Tutorial:Cluster Maker

clusterMaker is a Cytoscape plugin that unifies different clustering techniques and displays into a single interface. Current clustering algorithms include Hierarchical and k-Means for clustering expression or genetic data, and MCL and FORCE for clustering similarity networks to look for protein families.

ClusterMaker

Biological Use Case: Find possible complexes, protein families, functional relationships and view in biological context.

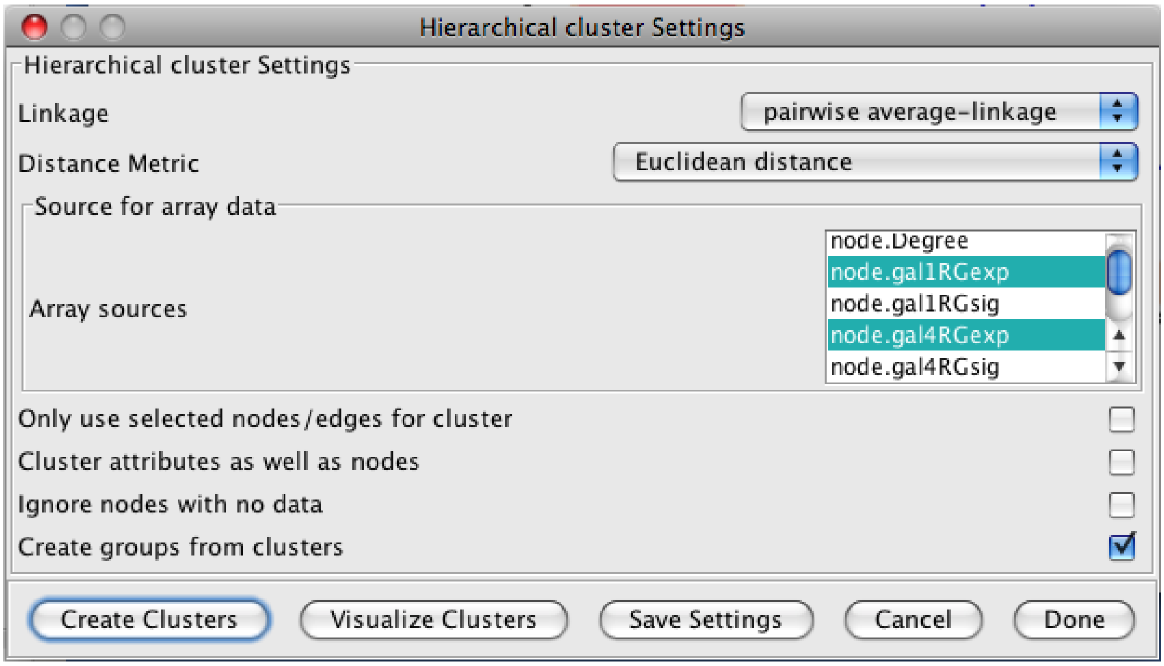
Dependencies: For group features, please also install the MetaNodePlugin2 and the NamedSelection plugin.

Procedure

1. Start with expression data for studies into mechanism for galactose utilization. Go to **File->Open** and select *galfiltered.cys* to load a session.

Run clustering to determine interesting subnets

1. Select **Plugins->Cluster->Hierarchical cluster**.
2. In the **Source for array data** box, select *node.gal1RGexp, node.gal4RGexp*, and *node.gal80Rexp*.
3. Deselect **Only use selected nodes/edges for cluster**.
4. Click **Create Clusters**.
5. When you have created the clusters, the **Visualize Clusters** clusters button should become active. Click **Visualize Clusters**.



Hierarchical cluster Settings

Hierarchical cluster Settings

Linkage: pairwise average-linkage

Distance Metric: Euclidean distance

Source for array data

Array sources: node.Degree, node.gal1RGexp (selected), node.gal1RGsig, node.gal4RGexp (selected), node.gal4RGsig

Only use selected nodes/edges for cluster ☐

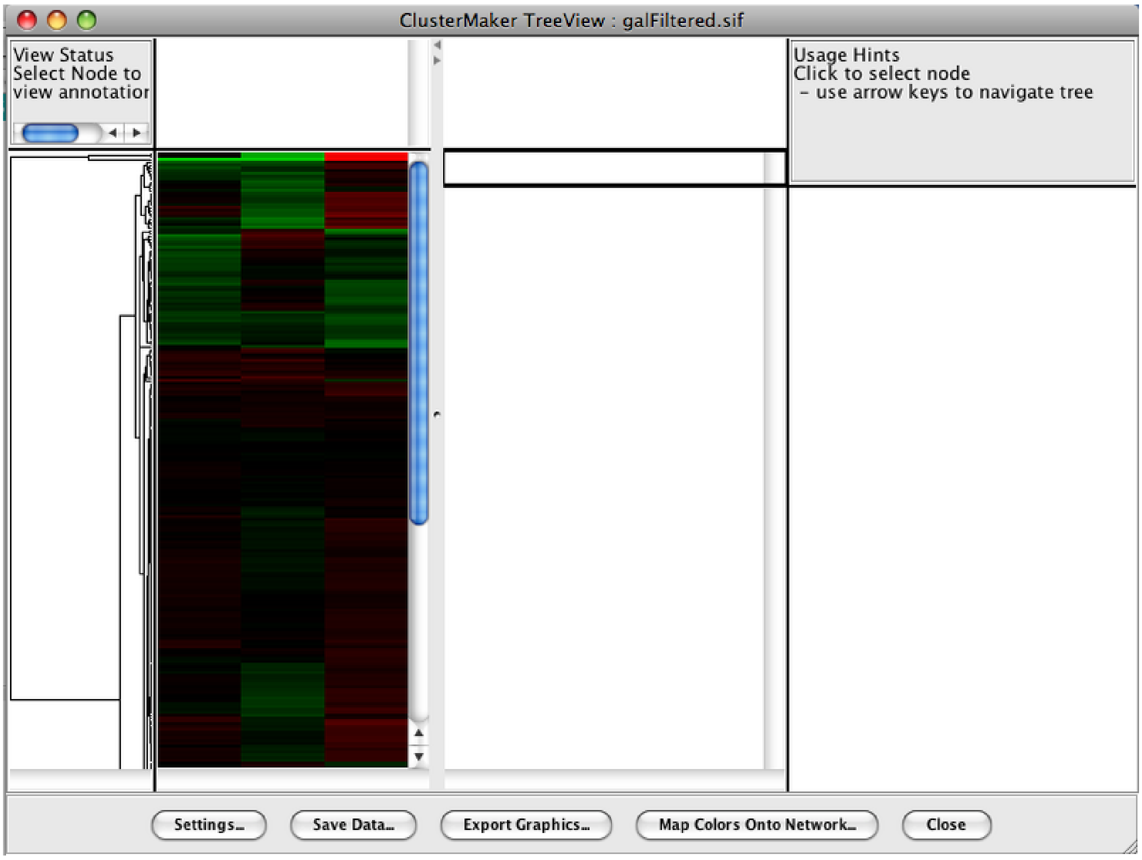
Cluster attributes as well as nodes ☐

Ignore nodes with no data ☐

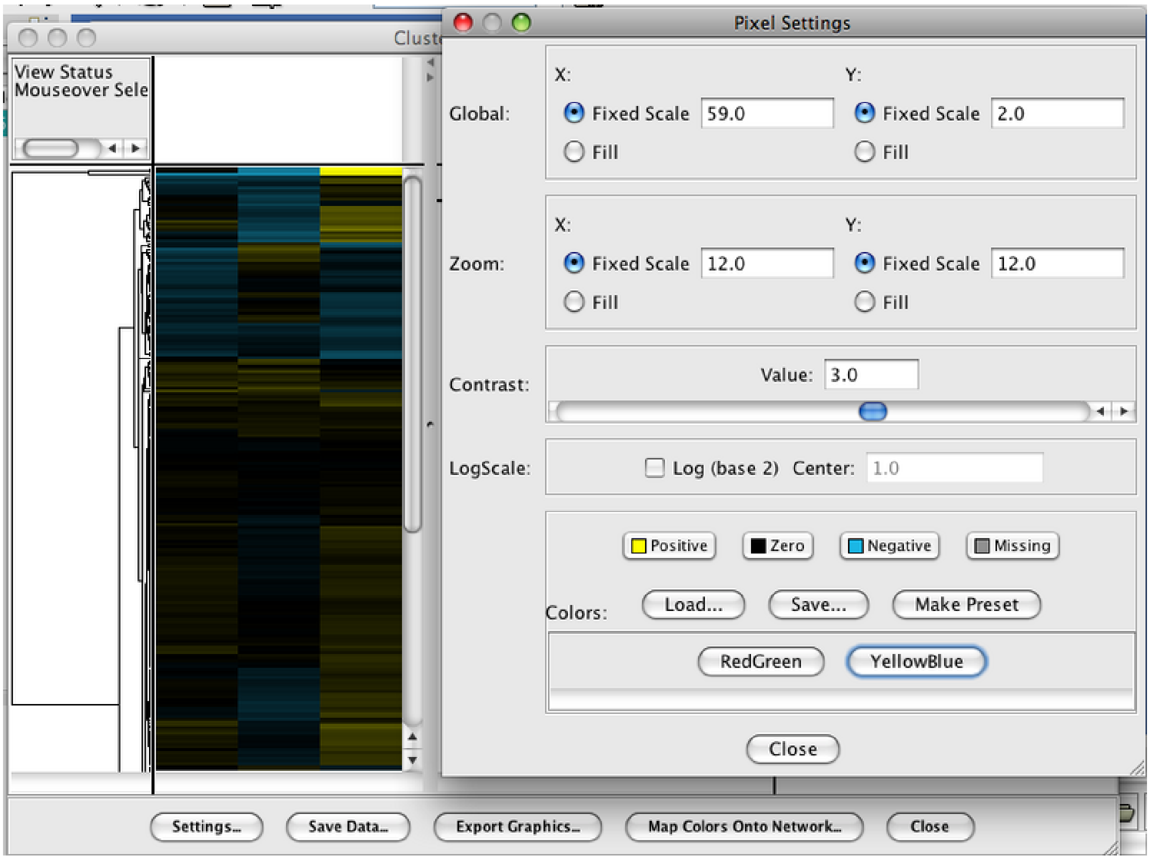
Create groups from clusters ☑

Visualize and navigate the clusters

1. You will now see an Eisen treeview visualization. On the treeview window, explore by clicking on points on the dendogram. Clicking/selecting a particular row in the heatmap will result in the expression values for that column being overlaid on the network view.



1. Use **shift-drag** to draw a box and see results on network.
2. Use **shift-click** to pick individual columns.
3. Select an individual row by clicking on it.
4. You can adjust the color scheme and contrast by going to **Settings**. For this demo, select **YellowBlue** in the colors window. This will change the Red/Green color scheme to Yellow/Blue. Click **Close**.



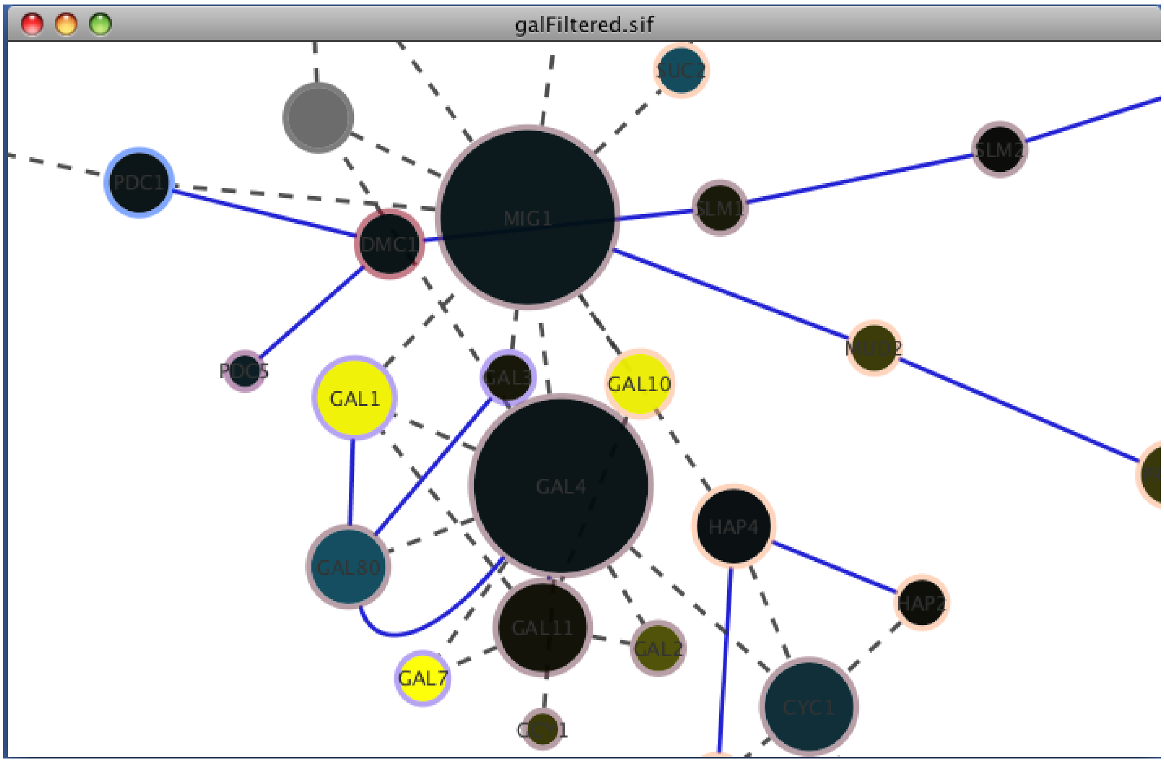
Global: X: ● Fixed Scale 59.0 ○ Fill Y: ● Fixed Scale 2.0 ○ Fill

Zoom: X: ● Fixed Scale 12.0 ○ Fill Y: ● Fixed Scale 12.0 ○ Fill

Contrast: Value: 3.0

LogScale: ☐ Log (base 2) Center: 1.0

1. Press **Map Colors Onto Network** and select one of the options from the *Attribute List*.
2. Click **Create Vizmap**. This will map the colors onto the network.



Animate expression values over time

1. Go to **Map colors onto network**.
2. On the pop-up screen, click on specific attributes to select. For this example, select *gal4RGexp* and *gal80Rexp*.
3. Press **Animate Vizmap**. This will animate the image on the main Cytoscape session screen.

Finding modules and complexes

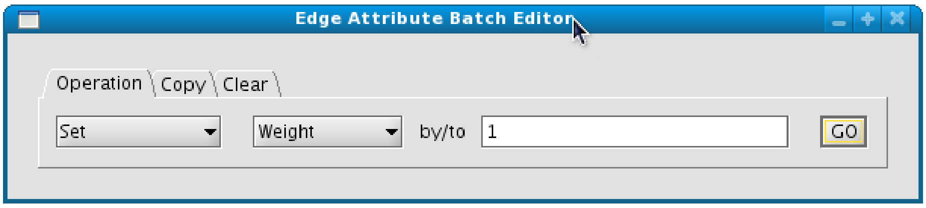
Now we're going to use *clusterMakers* **'MCL** algorithm to search for modules in the galFiltered network.

Procedure

1. Start with galFiltered open, as before.
2. Add a new edge attribute to provide a weight
3. Cluster with MCL
4. Visualize clusters

Add a new edge attribute

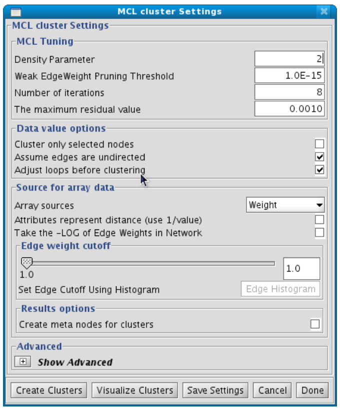
1. In the **Data Panel** click on the **Edge Attribute Browser** tab.
2. Now click on the **Create New Attribute** icon and create a new Integer attribute. Name the attribute *Weight*.
3. We're going to set all of our weights to be equal. To do this, select the **Attribute Batch Editor** icon located at the right of the **Data Panel**.
4. Under operation, select **Set** and *Weight* to 1. Then click **GO**.



Set
Weight
by/to 1

Create Clusters

1. Now that we have weights on our edges, we can use **MCL**: Select **Plugins->Cluster->MCL cluster** to bring up the **MCL cluster Settings** dialog.

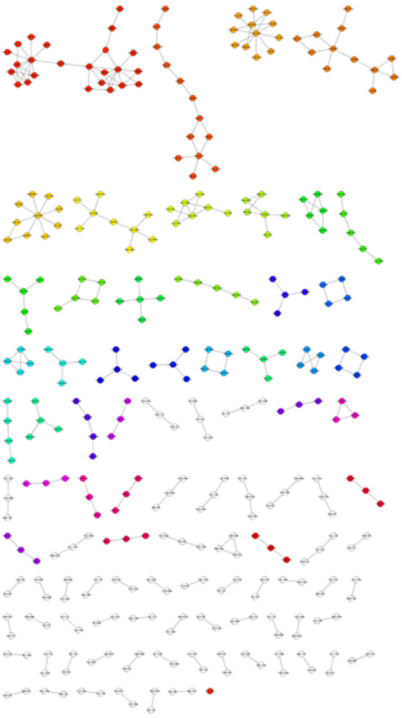


Density Parameter 2
Weak EdgeWeight Pruning Threshold 1.0E-15
Number of iterations 8
The maximum residual value 0.0010
Cluster only selected nodes ☐
Assume edges are undirected ☑
Adjust loops before clustering ☑
Array sources Weight
Attributes represent distance (use 1/value) ☐
Take the -LOG of Edge Weights in Network ☐
1.0 1.0
Set Edge Cutoff Using Histogram
Create meta nodes for clusters ☐

1. If it's not already set: change the **Array sources** to *Weight* and click **Create Clusters**.
2. After the algorithm has finished, MCL will display a dialog with the summary results.

Visualizing Clusters

1. To see the clusters in a new network, click on **Visualize Clusters**.
2. *clusterMaker* adds a new attribute (*0_MCL_cluster* in this case) to the network. Each cluster has a unique number for this attribute that may be used to change the graphics attributes in the **VizMapper**



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