

CYTOSCAPE PART II

3 types of network integration : integration with knowledge (enrichmap), integration of different networks, integration of expression and networks (jActive)

Integration of different networks : Networks of Networks

- Load the 3 different networks available in Github in Cytoscape (PPI.gr, Pathways.gr, Complexes.gr)
- What is the intersection between the 3 networks ? Between PPI and Complexes ?

Use Tools -> Merge -> Intersection

- Focus on the PPI_Complex intersection network, extract the largest connected component (with NetworkAnalyzer) and run an partitioning algorithm (with Clustermaker -> Network Cluster Algorithm -> MCL Cluster)
- See clusters with Clustermaker -> clusterMaker Visualization -> create network from cluster. You can also use create Results Panel from Clusters, or use the "Style" table to color clusters (Discrete mapping => right click, Mapping value generator)
- (If we have time), repeat with MCODE algorithm to see the different clusters obtained

Integration of Expression and Networks (jActive)

(this tutorial is inspired from

http://opentutorials.cgl.ucsf.edu/index.php/Tutorial:JActiveModules_3)

- Install the jActiveModules App either from within Cytoscape 3 (**Apps** → **App Manager**) or directly from <http://apps.cytoscape.org/>
- Open the **galFiltered.sif** network via **File** → **Import** → **Network from File....**
- Some of the network edges are directed ('pd'), other are not ('pp'), draw the directed edges with an arrow
- Load the expression data matrix **galExpData.csv** using the **File** → **Import** → **Table from File....** This file contains expression results for three sets of expression analysis, involving perturbation of three transcription factors involved in the yeast galactose utilization pathway.

This file also contains a necessary ingredient for jActiveModules: p-values indicating the significance of each expression value.

- Color nodes according to gal80RGexp
 - Node fill color
 - Continuous mapping

- Go to **Apps** → **jActiveModules....** The jActiveModules interface will appear as a tab in the **Control Panel**.

- Select gal80Rsig, Expand the **Advanced** panel, and run the algo with **Anneal** option. Notice that the **Number of Modules** is set to 5. This means that five putative hits will be returned, even if only one good one is found.

Target Network
galFiltered.sif_1

Numeric Node Attributes

Name	Most sig	Least sig	Reverse sig	Scaling
gal80Re...	-1.373	3.126	<input type="checkbox"/>	r...
gal1RG...	0	0.964	<input type="checkbox"/>	n...
gal1RG...	-2.426	2.058	<input type="checkbox"/>	r...
gal4RG...	0	1	<input type="checkbox"/>	n...
gal4RG...	-2.406	1.224	<input type="checkbox"/>	r...
gal80Rsig	0	1	<input type="checkbox"/>	n...

Advanced ▾

General Parameters

Number of Modules (1-1000): 5

Overlap Threshold: 0.8

☒ Adjust score for size?

☒ Regional Scoring?

Strategy

☒ Anneal ☐ Search

Annealing Parameters

Iterations (0-10⁸): 100000

Start Temp (0.0001 - 100): 1.0

Search

- When the results are ready, you will see 5 new subnetworks, as well as a network illustrating the search results.
- Explore the 2 subnetworks with the highest scores, and check their functions, for instance with the BINGO plugin