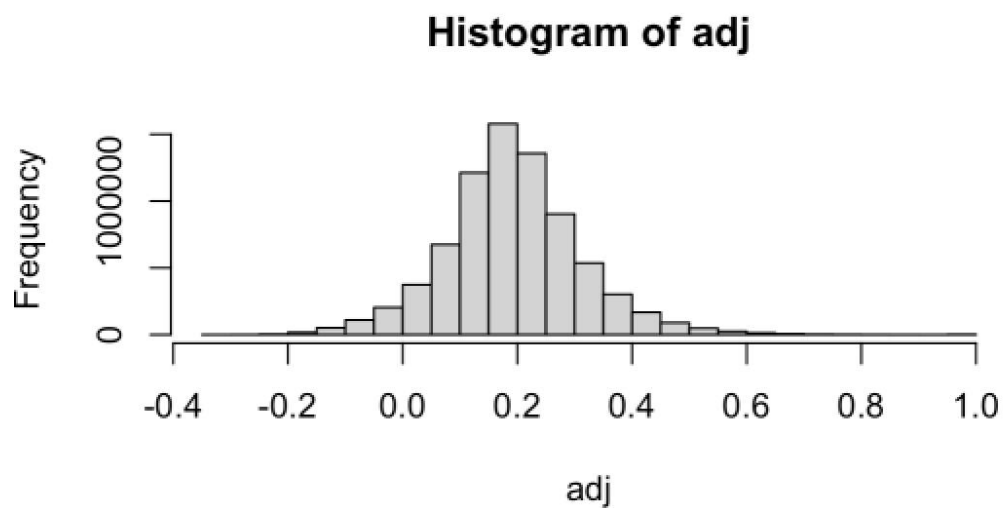


Please download the data

“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.



3. Keep edges whose $\text{adj}(\text{correlation}) > 0.5$ (see `which()` in R). Save adjacency edge list as a ".csv" file (see `write.csv()`)

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

node_list=rownames(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)
```

in R, set `quote=F`)

4. Convert the adjacency matrix into distance matrix by $1-\text{abs}(\text{correlation})$
5. Apply community detection (see `cluster_louvain()` in R

```
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")
```

package `igraph`).

6. Save the community detection result as node_label.csv

	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

file as below (different number
for different community)