

# GraphVar: a brief tutorial for getting started



## Hypothesis:

1. Chilli eating champs probably have more efficient brains... otherwise they could not deal with all the pain!
2. Probably orbito frontal gyrus and supplementary motor area contribute here... something like value representations and motor inhibition (... „don't spit out these delicious chillies“)



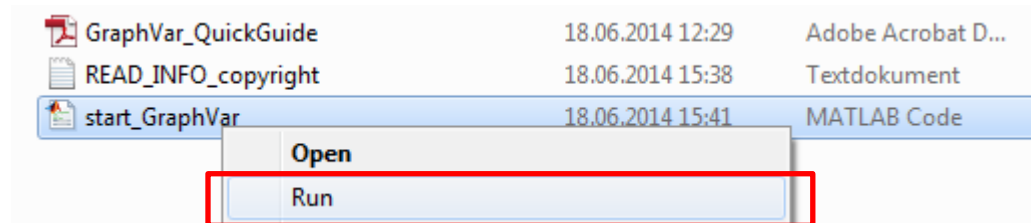


## Hypothesis:

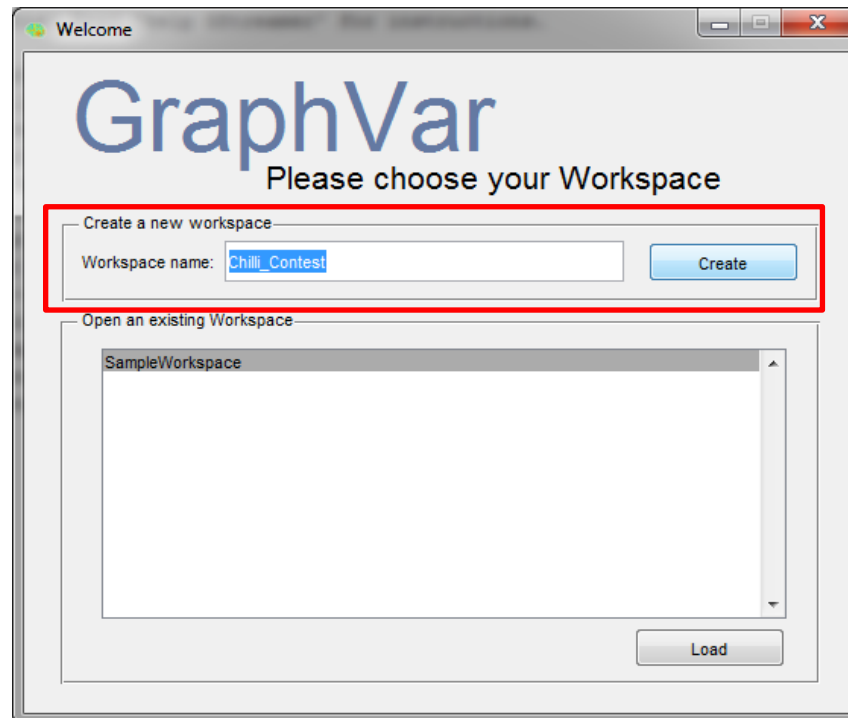
... a potential confound could be how much beer somebody had to drink before (i.e., cooling effect on the brain)

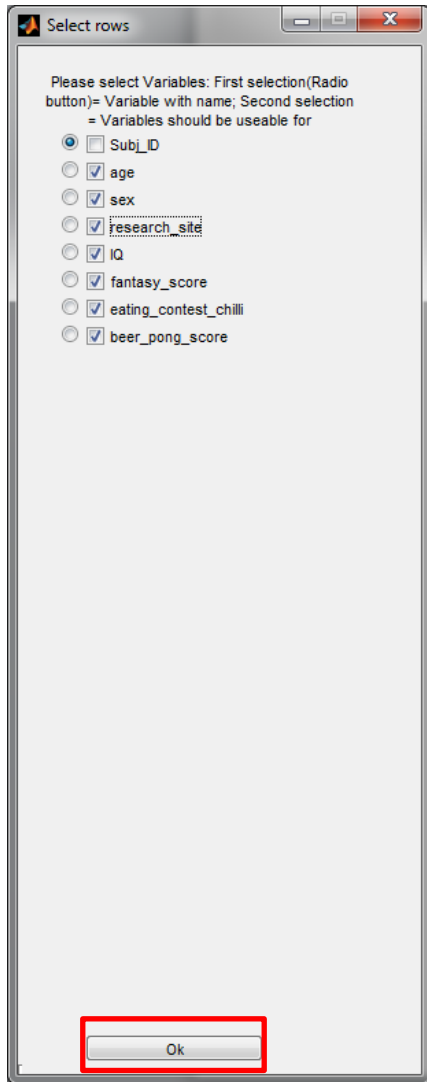


1. Use the right mouse to start GraphVar by clicking RUN on the „start\_GraphVar“ script in the main folder

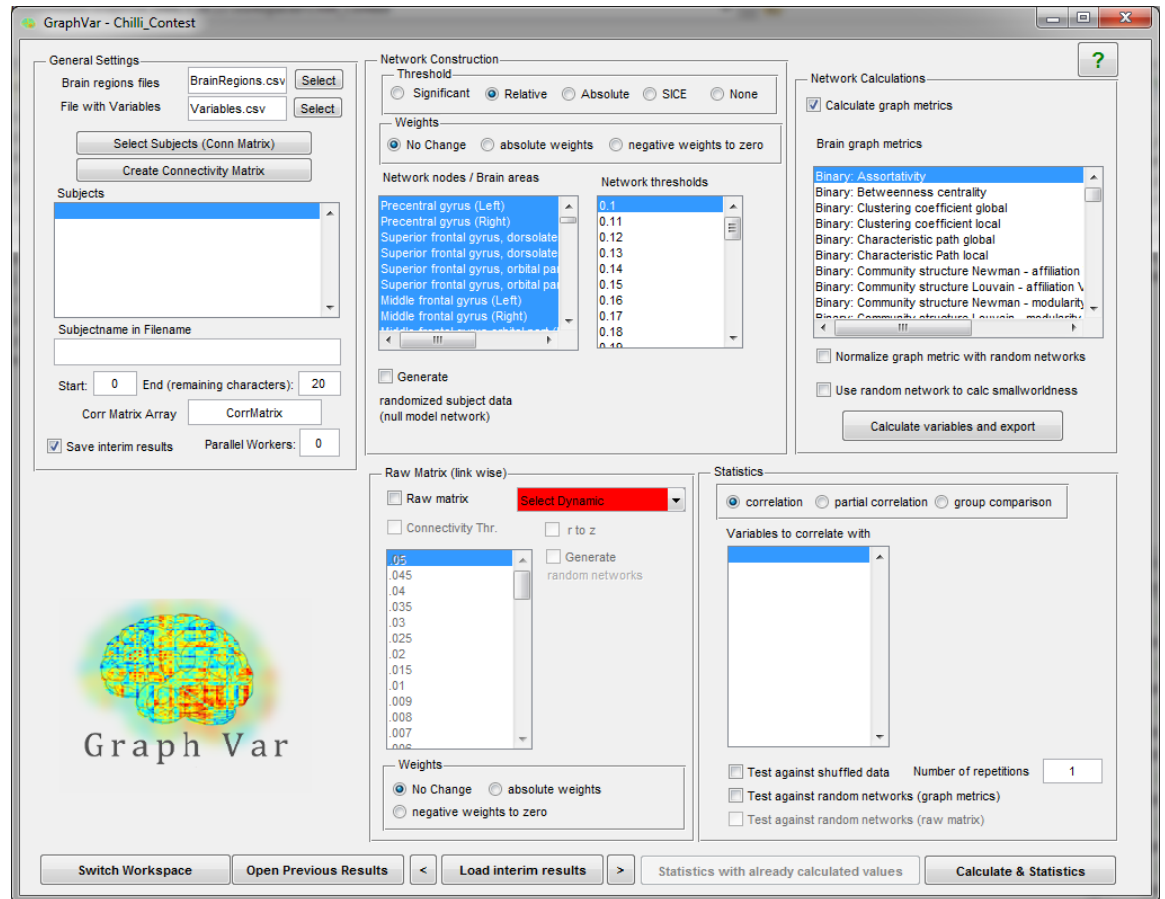


2. Create a new Workspace „Chilli\_Contest“





- The demo (default) data selection window appears (refer to the manual for how to change this)
- Research\_site and sex are initially not selected as these variables are encoded as strings in the variable spread sheet ... you may select them if you want
- Hit the okay button



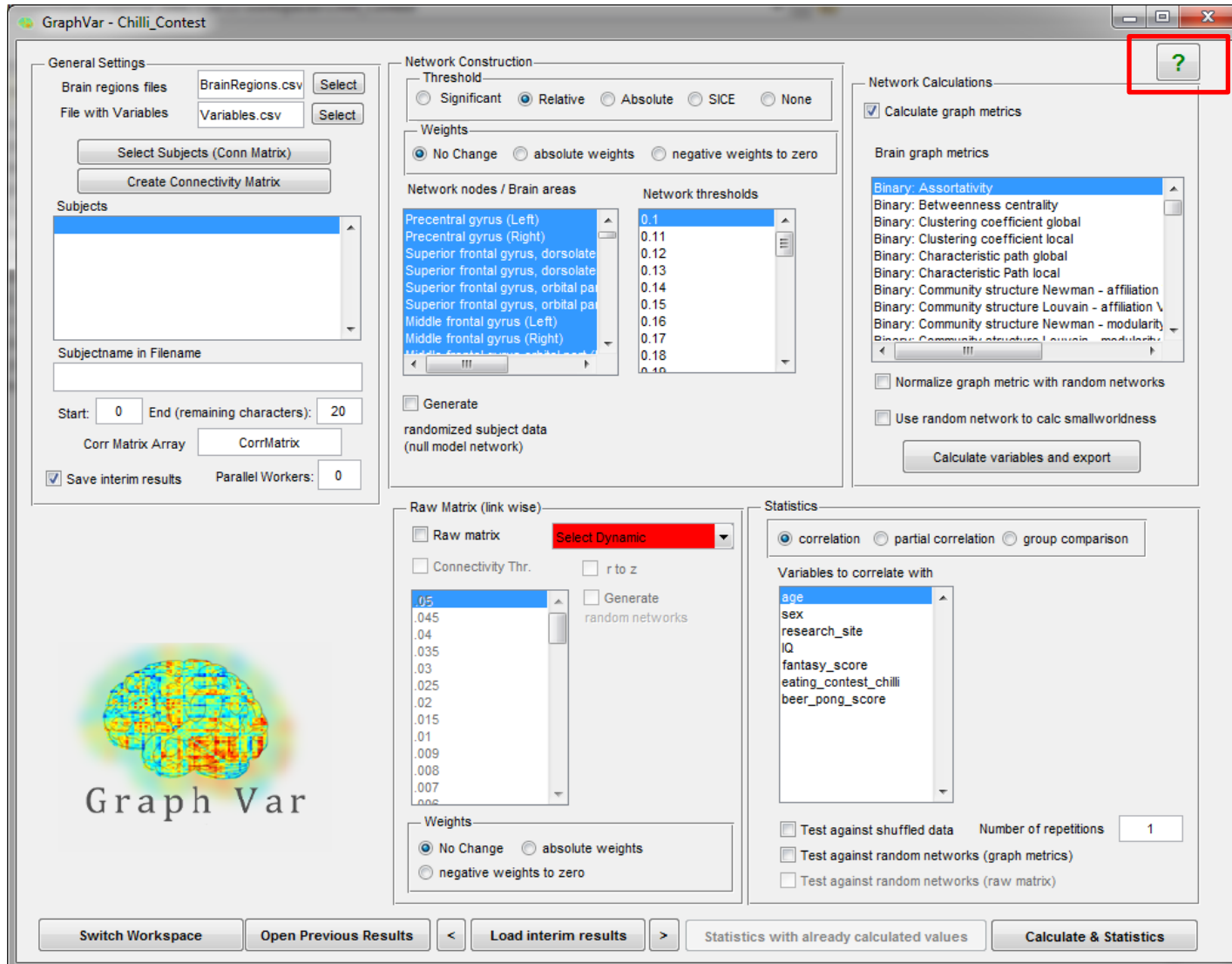
- Selected variables will be loaded in the „statistics window“

The screenshot displays the GraphVar software interface with the following components:

- General Settings:** Includes fields for 'Brain regions files' (BrainRegions.csv) and 'File with Variables' (Variables.csv), along with buttons for 'Select Subjects (Conn Matrix)' and 'Create Connectivity Matrix'.
- Subjects:** A list of subjects with a text field for 'Subjectname in Filename' and input fields for 'Start' (0) and 'End (remaining characters):' (20).
- Network Construction:** Features a 'Threshold' section with radio buttons for 'Significant', 'Relative' (selected), 'Absolute', 'SICE', and 'None'. It also has a 'Weights' section with 'No Change' (selected), 'absolute weights', and 'negative weights to zero'. A table lists 'Network nodes / Brain areas' and their corresponding 'Network thresholds'.
- Network Calculations:** Includes a checked 'Calculate graph metrics' option and a list of 'Brain graph metrics' such as 'Binary: Assortativity', 'Binary: Betweenness centrality', etc.
- Raw Matrix (link wise):** Contains a 'Raw matrix' section with a 'Select Dynamic' dropdown, a list of values, and checkboxes for 'Connectivity Thr.', 'r to z', and 'Generate random networks'. It also has a 'Weights' section.
- Statistics:** A red box highlights this section, which includes radio buttons for 'correlation' (selected), 'partial correlation', and 'group comparison'. It features a list of 'Variables to correlate with' (age, sex, research\_site, IQ, fantasy\_score, eating\_contest\_chilli, beer\_pong\_score) and checkboxes for testing against shuffled data, random networks (graph metrics), and random networks (raw matrix).
- Bottom Panel:** Contains navigation buttons like 'Switch Workspace', 'Open Previous Results', 'Load interim results', and 'Calculate & Statistics'.



- FYI: there is also a help button in the top right!
- When help is enabled, you will have a mouse over info for each function of the GUI



- Now, select the subjects (in general settings)
- Navigate to the „Sample Workspace“ and select subject 20-30
- Path: ...GraphVar/workspaces/SampleWorkspace/data/CorrMatrix

The screenshot displays the GraphVar software interface. The 'General Settings' panel on the left includes a 'Select Subjects (Conn Matrix)' button highlighted with a red box. Below it, a list of subjects is visible, and a 'Subjectname in Filename' field is present. The 'Network Construction' panel shows 'Threshold' set to 'Relative' and 'Weights' set to 'No Change'. The 'Network Calculations' panel has 'Calculate graph metrics' checked. The 'Select file(s)' dialog box is open, showing a list of files in the 'CorrMatrix' folder. The files are listed in a table with columns for Name, Änderungsdatum, Typ, and Größe. The files 'CorrMatrix\_sample\_20' through 'CorrMatrix\_sample\_30' are highlighted with a red box. The dialog box also shows the 'Dateiname' and 'Datentyp' fields.

**General Settings**

Brain regions files: BrainRegions.csv [Select]  
 File with Variables: Variables.csv [Select]  
 Select Subjects (Conn Matrix) [Red Box]  
 Create Connectivity Matrix

**Subjects**

Subjectname in Filename: \_\_\_\_\_  
 Start: 0 End (remaining characters): 20  
 Corr Matrix Array: CorrMatrix  
 Save interim results Parallel Workers: 0

**Network Construction**

Threshold:  Significant  Relative  Absolute  SICE  None  
 Weights:  No Change

**Network Calculations**

Calculate graph metrics

**Select file(s)**

Suchen in: CorrMatrix

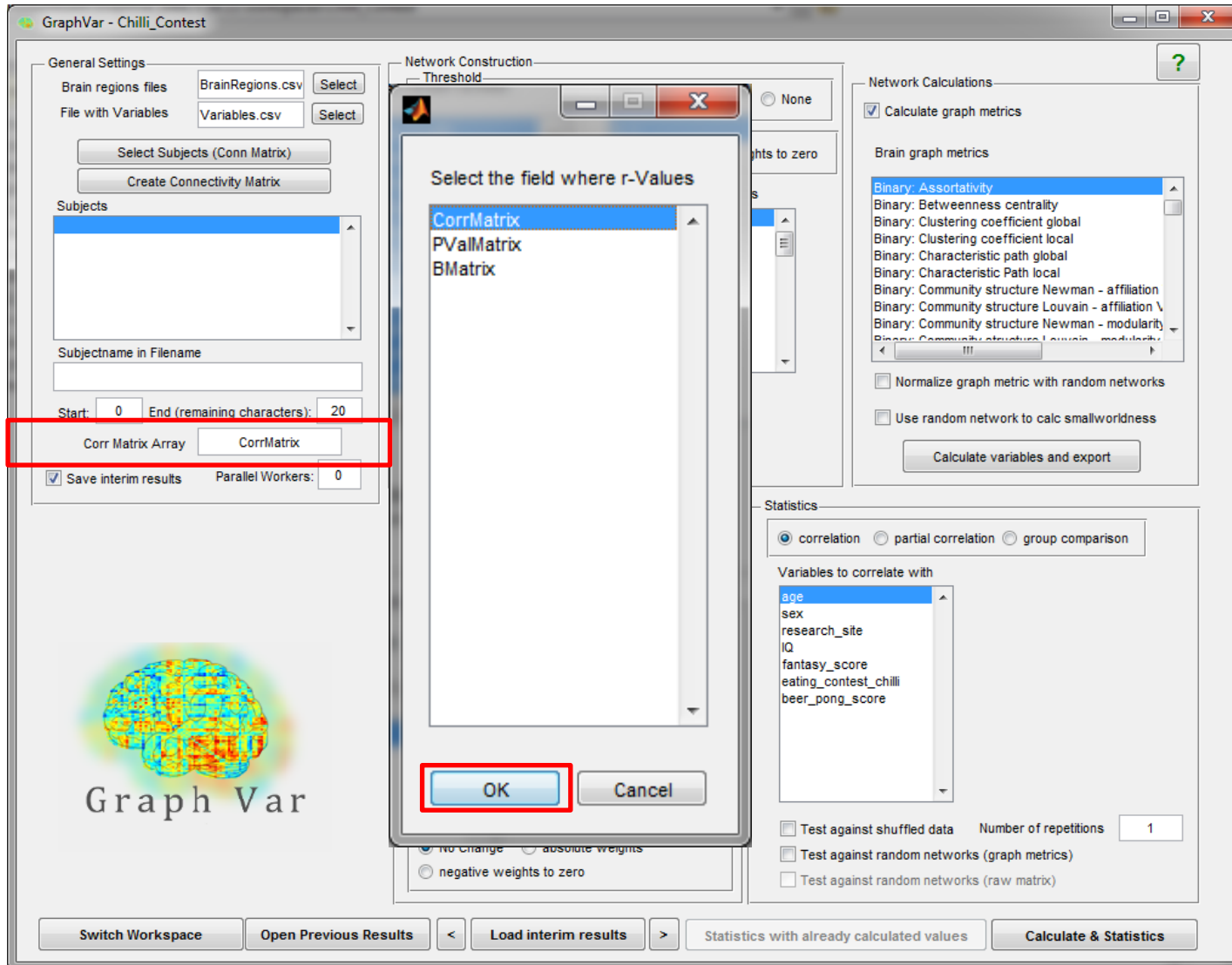
Name	Änderungsdatum	Typ	Größe
CorrMatrix_sample_08	17.06.2014 17:27	Microsoft Access ...	199 KB
CorrMatrix_sample_09	17.06.2014 17:27	Microsoft Access ...	200 KB
CorrMatrix_sample_10	17.06.2014 17:27	Microsoft Access ...	200 KB
CorrMatrix_sample_11	17.06.2014 17:27	Microsoft Access ...	200 KB
CorrMatrix_sample_12	17.06.2014 17:27	Microsoft Access ...	199 KB
CorrMatrix_sample_13	17.06.2014 17:27	Microsoft Access ...	200 KB
CorrMatrix_sample_14	17.06.2014 17:27	Microsoft Access ...	200 KB
CorrMatrix_sample_15	17.06.2014 17:27	Microsoft Access ...	200 KB
CorrMatrix_sample_16	17.06.2014 17:27	Microsoft Access ...	199 KB
CorrMatrix_sample_17	17.06.2014 17:27	Microsoft Access ...	199 KB
CorrMatrix_sample_18	17.06.2014 17:27	Microsoft Access ...	200 KB
CorrMatrix_sample_19	17.06.2014 17:27	Microsoft Access ...	200 KB
CorrMatrix_sample_20	17.06.2014 17:27	Microsoft Access ...	199 KB
CorrMatrix_sample_21	17.06.2014 17:27	Microsoft Access ...	199 KB
CorrMatrix_sample_22	17.06.2014 17:27	Microsoft Access ...	199 KB
CorrMatrix_sample_23	17.06.2014 17:27	Microsoft Access ...	200 KB
CorrMatrix_sample_24	17.06.2014 17:27	Microsoft Access ...	199 KB
CorrMatrix_sample_25	17.06.2014 17:27	Microsoft Access ...	200 KB
CorrMatrix_sample_26	17.06.2014 17:27	Microsoft Access ...	199 KB
CorrMatrix_sample_27	17.06.2014 17:27	Microsoft Access ...	199 KB
CorrMatrix_sample_28	17.06.2014 17:27	Microsoft Access ...	200 KB
CorrMatrix_sample_29	17.06.2014 17:27	Microsoft Access ...	199 KB
CorrMatrix_sample_30	17.06.2014 17:27	Microsoft Access ...	200 KB

Dateiname: "CorrMatrix\_sample\_30.mat" "CorrMatrix\_sample\_20.mat" "CorrMatrix\_sample\_21.mat" [Offnen]  
 Datentyp: MAT-files (\*.mat) [Abbrechen]

**Graph Var**

Switch Workspace Open Previous Results Load interim results Statistics with already calculated values Calculate & Statistics

- A selection windows appears asking for the array in the CorrMatrix .mat file in which the correlations are saved (here this is CorrMatrix)
- The name will subsequently appear in the Corr Matrix Array box





- Highlight the subject ID with the mouse to provide the reference between the CorrMatrices and the subject data in the variable spreadsheet (these should be identical)
- If you don't want to do statistics (only calculation of graph metrics and export) no spreadsheet is required

General Settings

Brain regions files (xls)

File with Variables (xls)

Subjects

C:\GraphVar\_beta\_v\_02\workspaces\SampleWc  
C:\GraphVar\_beta\_v\_02\workspaces\SampleWc  
C:\GraphVar\_beta\_v\_02\workspaces\SampleWc  
C:\GraphVar\_beta\_v\_02\workspaces\SampleWc  
C:\GraphVar\_beta\_v\_02\workspaces\SampleWc  
C:\GraphVar\_beta\_v\_02\workspaces\SampleWc

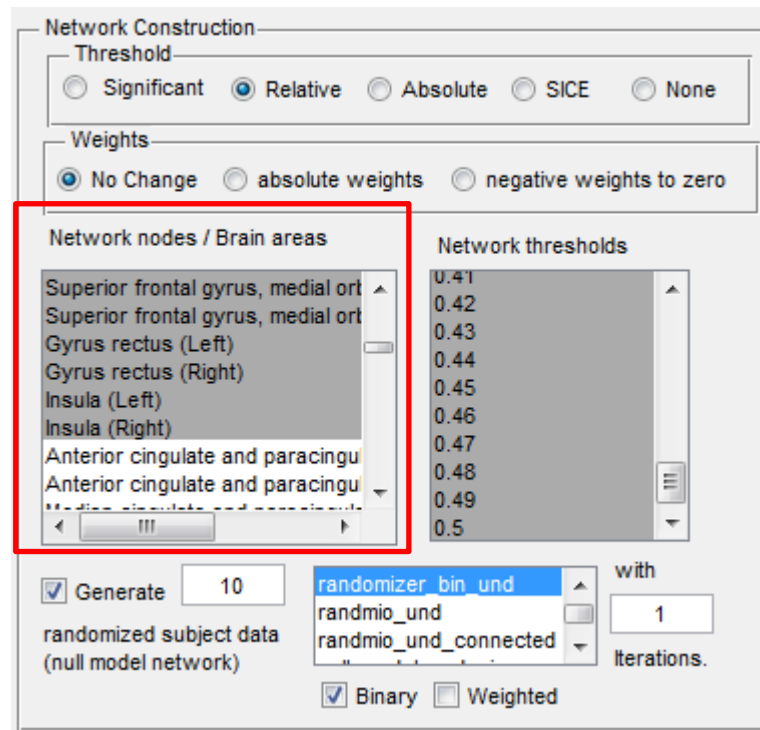
Subjectname in Filename

Start:  End (remaining characters):

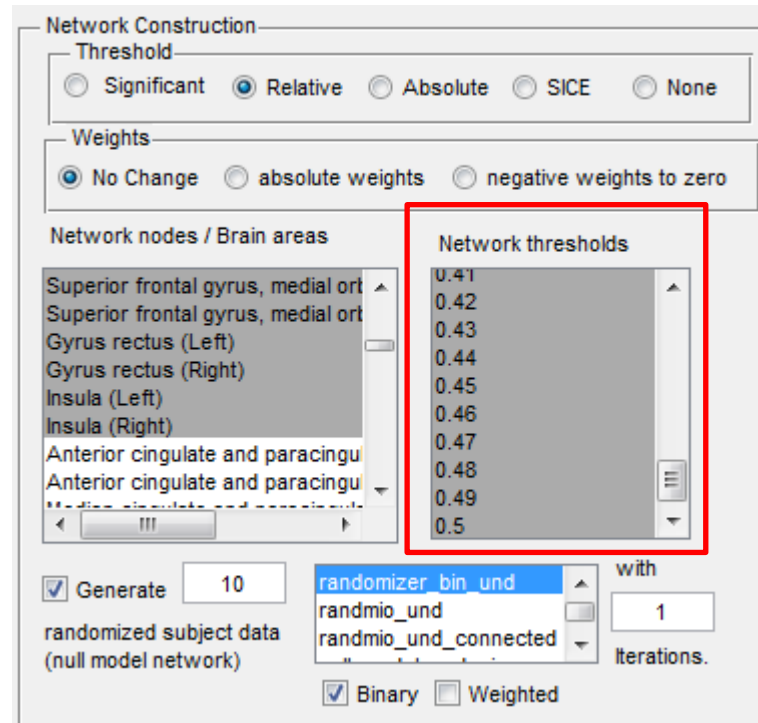
Corr Matrix Array

Save interim results

- Now, you'll have to specify a network in the network construction panel (by default AAL labels are loaded)  
-> the network nodes/brain areas refer to the „brain regions file“ (see manual)
  - For this tutorial we specify the „chilly-responsive-network“:  
starting from **Precentral gyrus (left)** until **Insula (right)**
- > select the 30 consecutive nodes with your mouse or keyboard

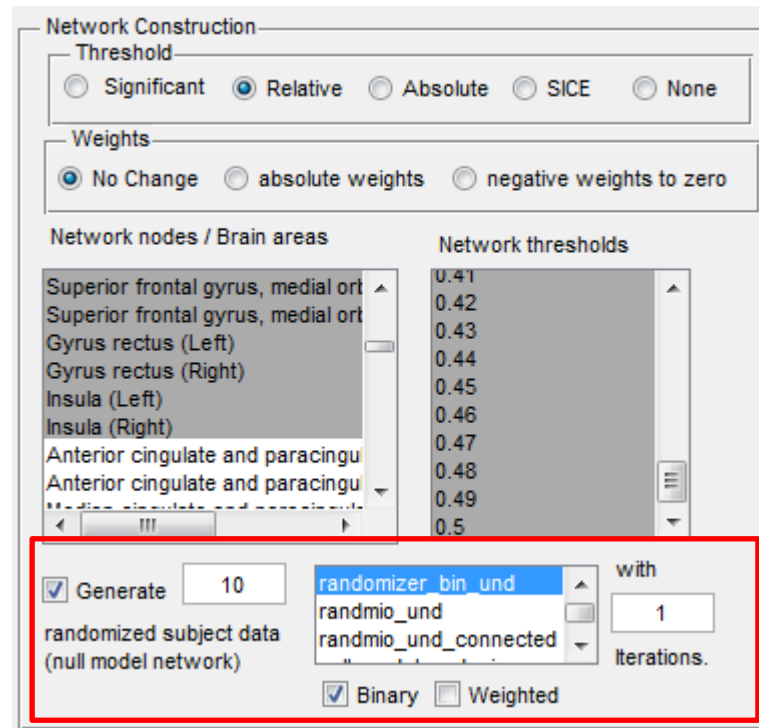


- Here, we want to construct different networks using relative thresholding (i.e., densities)
- Simply select all the thresholds in the box with „ctrl+A“ (see manual for how to add more thresholds)



- It is always a good idea to do statistics by also using subject specific null-model networks (i.e., non-parametric testing)
- For this example we ONLY generate **10 binary random networks** per subject per threshold using the „randomizer\_bin\_und“ BCT function

(normally you would use 100-1000 or even more ... but this will take a lot of time)

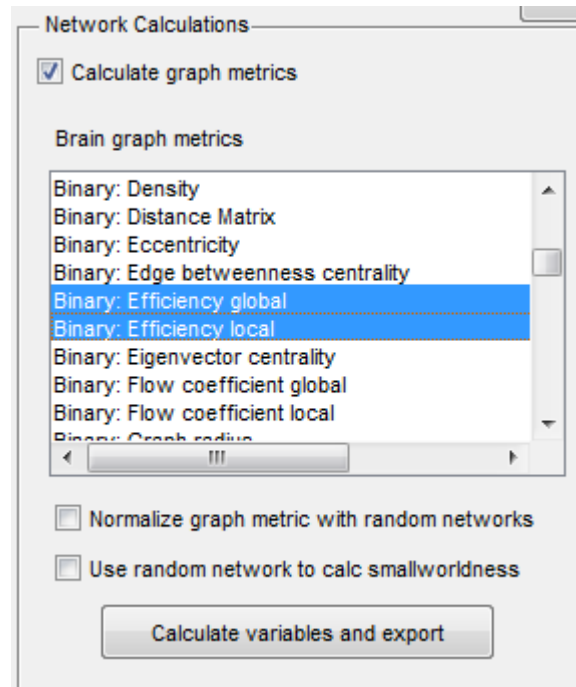


- As we have the hypothesis, that chilli eating champs probably have more efficient brains and that probably insula and orbito frontal cortex may contribute here, we select:

Binary: Efficiency global

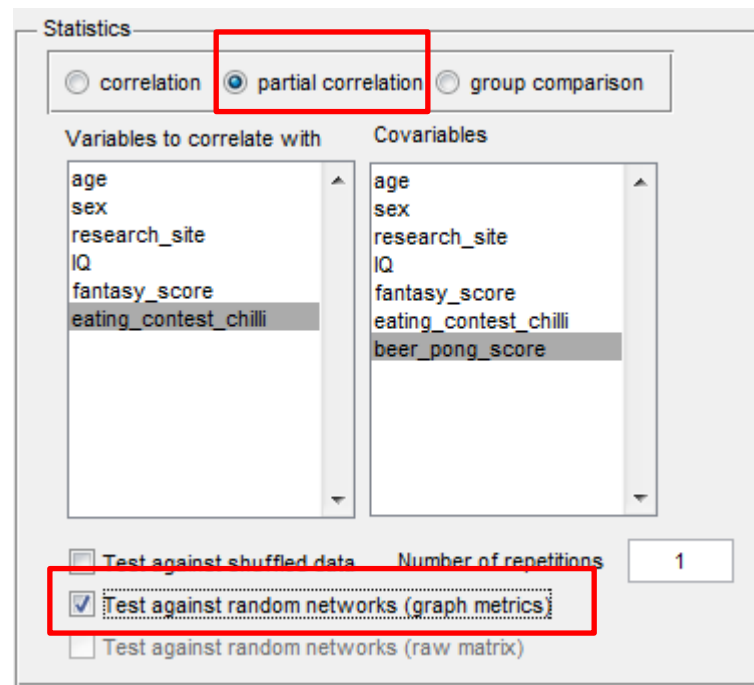
Binary: Efficiency local

- FYI: you can also add custom functions (see appendix in the manual); also note that for some of the functions it would not make sense to do statistics on (e.g., modularity affiliation vector; get components)

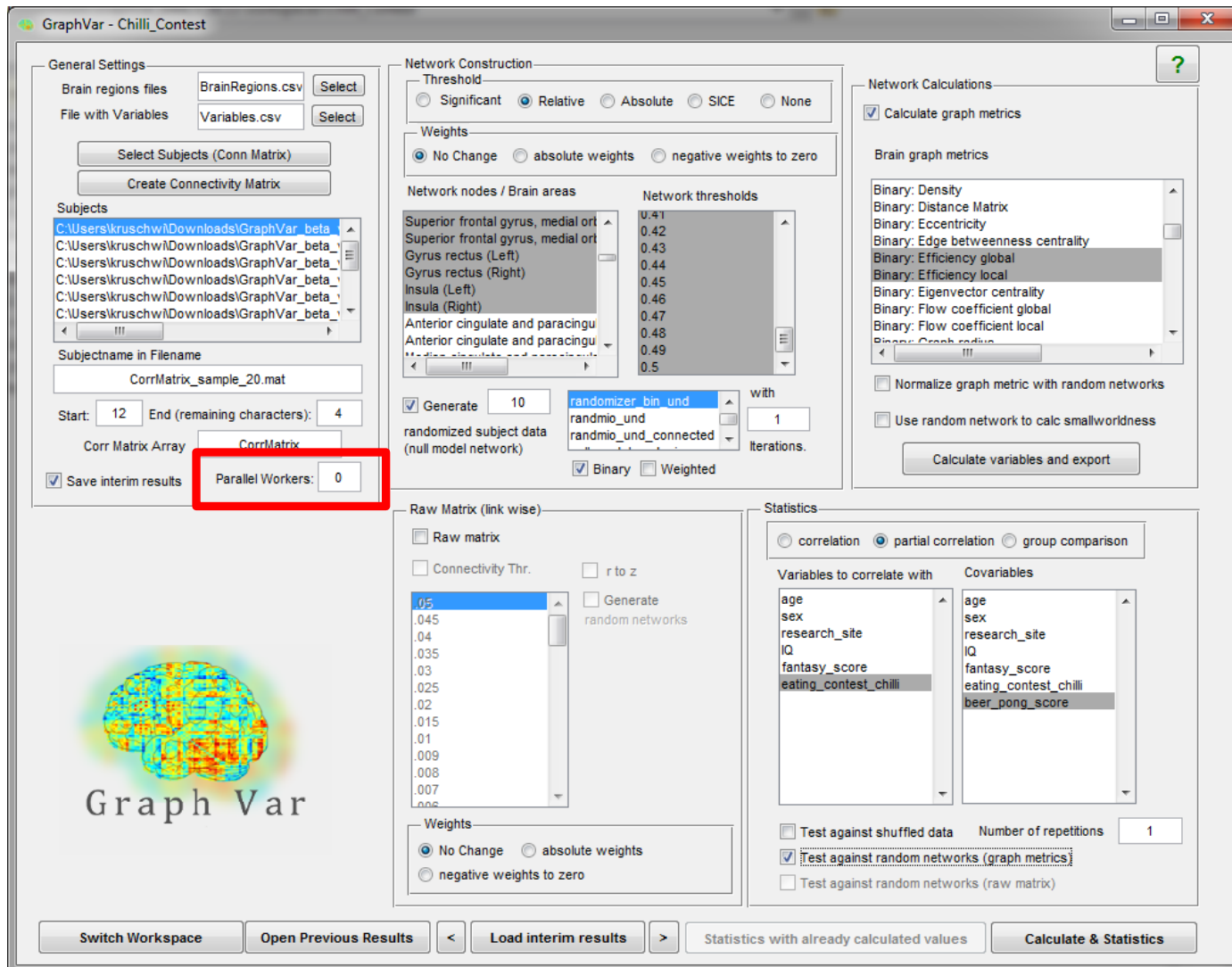




- In the statistics panel select „partial correlation“ and respectively „eating\_contest\_chilli“ and „beer\_pong\_score“
- Also select to test against the random networks (graph metrics)
- Note: if you have specified a variable as string in the spreadsheet (e.g., sex), it is not possible to use it as covariate (here you would have to specify as 0 and 1 respectively)



- If you have the parallel computing toolbox installed, you may want to use more workers (cores) to speed things up!



# Parallel Computing (with toolbox)

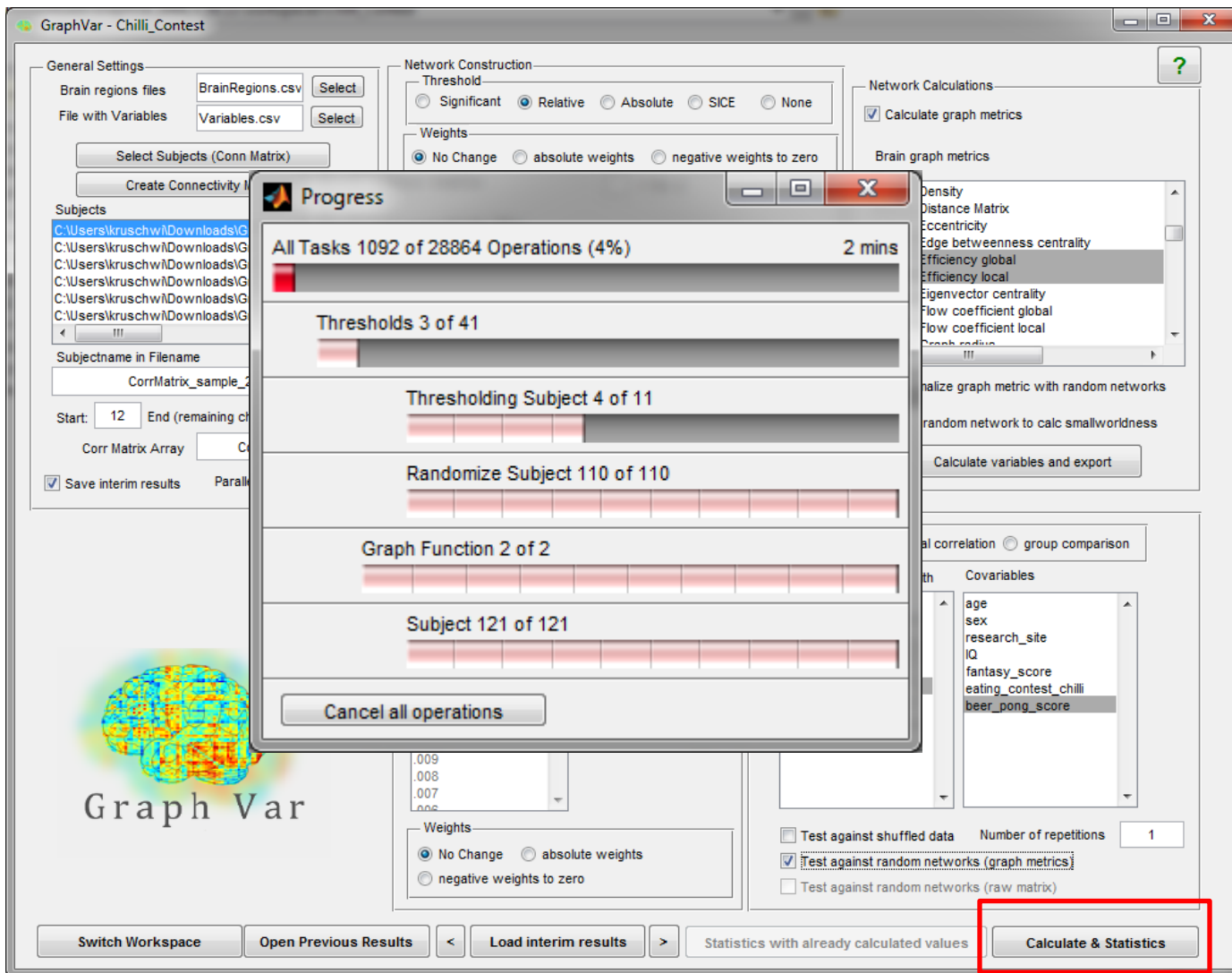
- You are ready to go and thus to test the hypothesis!
- Click on „Calculate & Statistics“

The screenshot shows the GraphVar software interface for the 'Chilli\_Contest' workspace. The interface is divided into several panels:

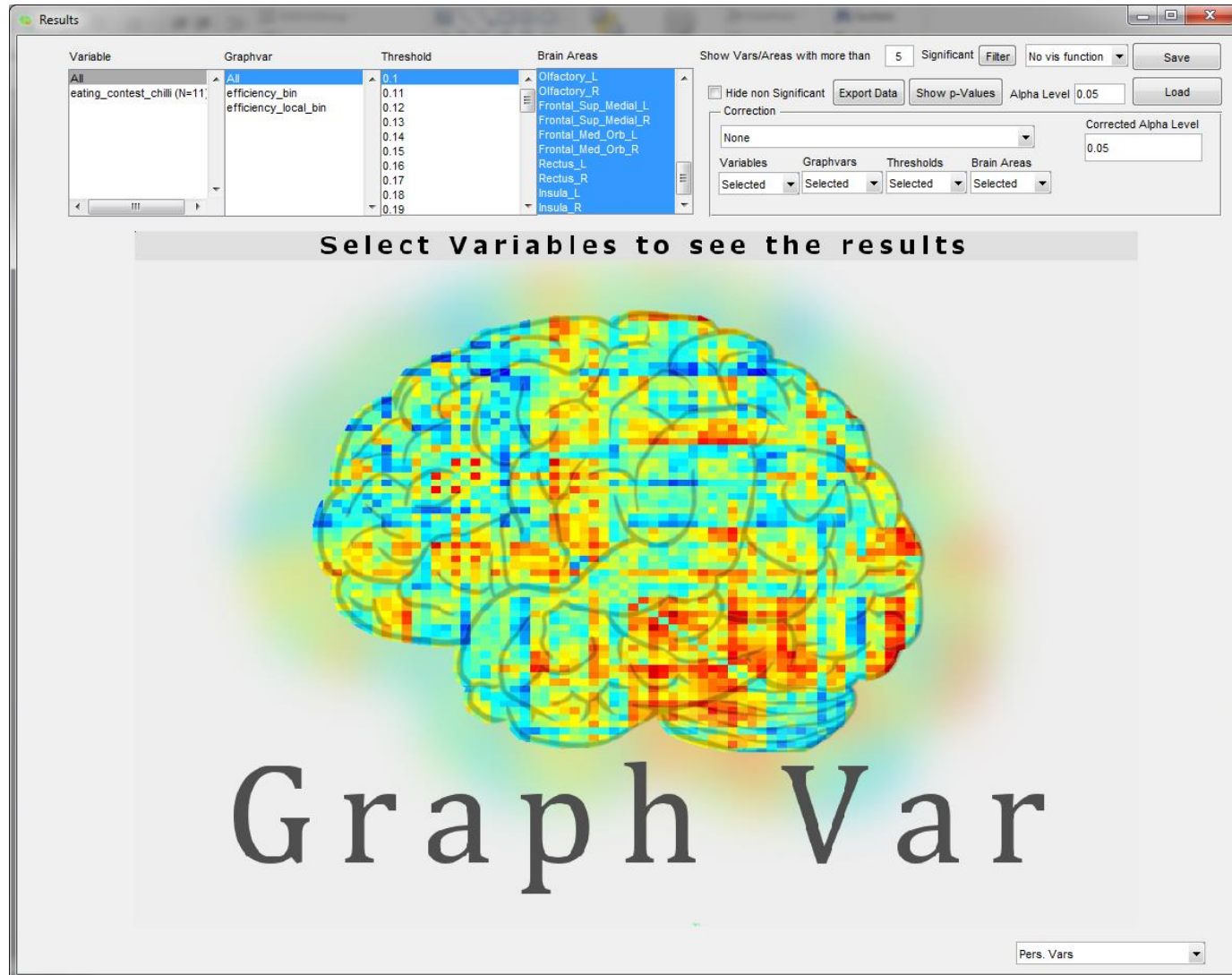
- General Settings:** Includes fields for 'Brain regions files' (BrainRegions.csv), 'File with Variables' (Variables.csv), and 'Subjectname in Filename' (CorrMatrix\_sample\_20.mat). It also has buttons for 'Select Subjects (Conn Matrix)' and 'Create Connectivity Matrix'.
- Subjects:** A list of subject files is shown, including 'C:\Users\kruschwi\Downloads\GraphVar\_beta\_...'.
- Network Construction:** Contains options for 'Threshold' (Significant, Relative, Absolute, SICE, None), 'Weights' (No Change, absolute weights, negative weights to zero), and 'Network nodes / Brain areas'. It also includes a 'Network thresholds' table and a 'Generate' button with a value of 10.
- Network Calculations:** Features a 'Calculate graph metrics' checkbox and a list of 'Brain graph metrics' such as 'Binary: Density', 'Binary: Distance Matrix', and 'Binary: Edge betweenness centrality'. There is a 'Calculate variables and export' button.
- Raw Matrix (link wise):** Includes a 'Raw matrix' checkbox, 'Connectivity Thr.' (0.05), and 'Weights' options (No Change, absolute weights, negative weights to zero).
- Statistics:** Contains options for 'correlation', 'partial correlation', and 'group comparison'. It has two lists: 'Variables to correlate with' (age, sex, research\_site, IQ, fantasy\_score, eating\_contest\_chilli) and 'Covariables' (age, sex, research\_site, IQ, fantasy\_score, eating\_contest\_chilli, beer\_pong\_score). It also includes a 'Test against random networks (graph metrics)' checkbox.

At the bottom of the interface, there are several buttons: 'Switch Workspace', 'Open Previous Results', 'Load interim results', and 'Calculate & Statistics'. The 'Calculate & Statistics' button is highlighted with a red box.

- This computation will take about 2-3 minutes ...



- This is the results viewer

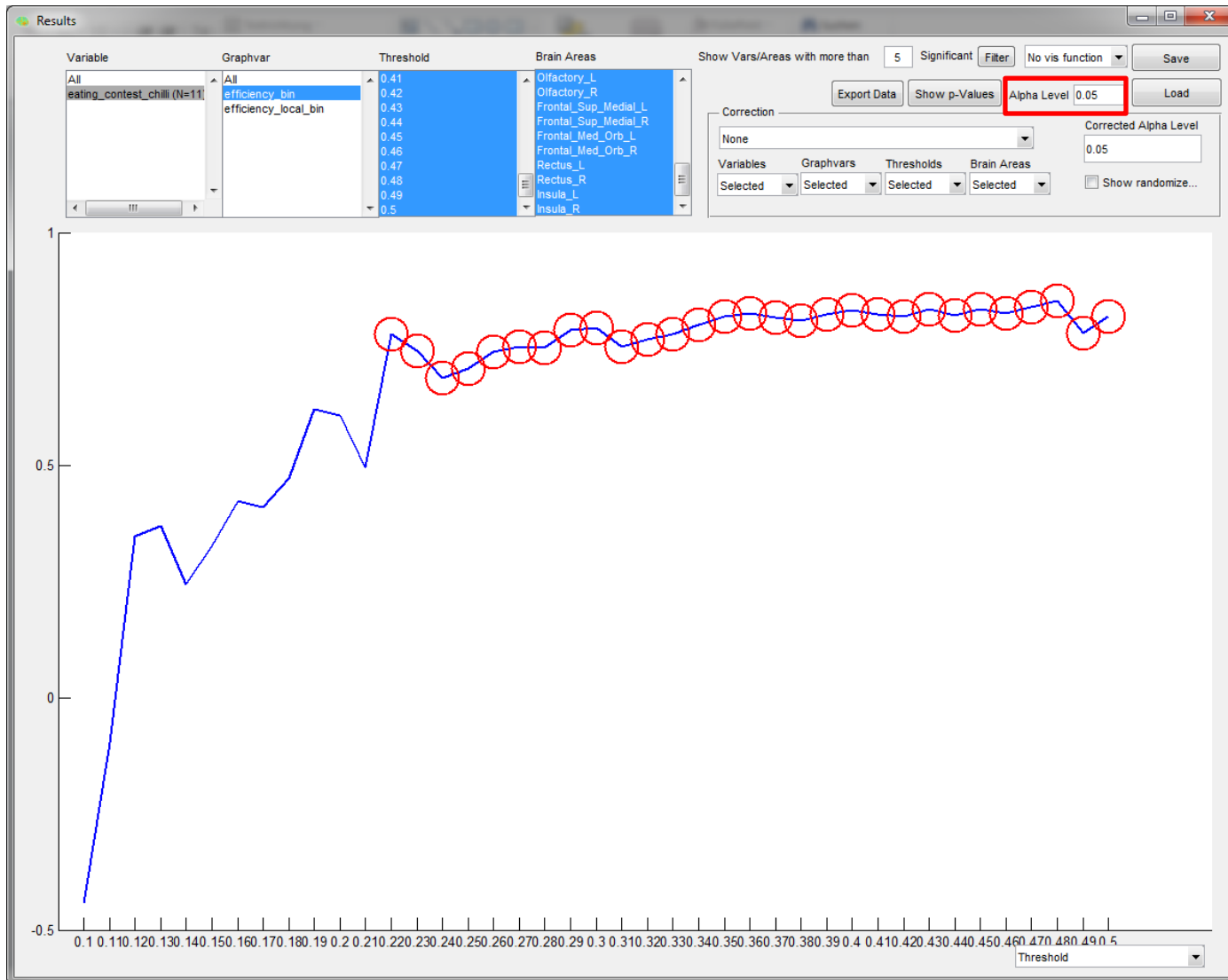




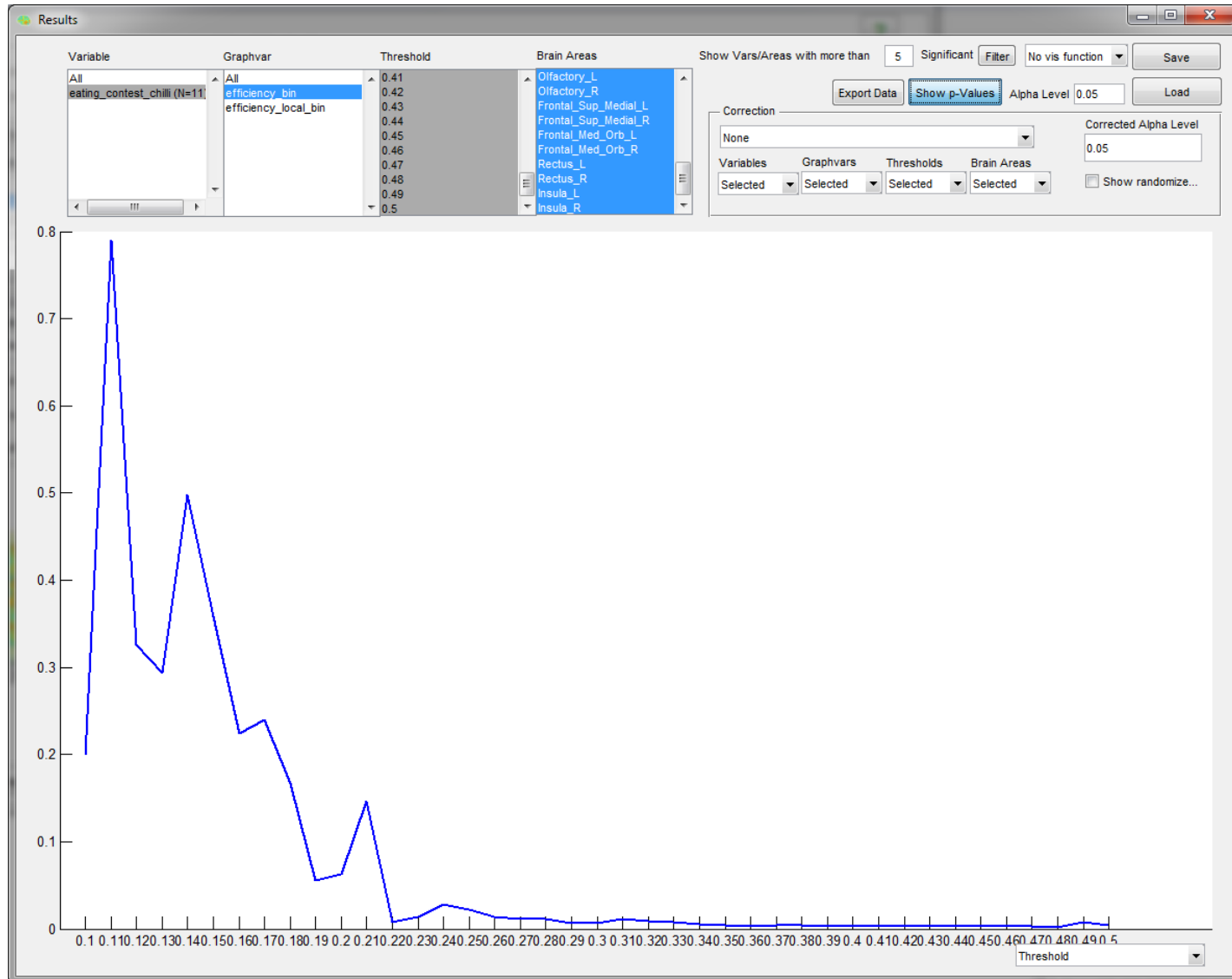
- To see the results for global efficiency across thresholds, select the chilli variable, „efficiency\_bin“, and all thresholds (ctrl+A)
- Selection of brain areas does not have an effect on global variables

Variable	Graphvar	Threshold	Brain Areas
All	All	0.41	Olfactory_L
eating_contest_chilli (N=11)	efficiency_bin	0.42	Olfactory_R
	efficiency_local_bin	0.43	Frontal_Sup_Medial_L
		0.44	Frontal_Sup_Medial_R
		0.45	Frontal_Med_Orb_L
		0.46	Frontal_Med_Orb_R
		0.47	Rectus_L
		0.48	Rectus_R
		0.49	Insula_L
		0.5	Insula_R

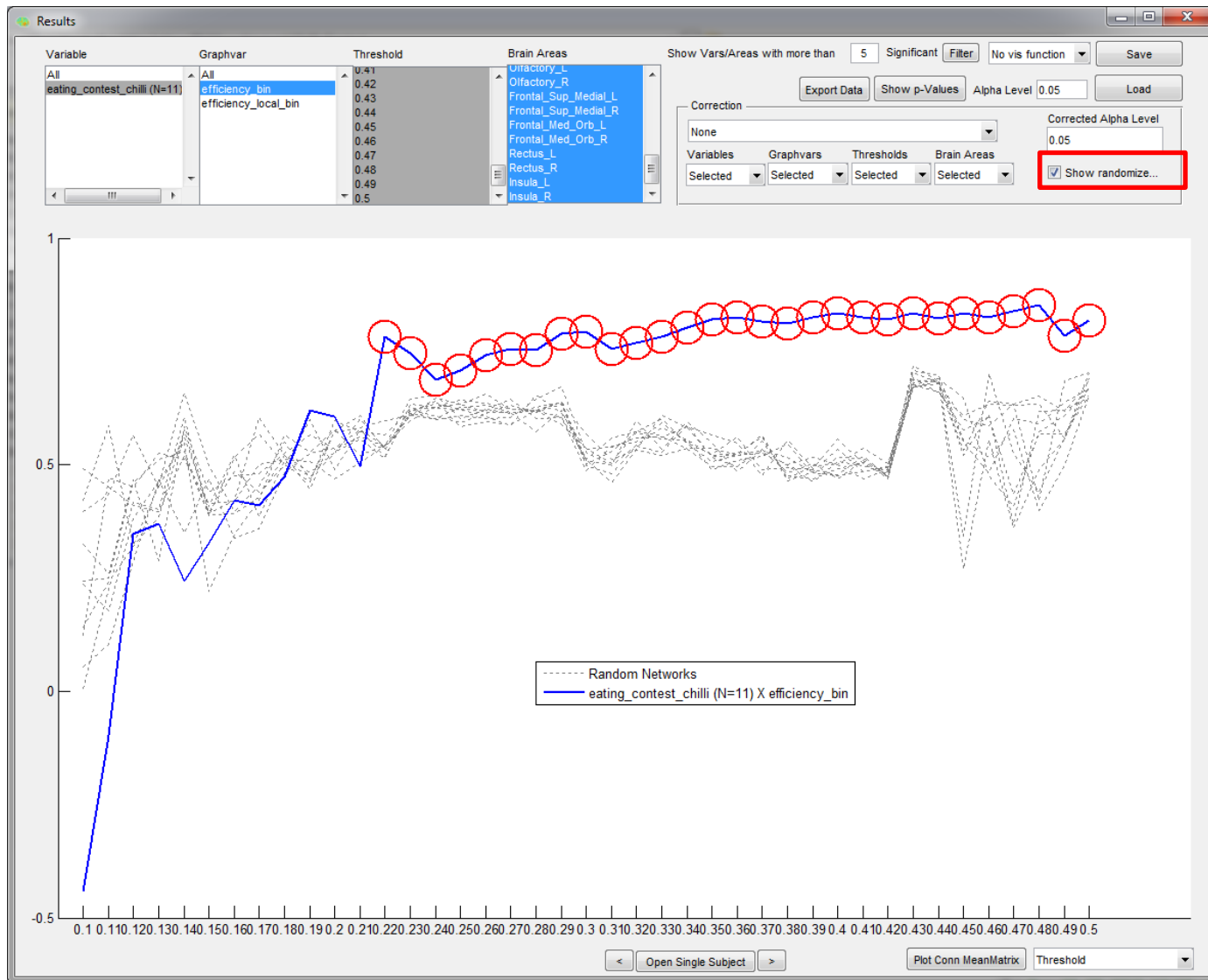
- Now, you should see the correlation of global efficiency and chilli eating contest scores
- The red dots indicate where the correlation is significant according to the desired alpha level (which you can change here)



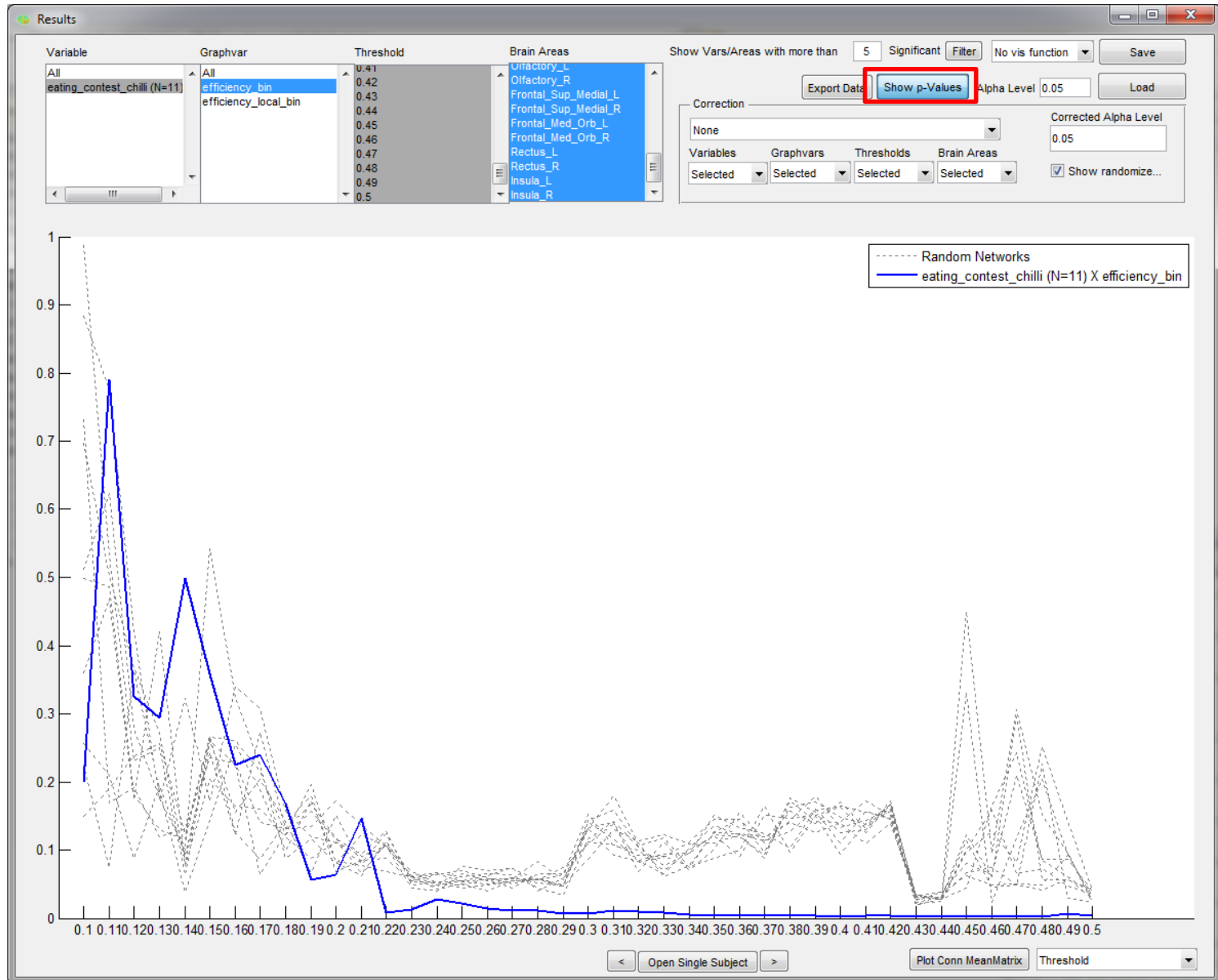
- To explore the p-values across thresholds select the „show p-Values“ button
- By hitting the button again the correlation appears again



- To plot the correlation of chilli scores and global efficiency derived from the random data (null-model distribution), click in „show randomize...“
- You can drag and drop the legend box

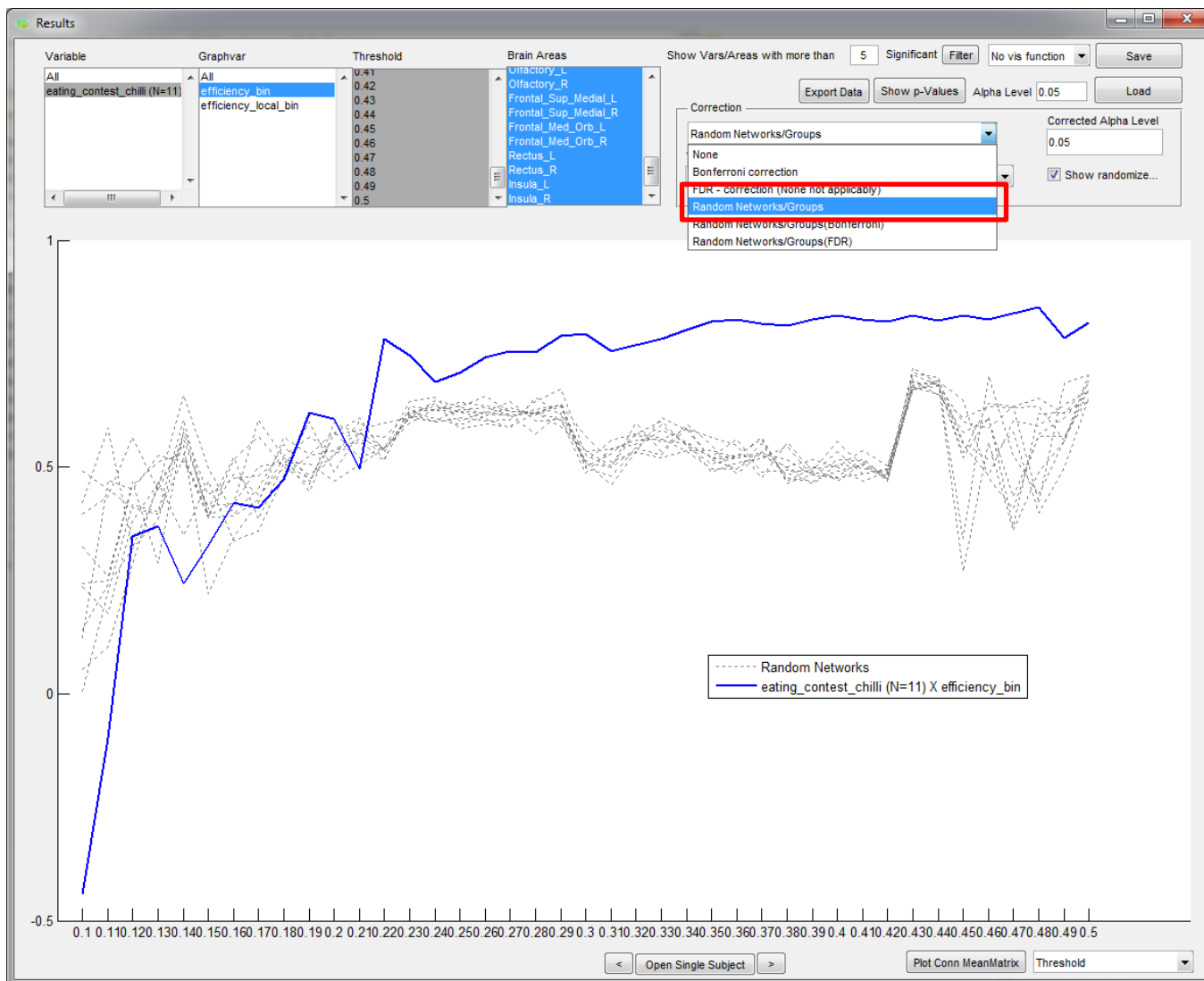


- You can also explore the p-value null-model distribution

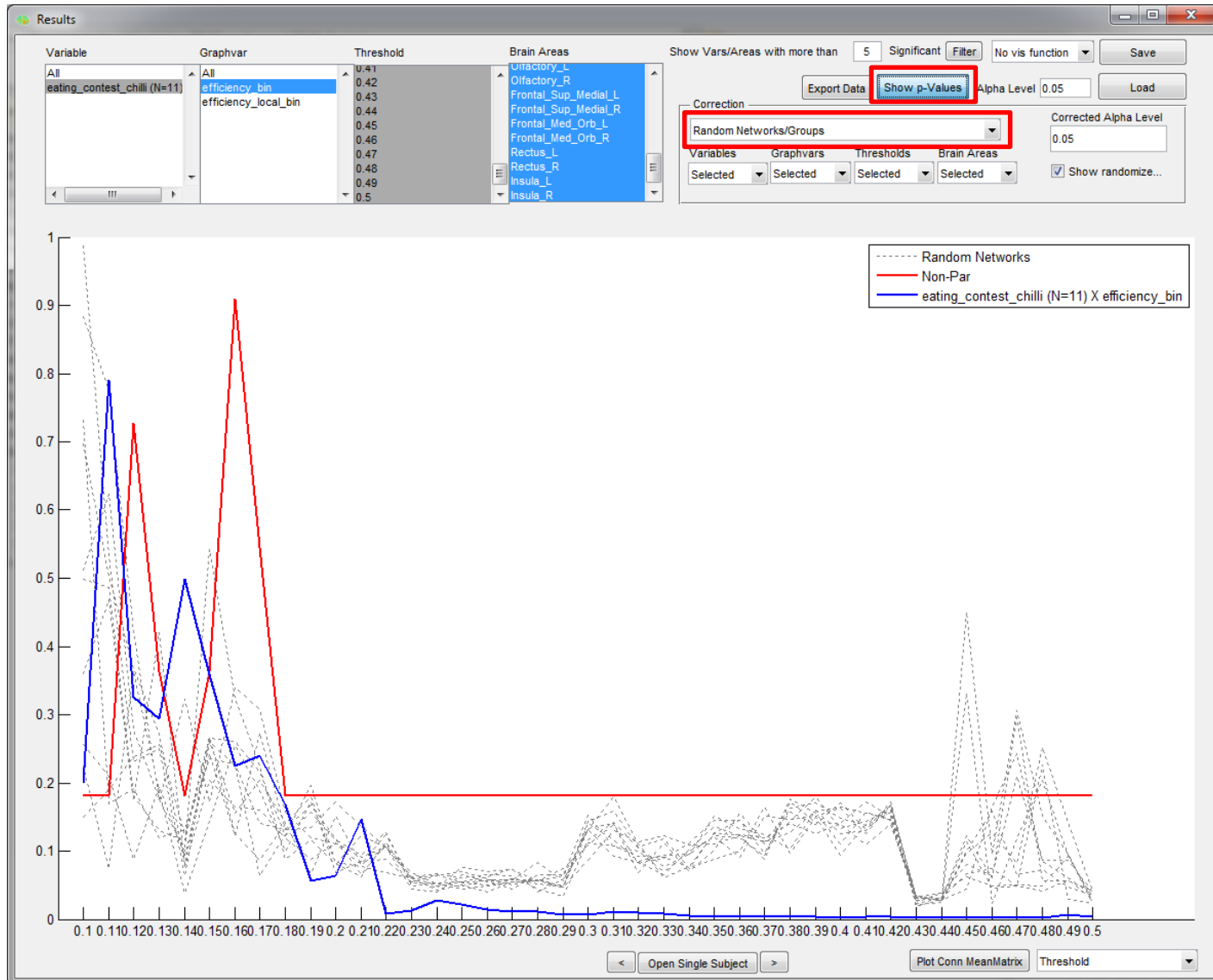




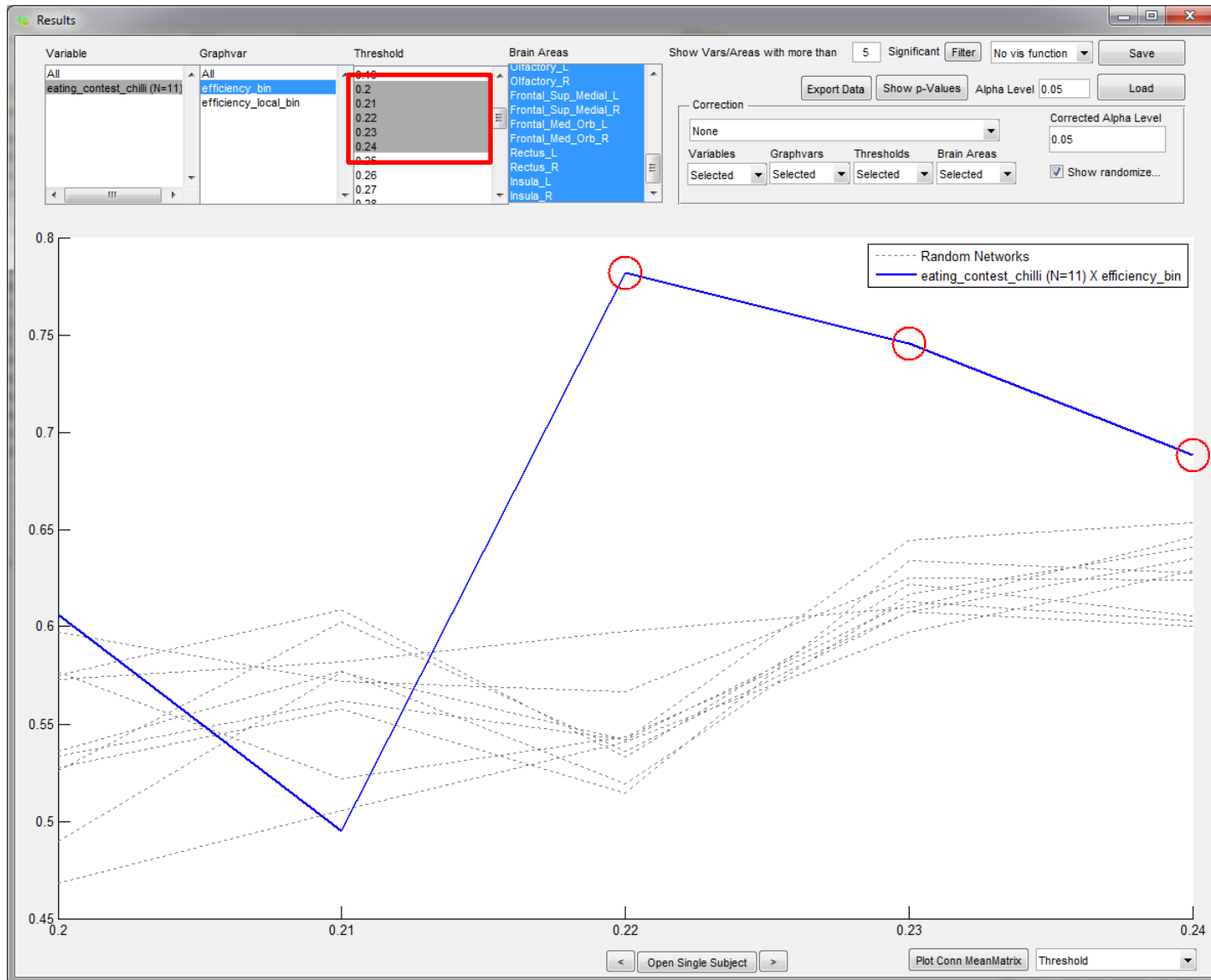
- Now, let's see if something is significant when using the non-parametric correlation testing (i.e., testing against null-models)
- NO .... Nothing is significant -> Why? Let's explore the non-parametric p-values!



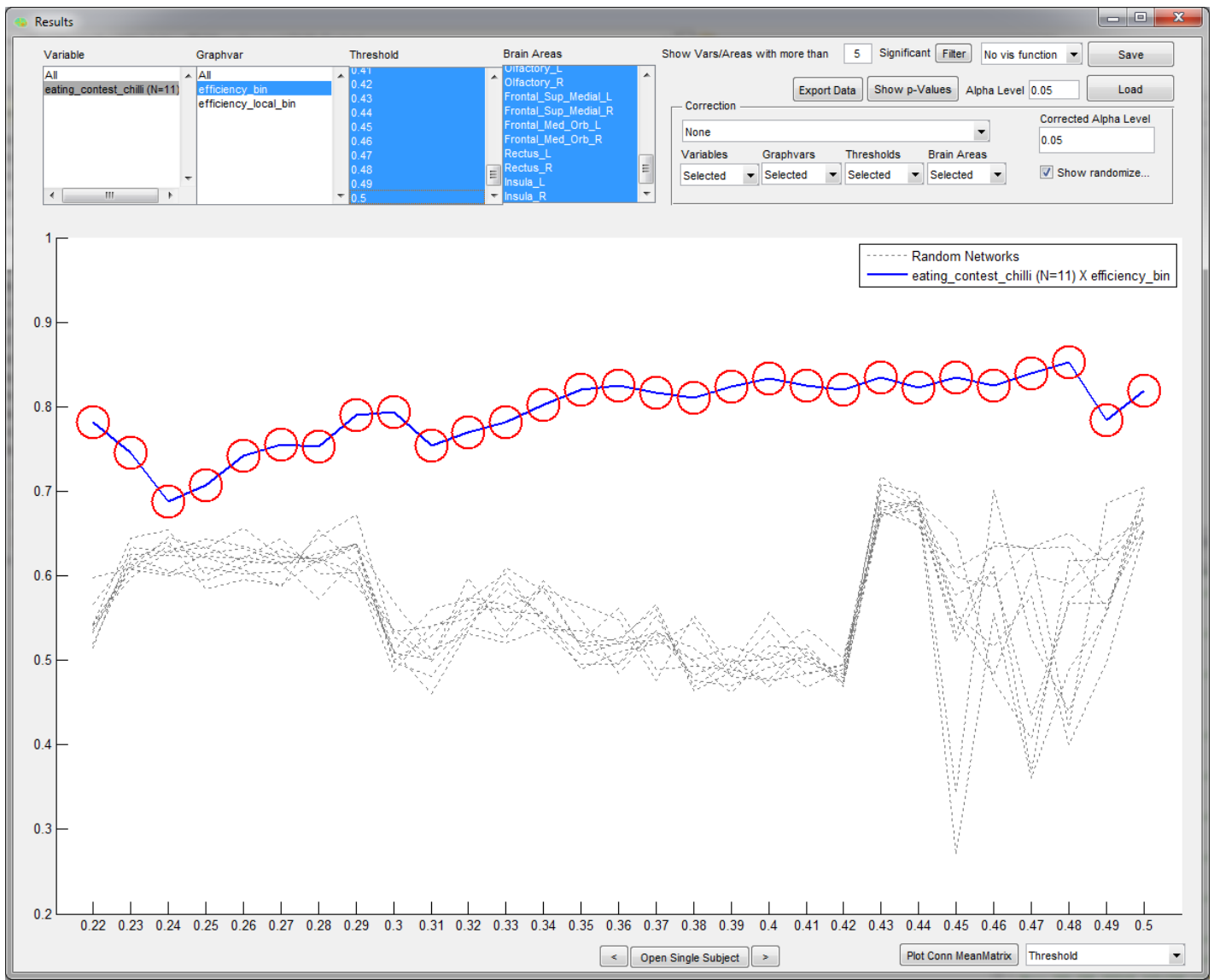
- Nothing is significant at  $p < 0.05$ , as we only generated 10 random networks per subject  
 -> thus, the non-parametric p-value can naturally never be 0.05
- Please refer to the manual for an explanation of all the correction methods (e.g., Bonferroni, FDR) and how to apply those!



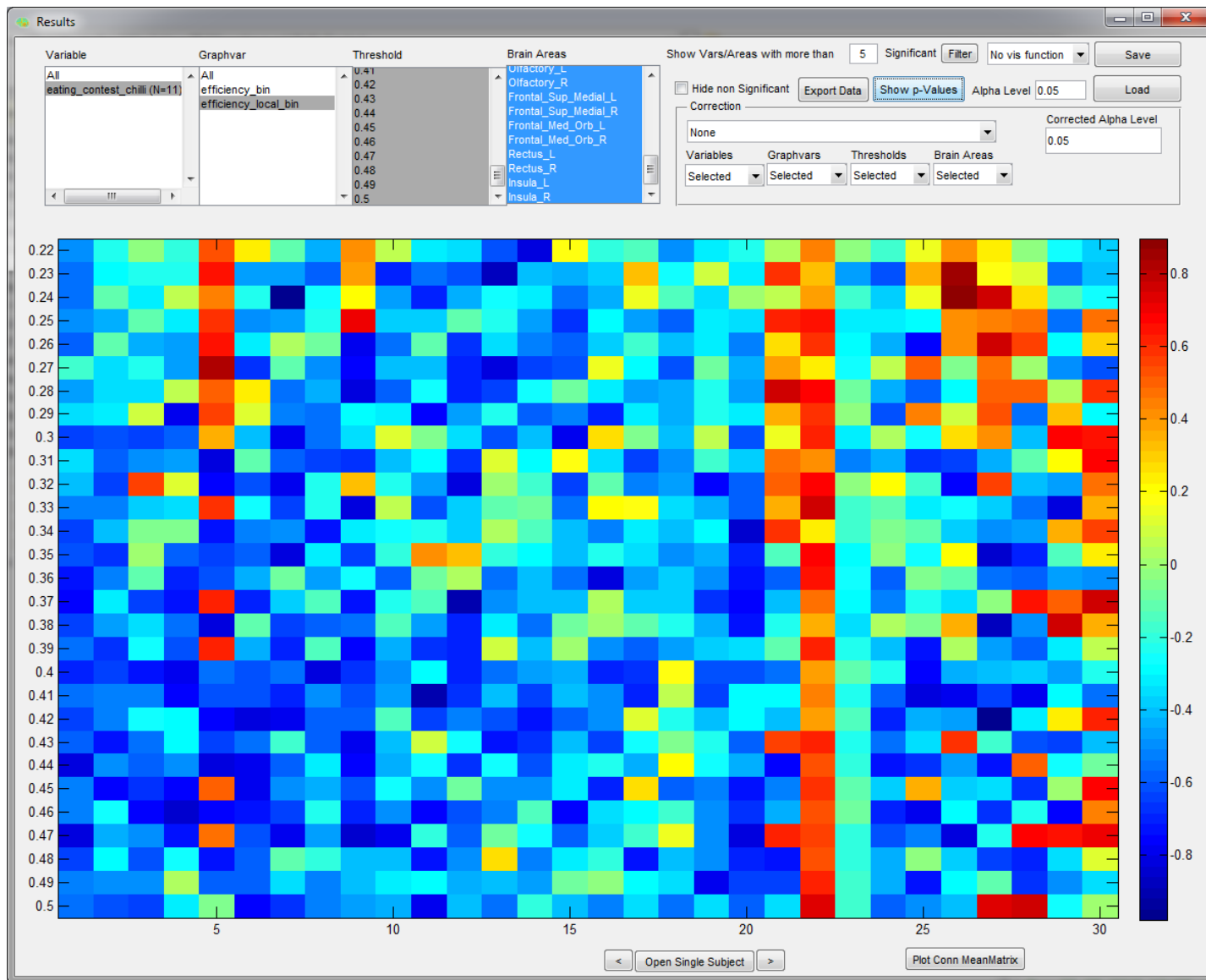
- By scaling down the thresholds, we notice that the association of global efficiency and chilli eating scores starts at a threshold of 0.22



- Driven by this beautiful association of global efficiency and chilli eating scores, we now decide to explore the local efficiencies of all the regions in our chilli-responsive-network across the threshold range 0.22-0.5
- Specify the threshold range and select the Graphvar „efficiency\_local\_bin“

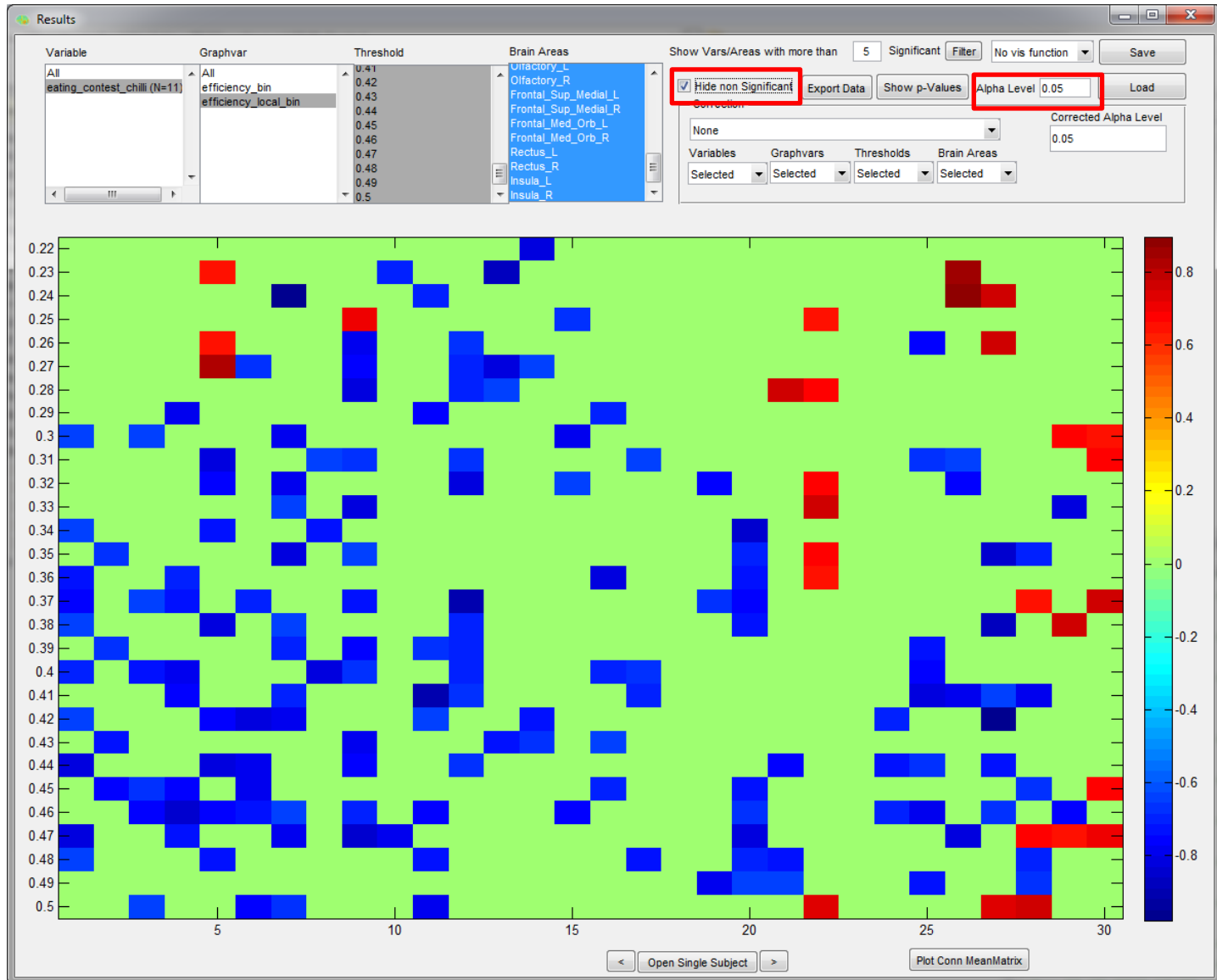


- Here you see the association of local efficiency of each of the 30 regions in the network to the chilli score
- Notice the mouse over box telling you the area, threshold, correlation, and p-value



The subsequent slides show some capabilities of the viewer... This is only for illustrational purposes!  
If your data looks like this please do not write a paper 😊

- FYI: it is possible to hide all non-significant associations
- In this example the associations DO NOT look meaningful (as associations on single thresholds should not be interpreted)
- For exemplary purposes let's put the alpha level to 0.1 (and let's pretend that it is 0.05)

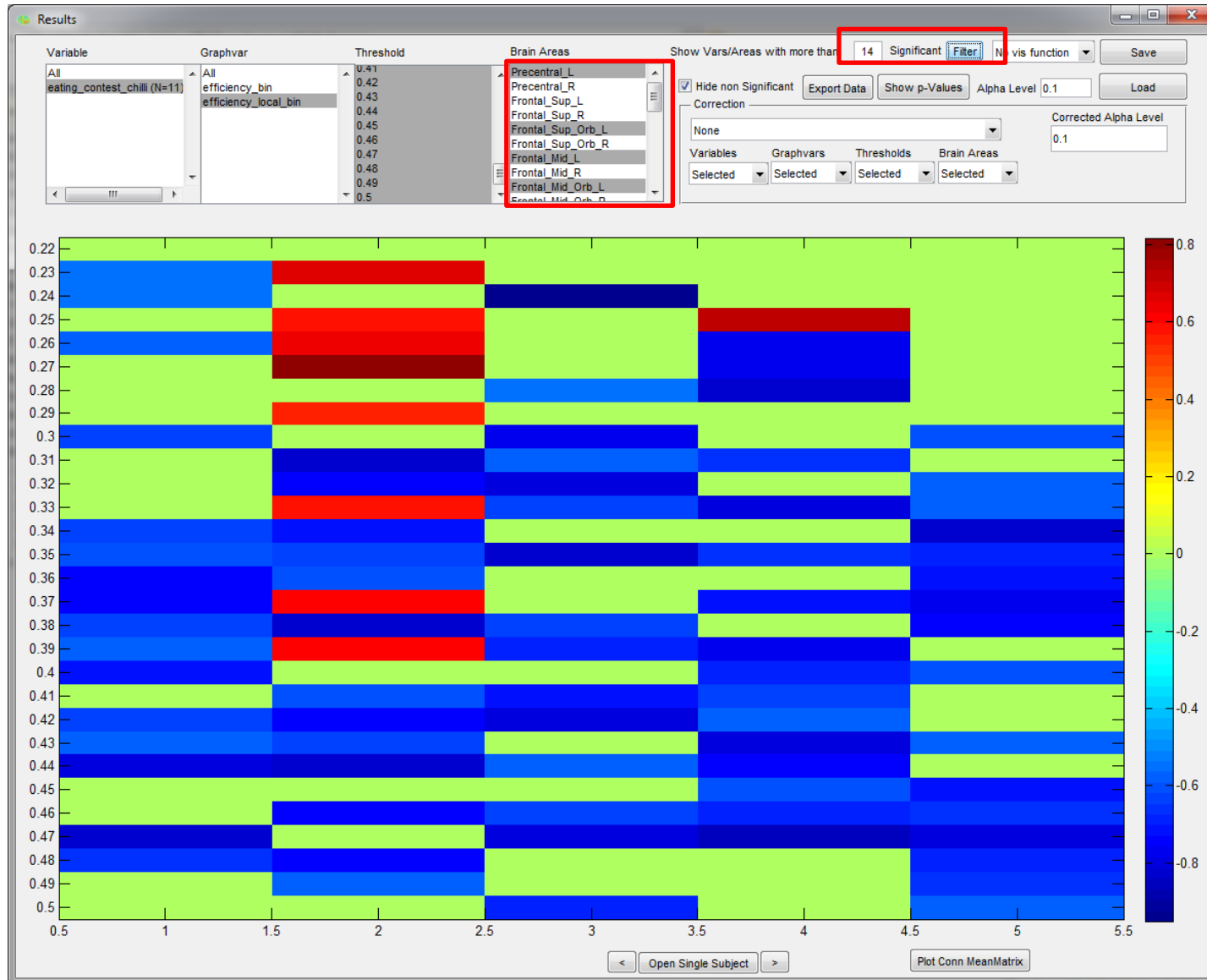


- This look a little bit better now 😊
- If we a-priori determined that only significant associations on minimally 15 thresholds would be meaningful, we can use the build in filter function and set the number on 14 (i.e.,  $\text{thr} > 14$ )

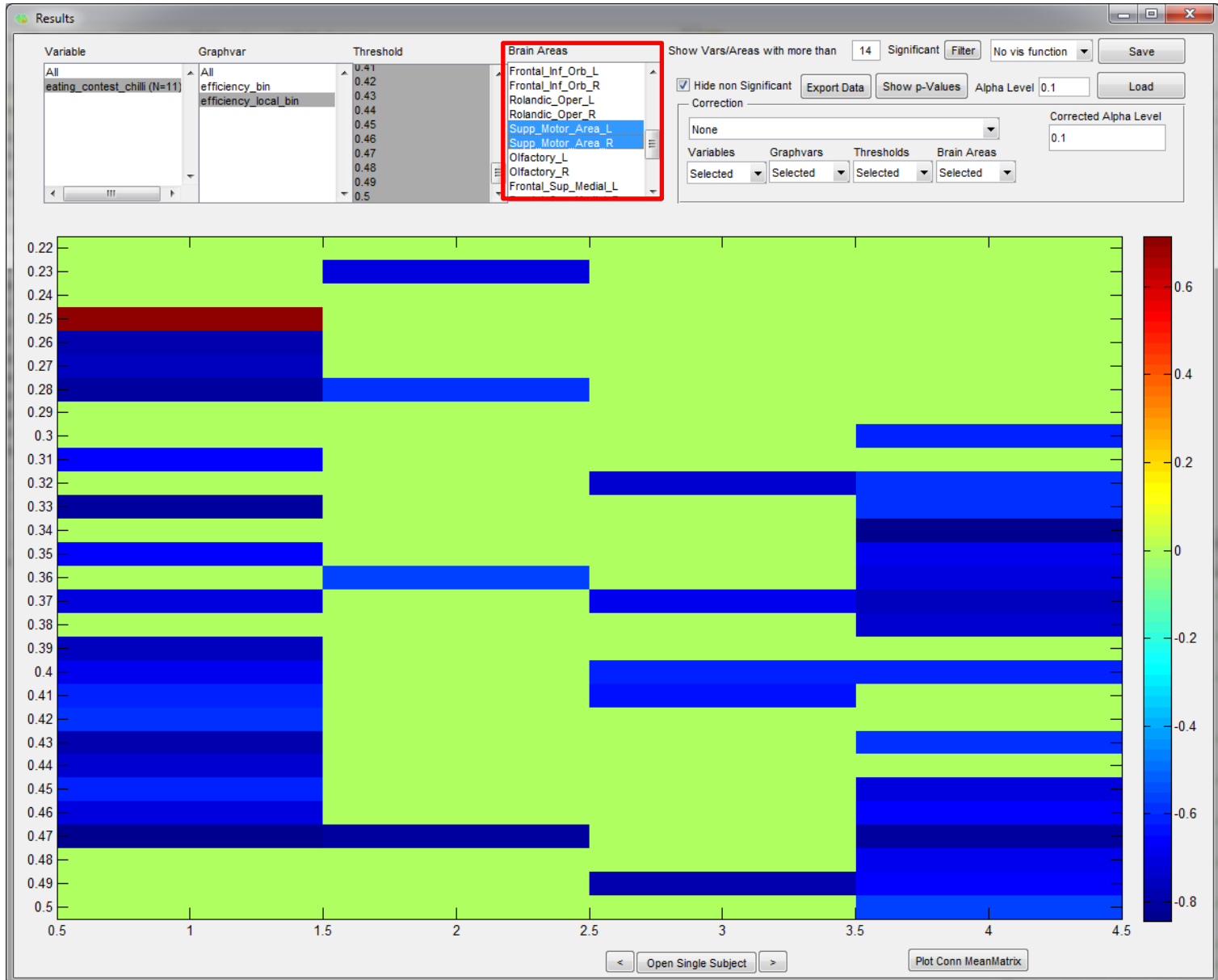




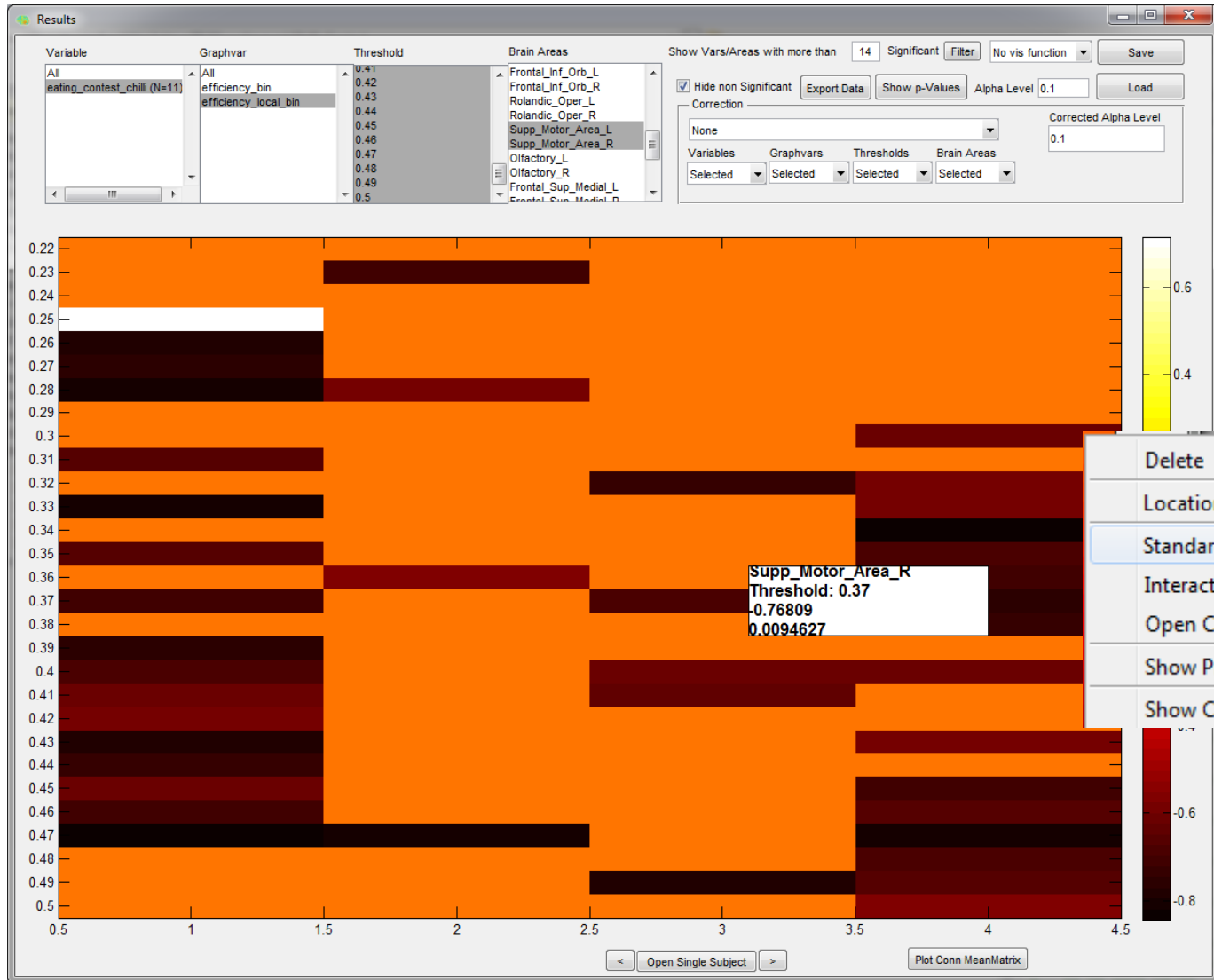
- Subsequently, the viewer will only show the areas with the specified criteria
- Note that these regions are highlighted in the „Brain Areas“ field.
- All subsequent actions will only apply to these regions (e.g. filtering)
- If you want the full network again you will have to select all nodes (ctrl+A)



- If you have an a-prior hypothesis on specific structures you can also simply select those in the „Brain Areas“ field
- We thought that orbito frontal gyrus and suppl motor area may play a role ...



- You can also change the properties of the colour map (right mouse click on the colour map)
- Also use the colour map editor to set the range of correlations in the colour bar (e.g., -1 to 1)



- We think that these results are meaningful (NOT) and decide to save and to export these to a csv file (which we open with excel later on)
- Only things that are visible in the results window will be exported (here Frontal\_Mid\_Orb L/R and Suppl\_Motor\_Area L/R across thresholds 0.22-0.5)
- Everything we have computed (global efficiency and local efficiency across thresholds) may be saved

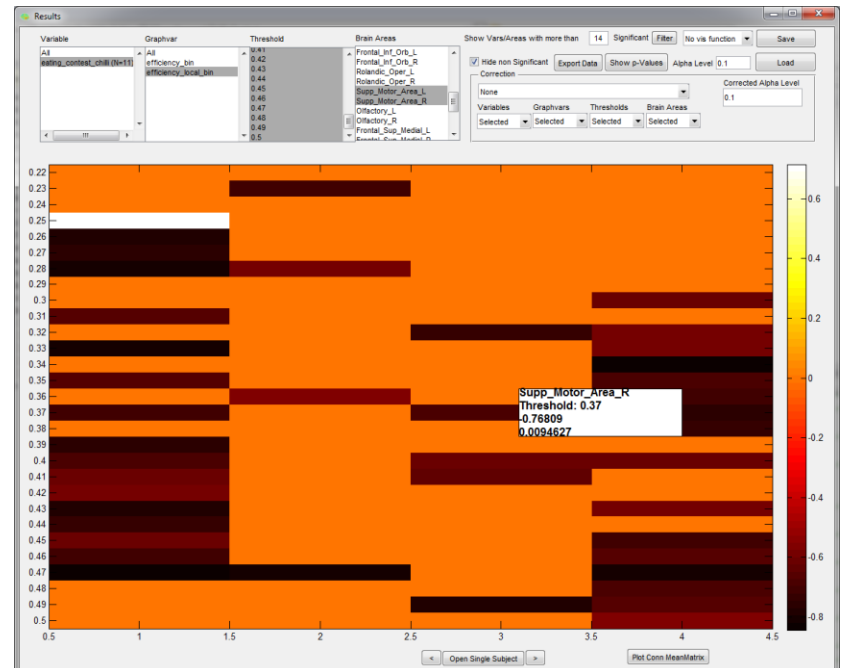
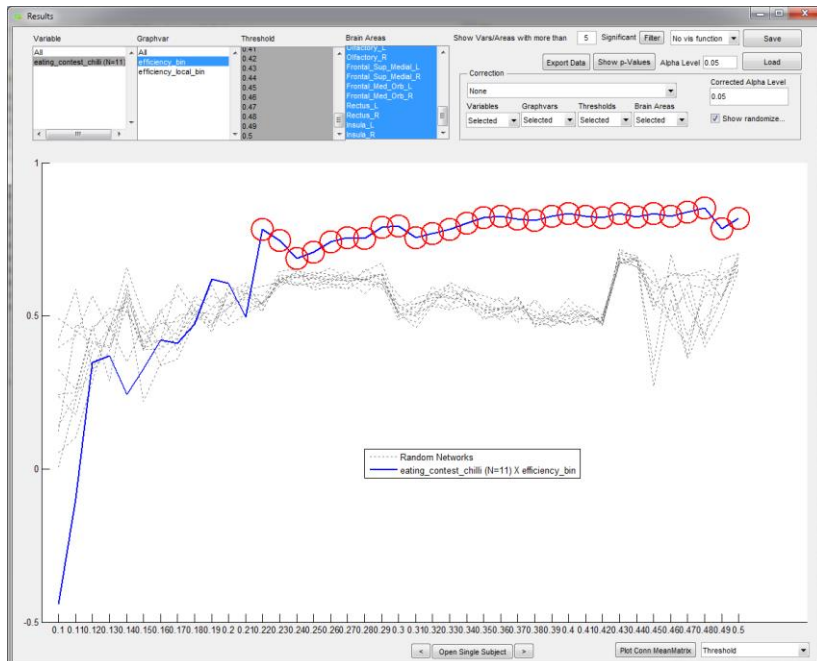
The image shows two overlapping windows. On the left is a Microsoft Excel spreadsheet titled 'TEST - Microsoft Excel'. The spreadsheet has columns A through F. Column A contains values from 0.22 to 0.5 in increments of 0.01. Column B is labeled 'eating\_conte X'. Column C is labeled 'Frontal\_Mid'. Column D is labeled 'Frontal\_Mid\_Suppl\_Motor'. Column E is labeled 'Suppl\_Motor\_Area\_R'. Column F is labeled 'Corrected AI' with a value of 0.1. The data in column F is constant at 0.1 for all rows.

On the right is a software interface window titled 'Brain Areas'. It has a 'Save' button highlighted with a red box. Below it is an 'Export Data' button also highlighted with a red box. There are checkboxes for 'Hide non Significant' and 'Show p-Values'. The 'Alpha Level' is set to 0.1. There are dropdown menus for 'Correction' (set to 'None') and 'Corrected Alpha Level' (set to 0.1). Below these are four dropdown menus labeled 'Variables', 'Graphvars', 'Thresholds', and 'Brain Areas', each with a 'Selected' dropdown. At the bottom of the window, there is a heatmap with a color scale from -0.8 to 0.6. A white box on the heatmap contains the text: 'Suppl\_Motor\_Area\_R', 'Threshold: 0.37', '-0.76809', and '0.0094627'. At the bottom of the heatmap window, there are buttons for 'Open Single Subject' and 'Plot Conn MeanMatrix'.

# Interpretation

## Hypothesis – confirmed!

1. YES - Chilli eating champs probably have more efficient brains... otherwise they could not deal with all the pain!
2. YES - orbito frontal gyrus and supplementary motor area contribute here...with a negative correlation of local efficiency to chilli eating ... much less spicy information transfer here!



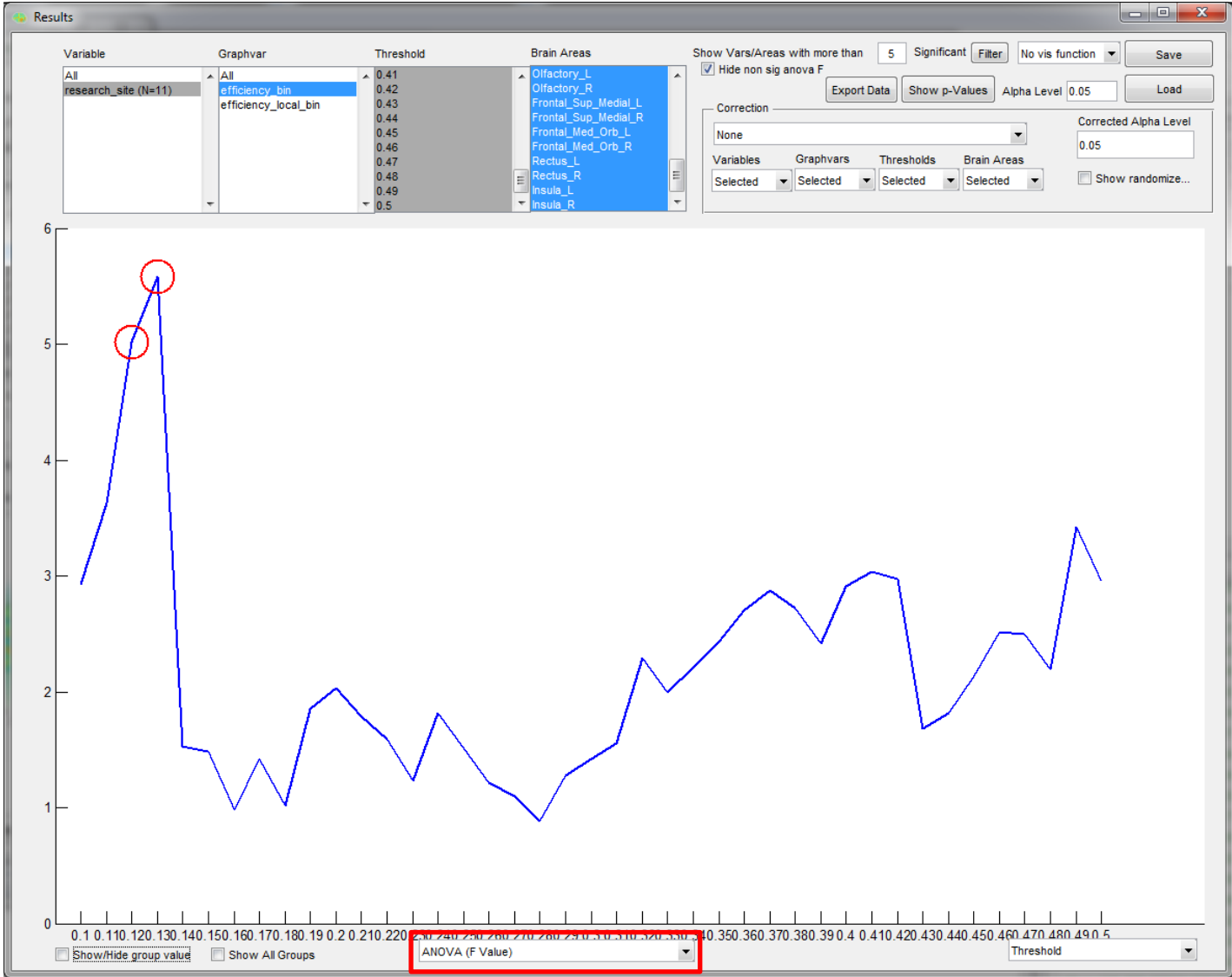
**Subsequent slides contain some  
more examples as group comparison or  
NBS**

- Now, we can also go back and decide to to a group comparison (ANOVA) on the previously calculated efficiencies
- Select group comparison with „research site“ and „test against random groups with 10 repetitions“
- Finally hit „Statistics with already calculated values“

The screenshot shows the GraphVar software interface with the following configurations:

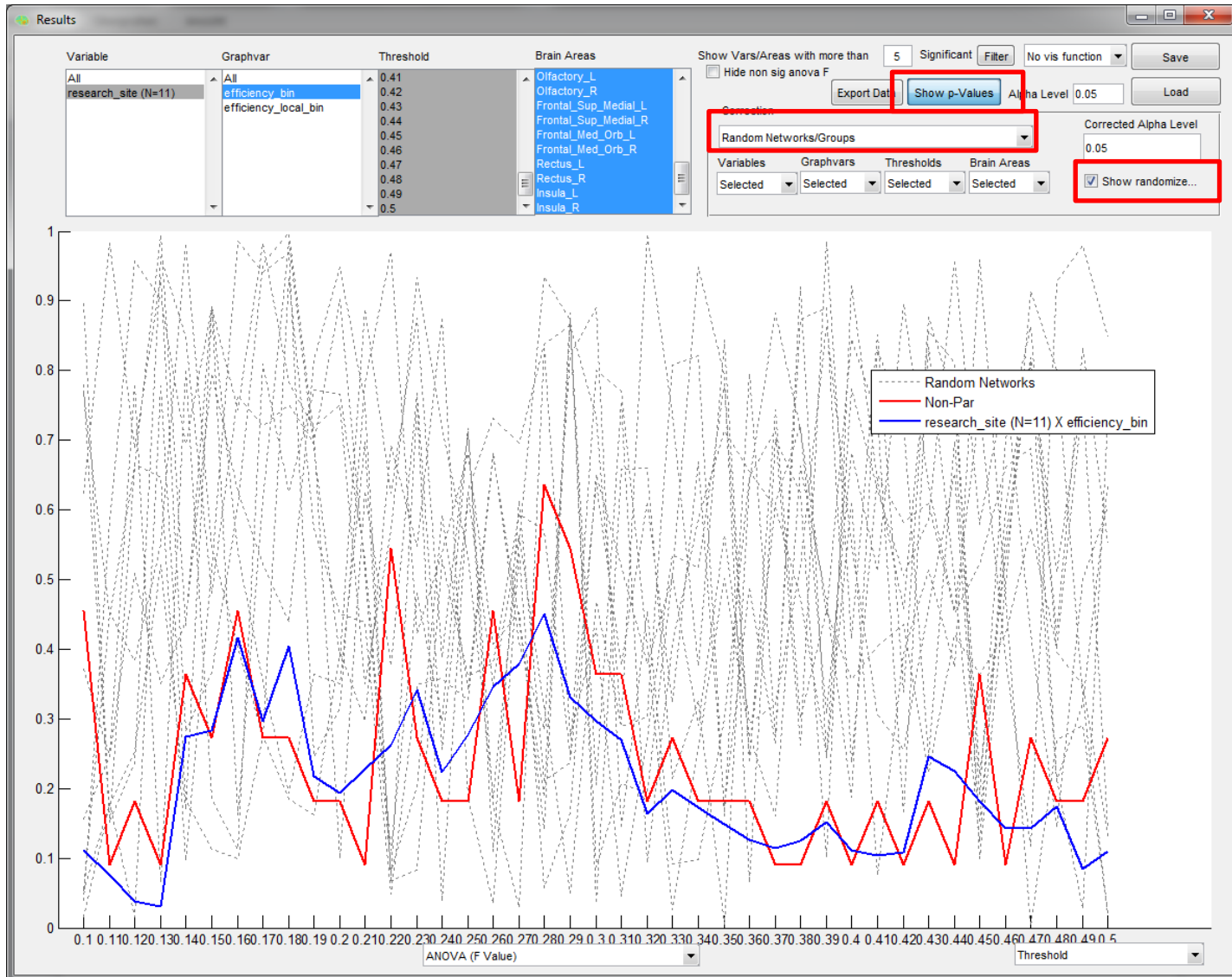
- General Settings:** Brain regions files: BrainRegions.csv; File with Variables: Variables.csv; Subjectname in Filename: CorrMatrix\_sample\_20.mat; Start: 12; End: 4; Corr Matrix Array: CorrMatrix; Save interim results: checked; Parallel Workers: 0.
- Network Construction:** Threshold: Relative; Weights: No Change; Network nodes / Brain areas: Superior frontal gyrus, medial orbit; Gyrus rectus (Left); Gyrus rectus (Right); Insula (Left); Insula (Right); Anterior cingulate and paracingulate; Network thresholds: 0.41 to 0.5; Generate: checked; 10 randomizer\_bin und randomio\_und randomized subject data (null model network) with 1 iteration; Binary: checked; Weighted: unchecked.
- Network Calculations:** Calculate graph metrics: checked; Brain graph metrics: Binary: Density, Distance Matrix, Eccentricity, Edge betweenness centrality, Efficiency global, Efficiency local, Eigenvector centrality, Flow coefficient global, Flow coefficient local, Graph radius; Normalize graph metric with random networks: unchecked; Use random network to calc smallworldness: unchecked; Calculate variables and export: button.
- Raw Matrix (link wise):** Raw matrix: unchecked; Connectivity Thr.: .05; r to z: unchecked; random networks: list of values from .05 to .005; Weights: No Change: checked; absolute weights: unchecked; negative weights to zero: unchecked.
- Statistics:** correlation: unchecked; partial correlation: unchecked; **group comparison: checked**; Variables Define Groups: age, sex, **research\_site**, IQ, fantasy\_score, eating\_contest\_chilli, beer\_pong\_score; Paired T-Test: unchecked; **Test against random groups: checked**; Number of repetitions: 10.
- Buttons:** Switch Workspace, Open Previous Results, Load interim results, **Statistics with already calculated values**, Calculate & Statistics.

- You see the distribution of ANOVA F values across thresholds for the group differences on global efficiency
- Red dots again indicate significance

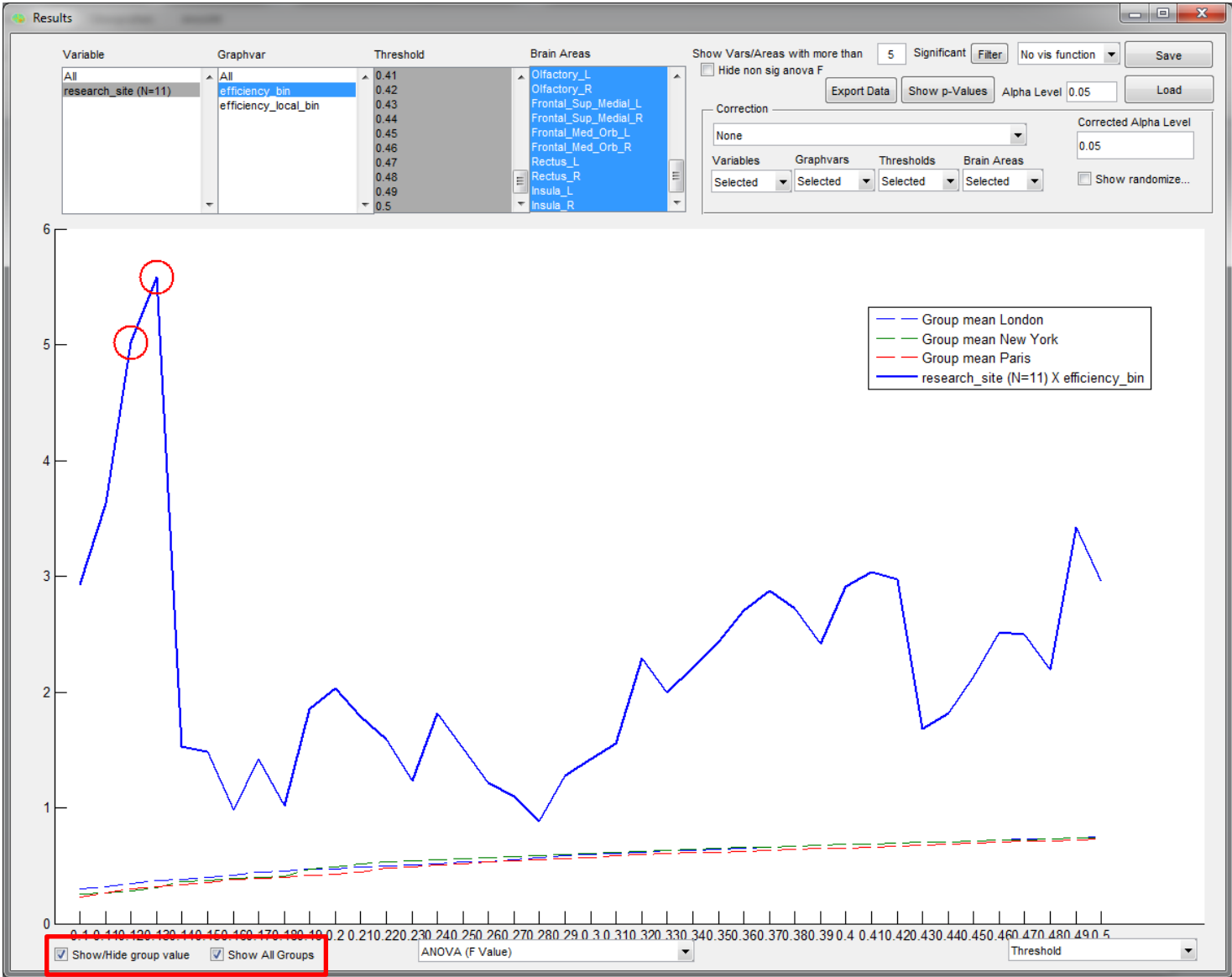




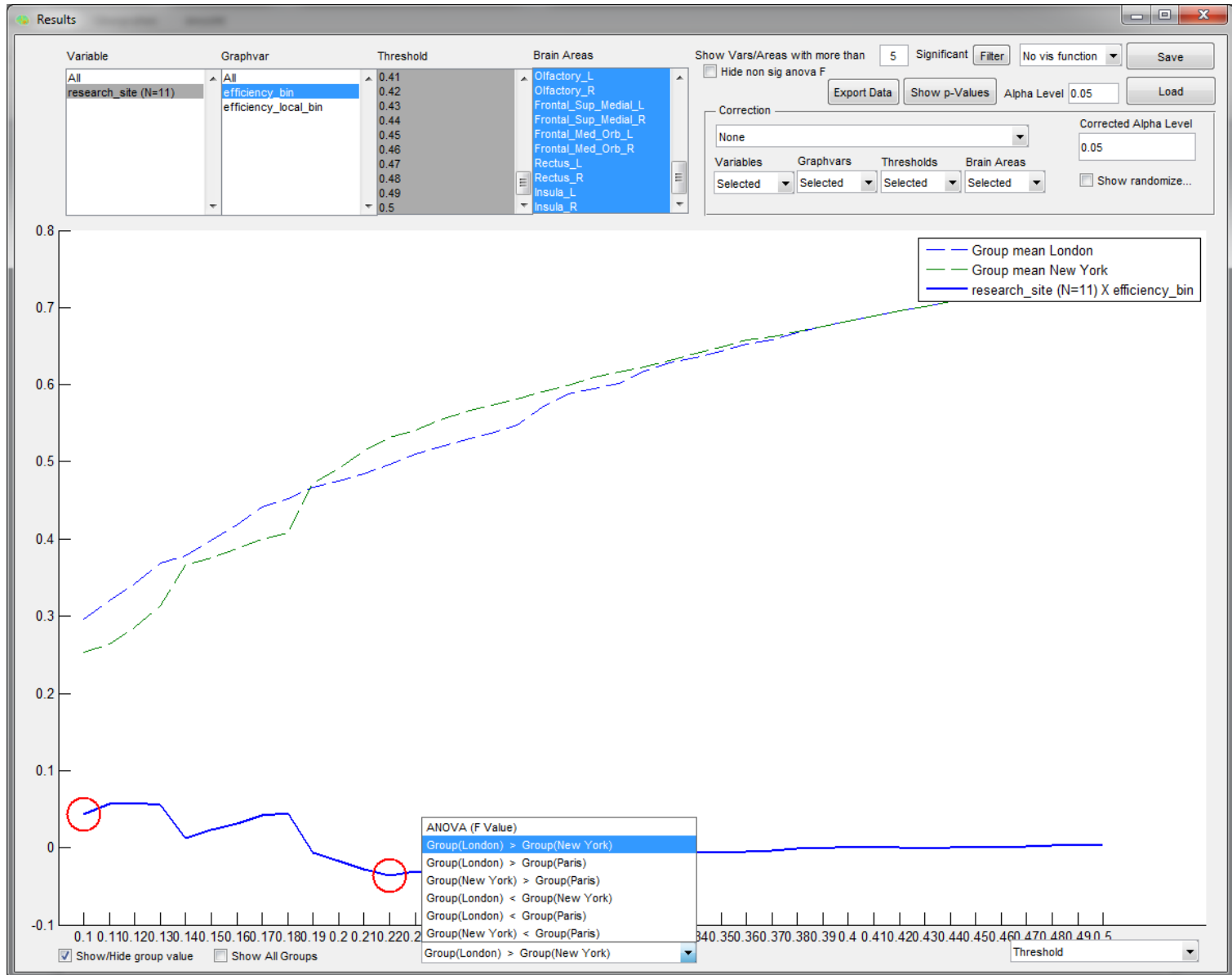
- Plot the parametric and non-parametric p-values ...



- Explore how the groups contribute to this effect by selecting „Show/Hide group value“ and „Show All Groups“



- Perform post-hoc t-tests by switching through the group contrasts
- The blue line shows the group difference for the specific contrast



- Finally, lets try some correlations on the raw correlation matrices!
- Deselect all other buttons and only use the following setting:

GraphVar - Chillli\_Contest

General Settings—  
 Brain regions files: BrainRegions.csv [Select]  
 File with Variables: Variables.csv [Select]  
 [Select Subjects (Conn Matrix)]  
 [Create Connectivity Matrix]

Subjects  
 C:\Users\kruschwi\Downloads\GraphVar\_beta\_...  
 C:\Users\kruschwi\Downloads\GraphVar\_beta\_...  
 C:\Users\kruschwi\Downloads\GraphVar\_beta\_...  
 C:\Users\kruschwi\Downloads\GraphVar\_beta\_...  
 C:\Users\kruschwi\Downloads\GraphVar\_beta\_...  
 C:\Users\kruschwi\Downloads\GraphVar\_beta\_...  
 Subjectname in Filename: CorrMatrix\_sample\_20.mat  
 Start: 12 End (remaining characters): 4  
 Corr Matrix Array: CorrMatrix  
 Save interim results Parallel Workers: 0

Network Construction—  
 Threshold—  
 Significant  Relative  Absolute  SICE  None  
 Weights—  
 No Change  absolute weights  negative weights to zero  
 Network nodes / Brain areas  

Network nodes / Brain areas	Network thresholds
Superior frontal gyrus, medial ort	0.41
Superior frontal gyrus, medial ort	0.42
Gyrus rectus (Left)	0.43
Gyrus rectus (Right)	0.44
Insula (Left)	0.45
Insula (Right)	0.46
Anterior cingulate and paracingu	0.47
Anterior cingulate and paracingu	0.48
Anterior cingulate and paracingu	0.49
Anterior cingulate and paracingu	0.5

 Generate randomized subject data (null model network)

Network Calculations—  
 Calculate graph metrics  
 Brain graph metrics  
 Binary: Density  
 Binary: Distance Matrix  
 Binary: Eccentricity  
 Binary: Edge betweenness centrality  
 Binary: Efficiency global  
 Binary: Efficiency local  
 Binary: Eigenvector centrality  
 Binary: Flow coefficient global  
 Binary: Flow coefficient local  
 Binary: Graph radius  
 Normalize graph metric with random networks  
 Use random network to calc smallworldness  
 [Calculate variables and export]

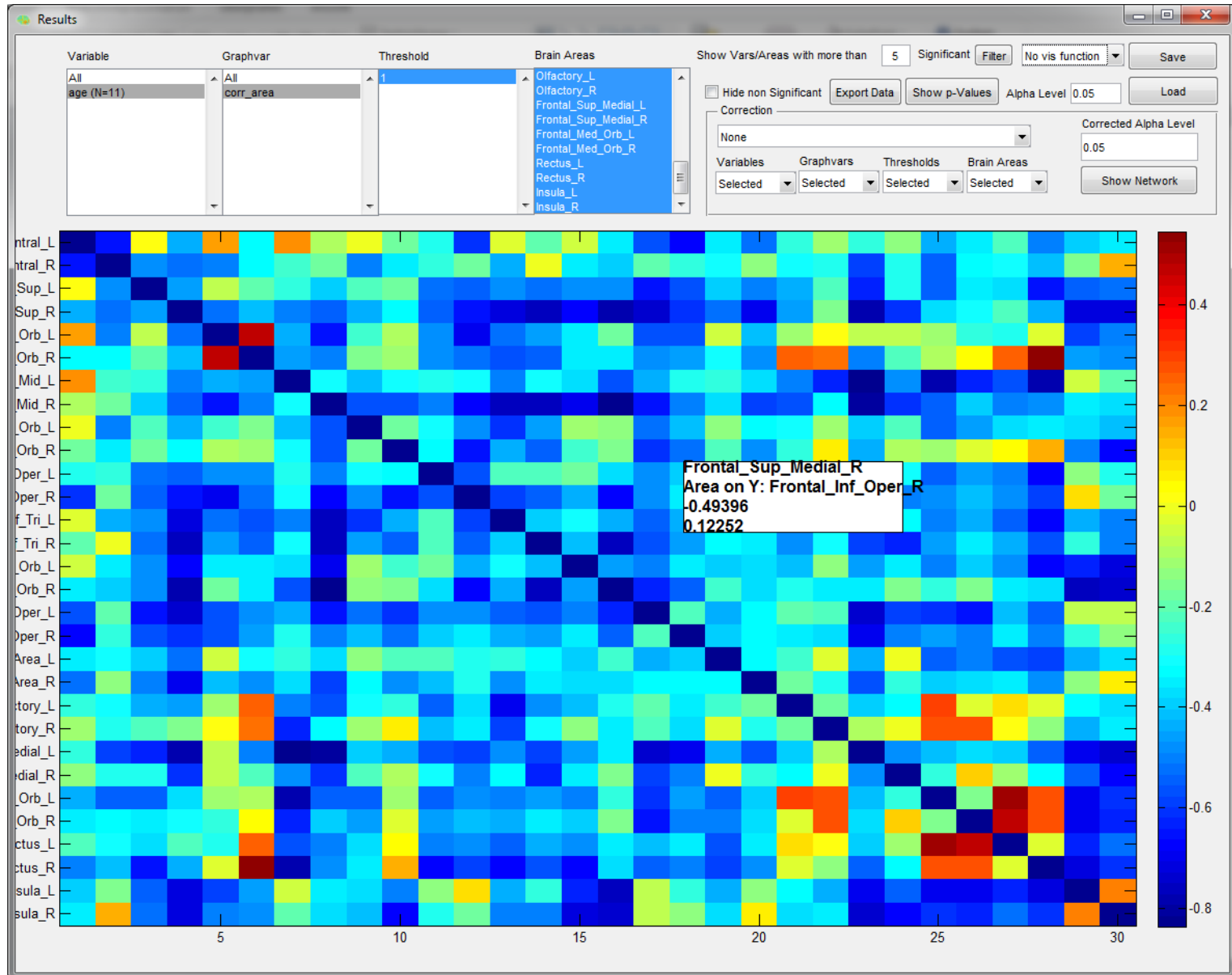
Raw Matrix (link wise)—  
 Raw matrix  
 Connectivity Thr.  r to z  
 Generate 10 random networks  
 random\_shuffle  
 null\_model\_und\_sigr  
 with 1 iterations for each subject.  
 Weights—  
 No Change  absolute weights  
 negative weights to zero

Statistics—  
 correlation  partial correlation  group comparison  
 Variables to correlate with  
 age  
 sex  
 research\_site  
 IQ  
 fantasy\_score  
 eating\_contest\_chilli  
 beer\_pong\_score  
 Test against shuffled data Number of repetitions: 1  
 Test against random networks (graph metrics)  
 Test against random networks (raw matrix)

Graph Var

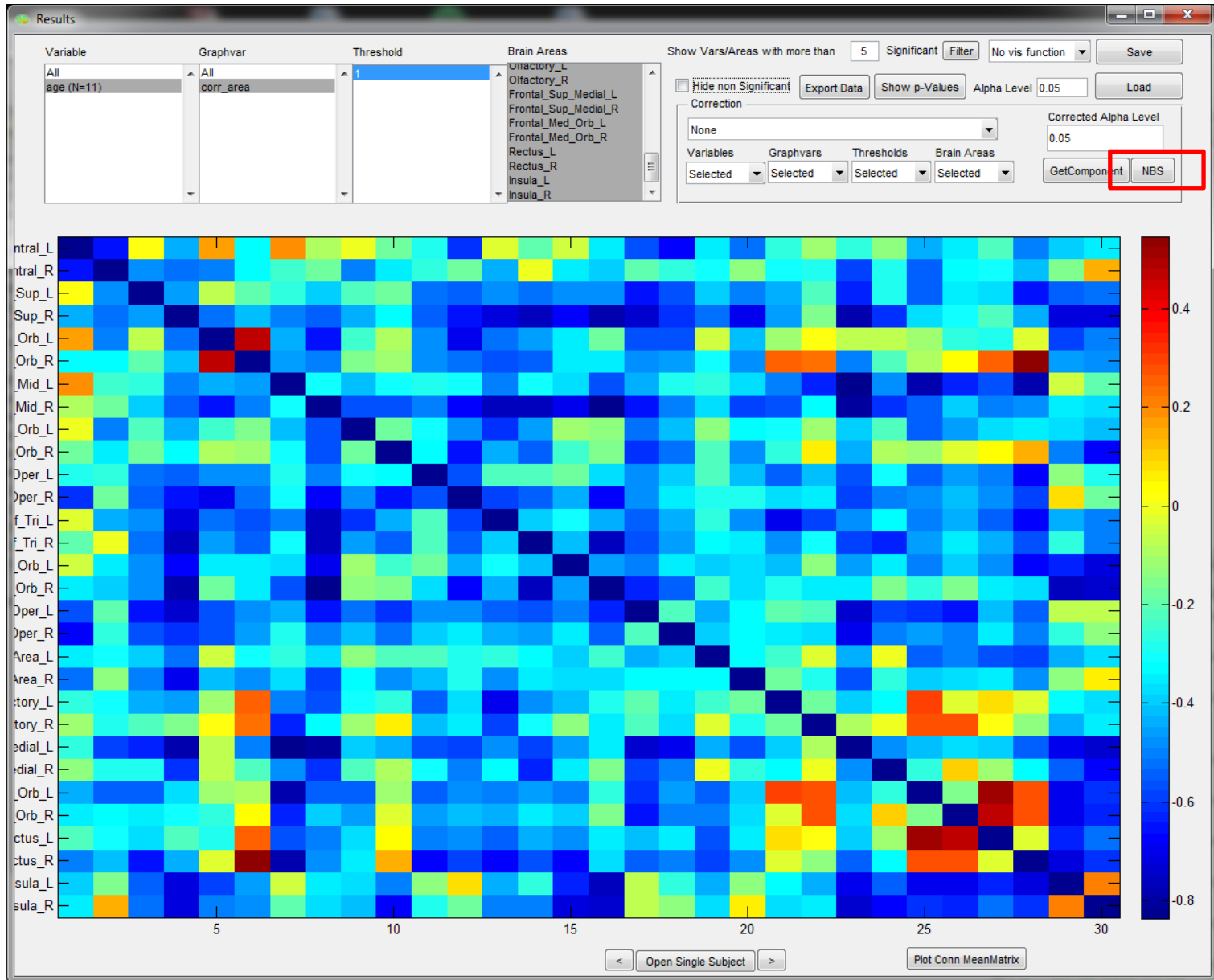
[Switch Workspace] [Open Previous Results] [Load interim results] [Statistics with already calculated values] [Calculate & Statistics]

- This is the correlation of age and the raw connectivities between the nodes in the 30x30 matrix

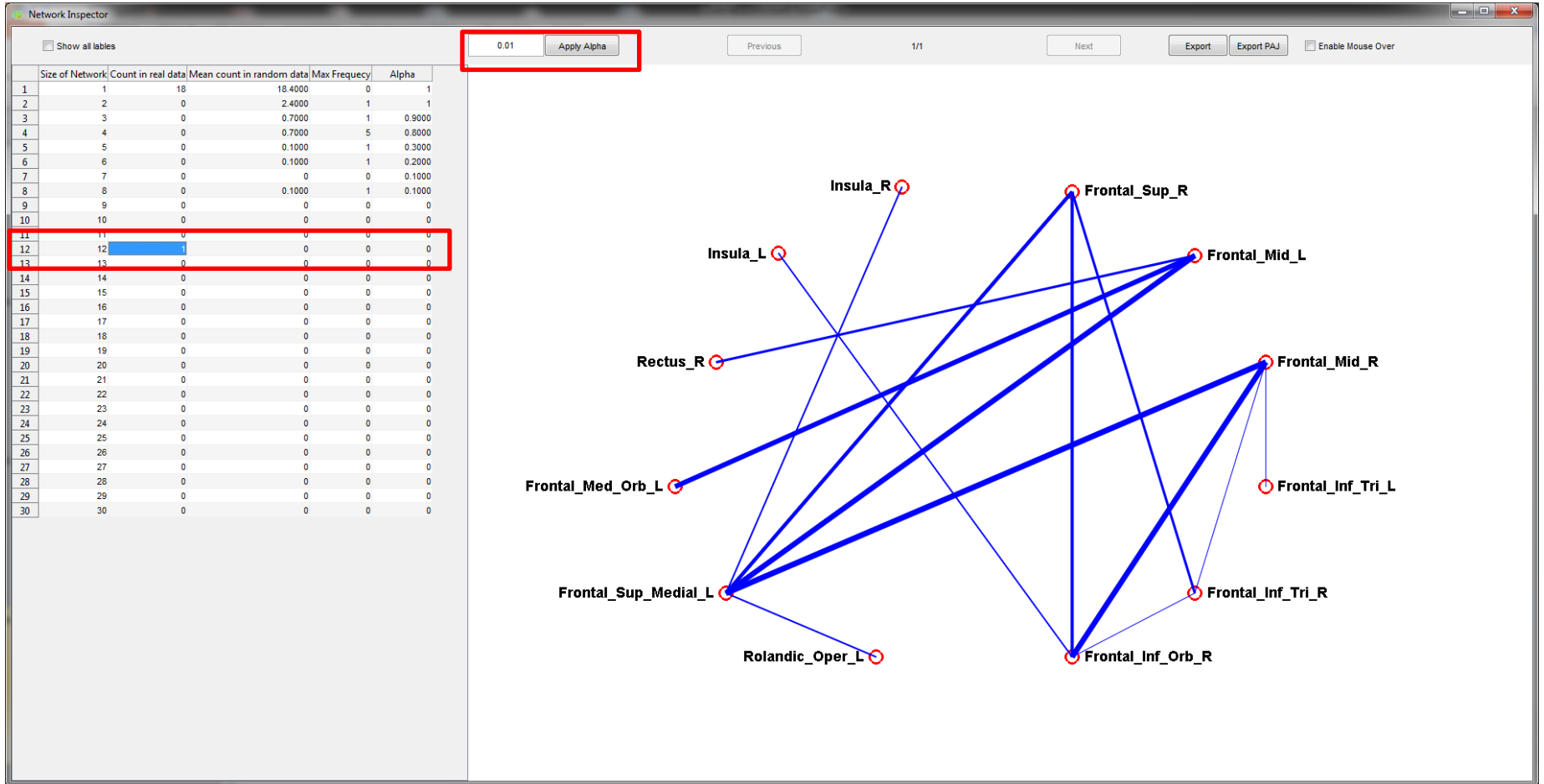




- Let's do network based statistics to identify a graph component that relates to age
- Hit the „NBS“ button

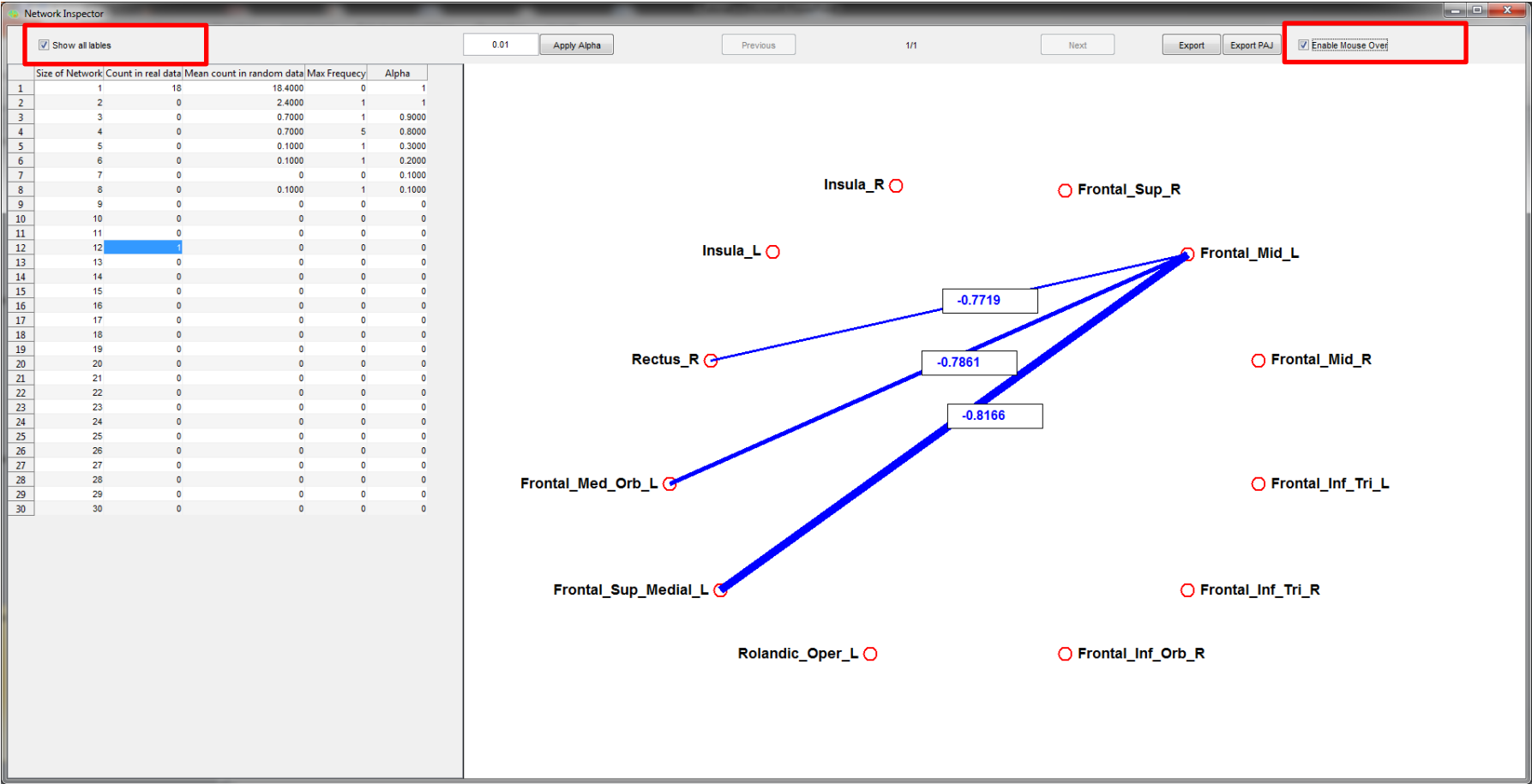


- Set the initial link threshold to 0.01
- And observe a significant graph component comprised of 12 nodes
- Please refer to the Manual for how to interpret and to use the Network Inspector





- Also use the „show all labels“ and „Enable Mouse Over“ to explore this component



- You can export the graph component in matrix format (.csv) but also in Pajek (PAJ) format for other visualization purposes

The screenshot displays the Network Inspector interface. On the left, a table shows network statistics. On the right, a network graph is visualized with nodes and edges. A red box highlights the 'Export' and 'Export PAJ' buttons. An Excel spreadsheet window is overlaid, showing a weight matrix for the network component.

Size of Network	Count in real data	Mean count in random data	Max Frequency	Alpha
1	1	18	18.4000	0
2	2	0	2.4000	1
3	3	0	0.7000	1
4	4	0	0.7000	5
5	5	0	0.1000	1
6	6	0	0.1000	1
7	7	0	0	0
8	8	0	0.1000	1
9	9	0	0	0
10	10	0	0	0
11	11	0	0	0
12	12	1	0	0
13	13	0	0	0
14	14	0	0	0
15	15	0	0	0
16	16	0	0	0
17	17	0	0	0
18	18	0	0	0
19	19	0	0	0
20	20	0	0	0
21	21	0	0	0
22	22	0	0	0
23	23	0	0	0
24	24	0	0	0
25	25	0	0	0
26	26	0	0	0
27	27	0	0	0

	Frontal_Sup	Frontal_Mid	Frontal_Mid	Frontal_Inf	Frontal_Inf	Frontal_Inf	Rolandic_Op	Frontal_Sup	Frontal_Mec	Rectus_R	Insula_L	Insula_R
1	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2	0.10861	0.084311	0.014581	0.0054916	0.0050639	0.010208	0.0043247	0.26486	0.18566	0.011261	0.012955	
3	0.10861	NaN	0.35322	0.12193	0.36113	0.065971	0.17005	0.0021601	0.0041195	0.0053841	0.89716	0.53985
4	0.084311	0.35322	NaN	0.0077671	0.0077944	0.0013347	0.031985	0.0025799	0.077524	0.13514	0.30529	0.25274
5	0.014581	0.12193	0.0077671	NaN	0.22023	0.17764	0.088324	0.13207	0.12049	0.024693	0.17427	0.11967
6	0.0054916	0.36113	0.0077944	0.22023	NaN	0.0070711	0.075507	0.058139	0.151	0.070663	0.43152	0.11865
7	0.0050639	0.065971	0.0013347	0.17764	0.0070711	NaN	0.04001	0.27635	0.45177	0.26136	0.0060546	0.010466
8	0.010208	0.17005	0.031985	0.088324	0.075507	0.04001	NaN	0.0084563	0.047716	0.077737	0.81679	0.83042
9	0.0043247	0.0021601	0.0025799	0.13207	0.058139	0.27635	0.0084563	NaN	0.19289	0.083149	0.017067	0.0084877
10	0.26486	0.0041195	0.077524	0.12049	0.151	0.45177	0.047716	0.19289	NaN	0.42423	0.019533	0.050757
11	0.18566	0.0053841	0.13514	0.024693	0.070663	0.26136	0.077737	0.083149	0.42423	NaN	0.013415	0.047003
12	0.011261	0.89716	0.30529	0.17427	0.43152	0.0060546	0.81679	0.017067	0.019533	0.013415	NaN	0.53035
13	0.012955	0.53985	0.25274	0.11967	0.11865	0.010466	0.83042	0.0084877	0.050757	0.047003	0.53035	NaN

- You can also directly open the graph component in BrainNetViewer (Xia et al.) if this nice viewer is installed
- **INFO: BrainNetViewer must be added to the MATLAB path with subfolders**

**Network Inspector**

Size of Network	Count in real data	Mean count in random data	Max Frequency	Alpha
1	1	18	19.2000	0
2	2	0	2	2
3	3	0	1	3
4	4	0	0.3000	1
5	5	0	0.2000	2
6	6	0	0.1000	1
7	7	0	0	0
8	8	0	0	0
9	9	0	0	0
10	10	0	0.1000	1
11	11	0	0	0
12	12	0	0	0
13	13	0	0	0
14	14	0	0	0
15	15	0	0	0
16	16	0	0	0
17	17	0	0	0
18	18	0	0	0
19	19	0	0	0
20	20	0	0	0
21	21	0	0	0
22	22	0	0	0
23	23	0	0	0
24	24	0	0	0
25	25	0	0	0
26	26	0	0	0
27	27	0	0	0
28	28	0	0	0
29	29	0	0	0
30	30	0	0	0

**BrainNet Viewer**

Please cite:  
 Xia M, Wang J, He Y (2013) BrainNet Viewer: A Network Visualization Tool for Human Brain Connectomics. PLoS ONE 8: e68910.

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 National Key Laboratory of Cognitive Neuroscience and Learning,  
 Beijing Normal University.

Contact Information:  
 Mingrui Xia: mingruixia@gmail.com  
 Yong He: yong.h.he@gmail.com

Rectus\_R

Frontal\_Inf\_Tri\_R

Frontal\_Inf\_Orb\_R