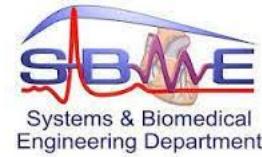




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心跳 Magnetic Resonant Imaging - SBE311-B 📸

MRI - TASK 2 - MRI & fMRI Visualization and Analysis 📈

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please let us know if we need to provide any additional data

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1 Preprocessing

1.1 Realigning and Unwarping the Data

Realign (Estimate & Reslice) Button.

Estimate: Estimating the amount that each volume is out of alignment with a reference volume.

Reslice: Indicates that these estimates will be used to nudge each of the volumes into alignment with the reference volume.

Steps: Realign and estimate button \Rightarrow Estimate and Reslice \Rightarrow Data (double click add session) \Rightarrow return to data and choose **new session** \Rightarrow click on each session and add all the 146 frame.

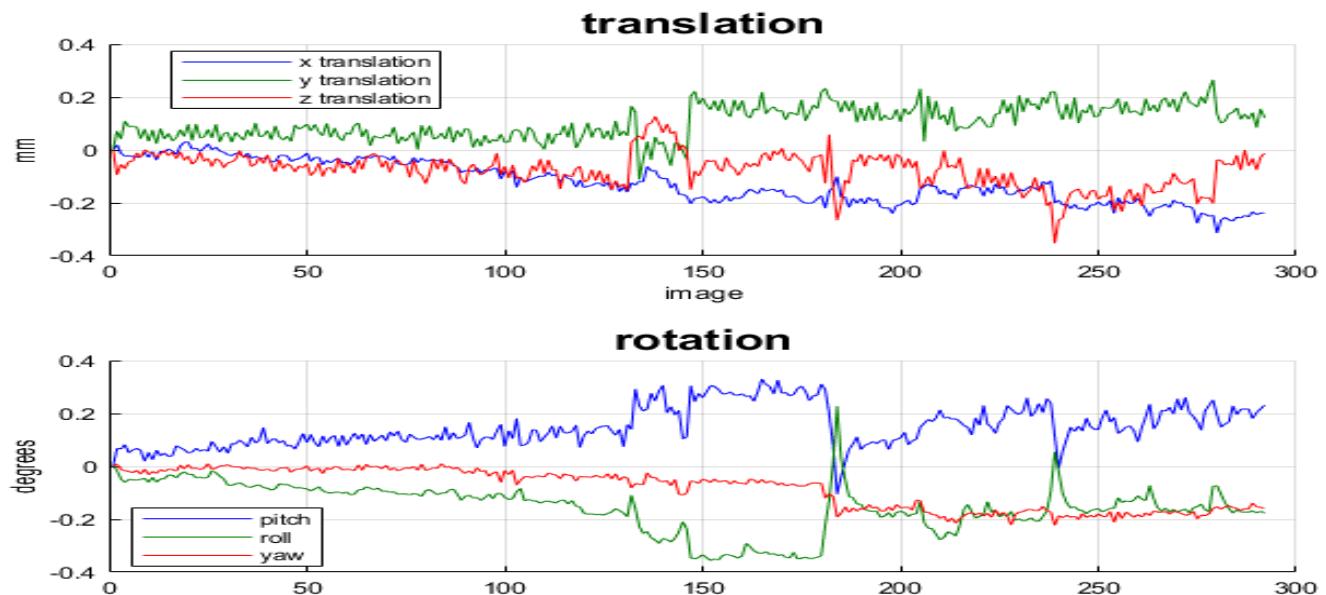


Figure 1: Realignment and Slicing

Traslation: is how the subject moves along each axes.

Rotation is how the subject rotates around each axes.

The guideline is to remove the runs in which the subject moves by more than one size voxel (3mm) for the entire run or half a size of a voxel (1.5mm) for a single volume.

The two runs are concatenated in one graph.

1.2 Slice-Timing Correction

FMRI volume is acquired in slices. Each of these slices takes time to acquire - from tens to hundreds of milliseconds. The two most commonly used methods for creating volumes are sequential and interleaved slice acquisition. Sequential slice acquisition acquires each adjacent slice consecutively, either bottom-to-top or top-to-bottom. Interleaved slice acquisition acquires every other slice, and then fills in the gaps on the second pass.

slice-timing correction can lead to significant increases in statistical power for studies with longer TRs (e.g., 2s or longer), and especially in the dorsal regions of the brain.

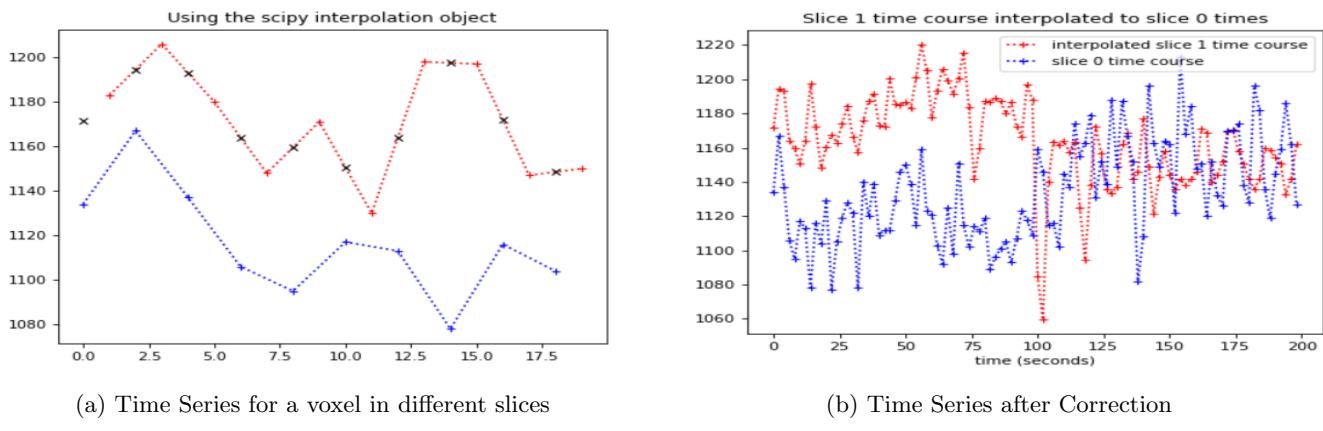


Figure 2: Slice Timing Correction

The scanner collected each volume slice by slice. That means that each slice corresponds to a different time. Knowing TR and the method used to create volumes; The time that the scanner takes to acquire a single slice will equal the TR/Number of slices.

We want to make a new 4D time series, where all the slices in each volume correspond to our best guess at what these slices would have looked like, if we had acquired them all at the same time.

We want to run some regression models on these data. We will make a predicted hemodynamic time course and regress the time series (slices over the 4th axis) against this time course so it would be convenient if all the voxels in one volume correspond to the same time.

Steps: Slice Timing Button \Rightarrow Data \Rightarrow add two sessions \Rightarrow use regular expression `^rsub-08-task-flanker-run-1.*` to filter your results \Rightarrow use regular expression `^rsub-08-task-flanker-run-2.*` choose all the 147 frame \Rightarrow write `V = spm-vol('sub-08-task-flanker-run-1-bold.nii')` to get the image header \Rightarrow write `V(1).dim` and get the number of slices in z direction \Rightarrow `TR = 2` , `TA = TR-(TR/Z slices) = 2-(2/40)` \Rightarrow Slice order enter `[1:2:40 2:2:40]`, and for the Reference Slice enter a value of 1 .

1.3 Coregistration

coregistration: Align the two sets of images (func, anat) as best we can. If we want to do a group analysis we need to ensure that each voxel for each subject corresponds to the same part of the brain. If we are measuring a voxel in the visual cortex, for example, we would want to make sure that every subject's visual cortex is in alignment with each other.

Coregister the functional data to the anatomical data(align the two sets of images as best we can).

This is done by Registering and Normalizing the images. Just as you would fold clothes to fit them inside of a suitcase, each brain needs to be transformed to have the same size, shape, and dimensions. We do this by normalizing (or warping) to a template. A template is a brain that has standard dimensions and coordinates - standard, because most researchers have agreed to use them when reporting their results.

Warp the images to a template, Affine transformation is used (translation, rotation, zoom, shear).

Registration and Normalization

Our goal is to warp the functional images to the template so that we can do a group-level analysis across all of our subjects.

Method:

- Align the outlines of the image.

- take advantage of anatomical and functional contrast weightings(CSF bright in functional data and dark in anatomical image) The registration algorithm moves the images around to test different overlays, matching the bright voxels on one image with the dark voxels of another image, and the dark with the bright, until it finds a match that cannot be improved upon. This procedure is also known as a cost function.
- the same transformations that were used to warp the anatomical image to the template are applied to the functional images.

Steps: Coregister (Estimate & Reslice) \Rightarrow input a Reference Image and a Source Image \Rightarrow The Reference Image is the image that will remain stationary(Functional) \Rightarrow The Source Image is moved around until a best fit is found between the Reference and the Source image using the cost function.(anatomical meansub-08).

Normalised Mutual Information Coregistration

$$X1 = -0.333*X + 0.002*Y + 0.000*Z + 61.309$$

$$Y1 = 0.002*X + 0.333*Y - 0.005*Z - 9.590$$

$$Z1 = 0.000*X + 0.004*Y + 0.250*Z - 8.345$$

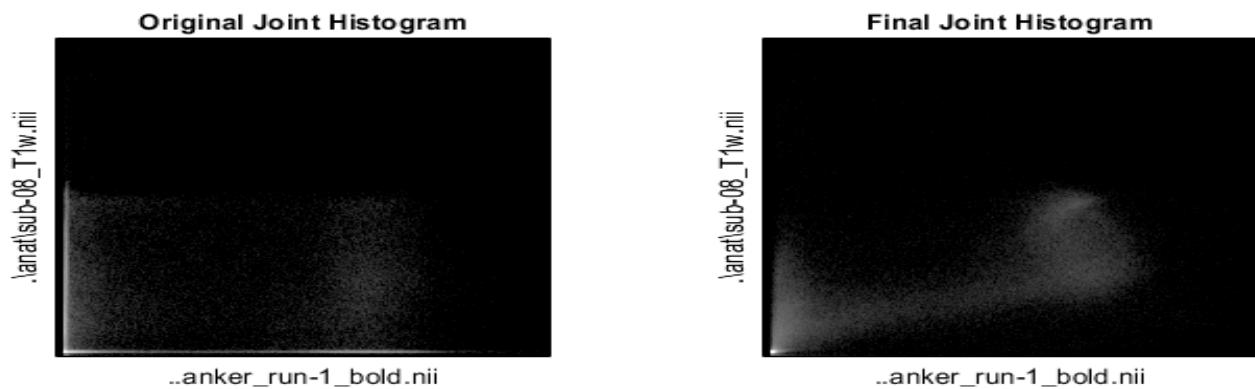


Figure 3: Coregistration

1.4 Segmentation

Mapping the tissues of anatomical image to the tissue of the template will increase the accuracy of the registration (CSF, Gray Matter, White Matter, Skull, Soft Tissue, All Other Tissues)

Steps: Segmentation \Rightarrow Volumes \Rightarrow rsub-08-T1W.nii \Rightarrow set save bias corrected to save bias corrected \Rightarrow Set Deformation Fields to Forward.

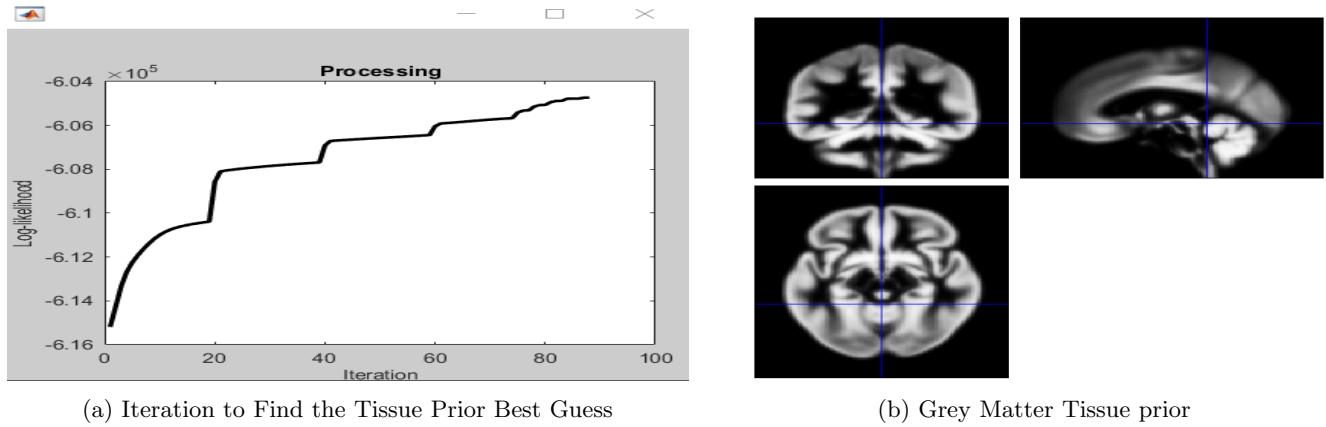


Figure 4: Segmentation

1.5 Normalization

We will use the output from segmentation to normalize our data.

Steps: Normalize (Write) \Rightarrow Data \Rightarrow create new subject \Rightarrow set deformation field to "y-rsub-08-T1w.nii" \Rightarrow images to write select all realigned and slice time corrected images (^ ar 1:146)

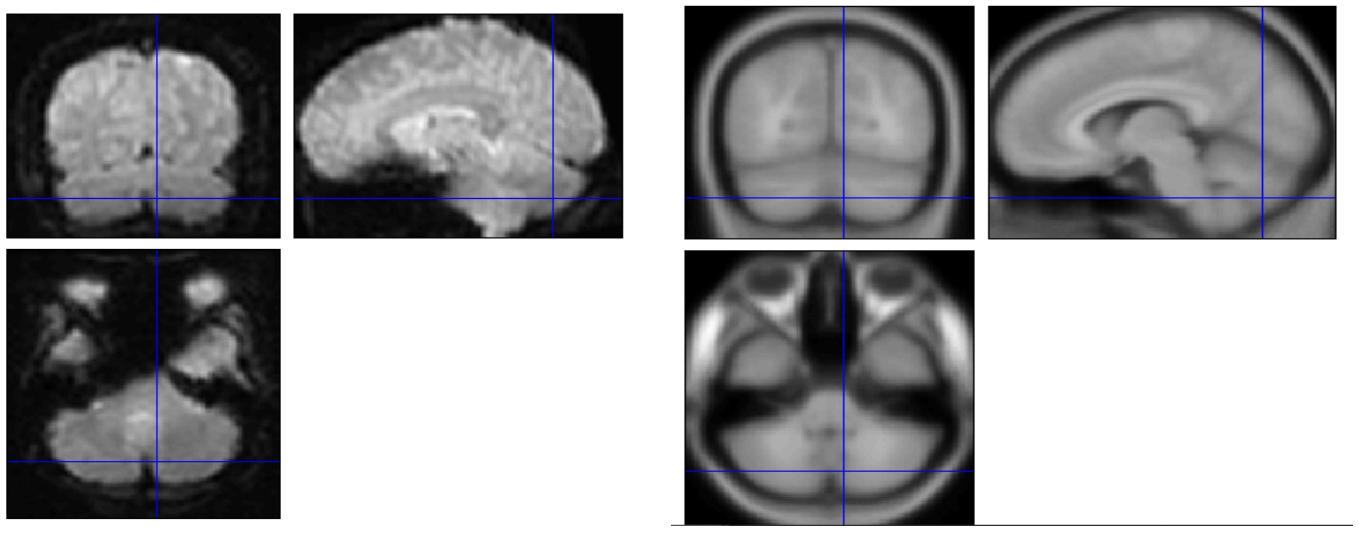


Figure 5: Normalization

The template singl-subj-1.nii will have the clearest spatial resolution. visualizing The results on this template may be slightly misleading, since each subject's anatomy has been warped and blurred; activation that appears to be in a specific location on the single-subj-T1 template may not be as specific as it appears.

It is recommended to visualize your activation on one of the averaged templates, or on an average image consisting of the mean of your subject's normalized anatomical images.

1.6 Smoothing

It is common to smooth the functional data, or replace the signal at each voxel with a weighted average of that voxel's neighbors. Smoothing does decrease the spatial resolution of your functional data. In fMRI noise to signal ratio is high so averaging over nearby voxels we can cancel out the noise and enhance the signal.

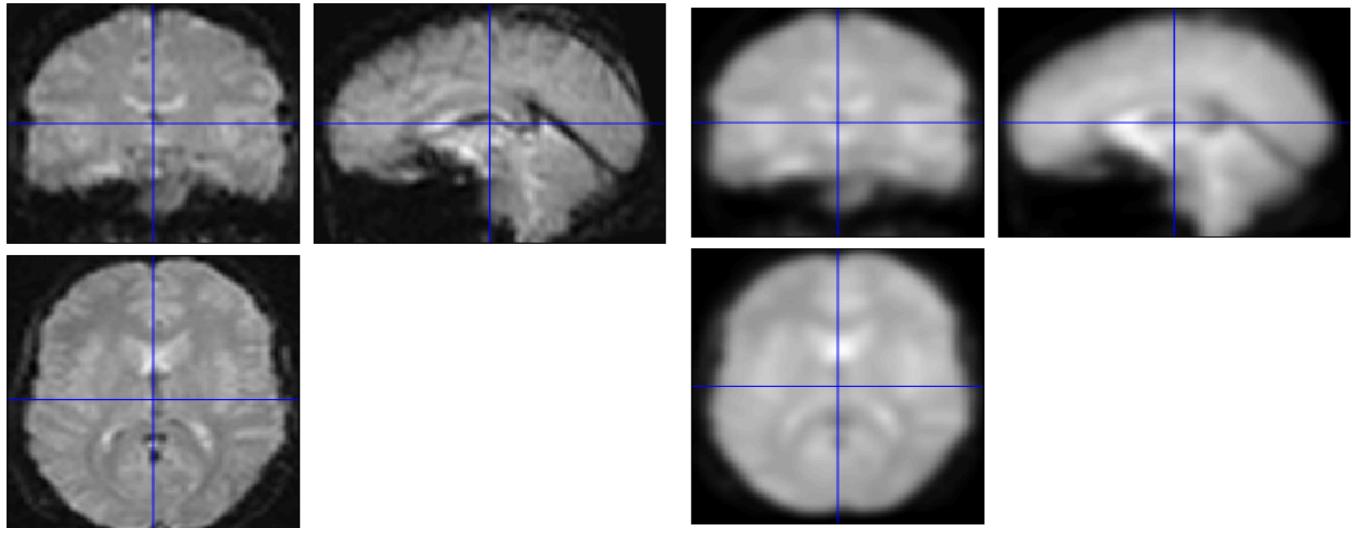


Figure 6: Smoothing

Steps: Smooth button \Rightarrow Images to Smooth \Rightarrow Select the warped functional images \Rightarrow expand them to include all 146 frames for each run.

2 Statistics and Modeling

After preprocessing the functional data we can fit a model to that data. To do that we need to understand some fundamentals such as the General Linear Model, the BOLD response, and what a time-series?

2.1 The Time-Series

fMRI datasets contain several volumes strung together like beads on a string; we call this concatenated string of volumes a run of data. The signal that is measured at each voxel across the entire run is called a time-series.

2.2 BOLD Signal as an Indirect Measure of Neural Firing

Whenever a stimulus is presented - such as a flash of light, or a sudden noise - that stimulus is transduced by the sensory organs into nerve impulses, which in turn stimulate neuronal firing in the brain. Neurons that fire require oxygen, and oxygen is delivered by the blood. That oxygenated blood in turn increases the signal from nearby hydrogen in the water in your body, which is what is measured in the scanner.

This is the measure used to infer whether a given region of the brain is “active” or not. And to make those inferences, we will need to take a closer look at the BOLD signal, experimental designs, and how we integrate the two with mathematical models.

2.3 The Hemodynamic Response Function (HRF)

This is important not only for modeling the link between neural activity and blood flow, and from there to the observed signal, but for how we define a model to test which brain regions show a significant change in their BOLD response to a given stimulus.

The BOLD signal also appeared to follow a consistent shape, peaking around six seconds and then falling back to baseline over the next several seconds. This shape can be modeled with a mathematical function called a Gamma Distribution. When the Gamma Distribution is created with parameters to best fit the BOLD response observed by the majority of empirical studies.

the Gamma Distribution is called a basis function. We call it a basis function because it is the fundamental element, or basis, of the model we will create and fit to the time series of the data. Furthermore, if we know what the shape of the distribution looks like in response to a very brief stimulus, we can predict what it should look like in response to stimuli of varying durations, as well as any combination of stimuli presented over time.

Figure 7: The Hemodynamic Response Function (HRF)

2.4 The General Linear Model

The General Linear Model. With a GLM, we can use one or more regressors, or independent variables, to fit a model to some outcome measure, or dependent variable. To do this we compute numbers called beta weights, which are the relative weights assigned to each regressor to best fit the data. Any discrepancies between the model and the data are called residuals.

GLM can be represented by this equation:

$$Y = \beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3 + \epsilon$$

where, Y(Dependant variable)(**Brain Activity**) can be predicted using X(independant variables) (**Incongruent , Congruent**) by computing the beta weights β_1, β_2 (**HRF Response**) scaled up and down relative to the contribution of congruent and incongruent conditions in predicting the Brain activity.

2.5 Creating Timing Files

Since every voxel has its own time-series, we do the procedure above for every voxel in the brain. This is known as a mass univariate analysis, since we estimate beta weights for each voxel's time-series.

Our goal is to create the fitted time-series so that we can use the estimated beta weights in a group-level analysis. But to do that, we first need to create our ideal time-series.

Within each subject's func directory are files labeled **events.tsv**. These files contain three pieces of information that we need to create our timing files (**onset Times**). This is very helpful in estiating the Design Matrix.

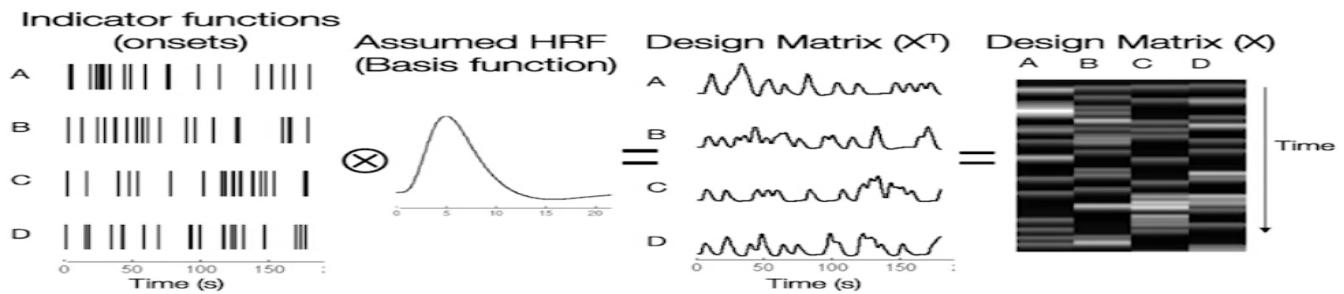


Figure 8: Convolution of HRF with Flanker Onset Times

The onset timing for each condition of each subject is created using a **Matlab Script** you can find this script in our submitted folder with name **convertOnsetTimes.m**

3 First Level Analysis

The timing files are used in conjunction with our imaging data to create statistical parametric maps. These maps indicate the strength of the correlation between our ideal time-series (which consists of our onset times convolved with the HRF) and the time-series that we collected during the experiment.

The amount of modulation of the HRF is represented by a beta weight, and this in turn is converted into a t-statistic when we create contrasts using the SPM contrast manager.

Steps: Specify 1st-Level \Rightarrow mkdir 1stLevel \Rightarrow choose the directory you just created \Rightarrow fill in the Timing parameters \Rightarrow select Seconds in Units for design, \Rightarrow enter a value of 2 for Interscan Interval \Rightarrow Data & Design \Rightarrow create two sessions \Rightarrow for each session(run) under Scan section filter your functional data to include all files begin with ^ swar \Rightarrow for each session(run) add two conditions Inc, Con \Rightarrow type **IncRun1 = importdata('incongruent(or congruent)- run1(2).txt');** **Inc(con)Run1(1)(:,1)**

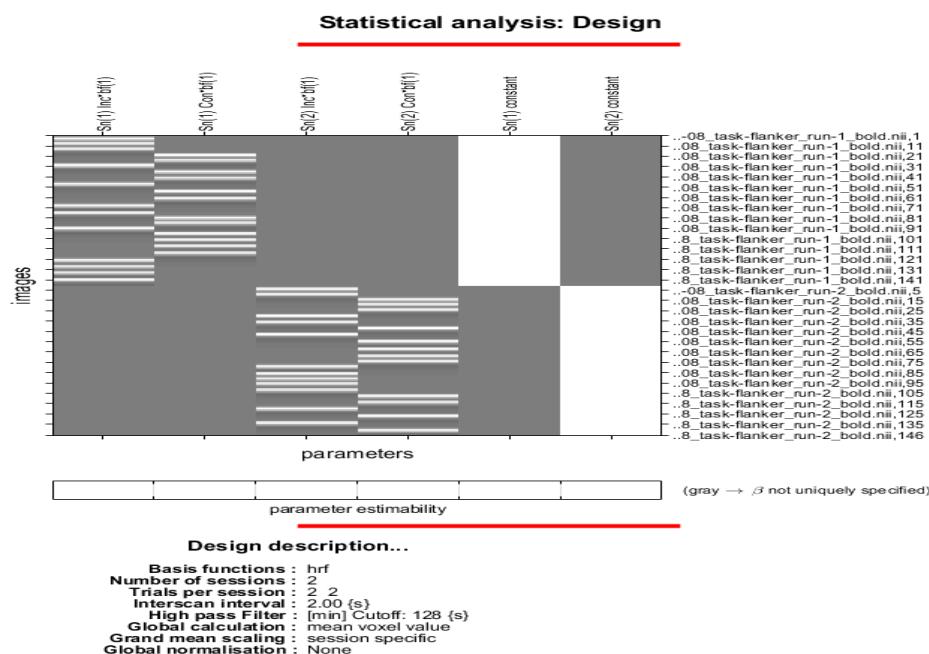


Figure 9: Design Matrix

3.1 Estimating The Model & The Contrast Manager

Steps: Estimate \Rightarrow Select SPM.mat (created from the last step) \Rightarrow Change Write residuals to Yes \Rightarrow Navigate to the 1stLevel directory and select the SPM.mat file.

Contrast Steps: Results \Rightarrow Define New Contrast \Rightarrow In the Name field type Inc-Con \Rightarrow In the contrast vector window, type 0.5 -0.5 0.5 -0.5, and then click submit.

Contrast weights of 0.5 and -0.5. instead of 1 and -1 because we are accounting for the number of runs in our study. We will divide our contrast weights of 1 and -1 by the number of runs that we have: e.g., $1/2 = 0.5$, and $-1/2 = 0.5$.

If we used a contrast vector of [1 -1 1 -1], the resulting **t-statistic would be the same**, but the **contrast estimate would be inflated** in proportion to the number of runs in our study.

3.2 Examining The Output

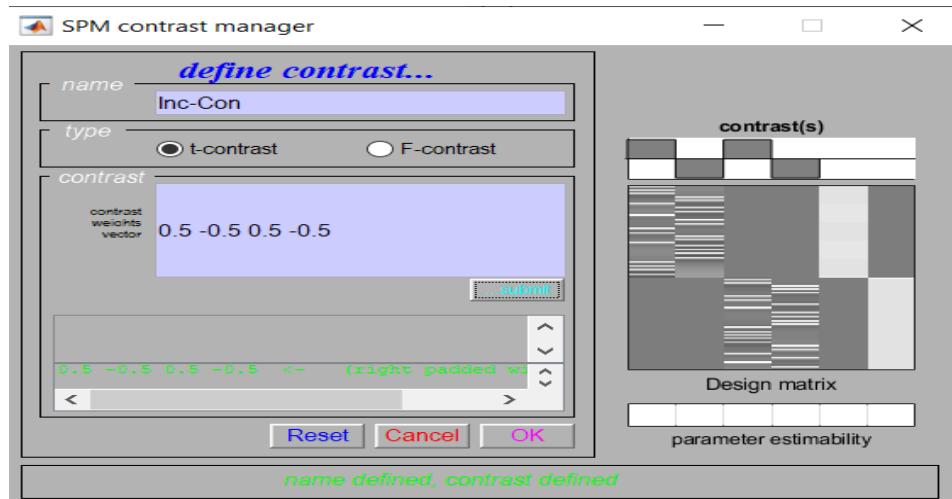
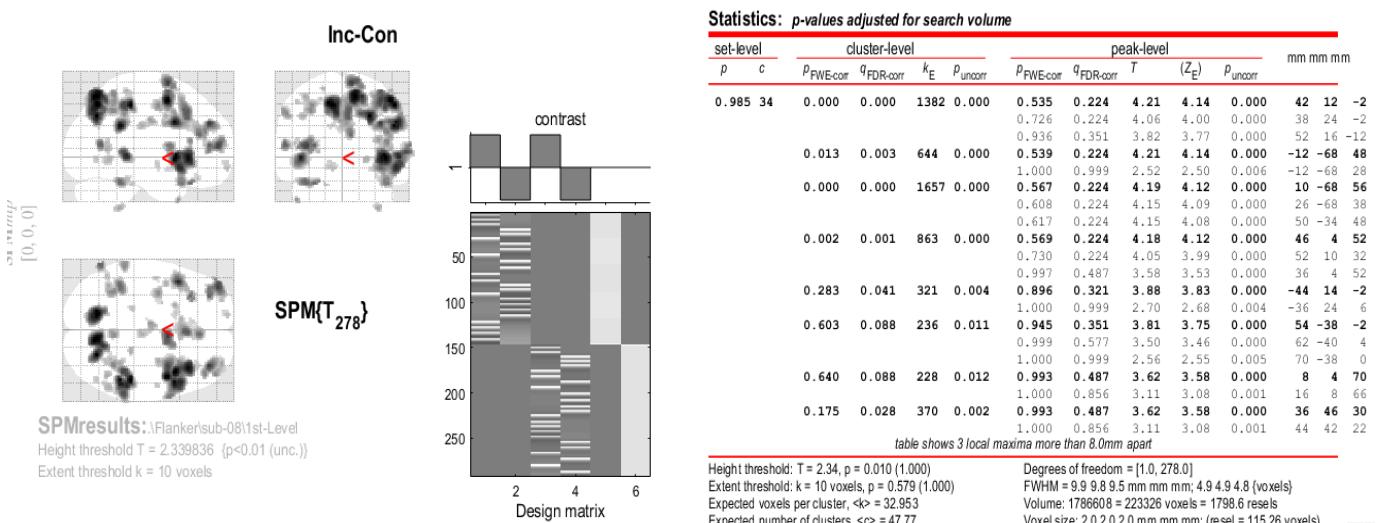


Figure 10: Contrast Estimation

Steps: apply masking: Set this to none (examine all of the voxels in the brain) \Rightarrow p value adjustment none \Rightarrow set the uncorrected p-value to 0.01 (**This will test each voxel individually at a p-threshold of 0.01.**) \Rightarrow extent threshold voxels Set to 10 which will only show clusters of 10 or more contiguous voxels.

This eliminate specks of voxels most likely found in noisy regions. Cluster correction will be done at the group level to appropriately control for the number of individual statistical tests.



(a) 1st Level Results on Glass Brain

(b) 1st Level Statistics Results

Figure 11: First Level Analysis

Results are displayed on a glass brain. Dark spots representing clusters of voxels that passed our statistical threshold.

The results can be also overlayed on an image other than the glass brain.

steps: Select overlays \Rightarrow select sections \Rightarrow Navigate to the spm12/canonical directory, and choose any of the T1 brains that you like. We will select **the avg152 brain**.

4 Scripting and Setting the Origin

Steps: open up the SPM GUI \Rightarrow click on the Batch button \Rightarrow From the top of the Batch Editor window \Rightarrow click on the SPM menu and select the following modules in this order to serve us as a template for all our subjects after generating the script.

All the steps are the same except making dependencies to take the output of each step as an input for the next. better [Read The Docs](#).

You can Find Our Own Script in our submitted directory **RunPreproc-TemplateAllsubjects-job.m**

An important step before running the script is to **Set the Origin** for all the anatomical data. The initial preprocessing steps, such as realignment and slice-timing correction, appear to have run without any errors. When we look at the output of coregistration Although the functional data looks normal, **the realigned anatomical image is flipped**.

If we look at the output of later stages, such as normalization or the 1st-level analysis, this error has been propagated to the functional data as well.

This originate due to **The centres of the anatomical and functional images are very far away from each other**, which causes the errors listed above.

To solve this error we need to set the origin at the anterior commissure, a bundle of white matter fibers that connect the anterior lobes of the brain.

Steps: point your crosshairs to the anterior commissure(see fig(12)) \Rightarrow click the Set Origin \Rightarrow click the Reorient button to permanently set this new origin of the anatomical image and any functional images. \Rightarrow run the script again the result will be correct.

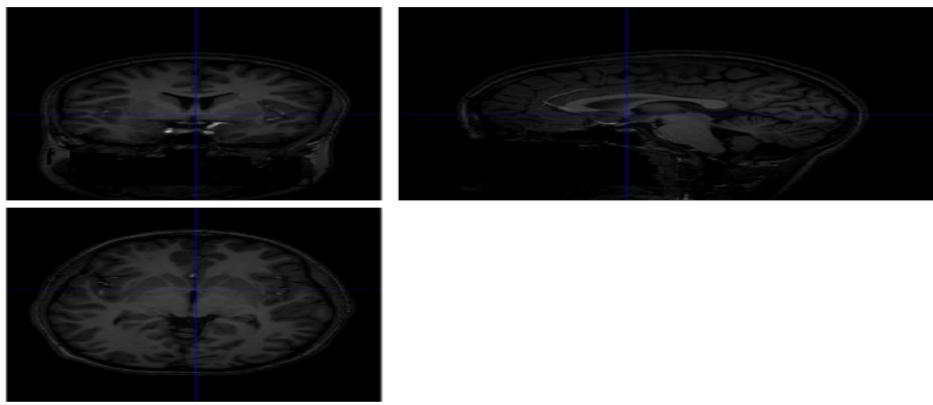


Figure 12: Anterior Commissure Near the Ventricles

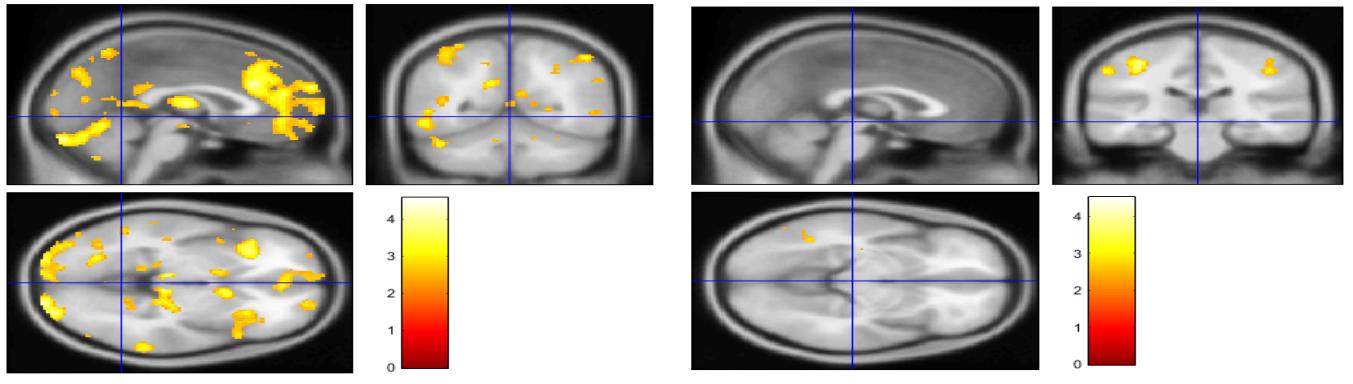
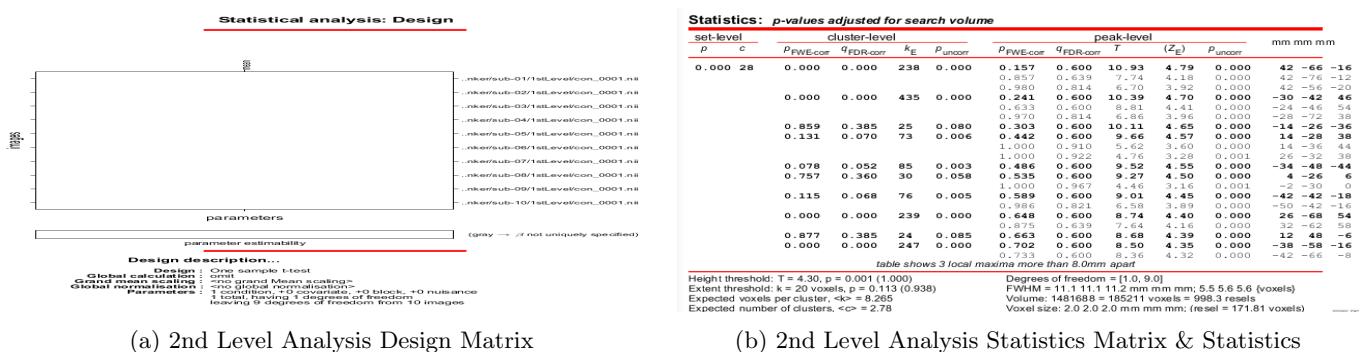


Figure 13: 1st Level Analysis sub-01 & sub-03

5 2nd Level Analysis



(a) 2nd Level Analysis Design Matrix

(b) 2nd Level Analysis Statistics Matrix & Statistics

Figure 14: 2nd Level Analysis

Group-Level Analysis: Calculate the standard error and the mean for a contrast estimate, and then test whether the average estimate is statistically significant. performs a t-test over the mean parameter estimates from each subject.

This design matrix looks like a white box. That indicates that there is only one regressor to test, namely the mean activation across all of the individual contrast images that went into the model.

Steps: mkdir 2ndLevel-Inc-Con \Rightarrow click on the button Specify 2nd-level \Rightarrow click on the Directory field, and select the 2ndLevel-Inc-Con folder \Rightarrow Scans : navigate to subjects 1stLevel directory, and select the Incongruent-Congruent contrast image, con-0001.nii .

For Contrast: Estimate button \Rightarrow Select the SPM.mat from 2ndLevel directory \Rightarrow overlay on avg152T1 brain template. \Rightarrow Results \Rightarrow Define new contrast \Rightarrow Contrast weight of 1.

We estimate congruent and incongruent contrast separately (1side t-test)

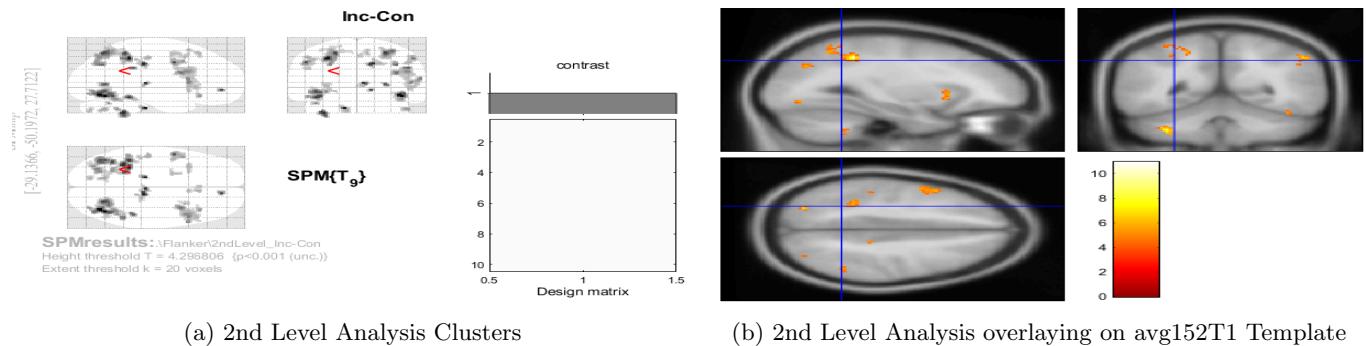


Figure 15: 2nd Level Analysis Clusters & Overlaying

6 Region of Interest Analysis - ROI

Group Level Analysis is called a whole-brain or exploratory analysis. These types of analyses are useful when the experimenter doesn't have a hypothesis about where the difference may be located.
we could restrict our analysis to this region and only extract data from voxels within that region. This is known as a region of interest (ROI) analysis(confirmatory analysis).

6.1 ROI Analysis Using Atlases from (WFU PickAtlas toolbox)

Steps: WFU PickAtlas toolbox \Rightarrow HUMAN ATLAS \Rightarrow From previous studies of cognitive control we would expect our study to show significant BOLD activity in the dorsal anterior cingulate (dACC) region \Rightarrow Brodmann Area 32 \Rightarrow In the left menu click the ADD \Rightarrow in the DILATE field \Rightarrow Enter a value of 1 and click 3D.

6.1.1 Extracting Data from the Anatomical Mask

There are two ways of extracting listed below:

- Extract the contrast estimate Incongruent-Congruent from our stats file; or
- Extract the individual beta weights for Incongruent and Congruent separately, and then take the difference between the two.

We will be focusing on the second method. This method allows you to determine what is driving the effect, whether a significant effect is due to both beta weights being positive but the Incongruent beta weights being more positive, both weights being negative but the Congruent betas more negative, or a combination of the two. It is only by extracting both sets of beta weights that we can determine this.

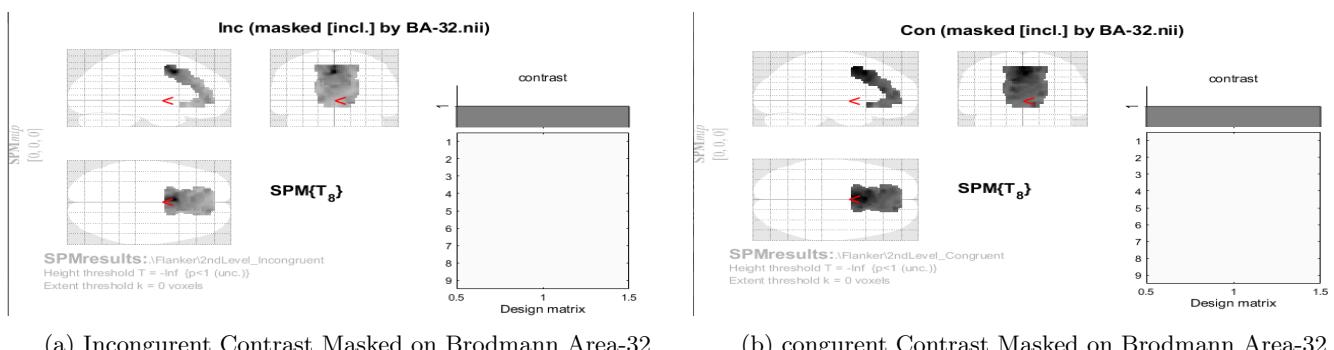


Figure 16: Incongruent & Congruent Contrasts Masked on Brodmann Area-32

Results: $h = 1$, $p = .0313$, $ci = 0.0240:0.3909$, $tstat = 2.6071$, $df = 8$, $sd = 0.2387$. The test was run on 9 subjects only. steps: list of contrast estimate for each subject for each voxel in the mask

6.2 ROI Analysis Using spherical ROI approach

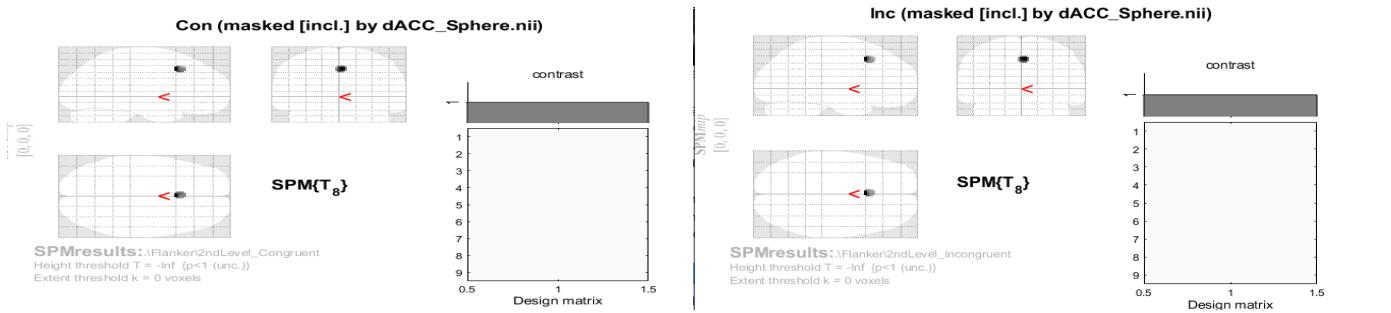


Figure 17: Incongruent & Congruent Contrasts Masked using Spherical ROI Approach

Results: $h = 1$, $p = .0337$, $ci= 0.0518:0.9945$, $tstat = 2.559$, $df = 8$, $sd = 0.6132$. The test was run on 9 subjects only. steps:..... list of contrast estimate for each subject for each voxel in the mask.