GIPC Toolbox

Walk Through

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Introduction

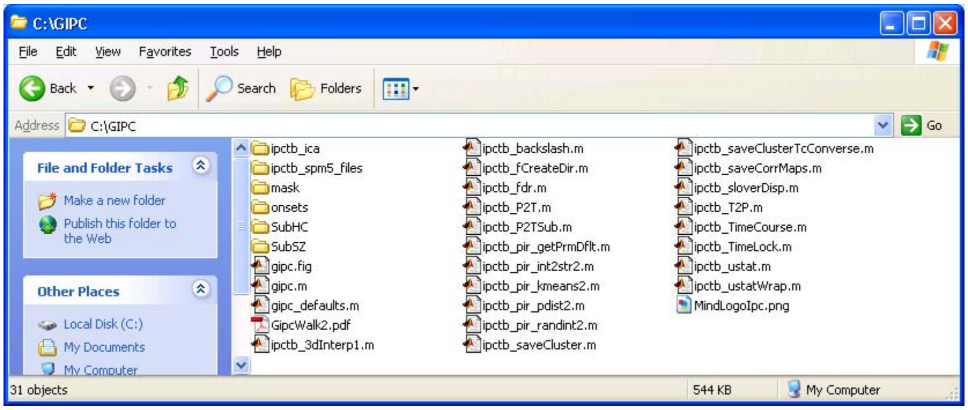
The GIPC (Group Inter-Participant Correlation) Toolbox (pronounced as the word Gypsy) finds the BOLD correlations between the same voxel among all participants within a group. In order for the time courses to correlate between participants the onsets of tasks has to be timed the same for each participant (hence this toolbox will not find any correlations for patients resting in scanner). The GIPC Toolbox compares two groups for differences and is computationally intense. It takes about 5.5 hours to run 6 controls and 6 subjects (every subject was scanned 1 session of 249 time points) using a PC with Intel Core 2 CPU 6600 @ 2.40GHz and 2GB RAM. More subjects increase computing time in proportion to the following exponential term $(grpMax^2 - grpMax) / 2$, where grpMax = max([controls, patients]). If you don't have enough computer memory (for amount of subjects chosen) the computer will suggest a change of the `gIpc.nSplit` variable which makes GIPC slower, but minimizes memory demands.

This GIPC method has proven success for separating a group of schizophrenics vs. healthy controls according to published study in Neuroimage in Feb 2008 (see reference at end).

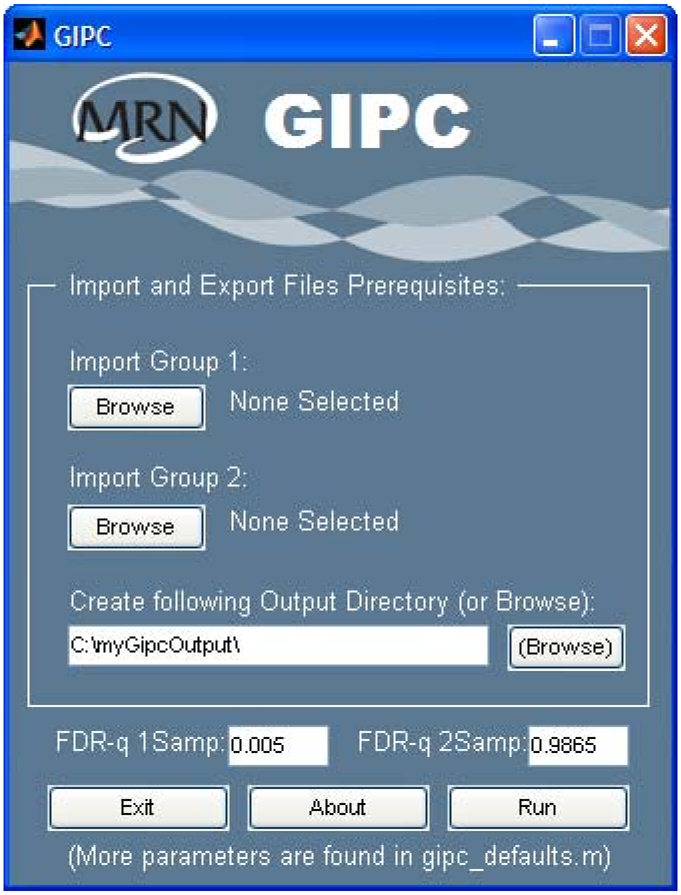
Installing GIPC Toolbox

GIPC Toolbox runs on a machine with MATLAB and works for both UNIX and WINDOWS. It is installed the following way.

1) Extract/unzip the files from "gipc1d.zip" to a folder where you want to store the GIPC Toolbox.
2) To run this walk through you also need our walk through subjects. To set up the sample subjects you need to unzip the "GipcSubjects.zip" file in the same directory as you unzipped "gipc1a.zip" creating the folders "SubHC" and "SubSZ" with contents. If "C:/GIPC" was chosen as folder to store GIPC in this folder would look as the following window.



3) To set MATLAB paths you need to run the graphical user interface once. After opening MATLAB you change the MATLAB directory to the folder where you unzipped the GIPC toolbox into. Type "gipc" at the command prompt of MATLAB which will result in the following form popping up on the screen.



C:\myGipcOutput\

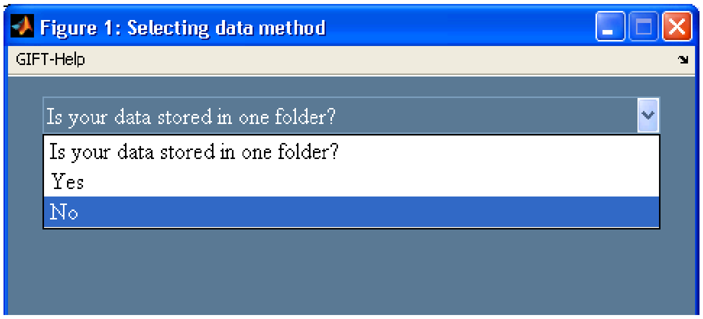
FDR-q 1Samp: 0.005

FDR-q 2Samp: 0.9865

Running the Sample Subjects

1) Start GIPC by typing "gipc" in the MATLAB command prompt (if not done already) as in step 2 below the "Installing GIPC Toolbox" header.

2) Click [Browse] for Group1 and the following image (Figure1: Selecting data method) will popup.



3) Select “No”.

4) After “No” option is selected the following window appear.

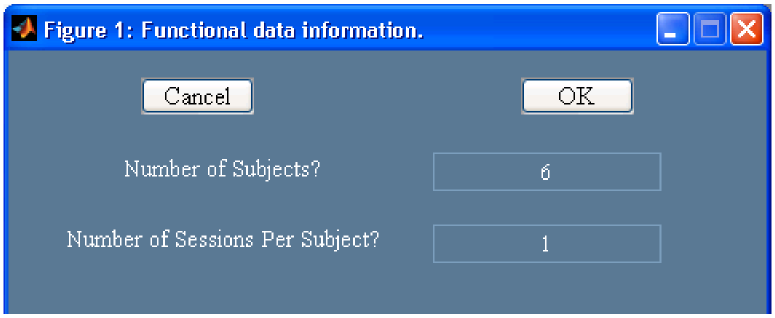


Figure 1: Functional data information.

Number of Subjects? 6

Number of Sessions Per Subject? 1

Enter 6 “Number of Subjects” (leave “Number of Sessions Per Subject” to 1) and click [OK].

5) Then the following figure pops up where you select the import files for each subject (and session).

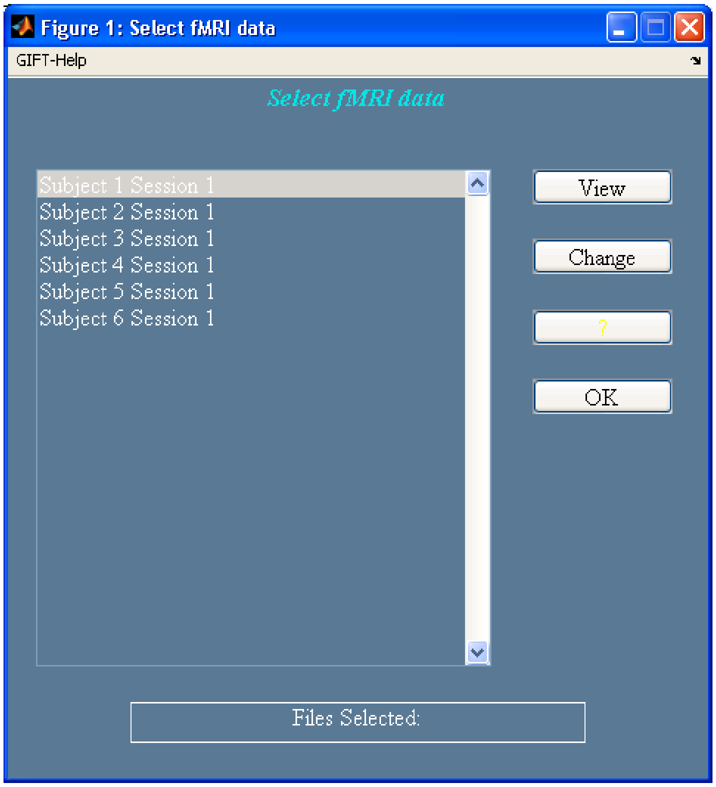


Figure 1: Select fMRI data

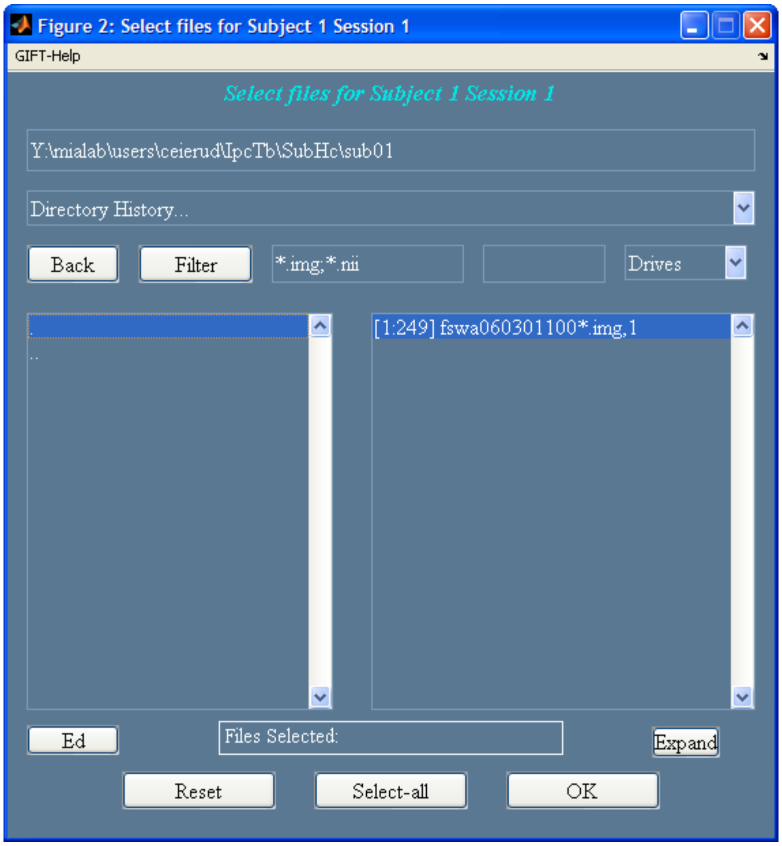
Select fMRI data

Subject 1 Session 1
Subject 2 Session 1
Subject 3 Session 1
Subject 4 Session 1
Subject 5 Session 1
Subject 6 Session 1

Files Selected:

Click “Subject 1 Session 1” in the list above.

6) Next a figure according to the following will popup.



Y:\mialab\users\ceierud\IpcTb\SubHc\sub01

.img;.nii

.
..

[1:249] fswa060301100*.img,1

By browsing directories in your left panel, click on folder the “SubHc” and then the “sub01” folder which contains the 249 files (one for each time point) in accordance to how the right panes looks like in figure above. Click on the entry in the right panel that holds the 249 img-files and the box above the [Select-all] button shows how many files you have selected (249).
After this you click the [OK] button.

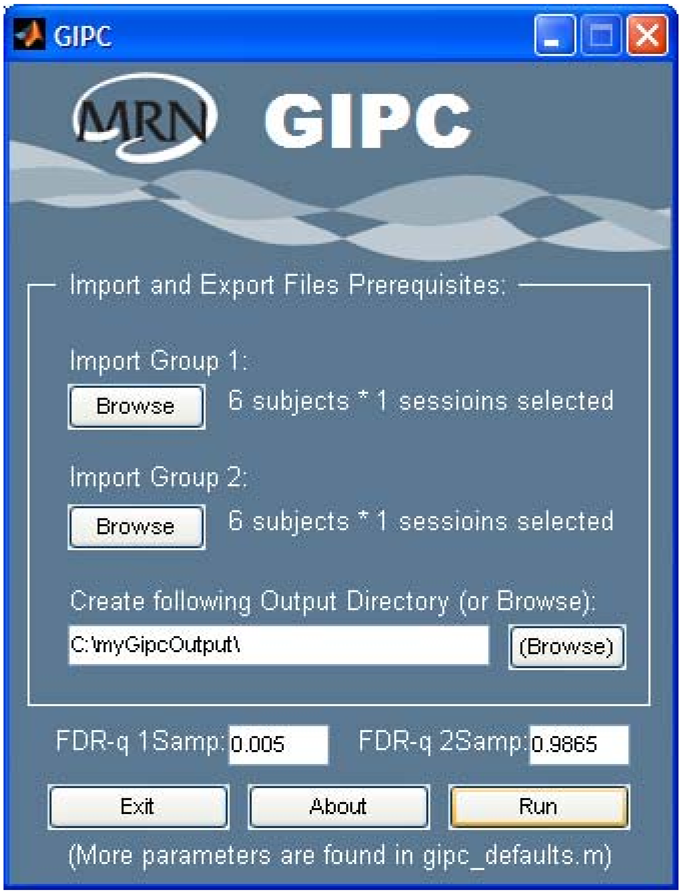
7) Analogous to step 5 and 6 select the following list entries and folders for files:

	List entries	Folder
2	Subject 2 Session 1	sub02
3	Subject 3 Session 1	sub03
4	Subject 4 Session 1	sub04
5	Subject 5 Session 1	sub05
6	Subject 6 Session 1	sub06

8) Analogous to steps 2-7 click browse for Group 2. Then select the following list entries and folders for files under the “SubSz” directory:

	List entries	Folder
1	Subject 1 Session 1	sub01
2	Subject 2 Session 1	sub02
3	Subject 3 Session 1	sub03
4	Subject 4 Session 1	sub04
5	Subject 5 Session 1	sub05
6	Subject 6 Session 1	sub06

9) Now the “Import Group1” and “Import Group2” should acknowledge your selected data and you may select the “Output Directory” to “c:\myGipcOutput”. The figure should now look as following.



Import and Export Files Prerequisites:

Import Group 1:
6 subjects * 1 sessioins selected

Import Group 2:
6 subjects * 1 sessioins selected

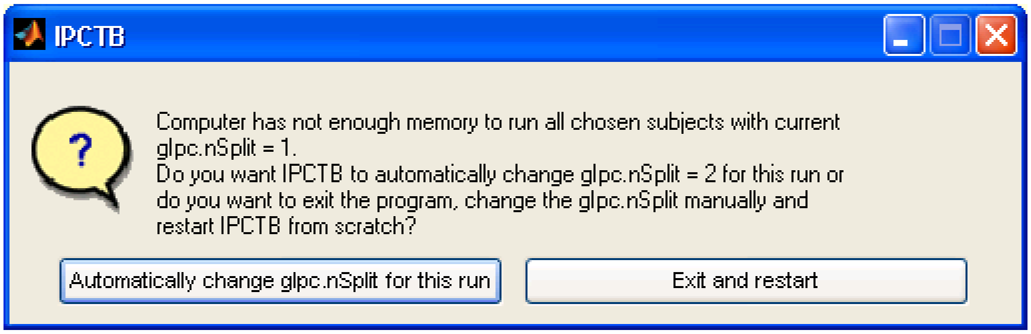
Create following Output Directory (or Browse):
C:\myGipcOutput\

FDR-q 1Samp: 0.005
FDR-q 2Samp: 0.9865

(More parameters are found in gipc_defaults.m)

10) If you want to change the FDR (False Discovery Rate) correction for the single group correlation maps (that you will get after the run) you can change the “FDR-q 1Samp” textbox and the correlation map that compares where the correlation of Group 1 > Group 2 by changing the “FDR-q 2Samp” textbox.

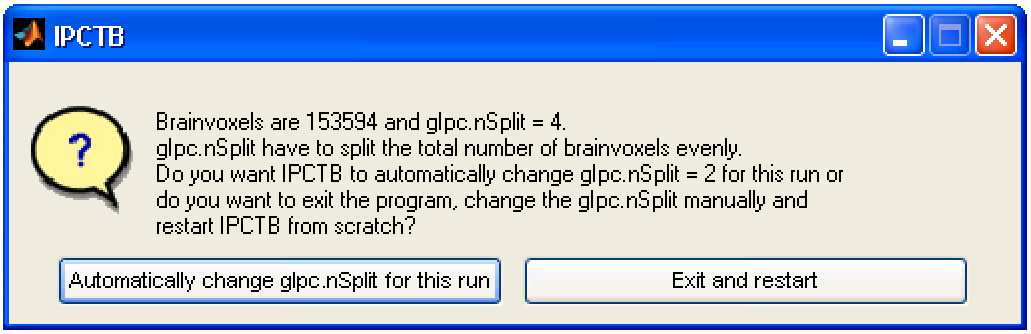
11) Now you are ready to run the application by clicking the [Run] button.
Note that the run may take several hours (or several days for studies over 35 subjects in a group). If a wait bar appears (estimating work done) you don't need to read the rest for this step. However, since the program is memory intensive (especially if you are running a study with more than 30 subjects in a single group) a memory test is run before computation begins. If the memory test proves your computer does not have enough memory for a specific number of subjects the following message box will display.



Computer has not enough memory to run all chosen subjects with current gIpc.nSplit = 1.
Do you want IPCTB to automatically change gIpc.nSplit = 2 for this run or do you want to exit the program, change the gIpc.nSplit manually and restart IPCTB from scratch?

If you click [Automatically change gIpc.nSplit for this run] GIPC will attempt to continue using the newly suggested gIpc.nSplit value. However GIPC will test if this new value really is sufficient for required memory need. If the memory test fails again the GIPC will suggest even a new value for gIpc.nSplit. This will go on until GIPC finds a gIpc.nSplit value that pass the memory requirement test. If you press [Exit and restart] you can increase the gIpc.nSplit value manually in the file ipctb_defaults.m. The downside of increasing gIpc.nSplit is that the higher `gIpc.nSplit` is the slower the GIPC gets.
If the memory test is passed it is no guarantee that you will not run out of memory anyway. The initial test is just a crude measurement that tests if the current `gIpc.nSplit` value for sure is not enough to run the program.

Another error you may encounter is the following message box:

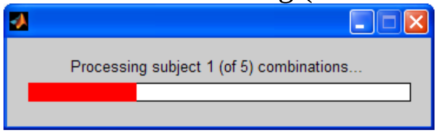


Brainvoxels are 153594 and gIpc.nSplit = 4.
gIpc.nSplit have to split the total number of brainvoxels evenly.
Do you want IPCTB to automatically change gIpc.nSplit = 2 for this run or do you want to exit the program, change the gIpc.nSplit manually and restart IPCTB from scratch?

If this is the case the chosen `gIpc.nSplit` does not divide the number of voxels in your imported images evenly which is a prerequisite. You may choose [Automatiucally change gIpc.nSplit for this run] to correct the value for this run.

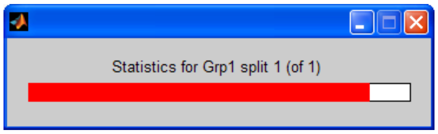
12) Wait bars will show calculations for hours…

First wait bars calculate the creation of the inter participant maps for each group and looks as following (this is usually the most time consuming process):



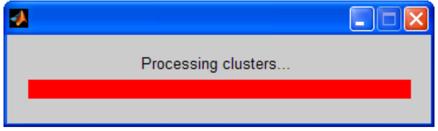
Processing subject 1 (of 5) combinations...

Then a wait bar shows status of statistics calculations for each group:



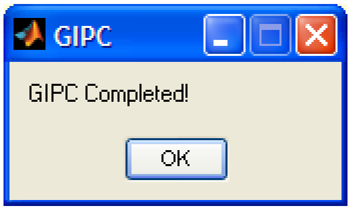
Statistics for Grp1 split 1 (of 1)

Finally a wait bar appears for each group.



Processing clusters...

After all wait bars have run through the following message box appears.



GIPC

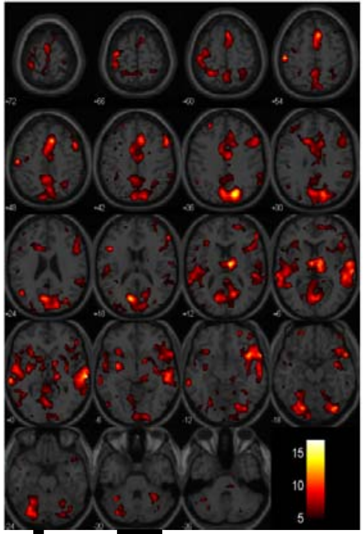
GIPC Completed!

Then you should find the following files in the "Export Path" you chose ("c:/myIpcOutput"):
* (Group1T.hdr), Group1T.img (files containing correlational T-scores for group 1)
* (Group2T.hdr), Group2T.img (files containing correlational T-scores for group 2)
* (Grp1Minus2T_Thresh.hdr), Grp1Minus2T_Thresh.img (files containing how much higher T-score group 1 has above group 2 and thresholded)
* The unthresholded version is stored in "Grp1Minus2T_UnthreshUncorr.*" which is always uncorrected as well to keep the negative difference if group 2 has a higher T-score than group 1.
* (ClustGrp1.hdr), ClustGrp1.img (files containing regions with same timecourses masked by grp1MoreThanGrp2.img originating from group 1).
* (ClustGrp2.hdr), ClustGrp2.img (files containing regions with same timecourses masked by grp1MoreThanGrp2.img originating from group 2).
* Timecourses and timelock-diagrams are stored in mat-files all starting with "ClustGrp".
* The Settings.mat file contains all your settings that were chosen at your last run. Keep track of this file if you want to check your settings for later use (if you forget any setting).

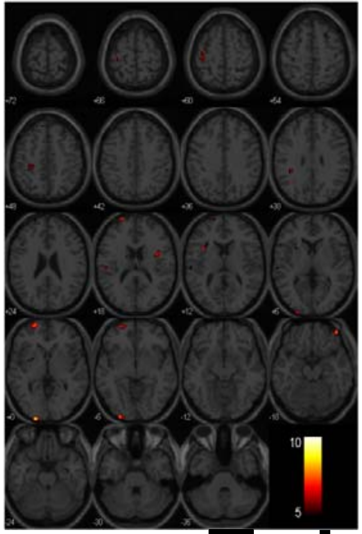
In the "c:/myGipcOutput/Images" directory however you have the following images (viewable with most image software or web browsers):

Image files after GIPC run in “c:/myGipcOutput/Images”:

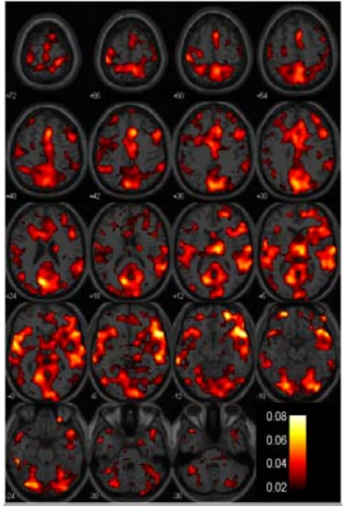
Group1T.png:



Group2T.png:

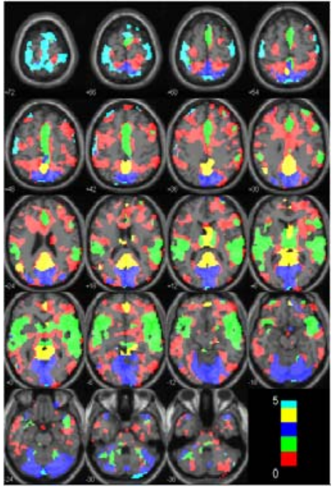


Grp1Minus2T_Thresh.png:

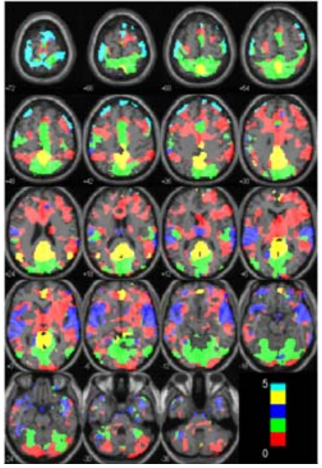


ClustGrp1.png:

*GIPC1d and later has solid colors.

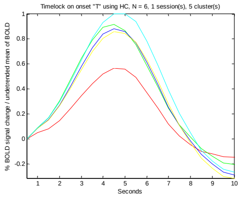


ClustGrp2.png:

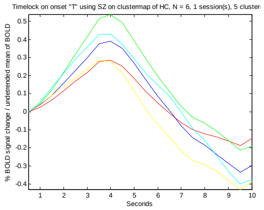


*GIPC1d and later has solid colors.

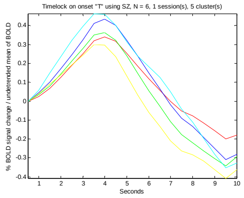
ClustGrp1_tcLock.fig



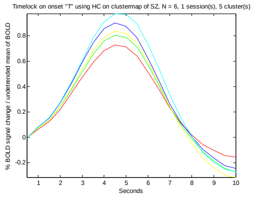
(ClustGrp1_tcLockConv.fig)



ClustGrp2_tcLock.fig



(ClustGrp2_tcLockConv.fig)



REFERENCE:

A method for multi-group inter-participant correlation: Abnormal synchrony in patients with schizophrenia during auditory target detection by Kim, D. / Pearlson, G.D. / Kiehl, K.A. / Bedrick, E. / Demirci, O. / Calhoun, V.D. , Neuroimage, 39 (3), p.1129-1141, Feb 2008

Hejnar MP, Kiehl KA, Calhoun VD. (2007): Interparticipant Correlations: A Model Free FMRI Analysis Technique. Hum.Brain Map. 28(9):860-867.