

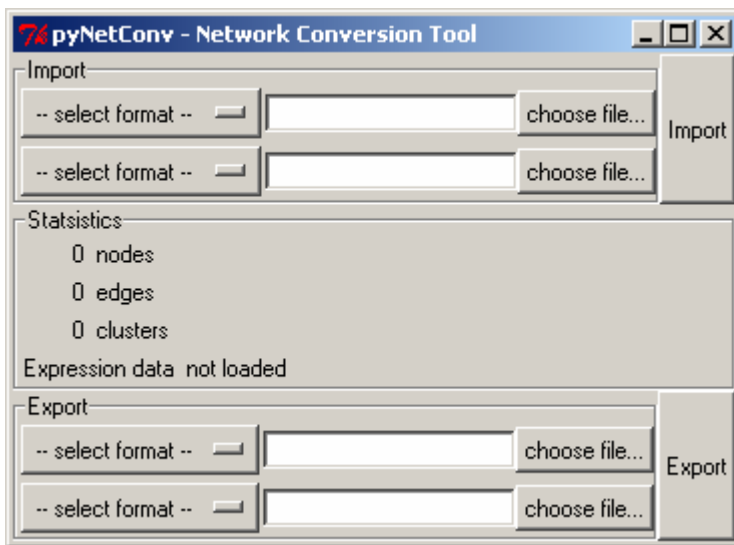
## Solution of exercise 2 from chapter 10

### Part 1: convert the networks

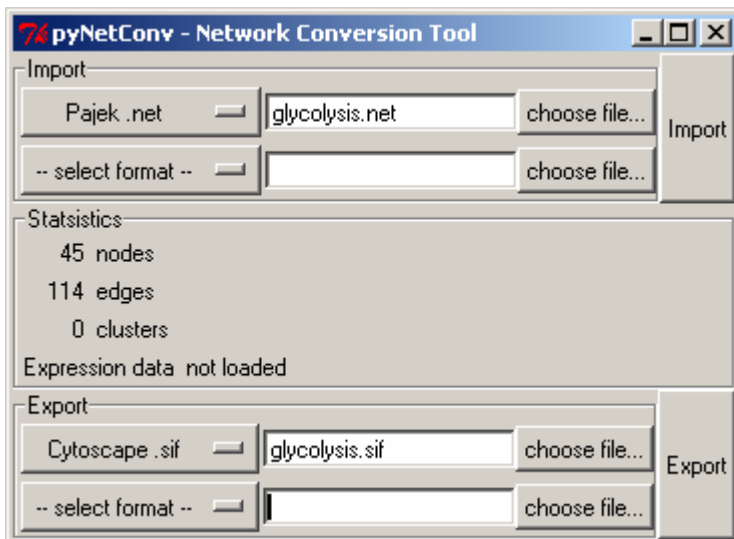
First, convert the networks using pyNetConv tool. You can use the command line tool or the GUI to achieve this. With the command:

```
$ netconv-gui .py
```

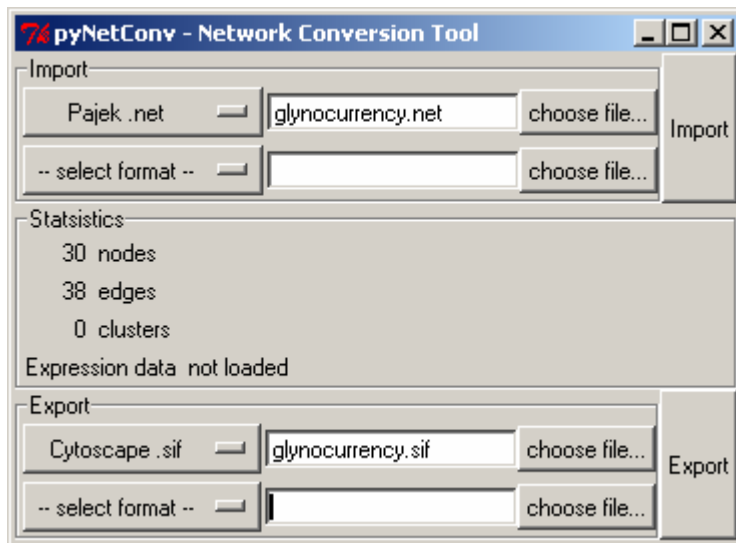
the GUI will show up as shown in the figure.



You can then load the network and convert it using the interface:

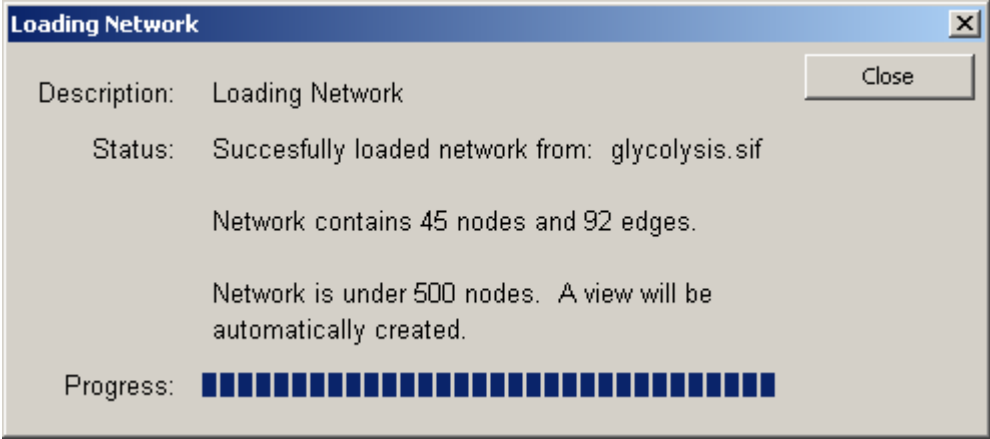


Then, you can do the same to the other network:

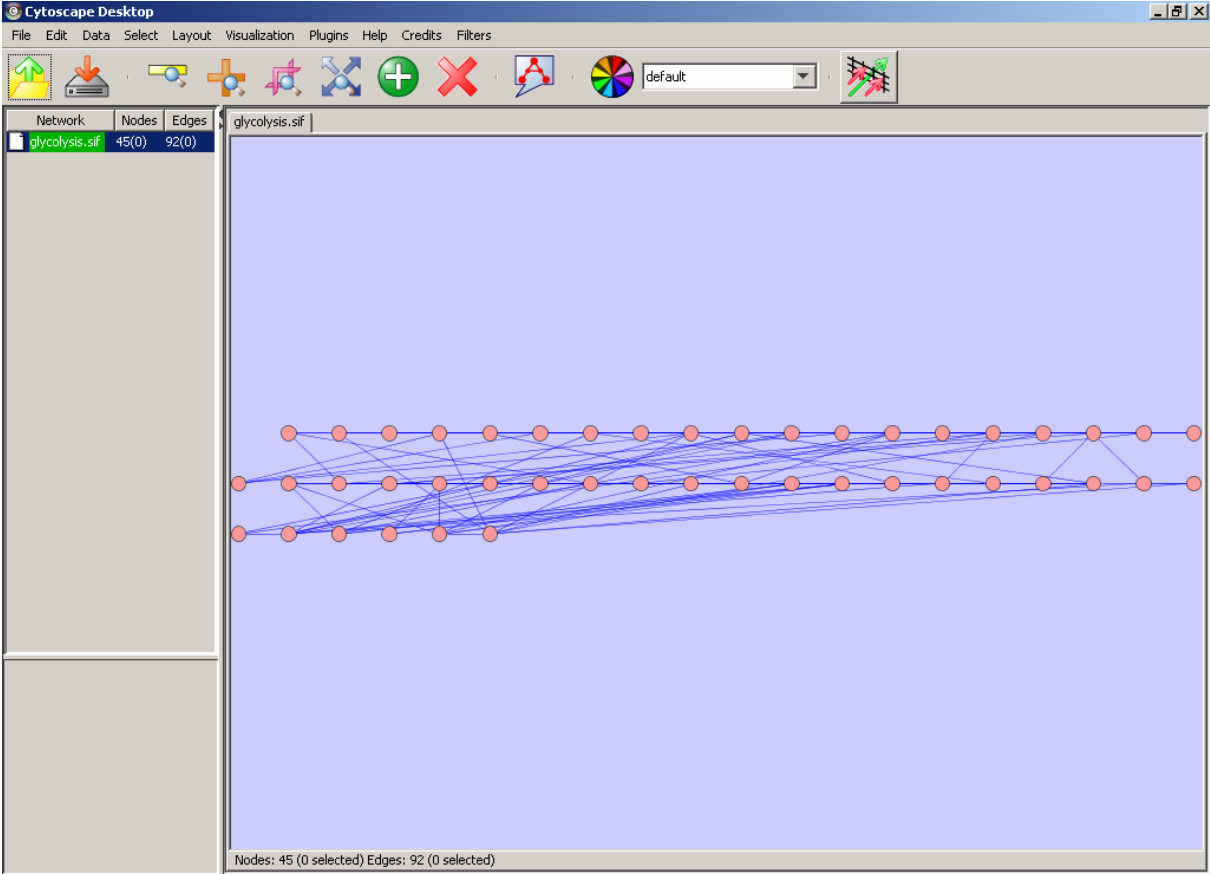


# Part 2: Viewing the networks in Cytoscape

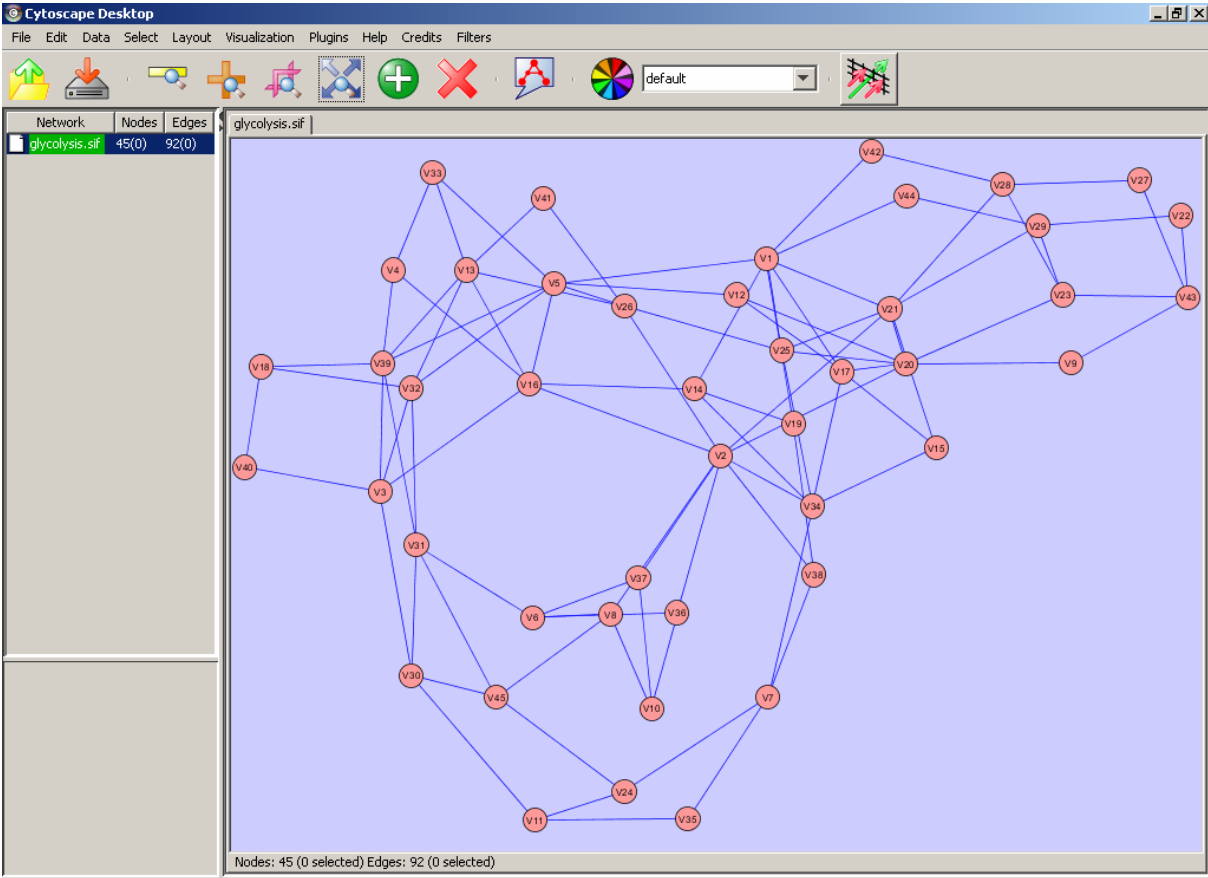
After loading the network in Cytoscape, you'll see an status like this:



The network is loaded:



And, after applying some layout to make it look better:



## Part 3: Network decomposition

To decompose, use the cluster tool. the command line and output of the commands are shown below.

```
$ ncluster.py glycolysis.sif
  Network prefix: glycolysis
  Network file: glycolysis.sif
(connected) nodes: 45
  (unique) edges: 92

Calculating centrality... done!
Calculating modularity |##### [100.0%]
Clustering (stage1) |##### [100.0%]
Clustering (stage2) |##### [100.0%]

Best modularity: 0.506793478261 with 5 modules.

Elapsed time: 0 seconds
```

```
$ ncluster.py glynocurrency.sif
  Network prefix: glynocurrency
  Network file: glynocurrency.sif
(connected) nodes: 30
  (unique) edges: 34

Calculating centrality... done!
Calculating modularity |##### [100.0%]
Clustering (stage1) |##### [100.0%]
Clustering (stage2) |##### [100.0%]

Best modularity: 0.647923875433 with 7 modules.

Elapsed time: 0 seconds
```

**Note:** All files generated in this tutorial are attached.