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Based off of the original by Ariel Sari & Evyatar Saias
Cytoscape 3.7.2

CyFinder User Guide

This is a modified version of the original User Guide by the previous group that worked on this project during Fall 2019. It has been significantly been more modified than the Developer Guide was as most of the screenshots and much of the text have been replaced and reorganized.

About

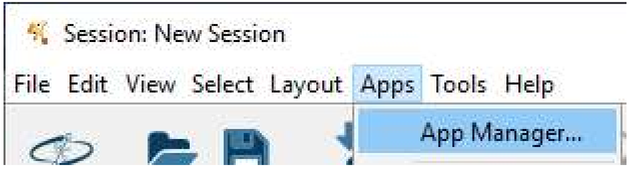
CyFinder is a Cytoscape app used for finding clique (complete) and bipartite subgraphs within a given network, which are then displayed in a visually meaningful way.

Getting Started

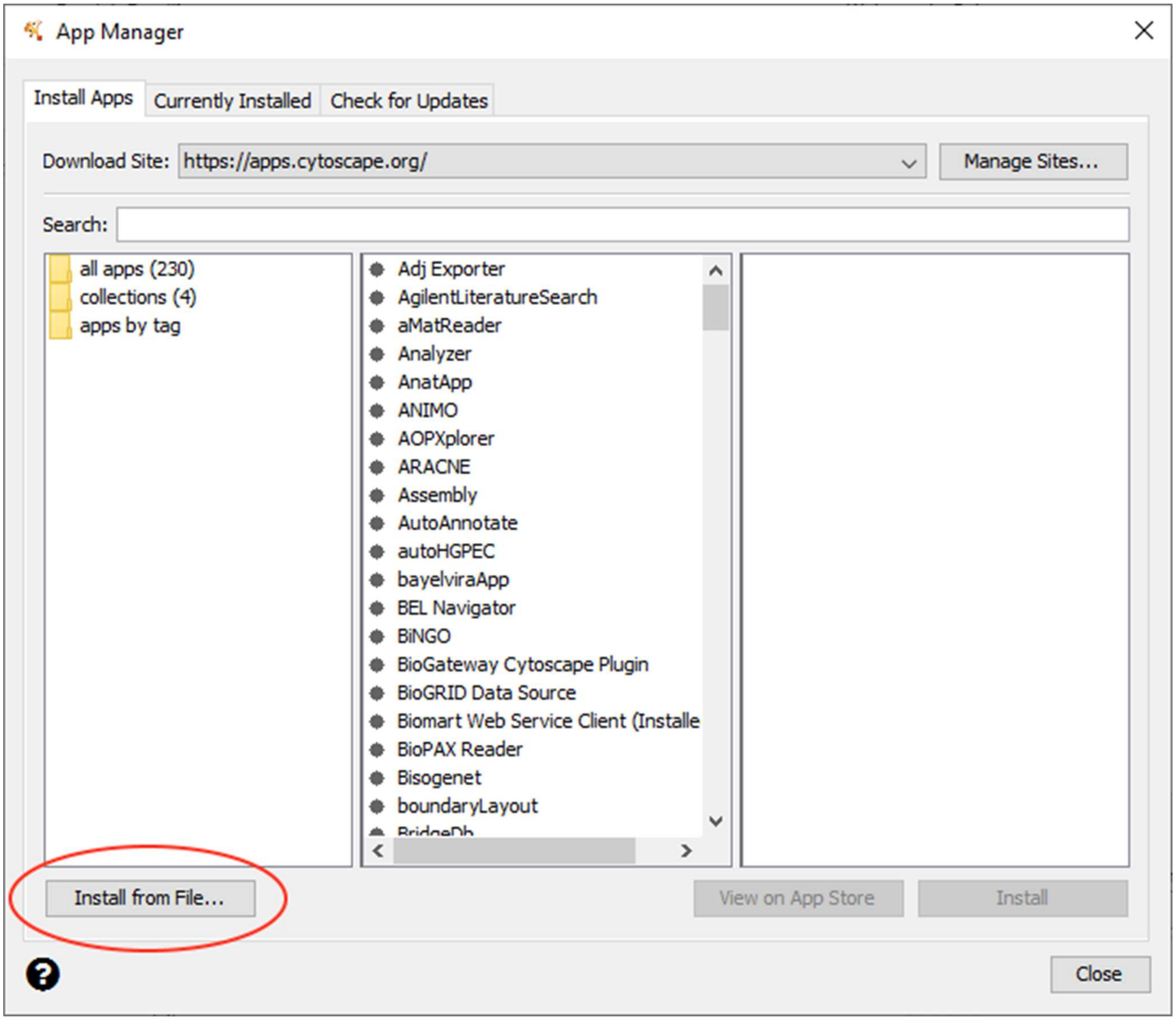
Step 1:

To get started we need to install the CyFinder app first. Instructions on building and installing the jar can be found in the Developer Guide. The installation steps are listed here for convenience.

Step 1a. Open Cytoscape and select Apps from the toolbar then click on "App Manager"



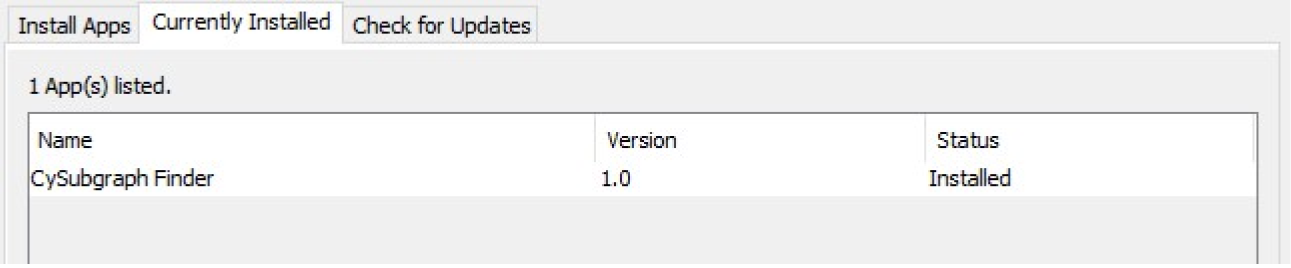
Step 1b: Click on the "Install from File…" button on the bottom left of the window. Then navigate to the location of the "CyFinder-1.0.jar" file.



Download Site: https://apps.cytoscape.org/

Search:

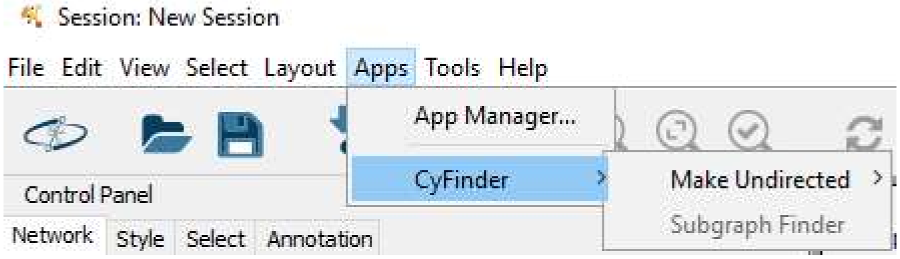
Step 1c: If no errors have occurred you should see the following window after selecting your jar file. The indication of success is if the word under Status says "Installed". You can now close this window.



1 App(s) listed.

Name	Version	Status
CySubgraph Finder	1.0	Installed

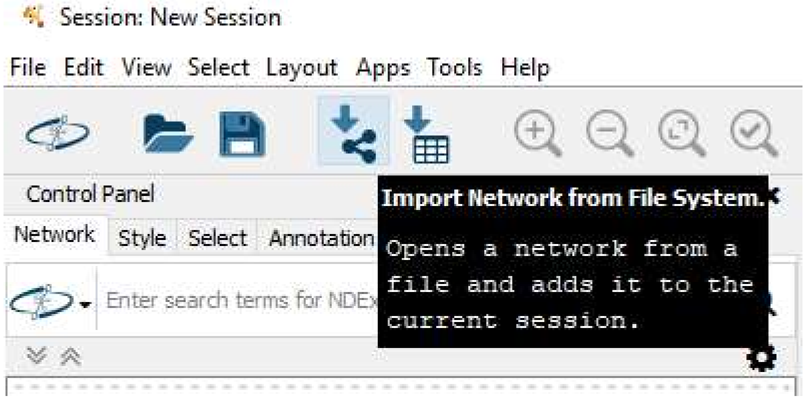
Step 1d: Lastly, confirm that you now have access to CyFinder. You should be able to see the CyFinder option from the Apps toolbar dropdown menu.



Step 2:

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.


Session: New Session
File Edit View Select Layout Apps Tools Help
Control Panel
Network Style Select Annotation
Enter search terms for NDEx

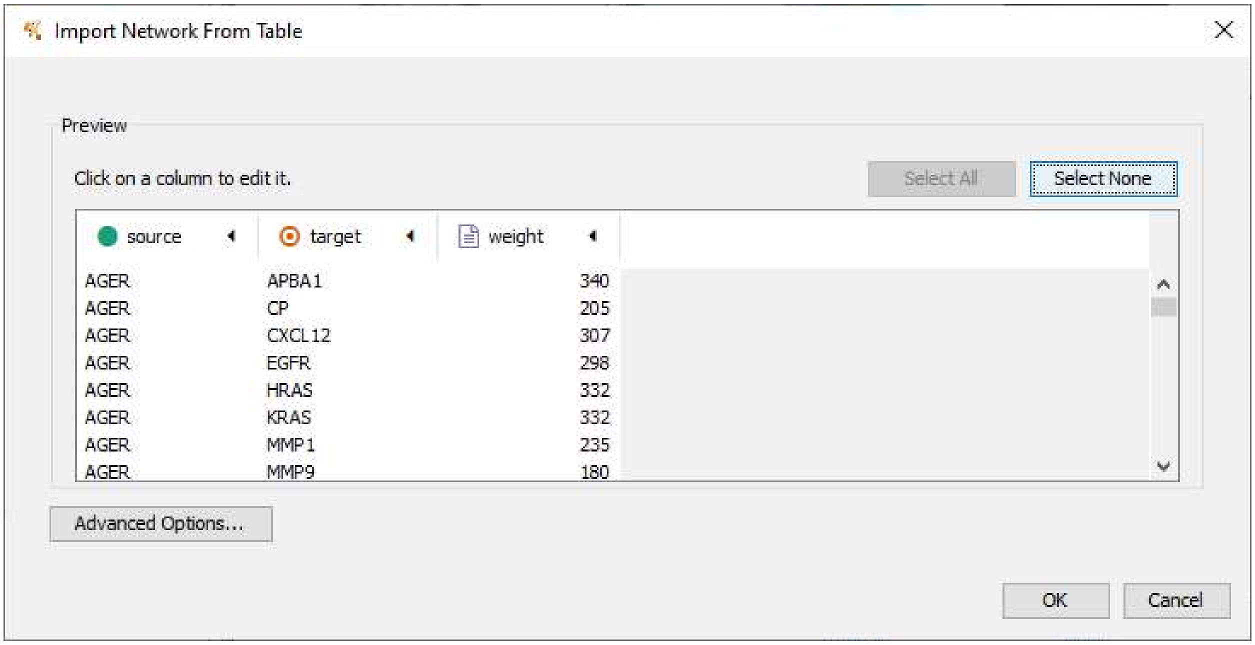
Import Network from File System.

Opens a network from a file and adds it to the current session.

Step 3:

After selecting your network file from the previous step, a window like this should appear. For this example, we are using the “Lung_Cancer.txt” graph that is included with the source, which has 82 nodes and 1062 edges.

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

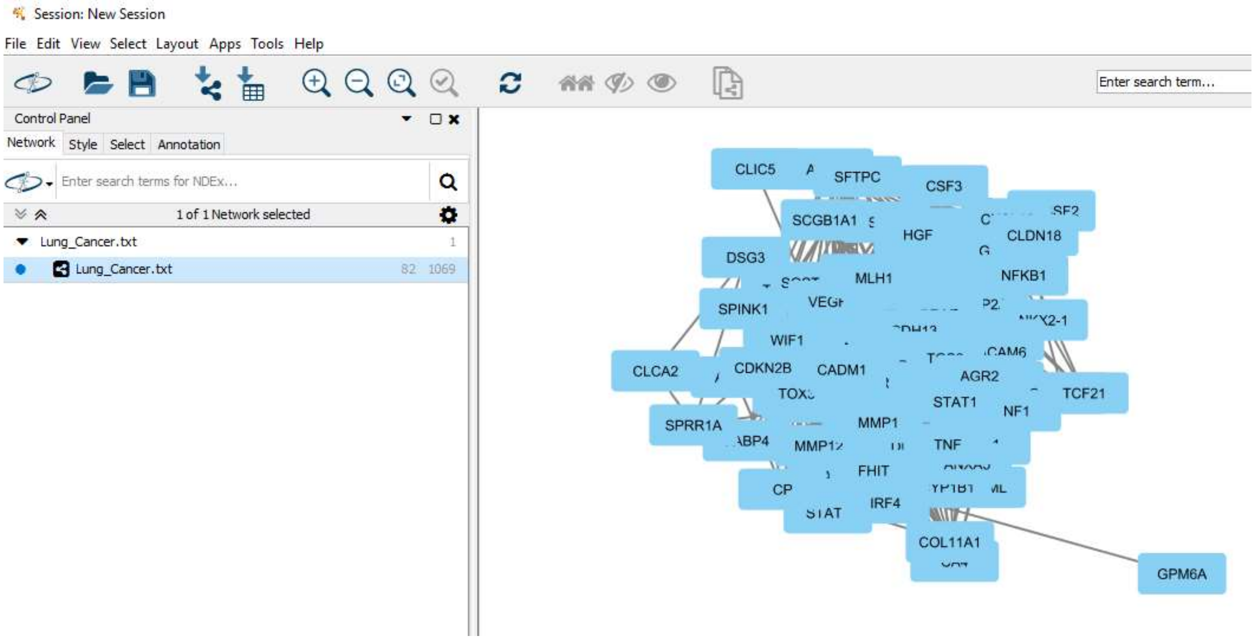


Click on a column to edit it.

source	target	weight
AGER	APBA1	340
AGER	CP	205
AGER	CXCL12	307
AGER	EGFR	298
AGER	HRAS	332
AGER	KRAS	332
AGER	MMP1	235
AGER	MMP9	180

Step 4:

Your network should now look similar to the graph below.



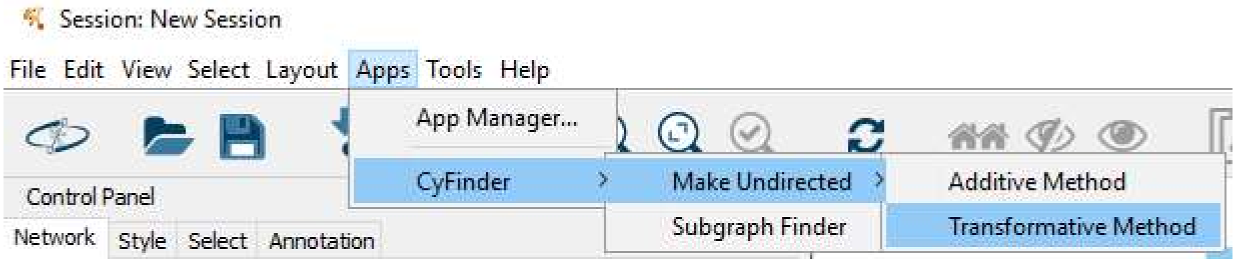
Now that you have your network imported into Cytoscape, we are ready to explore the options that the CyFinder app has to offer.

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.

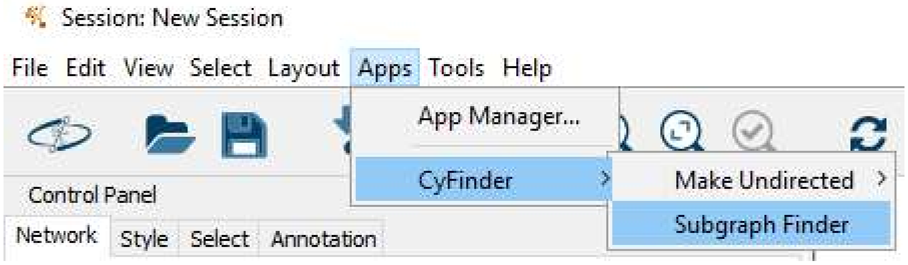
The transformative method makes the network undirected by altering the existing edges and replacing them with exact duplicates except they have the internal Cytoscape flag for directed-ness of edges set to false.

In this tutorial, we will be using the Transformative Method.
Click Apps -> CyFinder -> Make Undirected -> Transformative Method or Additive Method

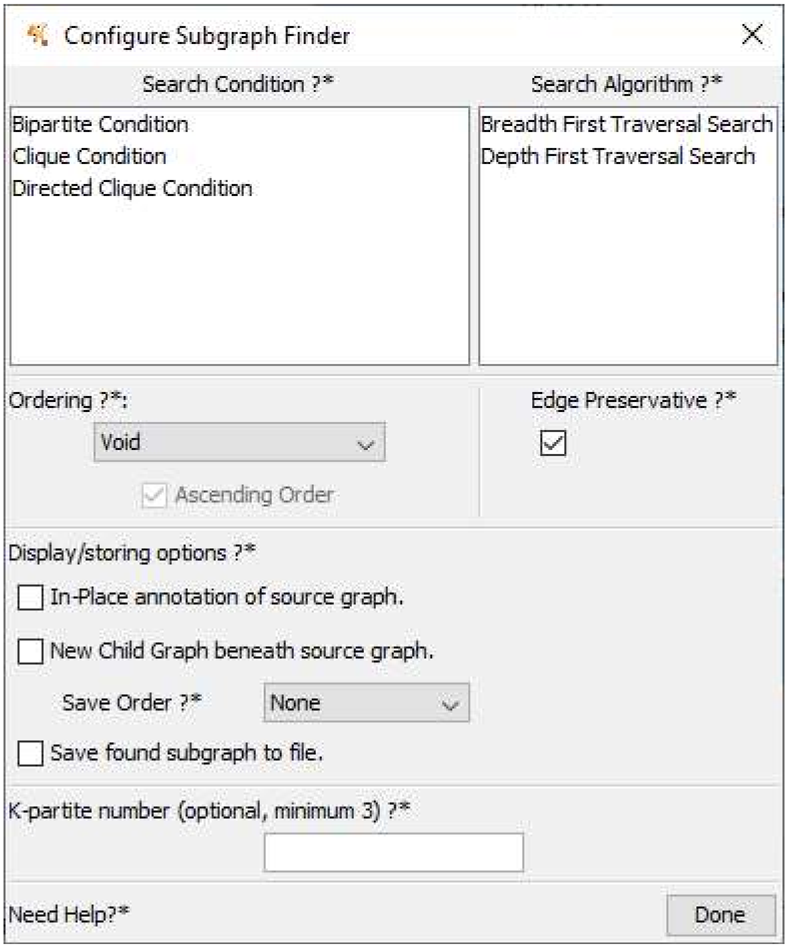


Step 5:
Now that our network is in an undirected state, we are ready to find meaningful subgraphs within this network. To do this, open the Subgraph Finder GUI.

Click on Apps -> CyFinder -> Subgraph Finder



Step 6:
After performing the previous step, the following window should appear:



Configure Subgraph Finder

Search Condition ?*

Bipartite Condition
Clique Condition
Directed Clique Condition

Search Algorithm ?*

Breadth First Traversal Search
Depth First Traversal Search

Ordering ?*: Void

☑ Ascending Order

Edge Preservative ?* ☑

Display/storing options ?*

□ In-Place annotation of source graph.

□ New Child Graph beneath source graph.

Save Order ?* None

□ Save found subgraph to file.

K-partite number (optional, minimum 3) ?*

Need Help?*

We are now ready to find Clique and Bipartite subgraphs.

It should be noted that any item marked with an asterisk can be hovered over to display a tooltip that tells you more about the item's functionality.

Step 7:

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 8:

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 9:

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. It is recommended that you keep this enabled, as disabling it may lead to some unexpected results.

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.

S**tep 10:**

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 second option. Check the "**New Child Graph beneath source graph**" checkbox by clicking on it.

Step 11:

There is a drop down box marked "Save Order" that is only applicable for "New Child Graph beneath source graph." When used it changes the order in which Cytoscape lists the graphs. There are currently four options:

- None: Do nothing. Displays graphs using the arbitrary traversal order.
- Ascending: Displays graphs from smallest to largest (node count).
- Descending: Displays graphs from largest to smallest (node count).
- Average Weight: Displays graphs from smallest to largest (average edge weight). There is currently no descending edge weight option.

For this tutorial we will be using the **Ascending** option. Select that from the combo box.

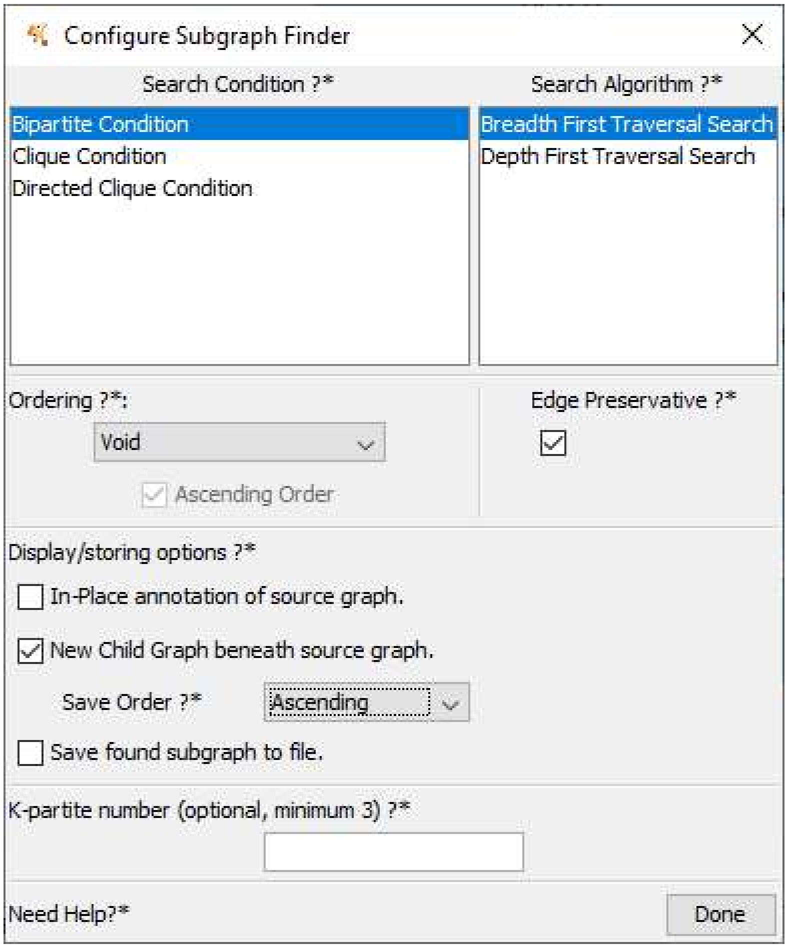
Step 12:

At the bottom of the GUI is a blank text field marked “k-partite number.” This field allows you to input any integer k (k > 2) to partition the graph into k partitions if it is possible to do so. A k-partite graph has k partitions, and a partition is a set of nodes that has no intra-set edges (that is, there is no edge between any two nodes in the same set).

However, if this is NOT selected, CyFinder will automatically assign partition numbers anyway. The difference is that these automatic partition numbers are assigned naturally through traversing. Partition 1 will consist of the arbitrary root vertex, partition 2 will consist of anything adjacent to partition 1 vertices that have not been visited yet, and so forth until all vertices are visited. As a result, the k value for the graph will vary by graph.

In order to show this functionality, we will **leave the text field blank** for now.

At this point, your window should look like this:



Configure Subgraph Finder

Search Condition ?*
- Bipartite Condition
- Clique Condition
- Directed Clique Condition

Search Algorithm ?*
- Breadth First Traversal Search
- Depth First Traversal Search

Ordering ?*: Void

☑ Ascending Order

Edge Preservative ?* ☑

Display/storing options ?*

☐ In-Place annotation of source graph.

☑ New Child Graph beneath source graph.

Save Order ?* Ascending

☐ Save found subgraph to file.

K-partite number (optional, minimum 3) ?*

Need Help?* Done

Select **Done** to find and display the subgraphs.

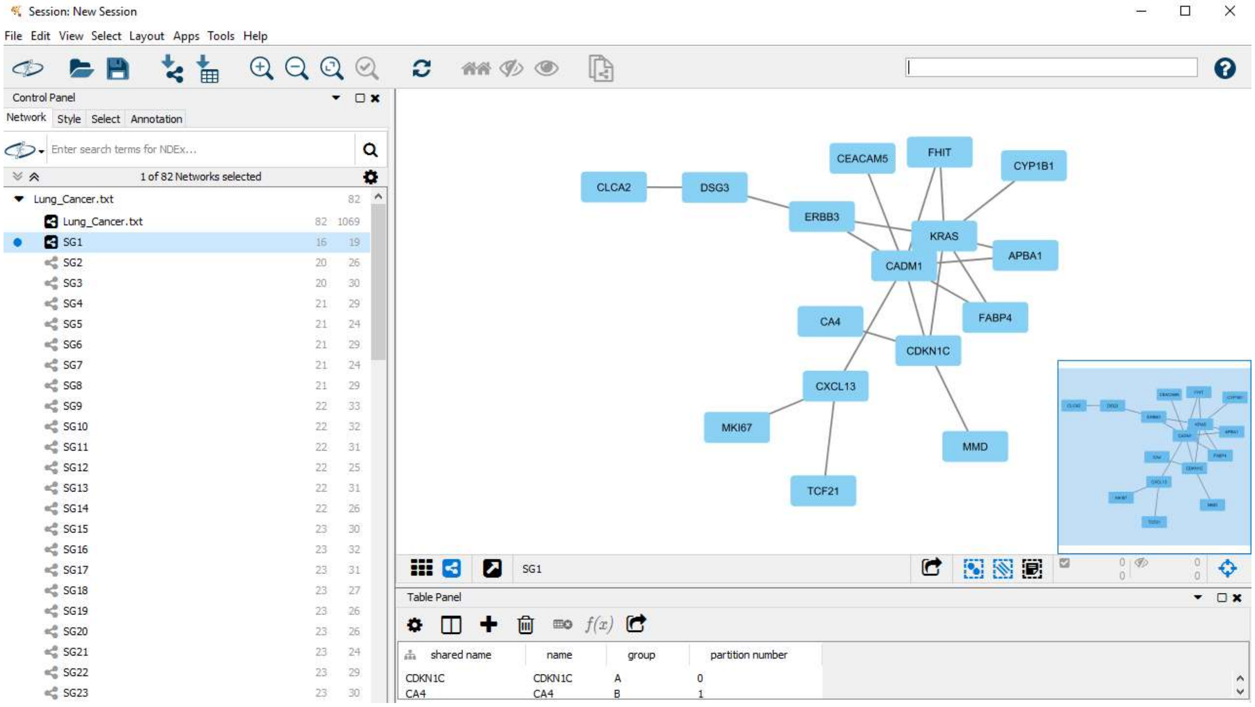
Step 13:

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. They are also sorted by node count in ascending order, with the smallest graph at the top and the largest graph at the bottom.

If you get an exception/error, make sure that you followed the instructions above. In particular, make sure that you transformed the graph into an undirected one.

Click the “Create View” button for any subgraph to display the graph, like in the screenshot below.


Session: New Session
File Edit View Select Layout Apps Tools Help
Control Panel
Network Style Select Annotation
Enter search terms for NDEx...
1 of 82 Networks selected
CLCA2
DSG3
CEACAM5
FHIT
CYP1B1
ERBB3
KRAS
APBA1
CADM1
CA4
FABP4
CDKN1C
CXCL13
MKI67
MMD
TCF21
SG1
Table Panel

Lung_Cancer.txt		82
Lung_Cancer.txt	82	1069
SG1	16	19
SG2	20	26
SG3	20	30
SG4	21	29
SG5	21	24
SG6	21	29
SG7	21	24
SG8	21	29
SG9	22	33
SG10	22	32
SG11	22	31
SG12	22	25
SG13	22	31
SG14	22	26
SG15	23	30
SG16	23	32
SG17	23	31
SG18	23	27
SG19	23	26
SG20	23	26
SG21	23	24
SG22	23	29
SG23	23	30

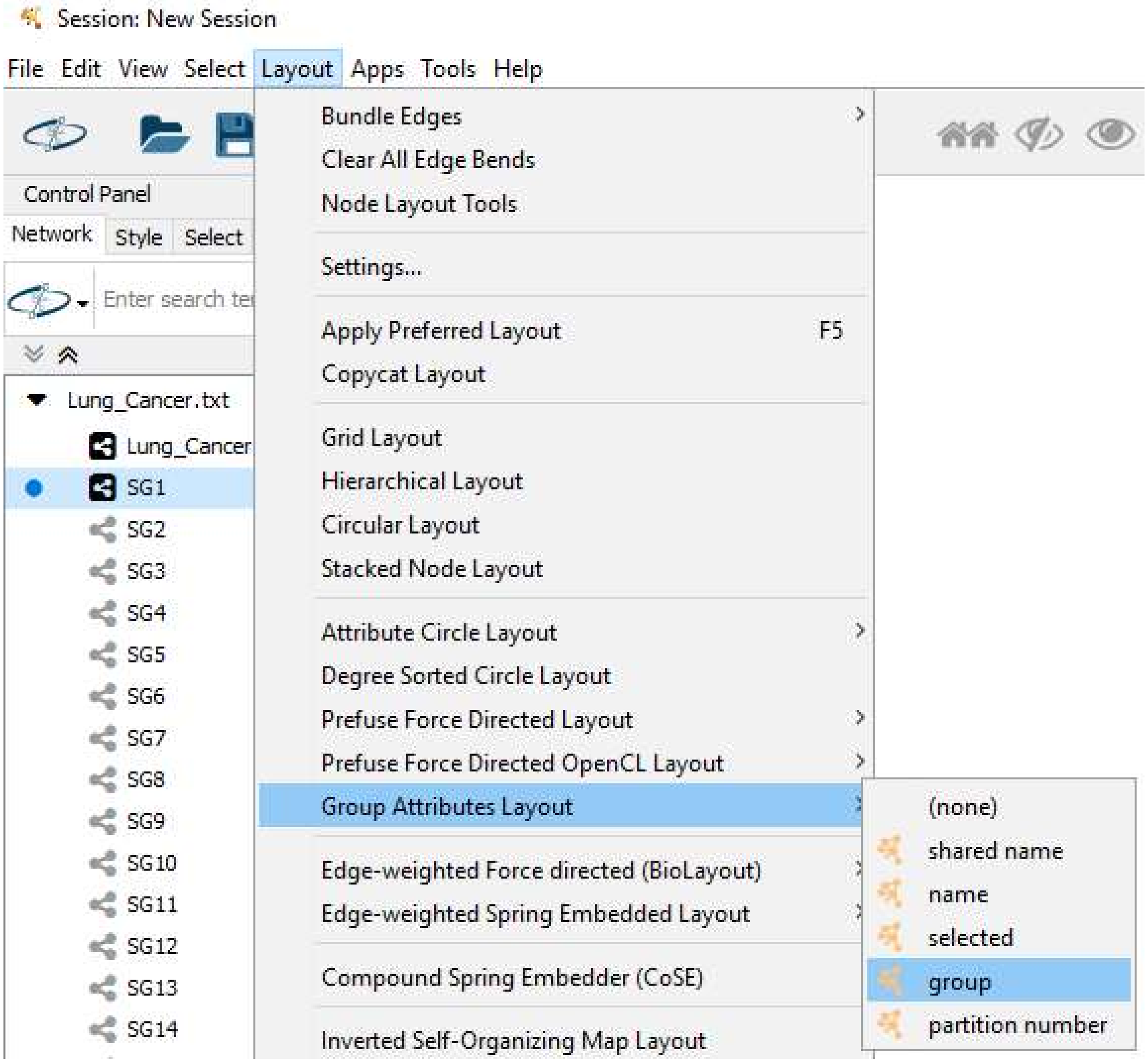
shared name	name	group	partition number
CDKN1C	CDKN1C	A	0
CA4	CA4	B	1

Step 14:

The algorithm has created two extra values for each node: group and partition number. These are used to display the graphs as bipartite and k-partite graphs, respectively. The idea is that any node with group A is in set A. Similar logic applies to partition numbers, except there are likely to be more than two sets.

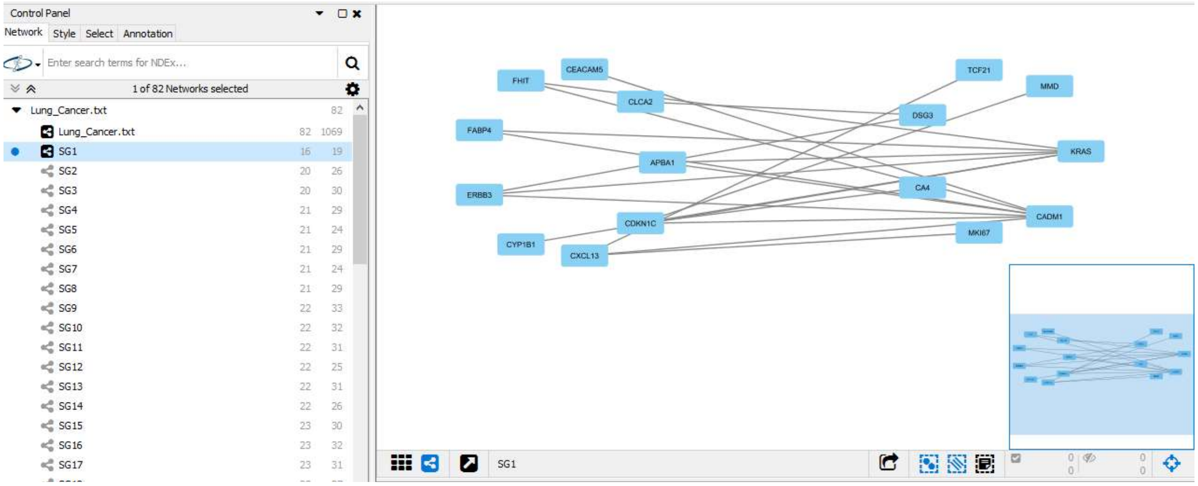
Cytoscape has a way to neatly display nodes in groups by group number.

Click Layout -> Group Attribute Layout -> group



Step 15:

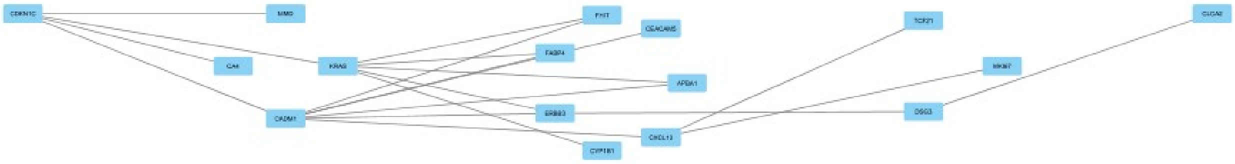
After performing the previous step correctly your bipartite subgraph should now be displayed in a similar format to the one in the figure below.



Lung_Cancer.txt	82	
Lung_Cancer.txt	82	1069
SG1	16	19
SG2	20	26
SG3	20	30
SG4	21	29
SG5	21	24
SG6	21	29
SG7	21	24
SG8	21	29
SG9	22	33
SG10	22	32
SG11	22	31
SG12	22	25
SG13	22	31
SG14	22	26
SG15	23	30
SG16	23	32
SG17	23	31

Note that each set lacks intra-set edges. That is, no two nodes in the same set are connected.

Step 16: A similar procedure can be followed with the partition number attribute, which displays the graph as described in Step 12. Go to **Layout -> Group Attributes Layout -> Partition Number** and the displayed graph should look like this.



Note that again, the graph is divided neatly into sets, and each set lacks multiple edges. In this case, the traversal produced a 5-partite graph, as the furthest vertex from the arbitrary root was five edges away.