GIPC Toolbox

Reference

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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).

Import Group 1, 2

This selects the files for the first group. Note that at least 2 subjects are needed for each group.

Browse

This calls a file browser to select the output folder, as opposed to simply typing it in the text box. This is also used to create a new folder for the output, if it didn't exist before.

Run

This starts GIPC. You must have both groups selected.

About

This gives information about GIPC.

Exit

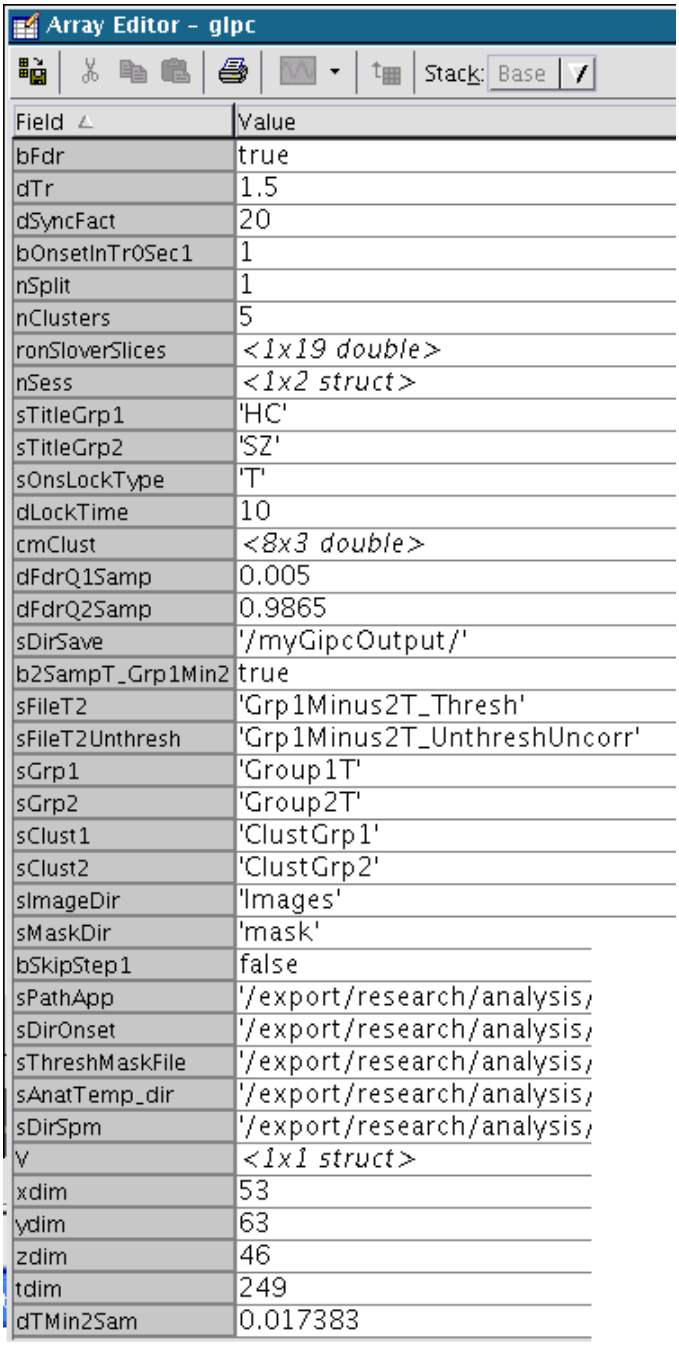
This exits GIPC.

GIPC Variables

pbRun_Callback:

gIpc

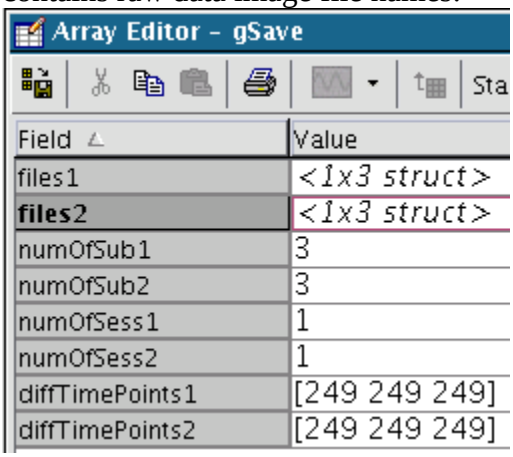
Has a lot of initiation variables (from gipc_defaults.m) and other important variables:



Field	Value
bFdr	true
dTr	1.5
dSyncFact	20
bOnsetInTr0Sec1	1
nSplit	1
nClusters	5
ronSloverSlices	*<1x19 double>*
nSess	*<1x2 struct>*
sTitleGrp1	'HC'
sTitleGrp2	'SZ'
sOnsLockType	'T'
dLockTime	10
cmClust	*<8x3 double>*
dFdrQ1Samp	0.005
dFdrQ2Samp	0.9865
sDirSave	'/myGipcOutput/'
b2SampT_Grp1Min2	true
sFileT2	'Grp1Minus2T_Thresh'
sFileT2Unthresh	'Grp1Minus2T_UnthreshUncorr'
sGrp1	'Group1T'
sGrp2	'Group2T'
sClust1	'ClustGrp1'
sClust2	'ClustGrp2'
sImageDir	'Images'
sMaskDir	'mask'
bSkipStep1	false
sPathApp	'/export/research/analysis/
sDirOnset	'/export/research/analysis/
sThreshMaskFile	'/export/research/analysis/
sAnatTemp_dir	'/export/research/analysis/
sDirSpm	'/export/research/analysis/
V	*<1x1 struct>*
xdim	53
ydim	63
zdim	46
tdim	249
dTMin2Sam	0.017383

gSave

contains raw data image file names:



ipctb_ustatWrap.m

Calculates the U-statistics (group statistics) for the groups

codRbAll

The mean of all subjects in selected group for every voxel (vector of 154000 in walk through)

codSe2All

The squared standard error of all subjects in selected group for every voxel (vector of 154000 in walk through)

codGrp

The one sample t-value for each voxel (after U-statistics)

codMnG1, codMnG2

A vector of means for each voxel for all subjects in group1 and group2

codT2Samp

A 2-sample ttest for every voxel

codT2Raw

Contains the Tvalues for all voxels for the 2 sample map

iMask

A mask index when switching from the complete 53*63*46 volume (about ~160 000 voxels) to the actual voxels that are in the brain (~71000)

ind

A variable is a vector masked to only select voxels inside of mask and above the t-value threshold

codT2Samp

All the voxels FDR corrected if FDR is chosen

hSlover

A handle to a slover figure (just for graphics with few properties different from a regular matlab figure)

ipctb_saveCluster.m

adTc

The clustered timecourses containing clusters, timepoints, and sessions in a 3D matrix saved in ClustGrp1_tc.mat and ClustGrp2_tc.mat for each group respectively

ipctb_TimeLock.m

dIntraTpsPerSec

Counts the number of time points per seconds that appear after interpolation

gIpc.dLockTime

Contains the time in seconds (usually 10 seconds) that will be displayed after the chosen onset (usually a target)

suTemp(iSess).rodOnsets

(only in ipctb_TimeLock.m) are the valid start times in seconds (of the onsets) that will be added to the time locked average timecourse (see fig. 6). Note that the variable is a structure of vectors per sessions, where rodOnsets are the vectors.

B

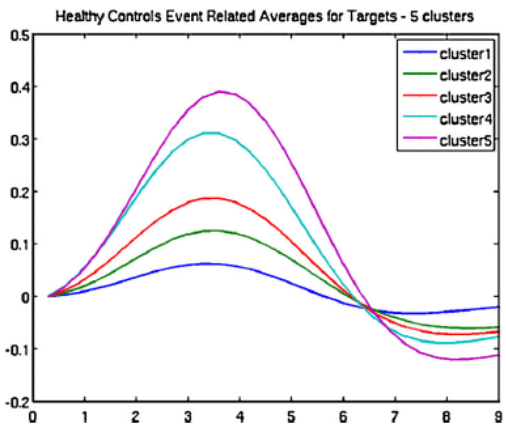


Fig. 6. Event-related averages for targets – five cluster results for healthy controls.

adTcTimeLocked

The two-dimensional array that stacks all windowed timecourses for a single cluster (onset derived timecourse part, the recorded timecourse are not in the secondstime dimension but in timeindex dimension)

adTcLockedMn

Collapses all the onset derived timcourse part by taking the mean of them all for each cluster (in walkthrough there are 5 clusters) and its dimensions are the clusters, timeindex

ipctb_sloverDisp.m

oSlover

The slover application object.

GIPC_Defaults.m

Note - All time is measured in seconds unless stated otherwise.

gIpc.bFdr

FDR (False Discovery Rate) Corrected or uncorrected
If uncorrected the p-threshholds are uncorrected.
(If group has too few subjects FDR-correction may sort away all results and therefore is better switched to uncorrected to get any results)

gIpc.dTr

Seconds per TR

gIpc.dSyncFact

Factor to interpolate TR more synchronized with seconds. Higher factor makes TR more interpolated to seconds and will find better match to onsets. However there are factors that interpolate TR to match the onsets exactly.

gIpc.bOnsetInTr0Sec1

Units used in the onset file

gIpc.nSplit

Memory splitter - higher integers makes ipctb run with less memory (and slower), but may need to be higher for computers with less memory.

gIpc.nClusters

Number of clusters for cluster images

gIpc.ronSloverSlices
Brain slices in Z direction (displayed in slover)

gIpc.nSess(1).susOnset, gIpc.nSess(2).susOnset
Onsets of 3 different types for 2 sessions/runs
Symbol used in graph, Line type and color (':k'=dotted black), filename of tab/commaseparated onset file in the onset directory of GIPC

gIpc.sTitleGrp1, gIpc.sTitleGrp2
Timelock Graph titles

gIpc.sOnsLockType
Onset type to lock to

gIpc.dLockTime
Time after lock that will be graphed (seconds)

gIpc.cmClust
Cluster colors (first has to be 0 0 0)

gIpc.dFdrQ1Samp, gIpc.dFdrQ2Samp
Defaults for p-val thresholds expressed as a decimal (1.0 = 100%)

gIpc.sDirSave
Default directory for output data (forward/backslash will depend on Windows/Unix platform convention)

gIpc.b2SampT_Grp1Min2
2 sample T-test order if b2SampT_Grp1Min2 = false, it means grp2 minus grp1 instead

gIpc.sFileT2, gIpc.sFileT2Unthresh
Filenames for 2 sample t-test

gIpc.sGrp1, gIpc.sGrp2
Names of resulting correlational image files

gIpc.sClust1, gIpc.sClust2
Cluster file names including start of time courses

gIpc.sImageDir
Default output directory name (not full path) for images

gIpc.sMaskDir
Directory name (not full path) for masks

gIpc.bSkipStep1

Set to true if all correlation maps are already saved (i.e. you have already run GIPC once on a set of data). This allows for quick re-computing of activation maps with different p-values without needlessly re-calculating the same correlation maps again. You may copy these files to an output directory (put the correlation maps in their sub folders Grp1 and Grp1) plus you need to copy the settings.mat to the new output folder. Note! The source nifti-files has to remain at location they existed at original run!

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