

GRAPH METRICS EXTRACTION PROTOCOL

The aim of this protocol is to extract graph metrics of external files (functional matrices of cGICA RSN networks) with GREYNA toolbox, that can be downloaded from this link <https://www.nitrc.org/projects/gretna/>, the user manual can be downloaded from this link https://www.nitrc.org/docman/view.php/668/2262/manual_v2.0.0.pdf

FILE STRUCTURE

There are two folders (G1 and G2) (the output of the previous protocol – signal extraction) with the functional matrices of each subject, there are the mean and the n windows per subject and every window is a functional matrix. These folder have the file structure shown in Figure 1 and Figure 2.

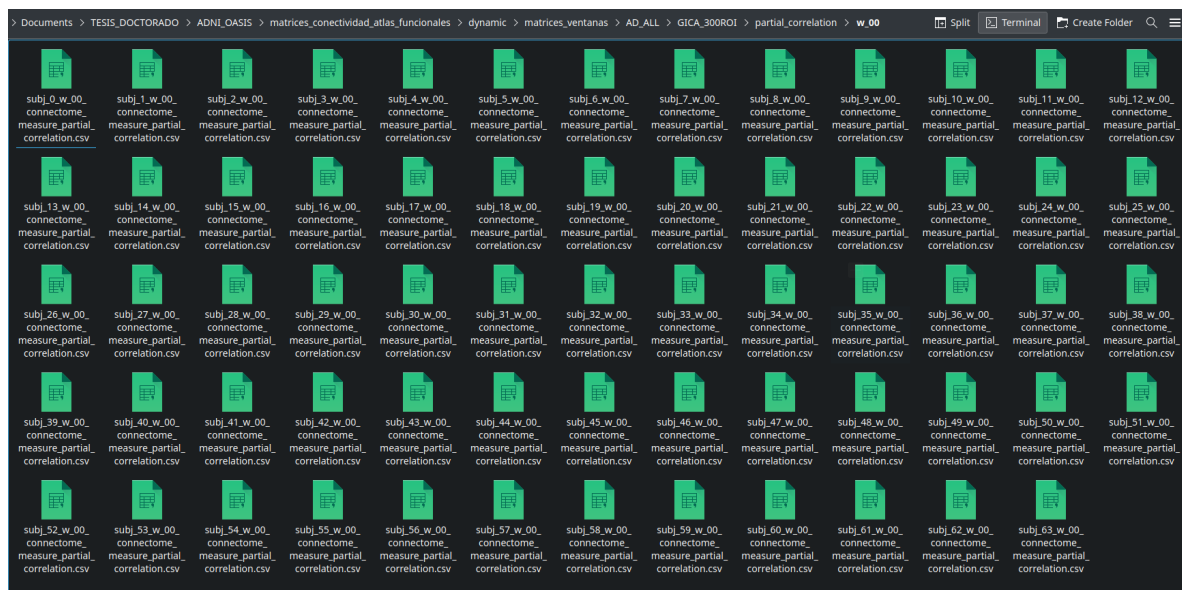


Figure 1: File structure, functional matrices per subject

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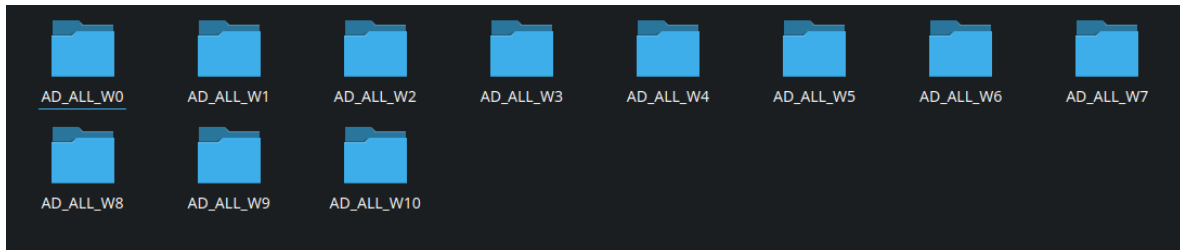


Figure 2: File structure, folder per window

GRETNA toolbox needs functional matrices to extract graph metrics. Click on NETWORK ANALYSIS to upload functional matrices Figure 3

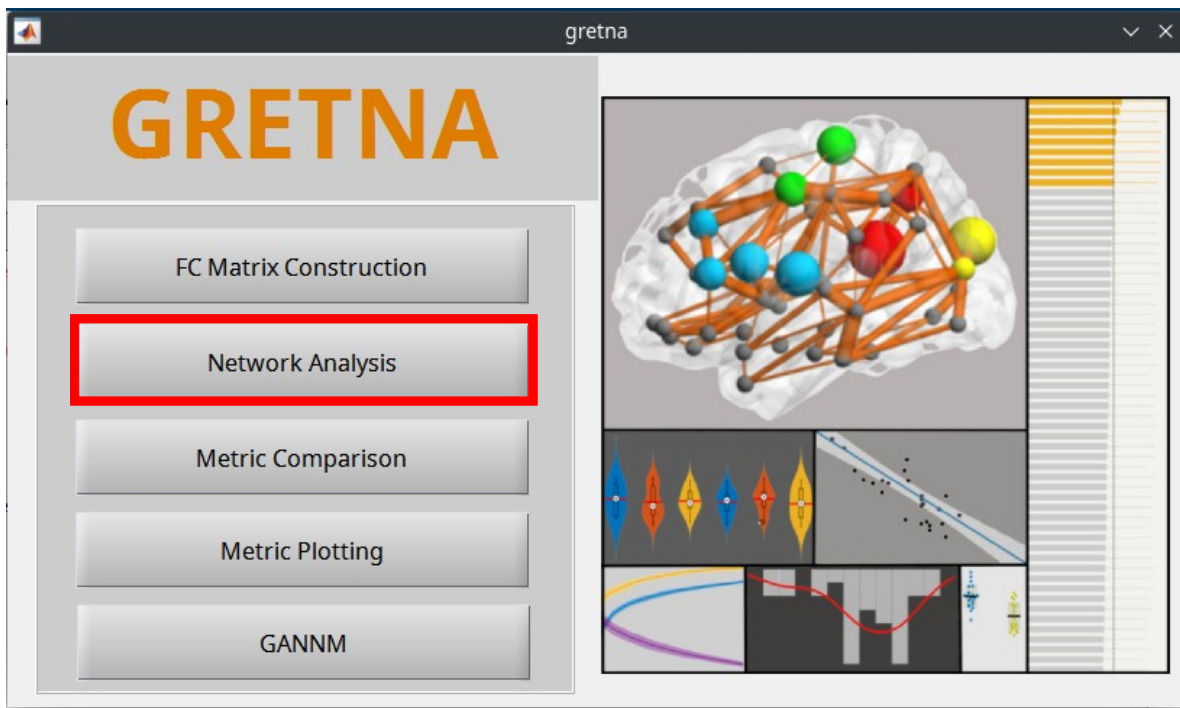


Figure 3: GRETNA initial interface.

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After click on “Network analysis” appears on the left of the window the graph metrics you can calculate and on the right the characteristics of those metrics when calculated. On the upper right side of the window were the functional matrices are going to be chosen Figure 4.

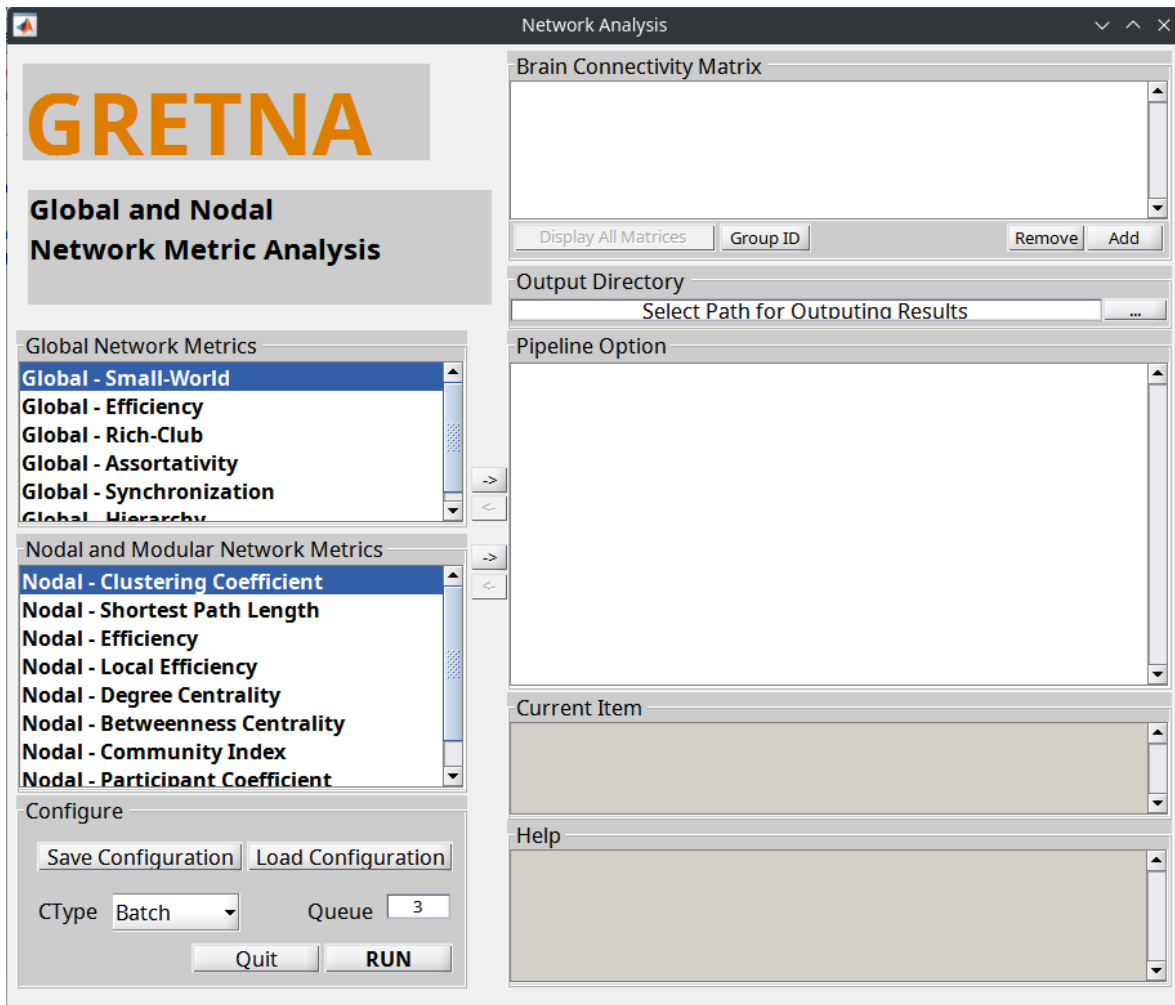


Figure 4: Network Analysis of GRETNA toolbox

The graph metrics we are going to analyze are Figure 5:

Nodal:

- Nodal Clustering Coefficient
- Nodal Shortest Path Length
- Nodal Efficiency
- Nodal Local Efficiency

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- Degree Centrality
- Betweenness Centrality
- Community Index

Global:

- Small World
- Global Efficiency
- Rich Club
- Assortativity
- Synchronization
- Hierarchy

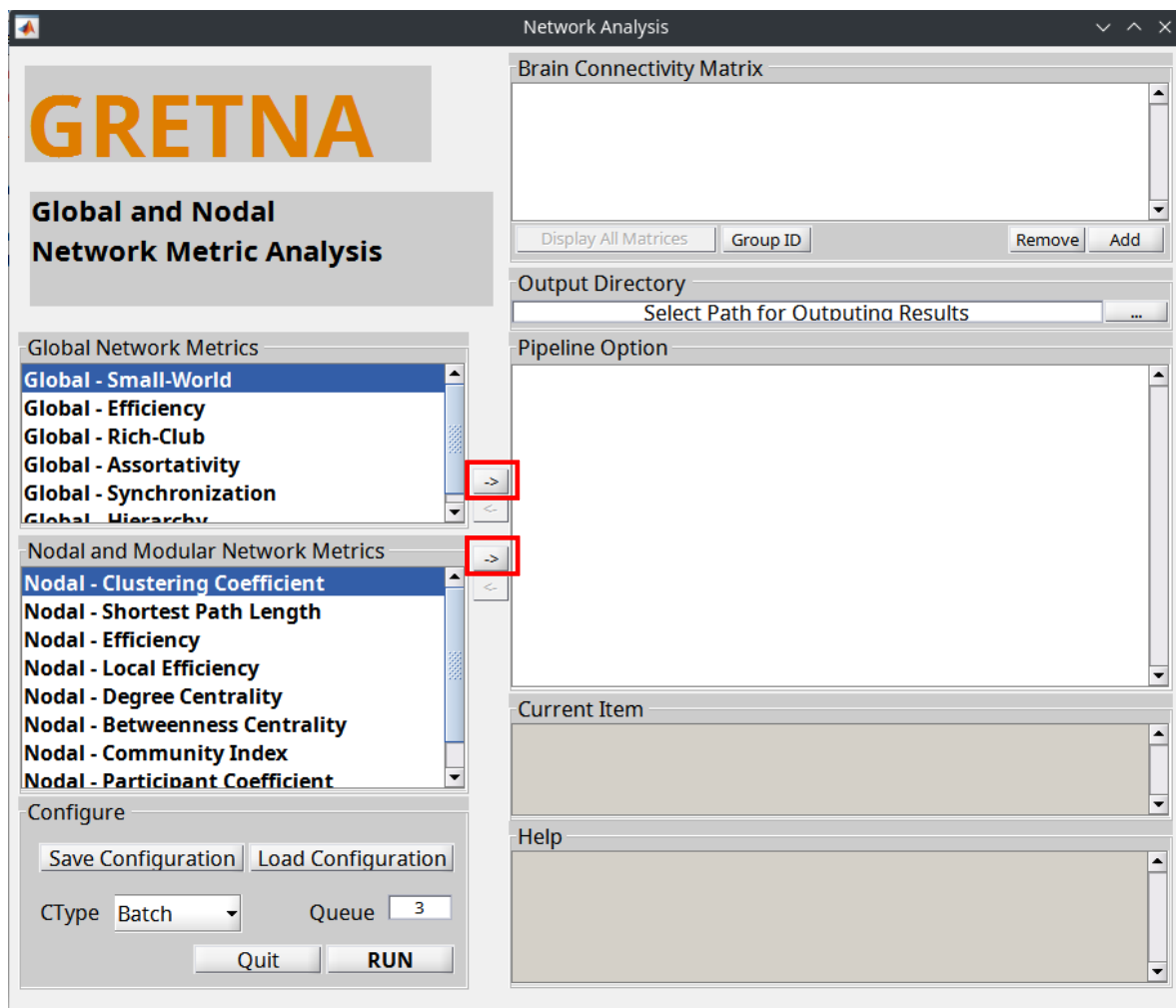


Figure 5: Global and Nodal graph metrics to analyze

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After the selection of the graph metrics to analyze, the characteristics of these are going to appear in the right side of the window and the metric is going to disappear on the left side
Figure 6

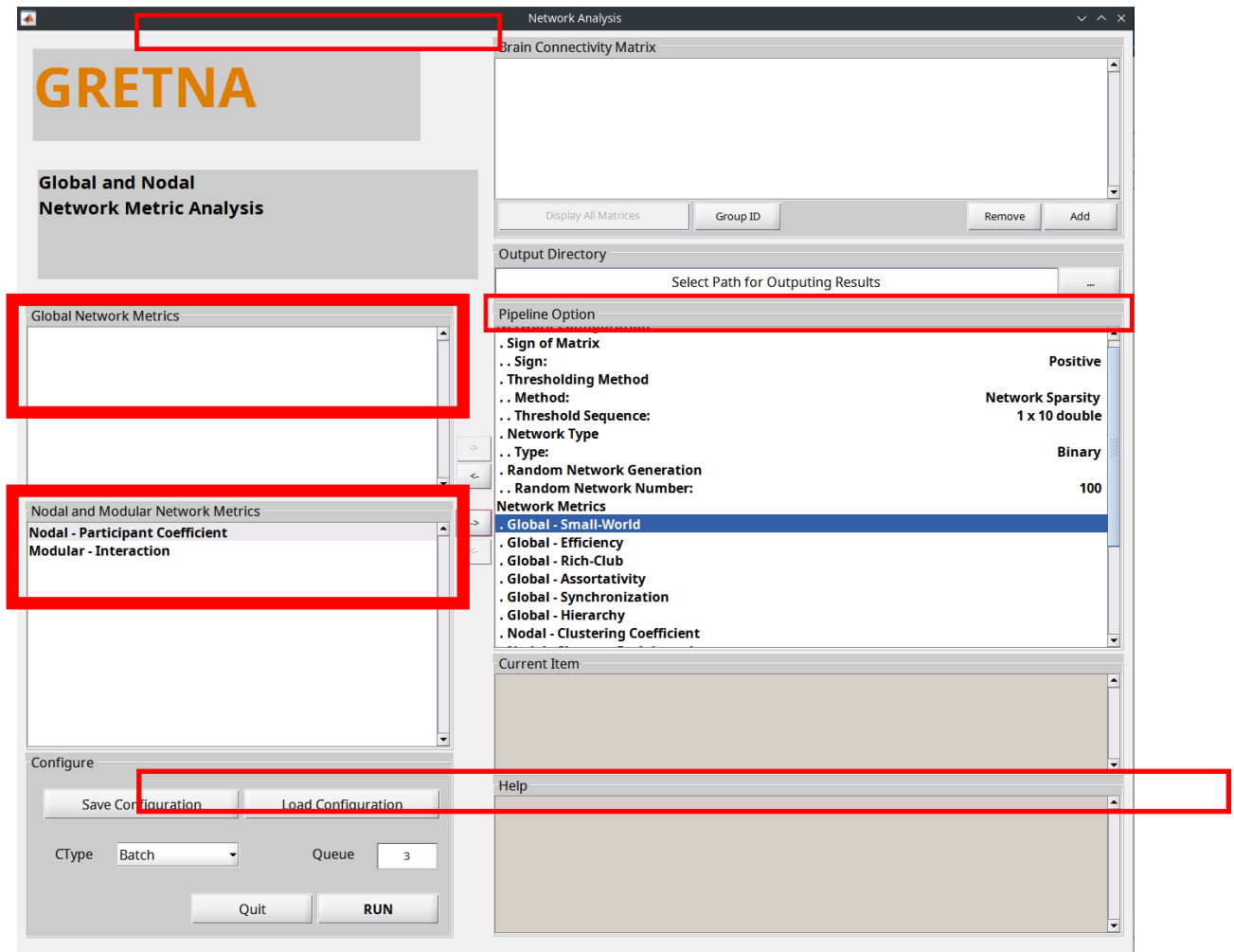


Figure 6: Selection of graph metrics



The characteristics of the metrics are left by default as proposed by GRETNA toolbox, no modifications are made Figure 7 and Figure 8.

Network Configuration	
. Sign of Matrix	
. . Sign:	Positive
. Thresholding Method	
. . Method:	Network Sparsity
. . Threshold Sequence:	1 x 10 double
. Network Type	
. . Type:	Binary
. Random Network Generation	
. . Random Network Number:	100
Network Metrics	
. Global - Small-World	
. Global - Efficiency	
. Global - Rich-Club	
. Global - Assortativity	
. Global - Synchronization	
. Global - Hierarchy	
. Nodal - Clustering Coefficient	

Figure 7: Characteristics of graph metrics

. Random Network Generation	
. . Random Network Number:	100
Network Metrics	
. Global - Small-World	
. Global - Efficiency	
. Global - Rich-Club	
. Global - Assortativity	
. Global - Synchronization	
. Global - Hierarchy	
. Nodal - Clustering Coefficient	
. Nodal - Shortest Path Length	
. Nodal - Efficiency	
. Nodal - Local Efficiency	
. Nodal - Degree Centrality	
. Nodal - Betweenness Centrality	
. Nodal - Community Index	
. . Modularity Algorithm:	Modified Greedy Optimization
. . Estimating Participant Coefficient:	TRUE

Figure 8: Characteristics of graph metrics

Functional matrices of every subject is going to be analyze, on BRAIN CONNECTIVITY MATRIX these are going to be chosen, click on ADD Figure 9.

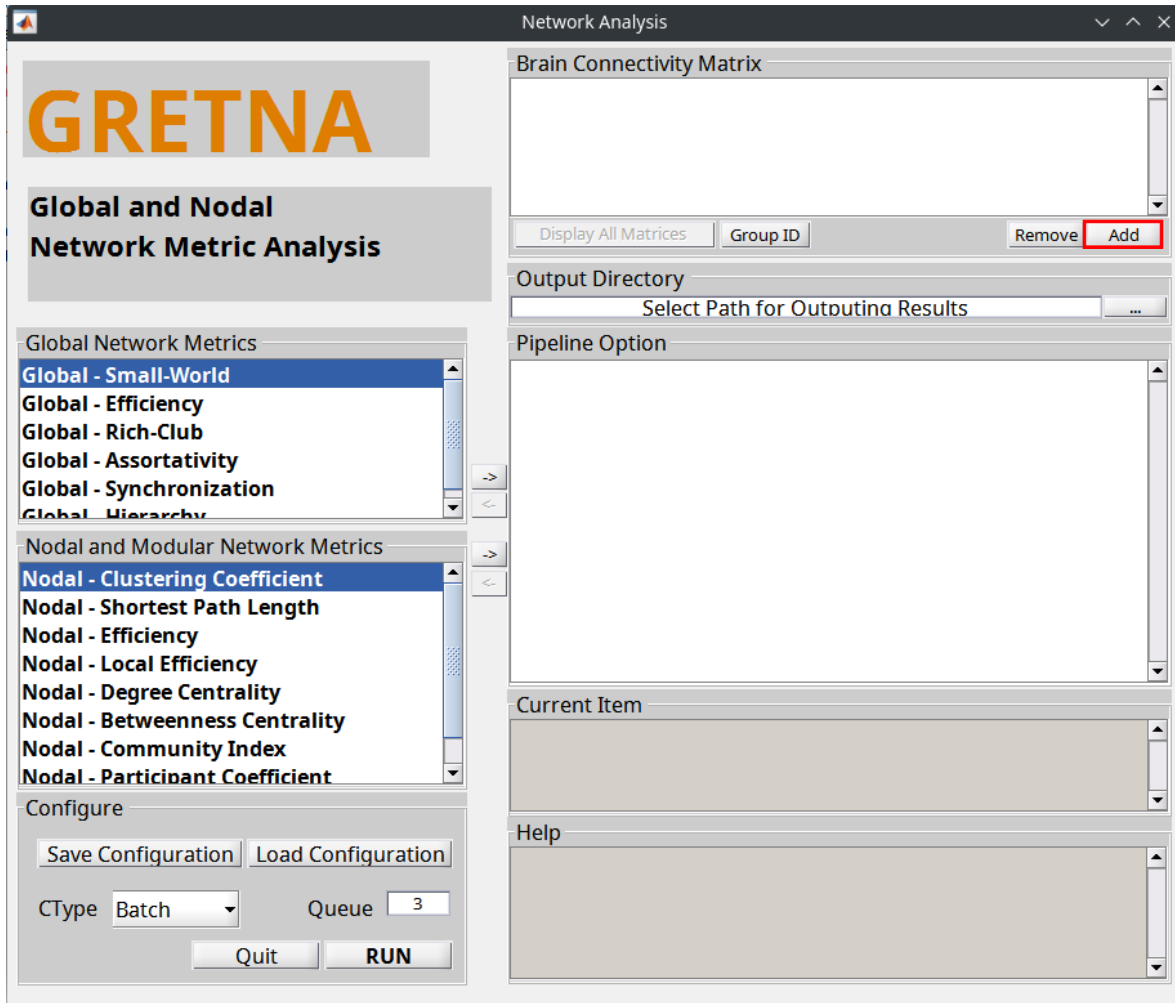


Figure 9: Brain Connectivity Matrix

After clicking on ADD an emergent window will appear where you must go to the folder where the functional matrices are saved Figure 10, Figure 11, Figure 12 and Figure 13.

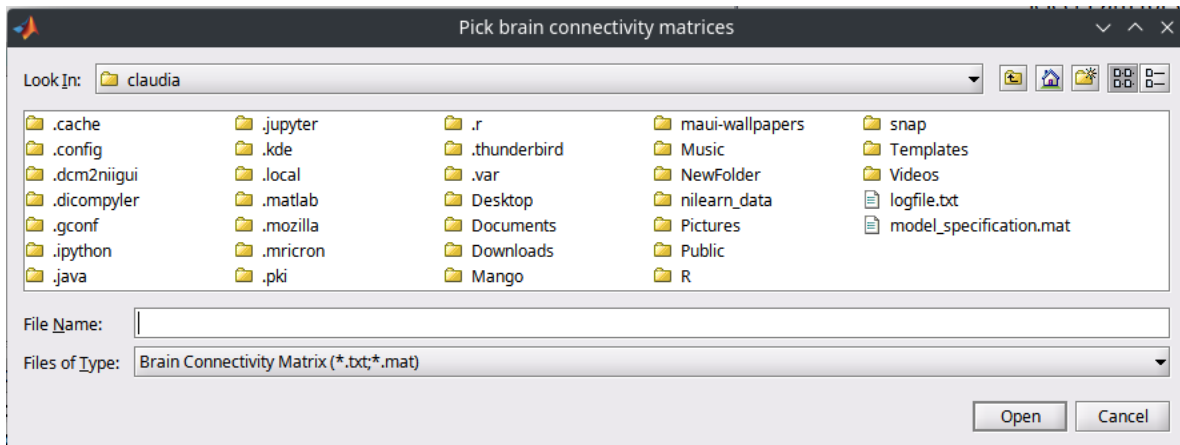


Figure 10: Selection of connectivity matrices

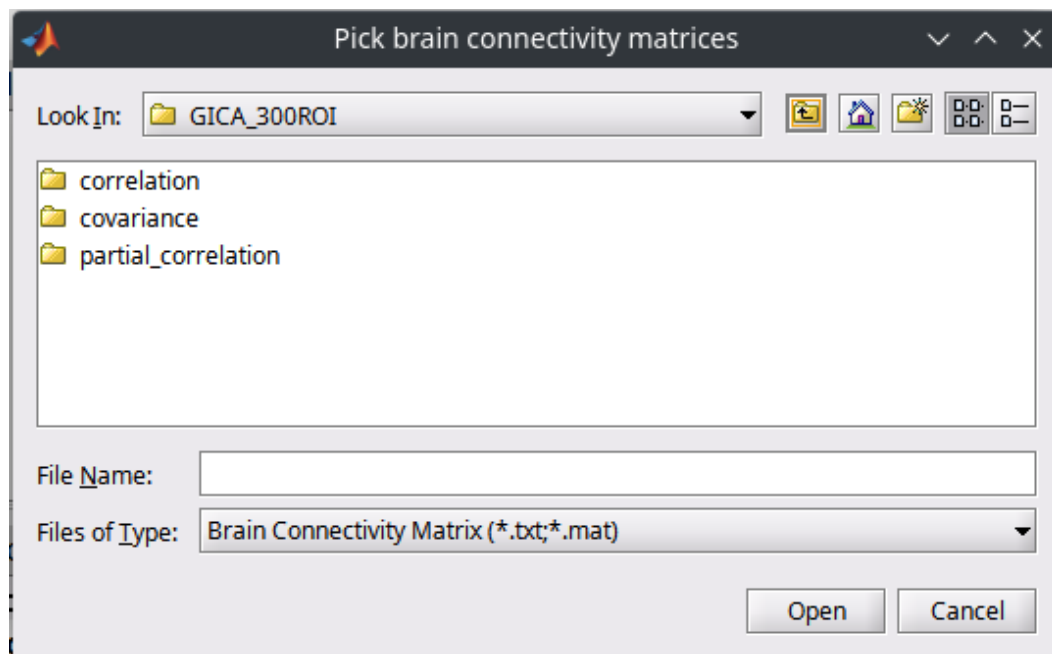


Figure 11: Selection of connectivity matrices

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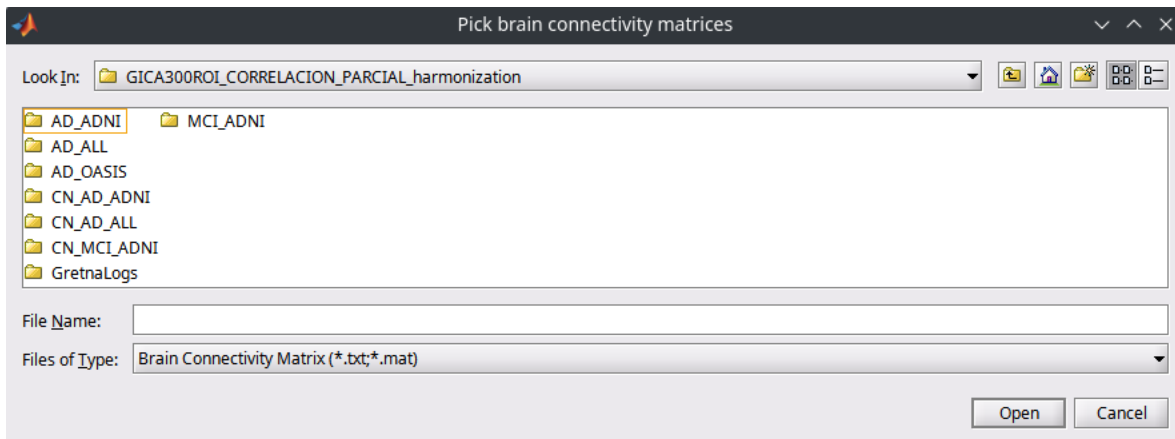


Figure 12: Selection of connectivity matrices

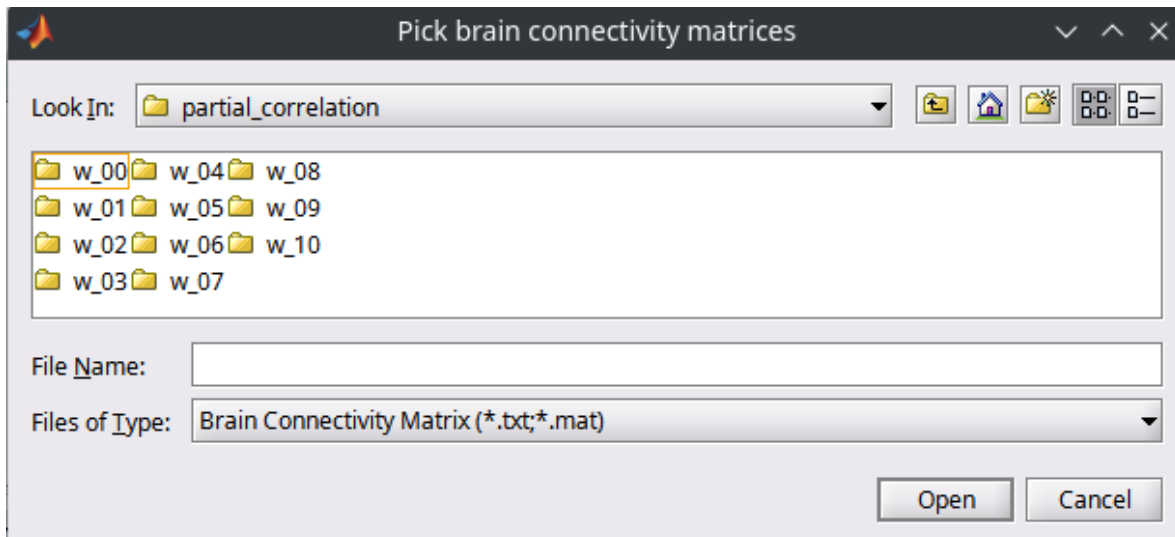


Figure 13: Selection of connectivity matrices

Open the folder of the first window in order to select the functional matrices that are saved there. When you do that no files you're going to find Figure 14.

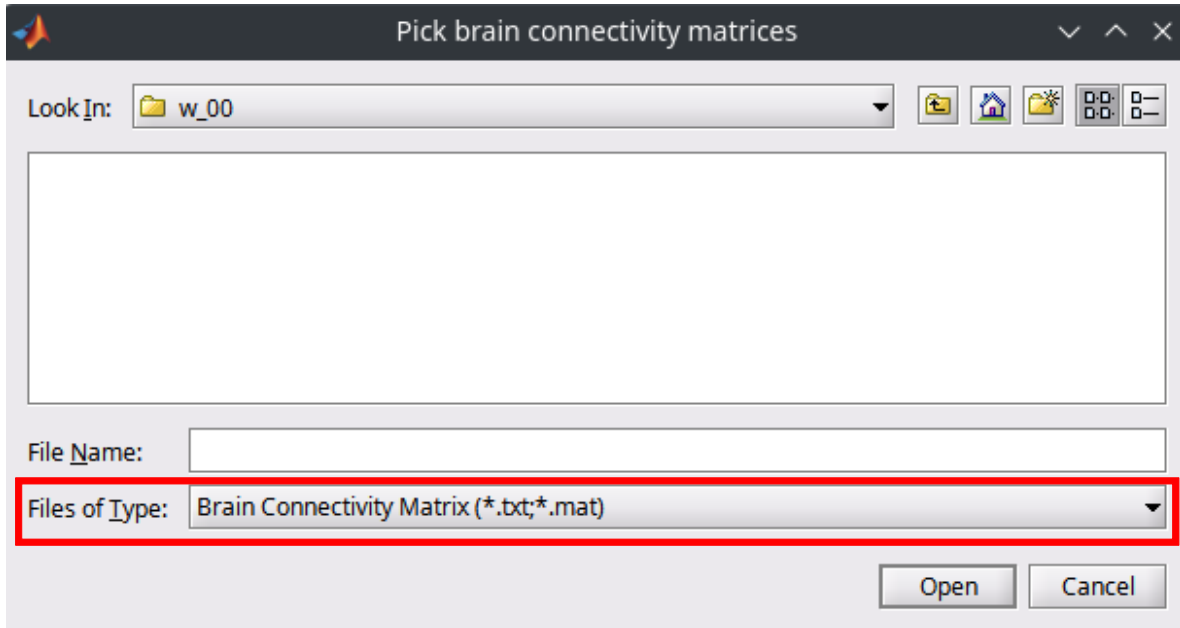


Figure 14: No files in folder selected

The functional matrices are in format .csv, so you must open “Files of Type” in order to select “All files” and the files in your folder are going to appear Figure 15.

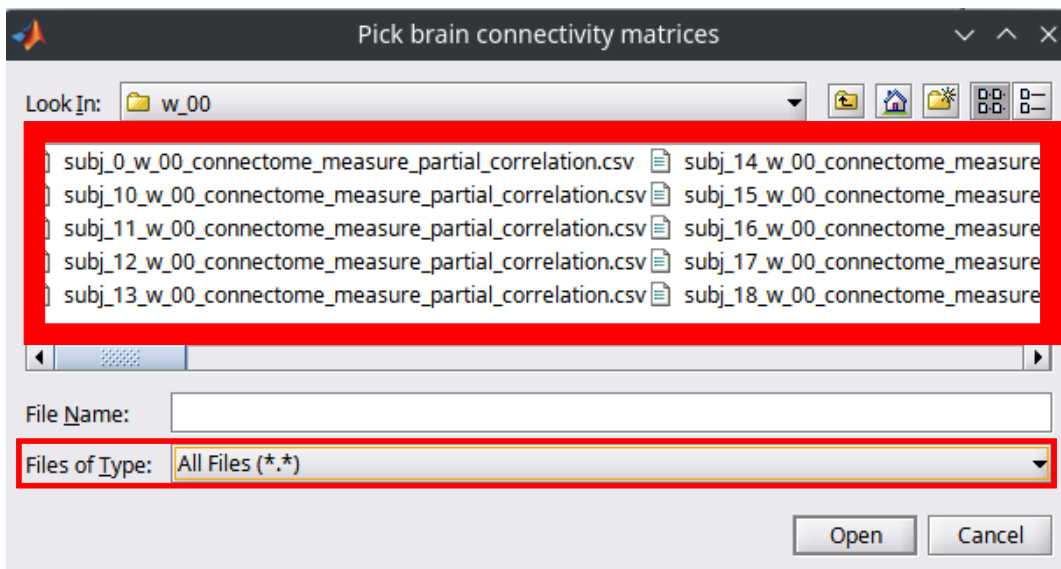


Figure 15: Selection of functional matrices files

When all files in the folder of the selected window appear (functional matrices per subject), you are going to select all files in that folder Figure 16. Make sure that you only select the windows per subject and not the window with the mean functional matrix.

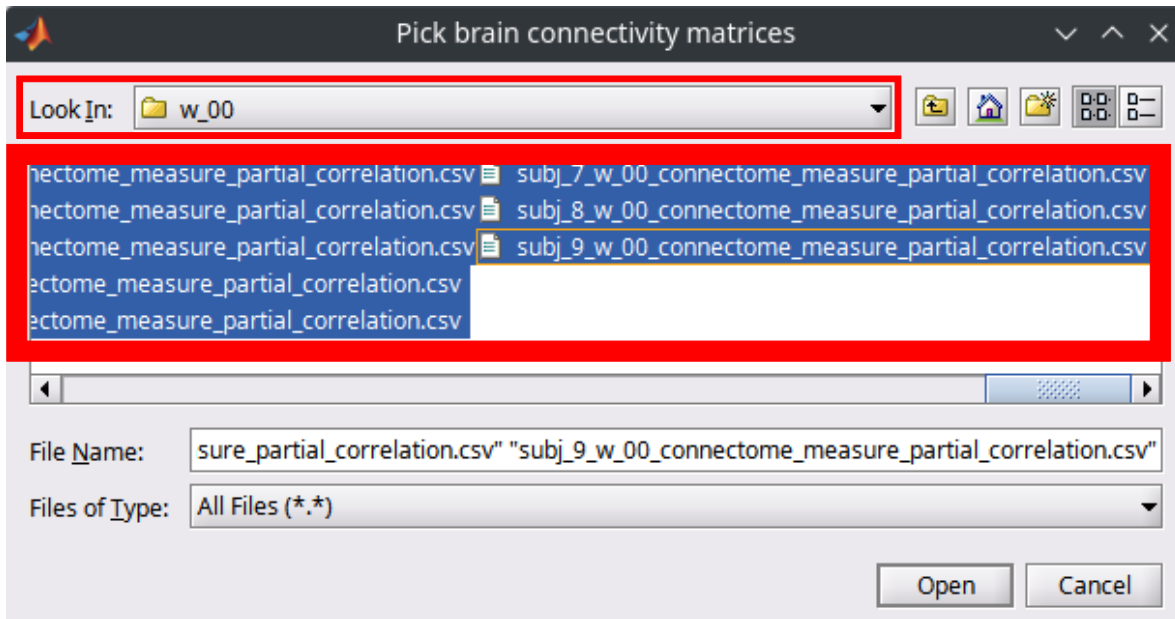


Figure 16: Selection of functional matrices per subject in the first window

After selecting the functional matrices per subject, you will see this matrices in the part Brain Connectivity Matrix, upper right in GRETNAt interface Figure 17. You can review if all files were selected.

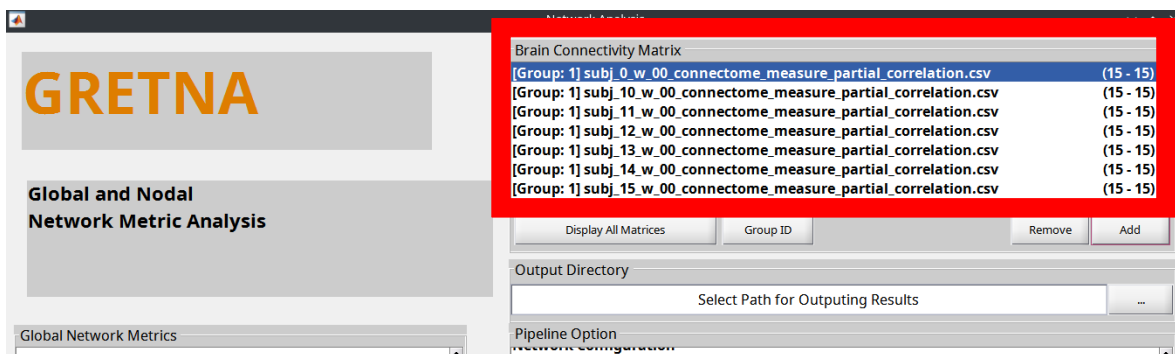


Figure 17: Selected functional matrices

As we have n windows with m functional connectivity matrices each one (window), you will have n groups as GRETNATM divides the information. If you add new functional connectivity matrices automatically GRETNATM will assigned it to Group 1 Figure 18.

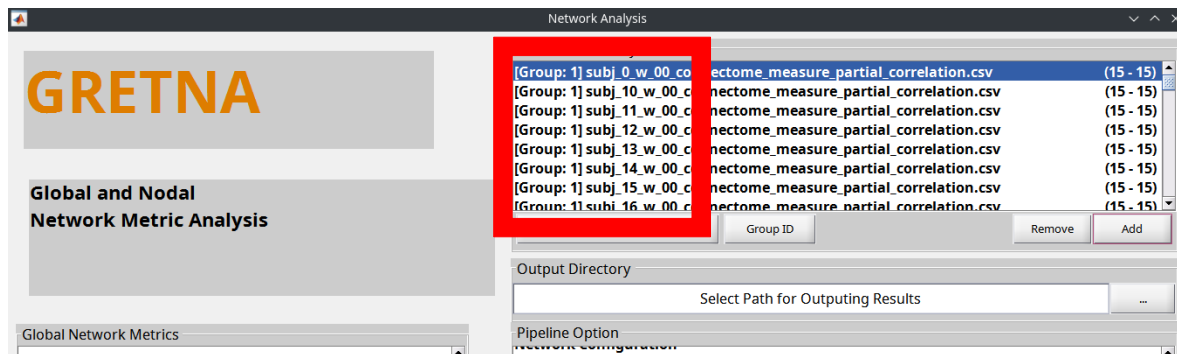


Figure 18: Name of groups

This is why you need to change the name of the groups when you add new functional connectivity matrices. Before adding a new window with its connectivity matrices, you must first change the group name of the one you immediately added before. Note that if you add the connectivity matrices of window 001, you don't need to change the group name, as GRETNATM will automatically name it as Group 1.

We suggest to name every group as the window.

Example:

Group:0 subj_xx_w_00
Group:1 subj_xx_w_01
Group:2 subj_xx_w_02
....
Group:10 subj_xx_w_10

To change the name of the group you need to make it manually, you could do it in a plain text before copying it in GRETNATM. In this guide we will show you how to do it manually and directly in the toolbox.

First, after you upload the functional matrices per subject of the first window, you must change the name of the group in order to match it with the window's name. To do this you click on "Group ID" and immediately a window opens where you can change the name of the group manually Figure 19.

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When you change some numbers, you can check how many numbers remain to be changed as you can see in Figure 21.

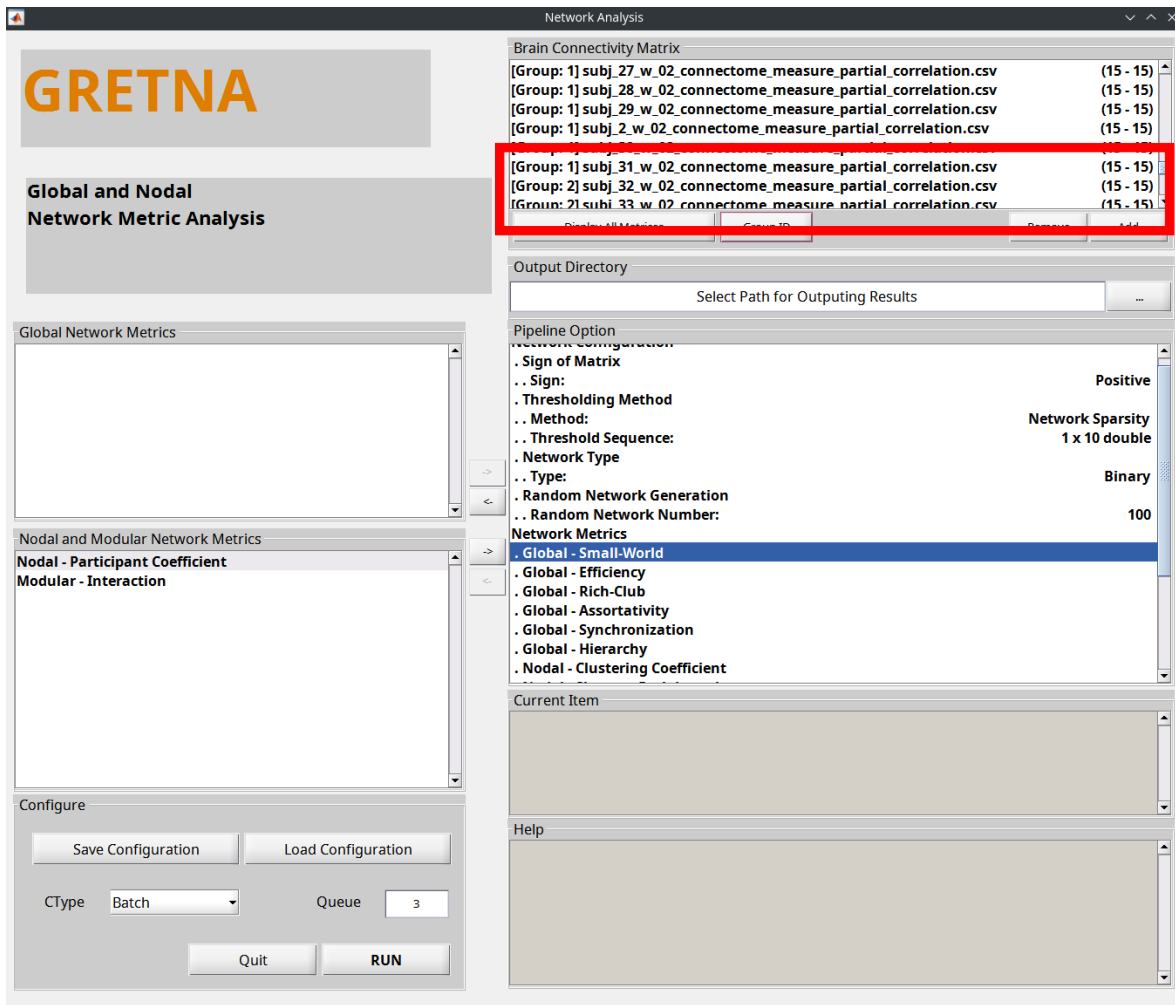


Figure 21: Checking the changes in the name of group

After you change the name of the group of every subject (functional connectivity matrix) in the window 0, you add the functional connectivity matrix per subject of window 1 Figure 22. Check that the number of subjects will be the same in every window per group, for example, if you have 121 in each group, you must have added 121 connectivity matrices per window.

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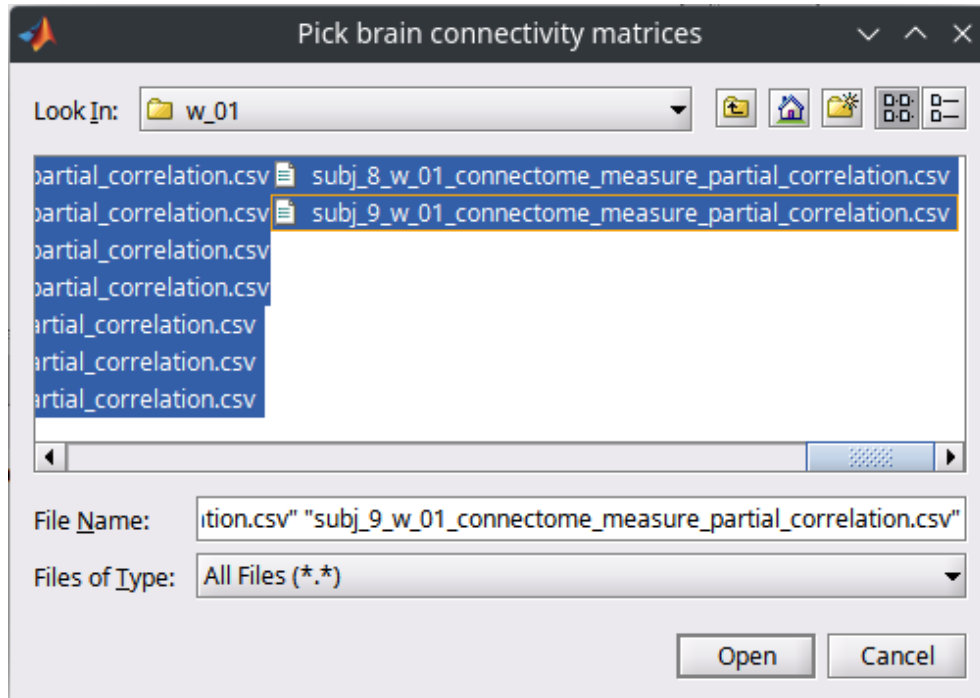


Figure 22: Adding the next files of functional connectivity matrix per subject of window1

As GRETNA labels every file as “Group 1” automatically you don’t need to change the name of this group of functional connectivity matrix Figure 23.

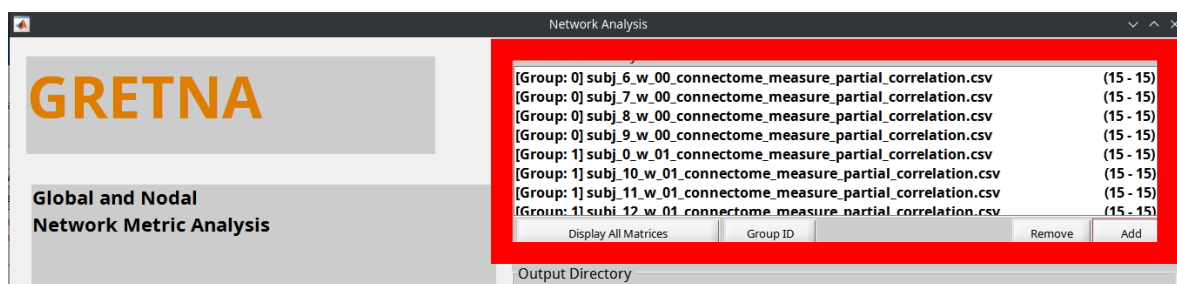


Figure 23: Automatic labeling of files in GRETNA toolbox

Then you add the functional connectivity matrix per subject of window 2, this is when you change the number of these files Figure 24 and Figure 25. Remember you can write the entire list of number per subject in a plain text and then paste it when you have added every file

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you're going to analyze and check that the group name corresponds with the number of the window.

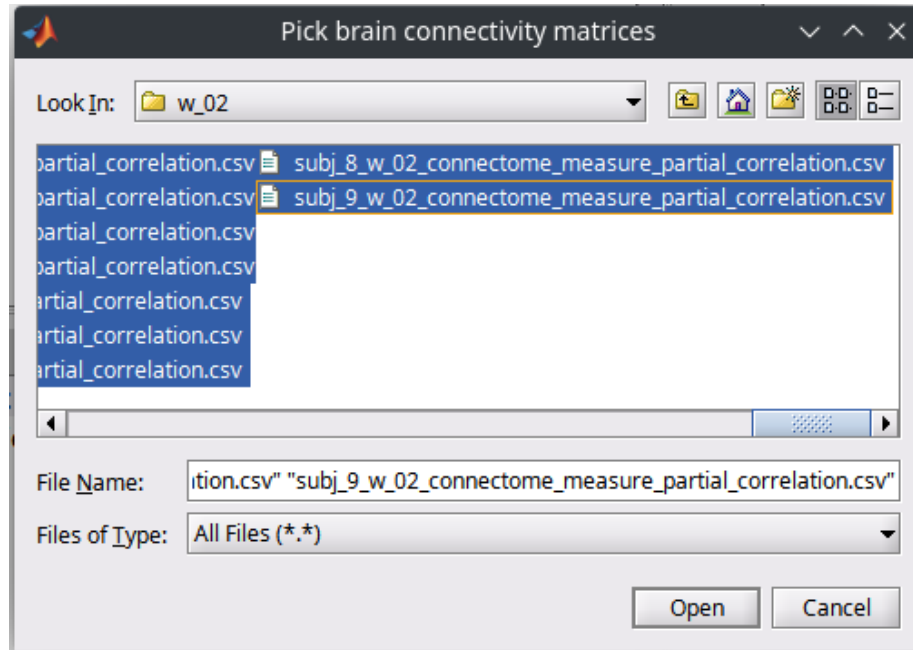


Figure 24: Adding the next files of functional connectivity matrix per subject of window2

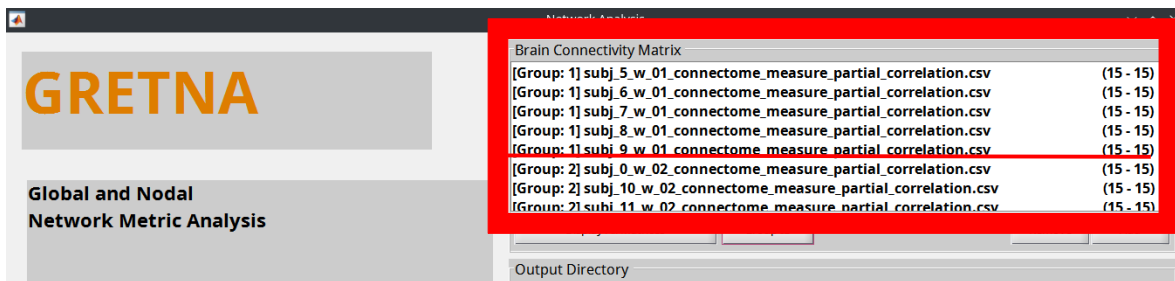


Figure 25: Checking the changes in the name of group 2

Keep doing step by step with all the remain files until you upload the functional connectivity matrices of the n windows. When you upload every file you're going to analyze, you must define the output directory Figure 26.

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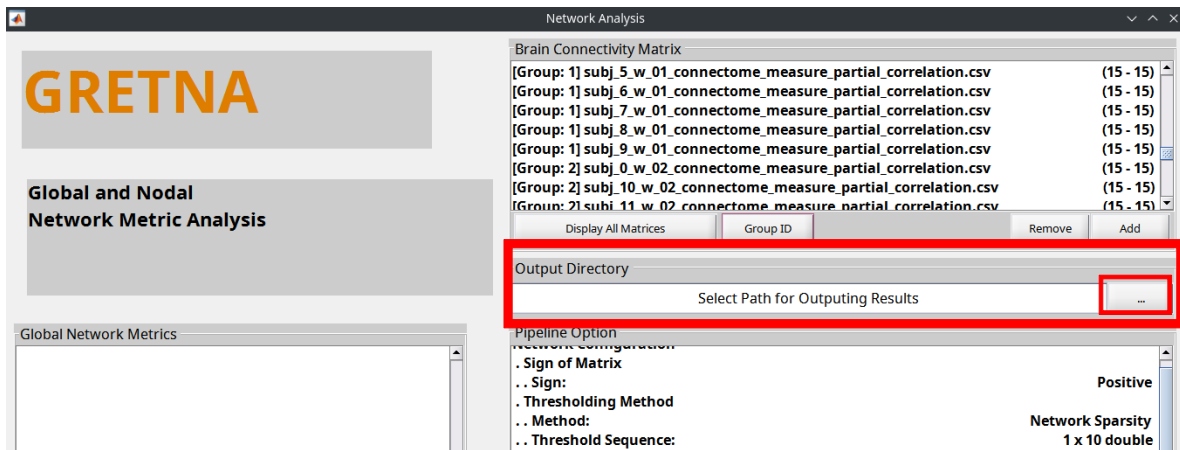


Figure 26: Select the output directory

Before you start the GRETNA algorithm with the selected files, you should select the maximum number of queues your computer has and you decide how many your going to run with this algorithm, in our case we use 20 Figure 27. Check how many CPU cores your computer has.

This process can take several hours of processing.

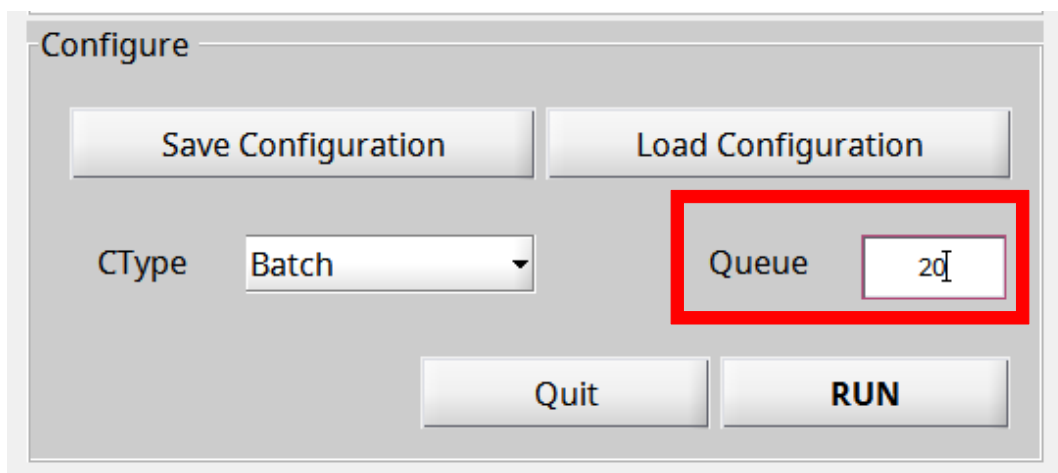


Figure 27: Define how many queues to use in graph metrics extraction



OUTPUT FOLDER STRUCTURE

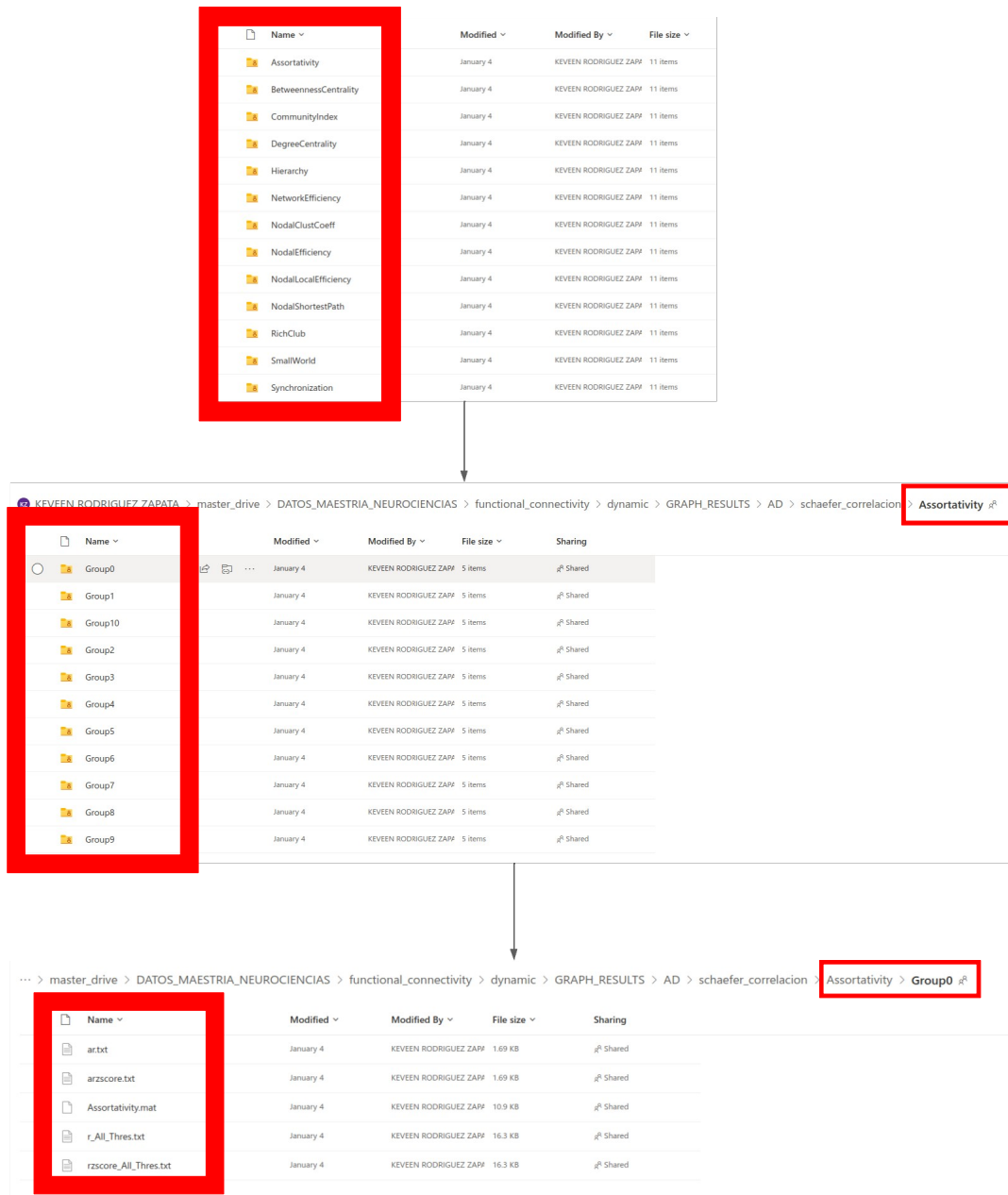


Figure 28: How the toolbox organizes the data in the output file.

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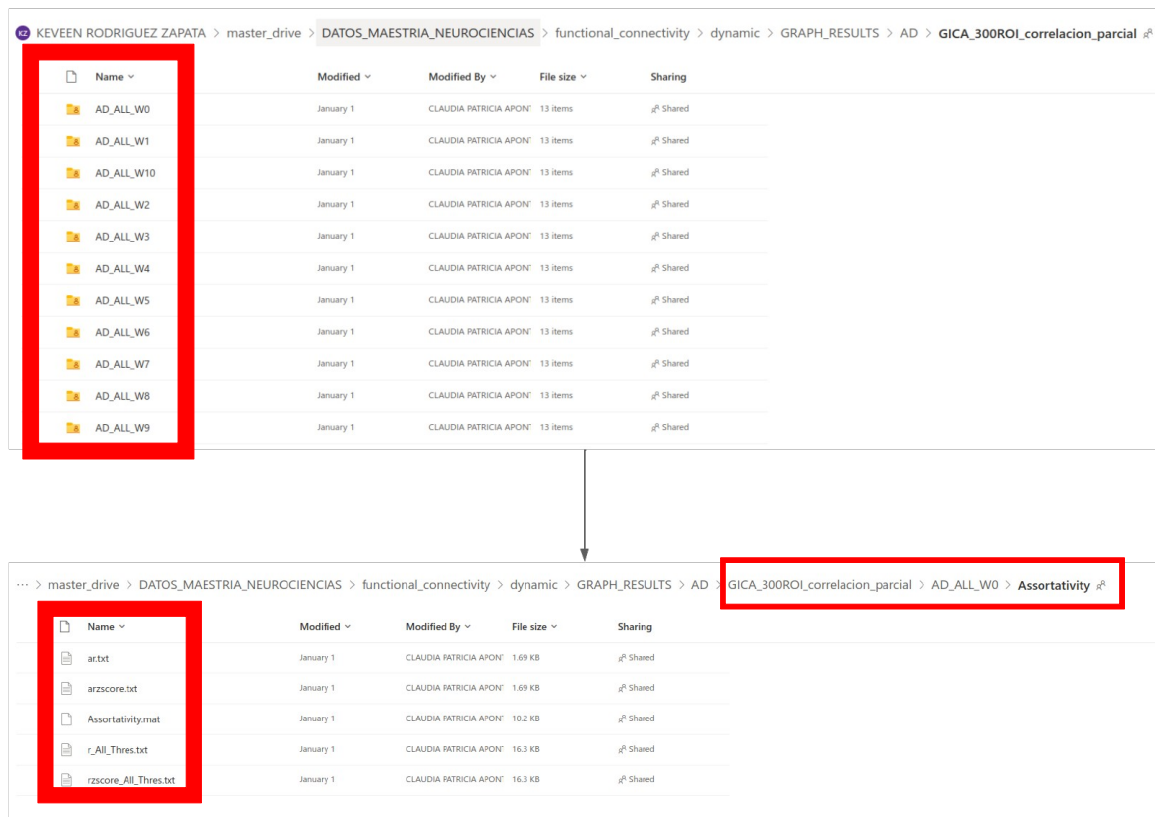
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As you can see in Figure 28, GRETNA has a distribution of folders and files that are not suitable for data analysis. The main folders are every graph metric and the files inside them are every group, in our case, every window.

The distribution of folders must be changed, the first folder must be the groups (11 windows) and inside every window folder must be the graph metrics, as shown in Figure 29.



Name	Modified	Modified By	File size	Sharing
AD_ALL_W0	January 1	CLAUDIA PATRICIA APONTE	13 items	Shared
AD_ALL_W1	January 1	CLAUDIA PATRICIA APONTE	13 items	Shared
AD_ALL_W10	January 1	CLAUDIA PATRICIA APONTE	13 items	Shared
AD_ALL_W2	January 1	CLAUDIA PATRICIA APONTE	13 items	Shared
AD_ALL_W3	January 1	CLAUDIA PATRICIA APONTE	13 items	Shared
AD_ALL_W4	January 1	CLAUDIA PATRICIA APONTE	13 items	Shared
AD_ALL_W5	January 1	CLAUDIA PATRICIA APONTE	13 items	Shared
AD_ALL_W6	January 1	CLAUDIA PATRICIA APONTE	13 items	Shared
AD_ALL_W7	January 1	CLAUDIA PATRICIA APONTE	13 items	Shared
AD_ALL_W8	January 1	CLAUDIA PATRICIA APONTE	13 items	Shared
AD_ALL_W9	January 1	CLAUDIA PATRICIA APONTE	13 items	Shared

Name	Modified	Modified By	File size	Sharing
ar.txt	January 1	CLAUDIA PATRICIA APONTE	1.69 KB	Shared
arscore.txt	January 1	CLAUDIA PATRICIA APONTE	1.69 KB	Shared
Assortativity.mat	January 1	CLAUDIA PATRICIA APONTE	10.2 KB	Shared
r_All_Thres.txt	January 1	CLAUDIA PATRICIA APONTE	16.3 KB	Shared
rzscores_All_Thres.txt	January 1	CLAUDIA PATRICIA APONTE	16.3 KB	Shared

Figure 29: File structure in the output file

The file structure must be like this:

Principal Folder:
Group Name

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Example:

G1

G2

Inside that folder, every window must be named:

Group_window number

Example:

G1_W0

G1_W1

G1_W2

.....

G1_W10

Folder of group2

G2_W0

G2_W1

G2_W2

....

G2_W10

Inside every window folder must be the individual folder for every graph metric, you can see an example of this in Figure 30. In this figure we have several groups, inside every group folder you can find a folder per window, and inside this latter, you should paste every metric result for that specific group and window.

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Figure 30: Folder structure

This is why, you take every graph metric as GRETNa gives you the output folder, for example Assortativity, within this metric there are 11 folders, one for each group. A folder is then created and named as suggested (group_#window), inside it a folder is copied with the name of the group (as GRETNa structures it), for example Group0 which will correspond to the name of the folder Gx_W0, then the name is changed (Gx_W0) and so on with each one of the groups until finishing with that metric. In this way, the folder Gx_W0 must contain the folder assortativity with the content of group 0.

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Inside every graph metric you will find specific files.

Nodal graph metrics:

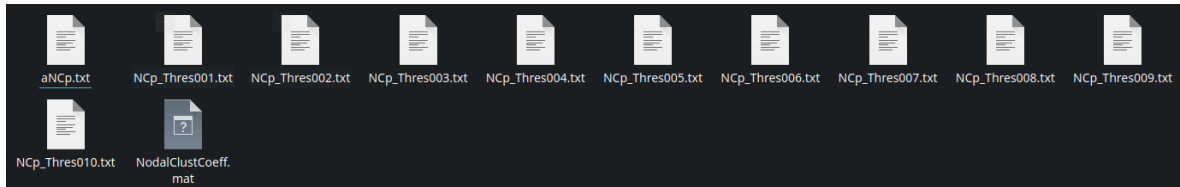


Figure 31: Nodal Clustering Coefficient folder

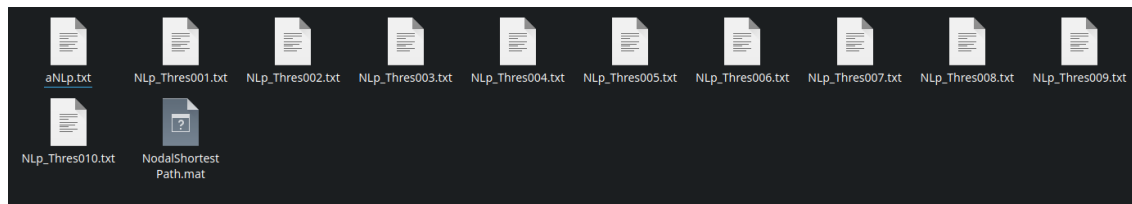


Figure 32: Nodal Shortest Path Length folder

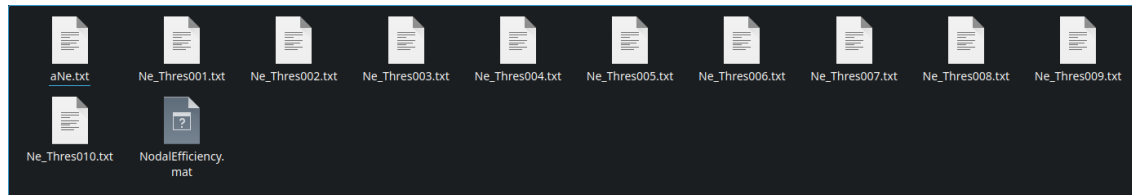


Figure 33: Nodal Efficiency folder

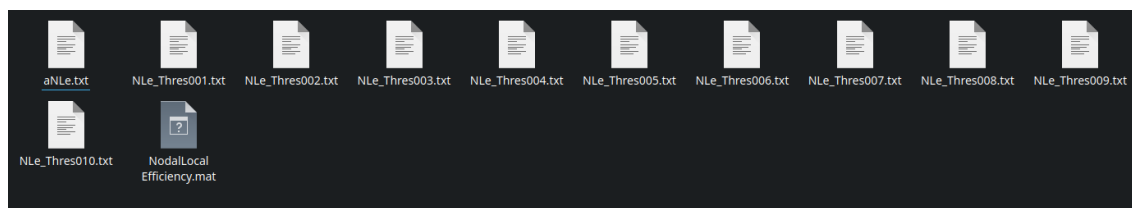


Figure 34: Nodal Local Efficiency folder

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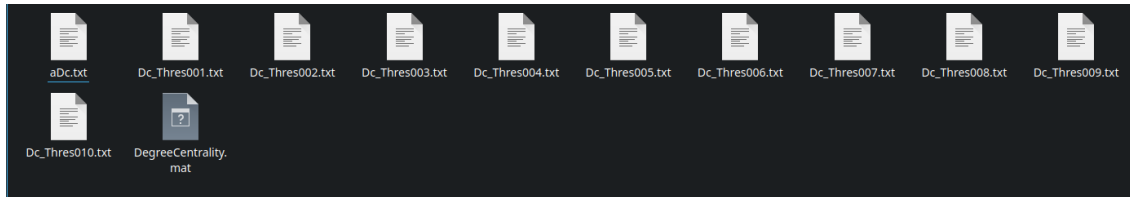


Figure 35: Degree Centrality folder

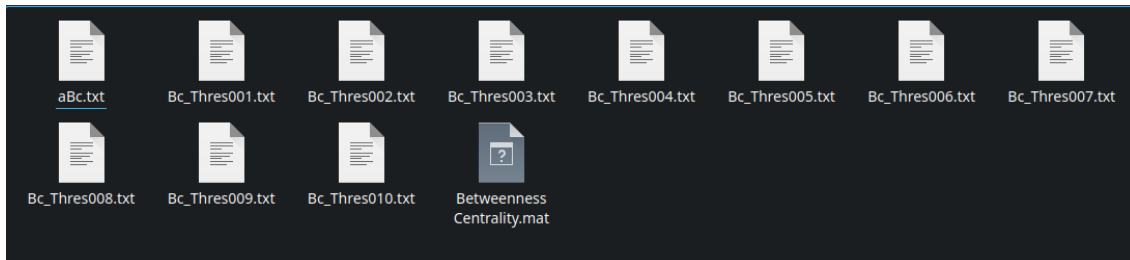


Figure 36: Betweenness Centrality folder

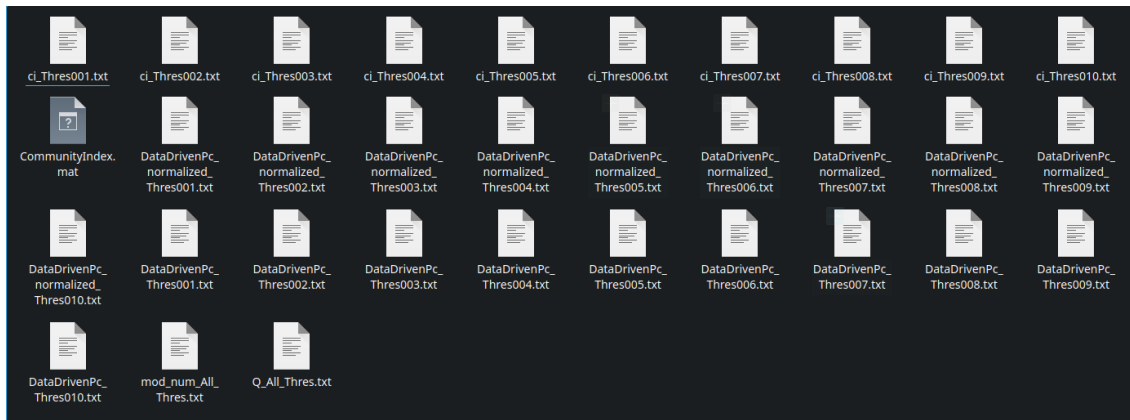


Figure 37: Community Index folder

Global graph metrics:

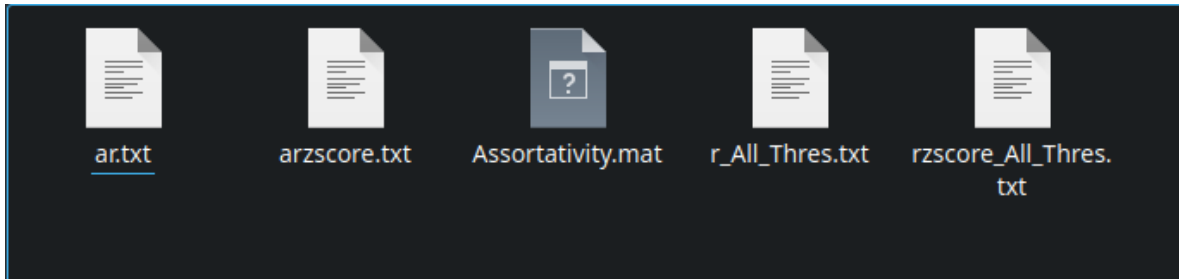


Figure 38: Assortativity folder

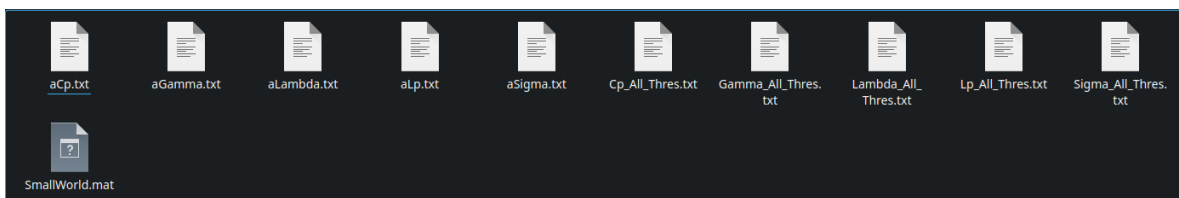


Figure 39: Small World folder

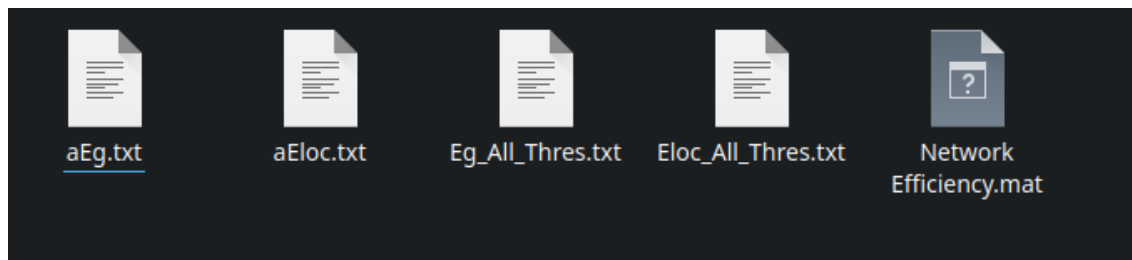


Figure 40: Network Efficiency folder

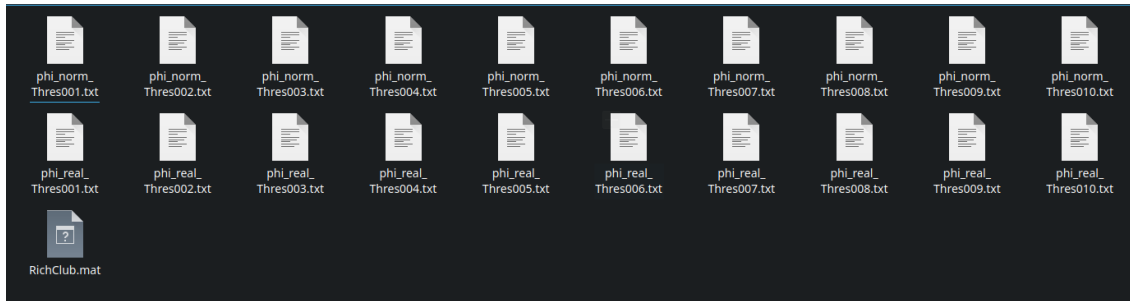


Figure 41: Rich Club folder

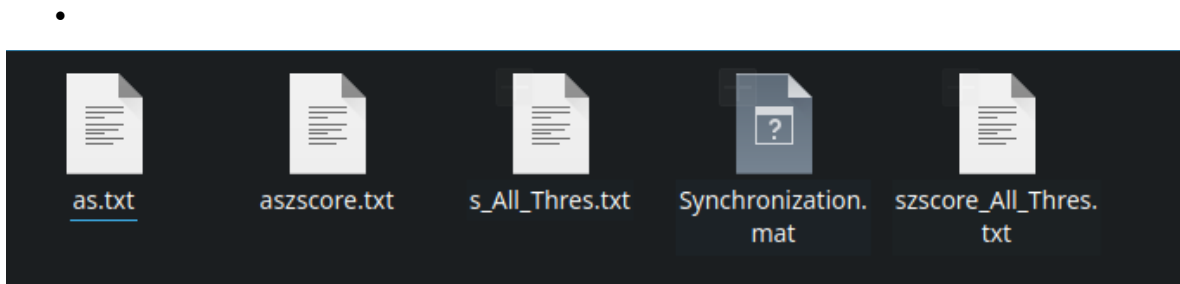


Figure 42: Synchronization folder

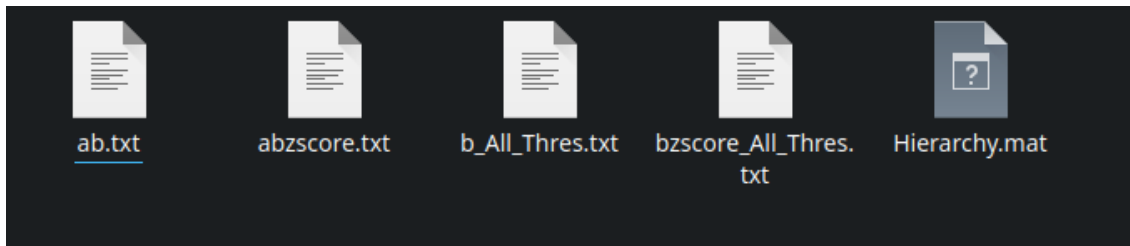


Figure 43: Hierarchy folder

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