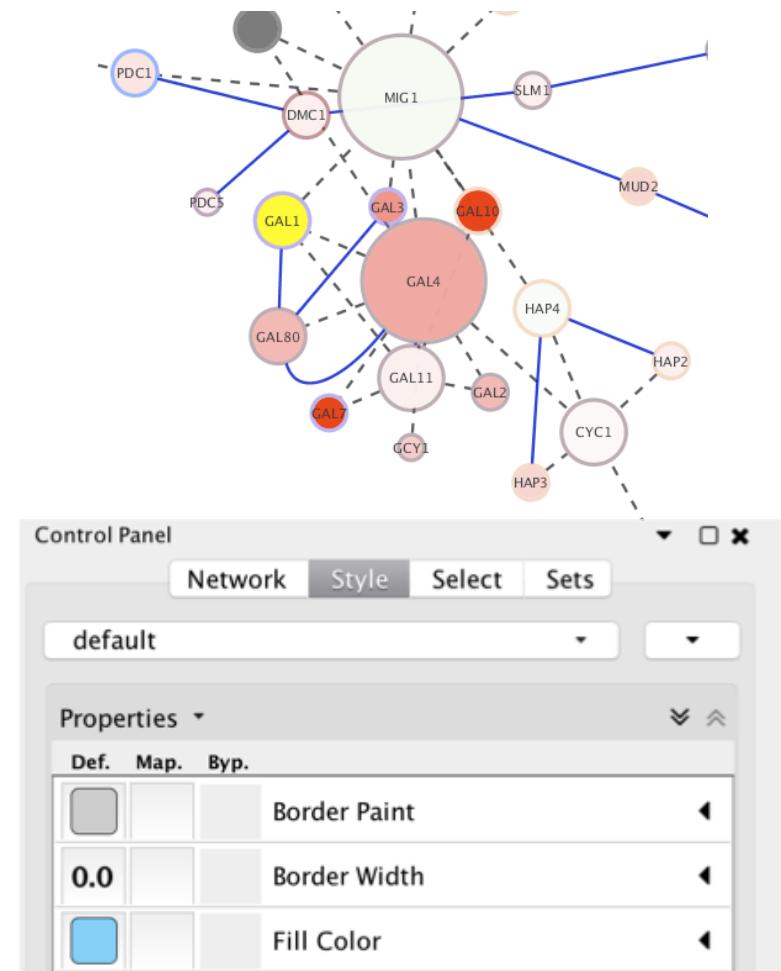




# Visualize data

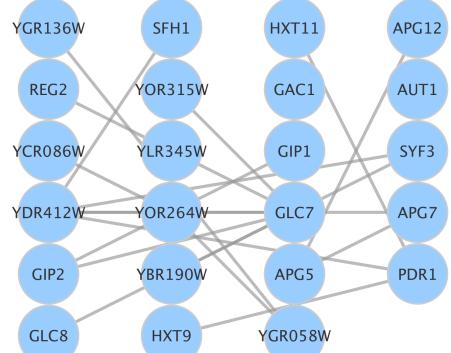
- **Layouts**
  - Hierarchical
  - Force-directed
  - ...
- **Data mapping**
  - Expression values to node color
  - Interaction type to edge line style



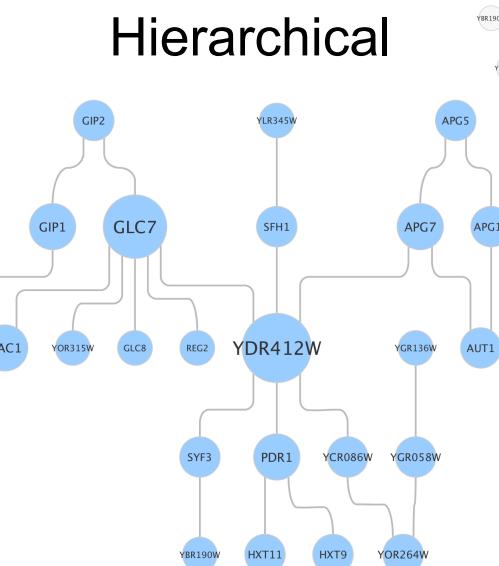


# Layouts

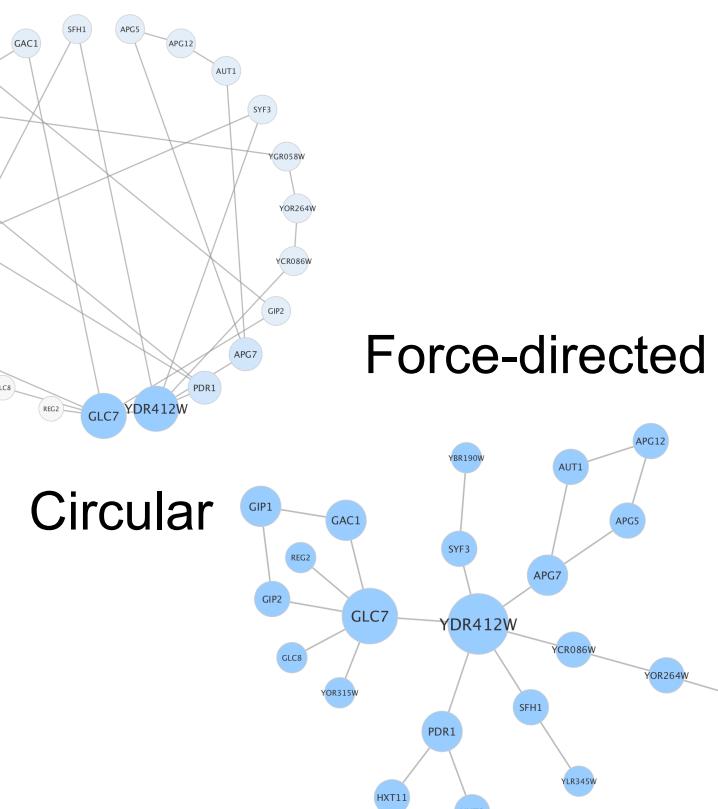
- Layouts determine the location of nodes and (sometimes) the paths of edges
- Recommended apps: yFiles Layout Algorithms, layoutSaver



Grid



Hierarchical



Circular



# Layouts: tips

- Use layouts to convey the relationships between nodes
- Layout algorithms may need to be “tuned” to fit your network
  - Check the *Layout Settings*
- Make use *Node Layout Tools*
  - Scale, align, rotate the network
- There is not one *correct* layout  
→ Try different things!

The image shows two overlapping dialog boxes from a software application.

**Layout Settings Dialog:**

- Layout Algorithm:** Prefuse Force Directed Layout
- Edge column that contains the weights:** (none)
- Edge Weight Settings:**
  - How to interpret weight values: Heuristic
  - The minimum edge weight to consider: 0E0
  - The maximum edge weight to consider: 1.79769E308
  - The default edge weight to consider: 0.5
- Number of Iterations:** 100
- Default Spring Coefficient:** 1E-4
- Default Spring Length:** 50
- Default Node Mass:** 3
- Force deterministic layouts (slower):**
- Standard Settings:**
  - Don't partition graph before layout:

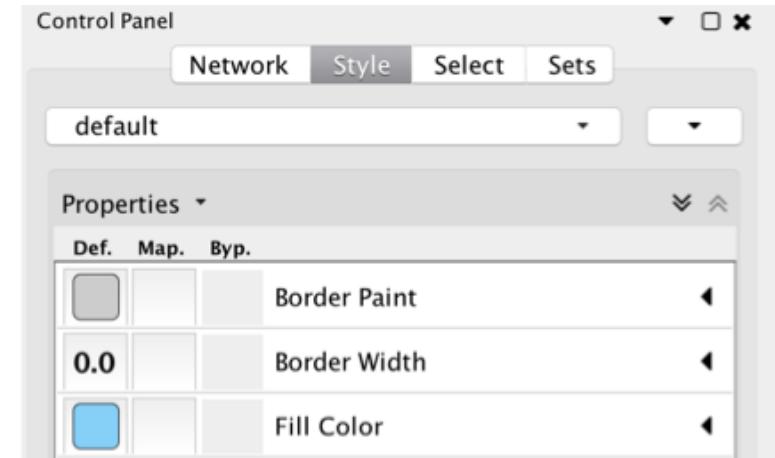
**Node Layout Tools Dialog:**

- Tool Panel:** Node Layout Tools
- Scale:** Width, Height, Selected Only (checkboxes checked)
- Align:** Horizontal alignment buttons (left, center, right).
- Distribute:** Horizontal distribution buttons (left, center, right).
- Stack:** Vertical stack buttons (top, middle, bottom).
- Rotate:** Rotation slider from -180 to 180 degrees, Selected Only (checkbox checked).



# Visualize data: mapping

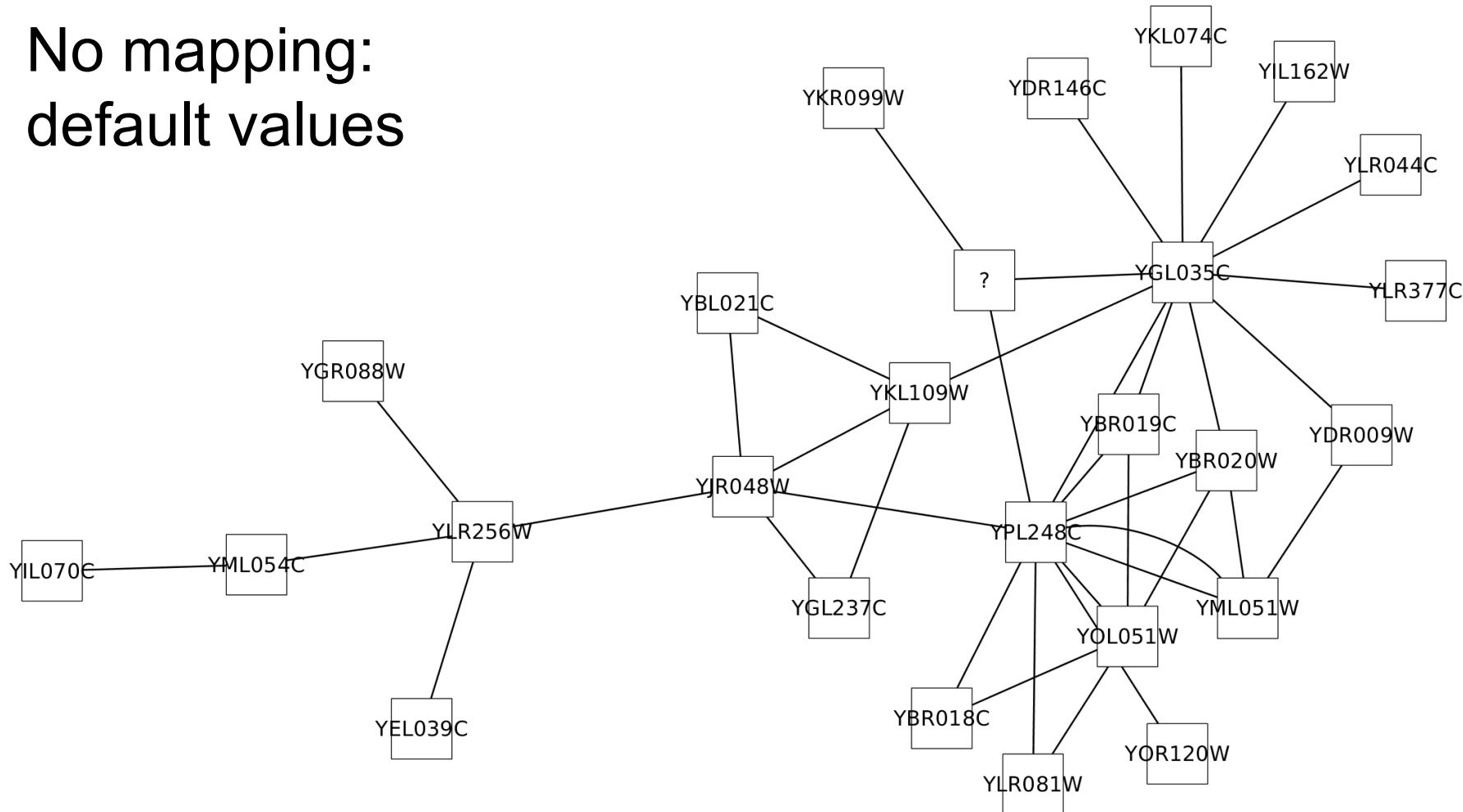
- Data mapping
  - Expression values to **node color**
  - Interaction type to edge **line style**
- Mapping types
  - Pass-through (usually **node/edge labels**)
  - **Discrete (categories)**
    - Type of interaction
  - **Continuous (numeric values)**
    - Node degree, expression values or interaction scores





# Data mapping

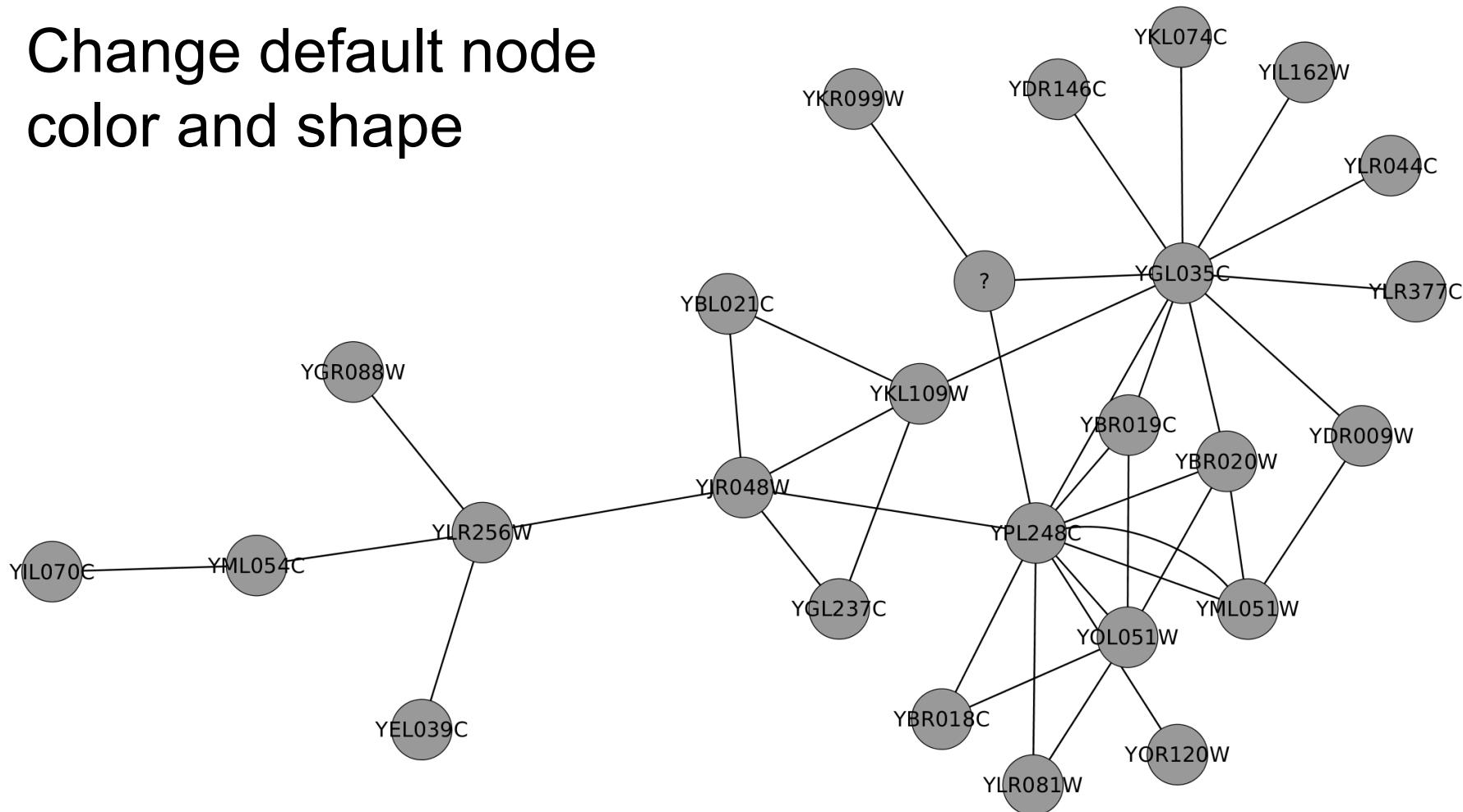
No mapping:  
default values





# Data mapping

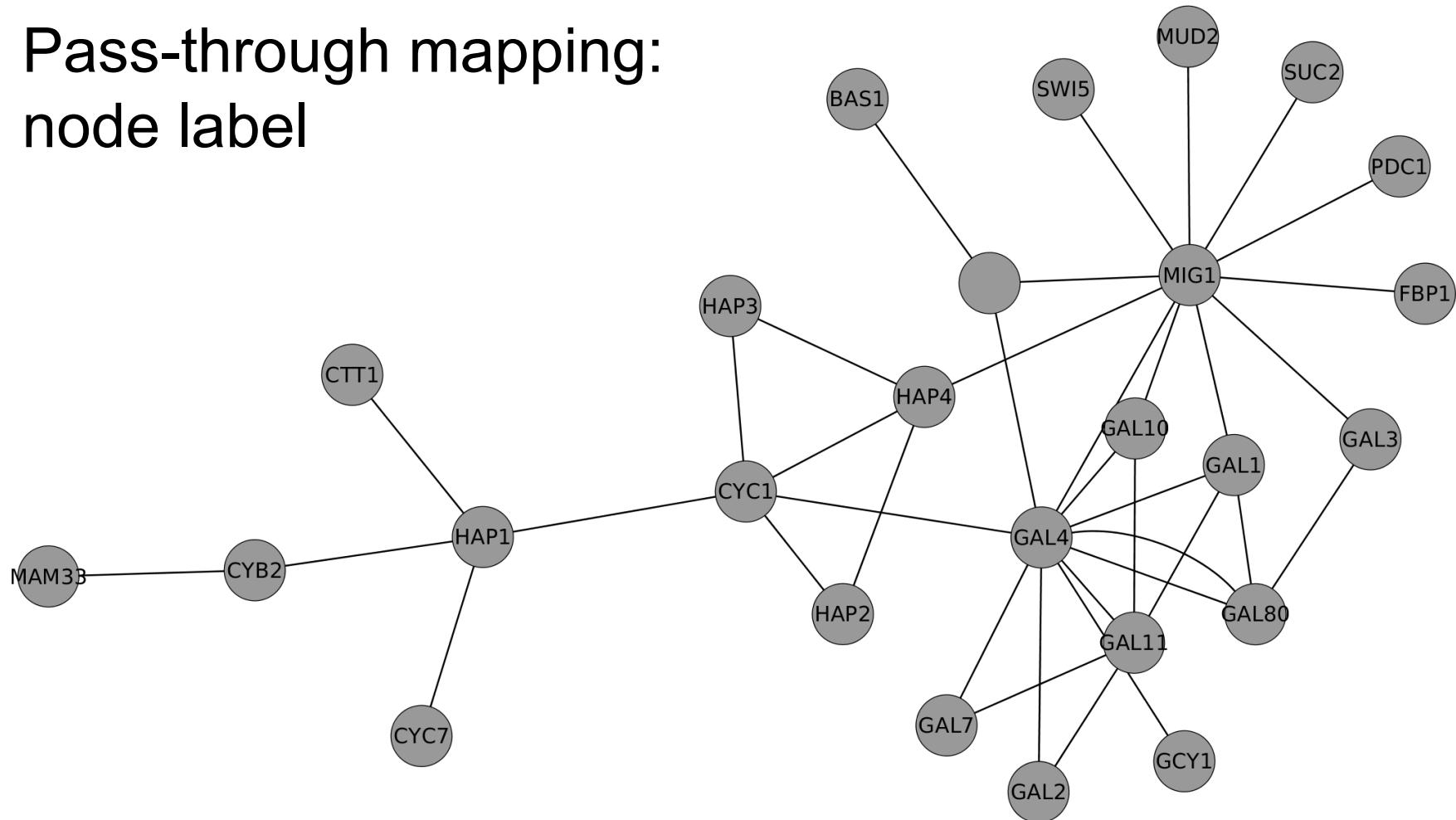
Change default node color and shape





# Data mapping

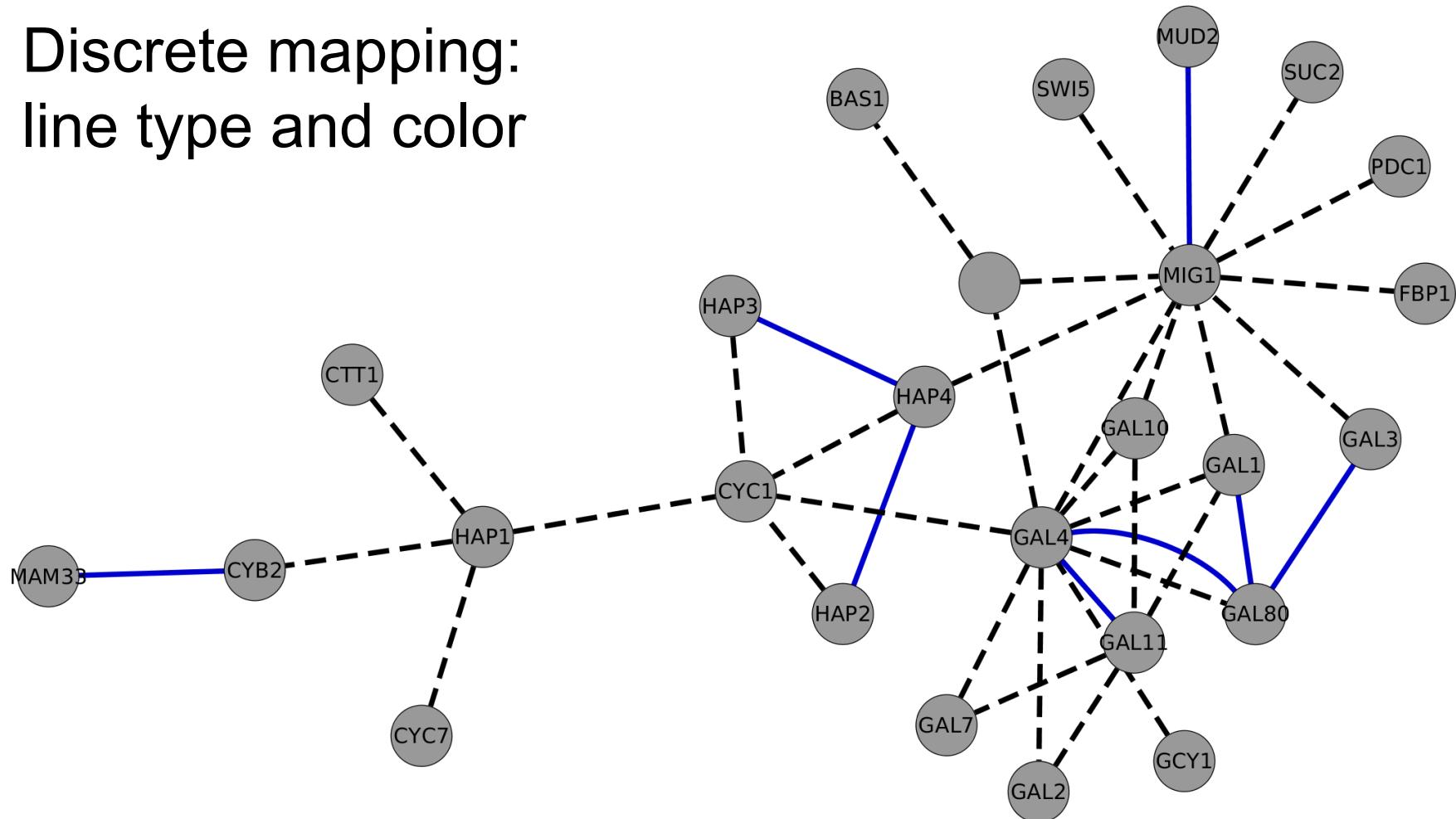
Pass-through mapping:  
node label





# Data mapping

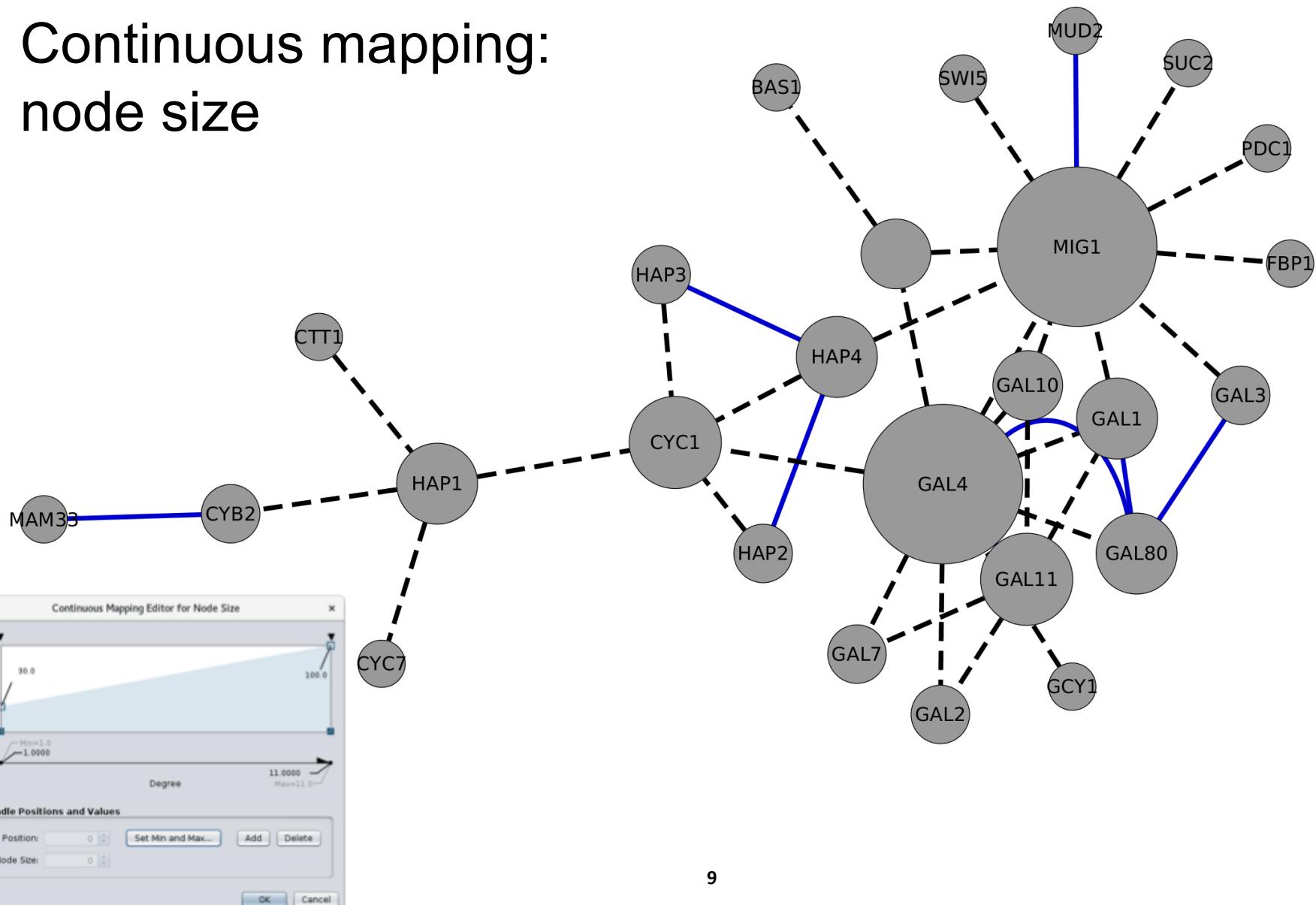
Discrete mapping:  
line type and color





# Data mapping

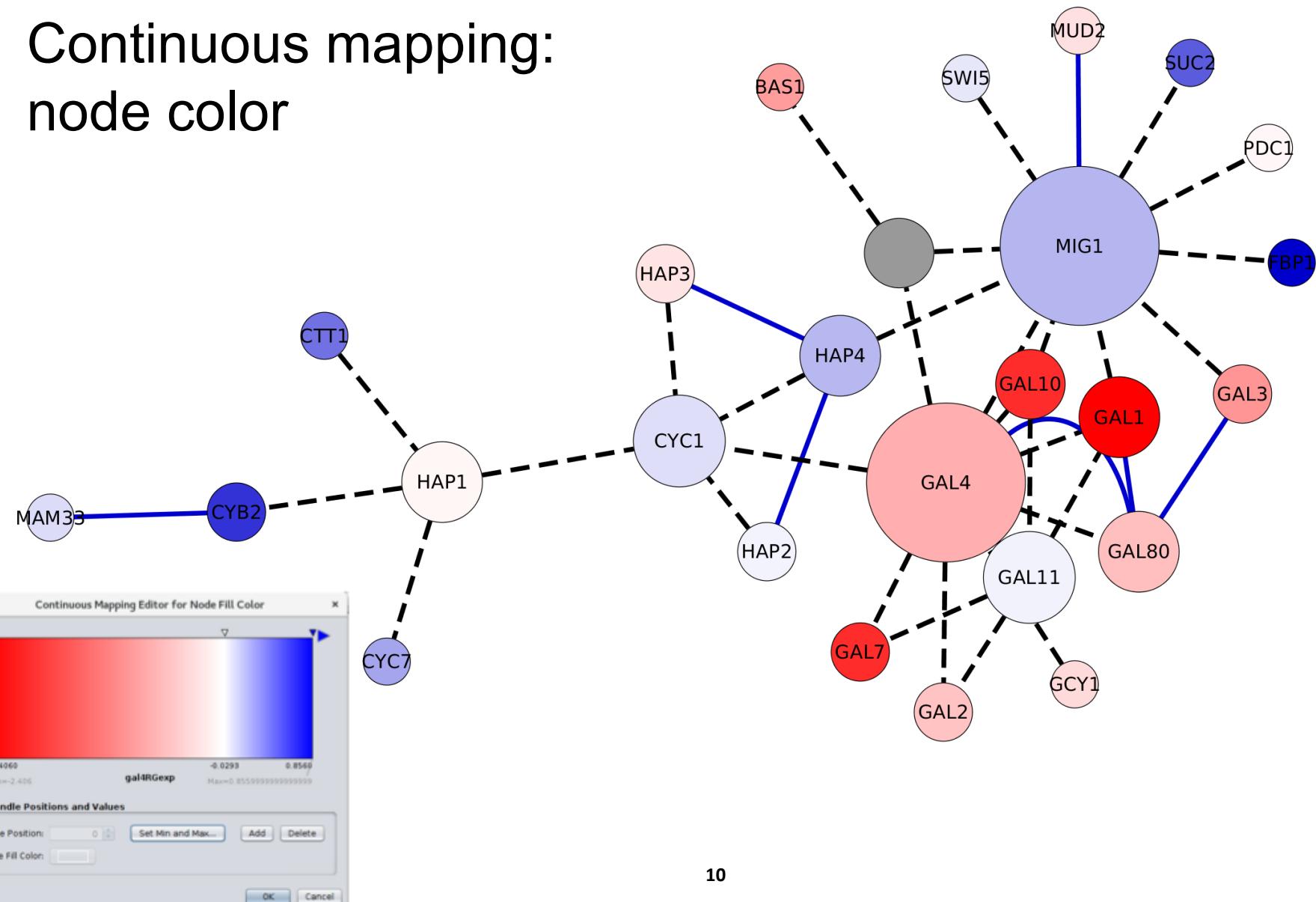
Continuous mapping:  
node size





# Data mapping

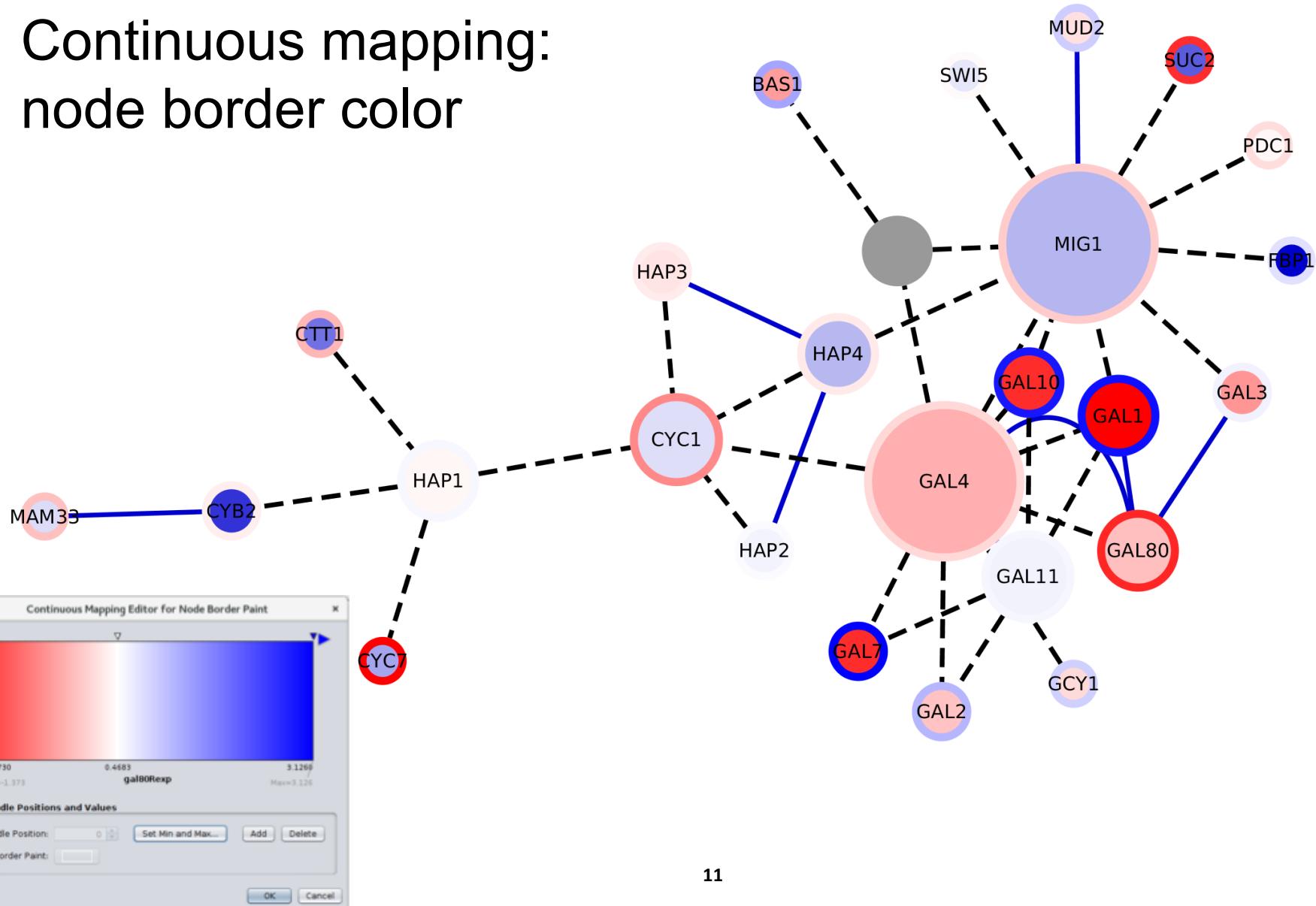
Continuous mapping:  
node color





# Data mapping

Continuous mapping:  
node border color





# Data mapping: tips

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



# Styles: User interface

Control Panel

Network Style Select Sets

STRING style - Parkinson's disease

Properties

Def. Map. Byp.

Border Paint	
0.0	Border Width
Fill Color	Height
45.0	Image/Chart 1
Image/Chart 2	Image/Chart 3
Image/Chart Position 3	Label
Label Color	Label Font Size
12	Shape
Size	Transparency
255	Width
Lock node width and height	

Node Edge Network

Styles tab

Default fill color: white

Node tab

Fill color mapping:  
rainbow colors

Bypass mapping

Edge tab



# Styles: examples

Session: New Session

Control Panel

Network Style Select

Jrce Target

Big Labels

BioPAX

BioPAX\_SIF

Curved

default

default black

Directed

Gradient1

Marquee

Minimal

Nested Network Style

Ripple

Sample1

Sample2

Sample3

Solid

Universe

Node Edge Network

Node Table Edge Table Network Table

Memory

The figure shows the Cytoscape interface with various network styles displayed in a panel on the left, a main network graph in the center, and a table at the bottom.

**Network Styles:**

- Jrce
- Target
- Big Labels
- BioPAX
- BioPAX\_SIF
- Curved
- default
- default black
- Directed
- Gradient1
- Marquee
- Minimal
- Nested Network Style
- Ripple
- Sample1
- Sample2
- Sample3
- Solid
- Universe

**Graph:**

A network graph with 10 nodes labeled Node 2 through Node 10. Node 2 is at the bottom, connected to Node 3, Node 4, and Node 5. Node 3 is connected to Node 4. Node 4 is connected to Node 5, Node 6, and Node 9. Node 5 is connected to Node 6, Node 7, and Node 10. Node 6 is connected to Node 7. Node 7 is connected to Node 10. Node 8 is also present in the graph area.

**Table:**

**Sheet1**

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



# Styles: examples

Session: New Session

Control Panel

Network Style Select

Jrce Target Big Labels Curved Directed Minimal Sample1 Solid

BioPAX default Gradient1 Nested Network Style Sample2 Universe

BioPAX\_SIF default black Marquee Ripple Sample3

Source Target Source Target Source Target Source Target Source Target Source Target

Sheet1

$f(x)$

Node Edge Network

Node Table Edge Table Network Table

Memory

The screenshot shows the Cytoscape interface with various network styles displayed in a grid. The styles include Jrce, Target, Big Labels, Curved, Directed, Minimal, Sample1, Solid, BioPAX, default, Gradient1, Nested Network Style, Sample2, Universe, BioPAX\_SIF, default black, Marquee, Ripple, and Sample3. The 'Style' tab is selected in the Control Panel.

The main workspace displays a network graph with 10 nodes (Node 2 to Node 10) and various edge types (solid, dashed, dotted) representing interactions like activates, inhibits, and interacts with. A zoomed-in view of the network is shown in a separate window.

A table below the network graph lists node names, their assigned complexes, and confidence values:

Node name	Belongs to	Confidence
Node 1	complex 1	0.9
Node 4	complex 1	0.9
Node 3	complex 1	0.9
Node 2	complex 1	0.5
Node 5	complex 2	0.8
Node 8	complex 2	0.8
Node 6	complex 2	0.7
Node 7	complex 2	0.7
Node 9	complex 1	0.1
Node 10	complex 1	0.1



# Styles: Discrete mapping

Session: New Session

Control Panel

Network Style Select

Properties

Def. Map. Byp.

Border Paint

Border Width

Fill Color

Column Belongs to

Mapping Type Discrete Mapping

complex 1 R:0 G:102 B:255 - #0064...

complex 2 R:255 G:153 B:0 - #FF99...

Height

Image/Chart 1

Label

Label Color

Label Font Size

Shape

Size

Transparency

Width

Lock node width and height

Node Edge Network

Sheet1

Table Panel

f(x)

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

Node Table Edge Table Network Table

Memory



# Styles: Continuous mapping





# Styles: Continuous mapping

Session: /Users/doncheva/Projects/Conferences/2017\_CourseAarhus/Materials/dem01.cys

Control Panel

Network Style Select Sets

Properties

Def. Map. Byp.

default cont

Border Paint

Border Width

Fill Color

Column Log ratio

Mapping Type Continuous Mapping

Current Mapping

Height

Image/Chart 1

Label

Label Color

Label Font Size

Shape

Size

Transparency

Width

Node Edge Network

Table Panel

Sheet1

$f(x)$

shared name	name	Node name	Belongs to	Complex	Log ratio
Node 7	Node 7	G	complex 2	0.7	4.0
Node 6	Node 6	F	complex 2	0.7	2.5
Node 10	Node 10	J	complex 1	0.1	2.0
Node 8	Node 8	H	complex 2	0.8	1.2
Node 4	Node 4	D	complex 1	0.9	0.4
Node 5	Node 5	E	complex 2	0.8	-0.5
Node 9	Node 9	I	complex 1	0.1	-1.4
Node 3	Node 3	C	complex 1	0.9	-1.5
Node 1	Node 1	A	complex 1	0.9	-2.0
Node 2	Node 2	B	complex 1	0.5	-2.5

Node Table Edge Table Network Table

Memory



# 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/>



# Annotate & analyze data

- Functional enrichment
- Clustering
- Topological analysis
- And many more...

Apps Tools Help

App Manager...

clusterMaker	▶
clusterMaker Dimensionality Reduction	▶
clusterMaker Ranking	▶
clusterMaker Visualizations	▶
LayoutMapper	▶
RINalyzer	▶
SetsApp	▶
STRING	▶
StructureViz	▶
BiNGO	▶

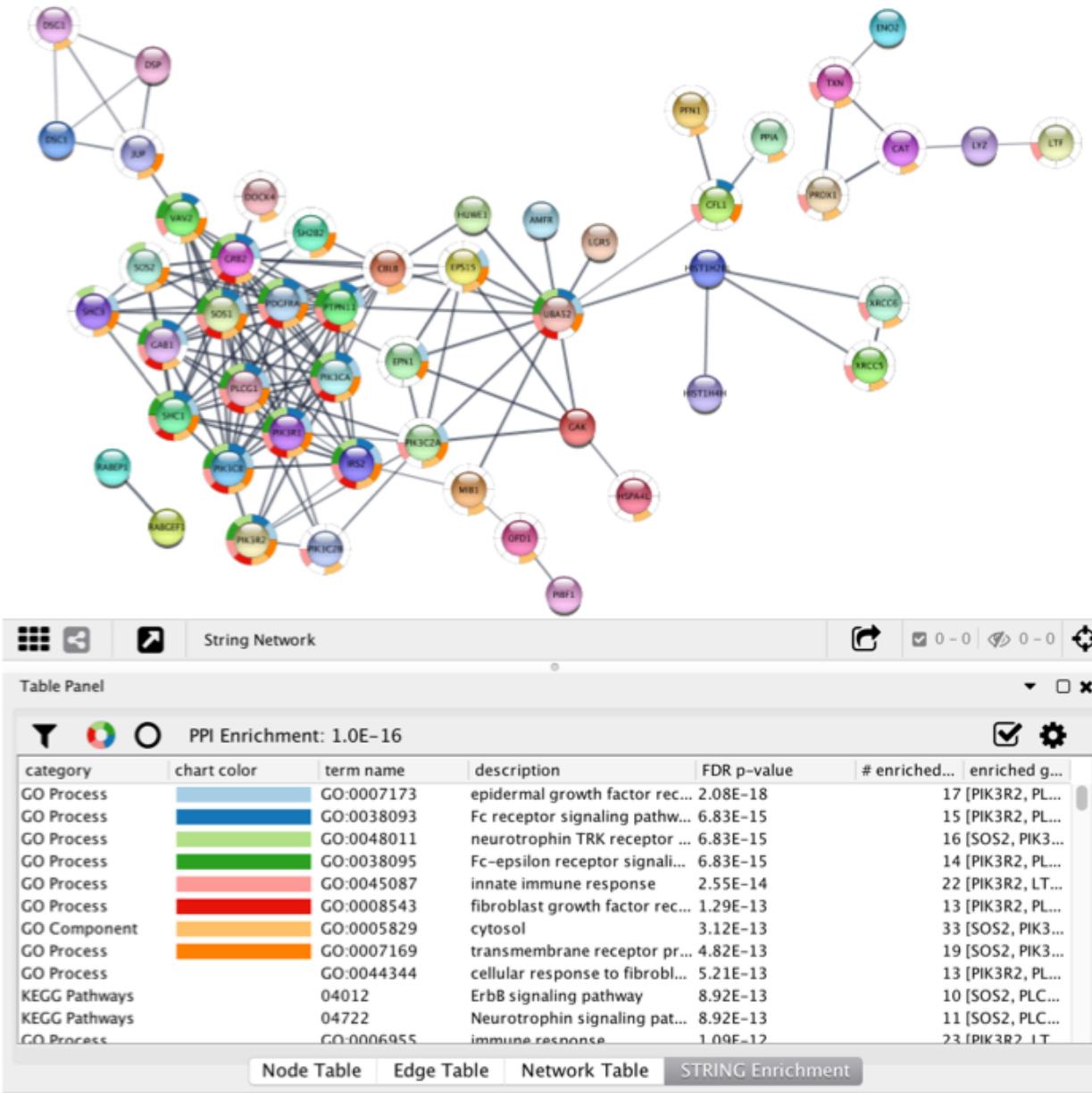


# Functional enrichment

- Find annotations that are **statistically overrepresented** in the network
- **Various sources** of annotation: Gene Ontology terms, KEGG & Reactome pathways, etc.
- Not really a network analysis technique
- **Very useful for visualization**



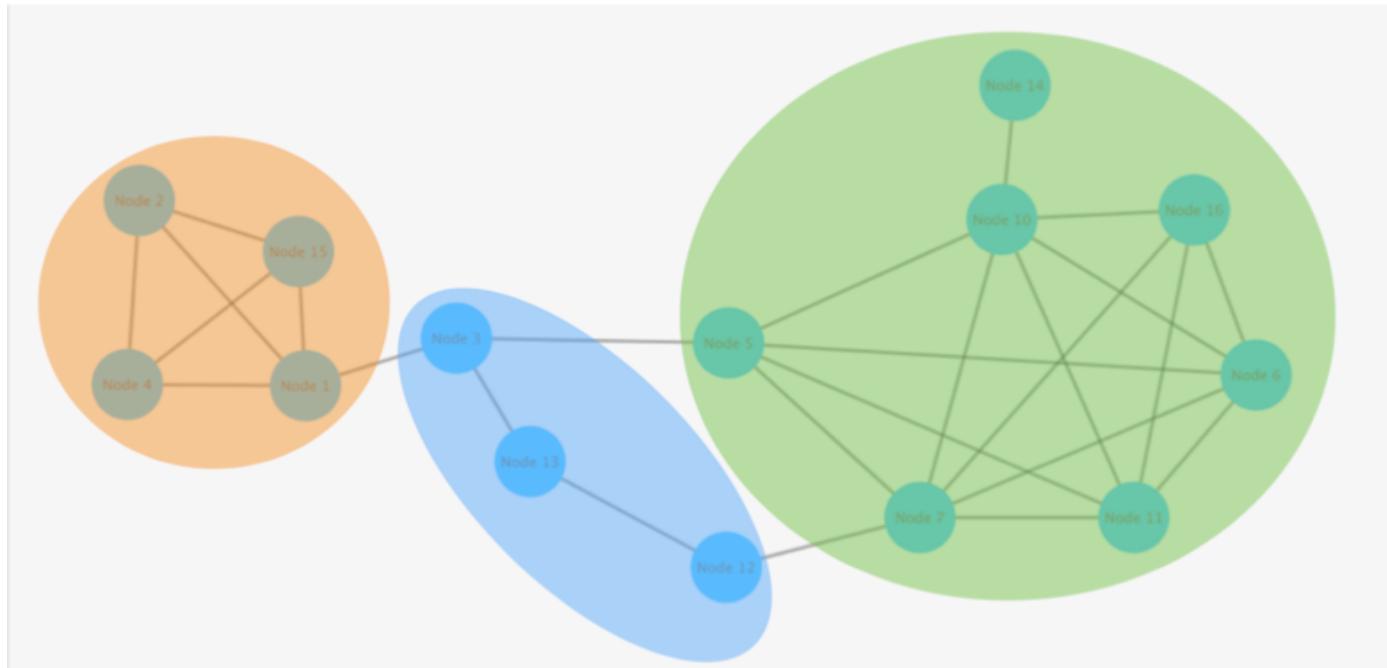
# Enrichment in Cytoscape





# Clustering

- Goal:
  - Group related items (typically nodes) together
  - Makes the network easier to understand





# Clustering

- Goal:
  - Group related items (typically nodes) together
  - Makes the network easier to understand
- Many ways to do it, but based on some measure of distance between the nodes



# Clustering

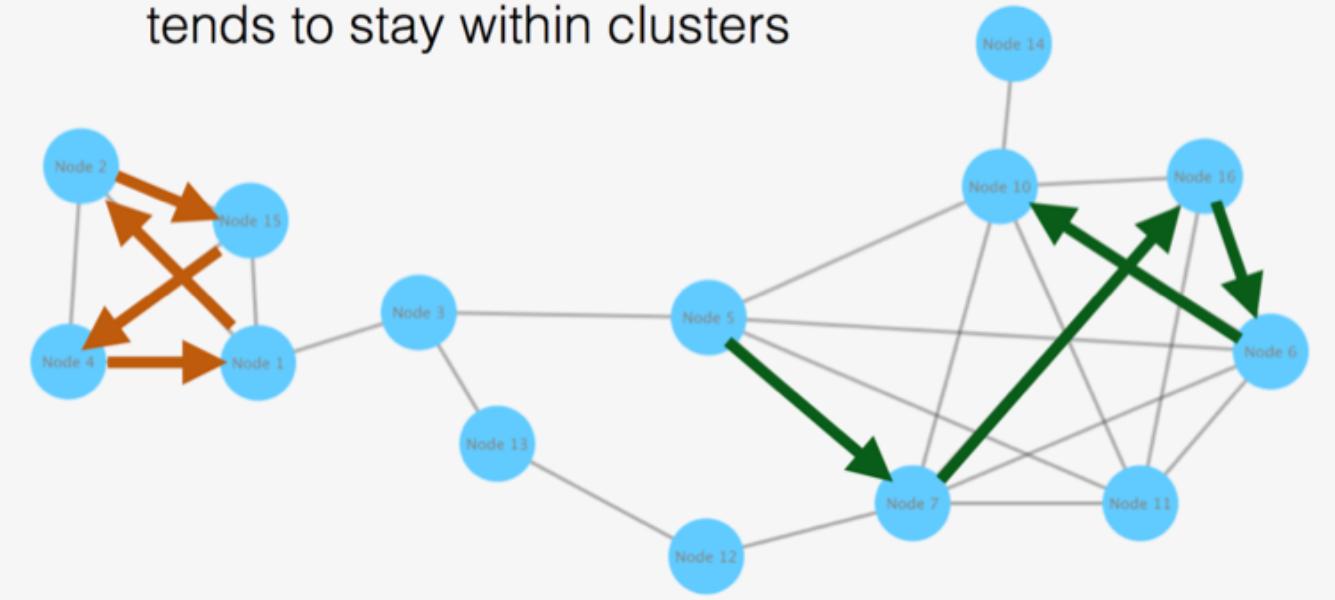
- Goal:
  - Group related items (typically nodes) together
  - Makes the network easier to understand
- Many ways to do it, but based on some measure of distance between the nodes
- Examples for biological networks:
  - Shown to represent protein complexes and parts of biological pathways in a protein-protein interaction network
  - Protein families in a protein similarity network



# Network Clustering

- Network clusters: highly interconnected sub-networks that may be partly overlapping
- Example: MCL clustering
  - Fast algorithm
  - No need to specify number of clusters

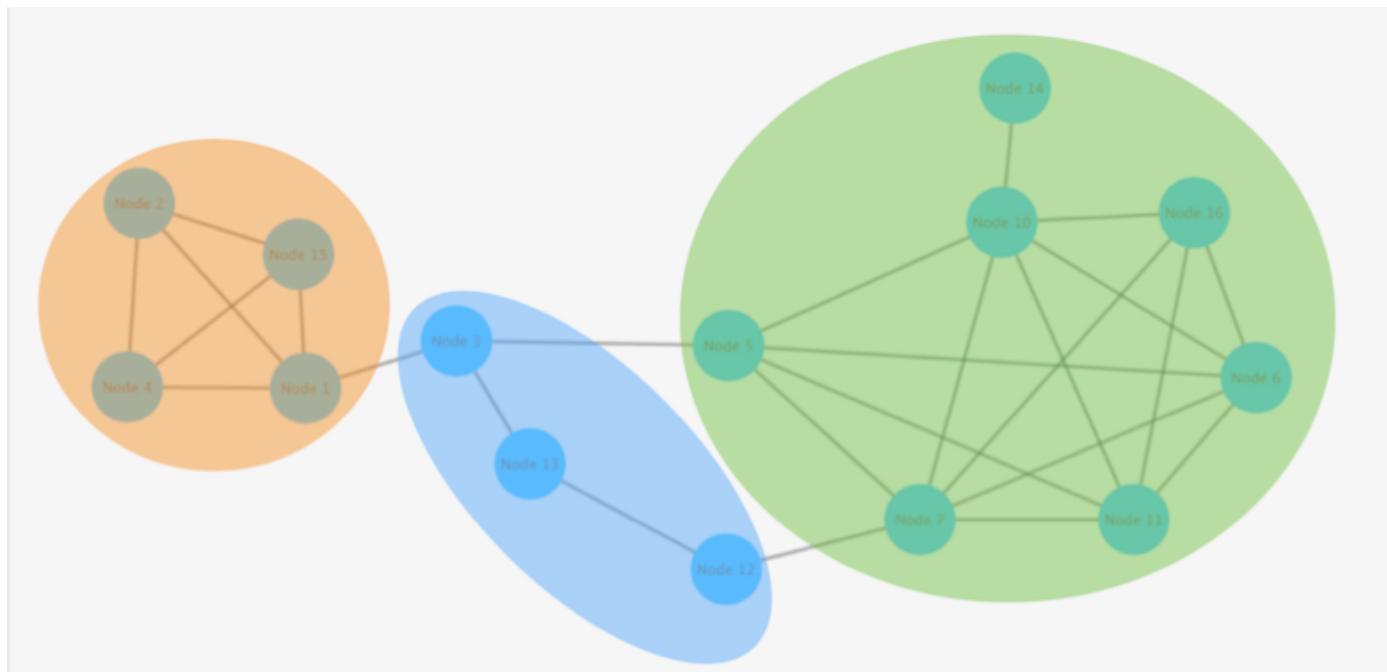
- Random walk between nodes tends to stay within clusters





# Network Clustering

- Network clusters: highly interconnected sub-networks that may be partly overlapping
- Example: MCL clustering
  - Fast algorithm
  - No need to specify number of clusters





# Clustering in Cytoscape



## clusterMaker2

Multi-algorithm clustering app for Cytoscape



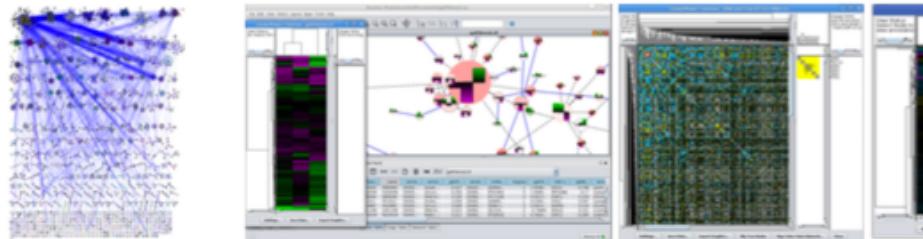
(17) 21408 downloads



Details

Release History

Categories: [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
- AutoSOME

CYTOSCAPE 3

✓ Installed

Version 1.1.0

Released 27 Apr 2017

Works with [Cytoscape 3.3](#)

[Download Stats](#) [Click here](#)

### RESOURCES

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[Tutorial](#)

[Cite this App](#)

[Code Repository](#)

[E-mail](#)



# Tutorials & Getting Help

- Alternative slides: <https://cytoscape.github.io/cytoscape-tutorials/presentations/embo-ppi-2019-bangalore.html>
- Cytoscape tutorials & presentations
  - [tutorials.cytoscape.org](http://tutorials.cytoscape.org)
  - <https://www.youtube.com/channel/UCv6auk9FK4NgXiXigrDLccw>
- Cytoscape helpdesk mailing list
  - [cytoscape-helpdesk@googlegroups.com](mailto:cytoscape-helpdesk@googlegroups.com)
- STRING & stringApp tutorials:
  - <https://jensenlab.org/training/>



**Thank you for your  
attention!**

**Questions?**