

CyFinder User Guide

About

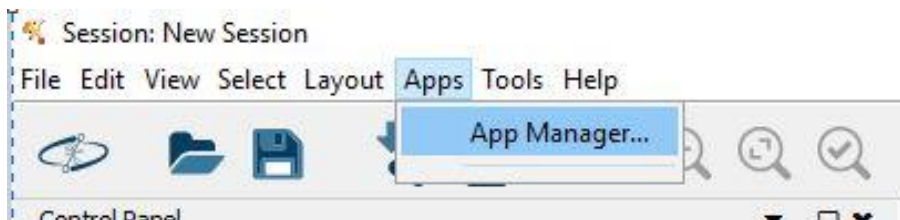
CyFinder is a Cytoscape app used for finding clique (complete) and bipartite subgraphs within a given network, which are then displayed in a visually meaningful way.

Getting Started

Step 1:

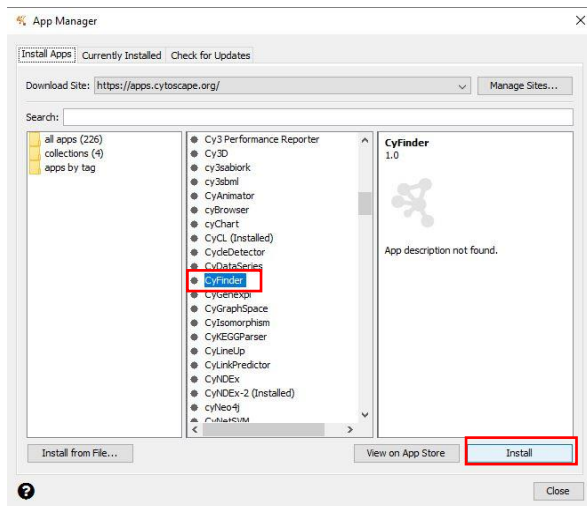
To get started we need to download the CyFinder app first.

To download CyFinder click the Apps toolbar and select the “App Manager...” option



Step 2:

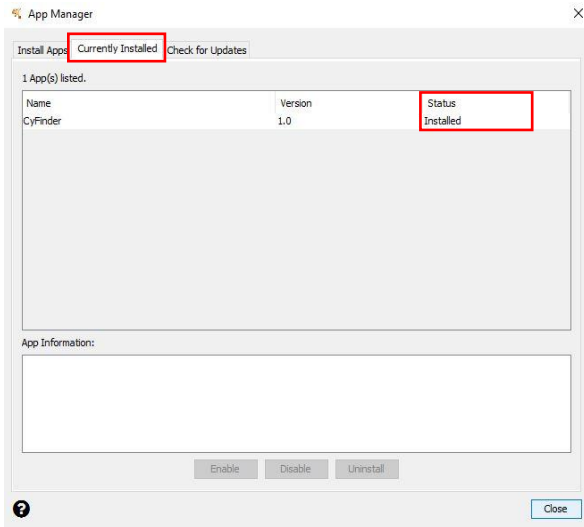
Next, locate the CyFinder app from the list of available apps and click install on the bottom right.



Step 3:

After clicking “Install”, click on the “Currently Installed” tab and a screen like this should appear.

If CyFinder has been installed successfully, you should see the word “Installed” under the “Status” column.

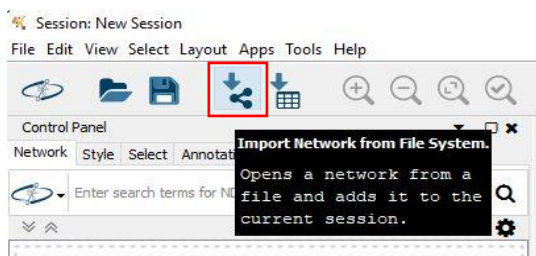


You may now close this window.

Step 4:

Now that we have CyFinder installed we are ready to import a network.

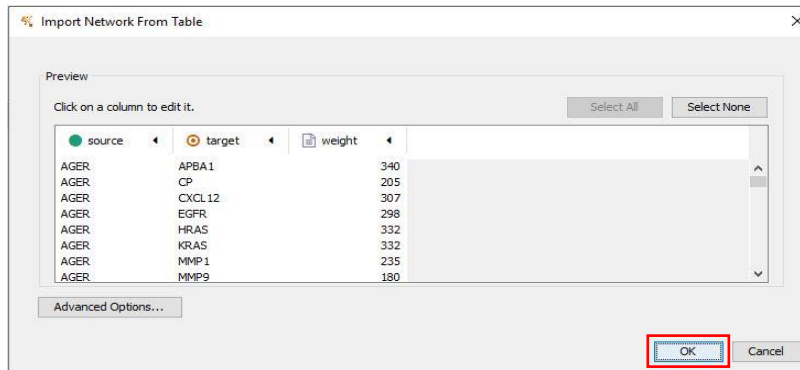
To import a network, click on the “Import Network from File System” button as shown below and navigate to the location of your network file then select it.



Step 5:

After selecting your network file from the previous step, a window like this should appear.

Make sure all your data has been processed successfully by Cytoscape and press “Ok” to import your network.

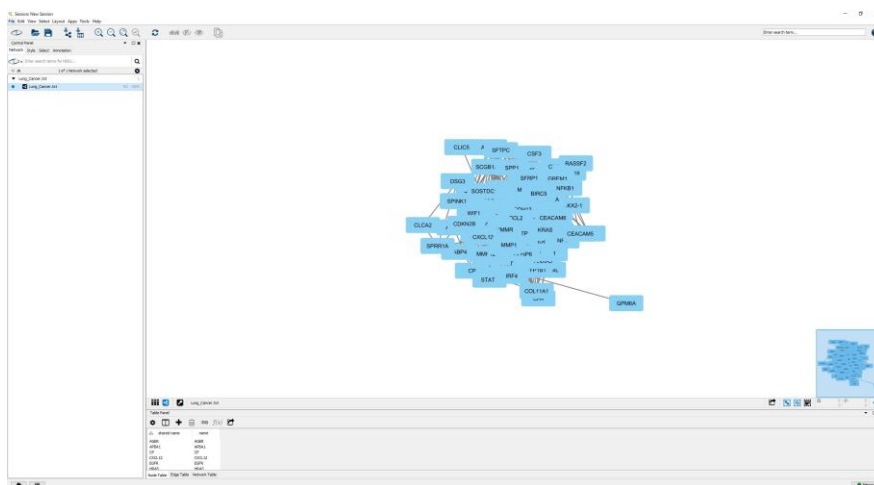


Step 6:

Now that you have imported your network it should look somewhat like the figure below.

In this example we are using “The Lung_Cancer.txt” data set which makes up our network.

This particular network contains 82 nodes and 1062 edges.



Now that you have your network imported into Cytoscape, we are ready to explore the options that the CyFinder app has to offer.

Step 7:

First, in order to find subgraphs within your network using the CyFinder app you will have to make your network undirected.

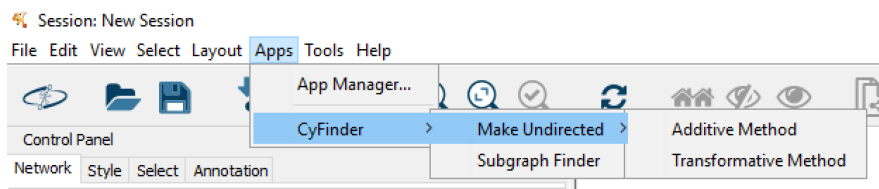
CyFinder provides two different options of doing this, the **additive method** and **transformative method**.

The additive method makes the network undirected by making a copy of every edge and reversing its source-target relationship.

The transformative method makes the network undirected by altering the existing edges and replacing them with exact duplicates except they have the internal Cytoscape flag for directed-ness of edges set to false.

In this tutorial, we will be using the Transformative Method.

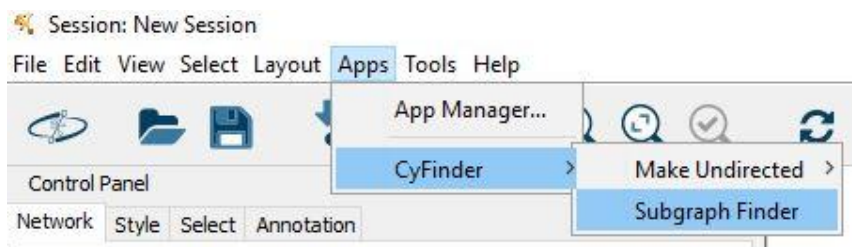
Click Apps -> CyFinder -> Make Undirected -> Transformative Method or Additive Method



Step 8:

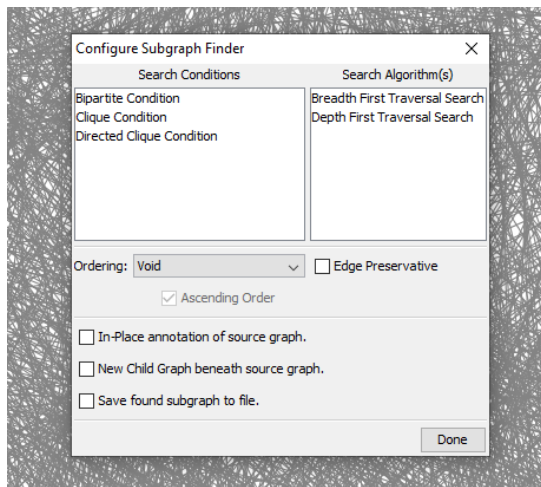
Now that our network is in an undirected state, we are ready to find meaningful subgraphs within this network.

Click on Apps -> CyFinder -> Subgraph Finder



Step 9:

After performing the previous step, the following window should appear:



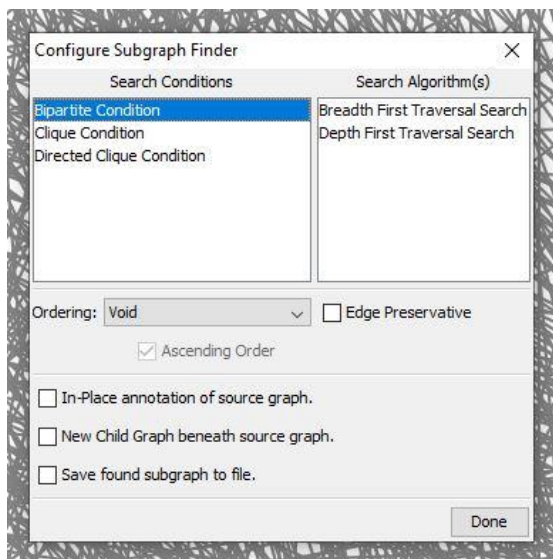
We are now ready to find Clique and Bipartite subgraphs.

Step 10:

As you can see CyFinder provides three search conditions to choose from, the **bipartite condition**, **clique condition**, and **directed clique condition**.

In this tutorial we will be showing the bipartite condition which is used to find bipartite subgraphs within the network, however the steps of using the clique condition and directed clique condition will be identical.

Select the **bipartite condition** by clicking on it.



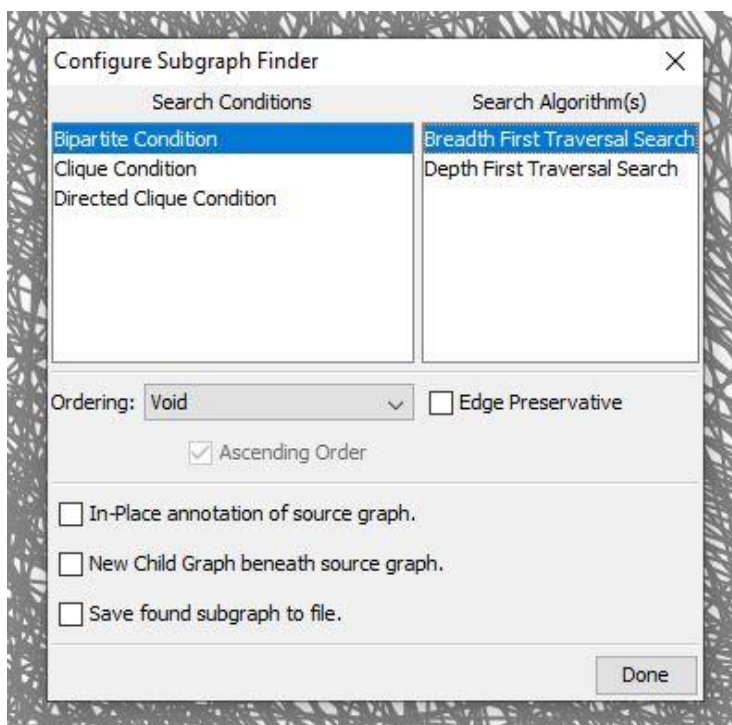
Step 11:

Now that we have specified which type of subgraphs should be searched for, we need to specify which search algorithm should be used to find them.

CyFinder provides us with two options to choose from, **breadth first traversal search**, and **depth first traversal search**.

In this tutorial we will be using the breadth first traversal search algorithm, however the steps of using the depth first traversal search algorithm will be identical.

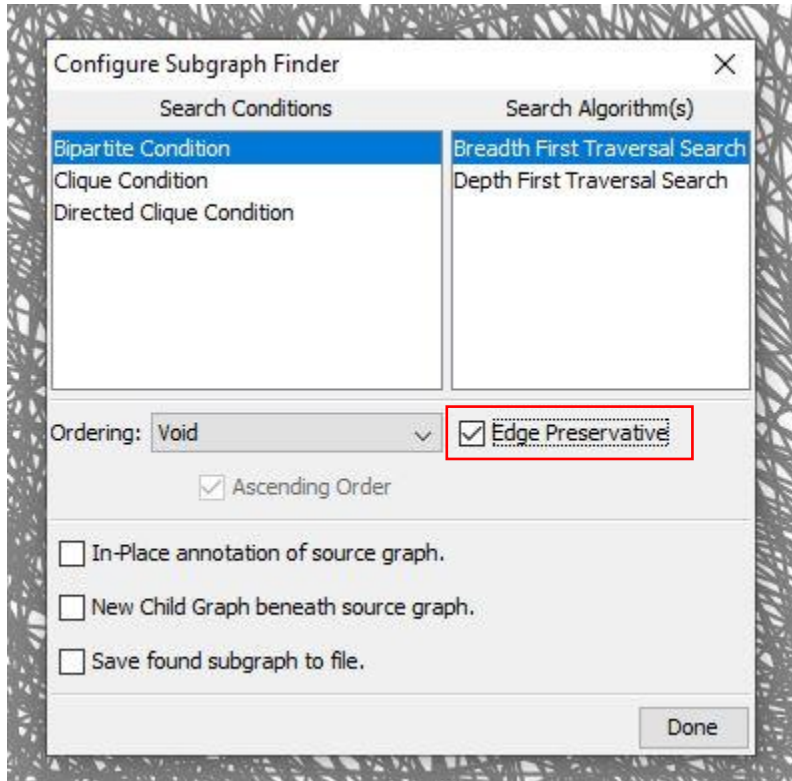
Select the **breadth first traversal search** algorithm by clicking on it.



Step 12:

Now that we have chosen our search condition and search algorithm, make sure the “**Edge Preservative**” checkbox is checked in order to preserve our edges.

Check the “**Edge Preservative**” checkbox by clicking on it.



Notice that there is a dropdown box for “Ordering” that we haven’t discussed yet that is currently is set to void.

We will leave it as void for the purposes of this tutorial since we are not interested in any particular ordering of our subgraphs.

Step 13:

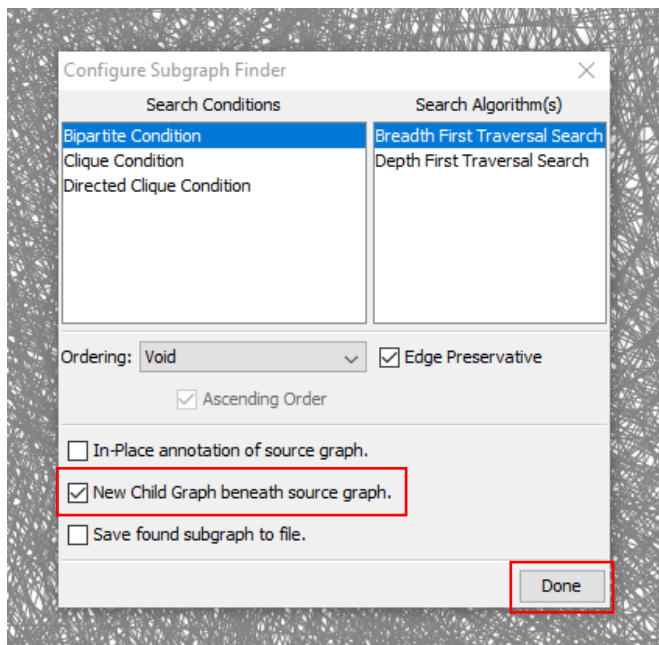
Now it is time to tell CyFinder how we want our results to be given to us. CyFinder provides us with three different options for how we would like to receive/display our results.

The three options are **“In-Place annotation of source graph”**, **“New Child Graph beneath source graph”**, and **“Save found subgraph to file”**, which we will now discuss.

In this tutorial we will be using the **“New Child Graph beneath source graph”**.

Check the **“New Child Graph beneath source graph”** checkbox by clicking on it.

Now that all of your options selected click the **“Done”** button.

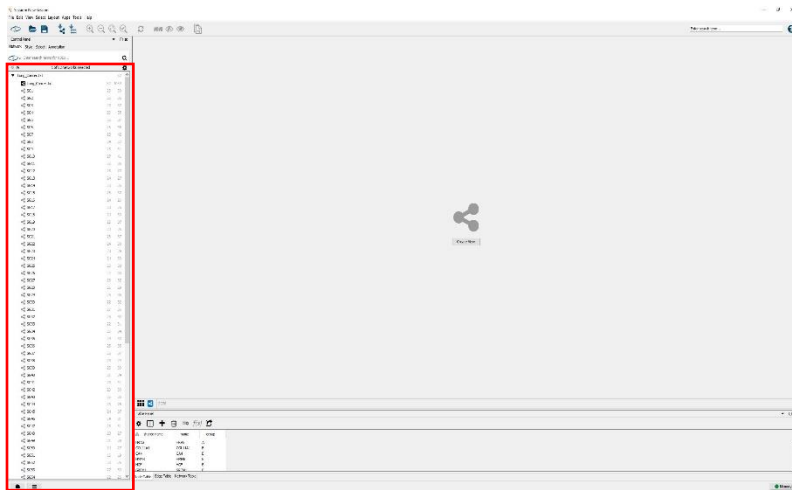


Step 14:

After you click on the “Done” button a new window will appear on left side of your Cytoscape window that will contain our results, as shown in the figure below.

The results are all of the subgraphs that were found given the conditions that we specified.

In our case, all of the subgraphs that were found are bipartite graphs using the breadth first search algorithm.

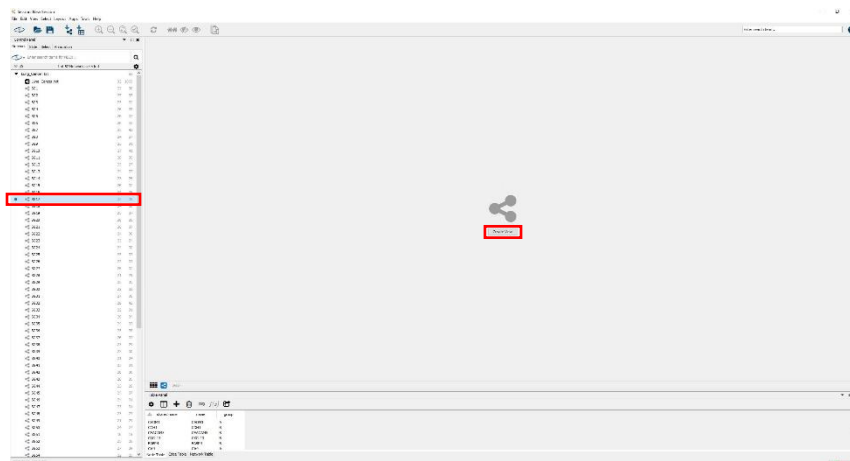


Step 15:

Now that we have all of our bipartite subgraphs available to us on the left window, we can simply select one.

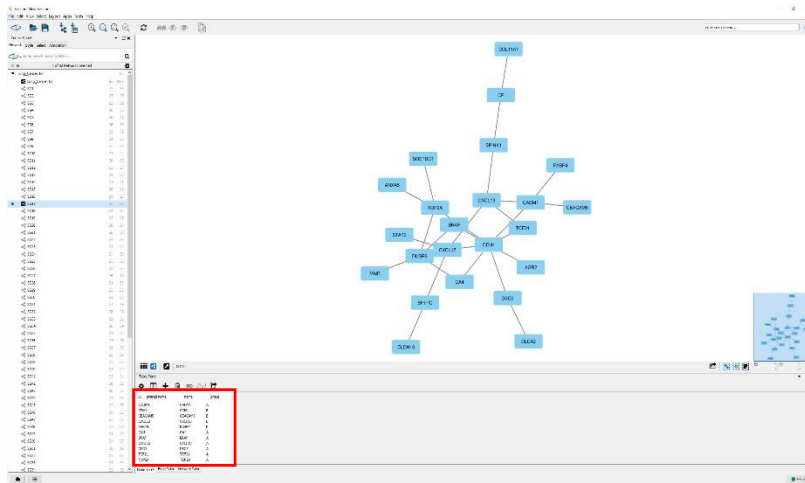
Then we can click on the “Create View” button in the center of the screen in order to view the selected subgraph.

In this tutorial we selected the “SG17” subgraph which stands for subgraph 17.



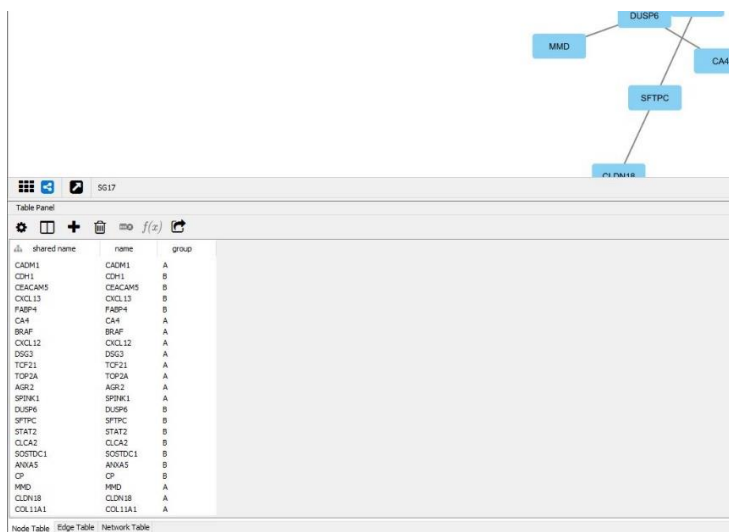
Step 16:

After clicking the “**Create View**” button your subgraph should be displayed. Notice the “Node Table” on the bottom of the window that CyFinder has populated particularly for this subgraph.



Step 17:

Still looking at the same subgraph “SG17” from our previous step. We can notice that it has a column called “group” in its node table. CyFinder has populated this column for us so we can easily be able to distinguish between the two different sets that make up this bipartite subgraph.



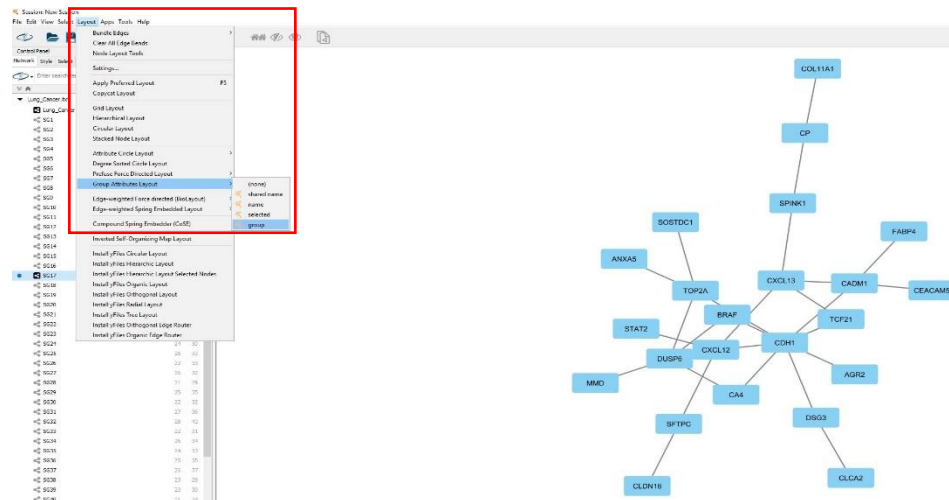
In the next step, we will show how to use the “group” attribute that CyFinder has provided to us in order to visually display the two distinct sets using the Cytoscape layout options.

Step 18:

To visually show the distinct sets using the “group” attribute that CyFinder has provided us with, we can take advantage of the “Group Attribute Layout” provided in Cytoscape by default.

As show in the figure below,

Click Layout -> Group Attribute Layout -> group



Step 19:

After performing the previous step correctly your bipartite subgraph should now be displayed in a similar format as shown in the figure below.

Now you should easily be able to distinguish between the two sets that make up the bipartite subgraph, where each distinct set is represented using a circular layout.

