

1. Demonstration of the Cytoscape Interface

Cytoscape Interface (version 2.8.3)

The screenshot displays the Cytoscape Desktop interface (Session: galFiltered.cys) with a network graph loaded from 'galFiltered.sif'. The interface is divided into several panels:

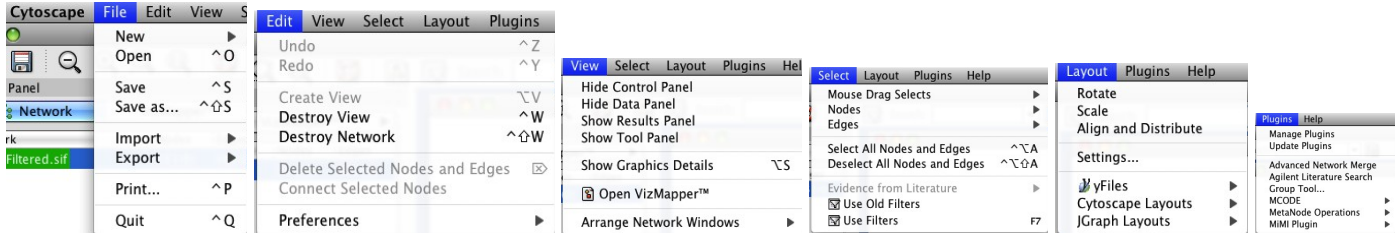
- Menu Bar:** Located at the top, containing File, Edit, View, Select, Layout, Plugins, and Help.
- Tool Bar:** Located below the menu bar, containing icons for file operations and navigation.
- Control Panel:** Located on the left side, showing the 'Network' tab with a table of nodes and edges.
- Navigator Panel:** Located below the Control Panel, showing a smaller view of the network graph.
- Graphic Panel:** The main central area displaying the network graph with nodes and edges.
- Data Panel:** Located at the bottom right, displaying a table of node attributes.
- Tool Panel:** Located at the bottom left, containing tools for rotating, scaling, and aligning/distributing nodes.

The Data Panel table contains the following data:

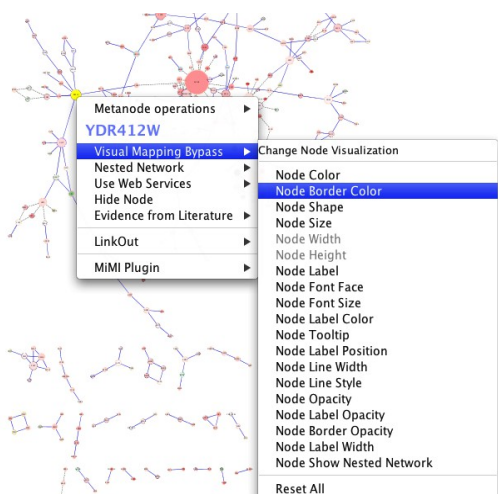
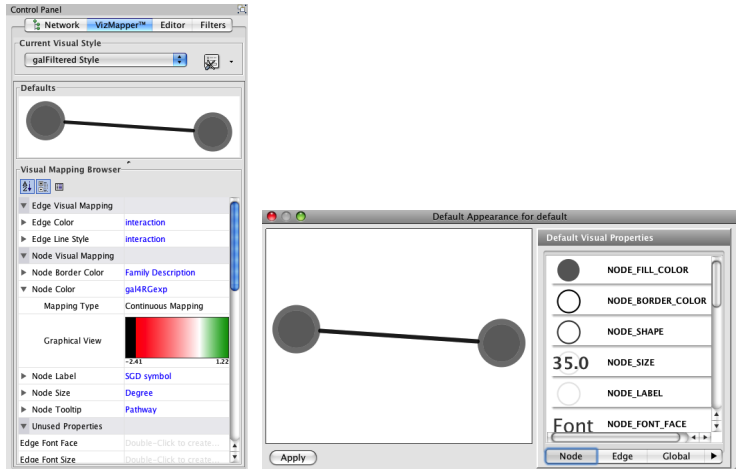
| ID | EntrezGene ID | Pathway | GeneRIF | SGD symbol | annotation.GO BIOLOGICAL_PROCESS | gal1RGexp |
|---------|---------------|-------------|---------------|------------|--|-----------|
| YDR244W | [851831] | [] | [Pex4p-d... | [PEX5] | [protein import into peroxisome matr... | 0.369 |
| YLR191W | [850888] | [] | [A novel P... | [PEX13] | [protein import into peroxisome matr... | 0.178 |
| YGL153W | [852724] | [] | [Pex14p i... | [PEX14] | [intracellular protein transport across... | 0.242 |
| YNL214W | [855507] | [] | [Pex19p... | [PEX17] | [protein import into peroxisome matr... | 0.122 |
| YDL078C | [851481] | [KEGG pa... | [] | [MDH3] | [NADH regeneration, carbohydrate m... | 0.217 |
| YDR142C | [851720] | [] | [appendi... | [PEX7] | [protein import into peroxisome matr... | -0.101 |

At the bottom of the interface, there are tabs for 'Node Attribute Browser', 'Edge Attribute Browser', and 'Network Attribute Browser'. A status bar at the very bottom provides instructions: 'Welcome to Cytoscape 2.7.0 Right-click + drag to ZOOM Middle-click + drag to PAN'.

Menu Bar



VizMapper



2. Demonstration of Network Visualization/Analysis in Cytoscape

2.1 Open and see network galFiltered.sif file, galFiltered.node.annotation.xls attribute file, Degree.NA node attribute file, galExpData.mrna file.

galFiltered.sif

Last Saved: 3/23/10 10:34:32 AM
File Path: /Volumes/nv/Cytoscape_v2.7.0/sampleData/galFiltered.sif

| | | | |
|---|---------|----|---------|
| 1 | YKR026C | pp | YGL122C |
| 2 | YGR218W | pp | YGL097W |
| 3 | YGL097W | pp | YOR204W |
| 4 | YLR249W | pp | YPR080W |
| 5 | YLR249W | pp | YBR118W |
| 6 | YLR293C | pp | YGL097W |
| 7 | YMR146C | pp | YDR429C |
| 8 | YDR429C | pp | YFL017C |
| 9 | YPR080W | pp | YAL003W |

galFiltered.node.annotation.xls

New Open Save Print Import Copy Paste Format Undo Redo AutoSum Sort A-Z Sort Z-A Gallery Toolbox Zoom Help

| ID | GeneName | Alias | Chromosome | Description |
|----|----------|--------|---------------|--|
| 2 | YGR085C | RPL11B | chromosome 7 | Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl11Ap; involved in ribosomal |
| 3 | YOR215C | AIM41 | chromosome 15 | Putative protein of unknown function; the authentic protein is detected in highly purified mitochondria in hig |
| 4 | YJR022W | LSM8 | chromosome 10 | Lsm (Like Sm) protein; forms heteroheptameric complex (with Lsm2p, Lsm3p, Lsm4p, Lsm5p, Lsm6p, and L |
| 5 | YGL044C | RNA15 | chromosome 7 | Cleavage and polyadenylation factor I (CF I) component involved in cleavage and polyadenylation of mRNA |
| 6 | YMR186W | HSC82 | chromosome 13 | Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and tog |
| 7 | YHR055C | CUP1-2 | chromosome 8 | Metallothionein, binds copper and mediates resistance to high concentrations of copper and cadmium; locus |

Degree.NA

Last Saved: 1/25/10 5:12:10 PM
File Path: /Volumes/nv/Cytoscape_v2.7.0/sampleData/Degree.NA

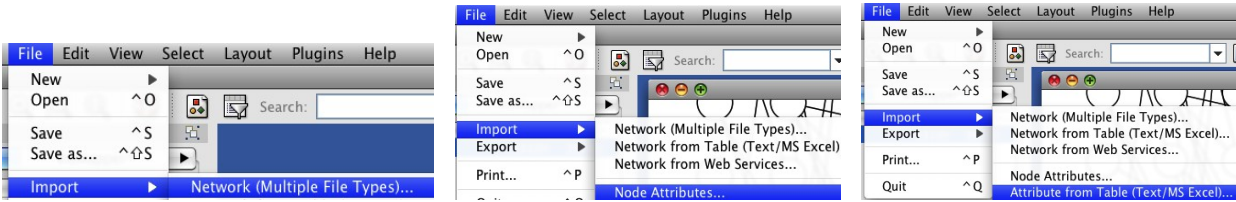
| | |
|---|----------------------------------|
| 1 | Degree (class=java.lang.Integer) |
| 2 | YDR309C = 1 |
| 3 | YLR264W = 4 |
| 4 | YJR060W = 2 |
| 5 | YPL201C = 1 |
| 6 | YDL088C = 2 |
| 7 | YLR116W = 2 |
| 8 | YEL041W = 1 |
| 9 | YNL216W = 17 |

galExpData.mrna

Last Saved: 1/21/10 11:23:50 AM
File Path: /Volumes/nv/Cytoscape_v2.7.0/sampleData/galExpData.mrna

| | |
|----|-------------------------------------|
| 1 | GENE COMMON gal1RG gal4RG gal80R |
| 2 | YHR051W COX6 -0.034 0.111 -0.304 |
| 3 | YHR124W NDT80 -0.090 0.007 -0.348 |
| 4 | YKL181W PRS1 -0.167 -0.233 0.112 |
| 5 | YGR072W UPF3 0.245 -0.471 0.787 |
| 6 | YHL020C OPI1 0.174 -0.015 0.151 |
| 7 | YGR145W YGR145W 0.387 -0.577 -0.088 |
| 8 | YGL041C YGL041C 0.285 -0.086 0.103 |
| 9 | YGR218W CRM1 -0.018 -0.001 -0.018 |
| 10 | YOR202W HIS3 0.432 -0.710 0.239 |
| 11 | YCR005C CIT2 0.085 0.392 0.464 |
| 12 | YER187W KHS1 0.159 0.139 -0.045 |
| 13 | YBR026C YBR026C 0.276 0.189 0.291 |

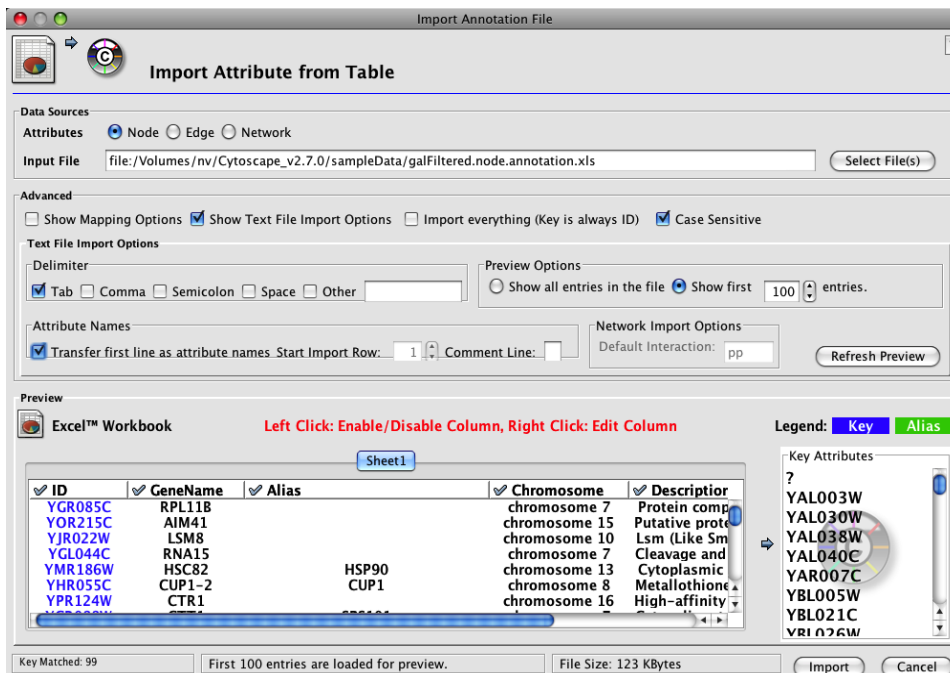
Visualization and Analysis Import:



Import galFiltered.sif file

Import Degree.NA file

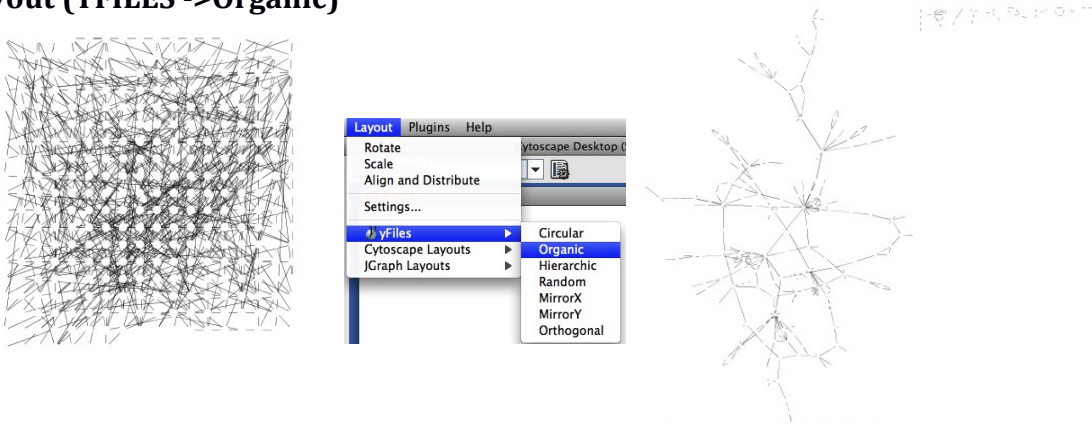
Import galFiltered.node.annotation.xls file



Above seen is the TABLE file import options

Use FILE->IMPORT->Attribute/Expression matrix file option to import expression data.

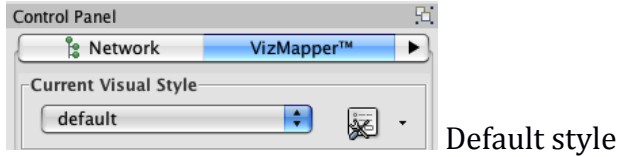
Layout (YFILES ->Organic)



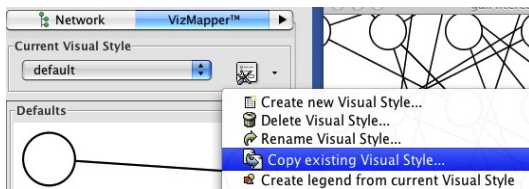
Visual mapping browser

Gene expression data (Gal1, Gal4, Gal80 Tfactors)

Create a new style – by copying existing one



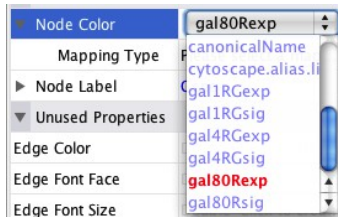
Default style



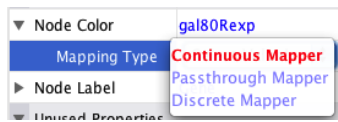
Copy existing style (give it a name)



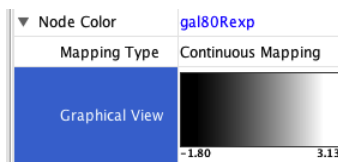
Double-click next to “Node Color” option in the Vizmapper window



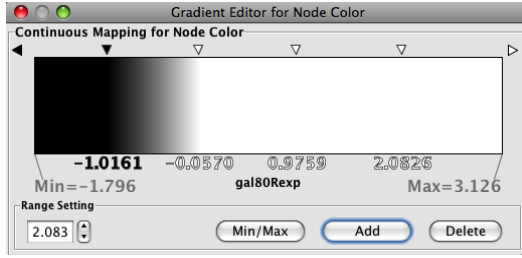
Choose “gal80Rexp” to color the nodes



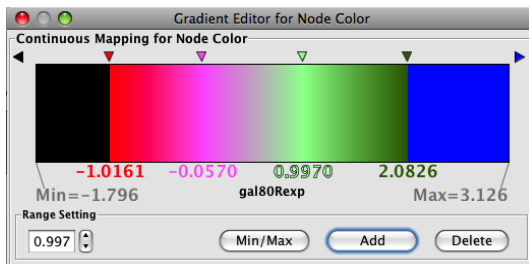
Choose “Continuous mapper” to set the type



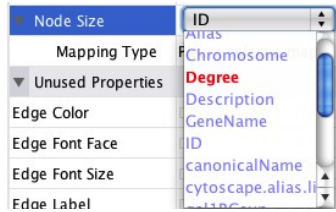
Click on the gradient to go to the gradient editor as seen below



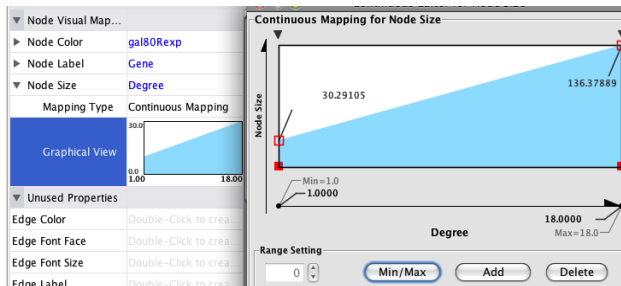
Click "Add" to add more little triangles (we need 6 here). Double click triangles to pick color



Set color for the gradient as = Black-red-pink-lightgreen-green-blue



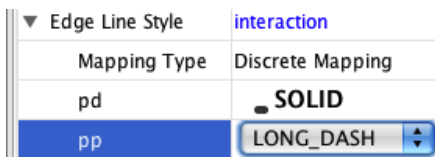
Node size = degree



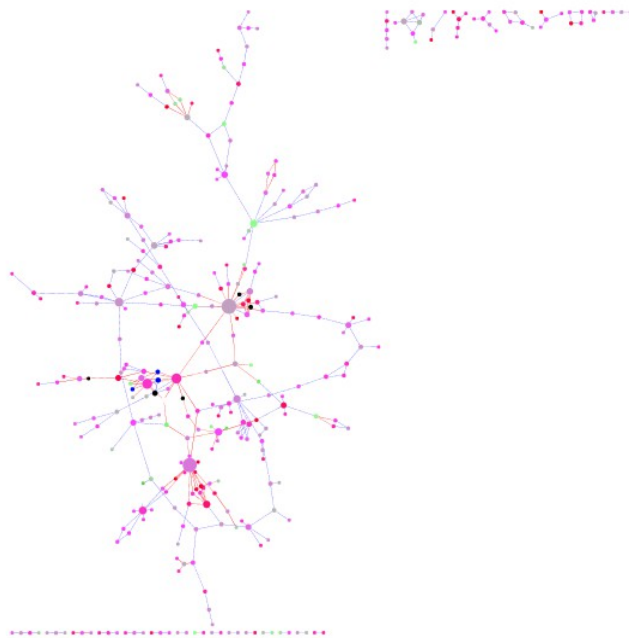
Continuous mapping (30 to 136)



Edge color = interaction

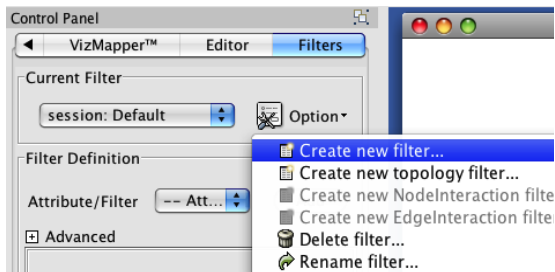


Edge line style = interaction

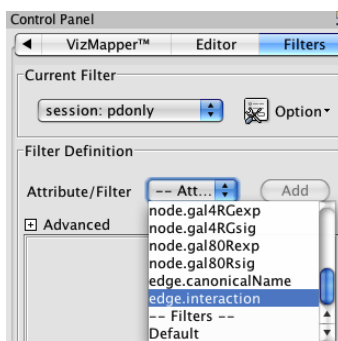


Filter

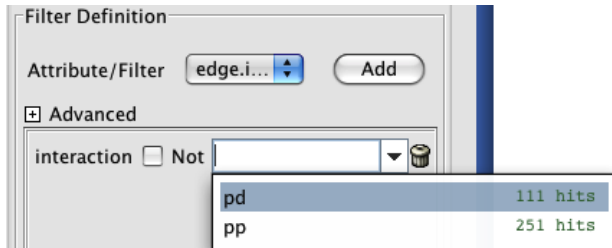
Lets work with pd only (filter and remove pp)



Create new Filter. When asked, give it a name

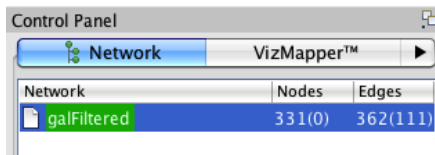


Select "Interaction", click button "Add"

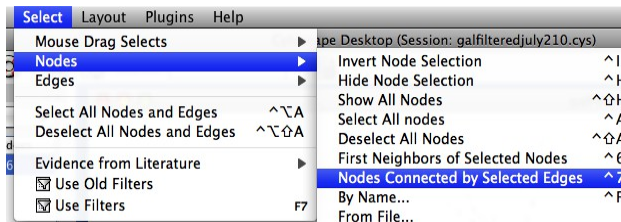


Click the little triangle, click “pd”, then “Apply Filter”.

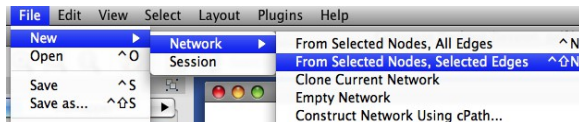
If you now go to the network tab in the “Control panel”, you will see that “111” edges are selected



111 edges are now selected.



Select nodes connected by selected edges



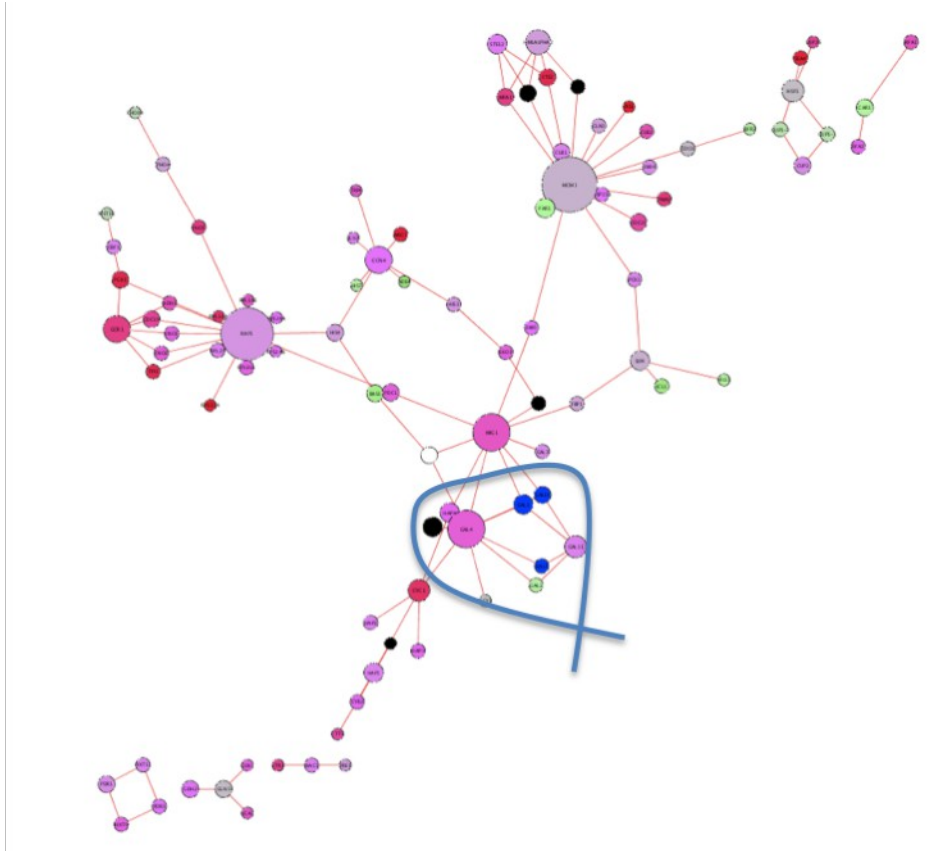
Create a new network, from selected nodes and selected edges

Layout -> Organic

Fit -> to screen

Vizmapper -> Node Label -> GeneName



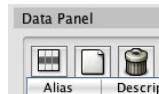


Some biology

3 blue nodes (highly induced)

See what they are by selecting them (clicking on the node and looking at the corresponding data

displayed in the data panel (click the first little icon that you can select to view in the data panel))

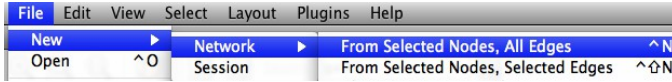


to see the list of attributes

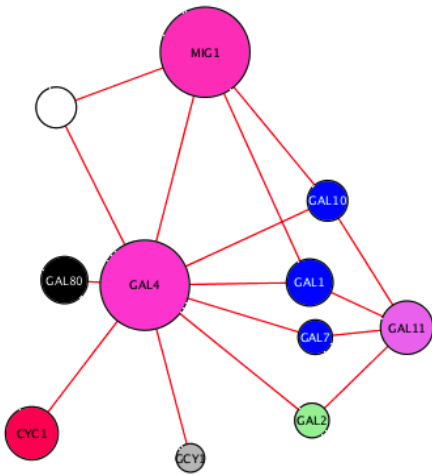
| Alias | Description | GeneName | ID |
|-------|-----------------|----------|---------|
| | Galactose-1... | GAL7 | YBR018C |
| | UDP-glucose... | GAL10 | YBR019C |
| | Galactokinas... | GAL1 | YBR020W |

Data corresponding to selected nodes

Select the two nodes that are connected to all 3 blue nodes (GAL4 and GAL1).
 From Menu bar, choose SELECT -> First neighbors of selected nodes.
 Create a new network from the selection, using all edges.



Create a new network from selected nodes and all edges



Gal4 is repressed by Gal80 (known).

So, if Gal80 is repressed, Gal4 becomes active

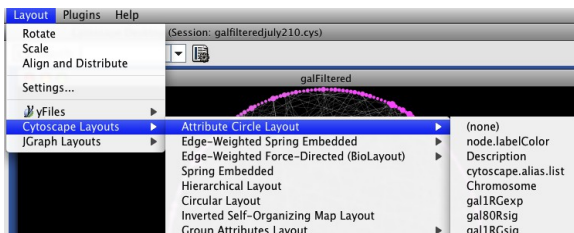
If Gal4 becomes active, it induces Gal genes (Gal1, Gal7, Gal10)

Layouts

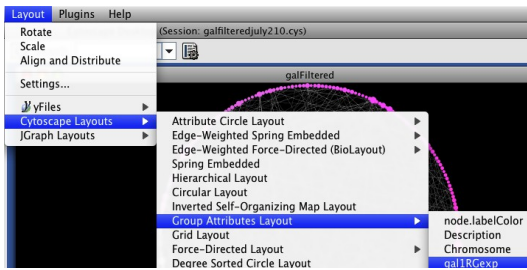
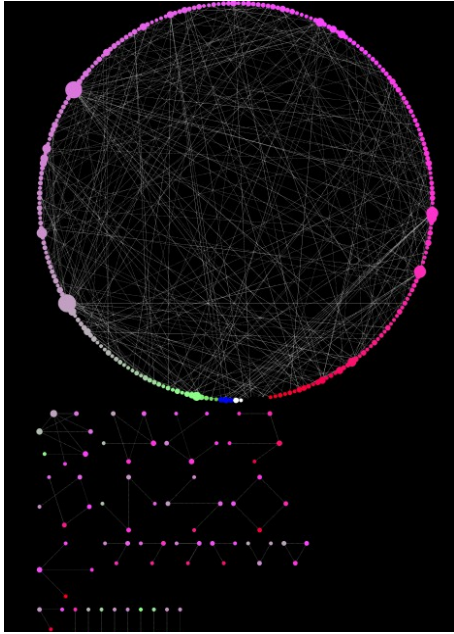
USE THE ABOVE NETWORK – full

Change background to black (use Vizmapper – global preference option)

Change edge color to white



Layout using "Attribute Circle Layout" using gal80RExp



Group attribute -> Use Chromosomes

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3. Demonstration of Building Networks using Cytoscape

Open a new Cytoscape window.

We are going to build a network of proteins interacting with itpr2 (IP3 receptor type2) – calcium channel protein.

Few interactions – takes less time to demonstrate online, use similar method for any proteins

Import – from web services

Choose pathway commons

Search for “itpr2”

Retrieve interactions (7)

Options to filter

Zoom out

Layout – organic

Reduce font size

Right click one – can grow network by adding neighbors

Set visual node attribute browser to show entrez gene id

Name network

STRING data for itpr2

Search for itpr2 at the STRING database site;

<http://string-db.org/>

Reduce score threshold and refresh network

Save network as .txt file

Import network

Layout – organic

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PLUGIN – Advanced Merge

Merge networks from multiple sources based on a common attribute.

Pathway commons nodes – have gene symbols

STRING – also have gene symbols

Select “union”...

Choose pathwaycommons and string networks

Set the matching attributes to “entrez gene” – “canonicalname”

Click “merge”

Zoom out
Layout – organic
Click on one of the pathway common node – showing both ids
See if those two are merged in the new network

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THAT'S IT....

Building networks by Merging data from various sources - tricky.
You will come across several situations....

Do email scienceapps@niaid.nih.gov for any help with Cytoscape or building and analyzing networks, you can mention my name if you want.

We could provide assistance from simple trouble shooting to fruitful collaborations.