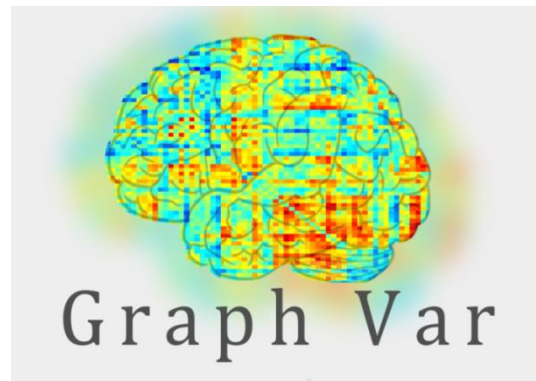


# GraphVar: a brief tutorial for getting started



## Outline:

1. **Example investigation:** „chilli contest“ (global and local efficiency)
2. **Group comparison** (global efficiency)
3. **Raw connectivity matrix** and **Network Based Statistics**
4. **Within design I** (change of efficiency T1 T2 between sex)
5. **Within design II** (change of efficiency and behavior T1 T2)

Frontal\_Sup\_Orb\_L  
Variable: sex  
d = 0.067693  
t(16) = 0.365046  
p = 0.719857

**d**: Difference between Group Means  
**F(df1,df2)**: F-value

Frontal\_Inf\_Orb\_L  
Variable: age\*sex  
d(b) = 0.047272  
t(16) = 0.090257  
p = 0.929203

**d(b)**: Difference between Standardized Regression Weights

Cingulum\_Ant\_R  
Variable: beer\_pong\_score  
b = 0.491152  
t(13) = 2.032979  
p = 0.062999

**b**: Standardized Regression Weight

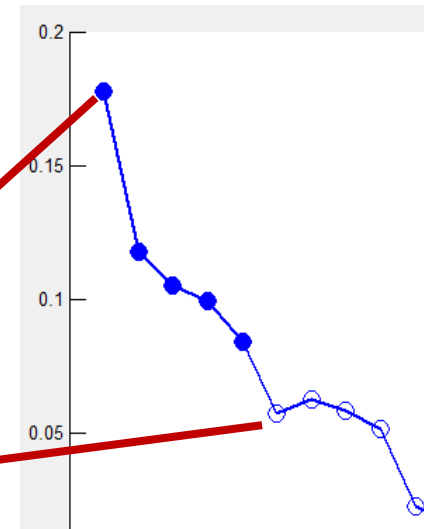
**t(df)**: t-Value

**p**: p-Value

Rolandic\_Oper\_R  
Variable: Intercept  
m = 0.688668  
t(16) = 6.904489  
p = 0.000004

**m**: Mean

significant  
not-significant



# Interpreting GraphVar output

# 1. Example investigation: „chilli contest“ (global and local efficiency)



## 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“)



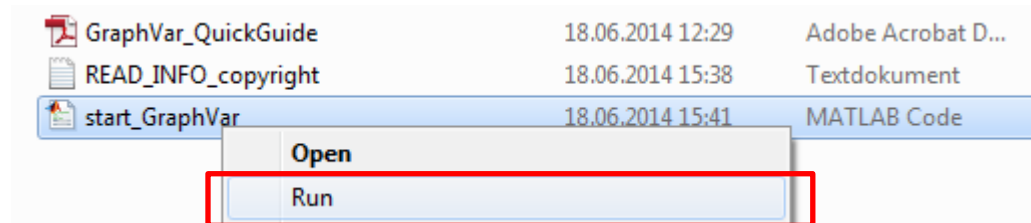


## Hypothesis:

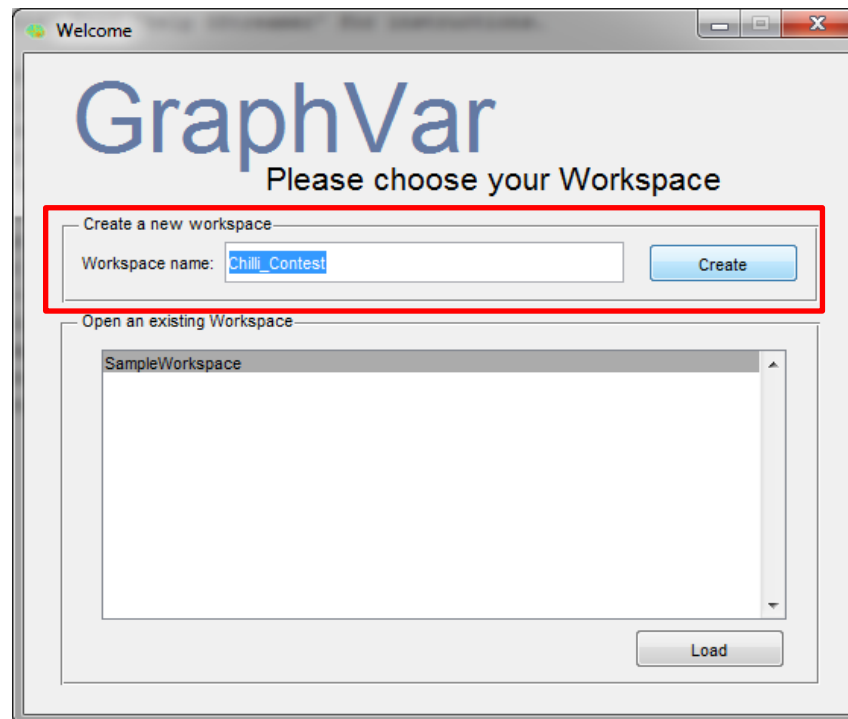
... a potential confound could be how much beer somebody had to drink before (i.e., cooling effect on the brain)

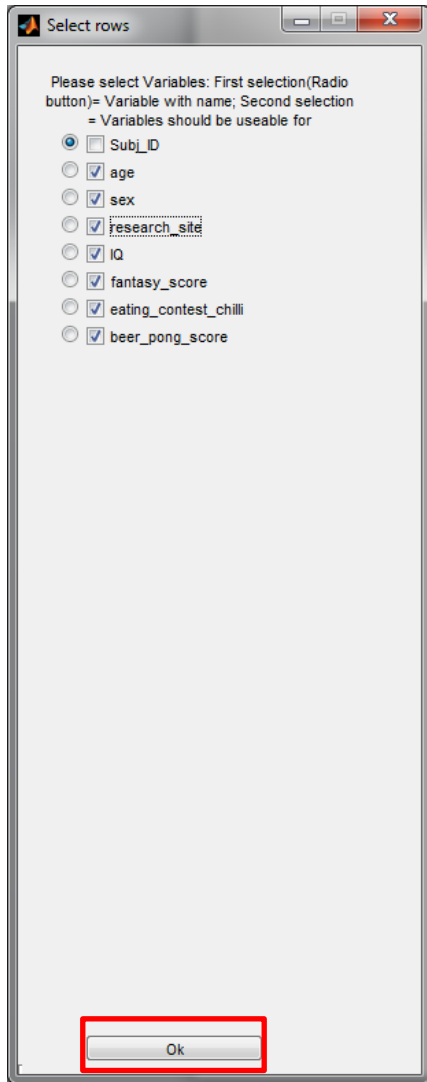


1. Use the right mouse to start GraphVar by clicking RUN on the „start\_GraphVar“ script in the main folder

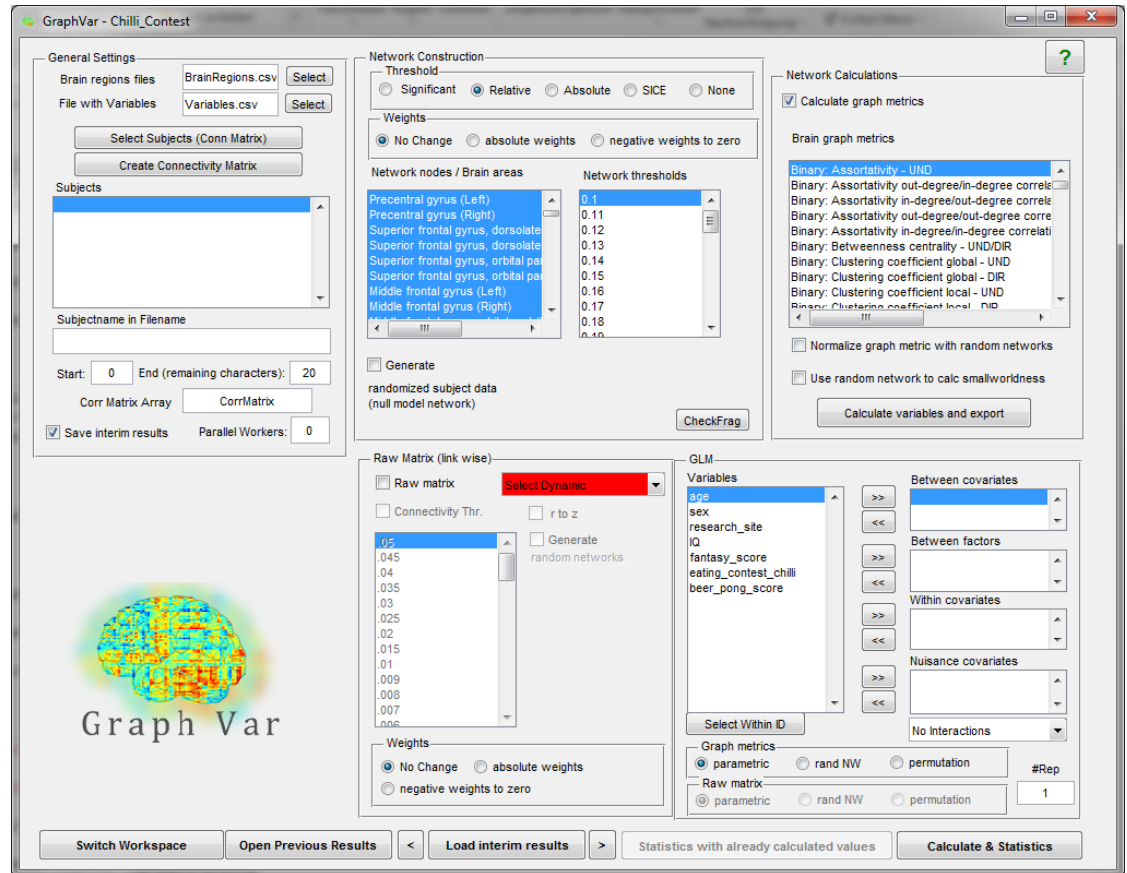


2. Create a new Workspace „Chilli\_Contest“





- 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 (or simply close the window)





- 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 brain regions including 'Precentral gyrus (Left)', 'Precentral gyrus (Right)', 'Superior frontal gyrus, dorsolate', 'Superior frontal gyrus, orbital pa', 'Middle frontal gyrus (Left)', and 'Middle frontal gyrus (Right)'. A 'Subjectname in Filename' field and 'Start'/'End' character limits are also present.
- Network Construction:** Features a 'Threshold' section with radio buttons for 'Significant', 'Relative' (selected), 'Absolute', 'SICE', and 'None'. A 'Weights' section has radio buttons for 'No Change' (selected), 'absolute weights', and 'negative weights to zero'. Below are two lists: 'Network nodes / Brain areas' and 'Network thresholds' (0.1 to 0.20).
- Network Calculations:** A 'Calculate graph metrics' section with a checked box. A list of 'Brain graph metrics' includes 'Binary: Assortativity - UND' (highlighted), 'Binary: Assortativity out-degree/in-degree correle', 'Binary: Assortativity in-degree/out-degree correle', 'Binary: Assortativity out-degree/out-degree corre', 'Binary: Assortativity in-degree/in-degree correlati', 'Binary: Betweenness centrality - UND/DIR', 'Binary: Clustering coefficient global - UND', 'Binary: Clustering coefficient global - DIR', 'Binary: Clustering coefficient local - UND', and 'Binary: Clustering coefficient local - DIR'. There are also checkboxes for 'Normalize graph metric with random networks' and 'Use random network to calc smallworldness', and a 'Calculate variables and export' button.
- Raw Matrix (link wise):** Includes a 'Raw matrix' checkbox, a 'Connectivity Thr.' list (0.05 to 0.2), and options for 'r to z' and 'Generate random networks'.
- GLM:** A 'Variables' list (age, sex, research\_site, IQ, fantasy\_score, eating\_contest\_chilli, beer\_pong\_score) is highlighted with a red box. It includes 'Between covariates', 'Between factors', 'Within covariates', and 'Nuisance covariates' sections. There are also 'Select Within ID', 'Graph metrics' (parametric selected, rand NW, permutation), and 'Raw matrix' (parametric selected, rand NW, permutation) options, along with a '#Rep' field set to 1.
- Weights:** Radio buttons for 'No Change' (selected), 'absolute weights', and 'negative weights to zero'.
- Brain Visualization:** A 3D brain model with a network overlay is shown with the text 'Graph Var' below it.
- Bottom Panel:** Contains buttons for 'Switch Workspace', 'Open Previous Results', 'Load interim results', 'Statistics with already calculated values', 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 most functions of the GUI

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

- General Settings:** Includes fields for 'Brain regions files' (BrainRegions.csv), 'File with Variables' (Variables.csv), and buttons for 'Select Subjects (Conn Matrix)' and 'Create Connectivity Matrix'. It also features a 'Subjects' list, 'Subjectname in Filename' field, 'Start' and 'End' character limits, 'Corr Matrix Array' and 'CorrMatrix' fields, and checkboxes for 'Save interim results' and 'Parallel Workers'.
- Network Construction:** Contains 'Threshold' options (Significant, Relative, Absolute, SICE, None), 'Weights' options (No Change, absolute weights, negative weights to zero), and two lists: 'Network nodes / Brain areas' and 'Network thresholds'. A 'Generate' button and 'randomized subject data (null model network)' text are also present.
- Network Calculations:** Features a checked 'Calculate graph metrics' option and a list of 'Brain graph metrics' including Binary Assortativity and Betweenness centrality. It also has checkboxes for 'Normalize graph metric with random networks' and 'Use random network to calc smallworldness', along with a 'Calculate variables and export' button.
- Raw Matrix (link wise):** Includes a 'Raw matrix' checkbox, a 'Connectivity Thr.' field, and a 'Weights' section with 'No Change', 'absolute weights', and 'negative weights to zero' options.
- GLM:** Contains a 'Variables' list, 'Between covariates', 'Between factors', 'Within covariates', and 'Nuisance covariates' sections. It also has 'Select Within ID', 'Graph metrics' (parametric, rand NW, permutation), and 'Raw matrix' (parametric, rand NW, permutation) options, along with a '#Rep' field.
- Bottom Panel:** Includes buttons for 'Switch Workspace', 'Open Previous Results', 'Load interim results', 'Statistics with already calculated values', and 'Calculate & Statistics'.
- Help Button:** A red box highlights a question mark icon in the top right corner of the window.



- 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. In the 'General Settings' panel, the 'Select Subjects (Conn Matrix)' button is highlighted with a red rectangle. Below it, the 'Subjects' list is empty, and the 'Subjectname in Filename' field is blank. The 'Start' field is set to 0 and the 'End (remaining characters)' field is set to 20. The 'Corr Matrix Array' is set to 'CorrMatrix'. The 'Save interim results' checkbox is checked, and 'Parallel Workers' is set to 0.

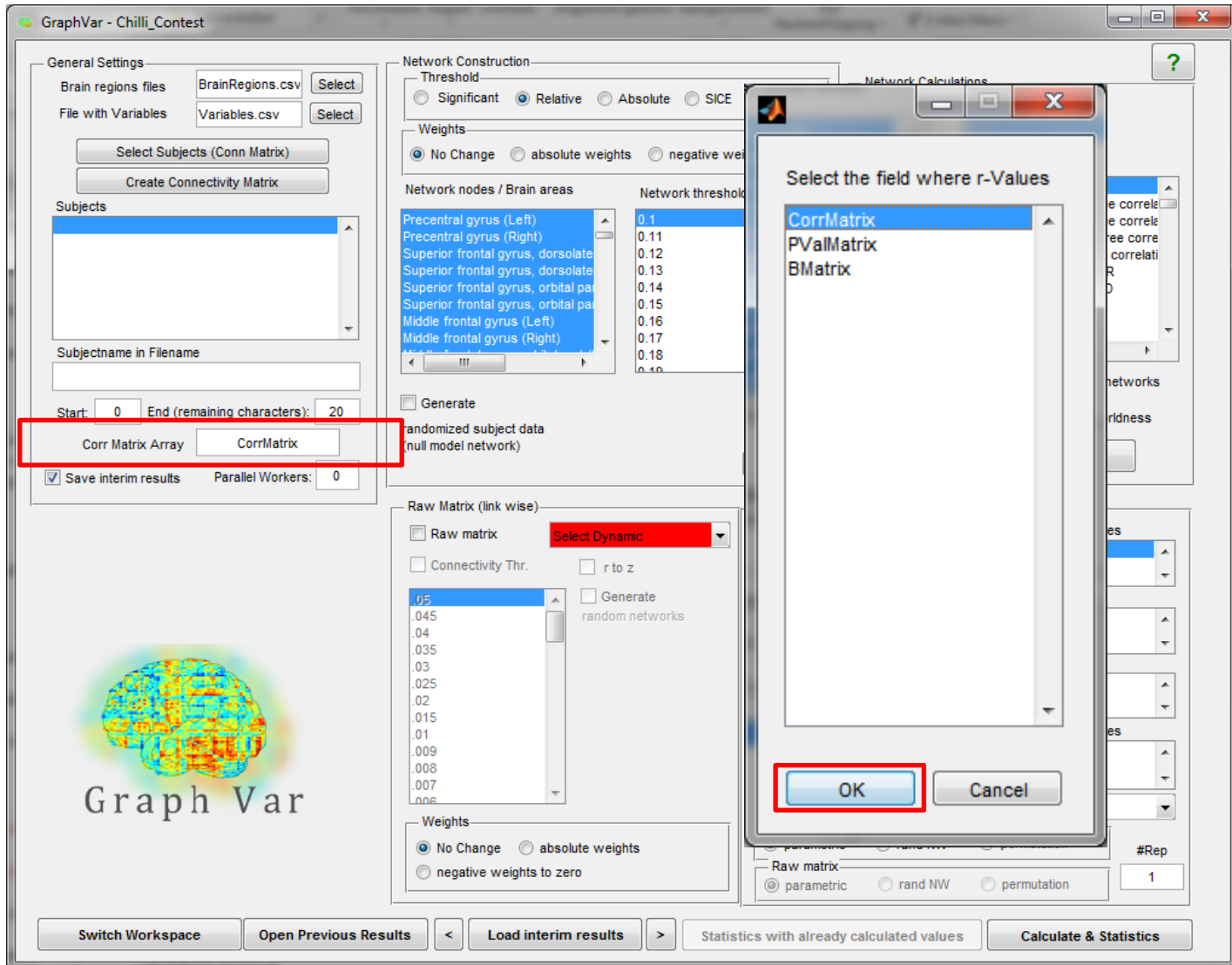
A file selection dialog is open, showing the 'CorrMatrix' folder. The list of files is as follows:

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

The files from 'CorrMatrix\_sample\_20' to 'CorrMatrix\_sample\_30' are highlighted in blue, and a red box surrounds this selection. The 'Dateiname' field is set to '"CorrMatrix\_sample\_30.mat" "CorrMatrix\_sample\_20.mat" "CorrMatrix\_sample\_21.mat"' and the 'Dateityp' is set to 'MAT-files (\*.mat)'. The 'Offnen' and 'Abbrechen' buttons are visible at the bottom right of the dialog.

At the bottom of the GraphVar window, there are buttons for 'Switch Workspace', 'Open Previous Results', 'Load interim results', 'Statistics with already calculated values', and 'Calculate & Statistics'. The GraphVar logo and a brain network visualization are visible at the bottom left.

- 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

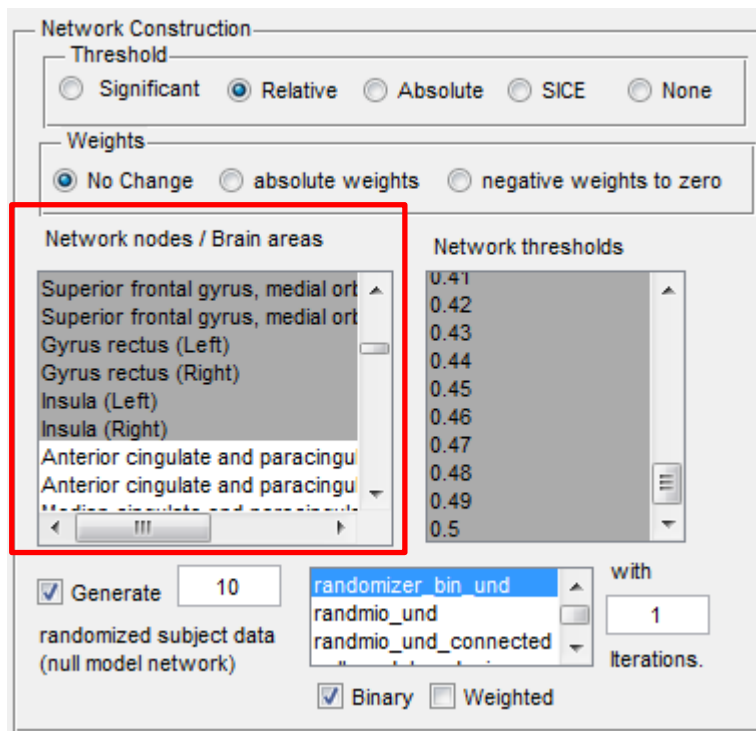
**Subjectname in Filename**

Start:  End (remaining characters):

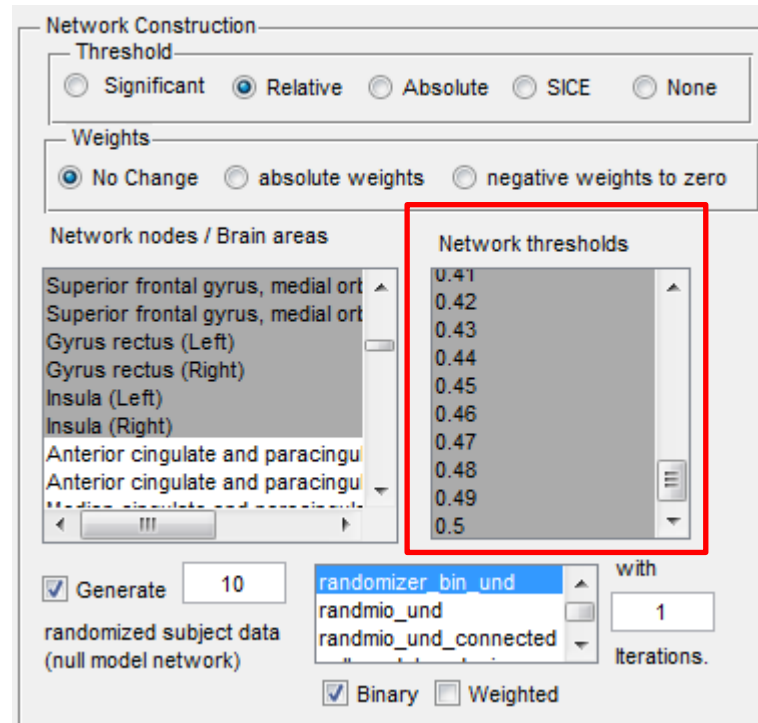
Corr Matrix Array

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

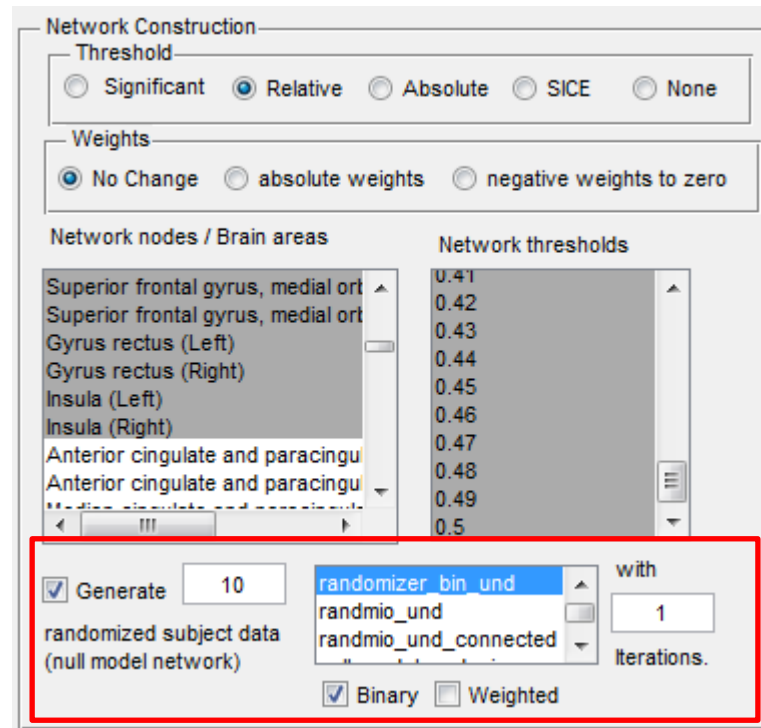


- Here, we want to construct different networks using relative thresholding (i.e., densities)
- Simply select all the thresholds in the box with „ctrl+A“ (see manual for how to add more thresholds)



- For this investigation let's construct subject specific null-model networks to calculate „small-worldness“
- Here, we ONLY generate **10 binary random networks** per subject per threshold using the „randomizer\_bin\_und“ BCT function

(for small-worldness, normalization purposes, or non-parametric testing you would normally use 100-1000 or even more ... but this will take a lot of time)



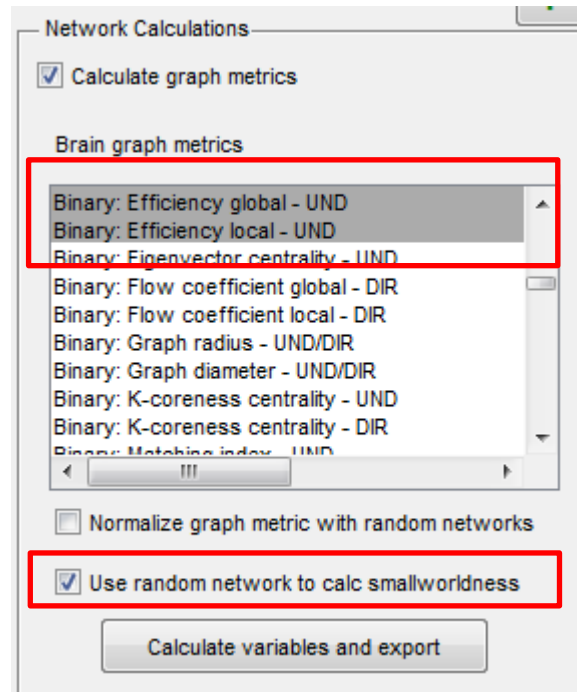


- As we have the hypothesis, that chilli eating champs probably have more efficient brains and that probably insula and orbito frontal cortex may contribute here, we select:

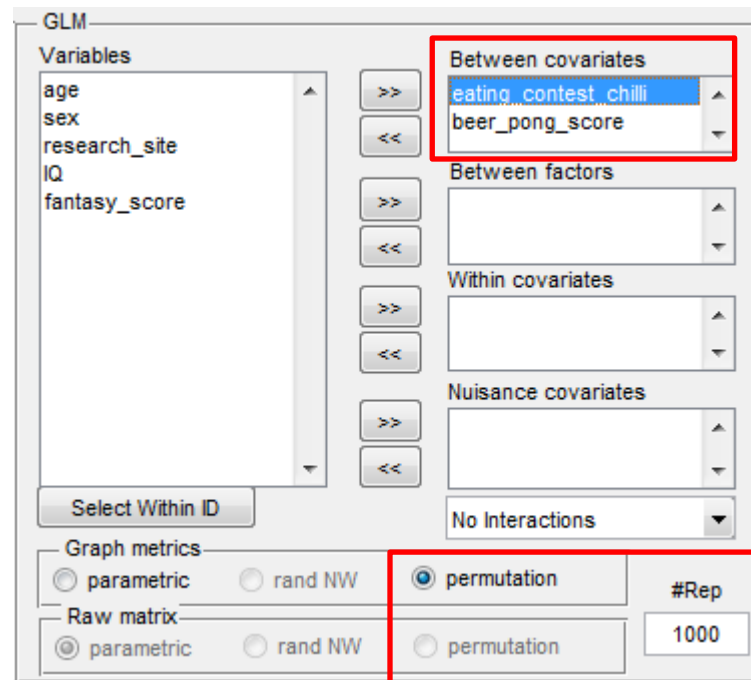
Binary: Efficiency global

Binary: Efficiency local

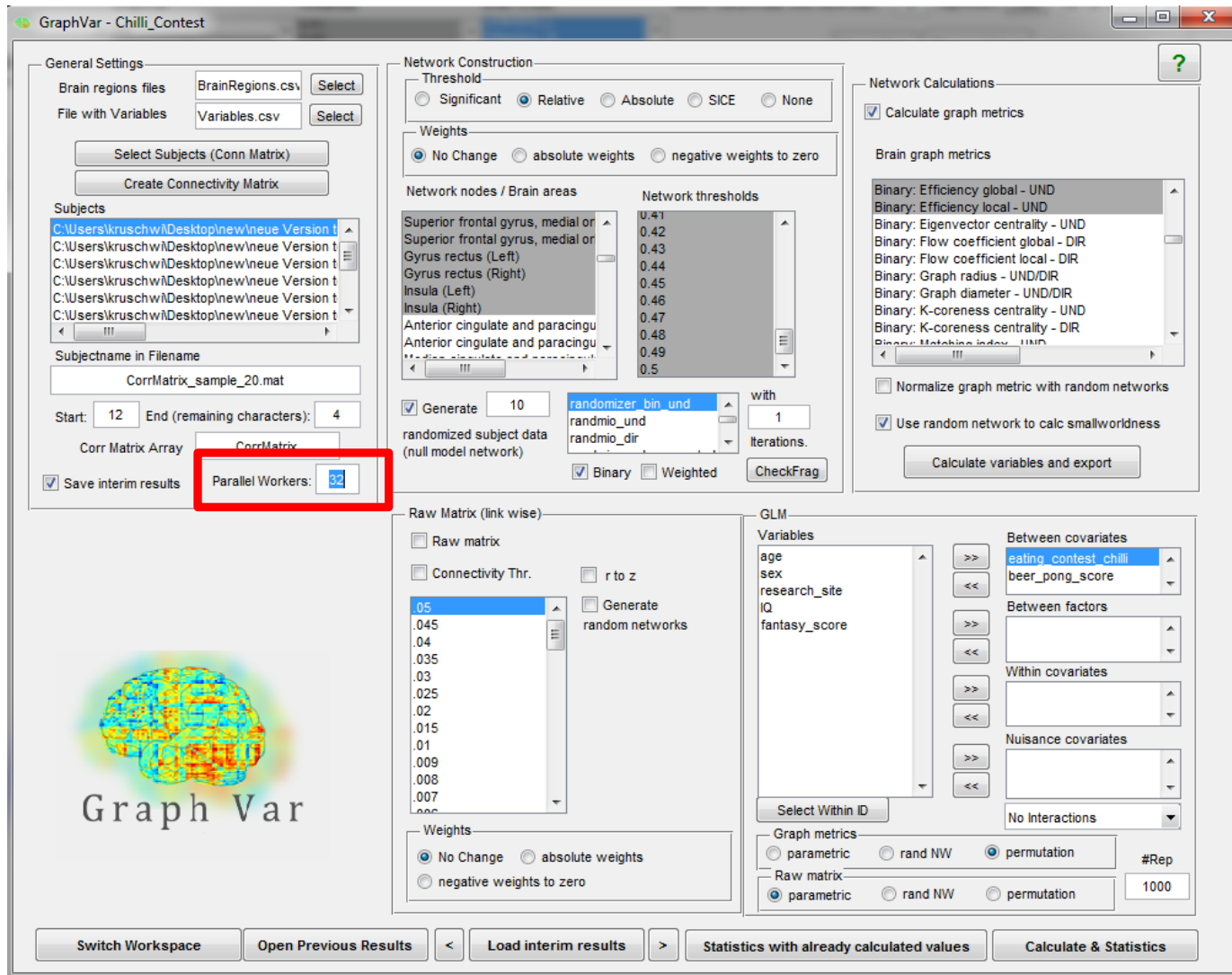
- Select also “Use random network to calc smallworldness”
- FYI: you can also add custom functions (see appendix in the manual); also note that for some of the functions it would not make sense to do statistics on (e.g., modularity affiliation vector; get components)



- In the GLM panel add „eating\_contest\_chilli“ and „beer\_pong\_score“ as predictors in the between covariates field
- Also select the option to perform permutation testing with 1000 permutations per threshold



- If you have the parallel computing toolbox installed, you may want to use more workers (cores) to speed up the generation of null-model networks!



# 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' project. The interface is divided into several panels:

- General Settings:** Includes fields for 'Brain regions files' (BrainRegions.csv), 'File with Variables' (Variables.csv), and 'Subjects' (a list of file paths). It also has a 'Subjectname in Filename' field (CorrMatrix\_sample\_20.mat), 'Start' (12) and 'End' (4) fields, and a 'Corr Matrix Array' (CorrMatrix) field.
- Network Construction:** Includes a 'Threshold' section with radio buttons for 'Significant', 'Relative' (selected), 'Absolute', 'SICE', and 'None'. It also has a 'Weights' section with radio buttons for '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 'Calculate graph metrics' checkbox (checked) and a list of 'Brain graph metrics' such as 'Binary: Efficiency global - UND', 'Binary: Efficiency local - UND', etc. It also has a 'Calculate variables and export' button.
- Raw Matrix (link wise):** Includes a 'Raw matrix' checkbox (unchecked), a 'Connectivity Thr.' field (.05), and a 'Weights' section with radio buttons for 'No Change' (selected), 'absolute weights', and 'negative weights to zero'.
- GLM:** Includes a 'Variables' list (age, sex, research\_site, IQ, fantasy\_score), a 'Between covariates' list (eating\_contest\_chilli, beer\_pong\_score), and a 'Between factors' list. It also has a 'Within covariates' list, a 'Nuisance covariates' list, and a 'No Interactions' dropdown.

At the bottom of the interface, there are several buttons: 'Switch Workspace', 'Open Previous Results', 'Load interim results', 'Statistics with already calculated values', and 'Calculate & Statistics' (highlighted with a red box).

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

The screenshot displays the GraphVar software interface with a progress dialog box overlaid. The main window is titled "GraphVar - Chilli\_Context" and contains several panels:

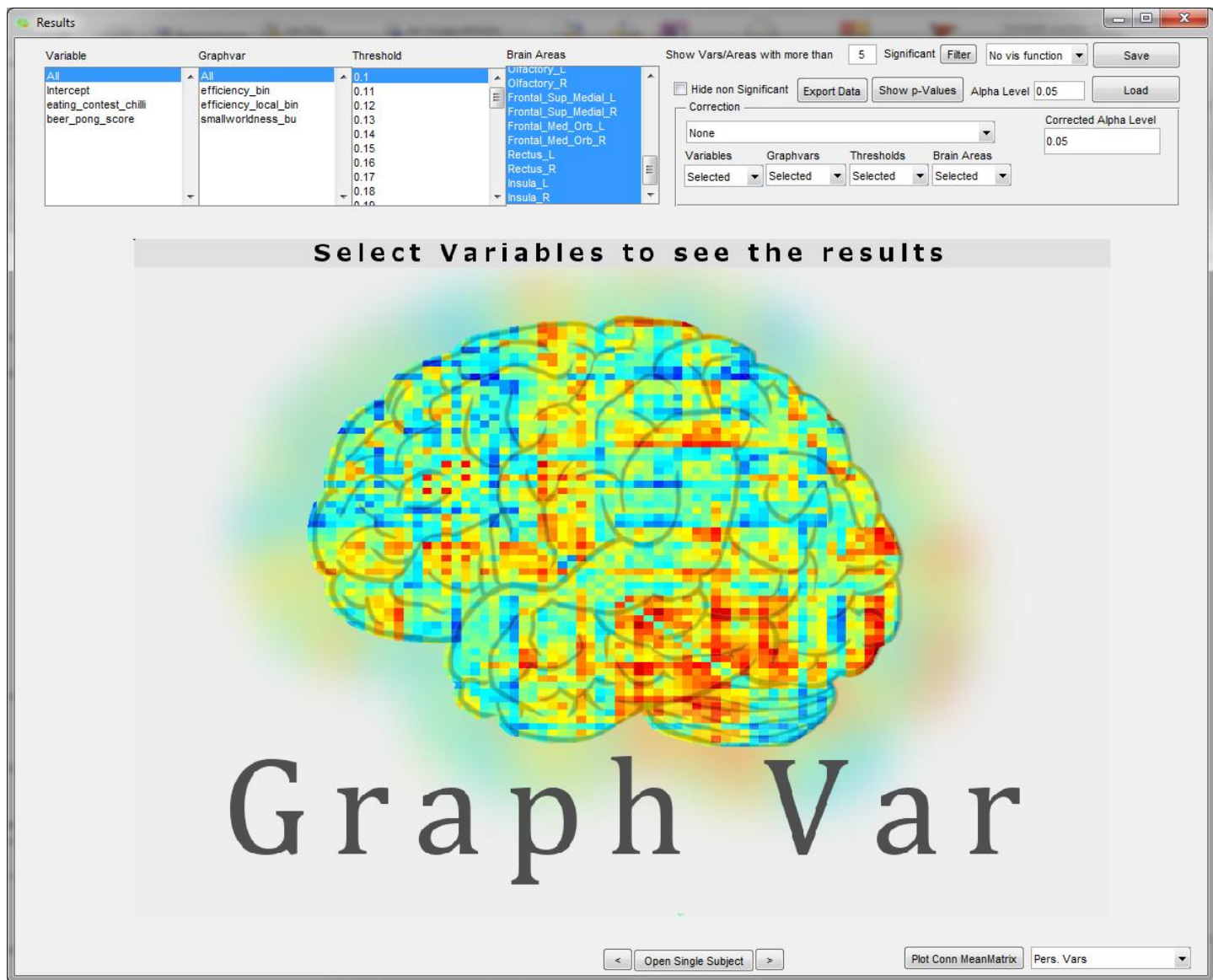
- General Settings:** Includes fields for "Brain regions files" (BrainRegions.csv), "File with Variables" (Variables.csv), and "Subjectname in Filename" (CorrMatrix\_sample\_20.mat). It also has checkboxes for "Save interim results" and "Parallel Workers".
- Network Construction:** Features a "Threshold" section with radio buttons for "Significant", "Relative" (selected), "Absolute", "SICE", and "None". It also has a "Weights" section with radio buttons for "No Change" (selected), "absolute weights", and "negative weights to zero".
- Network Calculations:** Includes a checked box for "Calculate graph metrics" and a list of "Brain graph metrics" such as "Binary: Efficiency global - UND", "Binary: Efficiency local - UND", "Binary: Eigenvector centrality - UND", "Binary: Flow coefficient global - DIR", "Binary: Flow coefficient local - DIR", "Binary: Graph radius - UND/DIR", "Graph diameter - UND/DIR", "K-core-ness centrality - UND", "K-core-ness centrality - DIR", and "Matching index - UND".
- Between covariates:** A list containing "eating\_contest\_chilli" (selected) and "beer\_pong\_score".
- Between factors:** An empty dropdown menu.
- Within covariates:** An empty dropdown menu.
- Nuisance covariates:** An empty dropdown menu.
- No Interactions:** A dropdown menu.
- Method:** Radio buttons for "permutation" (selected) and "Monte Carlo".
- #Rep:** A text field containing "1000".
- Calculate & Statistics:** A button highlighted with a red rectangle.

The progress dialog box, titled "Progress", shows the following status:

- All Tasks 15333 of 14883 Operations (100%)
- Thresholds 41 of 41
- Thresholding Subject 11 of 11
- Randomize Subject 110 of 110
- Graph Function 2 of 2
- Subject 121 of 121
- GLM
- Variable 2 of 3
- Threshold 25 of 41
- Chunk 1 of 1

At the bottom of the progress dialog is a "Cancel (or MainWin:Ctrl+C)" button.

- This is the results viewer

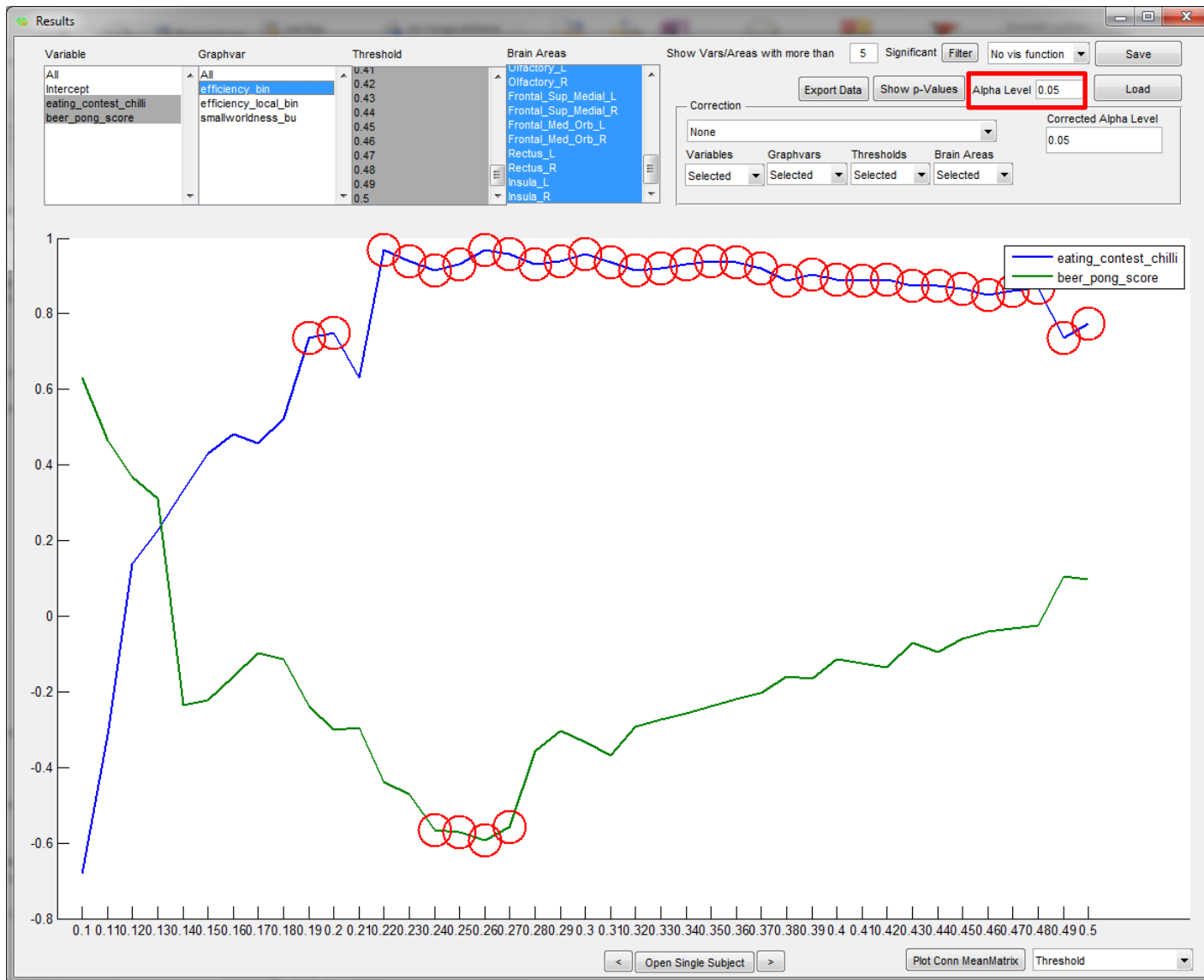




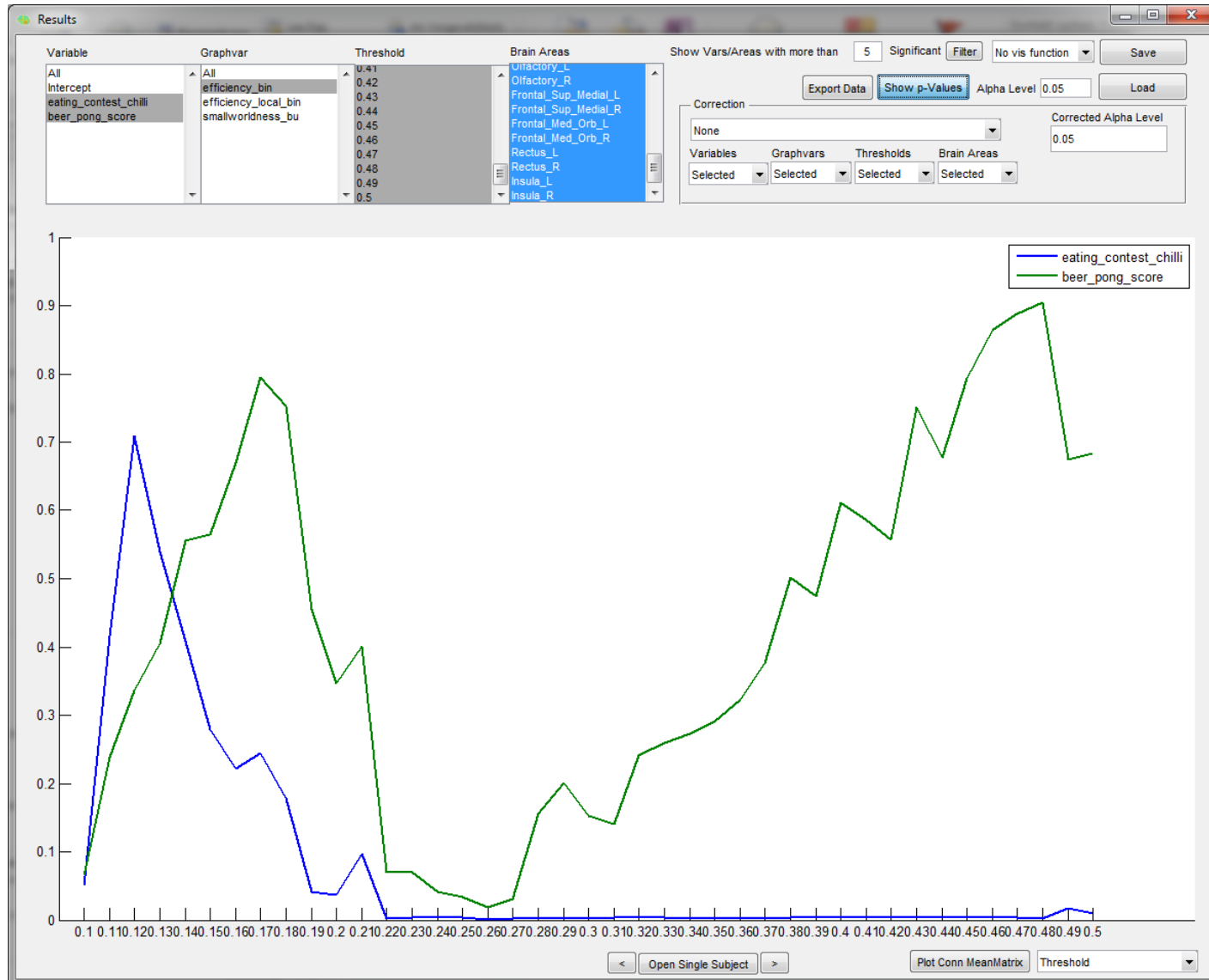
- To see the results for global efficiency across thresholds, select the „eating\_contest\_chilli“, „beer\_pong\_score“, „efficiency\_bin“, and all thresholds (ctrl+A)
- Selection of brain areas does not have an effect on global variables
- FYI: the „Intercept“ is the constant in the GLM (i.e., expected mean value of Y when all X=0)

Variable	Graphvar	Threshold	Brain Areas
All	All	0.41	Olfactory_L
Intercept	efficiency_bin	0.42	Olfactory_R
eating_contest_chilli	efficiency_local_bin	0.43	Frontal_Sup_Medial_L
beer_pong_score	smallworldness_bu	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

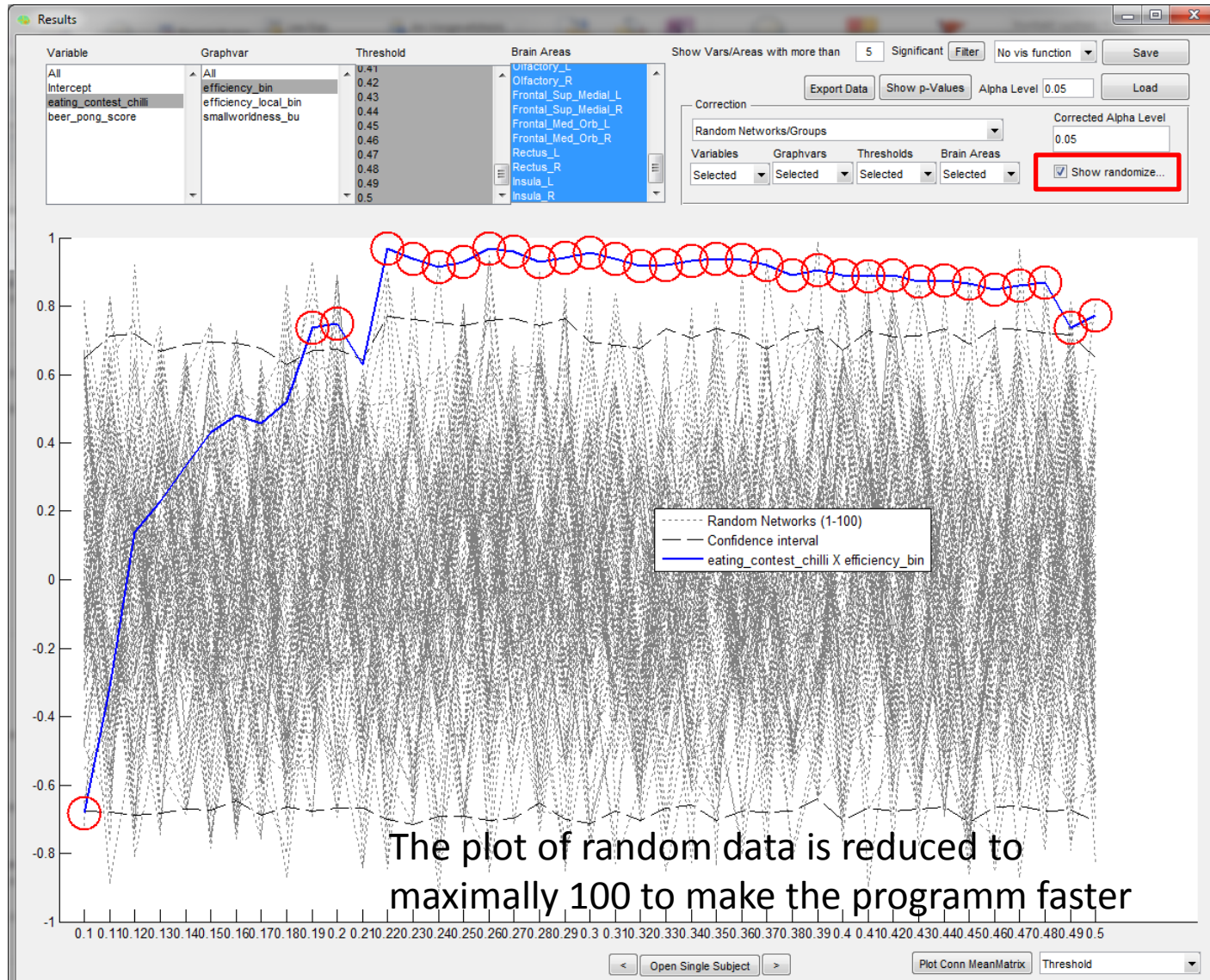
- Now, you should see the association of chilli eating contest scores, beer pong scores to global efficiency
- The red dots indicate where the correlation is significant according to the desired alpha level (which you can change here)



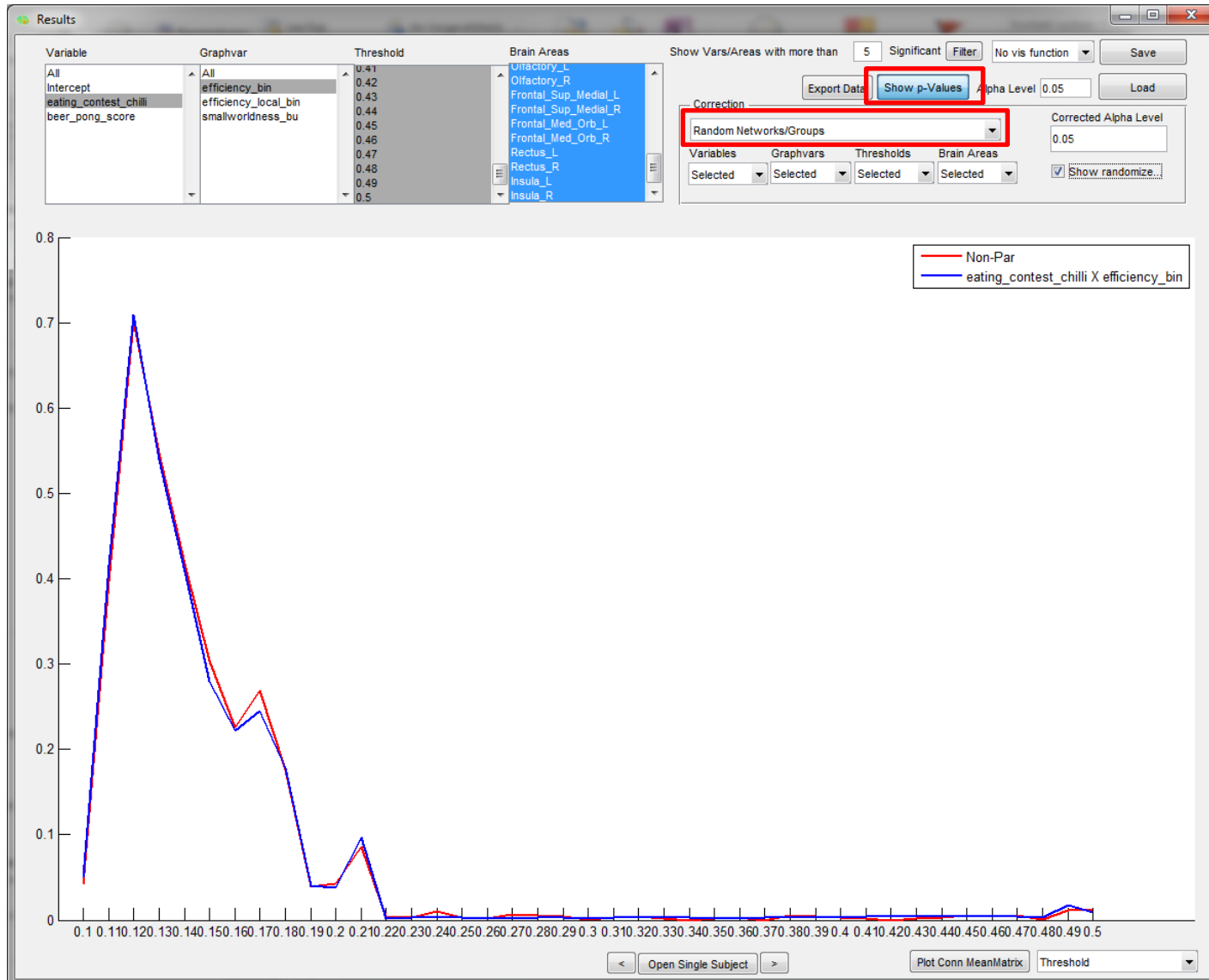
- To explore the p-values across thresholds select the „show p-Values“ button
- By hitting the button again the correlation appears again



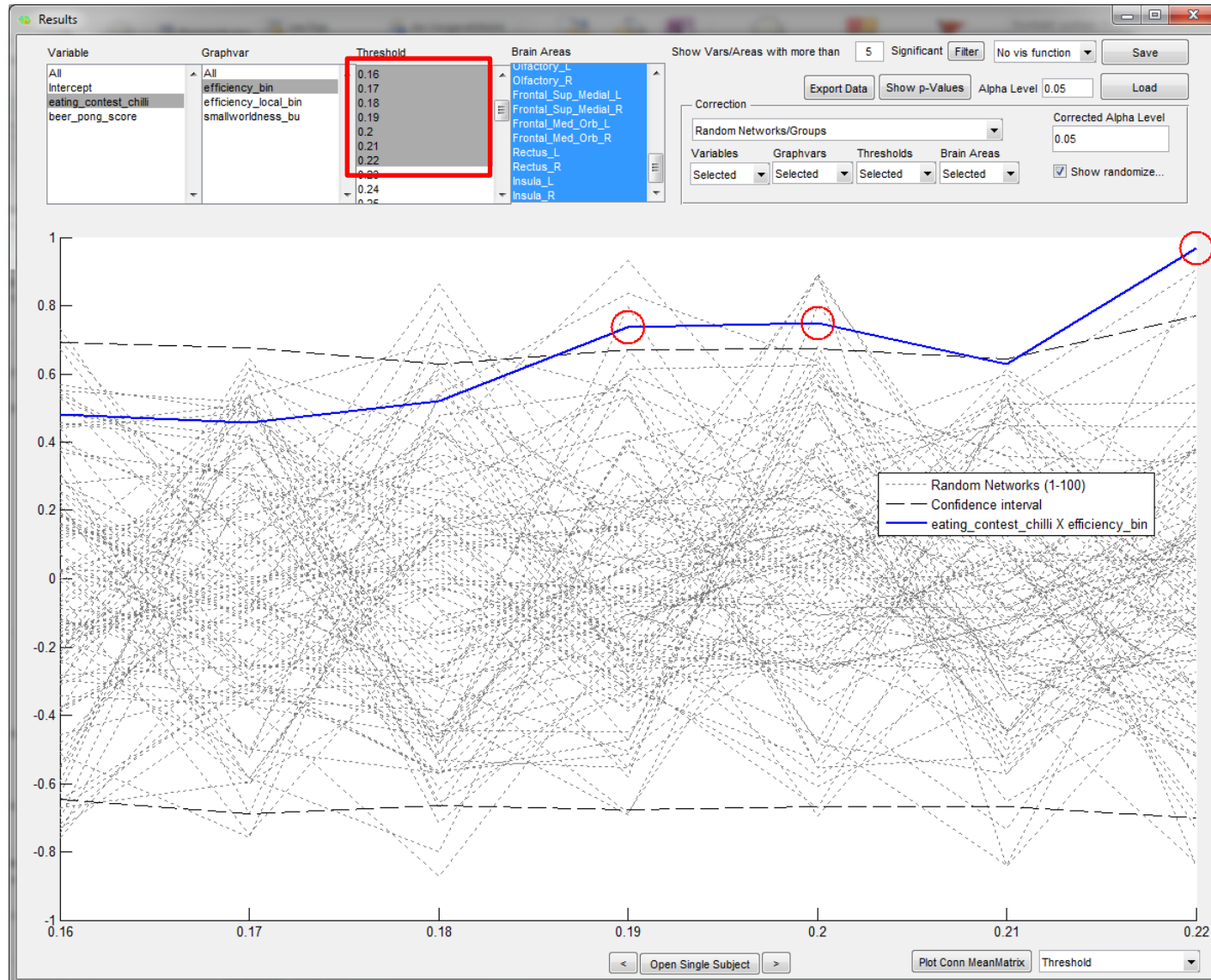
- To plot the non-parametric prediction of chilli scores and global efficiency derived from the random data (null-model distribution with 1000 permutations per threshold), select only „eating\_contest\_chilli“, select the correction method „Random Networks/Groups“ and click in „show randomize...“
- The confidence intervall (according to the selected alpha) and the null-model distribution appears
- You can drag and drop the legend box



- You can also explore the overlap of the parametric and non-parametric p-values
- Here, non-parametric p-values are nearly identical to the parametric distribution

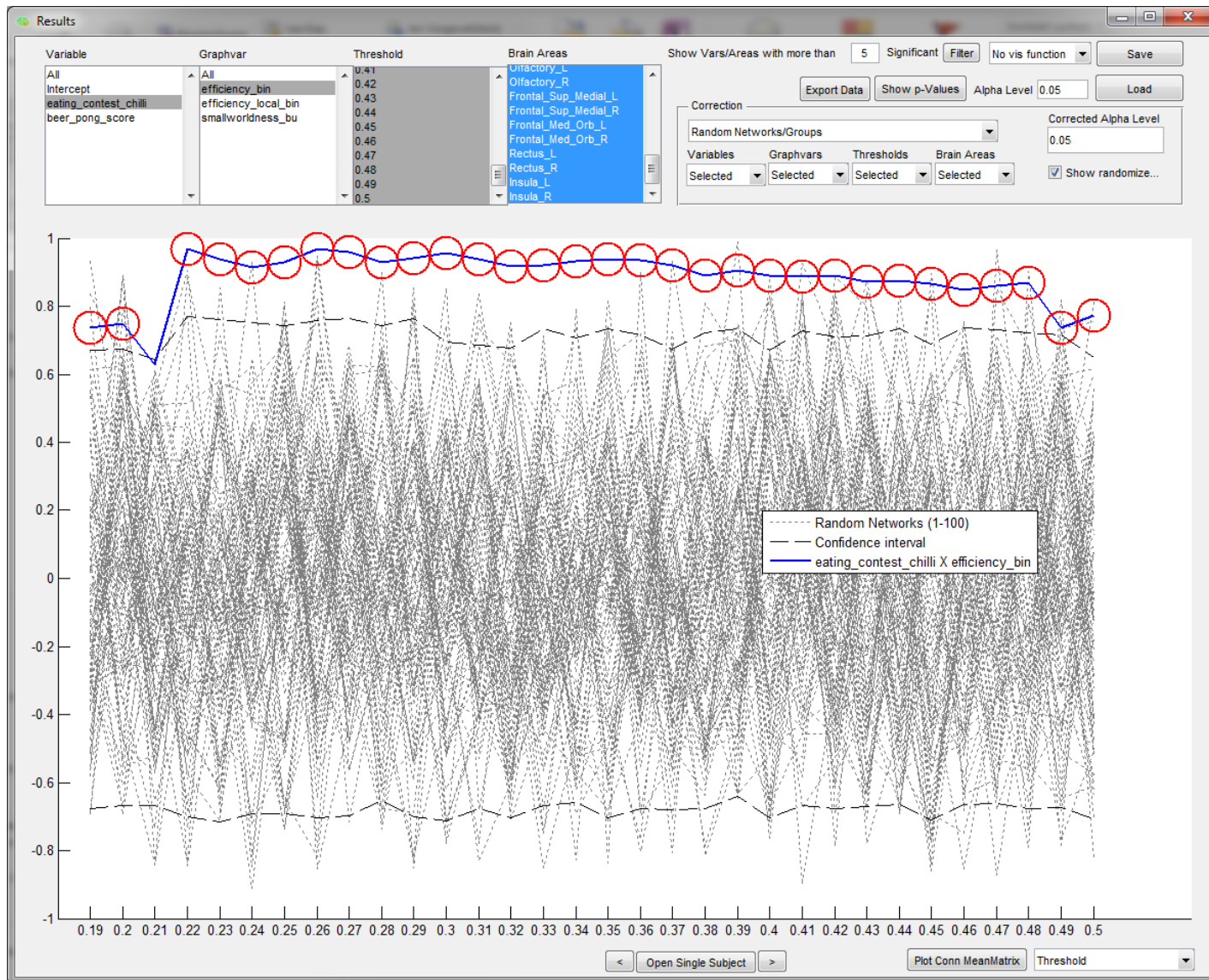


- By scaling down the thresholds, we notice that the association of global efficiency and chilli eating scores starts at a threshold of 0.19

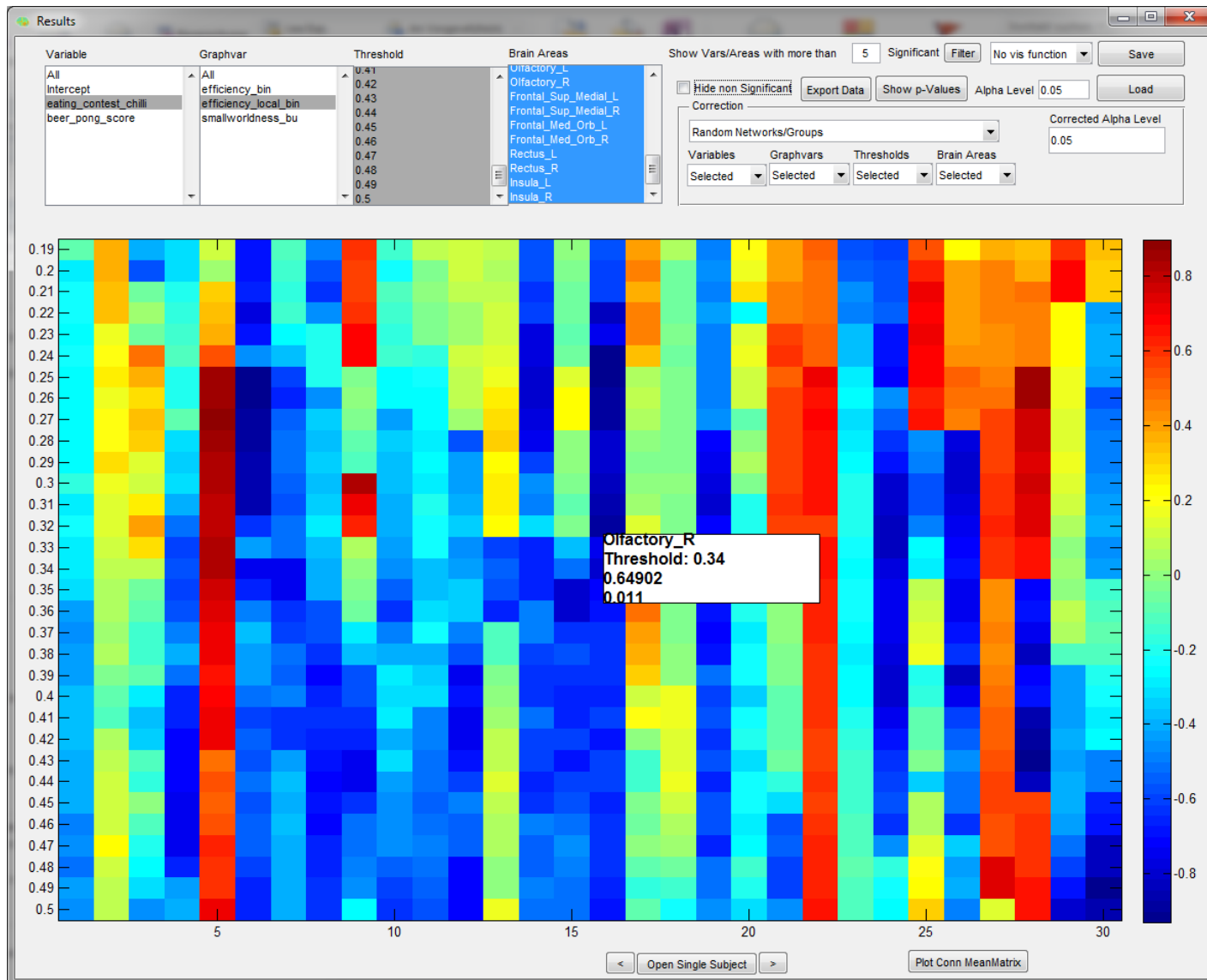




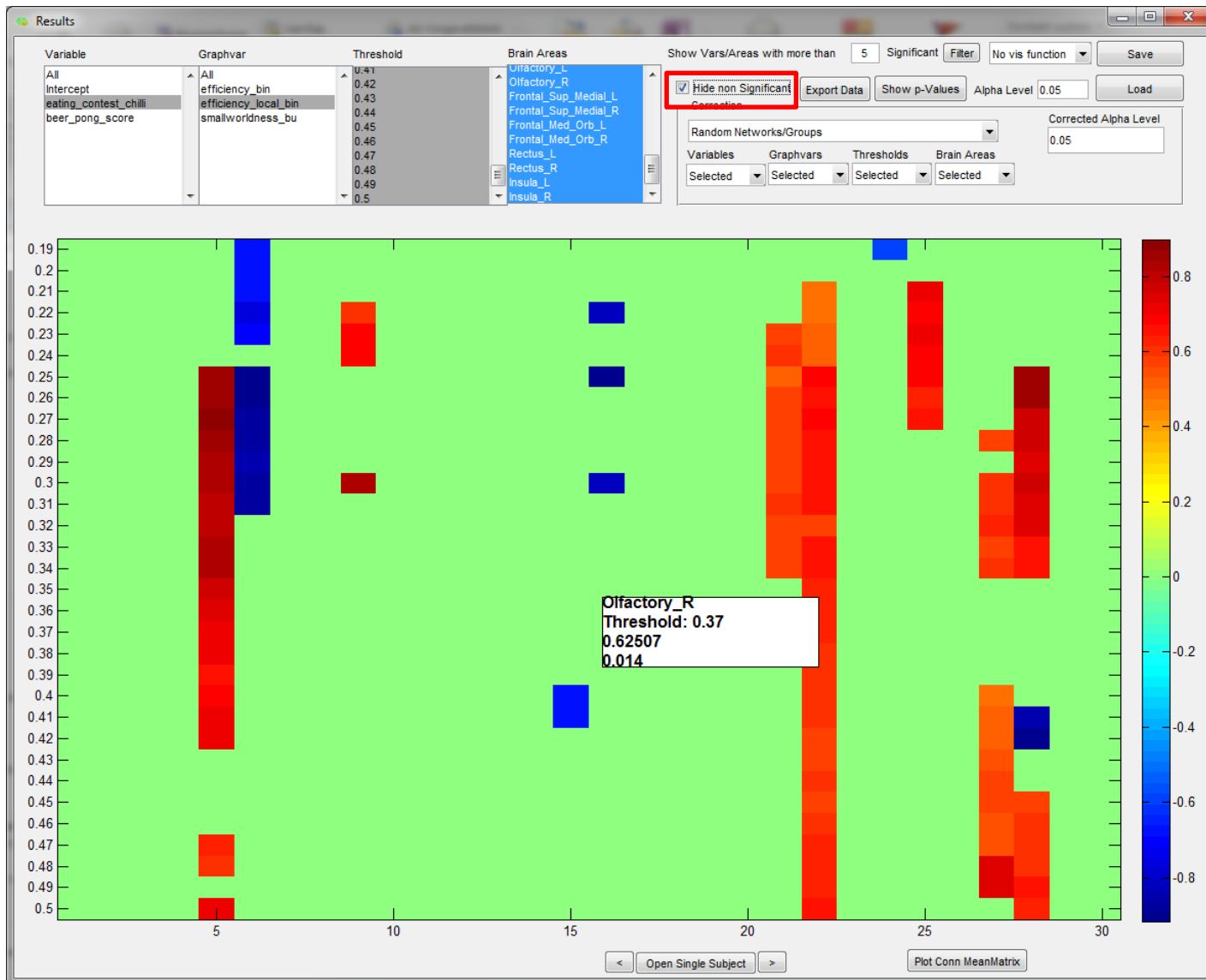
- Driven by this beautiful association of global efficiency and chilli eating scores, we now decide to explore the local efficiencies of all the regions in our chilli-responsive-network across the threshold range 0.19-0.5
- Specify the threshold range and select the Graphvar „efficiency\_local\_bin“



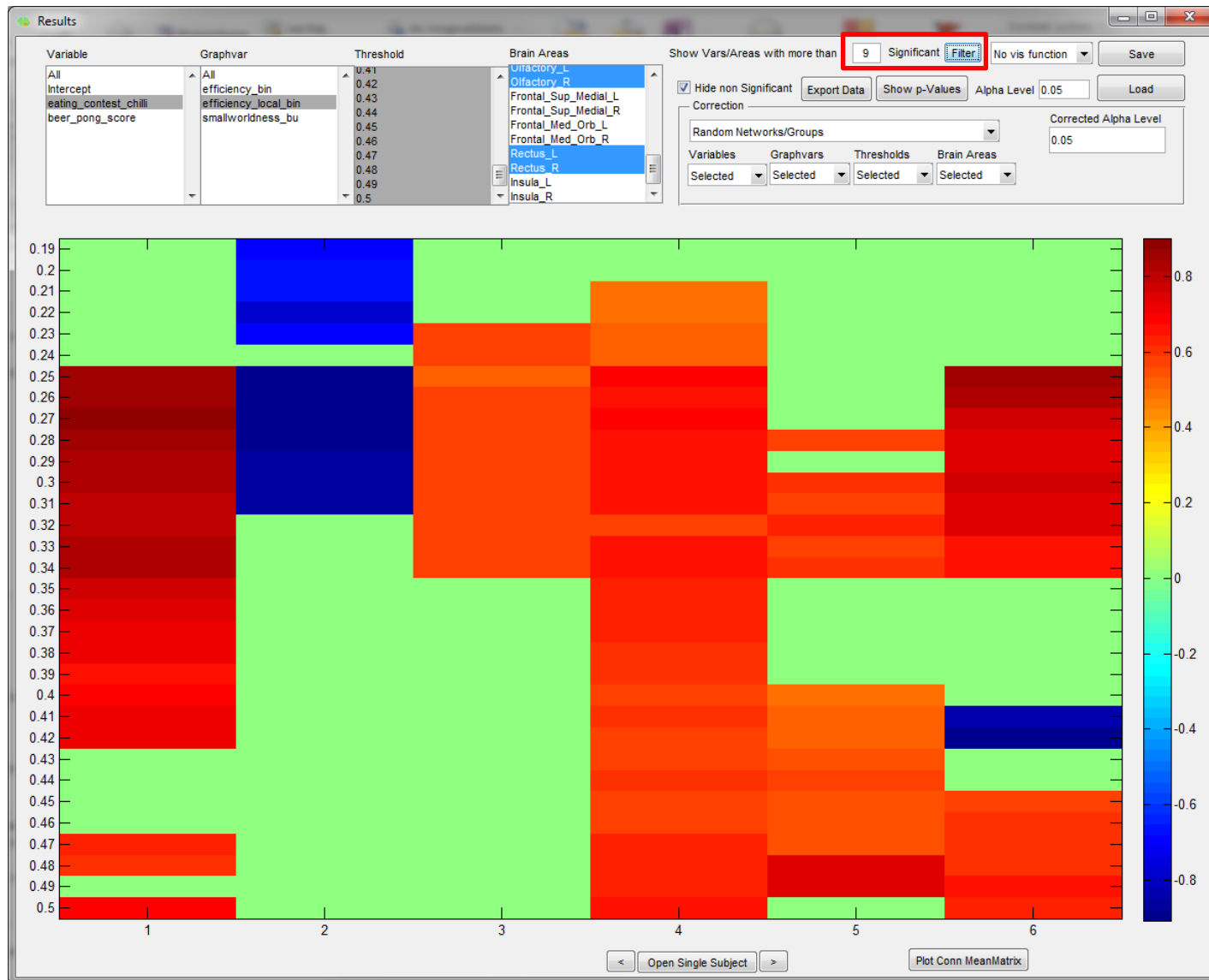
- Here you see the association of local efficiency of each of the 30 regions in the network to the chilli score
- Notice the mouse over box telling you the area, threshold, beta, and p-value



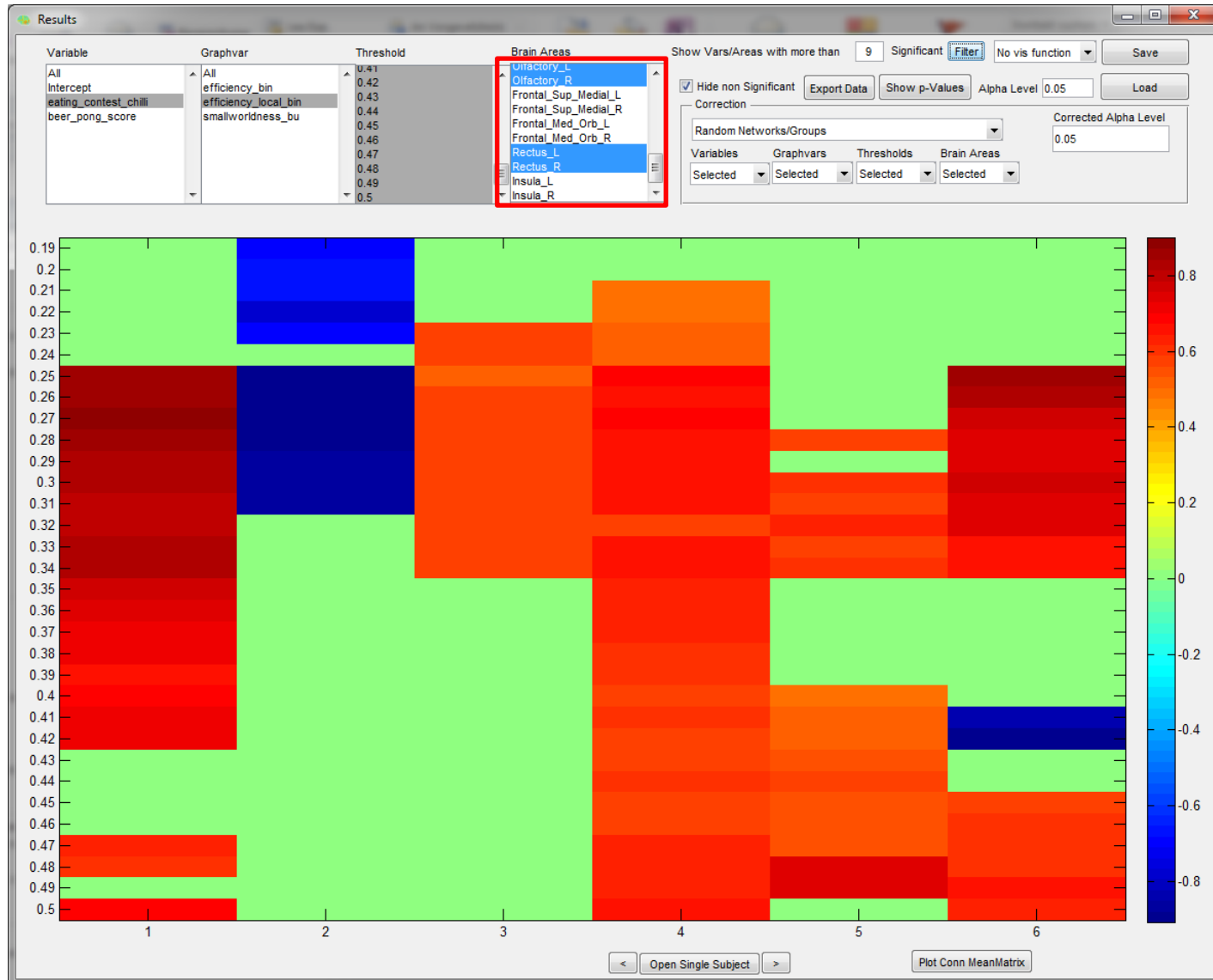
- FYI: it is possible to hide all non-significant associations



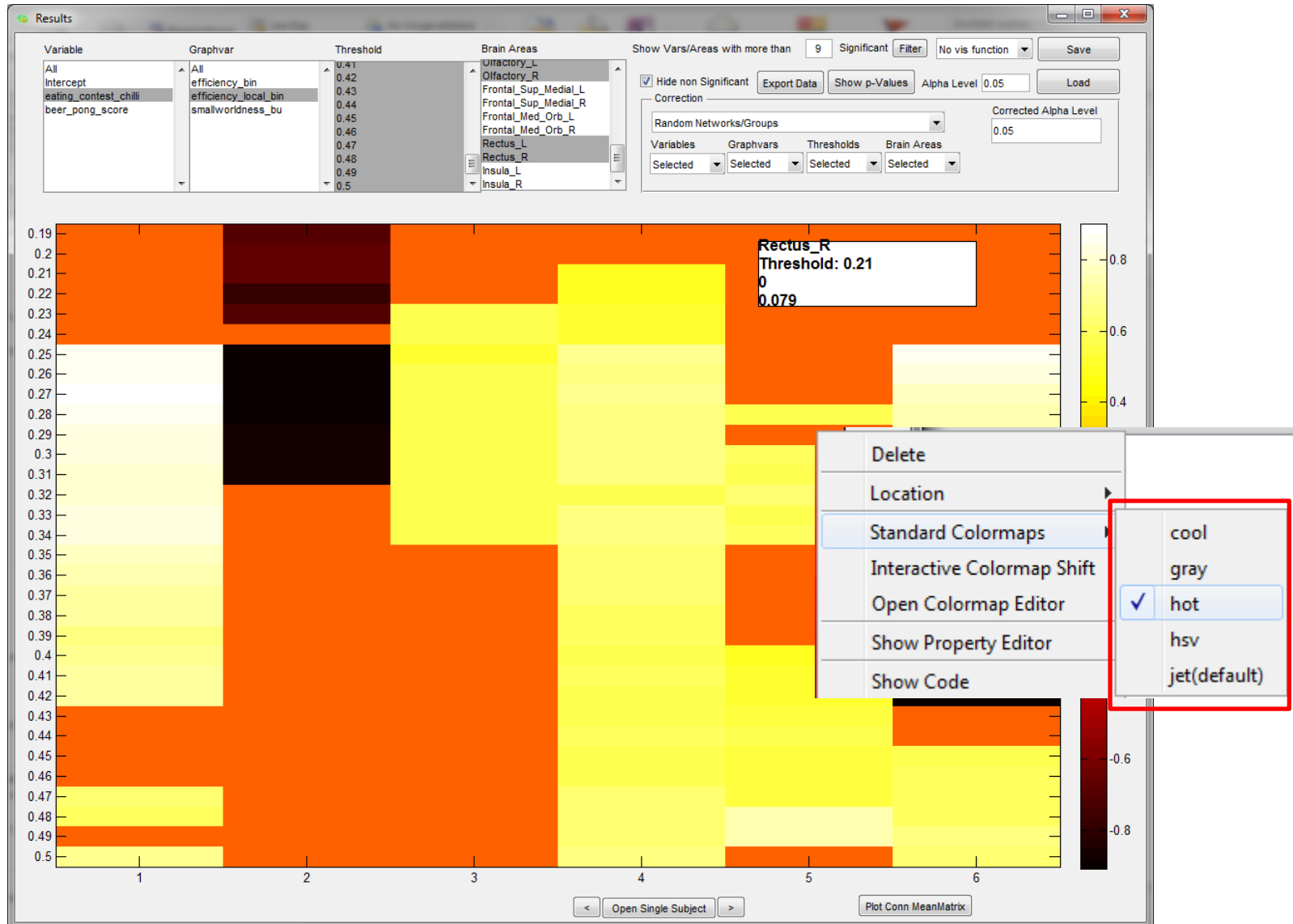
- If we a-priori determined that only significant associations on minimally 10 thresholds would be meaningful, we can use the build in filter function and set the number on 9 (i.e.,  $\text{thr} > 9$ )



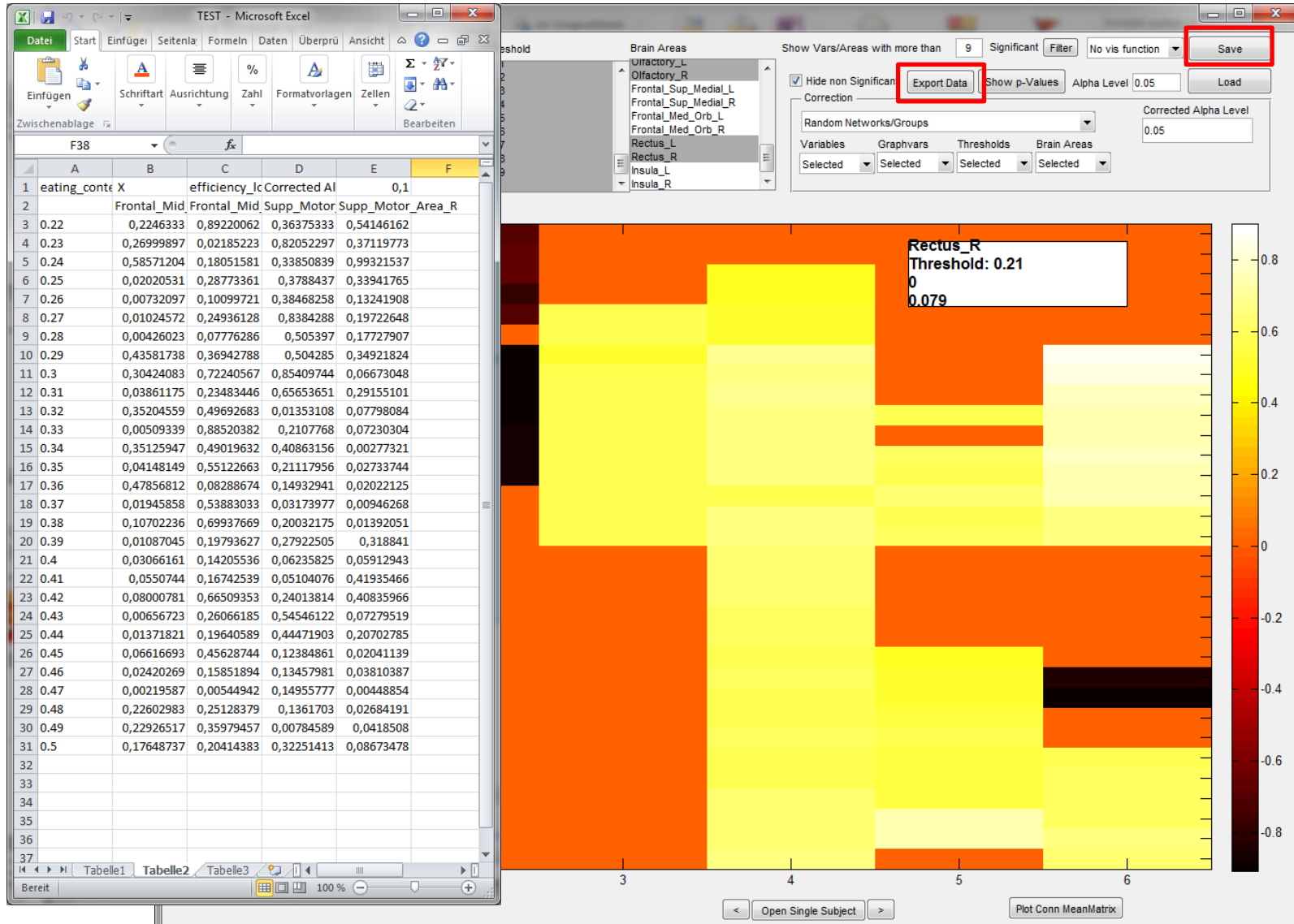
- Subsequently, the viewer will only show the areas with the specified criteria
- Note that these regions are highlighted in the „Brain Areas“ field.
- All subsequent actions will only apply to these regions (e.g. filtering)
- If you want the full network again you will have to select all nodes (ctrl+A)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



- 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 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  
Everything we have computed (global efficiency and local efficiency across thresholds) may be saved



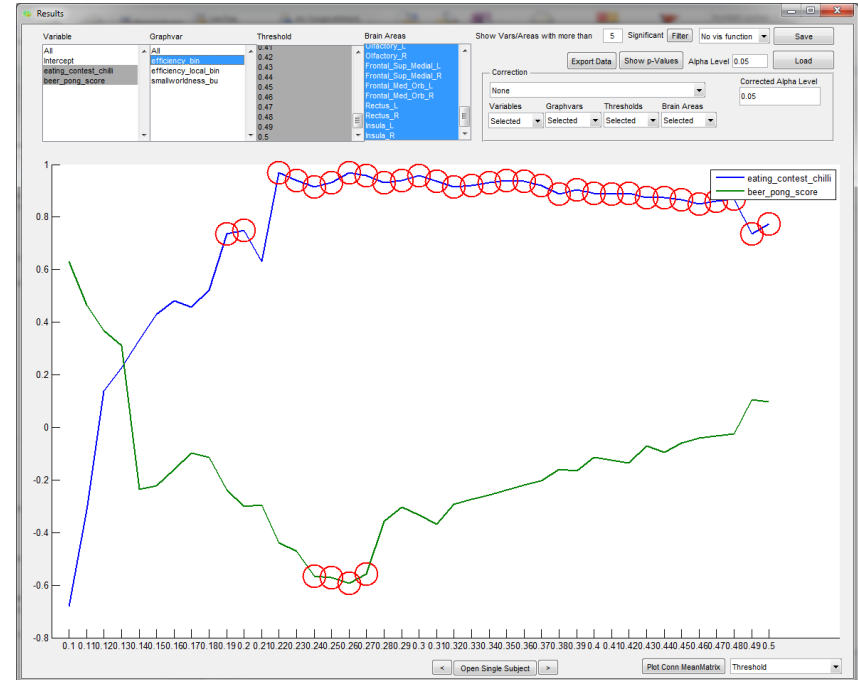
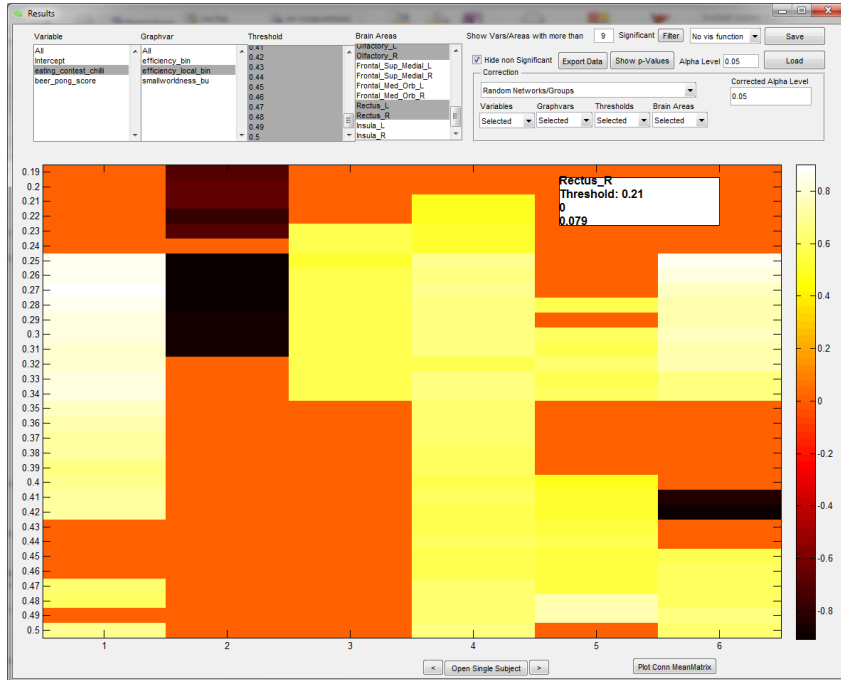


# Interpretation



## 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 the olfactory gyrus contribute here...with a positive correlation of local efficiency to chilli eating ... much more spicy information transfer here!



## **2. Group comparison (global efficiency)**

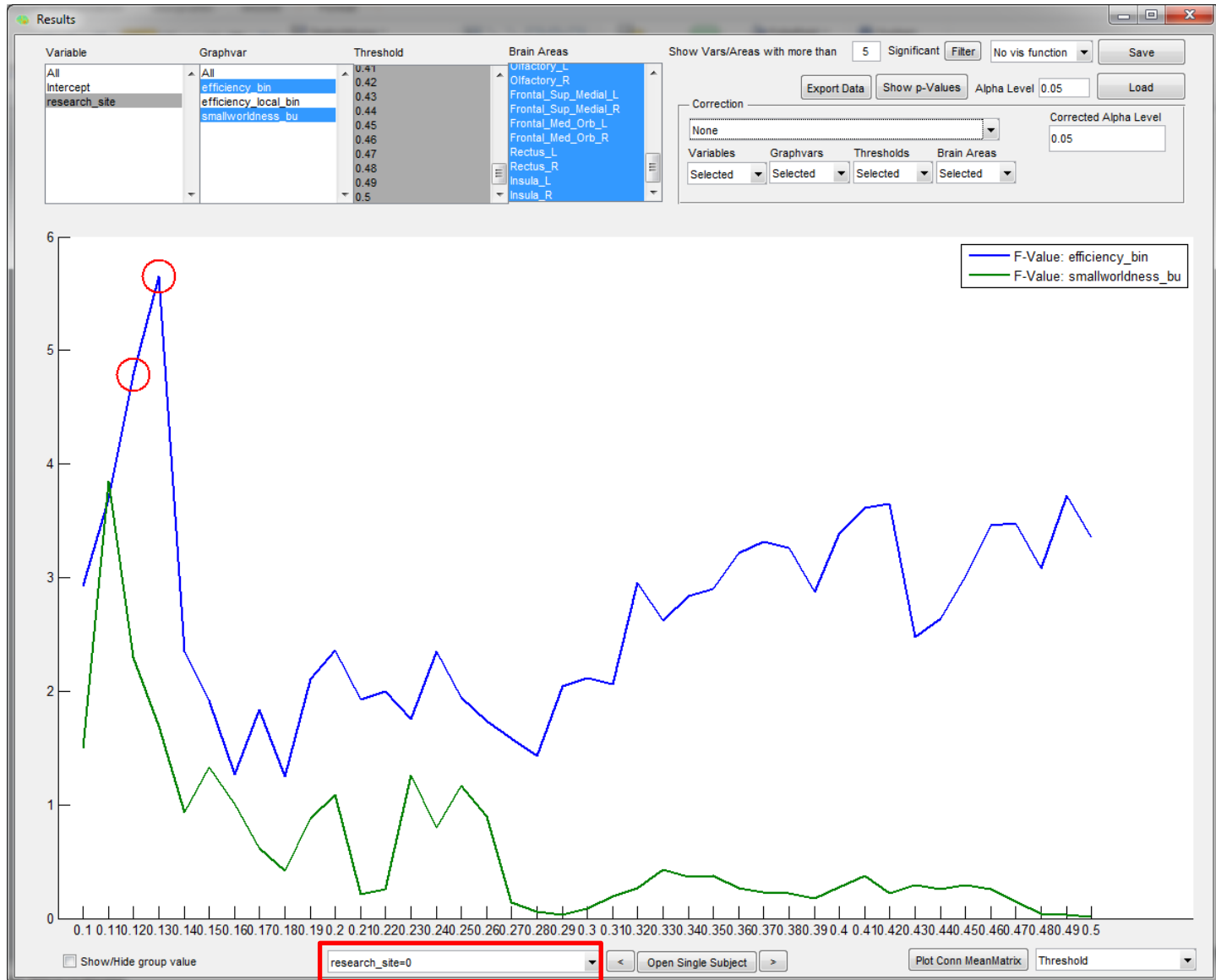
- Now, we can also go back and decide to do a group comparison (ANOVA) on the previously calculated efficiencies, where we regress out the influence of IQ and compute the model on the residuals
- Add „research site“ as a „between factor“, add „IQ“ as „nuisance covariate“ and „test against 1000 perm“
- Finally hit „Statistics with already calculated values“

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

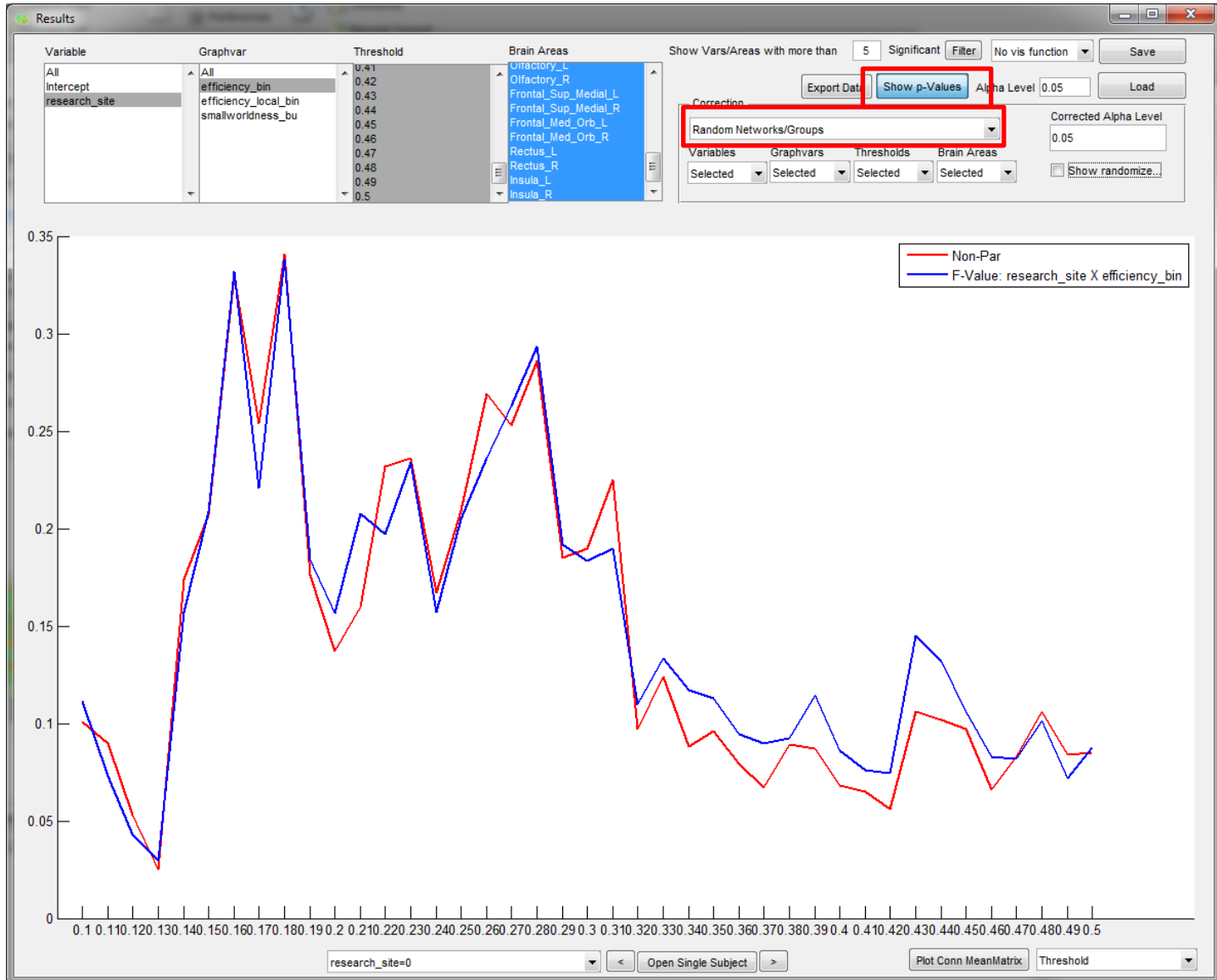
- General Settings:** Includes fields for 'Brain regions files' (BrainRegions.csv), 'File with Variables' (Variables.csv), and buttons for 'Select Subjects (Conn Matrix)' and 'Create Connectivity Matrix'. A list of subjects is shown, with the first one selected. 'Subjectname in Filename' is set to 'CorrMatrix\_sample\_20.mat'. 'Start' is 12, 'End' is 4. 'Corr Matrix Array' is 'CorrMatrix'. 'Save interim results' is checked, and 'Parallel Workers' is 32.
- Network Construction:** 'Threshold' is set to 'Relative'. 'Weights' are set to 'No Change'. 'Network nodes / Brain areas' includes 'Superior frontal gyrus, medial or', 'Gyrus rectus (Left)', 'Insula (Left)', and 'Insula (Right)'. 'Network thresholds' range from 0.41 to 0.5. 'Generate' is checked with 10 iterations. 'randomizer\_bin\_und' is selected. 'with' is 1. 'randomized subject data' is 'null model network'. 'Binary' is checked.
- Network Calculations:** 'Calculate graph metrics' is checked. A list of metrics is shown, including 'Binary: Efficiency global - UND', 'Binary: Eigenvector centrality - UND', etc. 'Normalize graph metric with random networks' is unchecked. 'Use random network to calc smallworldness' is checked. A 'Calculate variables and export' button is present.
- Raw Matrix (link wise):** 'Raw matrix' and 'Connectivity Thr.' are unchecked. 'r to z' is checked. 'Generate random networks' is unchecked. A list of values from .05 to .006 is shown.
- GLM:** 'Variables' include 'age', 'sex', 'fantasy\_score', 'eating\_contest\_chilli', and 'beer\_pong\_score'. 'Between covariates' is empty. 'Within covariates' is empty. 'Nuisance covariates' is 'IQ'. 'No Interactions' is selected. 'Graph metrics' are 'parametric' and 'rand NW'. 'Raw matrix' is 'parametric' and 'rand NW'. 'permutation' is selected for both, and '#Rep' is 1000.

At the bottom, there are buttons for 'Switch Workspace', 'Open Previous Results', 'Load interim results', 'Statistics with already calculated values' (highlighted with a red box), and 'Calculate & Statistics'.

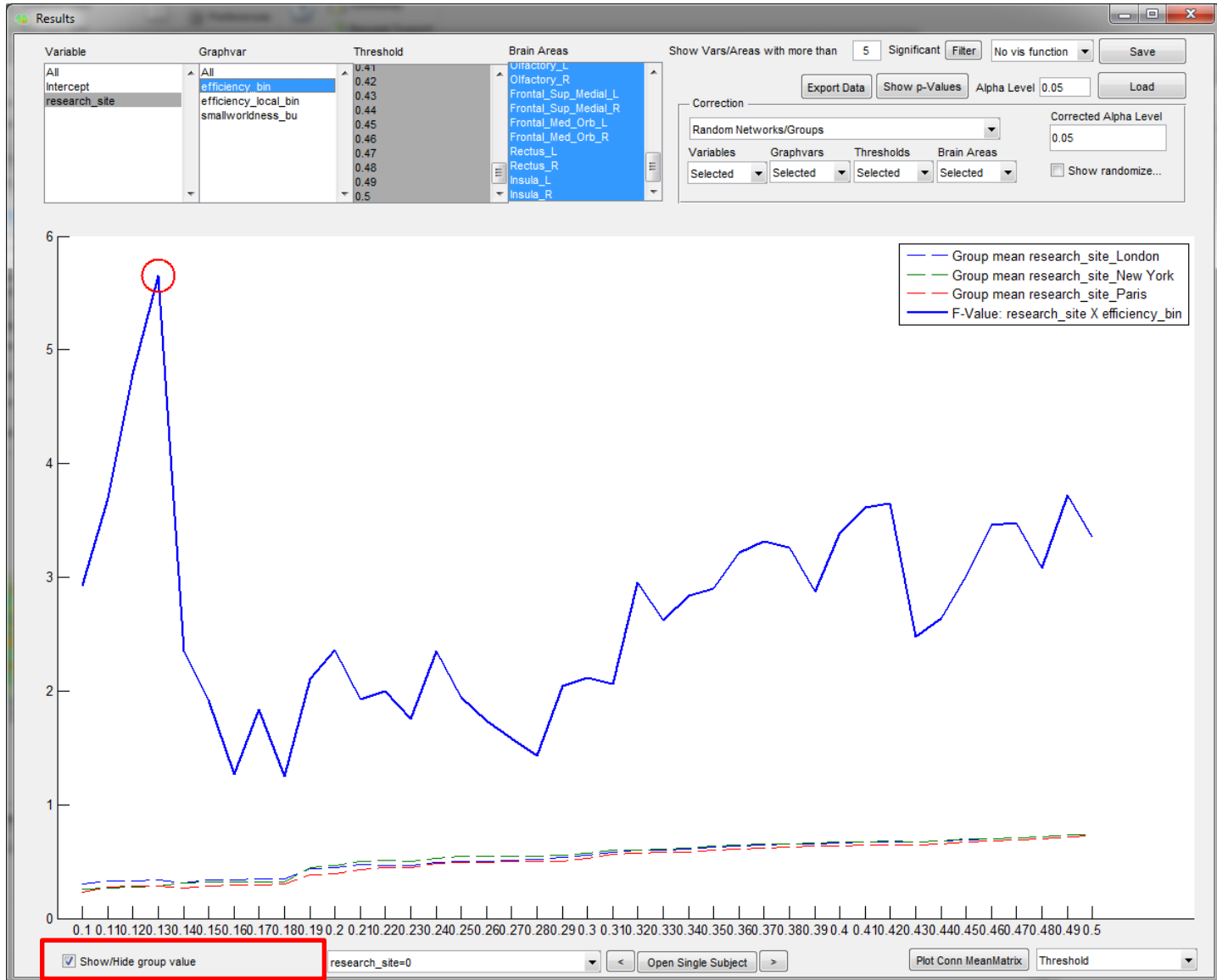
- You see the distribution of F values across thresholds for the group differences (i.e., factor research site) on global efficiency and small-worldness
- Red dots again indicate significance



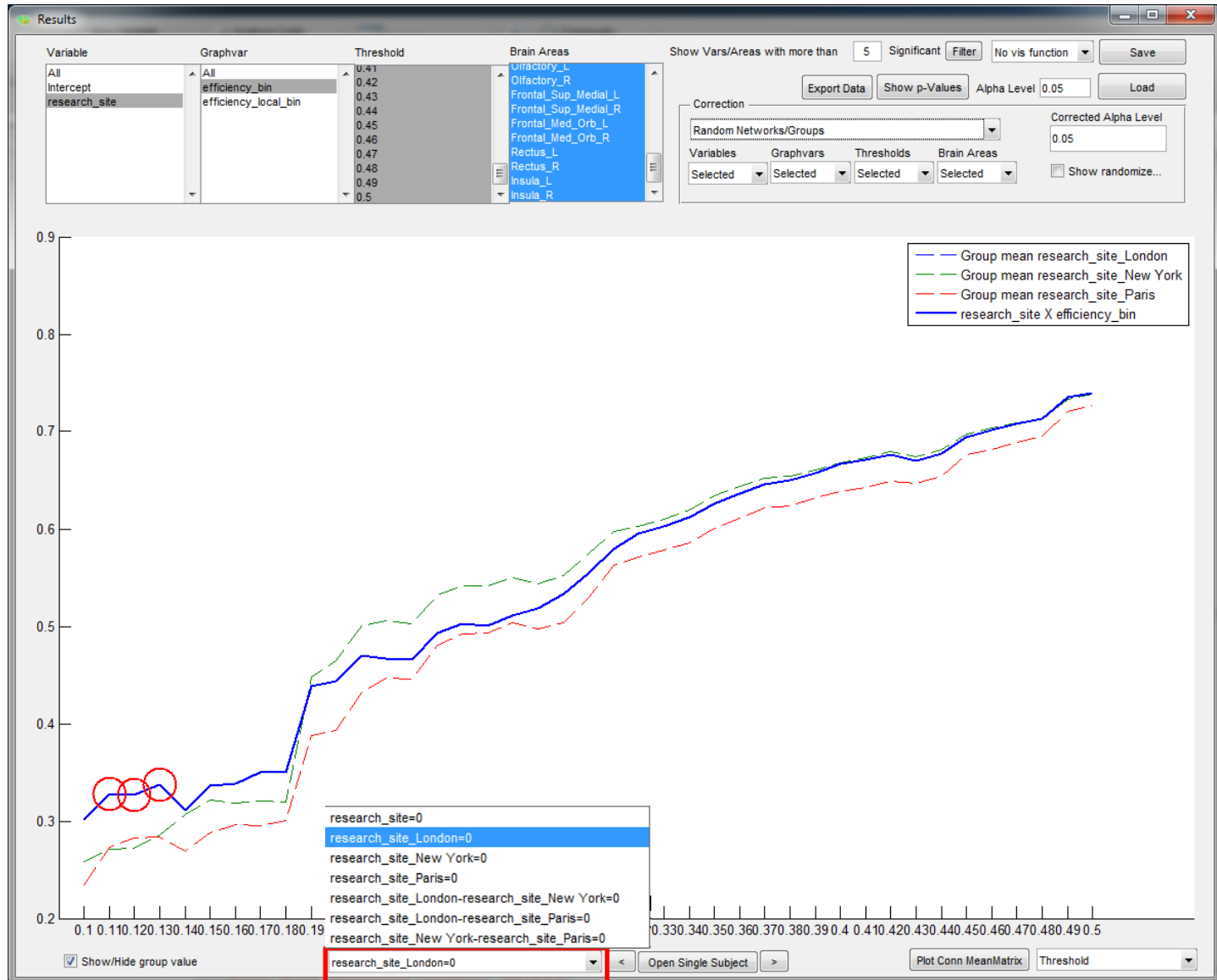
- Plot the parametric and non-parametric p-values ...



- Select only „efficiency\_bin“
- Explore how the groups contribute to this effect by selecting „Show/Hide group value“

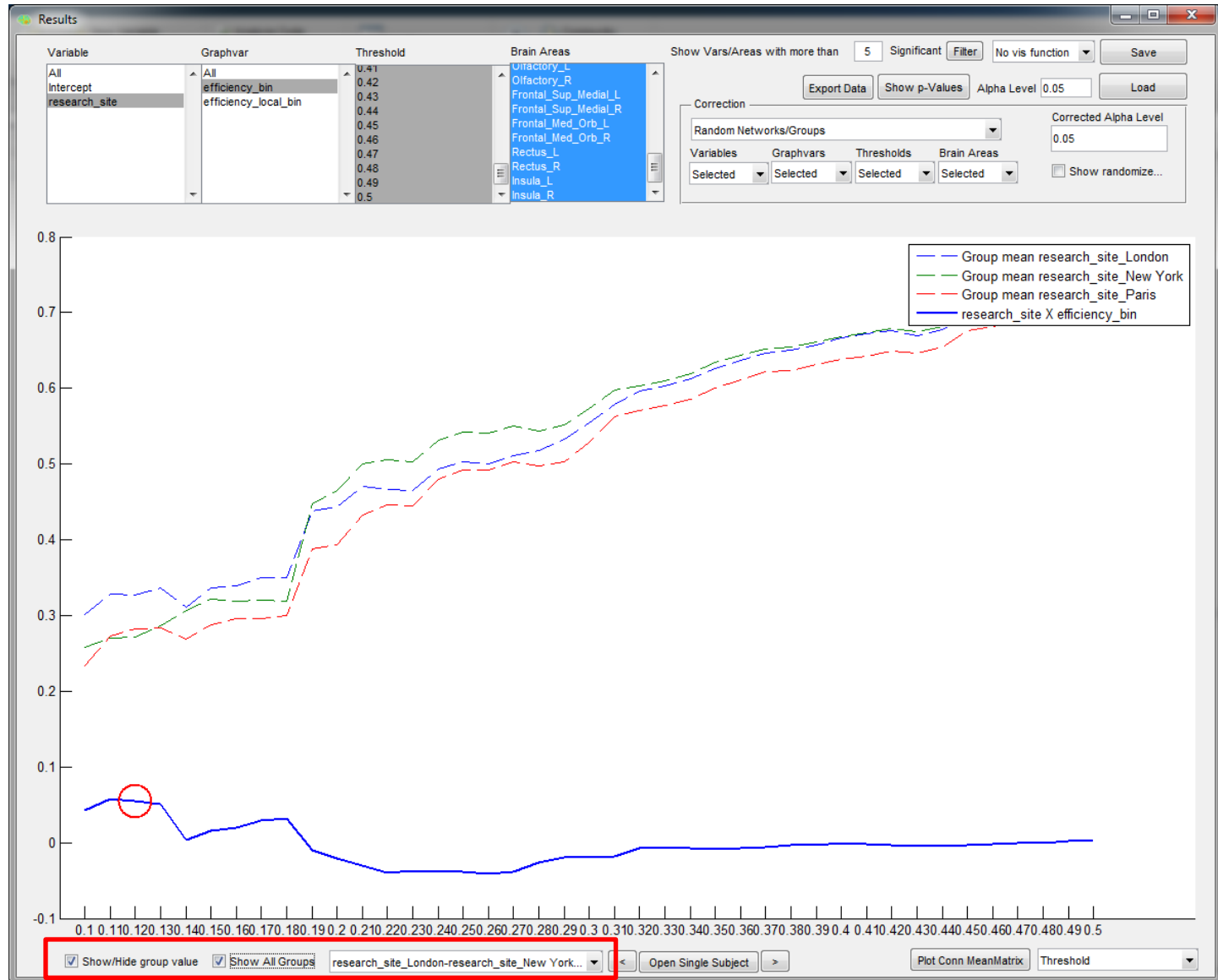


- Examine the mean of „efficiency\_bin“ for each single group (i.e., significance test against zero)
- The blue line shows the group mean for the selected group

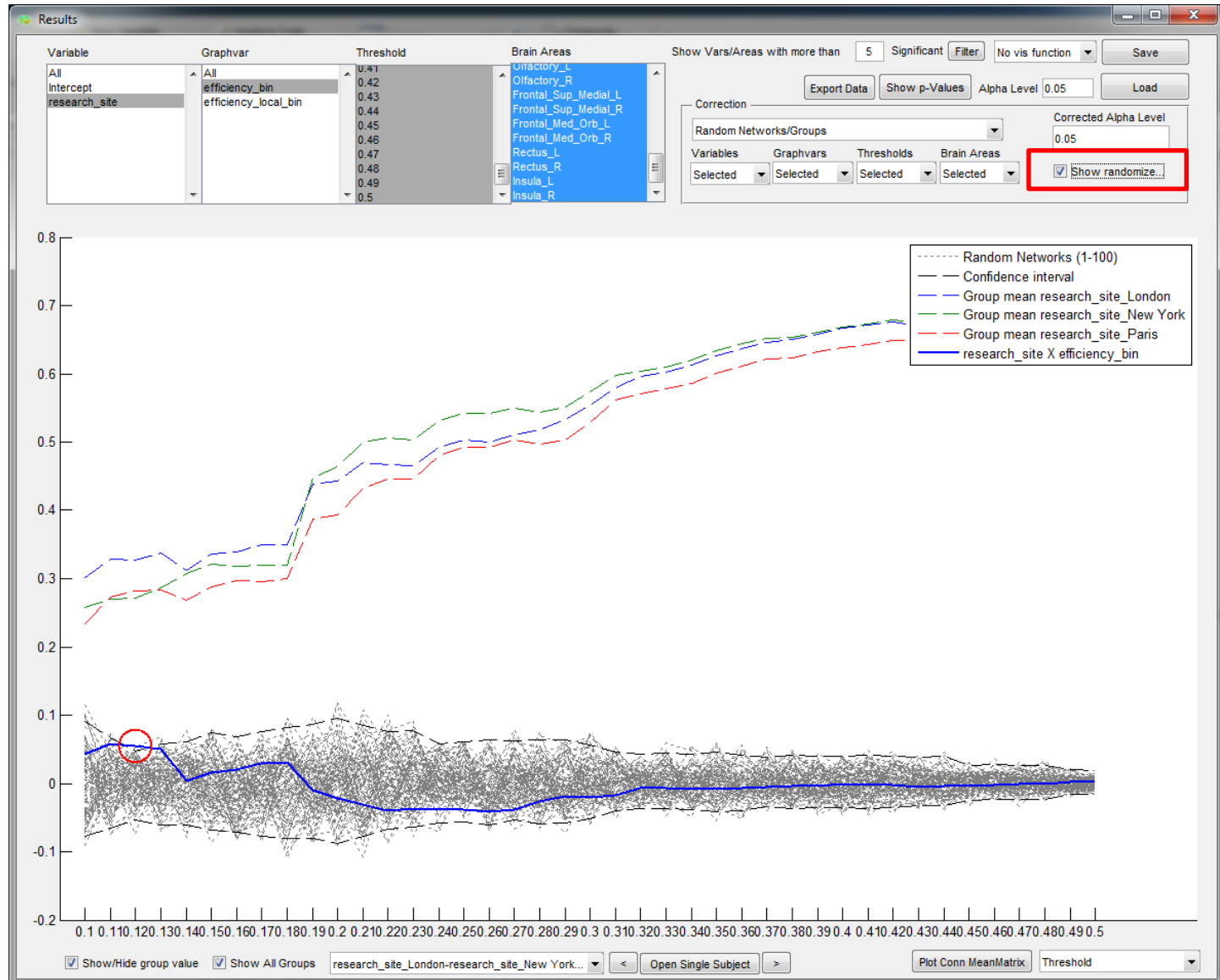




- Perform pair-wise comparisons by switching through the group contrasts (here: London vs. NewYork)
- The blue line shows the group difference for the specific contrast



- Examine the permutation testing derived null-model distribution for the selected contrast
- You can see how the confidence interval will change with decreasing alpha values (e.g. 0.001)



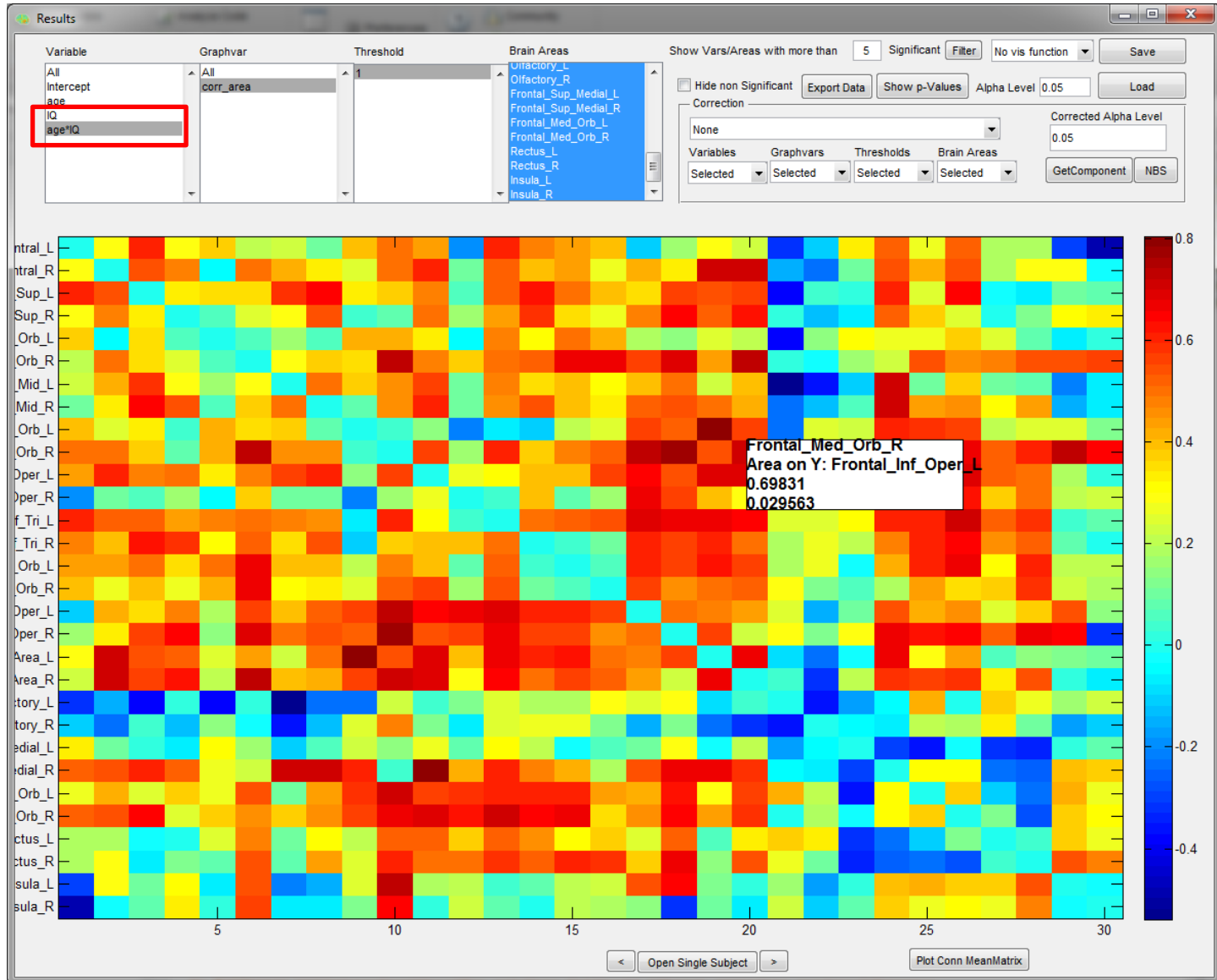
# **3. Raw Conn Matrix and Network Based Statistics**

- Let's try some computations on the raw correlation matrices!
- Deselect „Calculate graph metrics“ and only use the following setting in:

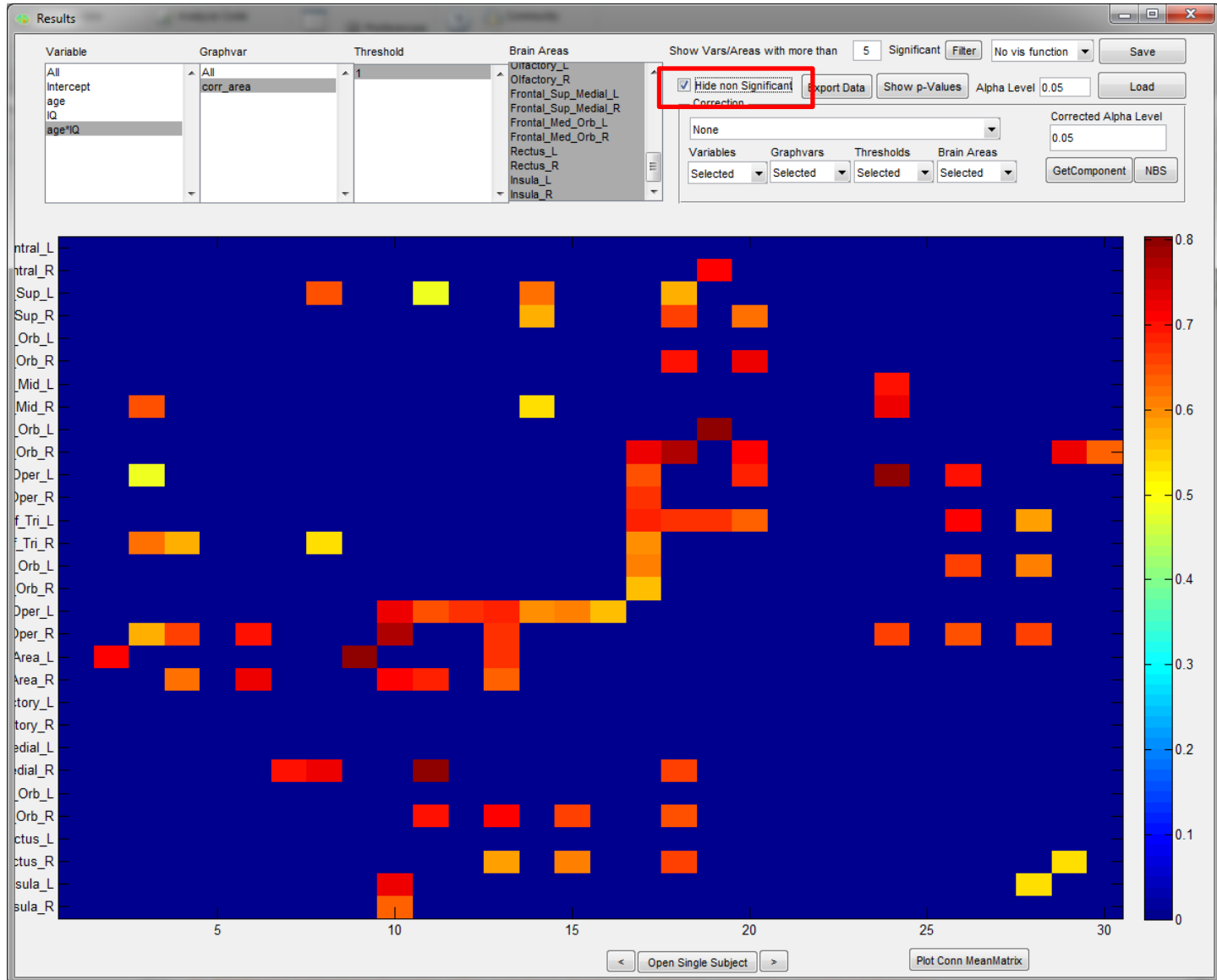
The screenshot shows the GraphVar software interface with the following settings:

- General Settings:** Brain regions files: BrainRegions.csv; File with Variables: Variables.csv; Subjects: C:\Users\kruschwi\Desktop\new\neue Version t; Subjectname in Filename: CorrMatrix\_sample\_20.mat; Start: 12; End (remaining characters): 4; Corr Matrix Array: CorrMatrix; Save interim results: checked; Parallel Workers: 32.
- Network Construction:** Threshold: Relative; Weights: No Change; Network nodes / Brain areas: Superior frontal gyrus, medial (R), Superior frontal gyrus, medial or, Superior frontal gyrus, medial or, Gyrus rectus (Left), Gyrus rectus (Right), Insula (Left), Insula (Right), Anterior cingulate and paracingu; Network thresholds: 0.1, 0.11, 0.12, 0.13, 0.14, 0.15, 0.16, 0.17, 0.18, 0.19; Generate: unchecked; randomized subject data (null model network): unchecked; CheckFrag: button.
- Network Calculations:** Calculate graph metrics: checked; Brain graph metrics: Binary: Cost efficiency global (Absolute or Signif), Binary: Degree - UND, Binary: Degree - DIR, Binary: Density - UND, Binary: Density - DIR, Binary: Distance Matrix - UND/DIR, Binary: Eccentricity - UND/DIR, Binary: Edge betweenness centrality - UND/DIR, Binary: Efficiency global - UND, Binary: Efficiency local - UND; 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: checked; Connectivity Thr.: unchecked; r to z: checked; Generate random networks: unchecked; Weights: No Change; GLM: Variables: sex, research\_site, beer\_pong\_score, fantasy\_score, eating\_contest\_chilli; Between covariates: age, IQ; Between factors: ; Within covariates: ; Nuisance covariates: ; Interactions 1st order; Graph metrics: parametric, rand NW, permutation; Raw matrix: parametric, rand NW, permutation; #Rep: 1000.

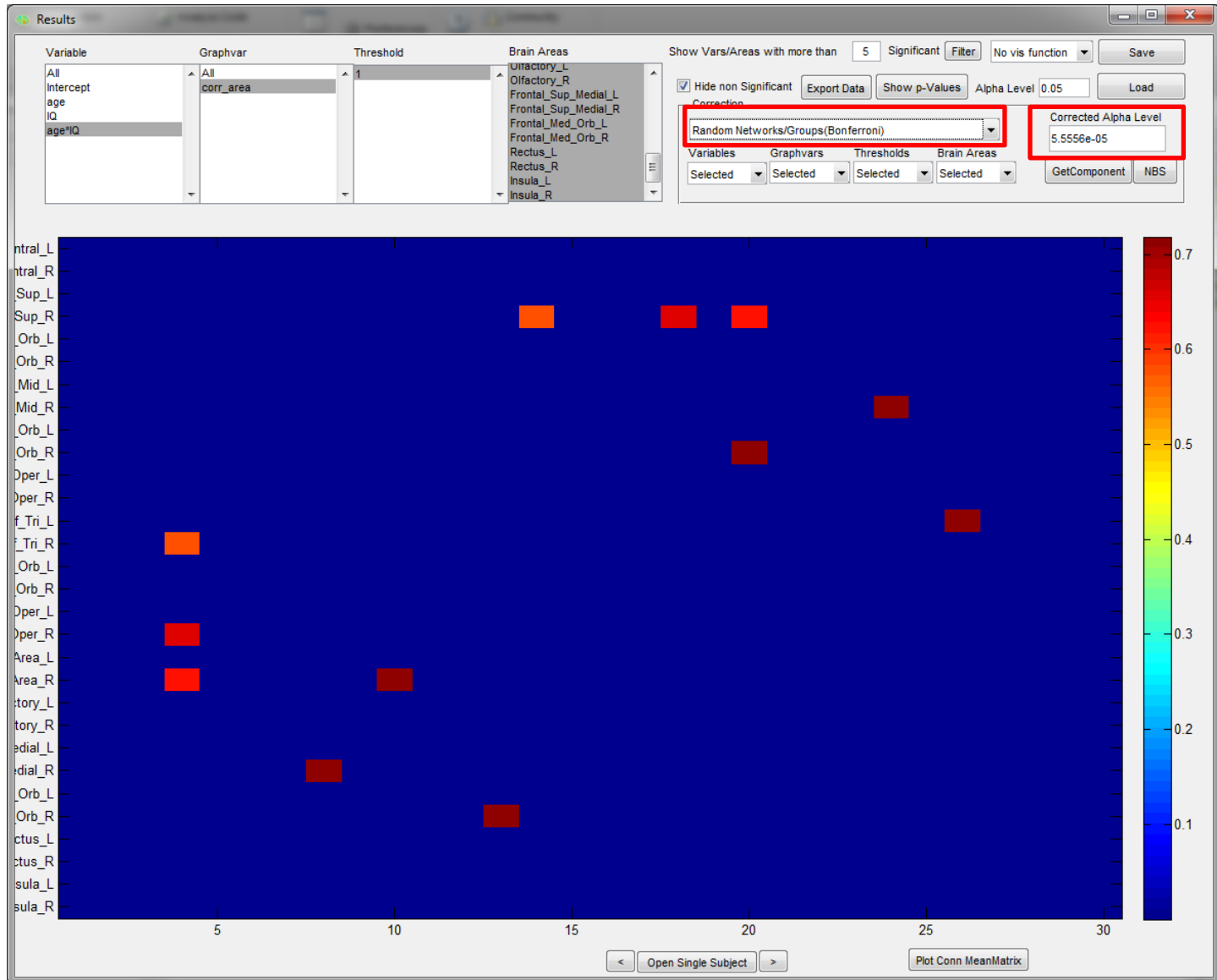
- This is the interaction of age and IQ and the raw connectivities between the nodes in the 30x30 matrix



- Show only the significant brain areas for the selected interaction by selecting the „hide non significant“ button
- FYI: in the „brain areas field“ you can also select only some areas to be plotted

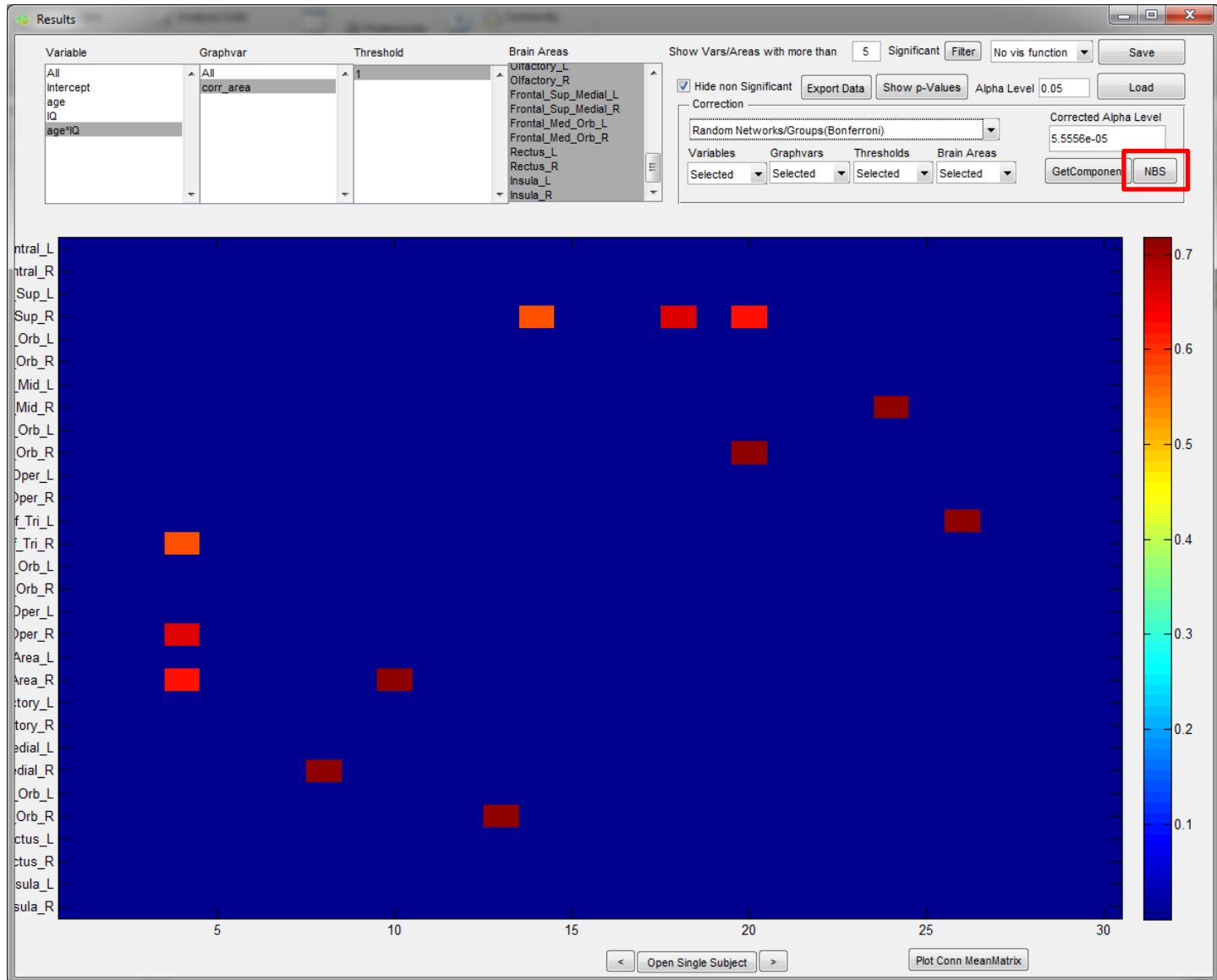


- Select the non-parametric results and apply the Bonferroni correction method: observe also the corresponding corrected alpha level (you may also try FDR correction)

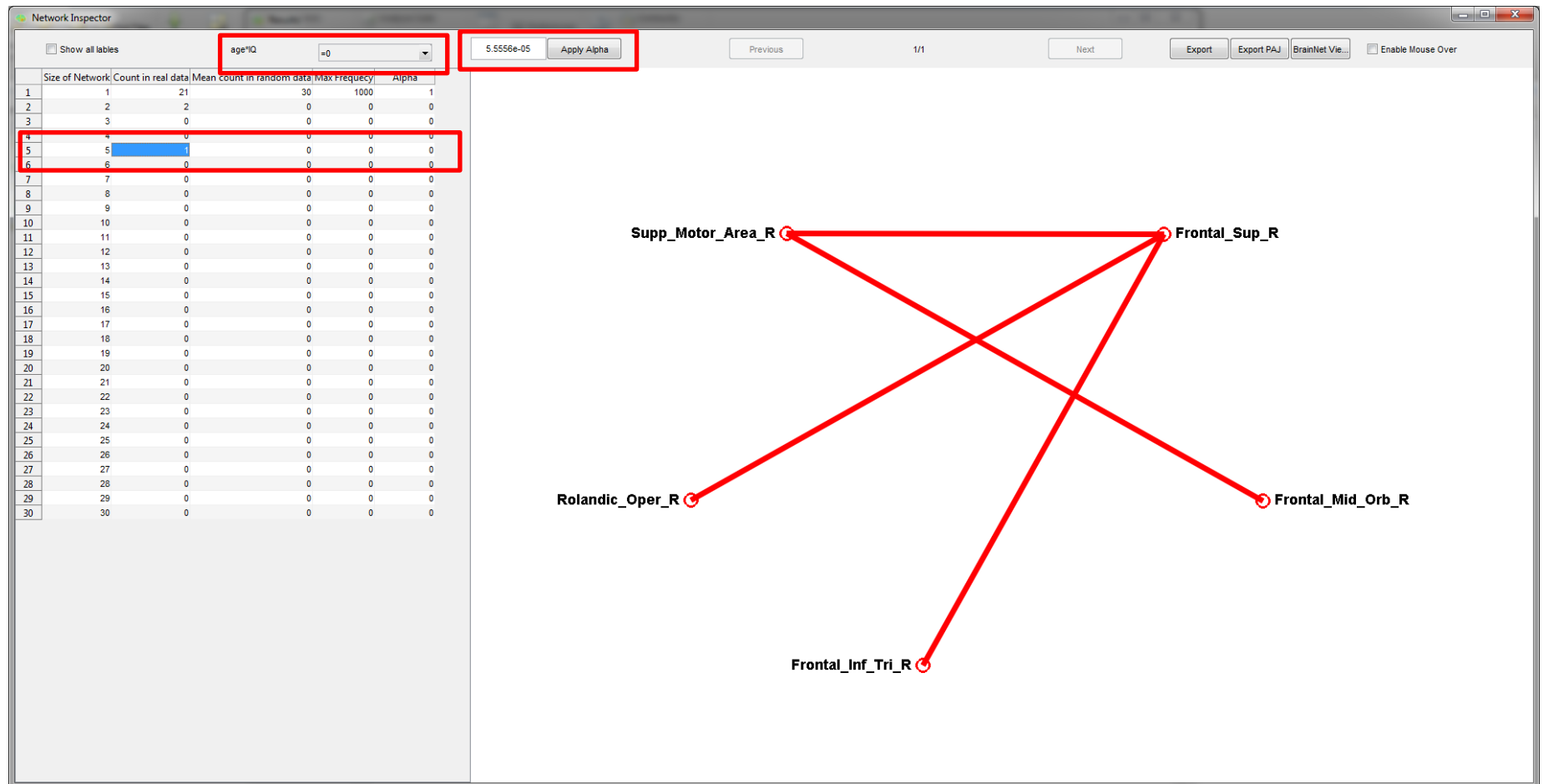




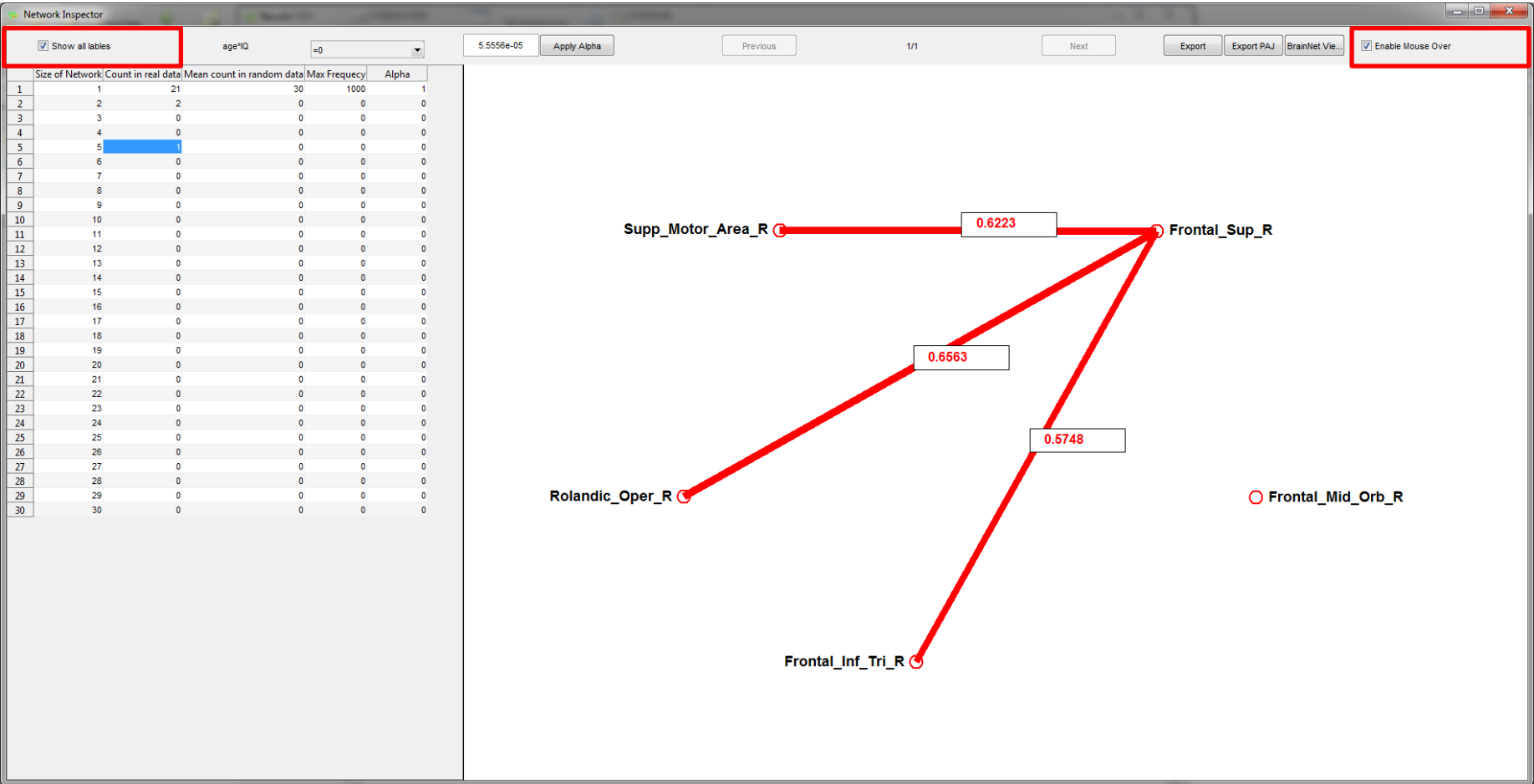
- You can now perform NBS! Note that for NBS the selected correction method will provide the p-values for the „initial-link-thresholding“ (here we take the non-parametric Bonferroni corrected p-values)
- Hit the „NBS“ button (for the „get component button please refer to the PDF „new features beta 0.62“)



- The initial-link threshold is carried over from the results viewer (here: non-parametric)
- And observe a significant graph component comprised of 12 nodes for the interaction
- The selection box allows you to plot positive and/or negative associations (here we only have positive)
- 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 shows the Network Inspector interface. On the left is a table with network statistics. On the right is a graph with three nodes: Supp\_Motor\_Area\_R, Frontal\_Sup\_R, and Frontal\_Mid\_Orb\_R, connected by red lines. An 'Export' button is highlighted with a red box in the top right. A 'component-r - Editor' dialog is open in the foreground, displaying a matrix of connectivity values.

Size of Network	Count in real data	Mean count in random data	Max Frequency	Alpha
1	1	21	30	1000
2	2	2	0	0
3	3	0	0	0
4	4	0	0	0
5	5	0	0	0
6	6	0	0	0
7	7	0	0	0
8	8	0	0	0
9	9	0	0	0
10	10	0	0	0
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

component-r - Editor

	Frontal_Sup_R	Frontal_Mid_Orb_R	Frontal_Inf_Tri_R	Rolandic_Oper_R	Supp_Motor_Area_R
Frontal_Sup_R	0	0.778	0	0	0
Frontal_Mid_Orb_R	0.778	0	0.146	0.001	0
Frontal_Inf_Tri_R	0	0.146	0	0.061	0.083
Rolandic_Oper_R	0.001	0.061	0	0.414	0
Supp_Motor_Area_R	0	0	0.083	0.414	0

- 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**

The screenshot displays the BrainNet Viewer software interface. On the left, the 'Network Inspector' window shows a table with network statistics. The 'BrainNet Viewer' window shows a 3D brain model with a network graph overlaid. A red box highlights the 'BrainNet Vie...' button in the top right corner of the Network Inspector window. A red arrow points from the 'Supp\_Motor\_Area\_R' node in the network graph to the BrainNet Viewer window.

Size of Network	Count in real data	Mean count in random data	Max Frequency	Alpha
1	21	30	1000	1
2	2	0	0	0
3	0	0	0	0
4	0	0	0	0
5	1	0	0	0
6	0	0	0	0
7	0	0	0	0
8	0	0	0	0
9	0	0	0	0
10	0	0	0	0
11	0	0	0	0
12	0	0	0	0
13	0	0	0	0
14	0	0	0	0
15	0	0	0	0
16	0	0	0	0
17	0	0	0	0
18	0	0	0	0
19	0	0	0	0
20	0	0	0	0
21	0	0	0	0
22	0	0	0	0
23	0	0	0	0
24	0	0	0	0
25	0	0	0	0
26	0	0	0	0
27	0	0	0	0
28	0	0	0	0
29	0	0	0	0
30	0	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.

Version 1.43 Released 20131227  
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# 4. Within design I (change of efficiency T1 T2)

## **Research option 1 - example:**

*investigate the association between a constant independent variable (e.g. sex or genotype) and a changing dependent network variable (e.g. efficiency in T1 and T2)*

- Select the „Variables\_Within\_Design“ sheet under .../workspaces/SampleWorkspace
- Notice: **Scan\_ID** (one subject = T1: sample\_01a, T2: sample\_01b) and **Subj\_ID** (sample 1)

**GraphVar - Chilli\_Contest**

General Settings

Brain regions files: BrainRegions.csv [Select]

File with Variables: Variables.csv [Select]

Select Subjects (Conn Matrix)

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  No Change

Weights

No Change  negative weights

Network nodes / Brain

Precentral gyrus (Left)

Precentral gyrus (Right)

Superior frontal gyrus

Superior frontal gyrus

Superior frontal gyrus

Middle frontal gyrus (Left)

Middle frontal gyrus (Right)

Generate

randomized subject data (null model network)

Raw Matrix (link wise)

Raw matrix

Connectivity Thr.

Weights

No Change  negative weights

Load in

**Variables\_Within\_Design\_15 - Microsoft Excel**

	A	B	C	D	E	F	G	H	I
1	Scan_ID	Subj_ID	age	sex	research_site	IQ	eating_content	beer_pong_score	fantasy_score
2	sample_01a	sample_01	2	female	New York	100	13	13	68,1
3	sample_02a	sample_02	4	female	New York	130	15	15	23,9
4	sample_03a	sample_03	2	female	New York	115	21	21	28,8
5	sample_04a	sample_04	2	female	Paris	98	10	10	40,2
6	sample_05a	sample_05	2	female	Paris	55	20	20	48,4
7	sample_06a	sample_06	3	female	Paris	120	17	17	43,5
8	sample_07a	sample_07	3	female	Paris	80	16	16	32,1
9	sample_08a	sample_08	3	male	Paris	99	15	15	37
10	sample_09a	sample_09	3	male	Paris	65	25	25	46,8
11	sample_10a	sample_10	4	male	Paris	140	23	23	43,5
12	sample_11a	sample_11	3	male	London	122	18	18	48,4
13	sample_12a	sample_12	4	male	London	130	23	23	46,8
14	sample_13a	sample_13	4	male	London	111	19	19	46,8
15	sample_14a	sample_14	4	male	London	82	14	14	41,9
16	sample_15a	sample_15	3	male	New York	79	16	16	40,2
17	sample_01b	sample_01	2	female	New York	48	13	25	68,1
18	sample_02b	sample_02	4	female	New York	47	15	23	23,9
19	sample_03b	sample_03	2	female	New York	53	21	18	28,8
20	sample_04b	sample_04	2	female	Paris	56	10	23	40,2
21	sample_05b	sample_05	2	female	Paris	62	20	19	48,4
22	sample_06b	sample_06	3	female	Paris	66	17	14	43,5
23	sample_07b	sample_07	3	female	Paris	68	16	47	32,1
24	sample_08b	sample_08	3	male	Paris	73	15	53	37
25	sample_09b	sample_09	3	male	Paris	63	25	47	46,8
26	sample_10b	sample_10	4	male	Paris	48	23	53	43,5
27	sample_11b	sample_11	3	male	London	64	18	56	48,4
28	sample_12b	sample_12	4	male	London	58	23	62	46,8
29	sample_13b	sample_13	4	male	London	51	19	66	46,8
30	sample_14b	sample_14	4	male	London	46	14	68	41,9
31	sample_15b	sample_15	3	male	New York	71	16	31	40,2

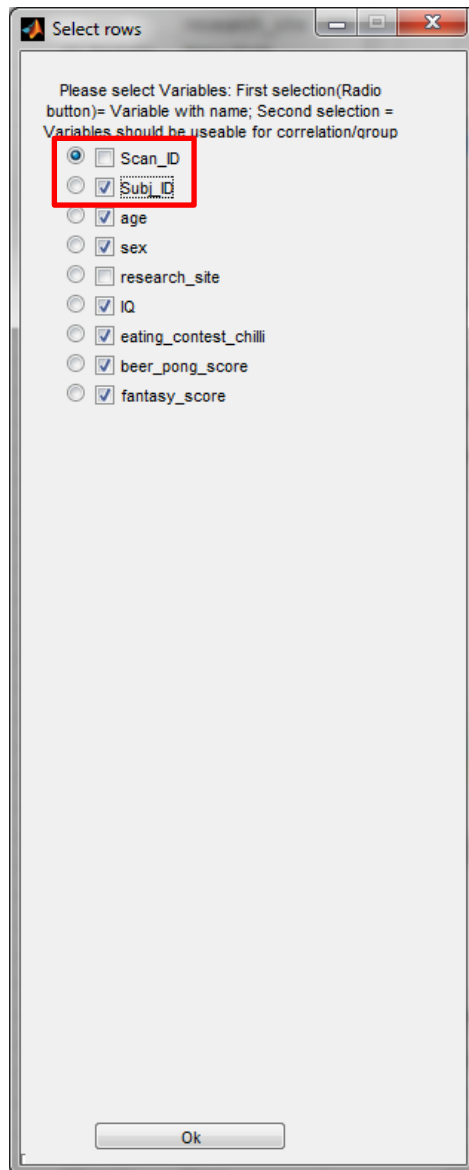
**Within Variables**

**Yellow:** constant variables repeated

**Purple:** changing variables T1 T2



- Select the „Variables\_Within\_Design“ sheet under .../workspaces/SampleWorkspace
- Notice: **Scan\_ID** (one subject = T1: sample\_01a, T2: sample\_01b) and **Subj\_ID** (sample 1)



- Select the „Scan\_ID“ as file identifier
- Select also „Subj\_ID“ as subject ID
  
- Select: age, sex, and IQ

- Navigate to GraphVar/workspaces/SampleWorkspace/data/CorrMatrix\_Within\_Design
- Select all 15 subjects (i.e., 30 files as 1 subject = T1: sample\_01a, T2: sample\_01b)

The screenshot displays the GraphVar software interface with a 'Select file(s)' dialog box open. The dialog shows the directory 'data \ CorrMatrix\_Within\_Design' containing 30 files. The main window shows the 'General Settings' and 'Network Construction' panels.

**General Settings:**

- Brain regions files: BrainRegions.csv
- File with Variables: Variables.csv
- Select Subjects (Conn Matrix)** (highlighted in red)
- Create Connectivity Matrix
- Subjects: (empty list)
- Subjectname in Filename: (empty text box)
- Start: 0, End (remaining characters): 20
- Corr Matrix Array: CorrMatrix
- Save interim results:
- Parallel Workers: 0

**Network Construction:**

- Threshold:  Relative
- Weights:  No Change
- Network nodes / Brain areas:
 

Network nodes / Brain areas	Network thresholds
Precentral gyrus (Left)	0.1
Precentral gyrus (Right)	0.11
Superior frontal gyrus, dorsolate	0.12
Superior frontal gyrus, dorsolate	0.13
Superior frontal gyrus, orbital pa	0.14
Superior frontal gyrus, orbital pa	0.15
Middle fronta	
Middle fronta	
Middle fronta	

**Network Calculations:**

- Calculate graph metrics:
- Brain graph metrics:
  - Binary: Assortativity
  - Binary: Betweenness centrality
  - Binary: Clustering coefficient global
  - Binary: Clustering coefficient local
  - Binary: Characteristic path global
  - Binary: Characteristic Path local
  - Binary: Community structure Newman - affiliation
  - Binary: Community structure Louvain - affiliation

**Select file(s) dialog box:**

Name	Änderungsdatum	Typ	Größe
CorrMatrix_sample_01a	03.09.2014 18:06	Microsoft Access ...	199 KB
CorrMatrix_sample_01b	03.09.2014 18:06	Microsoft Access ...	199 KB
CorrMatrix_sample_02a	03.09.2014 18:06	Microsoft Access ...	200 KB
CorrMatrix_sample_02b	03.09.2014 18:06	Microsoft Access ...	199 KB
CorrMatrix_sample_03a	03.09.2014 18:06	Microsoft Access ...	199 KB
CorrMatrix_sample_03b	03.09.2014 18:06	Microsoft Access ...	200 KB
CorrMatrix_sample_04a	03.09.2014 18:06	Microsoft Access ...	199 KB
CorrMatrix_sample_04b	03.09.2014 18:06	Microsoft Access ...	200 KB
CorrMatrix_sample_05a	03.09.2014 18:06	Microsoft Access ...	200 KB
CorrMatrix_sample_05b	03.09.2014 18:06	Microsoft Access ...	199 KB
CorrMatrix_sample_06a	03.09.2014 18:06	Microsoft Access ...	199 KB
CorrMatrix_sample_06b	03.09.2014 18:06	Microsoft Access ...	199 KB
CorrMatrix_sample_07a	03.09.2014 18:06	Microsoft Access ...	199 KB
CorrMatrix_sample_07b	03.09.2014 18:06	Microsoft Access ...	199 KB
CorrMatrix_sample_08a	03.09.2014 18:06	Microsoft Access ...	199 KB
CorrMatrix_sample_08b	03.09.2014 18:06	Microsoft Access ...	200 KB
CorrMatrix_sample_09a	03.09.2014 18:06	Microsoft Access ...	200 KB

File type filter: MAT-files (\*.mat)

- Highlight the Scan\_ID
- Select all nodes, threshold 0.1, and local efficiency
- GLM: sex as between factor

The screenshot displays the GraphVar software interface with several key settings highlighted in red boxes:

- General Settings:**
  - Brain regions files: BrainRegions.csv
  - File with Variables: /fthin\_Design.xlsx
  - Subjects list: Includes 'matrix\_Within\_Design\CorrMatrix\_sample\_01a.mat'.
  - Subjectname in Filename: CorrMatrix\_sample\_01a.ma
- Network Construction:**
  - Threshold: Relative
  - Weights: No Change
  - Network nodes / Brain areas: cerebellum\_10\_K, Vermis\_1\_2, Vermis\_3, Vermis\_4\_5, Vermis\_6, Vermis\_7, Vermis\_8, Vermis\_9, Vermis\_10
  - Network thresholds: 0.1, 0.11, 0.12, 0.13, 0.14, 0.15, 0.16, 0.17, 0.18, 0.19
- Network Calculations:**
  - Calculate graph metrics: Checked
  - Brain graph metrics: Binary: Efficiency local - UND
- Raw Matrix (link wise):**
  - Connectivity Thr.: .05
  - Weights: No Change
- GLM:**
  - Variables: Subj\_ID, age, IQ, eating\_contest\_chilli, beer\_pong\_score, fantasy\_score
  - Between covariates: sex

At the bottom of the interface, there are buttons for 'Switch Workspace', 'Open Previous Results', 'Load interim results', 'Statistics with already calculated values', and 'Calculate & Statistics'.

- Click on „Select Within ID“
- And highlight the „Subj\_ID“

The screenshot shows the GraphVar - Chilli\_Context software interface. The main window has several panels:

- General Settings:** Includes fields for 'Brain regions files' (BrainRegions.csv) and 'File with Variables' (C:\Users\kruschv...), along with buttons for 'Select Subjects (Conn Matrix)' and 'Create Connectivity Matrix'.
- Subjects:** A list of subject IDs and file paths, with 'C:\Users\kruschv\Desktop\new\neue Version t' selected.
- Network Construction:** Includes 'Threshold' (Relative selected), 'Weights' (No Change selected), and a table of 'Network nodes / Brain areas' with 'Network thresh' values.
- Raw Matrix (link wise):** Includes 'Raw matrix' and 'Connectivity Thr.' (0.05 selected) options.
- Graph metrics:** Includes 'parametric' selected and '#Rep' set to 1.

An overlay dialog box titled 'Select within ID field' is open, showing a list of variables: age, sex, research\_site, IQ, eating\_contest\_chilli, beer\_pong\_score, and fantasy\_score. 'Subj\_ID' is highlighted in blue. The 'OK' and 'Cancel' buttons are at the bottom of the dialog.

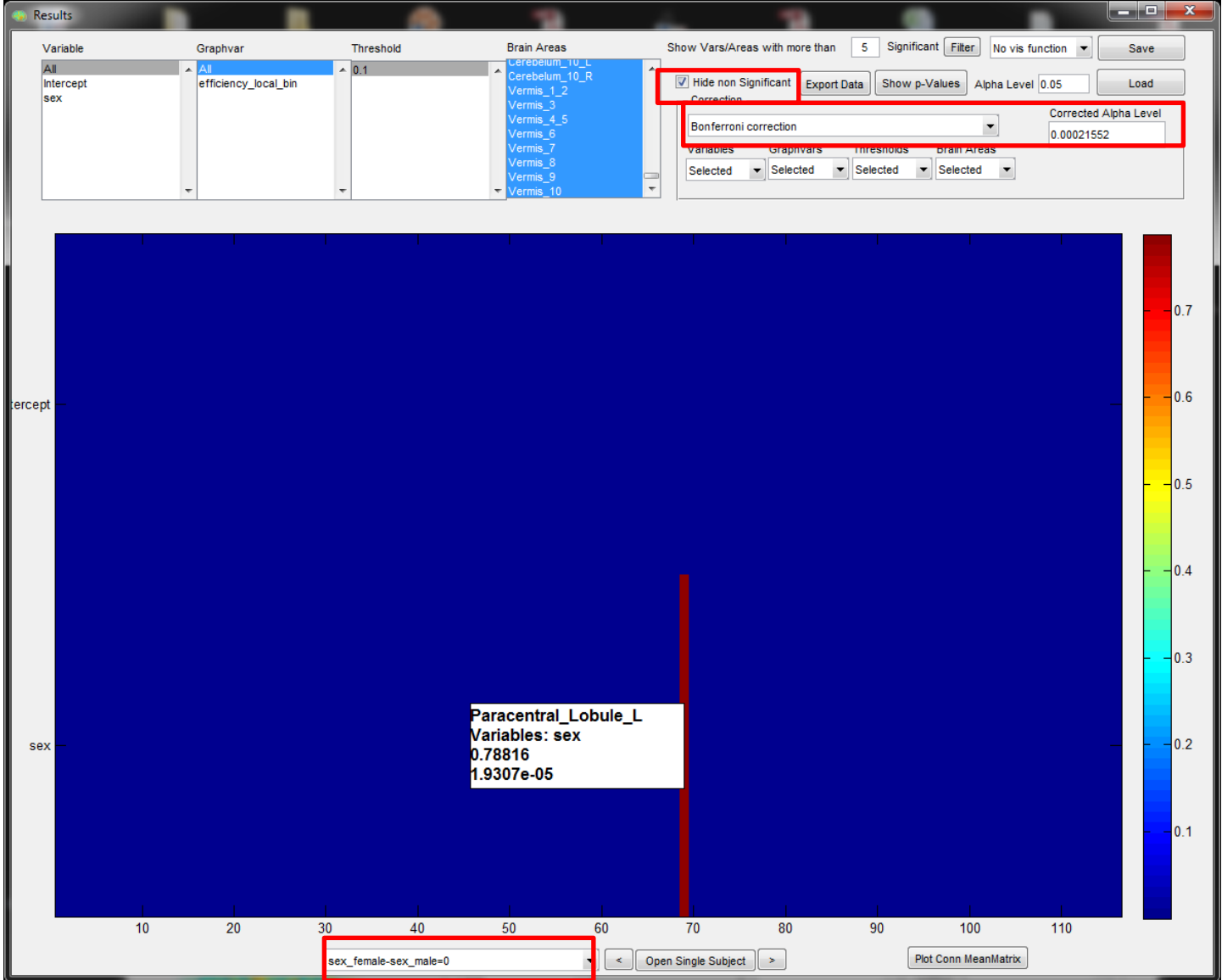
In the main window, the 'Select Within ID' button is highlighted with a red box.

- The Within deviding field will appear as such on the button
- „Calculate & Statistics“

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

- General Settings:** Includes fields for 'Brain regions files' (BrainRegions.csv), 'File with Variables' (rthin\_Design.xlsx), and buttons for 'Select Subjects (Conn Matrix)' and 'Create Connectivity Matrix'. A list of subject files is shown, with 'matrix\_Within\_Design\CorrMatrix\_sample\_01a.mat' selected. The 'Subjectname in Filename' is set to 'CorrMatrix\_sample\_01a.mat'. Start and End values are 12 and 4 respectively. 'Corr Matrix Array' is 'CorrMatrix'. 'Save interim results' is checked, and 'Parallel Workers' is 0.
- Network Construction:** 'Threshold' is set to 'Relative'. 'Weights' are set to 'No Change'. 'Network nodes / Brain areas' includes 'Cerebellum\_10\_K', 'Vermis\_1\_2', 'Vermis\_3', 'Vermis\_4\_5', 'Vermis\_6', 'Vermis\_7', 'Vermis\_8', 'Vermis\_9', and 'Vermis\_10'. 'Network thresholds' range from 0.1 to 0.19. A 'CheckFrag' button is present.
- Network Calculations:** 'Calculate graph metrics' is checked. A list of metrics is shown, including 'Binary: Eccentricity - UND/DIR', 'Binary: Edge betweenness centrality - UND/DIR', 'Binary: Efficiency global - UND', 'Binary: Efficiency local - UND', 'Binary: Eigenvector centrality - UND', 'Binary: Flow coefficient global - DIR', 'Binary: Flow coefficient local - DIR', 'Binary: Graph radius - UND/DIR', 'Binary: Graph diameter - UND/DIR', and 'Binary: K-coreness centrality - UND'. 'Normalize graph metric with random networks' and 'Use random network to calc smallworldness' are unchecked. A 'Calculate variables and export' button is at the bottom.
- Raw Matrix (link wise):** 'Raw matrix' and 'Connectivity Thr.' are unchecked. 'r to z' is checked. 'Generate random networks' is unchecked. A list of values from .05 to .006 is shown.
- GLM:** 'Variables' include 'Subj\_ID', 'age', 'IQ', 'eating\_contest\_chilli', 'beer\_pong\_score', and 'fantasy\_score'. 'Between covariates', 'Between factors' (with 'sex' selected), 'Within covariates', and 'Nuisance covariates' are empty. 'No Interactions' is selected. 'Graph metrics' and 'Raw matrix' are both set to 'parametric'. '#Rep' is 1. A red box highlights the 'Within ID - Subj\_ID' field and its 'Clear' button.
- Brain Visualization:** A 3D brain model is shown with a network overlay. The text 'Graph Var' is displayed below it.
- Bottom Panel:** Includes buttons for 'Switch Workspace', 'Open Previous Results', 'Load interim results', 'Statistics with already calculated values', and 'Calculate & Statistics' (highlighted with a red box).

- After Bonferroni correction we can observe a significant difference in change of local efficiency between T1 and T1 as a function of sex (i.e., females as compared to males have a stronger change in local efficiency between T1 and T2)



# 4. Within design II (change of efficiency and behavior T1 T2)

## **Research option 2 - example:**

*investigate the association between a changing independent variable (e.g. cognitive function in T1 and T2) and the change of a dependent network variable (e.g. network efficiency in T1 T2)*

- Select the „Variables\_Within\_Design“ sheet under .../workspaces/SampleWorkspace
- Notice: **Scan\_ID** (one subject = T1: sample\_01a, T2: sample\_01b) and **Subj\_ID** (sample 1)

**Within Variables**

**Yellow:** constant variables repeated  
**Purple:** changing variables T1 T2

	Scan_ID	Subj_ID	age	sex	research_site	IQ	eating_content	beer_pong_score	fantasy_score
1	Scan_ID	Subj_ID							
2	sample_01a	sample_01	2	female	New York	100	13	13	68,1
3	sample_02a	sample_02	4	female	New York	130	15	15	23,9
4	sample_03a	sample_03	2	female	New York	115	21	21	28,8
5	sample_04a	sample_04	2	female	Paris	98	10	10	40,2
6	sample_05a	sample_05	2	female	Paris	55	20	20	48,4
7	sample_06a	sample_06	3	female	Paris	120	17	17	43,5
8	sample_07a	sample_07	3	female	Paris	80	16	16	32,1
9	sample_08a	sample_08	3	male	Paris	99	15	15	37
10	sample_09a	sample_09	3	male	Paris	65	25	25	46,8
11	sample_10a	sample_10	4	male	Paris	140	23	23	43,5
12	sample_11a	sample_11	3	male	London	122	18	18	48,4
13	sample_12a	sample_12	4	male	London	130	23	23	46,8
14	sample_13a	sample_13	4	male	London	111	19	19	46,8
15	sample_14a	sample_14	4	male	London	82	14	14	41,9
16	sample_15a	sample_15	3	male	New York	79	16	16	40,2
17	sample_01b	sample_01	2	female	New York	48	13	25	68,1
18	sample_02b	sample_02	4	female	New York	47	15	23	23,9
19	sample_03b	sample_03	2	female	New York	53	21	18	28,8
20	sample_04b	sample_04	2	female	Paris	56	10	23	40,2
21	sample_05b	sample_05	2	female	Paris	62	20	19	48,4
22	sample_06b	sample_06	3	female	Paris	66	17	14	43,5
23	sample_07b	sample_07	3	female	Paris	68	16	47	32,1
24	sample_08b	sample_08	3	male	Paris	73	15	53	37
25	sample_09b	sample_09	3	male	Paris	63	25	47	46,8
26	sample_10b	sample_10	4	male	Paris	48	23	53	43,5
27	sample_11b	sample_11	3	male	London	64	18	56	48,4
28	sample_12b	sample_12	4	male	London	58	23	62	46,8
29	sample_13b	sample_13	4	male	London	51	19	66	46,8
30	sample_14b	sample_14	4	male	London	46	14	68	41,9
31	sample_15b	sample_15	3	male	New York	71	16	31	40,2



- Navigate to GraphVar/workspaces/SampleWorkspace/data/CorrMatrix\_Within\_Design
- Select all 15 subjects (i.e., 30 files as 1 subject = T1: sample\_01a, T2: sample\_01b)

The screenshot displays the GraphVar software interface with a 'Select file(s)' dialog box open. The dialog shows the directory 'data \ CorrMatrix\_Within\_Design' containing 30 files. The main interface has a red box around the 'Select Subjects (Conn Matrix)' button.

Name	Änderungsdatum	Typ	Größe
CorrMatrix_sample_01a	03.09.2014 18:06	Microsoft Access ...	199 KB
CorrMatrix_sample_01b	03.09.2014 18:06	Microsoft Access ...	199 KB
CorrMatrix_sample_02a	03.09.2014 18:06	Microsoft Access ...	200 KB
CorrMatrix_sample_02b	03.09.2014 18:06	Microsoft Access ...	199 KB
CorrMatrix_sample_03a	03.09.2014 18:06	Microsoft Access ...	199 KB
CorrMatrix_sample_03b	03.09.2014 18:06	Microsoft Access ...	200 KB
CorrMatrix_sample_04a	03.09.2014 18:06	Microsoft Access ...	199 KB
CorrMatrix_sample_04b	03.09.2014 18:06	Microsoft Access ...	200 KB
CorrMatrix_sample_05a	03.09.2014 18:06	Microsoft Access ...	200 KB
CorrMatrix_sample_05b	03.09.2014 18:06	Microsoft Access ...	199 KB
CorrMatrix_sample_06a	03.09.2014 18:06	Microsoft Access ...	199 KB
CorrMatrix_sample_06b	03.09.2014 18:06	Microsoft Access ...	199 KB
CorrMatrix_sample_07a	03.09.2014 18:06	Microsoft Access ...	199 KB
CorrMatrix_sample_07b	03.09.2014 18:06	Microsoft Access ...	199 KB
CorrMatrix_sample_08a	03.09.2014 18:06	Microsoft Access ...	199 KB
CorrMatrix_sample_08b	03.09.2014 18:06	Microsoft Access ...	200 KB
CorrMatrix_sample_09a	03.09.2014 18:06	Microsoft Access ...	200 KB

- Highlight the Scan\_ID
- Select all nodes, all thresholds, binary „Transitivity“

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

- General Settings:** Brain regions files: BrainRegions.csv; File with Variables: rthin\_Design.xlsx; Subjects list: matrix\_Within\_Design\CorrMatrix\_sample\_01a.mat (highlighted); Subjectname in Filename: CorrMatrix\_sample\_01a.mat (highlighted); Start: 12; End (remaining characters): 4; Corr Matrix Array: CorrMatrix; Save interim results: checked; Parallel Workers: 0.
- Network Construction:** Threshold: Relative; Weights: No Change; Network nodes / Brain areas: Cerebellum\_10\_A, Vermis\_1\_2, Vermis\_3, Vermis\_4\_5, Vermis\_6, Vermis\_7, Vermis\_8, Vermis\_9, Vermis\_10; Network thresholds: 0.41, 0.42, 0.43, 0.44, 0.45, 0.46, 0.47, 0.48, 0.49, 0.5; Generate randomized subject data: unchecked; CheckFrag button.
- Network Calculations:** Calculate graph metrics: checked; Brain graph metrics list: Binary: Rich club coefficient - DIR, Binary: Small World Propensity - UND, Binary: Subgraph centrality - UND, Binary: Topological overlap - UND, Binary: Transitivity - UND (highlighted), Binary: Transitivity - DIR, Binary: Within-module degree z-score - UND, Binary: Within-module out-neighbor degree z-score, Binary: Participation coefficient - UND, Binary: Participation out-neighbor coefficient - DIR; 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.: checked; r to z: unchecked; Generate random networks: unchecked; List of values: .05 (highlighted), .045, .04, .035, .03, .025, .02, .015, .01, .009, .008, .007, .006; Weights: No Change; Weights: absolute weights: unchecked; Weights: negative weights to zero: unchecked.
- GLM:** Variables list: Subj\_ID, age, eating\_contest\_chilli, fantasy\_score, sex, IQ, beer\_pong\_score; Between covariates: empty; Between factors: empty; Within covariates: empty; Nuisance covariates: empty; No Interactions: selected; Graph metrics: parametric: unchecked, rand NW: unchecked, permutation: checked; Raw matrix: parametric: checked, rand NW: unchecked, permutation: unchecked; #Rep: 1000.

At the bottom, there are buttons for: Switch Workspace, Open Previous Results, Load interim results, Statistics with already calculated values, and Calculate & Statistics.

- 1. GLM: select beer\_pong\_score as within covariate
- 2. Select „Subj\_ID“ as within dividing field in the automatic pop-up window

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

- General Settings:** Brain regions files (BrainRegions.csv), File with Variables (fthin\_Design.xlsx), and buttons for "Select Subjects (Conn Matrix)" and "Create Connectivity Matrix".
- Subjects:** A list of subject files including "matrix\_Within\_Design\CorrMatrix\_sample\_01a.mat".
- Subjectname in Filename:** CorrMatrix\_sample\_01a.mat
- Start:** 12, **End (remaining characters):** 4
- Corr Matrix Array:** CorrMatrix
- Save interim results:** Checked, **Parallel Workers:** 0
- Network Construction:** Threshold (Relative), Weights (No Change), and Network nodes / Brain areas (Cerebellum\_10\_A, Vermis\_1\_2, Vermis\_3).
- Network Calculations:** Calculate graph metrics (checked), Brain graph metrics (Binary: Rich club coefficient - DIR, Binary: Small World Propensity - UND, Binary: Subgraph centrality - UND, Binary: Topological overlap - UND, Binary: Transitivity - UND, Binary: Transitivity - DIR, Binary: Within-module degree z-score - UND, Binary: Within-module out-neighbor degree z-score - UND, Binary: Participation coefficient - UND, Binary: Participation out-neighbor coefficient - UND), Normalize graph metric with random networks (unchecked), Use random network to calc smallworldness (unchecked), and Calculate variables and export (button).
- GLM:** Variables (Subj\_ID, age, eating\_contest\_chilli, fantasy\_score, sex, IQ), Between covariates, Between factors, Within covariates (beer\_pong\_score), Nuisance covariates, No Interactions, Graph metrics (parametric, rand NW, permutation), Raw matrix (parametric, rand NW, permutation), #Rep (1000).
- Pop-up Dialog:** "Select within ID field" with a list of variables (Subj\_ID, age, sex, research\_site, IQ, eating\_contest\_chilli, beer\_pong\_score, fantasy\_score) and "OK" and "Cancel" buttons.

- Run 1000 permutations
- Calculate & Statistics

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

- General Settings:** Includes fields for 'Brain regions files' (BrainRegions.csv), 'File with Variables' (rthin\_Design.xlsx), and buttons for 'Select Subjects (Conn Matrix)' and 'Create Connectivity Matrix'. A list of subject files is shown, with 'matrix\_Within\_Design\CorrMatrix\_sample\_01a.mat' selected. The 'Subjectname in Filename' is 'CorrMatrix\_sample\_01a.mat'. Start/End characters are set to 12/4, and 'Corr Matrix Array' is 'CorrMatrix'. 'Save interim results' is checked, and 'Parallel Workers' is 0.
- Network Construction:** 'Threshold' is set to 'Relative'. 'Weights' are set to 'No Change'. A list of 'Network nodes / Brain areas' (Cerebellum\_10\_A to Vermis\_10) and their corresponding 'Network thresholds' (0.41 to 0.5) are shown. A 'CheckFrag' button is present.
- Network Calculations:** 'Calculate graph metrics' is checked. A list of 'Brain graph metrics' includes 'Binary: Transitivity - UND' (highlighted). 'Normalize graph metric with random networks' and 'Use random network to calc smallworldness' are unchecked. A 'Calculate variables and export' button is at the bottom.
- Raw Matrix (link wise):** 'Raw matrix' and 'Connectivity Thr.' are unchecked. 'r to z' and 'Generate random networks' are checked. A list of values (.05 to .006) is shown. 'Weights' are set to 'No Change'.
- GLM:** 'Variables' include 'Subj\_ID', 'age', 'eating\_contest\_chilli', 'fantasy\_score', 'sex', and 'IQ'. 'Between covariates', 'Between factors', and 'Within covariates' (with 'beer\_pong\_score' selected) are empty. 'Nuisance covariates' and 'No Interactions' are empty. 'Graph metrics' are set to 'parametric' and 'rand NW'. 'Raw matrix' is set to 'parametric' and 'rand NW'. 'permutation' is selected for both, and '#Rep' is set to 1000.
- Bottom Panel:** Includes buttons for 'Switch Workspace', 'Open Previous Results', 'Load interim results', 'Statistics with already calculated values', and 'Calculate & Statistics' (highlighted with a red box).

- You will observe a significant positive association between change in behavior and a change in transitivity in the low threshold range

