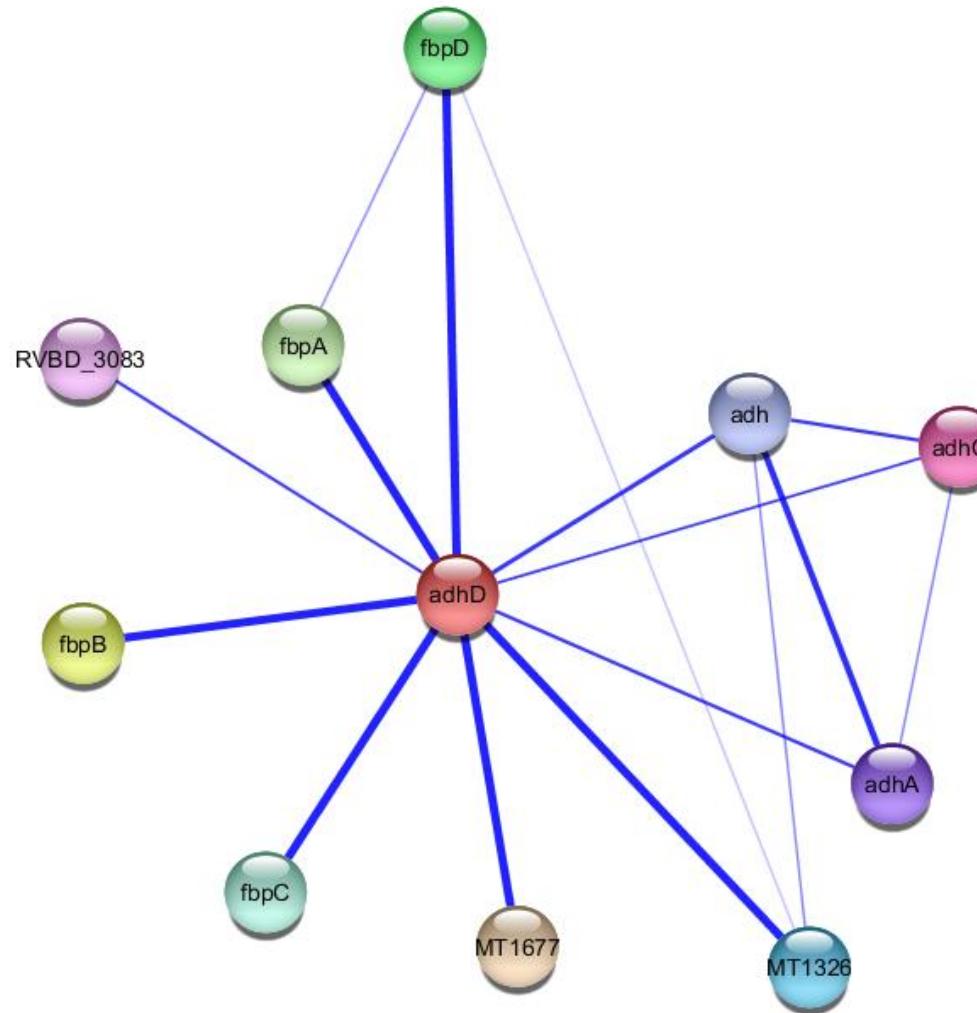


Some layouts in Cytoscape

- 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

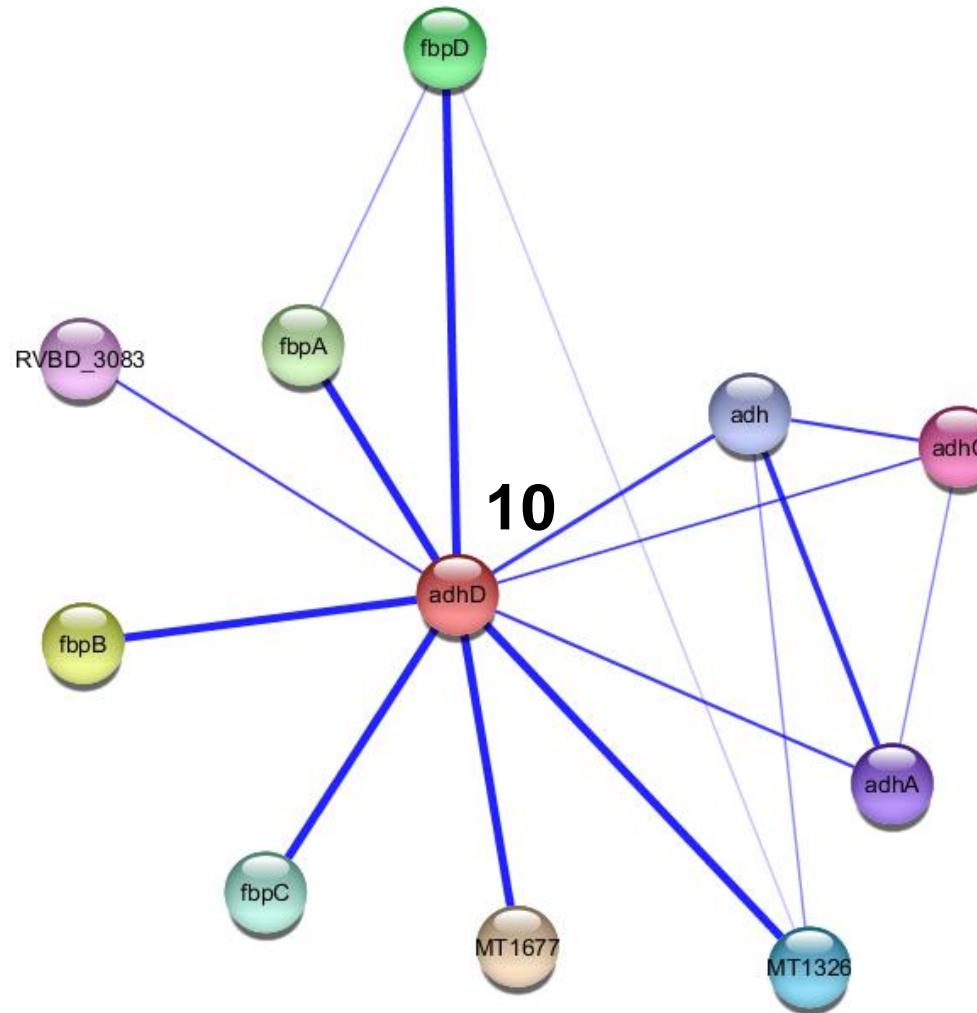


Some Analysis with Cytoscape - Degree



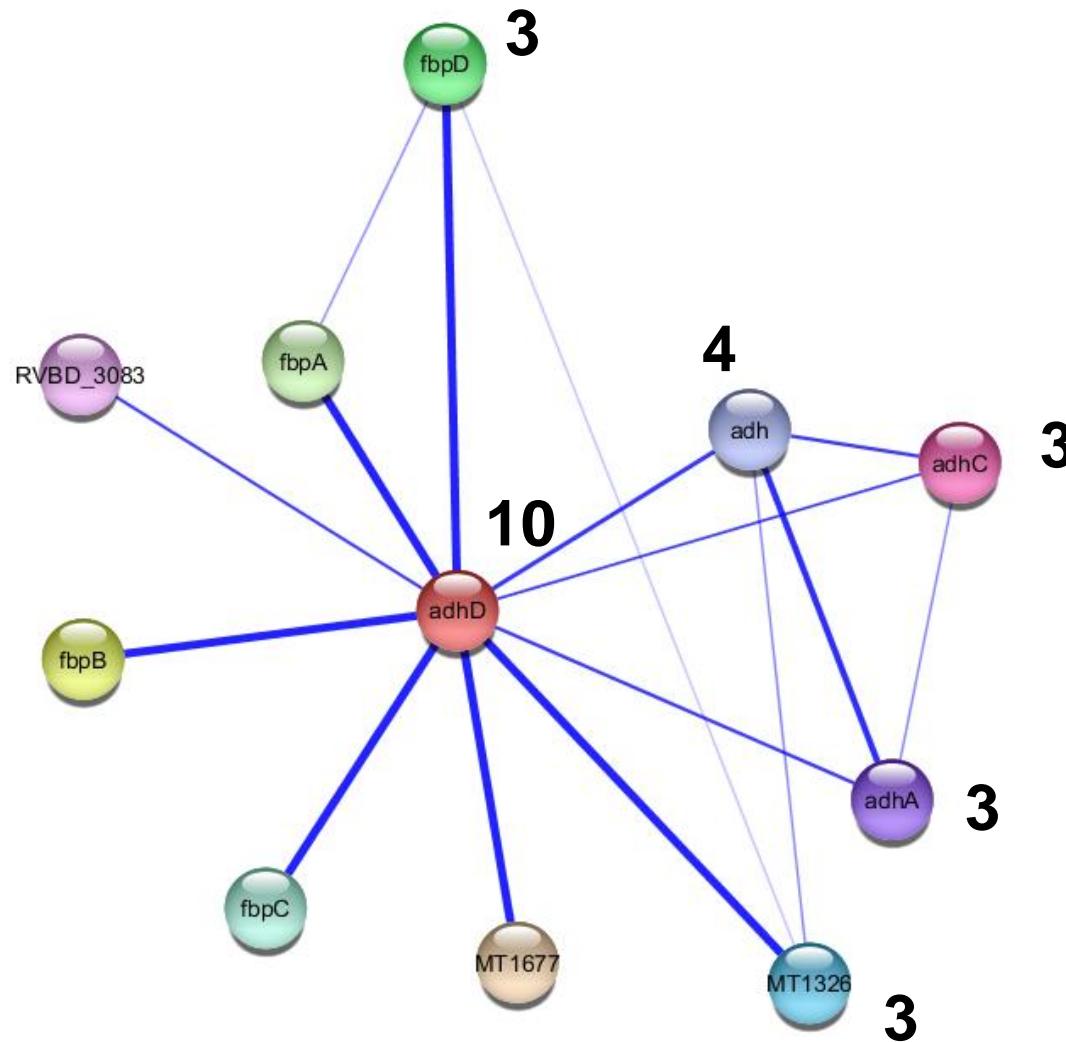


Some Analysis with Cytoscape - Degree





Some Analysis with Cytoscape - Degree



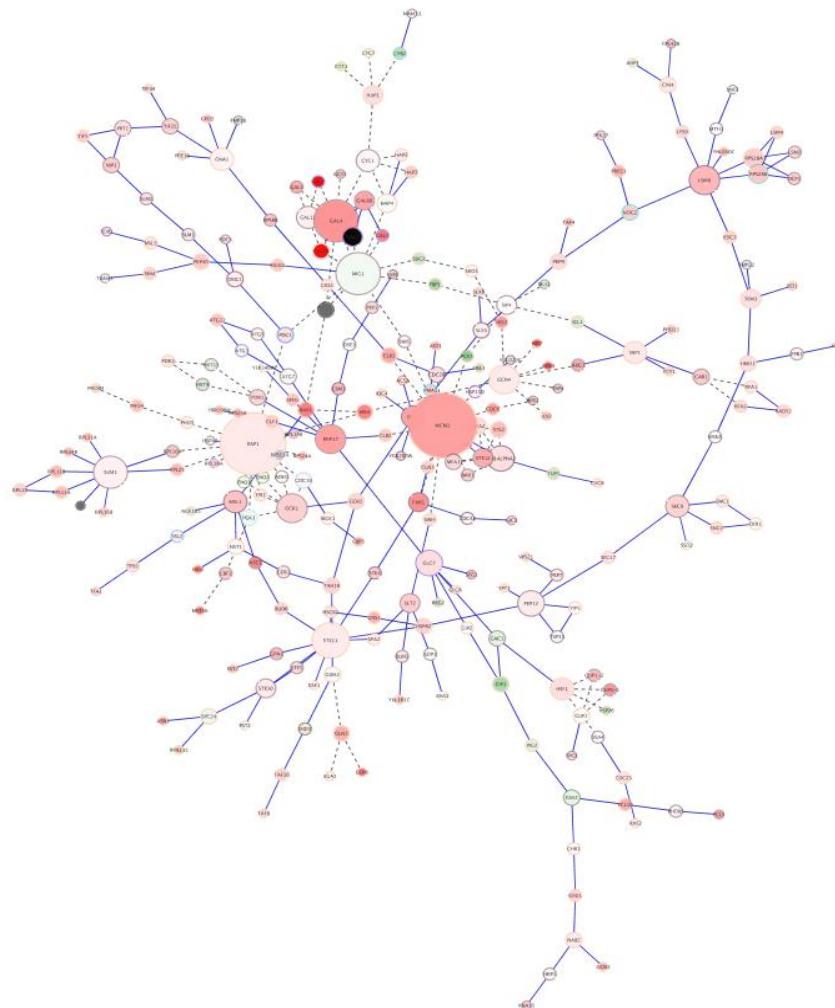
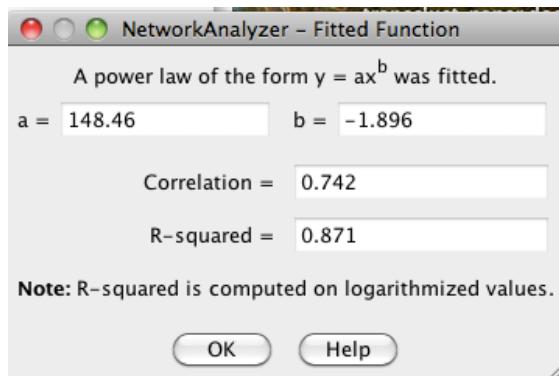
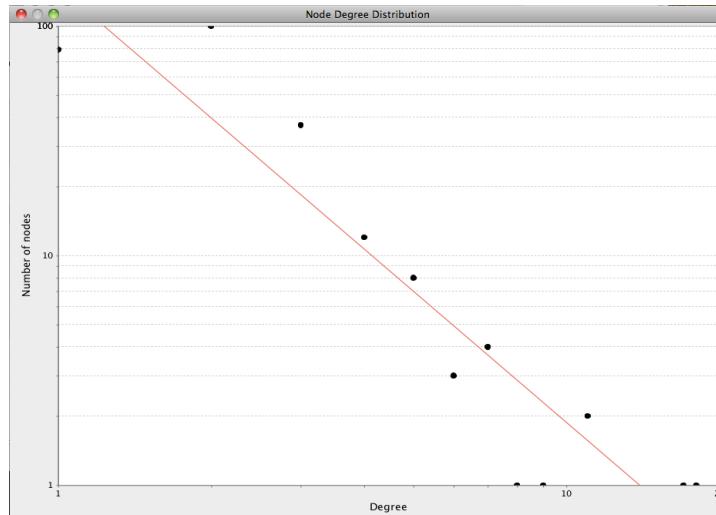


Some Analysis with Cytoscape - Scale-free

- Scale-free networks
 - Degree distribution follows power law:
$$P(k) \sim k^{-\gamma}$$
, where γ is a constant.
 - Result is that there are distinctive “hubs” (essential proteins?)
 - Overall, though, network is resilient to perturbation
 - Biological (and social) networks tend to be scale-free



Some Analysis with Cytoscape - Scale-free





Some Analysis with Cytoscape - Small-world

- 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)





Some Analysis with Cytoscape - Animation

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



Loading Tables

- Nodes and edges can have data associated with them
 - Gene expression data
 - Mass spectrometry data
 - Protein structure information
 - Gene Ontology terms, etc.
- Cytoscape supports multiple data types: Numbers, Text, Logical, Lists...

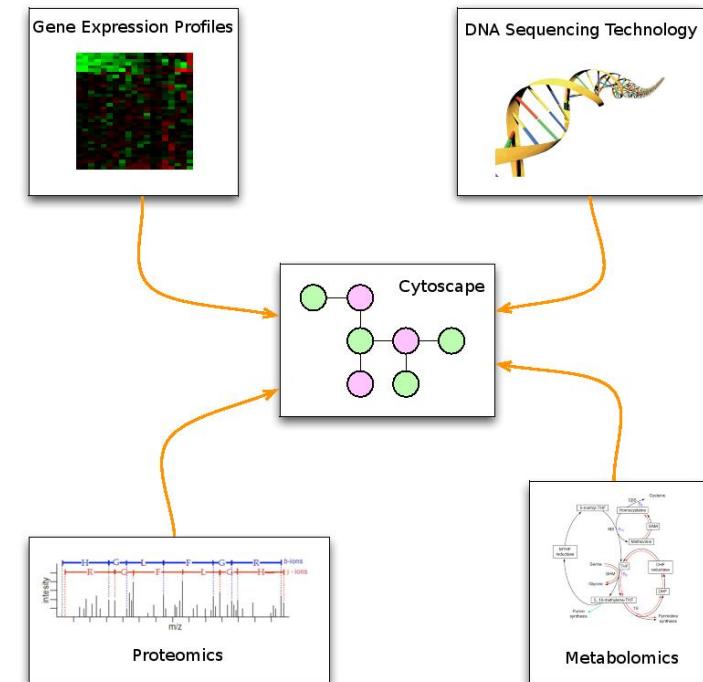




Table Loader

- Loading network data in Cytoscape:
 1. Load network and edge data from Excel spreadsheet
 2. Load attribute data from the same Excel spreadsheet
- Assign attribute data with the network data
- Column types guessed by Cytoscape often wrong



Table Loader

Import Network From Table

Preview

Click on a column to edit it.

Select All Select None

UniprotID1	Type of interaction	UniprotID2	EntrezID1	GeneSymbol1	EntrezID2	GeneSymbol2
Q9P2J5	hu-hu	UniprotID2	0	LARS	5859	QARS
Q9P2J5	hu-hu		0	LARS	9255	SCYE1
Q9P2J5	hu-hu		0	LARS	5917	RARS
Q9P2J5	hu-hu		0	LARS	4141	MARS
P14868	hu-hu		5	DARS	5859	QARS
P14868	hu-hu		5	DARS	3376	IARS
P14868	hu-hu		5	DARS	4141	MARS
P14868	hu-hu		5	DARS	5917	RARS
P14868	hu-hu		5	DARS	7965	JTV1
P14868	hu-hu		5	DARS	9255	SCYE1
P14868	hu-hu		5	DARS	51520	LARS
P14868	hu-hu	Q15046	1615	DARS	3735	KARS
P14868	hu-hu	O43324	1615	DARS	9521	EEF1E1
P14868	hu-hu	P07814	1615	DARS	2058	EPRS
P54136	hu-hu	Q12904	5917	RARS	9255	SCYE1
Q15046	hu-hu	P54136	3735	KARS	5917	RARS
Q15046	hu-hu	P47897	3735	KARS	5859	QARS
Q15046	hu-hu	Q12904	3735	KARS	9255	SCYE1
Q15046	hu-hu	P56192	3735	KARS	4141	MARS
Q15046	hu-hu	Q9P2J5	3735	KARS	51520	LARS
P47897	hu-hu	Q12904	5859	QARS	9255	SCYE1
P47897	hu-hu	P54136	5859	QARS	5917	RARS
P41252	hu-hu	Q13155	3376	IARS	7965	JTV1
P41252	hu-hu	Q15046	3376	IARS	3735	KARS
P41252	hu-hu	P56192	3376	IARS	4141	MARS
P41252	hu-hu	Q12904	3376	IARS	9255	SCYE1
P41252	hu-hu	Q9P2J5	3376	IARS	51520	LARS
P41252	hu-hu	P54136	3376	IARS	5917	RARS

List Delimiter: |

Advanced Options...

Cancel OK



Loading Tables

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



Loading Tables

Cytoscape

File Edit View Select Layout Apps Tools Help

Recent Session
New
Open...
Save
Save As...
Import
Export
Load Data Table
Merge Data Table...
Run...
Print Current Network...
⌘P

Session: New Session

Yeast Network Sheet 1

Network Table

Table File...
Vizmap File...
Ontology and Annotation...
WikiPathways

Yeast Network Sheet 1

Yeast Network Sheet 1

Table Panel

Yeast Network Sheet 1

shared... name isExclu...

Node Table Edge Table Network Table

Memory: OK

✓ Loading network from table

The screenshot shows the Cytoscape application interface. The main window displays a network graph titled "Yeast Network Sheet 1" with numerous nodes represented by blue rectangles and connecting edges. A context menu is open over the network, with the "Import" option highlighted. A submenu under "Import" is also open, showing options like "Table", "File...", and "URL...". Below the main window, a "Table Panel" is visible, showing a header row with columns for "shared...", "name", and "isExclu...". At the bottom of the screen, there is a status bar with the message "✓ Loading network from table" and a "Memory: OK" indicator.



Loading Tables

Cytoscape Import Column From Table

Target Network Data

Where to import Table Data To a Network Collection

Select a Network Collection

Network Collection Yeast Network Sheet 1

Key Column for Network: shared name

Importing Type

Import Data as: Node Table Columns

Advanced

Show Mapping Options Show Text File Import Options Case Sensitive

Annotation File to Table Mapping

Select the primary key column in table:

a b GENE

Preview

Text File Left Click: Enable/Disable Column, Right Click: Edit Column

newTable

GENE	COMMON	gal1RGexp	gal4RGexp	gal80Rexp
YHR051W	COX6	-0.034	0.111	-0.304
YHR124W	NDT80	-0.090	0.007	-0.348
YKL181W	PRS1	-0.167	-0.233	0.112
YGR072W	UPF3	0.245	-0.471	0.787
YHL020C	OPI1	0.174	-0.015	0.151
YGR145W	YGR145W	0.387	-0.577	-0.088
YGL041C	YGL041C	0.285	-0.086	0.103
YGR021W	SRM1	0.010	0.001	0.010

- - File Size: Unknown

Load OK Cancel Memory: OK



Loading Tables

Cytoscape File Edit View Select Layout Apps Tools Help

Session: New Session

Control Panel

Network

Network | No... | Ed...

Yeast Network Sheet 1
Yeast Network Sheet 33... 36...

Yeast Network Sheet 1

Table Panel

Yeast Network Sheet 1

shared...	name	isExclu...	COMM...	gal1R...	gal4R...	gal80R...	gal1R...	gal4R...

Node Table Edge Table Network Table

Memory: OK

Loading table data



Loading Tables

Cytoscape File Edit View Select Layout Apps Tools Help

Session: New Session

Control Panel

Network

Network No... Ed...

Yeast Network Sheet 1
Yeast Network Sheet 33... 36...

Yeast Network Sheet 1

Table Panel

Change Table Mode

Yeast Network Sheet 1

shared...	name	isExclu...	COMM...	gal1R...	gal4R...	gal80R...	gal1R...	gal4R...
YGL229C	YGL229C	false	SAP4	-0.521	0.171	-0.208	2.365E...	0.0208
YBR217W	YBR217W	false	APG12	0.088	-0.332	0.378	0.143	0.0110
YBR160W	YBR160W	false	CDC28	-0.016	-0.087	-0.405	0.7432	0.3210
YNL216W	YNL216W	false	RAP1	0.205	0.015	0.234	0.024692	0.9349
YLR249W	YLR249W	false	YEF3	-0.39	-0.394	-0.769	2.713E-8	0.0474
YGL202W	YGL202W	false	ARO8	-0.305	-0.286	-0.536	4.2677E...	4.2373
YML123C	YML123C	false	PHO84	0.283	-0.114	0.692	0.00151...	0.0194
YBR018C	YBR018C	false	GAL7	0.153	-1.995	3.126	7.8855E...	3.6284
YIL105C	YIL105C	false	YIL105C	0.106	0.023	0.107	6.0824E...	0.6670

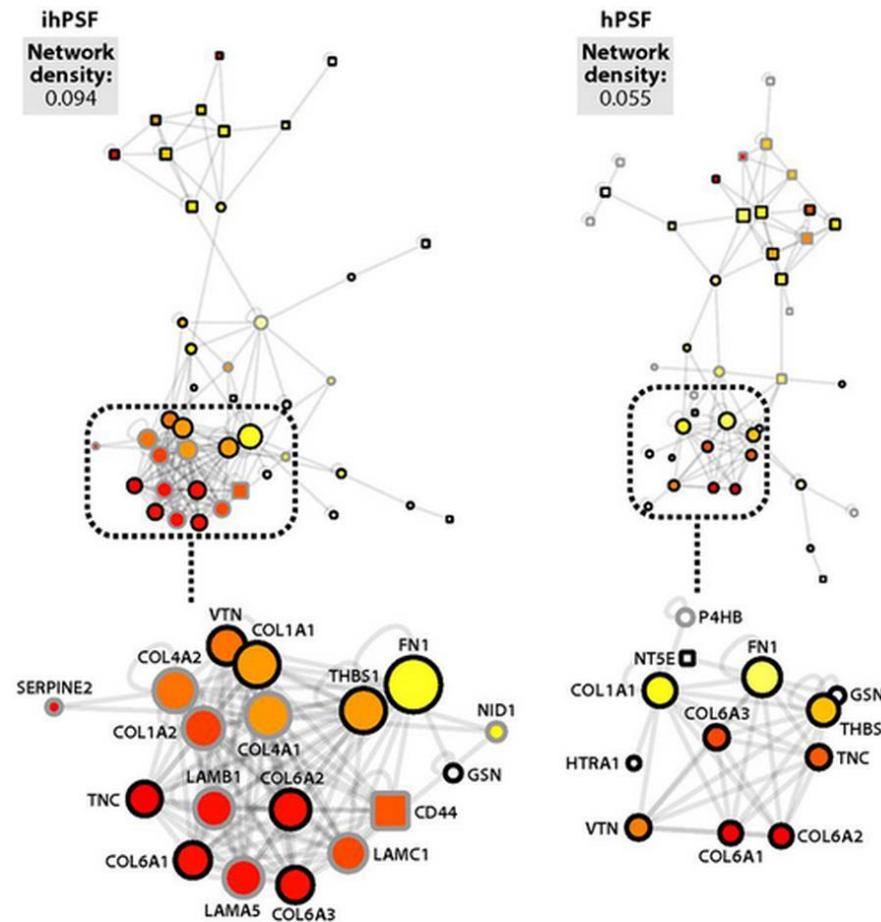
Node Table Edge Table Network Table

✓ Loading table data

Memory: OK



Some Papers

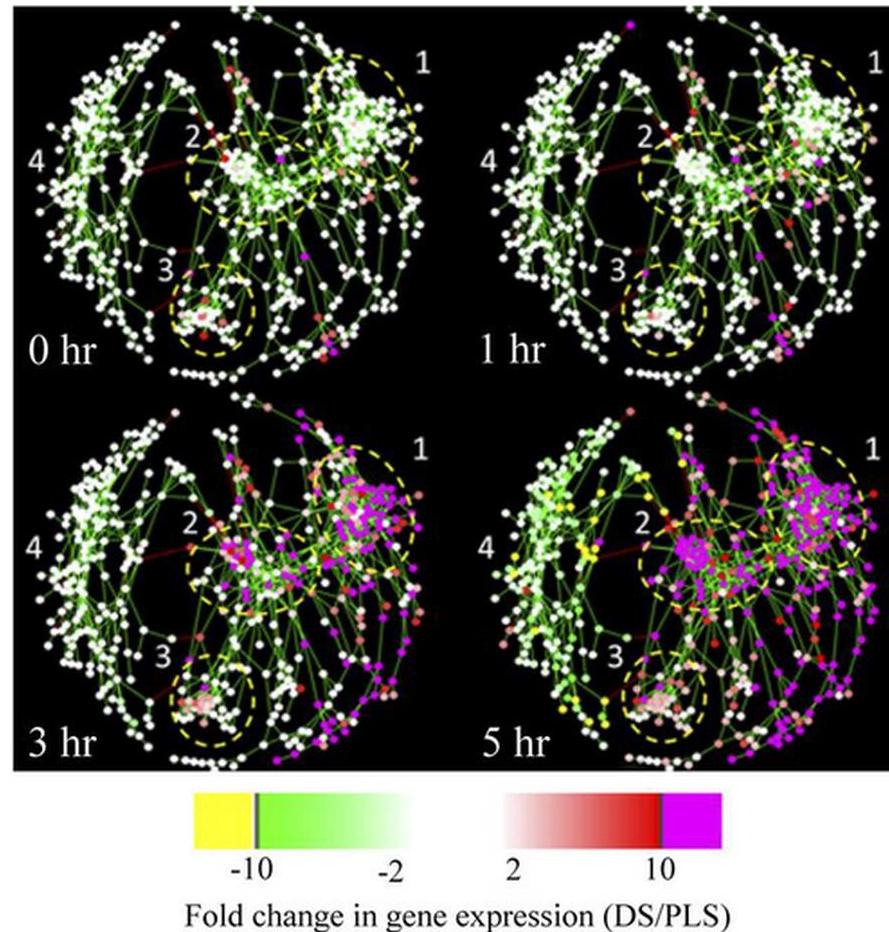


Comparative proteomic analysis of supportive and unsupportive extracellular matrix substrates for human embryonic stem cell maintenance.

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



Some Papers

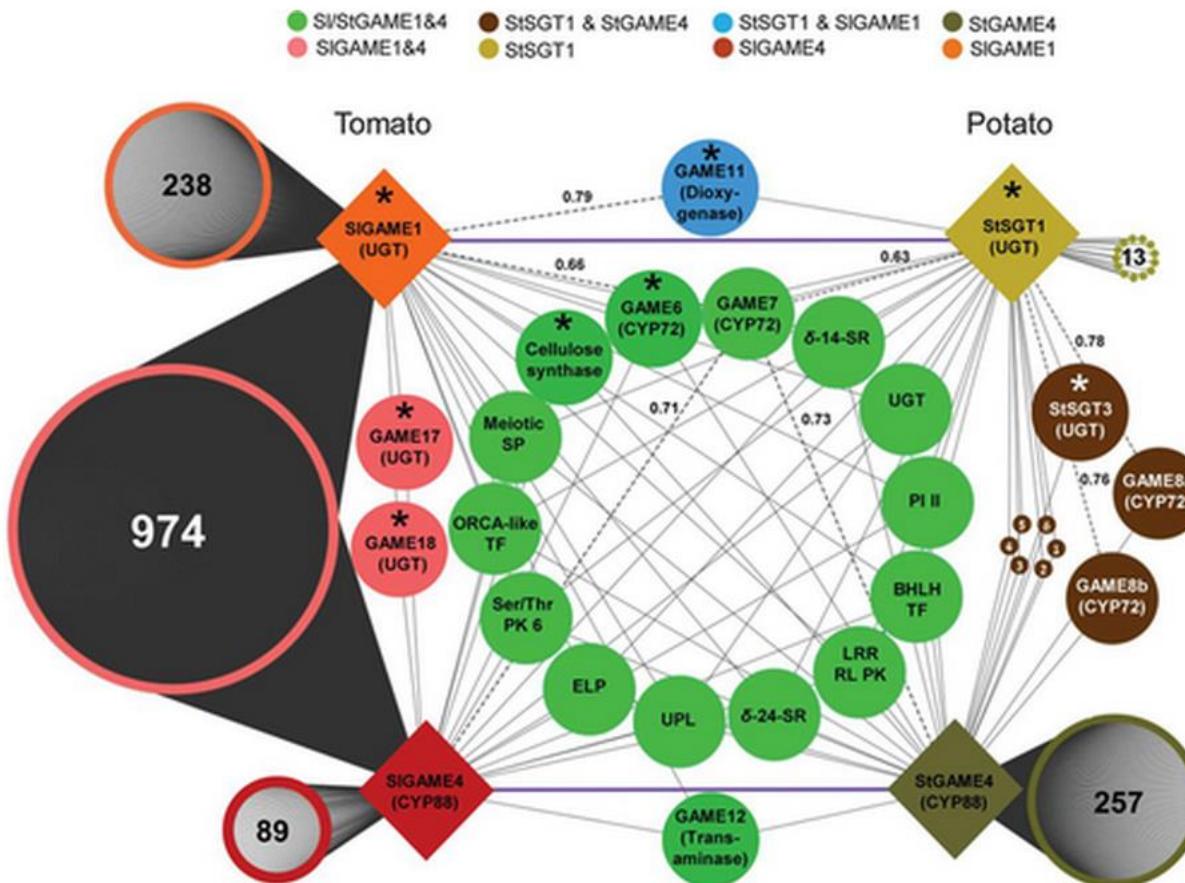


System-wide hypersensitive response-associated transcriptome and metabolome reprogramming in tomato.

Etalo et al, Plant Physiol. 2013 Jul;162(3):1599-617.



Some Papers

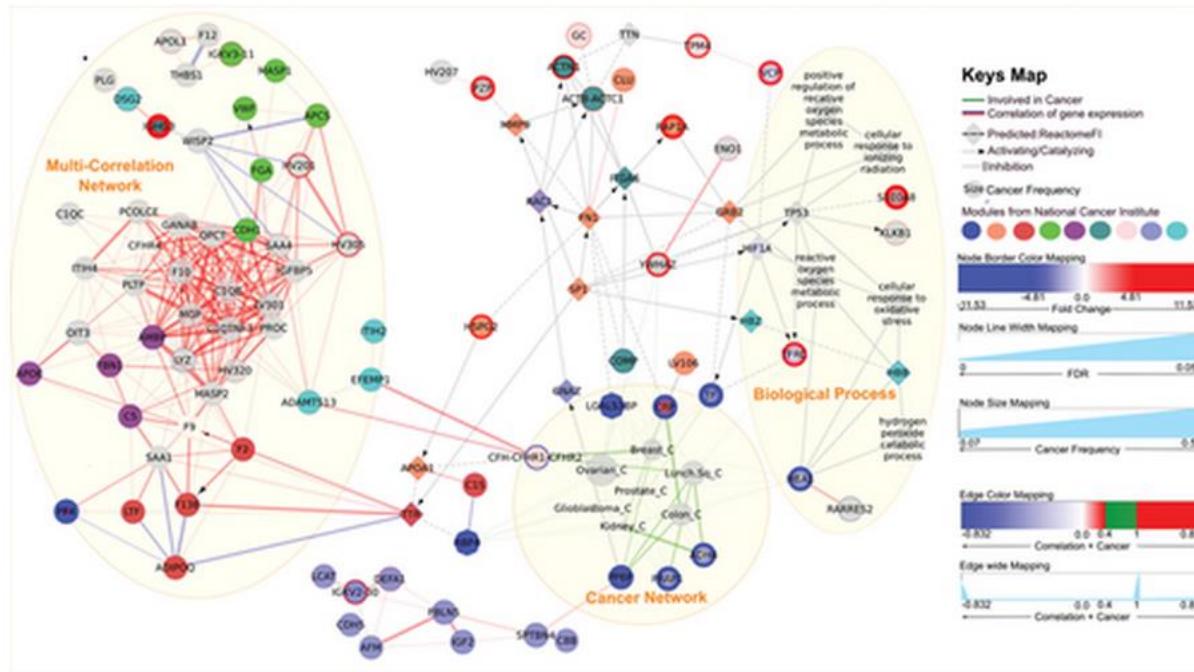


Biosynthesis of antinutritional alkaloids in solanaceous crops is mediated by clustered genes.

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



Some Papers

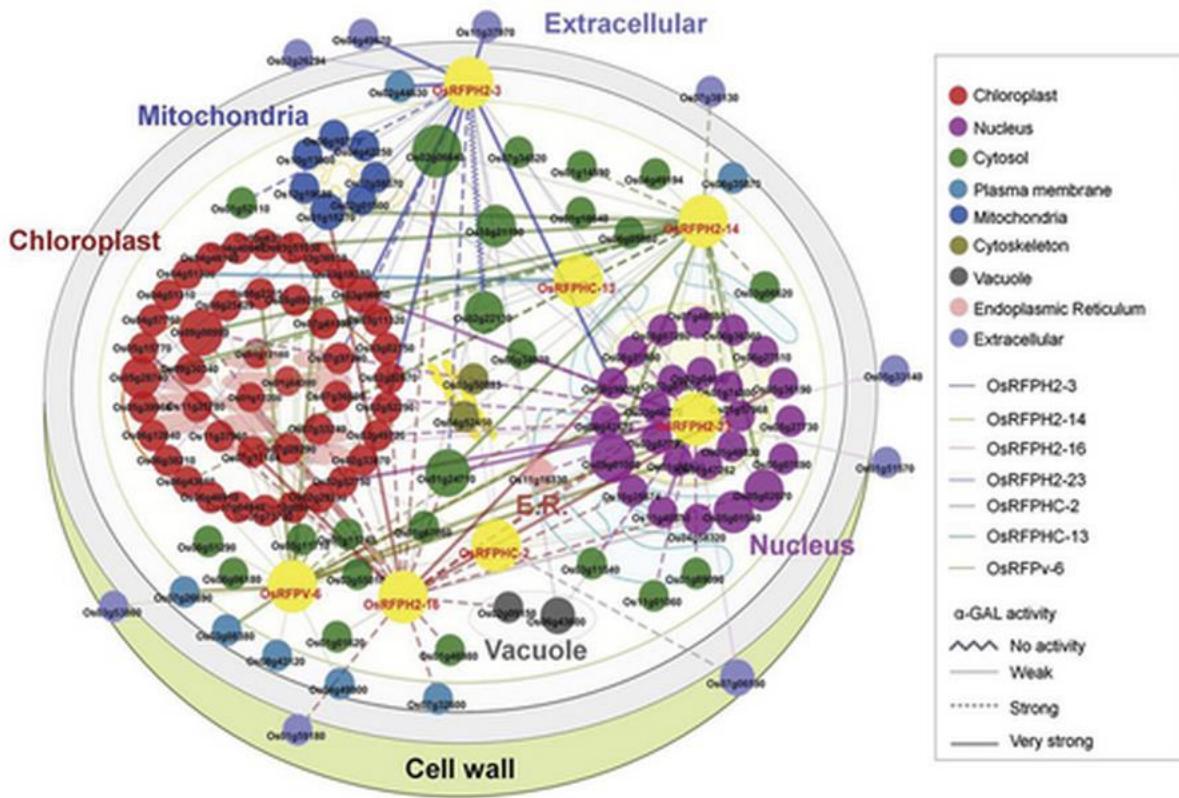


Graphical Identification of Cancer-Associated Gene Subnetworks Based on Small Proteomics Data Sets.

Mezhoud et al, OMICS. 2013 May 3.



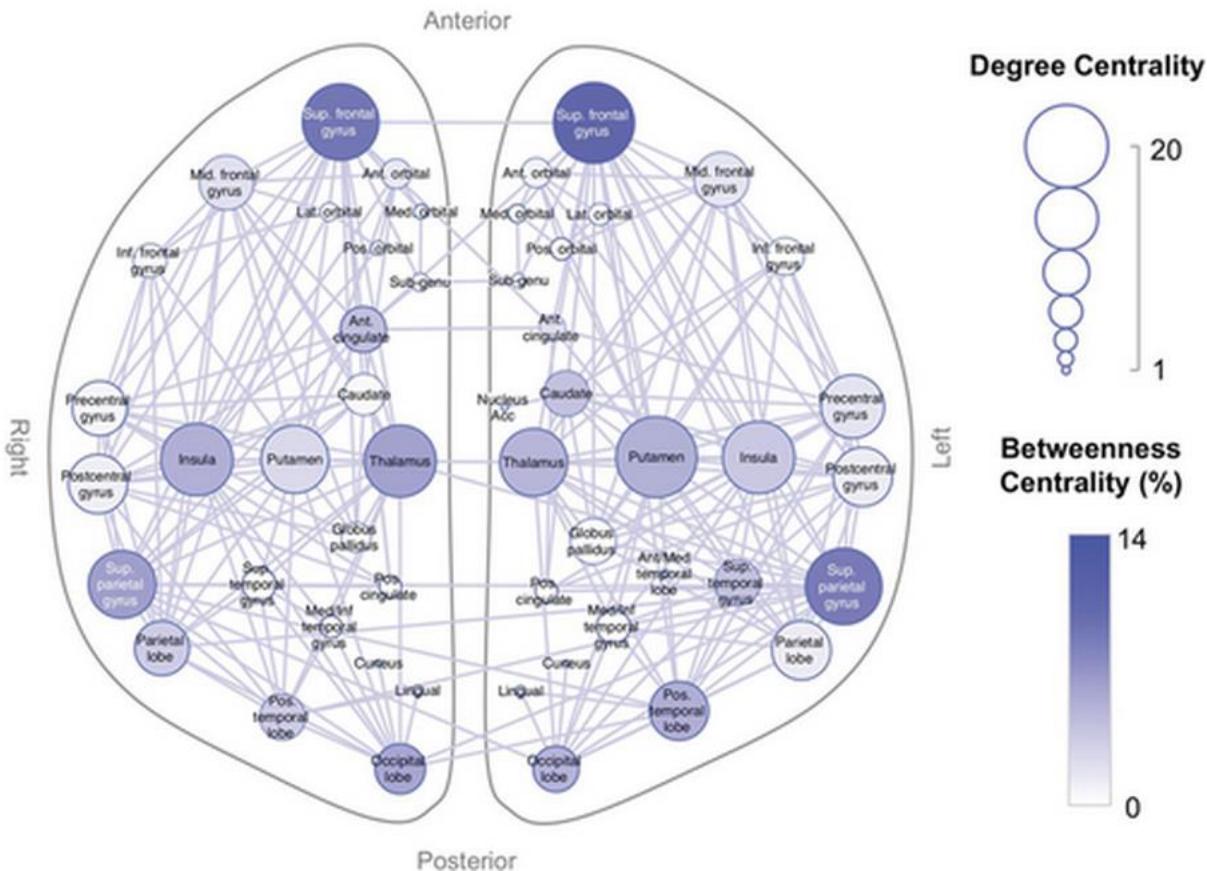
Some Papers



Comprehensive Analysis of the Rice RING E3 Ligase Family Reveals Their Functional Diversity in Response to Abiotic stress.
Lim et al, DNA Res. 2013 Apr 9.



Some Papers



Whole-Brain Mapping of Structural Connectivity in Infants Reveals Altered Connection Strength Associated with Growth and Preterm Birth.
Pandit et al, Cereb Cortex. 2013 Mar 31.

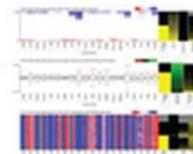


Some Papers

Matrix heatmaps



Gitools



UCSC/ Cancer Genetics Browser

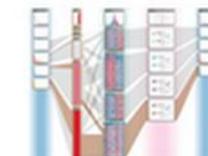
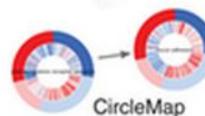
Genomic coordinates



IGV



Savant



Caleydo / StratomeX



Regulome explorer



Cytoscape

Networks

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



Questions?

