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Scripts that I have written for the manuscript titled "Efficient Identification of Multiple Pathways: RNA-Seq Analysis of Livers from 56Fe Ion Irradiated Mice"

Manual: WGCNA-M

This code performs unipartite network community detection, using modularity.
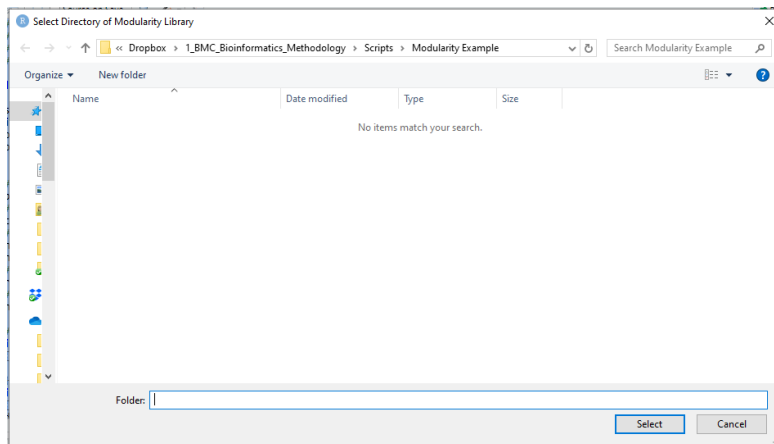
Dependencies:

- svDialogs

Input file requirements:

1. **Adjacency Matrix from WGCNA**

Running:

1. Run WGCNA-M.R script
2. Select the directory where the R script is located with the necessary library files as shown below

Name	Date modified	Type	Size
R_uni.c	8/22/2019 10:53 PM	C File	1 KB
R_uni.dll	8/22/2019 10:53 PM	Application exten...	49 KB
R_uni.h	8/22/2019 10:53 PM	H File	1 KB
R_uni.so	8/22/2019 10:53 PM	SO File	35 KB
uni_ft2.c	8/22/2019 10:53 PM	C File	16 KB
uni2.h	8/22/2019 10:53 PM	H File	2 KB

3. Select the Adjacency Matrix File:

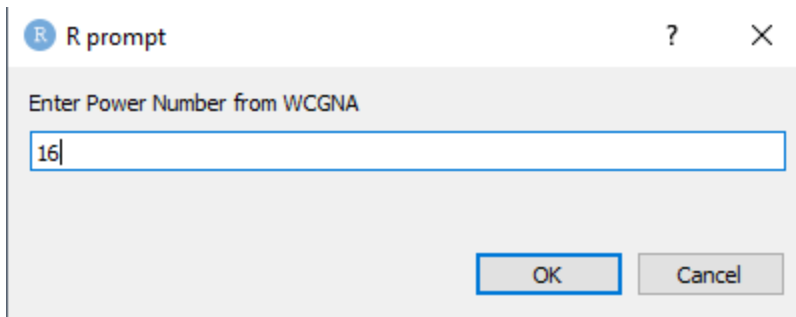a. In the example dataset it is "adjacency_1e5.txt"
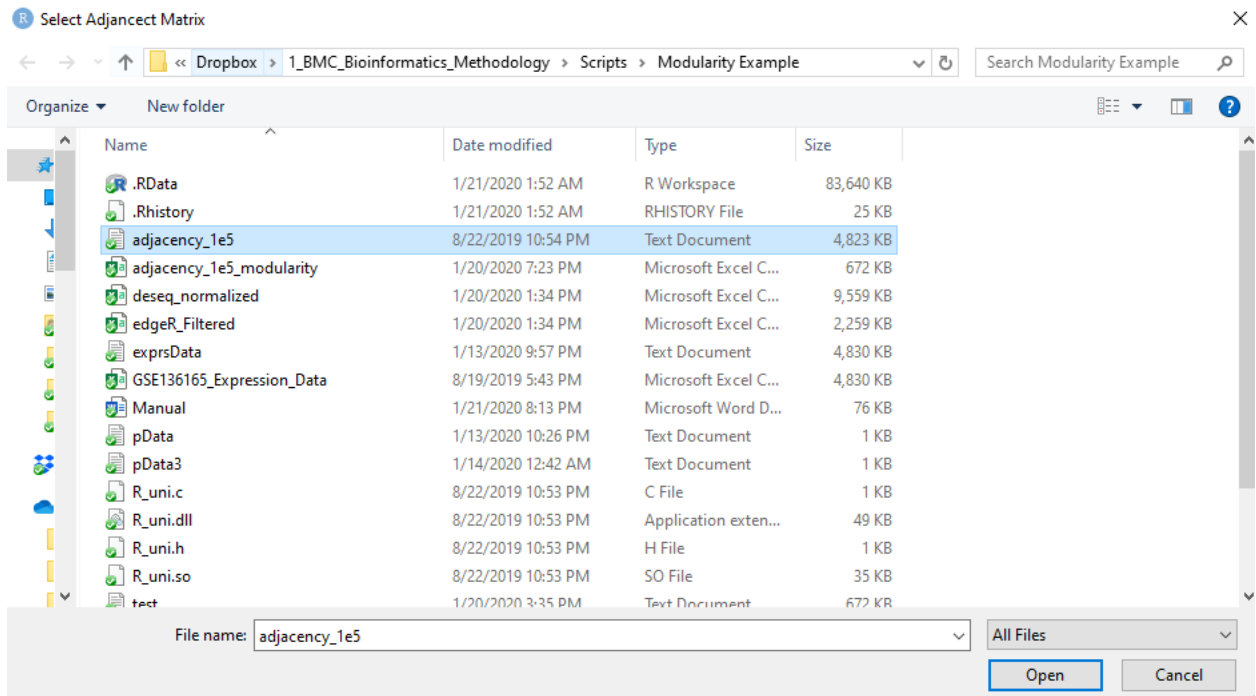
4. Select a File Name to Save the Modularity Network Algorithm Output in a comma separated values file format.
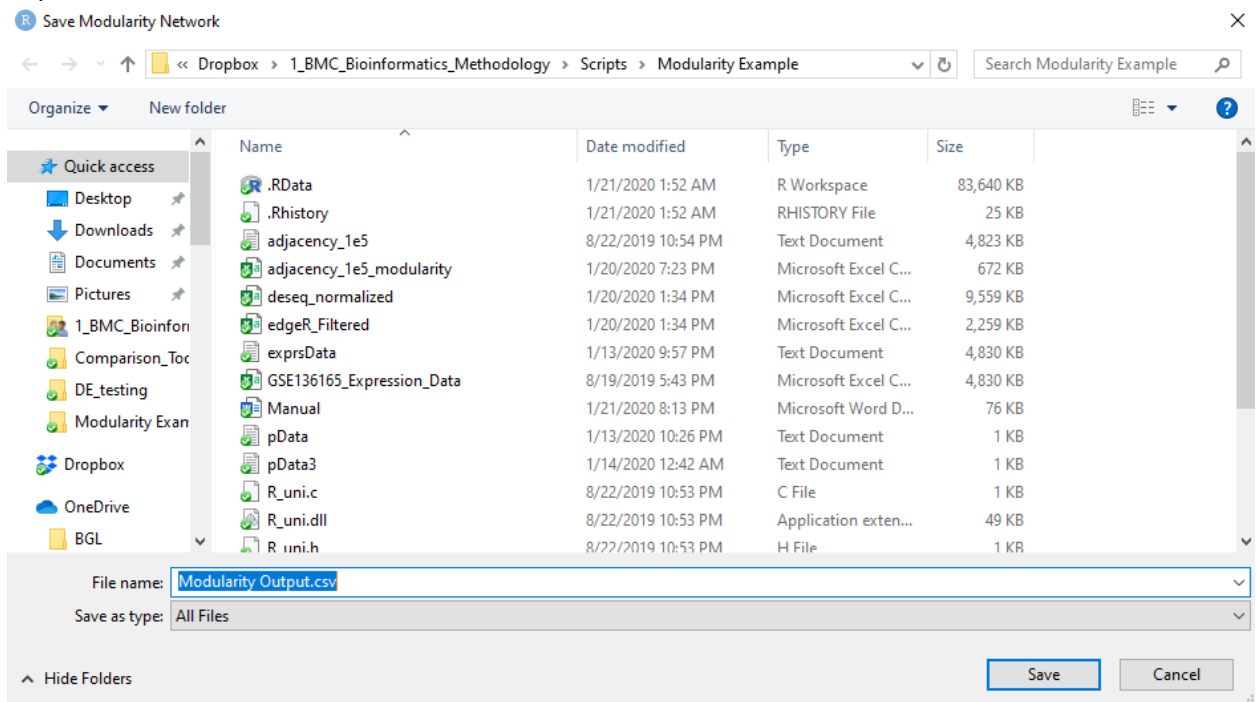
5. Pick the Soft Power Number based on how the adjacency matrix was generated by WCGNA
   a. A soft power threshold of 16 was chosen as optimal for the example dataset
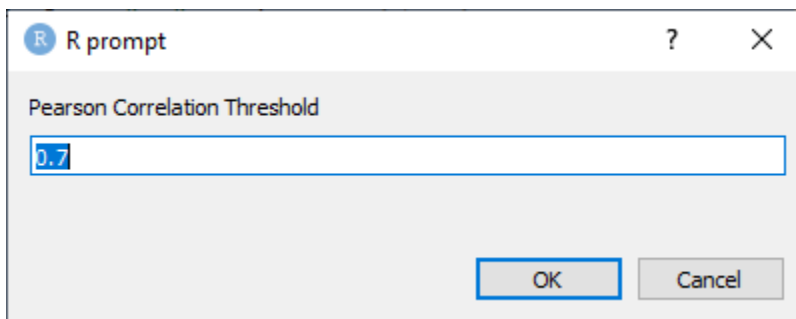
R prompt   ?   X

Enter Power Number from WCGNA

`16`

OK   Cancel

6. Pick the Pearson Correlation Threshold
    a. A Pearson correlation threshold of 0.7 was chosen as optimal for the example dataset
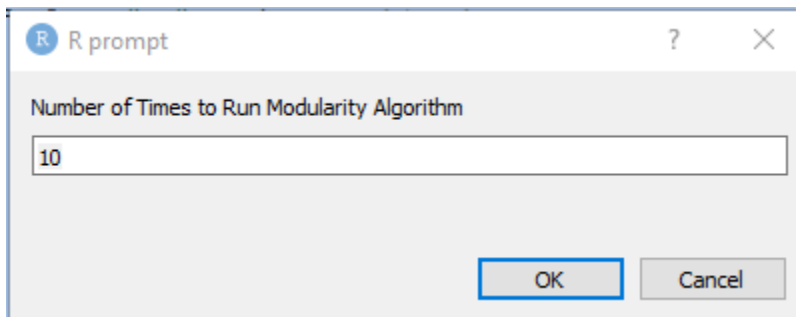7.

R prompt   ?   X

Pearson Correlation Threshold

`0.7`

OK   Cancel

8. Pick the number of times to run the modularity algorithm

R prompt   ?   X

Number of Times to Run Modularity Algorithm

`10`

OK   Cancel

9. When the algorithm finishes running it will print a summary

```
> #print network size
> print(n)
[1] 634
> #print modularity score
> print(modRes[[4]])
[1] 0.4829613
> #print number of clusters
> print(max(modRes[[5]]))
[1] 5
> #print median of cluster size
> print(median(table(modRes[[5]])))
[1] 128
> #print average cluster size
> print(mean(table(modRes[[5]])))
[1] 126.8
```