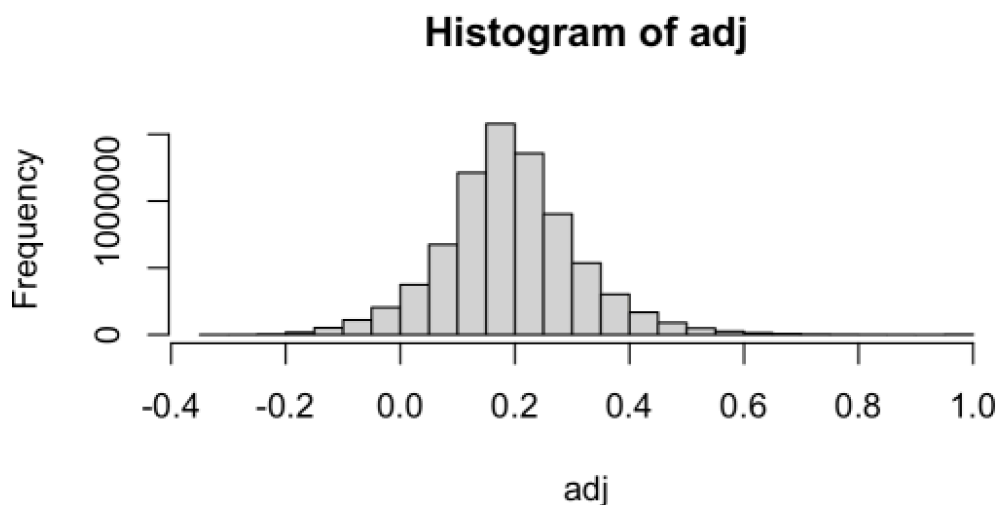# Lab4

Please download the data "Gene_expression_table_filtered.txt" from iSpace.

1. Reconstruct gene network adjacency matrix by Pearson correlation (see cor() in R)
2. Draw distribution for edge weight, select edge filter cutoff.

Histogram of adj

3. Keep edges whose adj(correlation)> 0.5 (see which() in R). Save adjacency edge list as a ".csv" file (see write.csv() in R, set quote=F)

```
A=which(abs(adj)>0.5,arr.ind=T)

node_list=colnames(data)

edges=cbind(node_list[A[,1]],node_list[A[,2]],adj[A])

colnames(edges)=c("source","target","weight")

write.csv(edges,file="mouse_retina_adj.csv",quote=F)
```

4. Convert the adjacency matrix into distance matrix by 1-abs(correlation)
5. Apply community detection (see cluster_louvain() in R package igraph).

```
G1 <- graph.adjacency(distancematrix, mode = "undirected",
                      weighted = TRUE, diag = TRUE)
clusterlouvain <- cluster_louvain(G1)

tmp=c()
label=c()
for(i in c(1:2))
{
  tmp=c(tmp,clusterlouvain[[i]])
  label=c(label,rep(i,length(clusterlouvain[[i]])))
}
result=cbind(tmp,label)

write.csv(result,file="mouse_retina_node_label.csv")
```
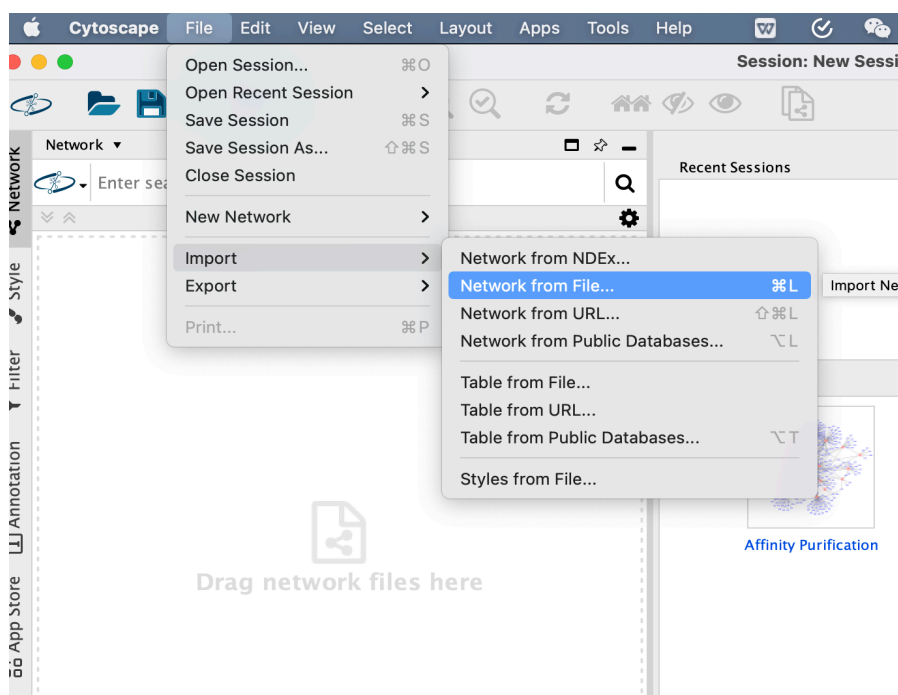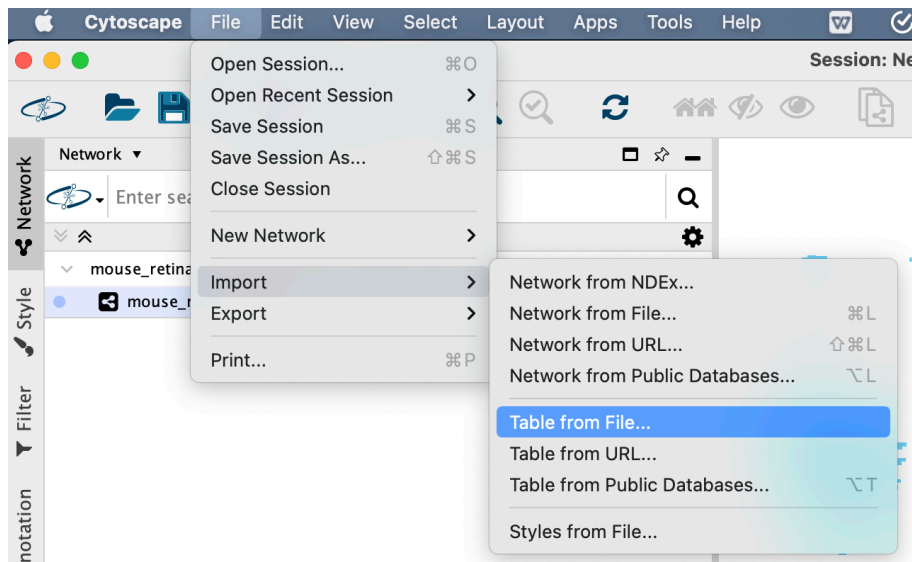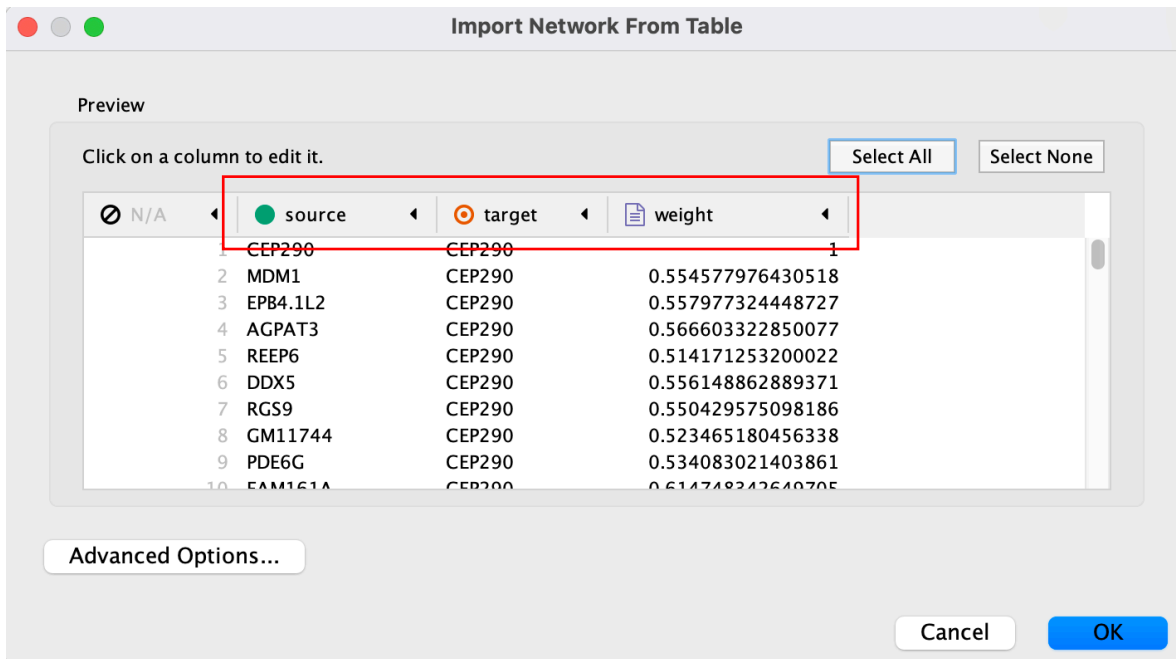
6. Save the community detection result as node_label.csv file as below (different number for different community)

	tmp	label
1	CCDC59	1
2	LIN7A	1
3	OSBPL8	1
4	NAP1L1	1
5	KRR1	1
6	ZFC3H1	1
7	YEATS4	1
8	CPSF6	1
9	DDIT3	1

7. Download Cytoscape from https://cytoscape.org/
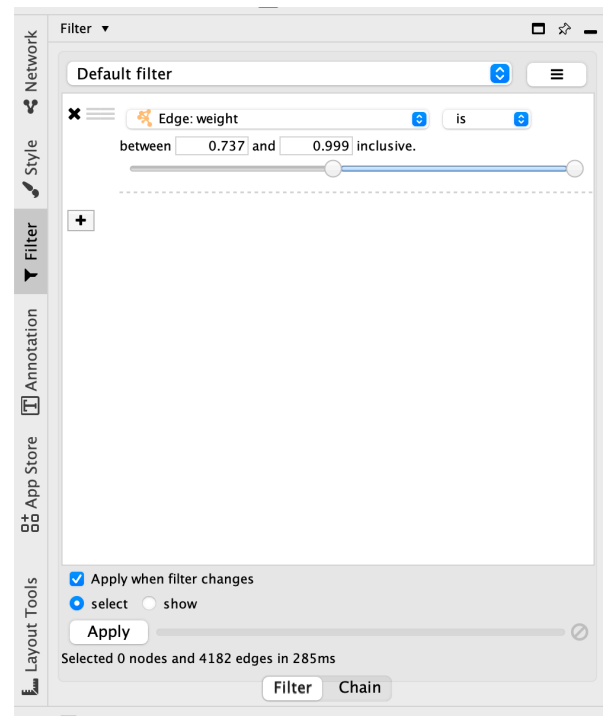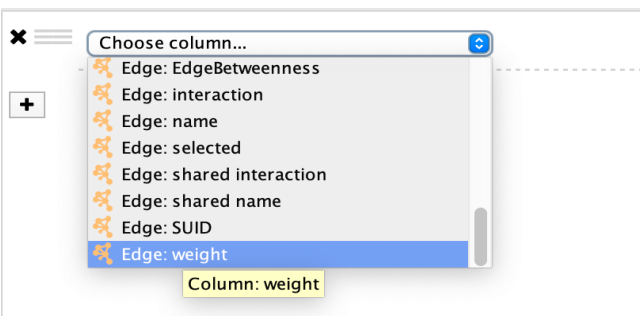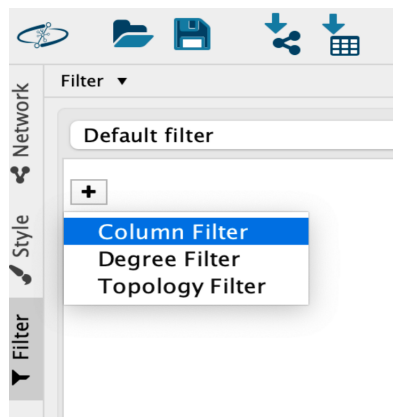8. Import network into Cytoscape

adjacency edge list

node label
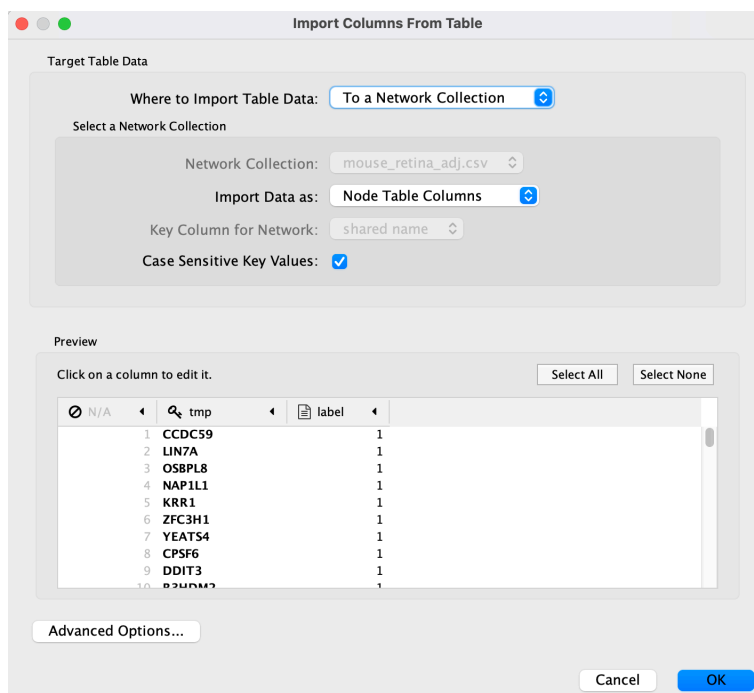
9. Tools-> analyze network
10. Apply filter according to edge weight, to select the edges and the connected nodes. Hide unselected edges and nodes.
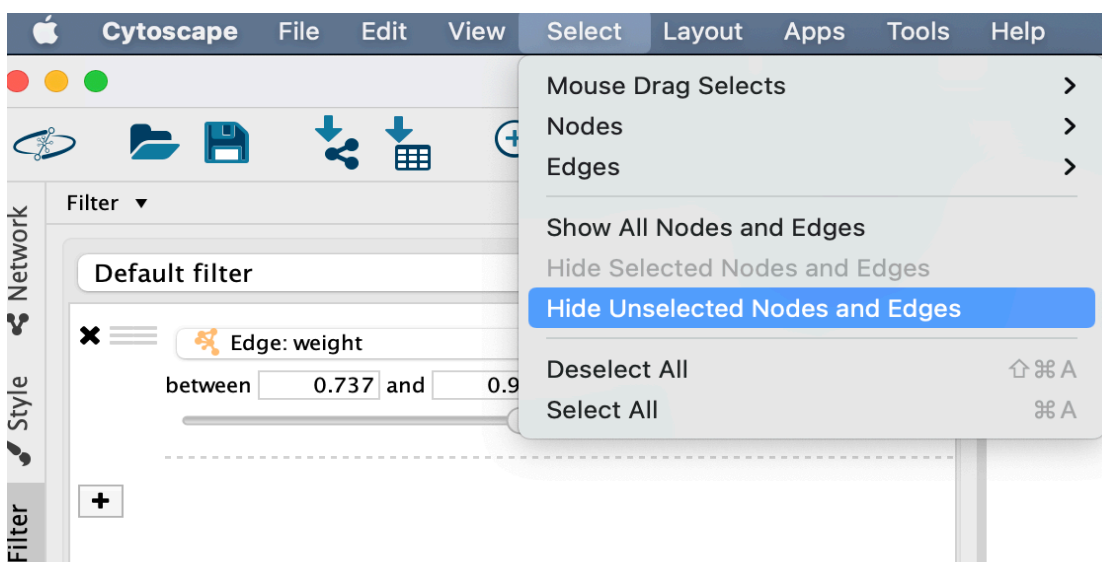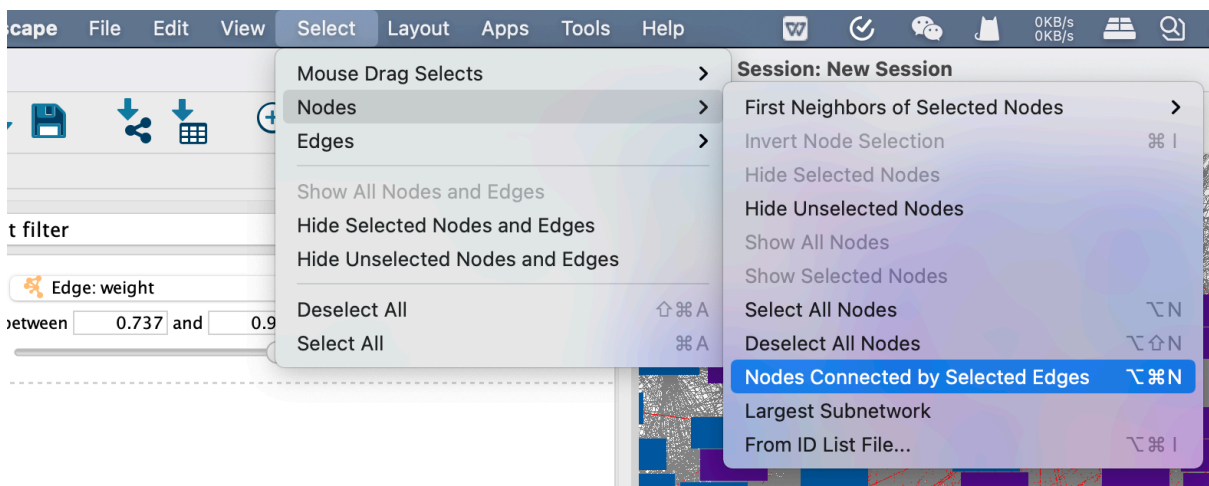
11. Do visualisation to identify the important genes. Try "yFile organic layout", "force directed layout" and other layout; change style to sample1; set node color for each community; set label size and node width according to degree.

12. Drag mouse to see the network, Observe and list the important genes. Find the gene annotation of the important genes from GeneCard.
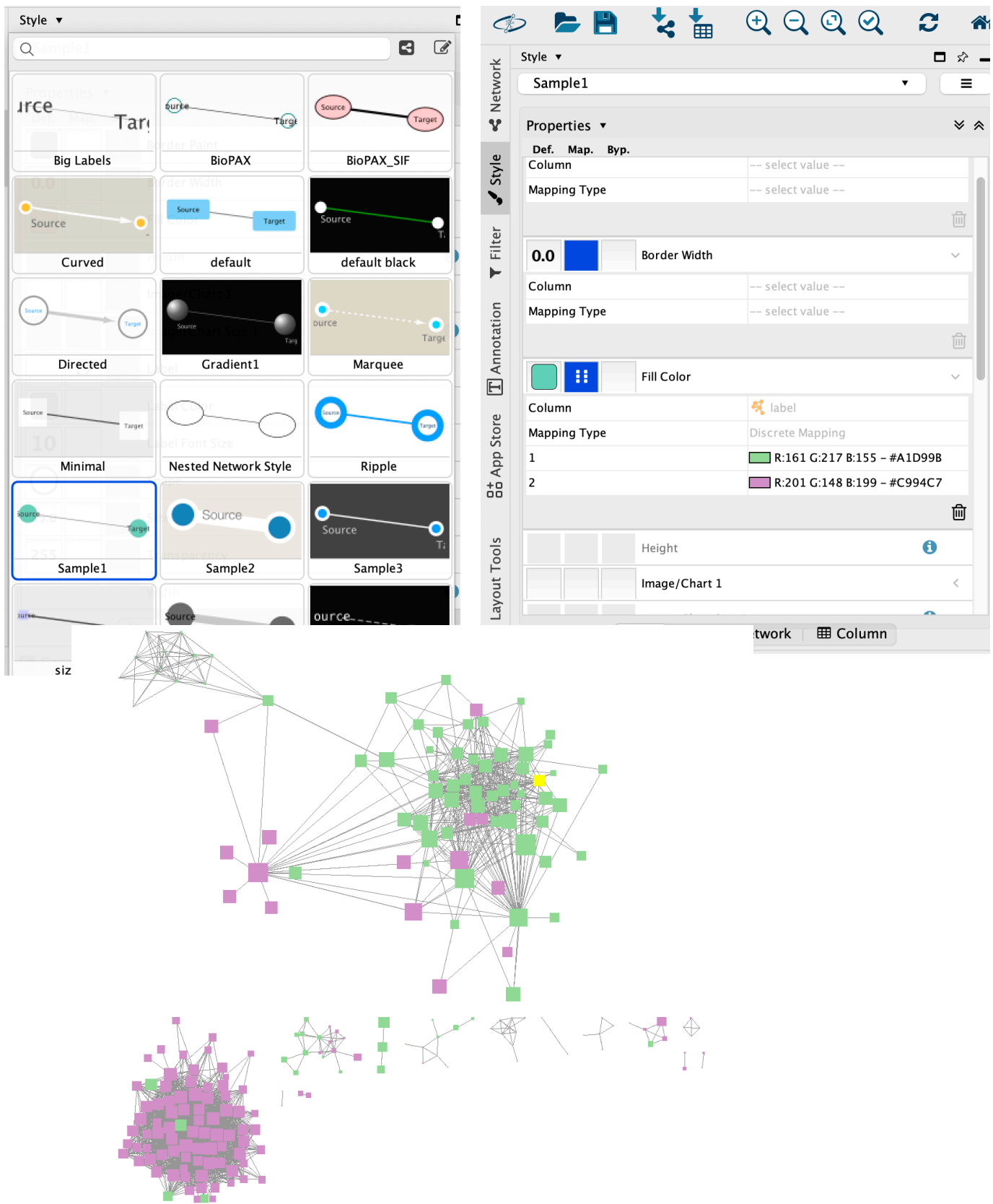
Style
Filter
Annotation
App Store
ut Tools

Def. Map. Byp.

10 Label Font Size

Column   Degree
Mapping Type   Continuous Mapping

90.0

Current Mapping

0.0
2.00   952.00

Shape

25.0 Size

Column   Degree
Mapping Type   Continuous Mapping

60.7

Current Mapping

0.0
2.00   952.00

Cytoscape File Edit View Select Layout Apps Too

Open Session...   ⌘O
Open Recent Session   >
Save Session   ⌘S
Save Session As...   ⇧⌘S
Close Session

New Network   >
Import   >
Export   >   Network to NDEx...

Print...   ⌘P   Network to File...
                                              Network to Image...
                                              Network to Web Pag

Style ▾   Table to File...

Sample1   Styles to File...

Properties ▾

Def. Map. By
Column
Mapping Type

0.0   Border Width

Column   -- select value
Mapping Type   -- select value