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.

**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.
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**.
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 top right of the Data Panel.
4. Under operation, select Set and Weight to 1. Then click GO.
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.

![MCL cluster Settings dialog]

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.
References

Article Sources and Contributors


Image Sources, Licenses and Contributors


License

Attribution-NonCommercial-ShareAlike 3.0 Unported
http://creativecommons.org/licenses/by-nc-sa/3.0/