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1. Demonstration of the Cytoscape Interface

Cytoscape Interface (version 2.8.3)

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.

Visualization and Analysis
Import:
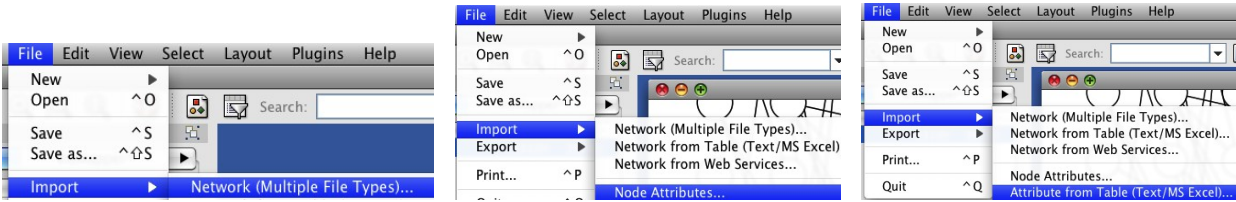
Import galFiltered.sif file   Import Degree.NA file   Import galFiltered.node.annotation.xls file
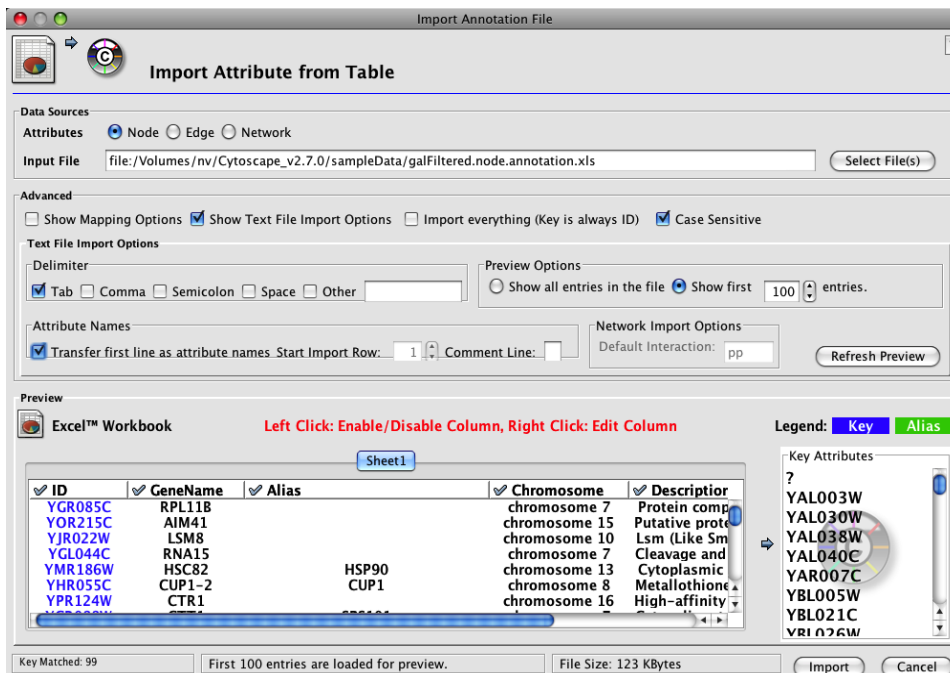
Above seen is the TABLE file import options

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

Layout (YFILES ->Organic)
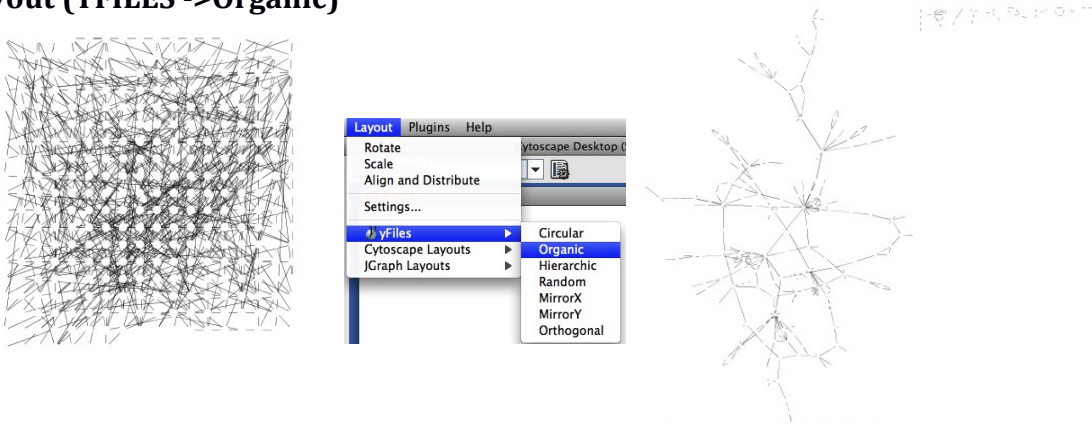
Visual mapping browser

Gene expression data (Gal1, Gal4, Gal80 Tfactors)

Create a new style – by copying existing one
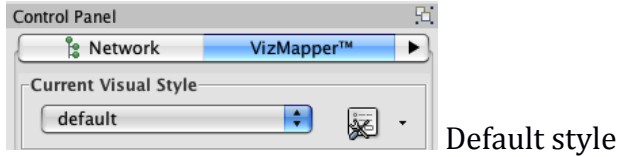
 Default style
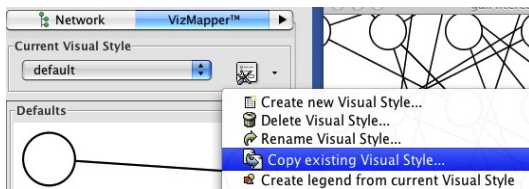
 Copy existing style (give it a name)

 Double-click next to "Node Color" option in the Vizmapper window
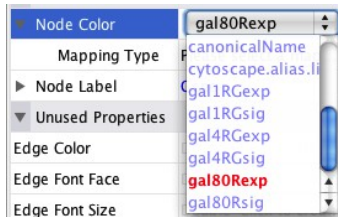
 Choose "gal80Rexp" to color the nodes
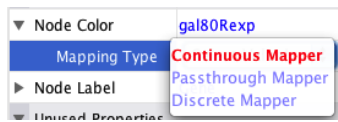
 Choose "Continuous mapper" to set the type
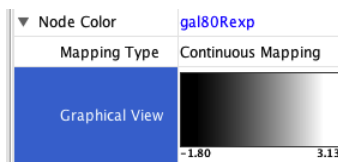
 Click on the gradient to go to the gradient editor as seen below
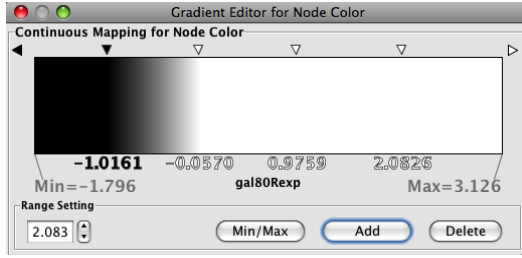
Click "Add" to add more little triangles (we need 6 here). Double click triangles to pick color
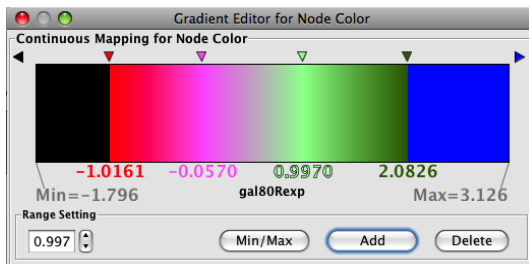
Set color for the gradient as = Black-red-pink-lightgreen-green-blue
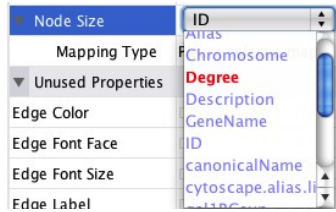
Node size = degree
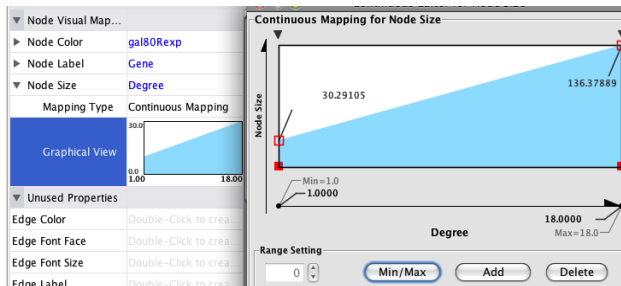
Continuous mapping (30 to 136)

Edge color = interaction
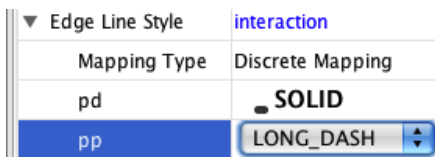
Edge line style = interaction
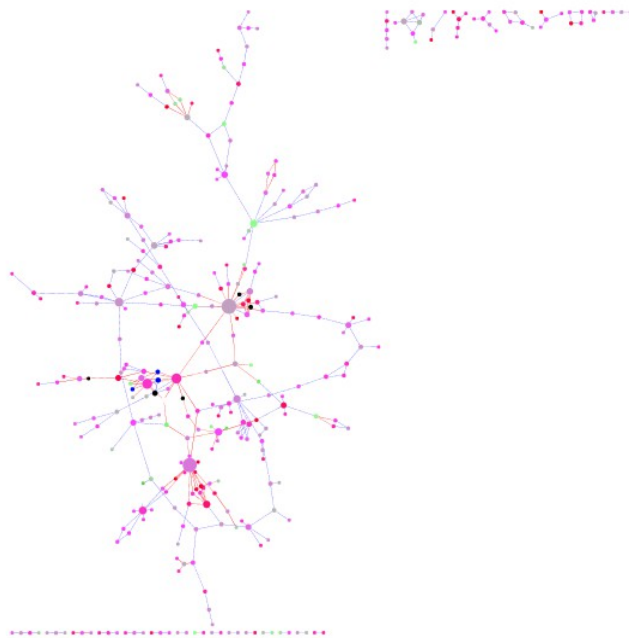
Filter

Lets work with pd only (filter and remove pp)
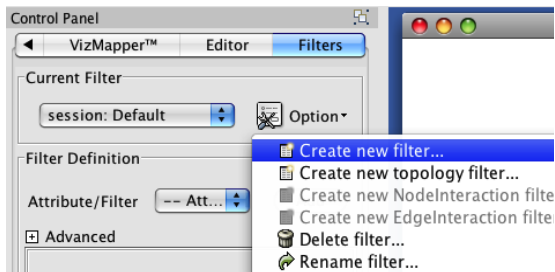
Create new Filter. When asked, give it a name
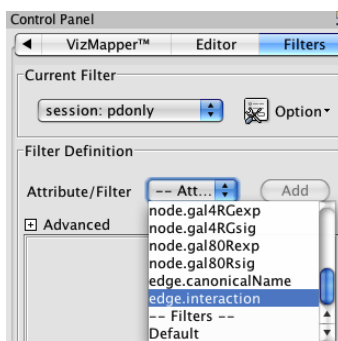
Select "Interaction", click button "Add"
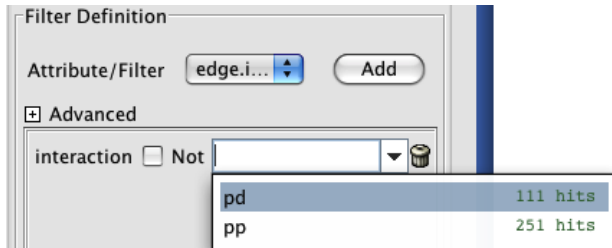
Click the little triangle, click "pd", then "Apply Filter".

If you now go to the network tab in the "Control panel", you will see that "111" edges are selected
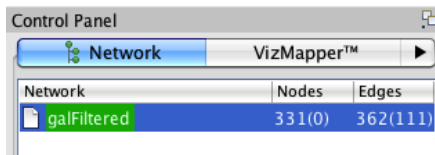
111 edges are now selected.
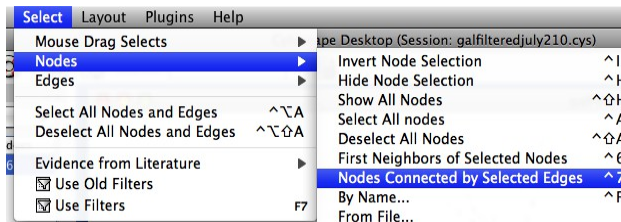
Select nodes connected by selected edges
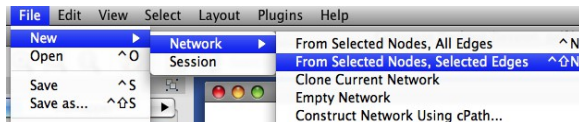
Create a new network, from selected nodes and selected edges

Layout -> Organic

Fit -> to screen

Vizmapper -> Node Label -> GeneName
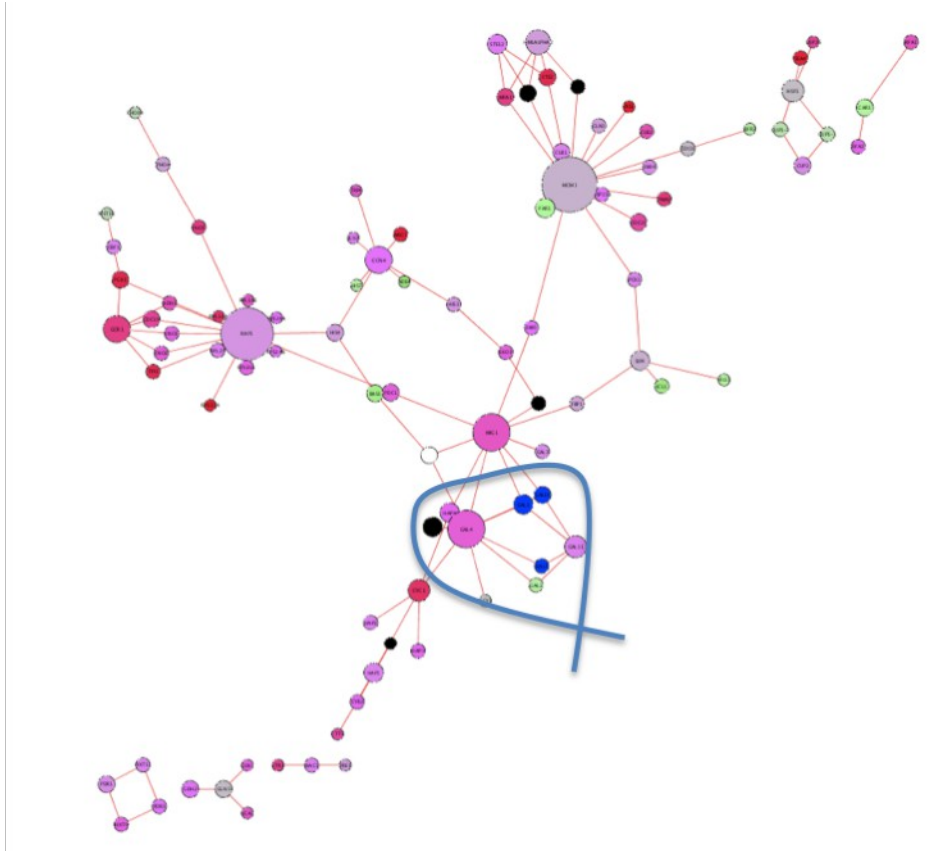
Some biology

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 to see the list of attributes that you can select to view in the data panel))

   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.
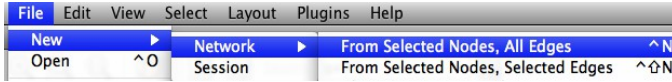
Create a new network from selected nodes and all edges
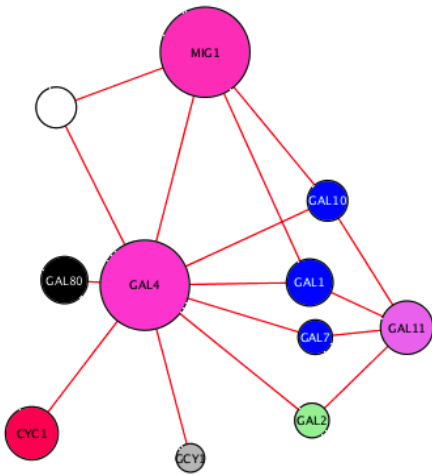
Gal4 is repressed by Gal80 (known).

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
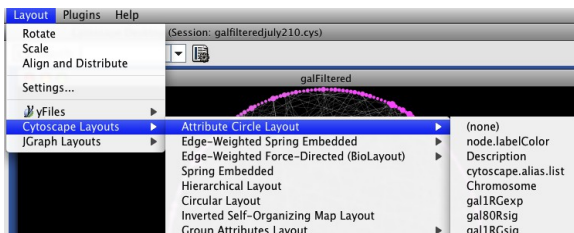
Layout using "Attribute Circle Layout" using gal80RExp
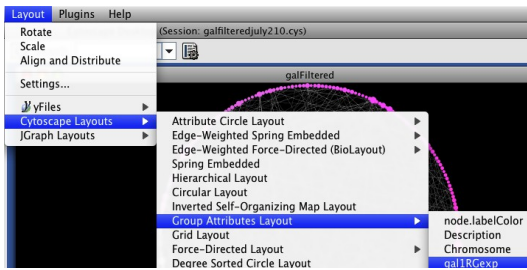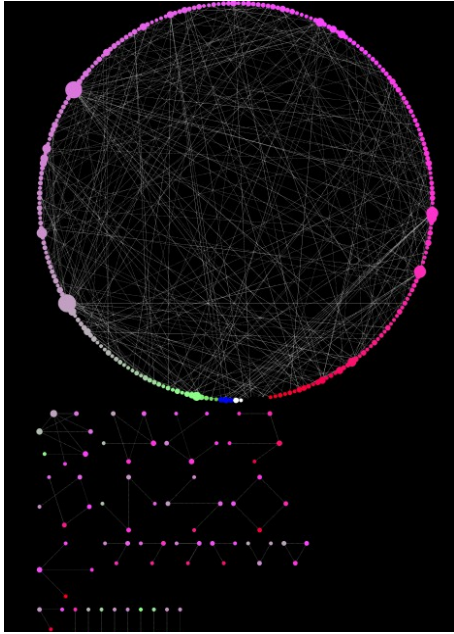
Group attribute -> Use Chromosomes

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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.