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Date: 01/13/2020

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:

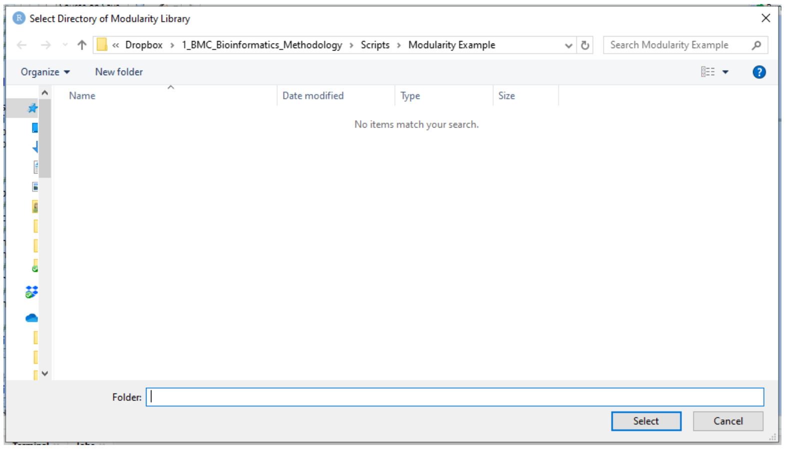
- svDialogs

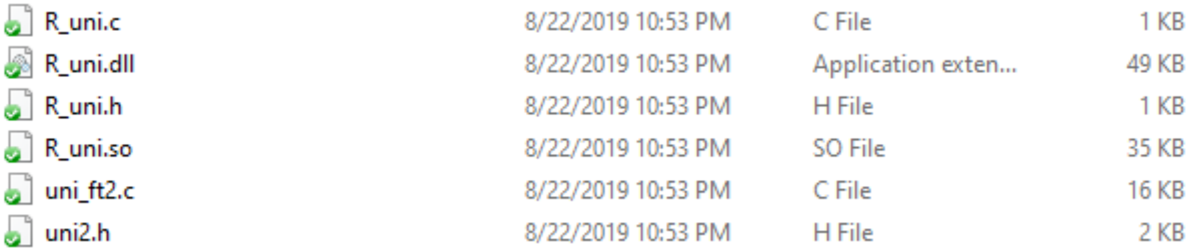
Input file requirements:

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

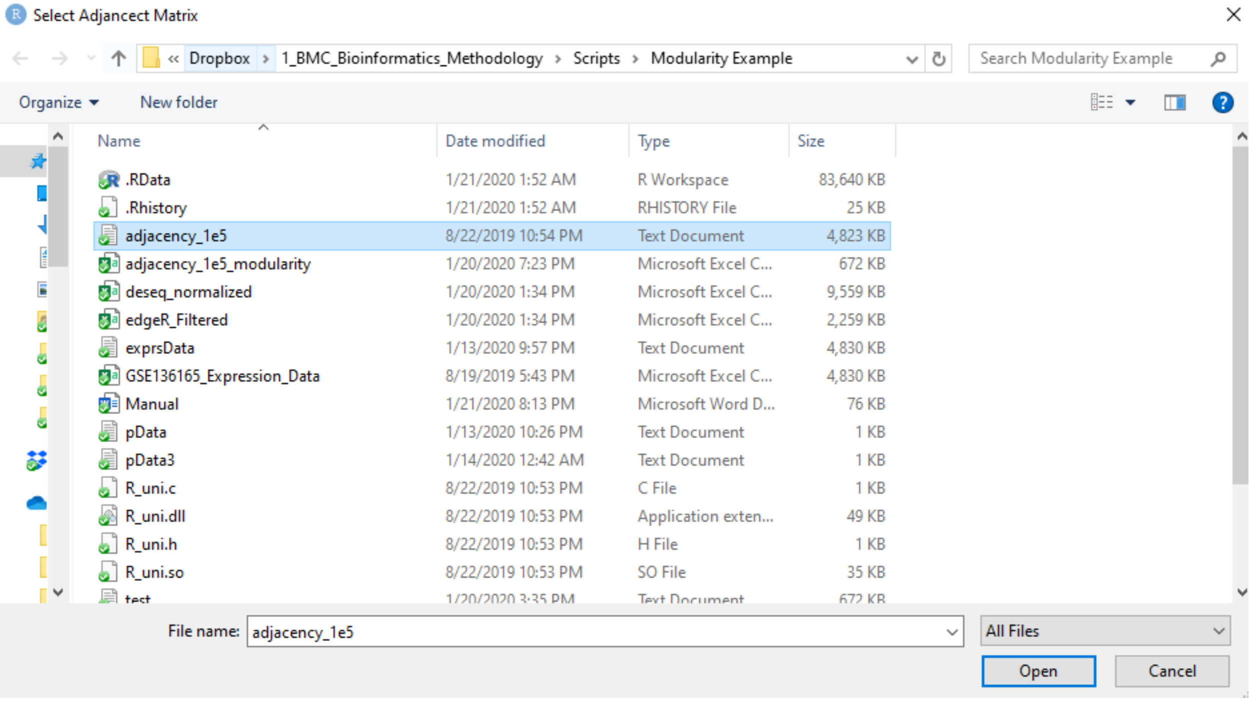

Select Directory of Modularity Library
« Dropbox › 1_BMC_Bioinformatics_Methodology › Scripts › Modularity Example
Search Modularity Example
Organize ▾
New folder
Name
Date modified
Type
Size
No items match your search.
Folder:
Select
Cancel



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”

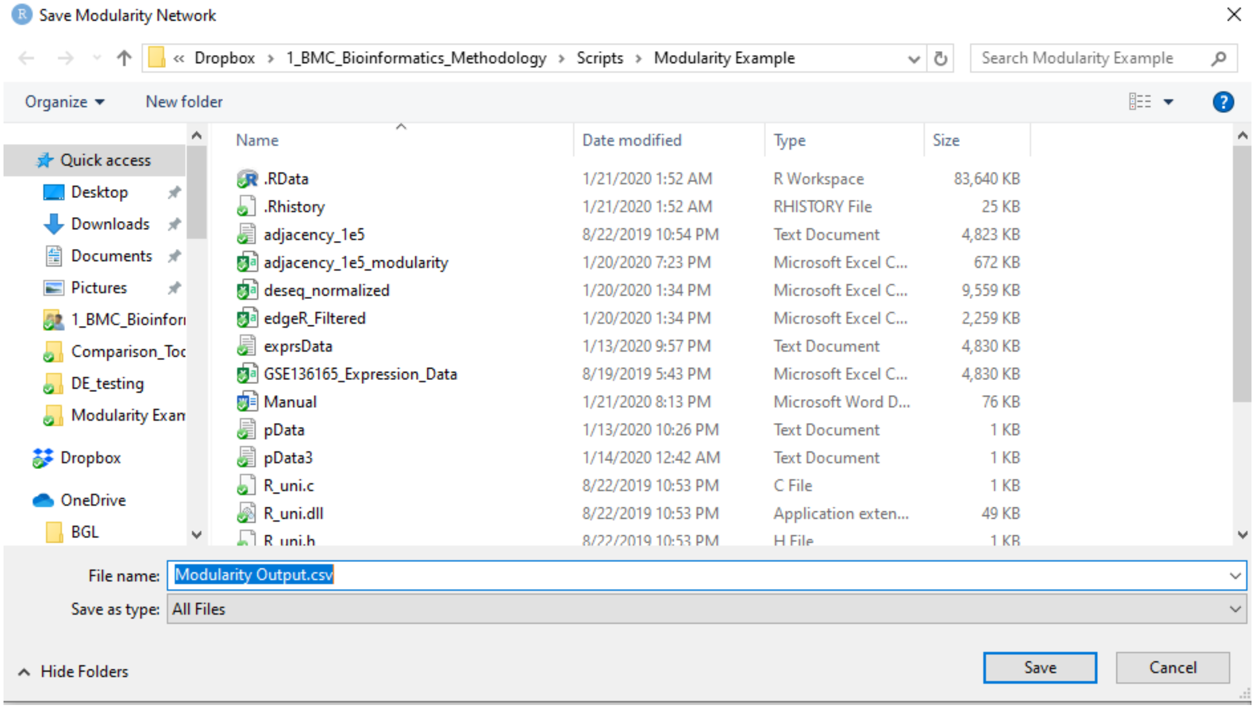


Select Adjancect Matrix
« Dropbox › 1_BMC_Bioinformatics_Methodology › Scripts › Modularity Example
Search Modularity Example
Organize ▾
New folder

Name	Date modified	Type	Size
.RData	1/21/2020 1:52 AM	R Workspace	83,640 KB
.Rhistory	1/21/2020 1:52 AM	RHISTORY File	25 KB
adjacency_1e5	8/22/2019 10:54 PM	Text Document	4,823 KB
adjacency_1e5_modularity	1/20/2020 7:23 PM	Microsoft Excel C...	672 KB
deseq_normalized	1/20/2020 1:34 PM	Microsoft Excel C...	9,559 KB
edgeR_Filtered	1/20/2020 1:34 PM	Microsoft Excel C...	2,259 KB
exprsData	1/13/2020 9:57 PM	Text Document	4,830 KB
GSE136165_Expression_Data	8/19/2019 5:43 PM	Microsoft Excel C...	4,830 KB
Manual	1/21/2020 8:13 PM	Microsoft Word D...	76 KB
pData	1/13/2020 10:26 PM	Text Document	1 KB
pData3	1/14/2020 12:42 AM	Text Document	1 KB
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
test	1/20/2020 3:35 PM	Text Document	672 KB

File name: adjacency_1e5

4. Select a File Name to Save the Modularity Network Algorithm Output in a commas separate file format.



Name	Date modified	Type	Size
.RData	1/21/2020 1:52 AM	R Workspace	83,640 KB
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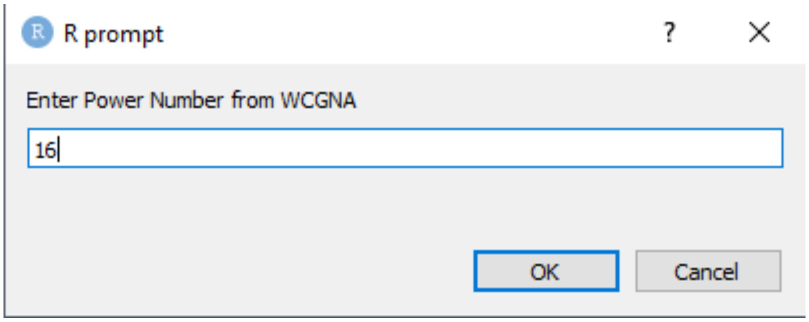
pData3	1/14/2020 12:42 AM	Text Document	1 KB
R_uni.c	8/22/2019 10:53 PM	C File	1 KB
R_uni.dll	8/22/2019 10:53 PM	Application exten...	49 KB
R_uni.h	8/22/2019 10:53 PM	H File	1 KB

File name: Modularity Output.csv

Save as type: All Files

5. Pick the Soft Power Number based on how the adjacency matrix was generated by WCGNA

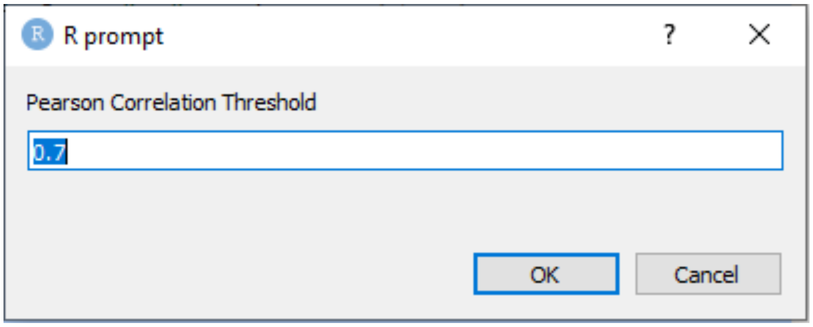
a. A soft power threshold of 16 was chosen as optimal for the example dataset



Enter Power Number from WCGNA

16

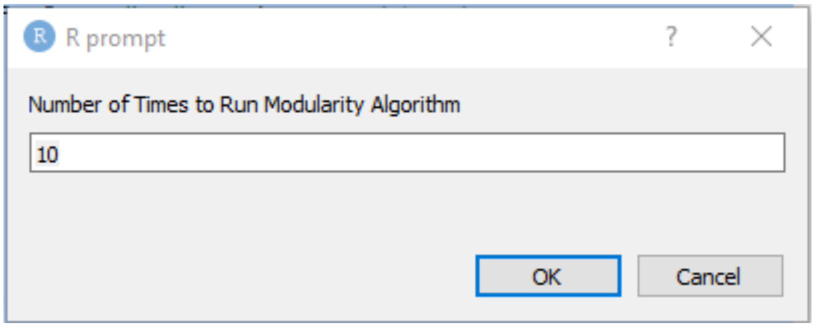
6. Pick the Pearson Correlation Threshold
    a. A Pearson correlation threshold of 0.7 was chosen as optimal for the example dataset
7.



Pearson Correlation Threshold

0.7

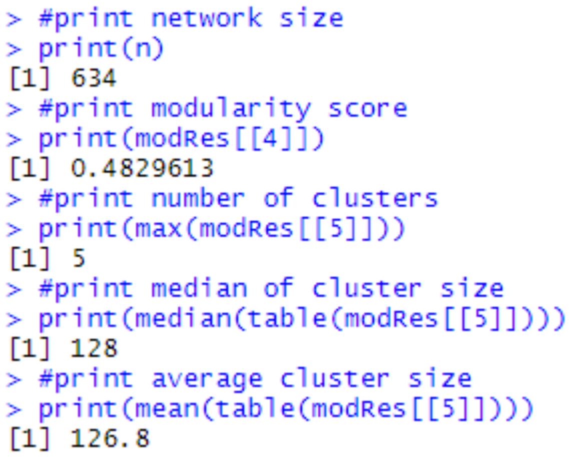
8. Pick the number of times to run the modularity algorithm



Number of Times to Run Modularity Algorithm

10

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
```