

FMRI Cognitive Control Analysis

Youssef Shawki

September 21, 2024

Abstract

A well-processed fMRI data could help tremendously in attaining reliable results, which could be useful for post-processing tasks. Towards that end, we would consider the applicable steps of the pre-processing stages involved in processing the Flanker dataset [1] by making use of FSL tool. In addition, we will systematically examine each pre-processing step, fine-tuning its parameters to gain a deeper understanding of their functionality. At the end, we would see the accumulated effect of such pre-processing step on the functional and anatomical MRI data of one subject. Afterwards, we would give an overview about the brain anatomy by exploring the FSL's atlases on the standard MNI space. After that, we would start modeling and conducting statistical analysis. Finally, we would conduct a ROI analysis to determine the clusters of high statistical significance.

Keywords: fMRI, Pre-processing, Flanker Dataset, Post-processing, FSL, anatomy, atlases, MNI space, statistical analysis, ROI analysis.

1 Introduction

As we might know, the fMRI signals stem from the variation in oxygenated blood in different regions in the brain in what is known as blood-oxygen-level-dependent (BOLD) signal, which in turn reflects the changes in the environmental magnetic properties of each region. The reason behind this changes arises from the nature of the oxygenated and deoxygenated blood. The oxygenated blood acts as diamagnetic material, due to the presence of oxygen ions, which introduce a shielding that prevent the magnetic flux from manipulating iron atoms in the hemoglobin. On the other hand, the deoxygenated blood acts as paramagnetic material which conducts magnetic flux very well. By detecting such difference in magnetic properties, we could measure the region of activation corresponding to specific task.

Practically, this measurement process is modulated with some fluctuations, or rather noise, that are not of our interest, such as head motion, random drifts, breathing, and heartbeats. These noisy signals are inevitable and we need to know how we could deal with them. Some of them are periodic in somehow and could be regressed out of the data by modelling, while others are not. This where the role of pre-processing comes in, which involves several steps including **brain extraction, Motion correction, slice time correction, smoothing and registration and normalization**. We would explore each one of them in the upcoming sections by applying such techniques on a real fMRI dataset using FSL. But before, we would consider the neuro-anatomy of the brain to build a solid background, upon which we would continue our exploration of the dataset. Finally, we would apply statistical analysis to extract valuable insights from the data.

The dataset used involves the Flanker task, which is designed to tap into a mental process known as cognitive control. Let us define we're going to define cognitive control as the ability to ignore irrelevant stimuli in order to do the task correctly. This dataset contains 26 subjects with each having structural MRI image (**T1-weighted**) and 2 sessions of functional MRI (**T2*-weighted**) each of 146 volumes with repetition time of 2sec and voxel dimension of 4mm. Throughout the paper, we would consider experimenting with subject (8). We could see part of the header file information of the run 1 fMRI data of that subject in [1].

```
joyou159@youssef:~/Downloads/Data/sub-08/fun$ fslhd sub-08_task-flanker_run-1_sub-08_task-flanker_run-1_bold.nii.gz sub-08_task-flanker_run-1_events.tsv
joyou159@youssef:~/Downloads/Data/sub-08/fun$ fslhd sub-08_task-flanker_run-1_bold.nii.gz
fslname          sub-08_task-flanker_run-1_bold.nii.gz

sizeof_hdr      348
data_type        INT16
dim0             4
dim1             64
dim2             64
dim3             40
dim4             146
dim5             1
dim6             1
dim7             1
vox_units        mm
```

Figure 1: The header file of fMRI data of run 1 for subject 8

2 Dataset Inspection

Before jumping into the pre-processing stage, it's a good practice to inspect your dataset to get some sense about its quality, in what is known as **Quality Control**. In this stage, we have explored the dataset manually to report any artifacts or noise in either the functional or structural MRI data. This might give us some overview about the data we are about to work on and provide guidelines of how to deal with it in the pre-processing stage. Furthermore, we could rely on that to assess how well we have done in the pre-processing stage, by looking at the data after being processed.

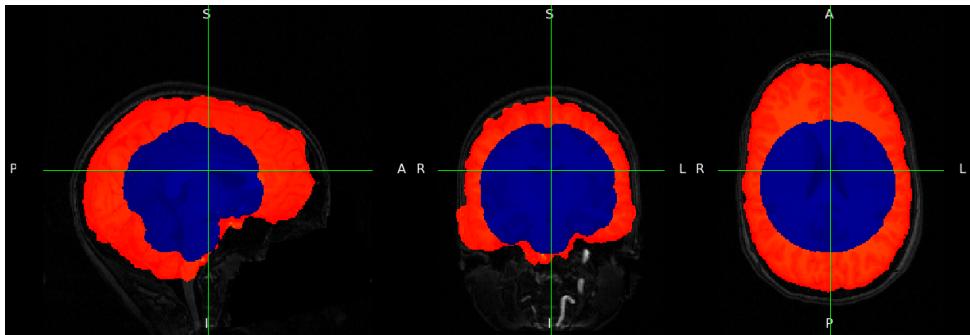


Figure 2: Skull stripping with different values of FIT, blue for (0.9) and red for (0.1)

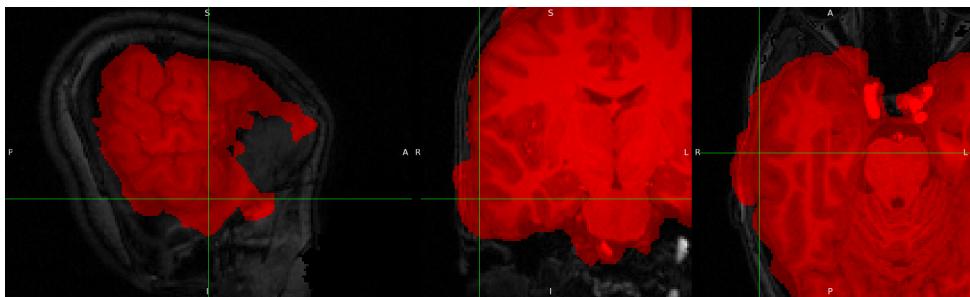


Figure 3: Bad skull stripping result due to conservative value of FIT (0.1)

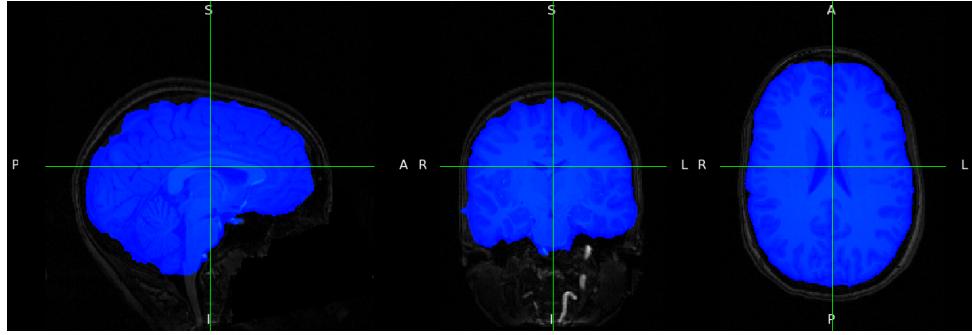


Figure 4: Best skull stripping at FIT value of (0.2)

Table 1: Quality Control Assessment of the 26 Subjects Included in the Dataset

Subject no	Structural		Functional	
	Artifacts	Facial Removal	Run 1	Run 2
1	--	++	+	+
2	--	+	+	+
3	--	-	++	++
4	--	-	+	+
5	--	-	+	+
6	--	+	+	+
7	--	++	+	+
8	--	++	--	--
9	--	-	--	--
10	--	+	+	--
11	--	+	+	+
12	--	+	--	+
13	--	++	+	+
14	+ (wrap around)	++	--	--
15	--	++	+	++
16	--	++	+	+
17	--	++	--	+
18	--	++	--	--
19	--	++	++	+
20	+ (wrap around)	-	+	--
21	+ (wrap around)	++	+	+
22	-	+	+	+
23	--	++	--	--
24	--	+	+	+
25	+ (wrap around)	++	+	+
26	--	-	+	+

The assessment criteria we have considered are as the following. For structural image, we have looked at the artifacts presented in this paper [2] besides facial removal. For functional

images, we have focused on motion artifacts. The assessment scheme has different levels, which are represented with these plus (+) and minus (-) symbols, where they mean **presence** and **lack of** respectively. Given that each one of them may be used to express different levels by its count, with 2 being the maximum. The assessment results are shown in table 1

3 Pre-processing Stage

3.1 Brain Extraction

Brain extraction or what is known as skull stripping is an essential step in our pre-processing stage, where it removes the bony cage and any non-brain areas from the structural image. The reason for that is being it a redundant data that we are not going to consider in fMRI study. For that purpose, we are going to use a tool in the FSL called BET (Brain Extraction Tool).

In order to get a satisfactory results, we are going to tune a threshold parameter used in the algorithm upon which the bet is built, namely the fractional intensity threshold (FIT) which ranges from 0 up to 1. Let's try with two different extreme values (0.1&0.9) on the structural image of subject (8) to get a sense of its effect.

As shown in figure 2, The higher the value of FIT the less conservative the algorithm about the brain tissue, this is clear in Blue-contrasted brain image. This high value of FIT (0.9) has resulted in losing a lot of info from the brain tissue, which worsens the situation further. On the other hand, the lower the value of the FIT, the more conservative the algorithm, which is obvious from red-contrasted brain image of FIT value of (0.1). The general rule is "*it is better to be on the side of leaving too much skull, as opposed to removing too much*".

From the previous trials, we could deduce that the best value for FIT is (0.2) as in figure 4. This value would prevent us from losing too much information about the brain, and at the same time would help us avoiding bad stripping as depicted in figure 3.

Manually iterating over all structural MRI data and adjusting the threshold value for skull stripping would not only be time-consuming but also prone to error. To streamline this process, we've developed a **Bash script** that automates the task, utilizing a default FIT value. While the script provides a baseline for processing, it's essential to review the results afterward. Variations in FIT accuracy across subjects may require adjustments, but the script offers a starting point for further refinement. The Bash script is provided in the Appendix.

3.2 Motion Correction

Movement during fMRI sessions could have severe consequences, potentially leading to misleading data and confounding variables. Excessive subject movement poses a significant risk, as it may result in the measurement of signals from voxels that have been shifted. Consequently, there is a danger of capturing signals from voxels located in different regions or tissue types during different parts of the experiment. Moreover, it gets worse if the experiment involves movement in response to stimuli, then we would not be able to distinguish the source of the signal. Therefore, motion correction step is very crucial for accurate results. For that purpose, we are going to use FEAT GUI of FSL tool, which indeed will last for the rest of pre-processing journey.

The motion correction is done using **MCFLIRT** algorithm, which indeed undo such motion

using rigid body transformation, including translation and rotation each of (3) degree of freedom, from some well-defined reference point in time. Let's run this algorithm on subject (8) and observe the results for both runs, given that the dimension of the voxel which included in the image header is 4mm. Therefore, we could use such piece of information as a measure of how powerful the movements in each run. We could use the following guidelines for checking "*If there is relative motion of more than half a voxel or absolute motion of more than a voxel, you may want to consider more advanced correction techniques such as scrubbing, or removing the run from the analysis altogether.*".

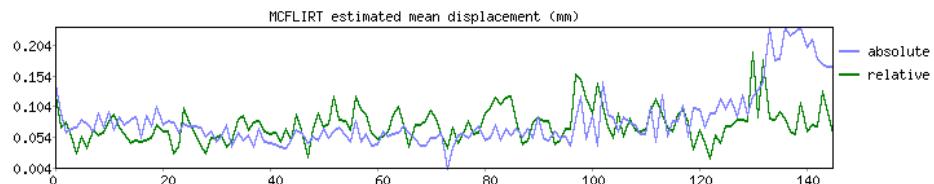


Figure 5: The absolute and relative mean displacement of each voxel in run 1 along all volumes

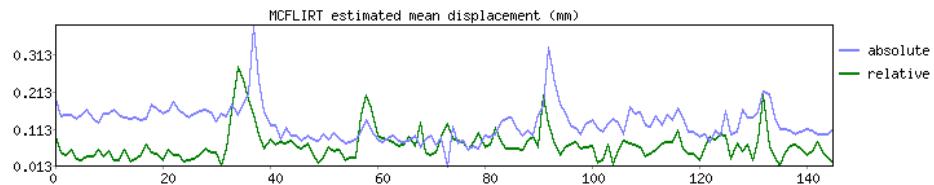


Figure 6: The absolute and relative mean displacement of each voxel in run 2 along all volumes

As depicted in figure 5, the maximum absolute and relative mean displacement in run 1 are extremely small, which indicates a good quality fMRI data as marked in the quality control table 1. The same applies to run 2 in figure 6, but in this case there are two peaks in the absolute and relative curves, indicating that the subject has moved slightly on wider period.

3.3 Slice-Time Correction

Unlike a photograph, in which the entire picture is taken in a single moment, an fMRI volume is acquired in slices. Each of these slices takes time to be acquired - from tens to hundreds of milliseconds. The two most common methods of acquiring volumes are sequential and interleaved slice acquisition. The sequential, as name implies, acquires the volume slice by slice from bottom to top or vice versa. On the other hand, the interleaved method, acquires slices intermittently and interpolate in-between.

This correction is very important only and only if the **TR** is high enough, (conventionally higher than 2 sec), otherwise it will be redundant computational cost. Fortunately, our dataset have been acquired at TR of (2), which exempts us from applying this pre-processing step.

3.4 Smoothing

For the sake of reducing the noise in the fMRI volumes, it's recommended to perform such filtration to suppress any sparks in the data. However, we need to keep in mind that if the

region of interest is expected to be small, it's better to leave smoothing out to avoid missing out important information.

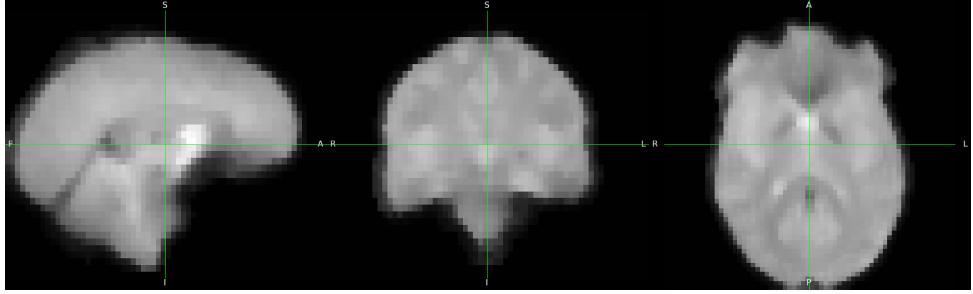


Figure 7: Smoothed fMRI data of run 1 with a kernel of size 3mm

As depicted in figures 7 through 9, as we increase the size of the filter used in smoothing, we get more blurred results, thus, more fine details about the brain vanish. Each filter size would be useful in specific context of interest, thus, we could not conclude from these results the best one to be used, however we would continue the rest pre-processing steps with the results of 5mm filter size.

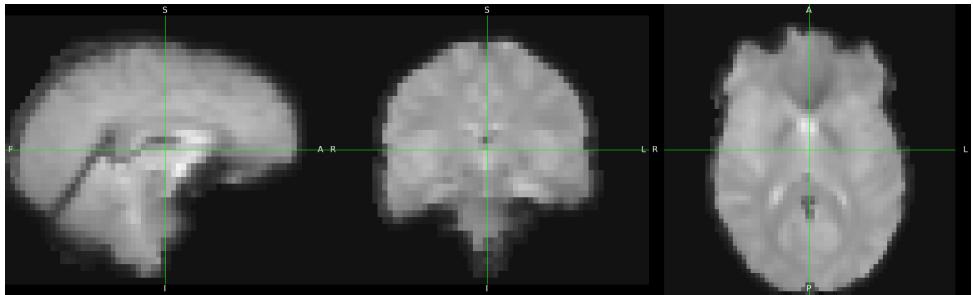


Figure 8: Smoothed fMRI data of run 1 with a kernel of size 5mm

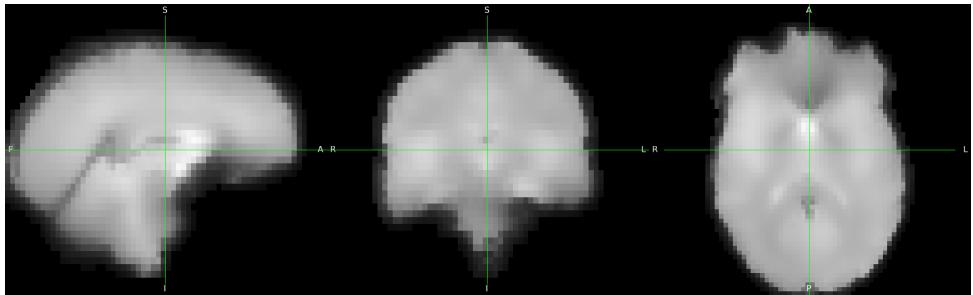


Figure 9: Smoothed fMRI data of run 1 with a kernel of size 12mm

3.5 Registration and Normalization

Although most people's brains are similar - everyone has a cingulate gyrus and a corpus callosum, for instance - there are also differences in brain size and shape. As a consequence, 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.

This is done by registering and normalizing the fMRI data. This is similar to folding clothes to fit them inside of a suitcase, each brain needs to be transformed to have the same size, shape,

and dimensions. Simply put, the meaning of registration is conducting alignment between the functional and structure images. The reason for this is to pave the way to transforming the functional to the **standardized space (MNI)** by means of the structural image as mediator, where we transform the structural MRI image to the MNI space and come up with the transformation matrix. since, thanks to registration, both structural and functional could speak the same spatial language. Now, what applies to the structural MRI could be applied to the functional MRI. Therefore we could make use of the transformation matrix used for structural and apply it to functional.

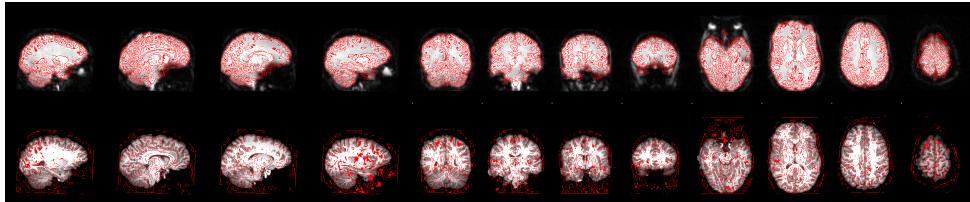


Figure 10: Registration of the functional MRI data of run 1 to the structural MRI data using full search & 12 DOF

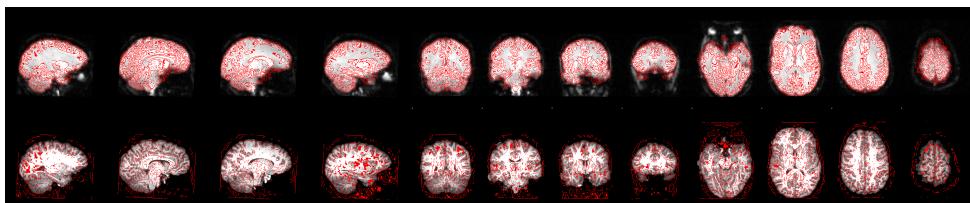


Figure 11: Registration of the functional MRI data of run 2 to the structural MRI data using full search & 12 DOF

The reason behind taking this far long way, is the low resolution of functional in contrast to functional. let's consider the output of this two steps to get a better sense of how it works.

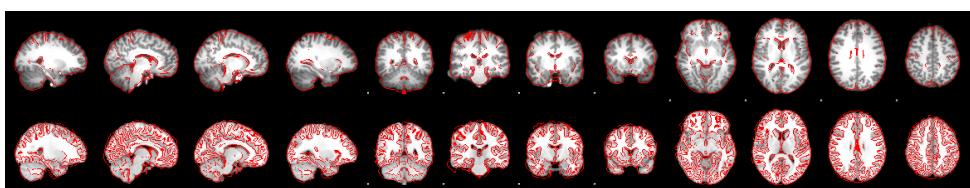


Figure 12: Normalization of structural MRI data onto the MNI space using full search & 12 DOF

As depicted by figures 10 & 11, the fMRI data (the gray scaled brain) of run 1 and run 2 is somehow well-aligned with the structural MRI data (red colored), which indicate a successful co-registration.

In figure 12, we could see the normalization of structural MRI data onto the MNI space. This normalization generates a transformation matrix that is required to transform the fMRI data to the MNI space.

In figures 13 & 14, we could see the normalization of the fMRI data (red scaled) of run 1 and run 2 on the standardized space or rather MNI space (gray colored), indicating successful

normalization of the data, and its readiness to contribute to the group analysis. This normalization has been done using the transformation matrix obtained from projecting structural MRI data onto the MNI space.

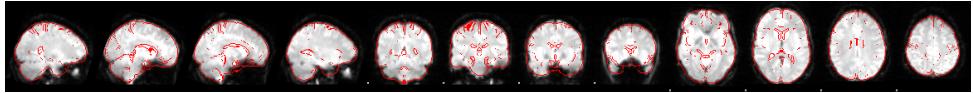


Figure 13: Normalization of fMRI data of run 1 onto the MNI space using full search & 12 DOF

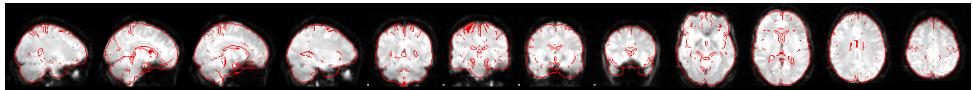


Figure 14: Normalization of fMRI data of run 2 onto the MNI space using full search & 12 DOF

To obtain the previous results, we have used a brute force technique to get the optimal starting point in both the registration the fMRI data to structural MRI data as well as in the normalization of structural MRI data to the template image (MNI space). This brute force technique is called full search. After getting the optimal starting point of matching, the mapping starts between the images and the templates. This mapping is done linearly using affine transformation of 12 degrees of freedom. This high degree of freedom has contributed to such successful alignment in both registration and normalization due to the high flexibility. Therefore, if we have decreased the degree of freedom, we would come up with somehow distorted alignments as depicted in figures 15 through 17. The registration alignment is the least affected, but both normalization of structural and functional MRI to MNI space are somehow distorted.

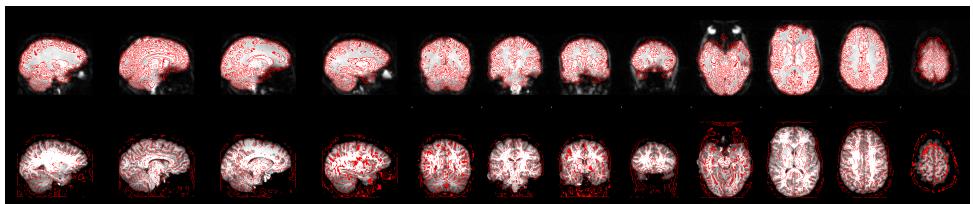


Figure 15: Registration of the functional MRI data of run 1 to the structural MRI data using full search & 3 DOF

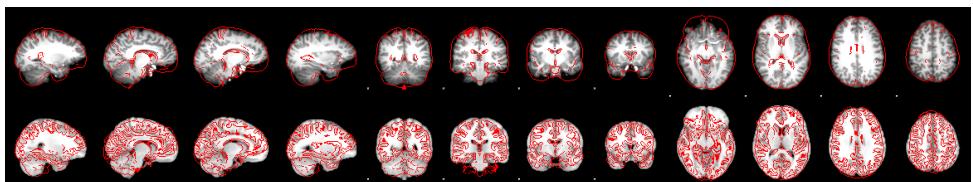


Figure 16: Normalization of structural MRI data onto the MNI space using full search & 3 DOF

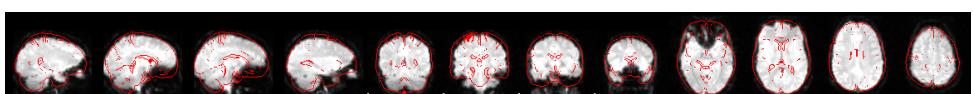


Figure 17: Normalization of fMRI data of run 1 onto the MNI space using full search & 3 DOF

The mapping or rather the affine transformation in case of registration could be fine tuned using an advanced registration technique called brain boundary registration. This technique uses the tissue boundaries to fine-tune the alignment between the functional and structural images. Figure 18 Shows the registration set of samples of fMRI data and structural MRI data using brain boundary registration (BBR). In order to highlight the fine tuning that involved in DDR. let us zoom in to specific sample in case of 12 DOF and BBR. Figures 19 & 20 set a comparison between 12-DOF and BBR for same sample of registration.

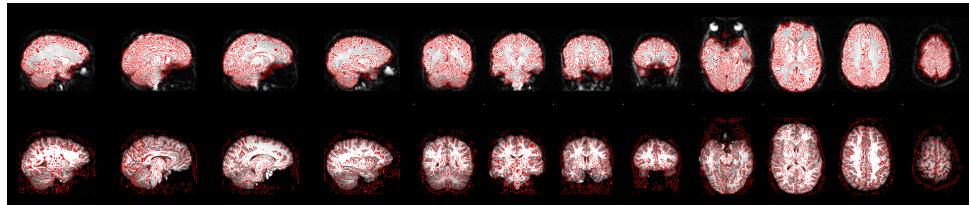


Figure 18: Registration of the functional MRI data of run 1 to the structural MRI data using full search & BBR

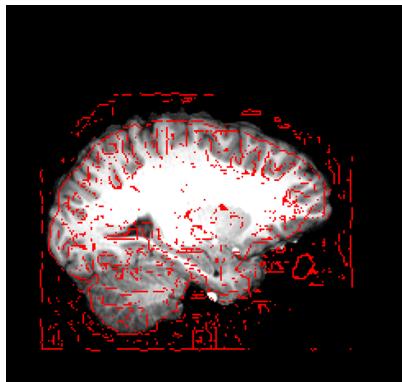


Figure 19: BBR registration sample

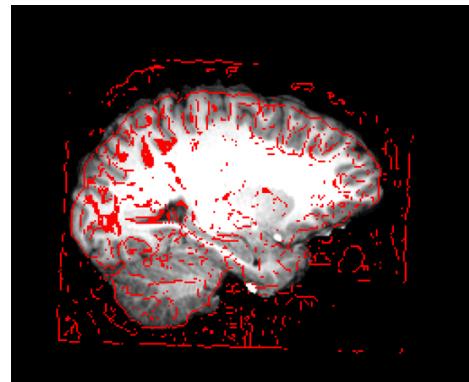


Figure 20: 12-DOF registration sample

4 Anatomy

Through our journey, understanding the anatomy of the brain besides function mapping is very critical. This could help in understanding the how normalization occurs, besides conducting a region of interest (ROI) analysis and localization of activation regions in fMRI. Therefore, over the following sub-sections, we would investigate the brain from the most high level structures up to the deeper structures. For the sake of this investigation, we would use FSL's atlases on the **MNI152_T1_1mm_brain** standard template.

4.1 High Level Investigation

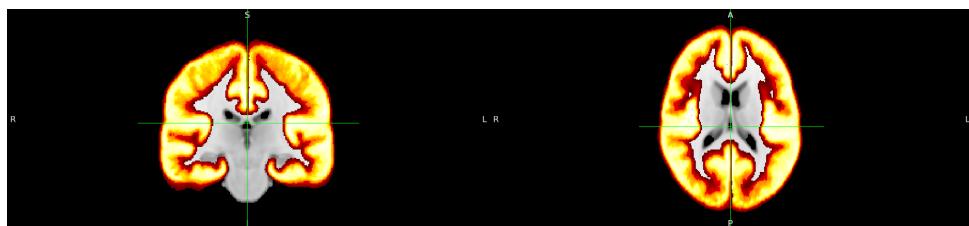


Figure 21: The gray matter (cerebral cortex)

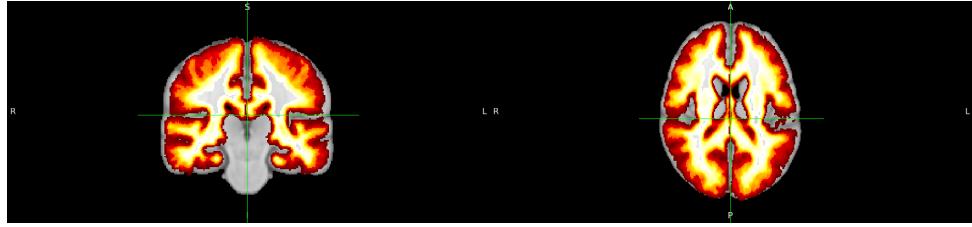


Figure 22: The cerebral white matter

4.1.1 Cerebrum

The cerebrum (front of brain) comprises gray matter [21] and white matter [22] at its center. The largest part of the brain, the cerebrum initiates and coordinates movement and regulates temperature. Other areas of the cerebrum enable speech, judgment, thinking and reasoning, problem-solving, emotions and learning. Other functions relate to vision, hearing, touch and other senses.

The cerebrum has four sections called lobes, namely **frontal**, **parietal**, **temporal** and **occipital**. Each lobe controls specific functions.

- **Frontal lobe [23]:** It's the largest lobe of the brain, located in the front of the head. The frontal lobe is involved in personality characteristics, decision-making, and movement. Recognition of smell usually involves parts of the frontal lobe. Additionally, the frontal lobe contains Broca's area, which is associated with speech ability.

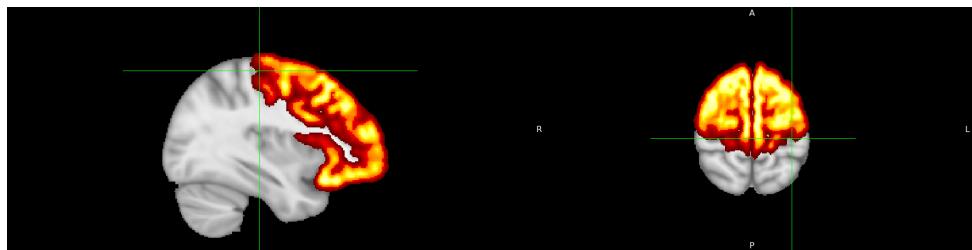


Figure 23: Frontal lobe

- **Parietal lobe [24]:** The middle part of the brain, the parietal lobe helps a person identify objects and understand spatial relationships (where one's body is compared with objects around the person). The parietal lobe is also involved in interpreting pain and touch in the body. The parietal lobe houses Wernicke's area, which helps the brain understand spoken language.

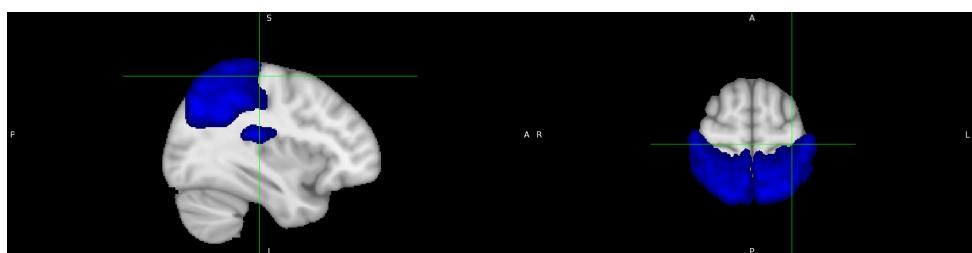


Figure 24: Parietal lobe

- **Occipital lobe [25]:** The occipital lobe is the back part of the brain that is involved with vision

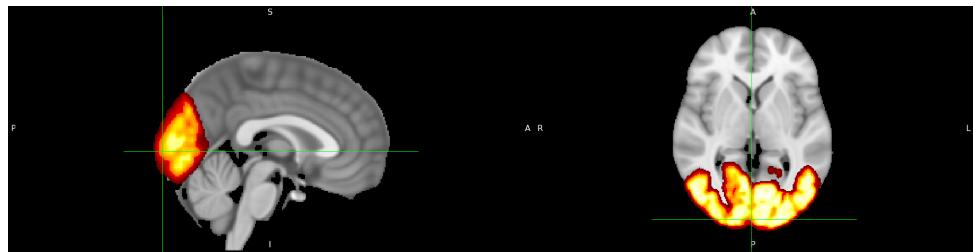


Figure 25: Occipital lobe

- **Temporal lobe [26]:** The sides of the brain, temporal lobes are involved in short-term memory, speech, musical rhythm and some degree of smell recognition. Deeper Structures Within the Brain

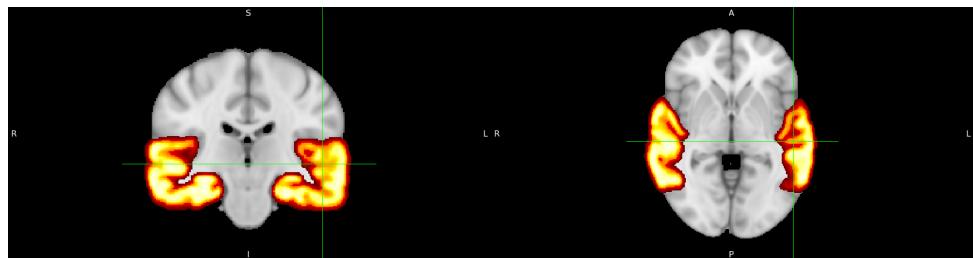


Figure 26: Temporal lobe

4.1.2 Brainstem

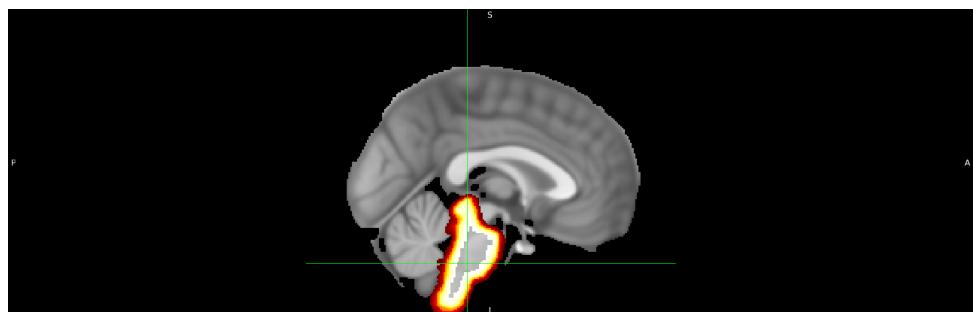


Figure 27: Brain stem

The brainstem [27] (middle of brain) connects the cerebrum with the spinal cord. The brainstem includes the **midbrain** [28], the **pons** [29] and the **medulla** [30].

The **midbrain**, also known as mesencephalon, involved into various functions from hearing and movement to calculating responses and environmental changes. It also contains the substantia nigra, an area affected by Parkinson's disease that is rich in dopamine neurons and part of the basal ganglia, which in turn enables movement and coordination.

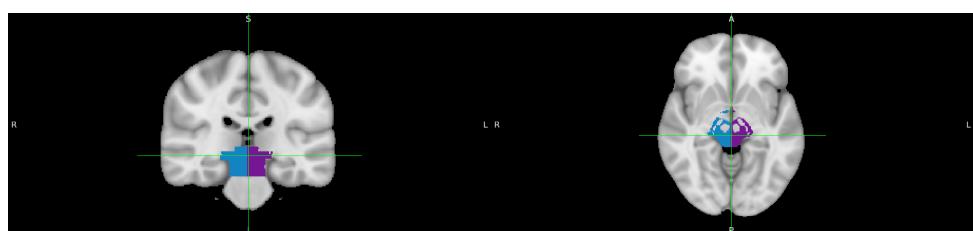


Figure 28: The left and Right midbrain (mesencephalon)

The **pons** is the origin for four of the 12 cranial nerves, which enable a range of activities such as tear production, chewing, blinking, focusing vision, balance, hearing and facial expression.

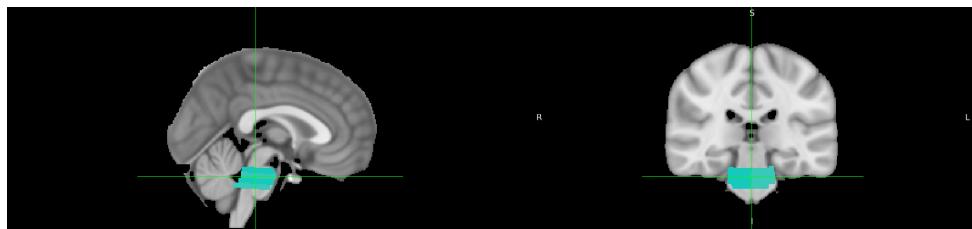


Figure 29: The left and right pons

The **medulla** regulate many bodily activities, including heart rhythm, breathing, blood flow, and oxygen and carbon dioxide levels. The medulla produces reflexive activities such as sneezing, vomiting, coughing and swallowing.



Figure 30: The left and right medulla

The spinal cord extends from the bottom of the medulla and through a large opening in the bottom of the skull. Supported by the vertebrae, the spinal cord carries messages to and from the brain and the rest of the body.

4.1.3 Cerebellum

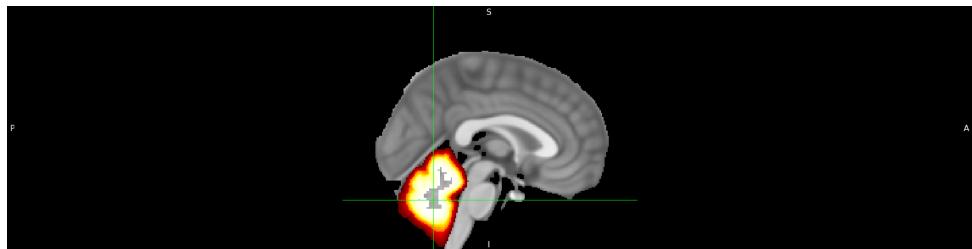


Figure 31: The cerebellum

The cerebellum [31] is involved in coordinating voluntary muscle movements and in maintaining posture, balance and equilibrium. New studies are exploring the cerebellum's roles in thought, emotions and social behavior, as well as its possible involvement in addiction, autism and schizophrenia.

4.2 Deep Level Investigation

4.2.1 Diencephalon

It contains two structures, namely thalamus [32] and hypothalamus [33]. The thalamus serves as a relay station for sensory information, directing signals from various sensory modalities (such

as vision, hearing, touch, and taste) to the appropriate areas of the cerebral cortex for further processing. It also plays a role in regulating consciousness, sleep, and alertness.

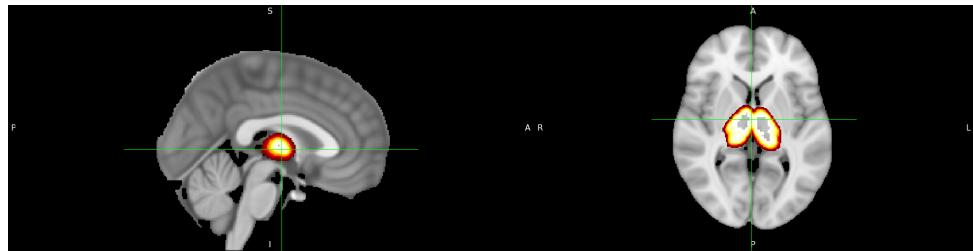


Figure 32: The thalamus

The hypothalamus, located below the thalamus, is involved in maintaining homeostasis by regulating various bodily functions such as temperature, hunger, thirst, and sleep-wake cycles. It controls the release of hormones from the pituitary gland, influencing functions such as growth, metabolism, and reproduction. Additionally, the hypothalamus is crucial for emotional responses and the expression of behaviors related to survival and reproduction.

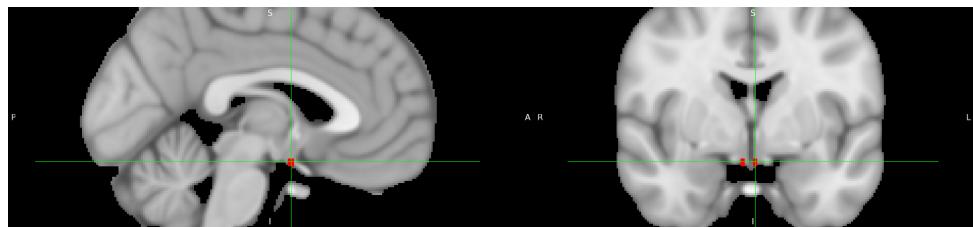


Figure 33: The hypothalamus

4.2.2 Limbic System

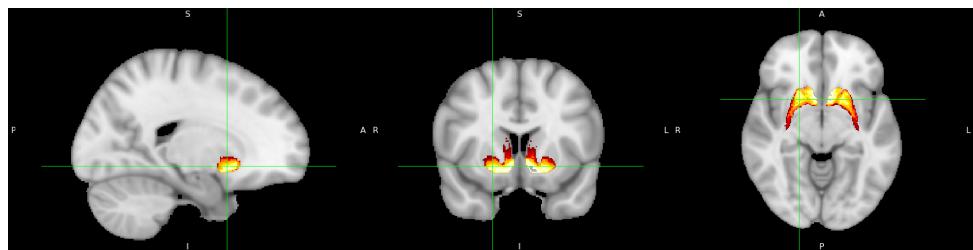


Figure 34: Limbic System

The limbic system [34] includes hippocampus [35] and amygdala [36]. The Hippocampus supports memory, learning, navigation and perception of space. It receives information from the cerebral cortex and may play a role in Alzheimer's disease.

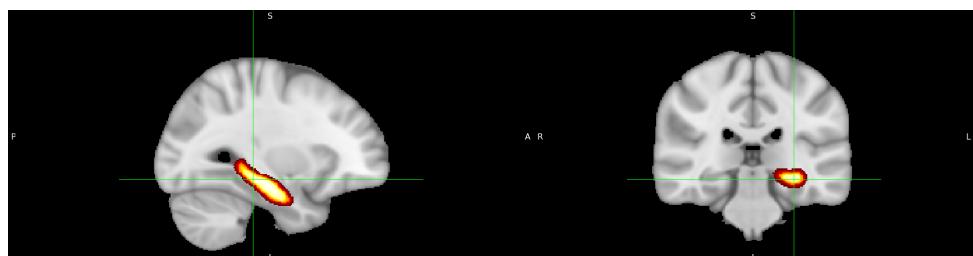


Figure 35: the hippocampus

The amygdalae regulate emotion and memory and are associated with the brain's reward system, stress, and the “fight or flight” response when someone perceives a threat.

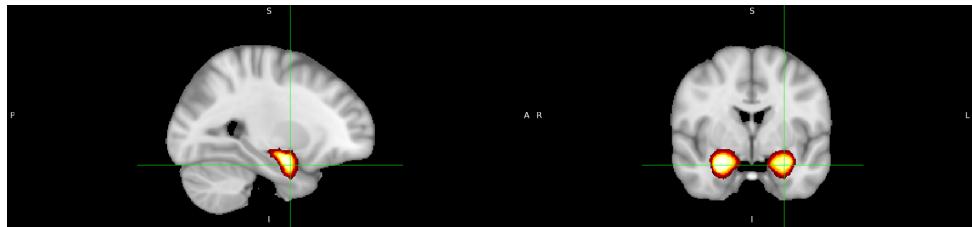


Figure 36: The left and right amygdalae

4.2.3 Caudate Nucleus

The caudate nucleus [37] plays a crucial role in motor control, procedural learning, and reward-related behaviors. It helps regulate voluntary movements and is involved in forming habits and integrating sensory and cognitive information to execute actions efficiently.

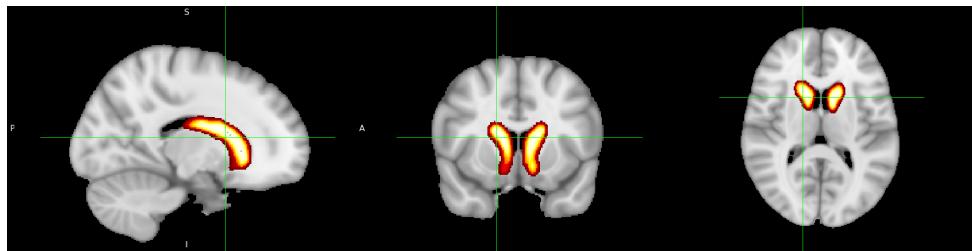


Figure 37: The caudate nucleus

4.2.4 Insula

the insula [38] is involved in various functions, including emotion regulation, self-awareness, and interoception, which is the perception of internal bodily states. It also plays a role in processing emotions, empathy, and social cognition, as well as in monitoring and responding to physiological sensations such as pain, hunger, and thirst. Additionally, the insula is implicated in decision-making processes and the integration of sensory information with emotional and cognitive states.

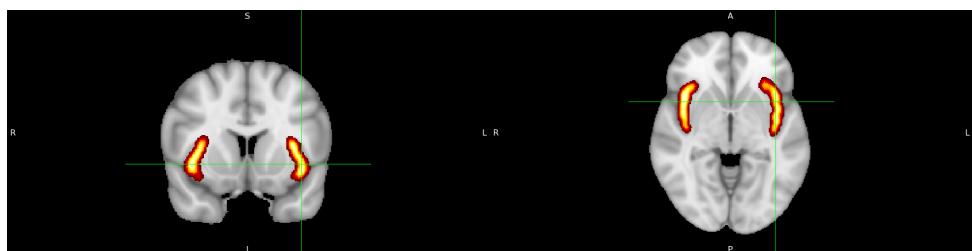


Figure 38: The insula

4.2.5 Corpus Callosum

The corpus callosum [39] is the largest white matter tract in the brain, connecting the left and right cerebral hemispheres. It facilitates communication between the hemispheres, enabling the integration of sensory, motor, and cognitive functions across both sides of the brain. This

interhemispheric connectivity supports tasks such as language processing, spatial awareness, and complex problem-solving.

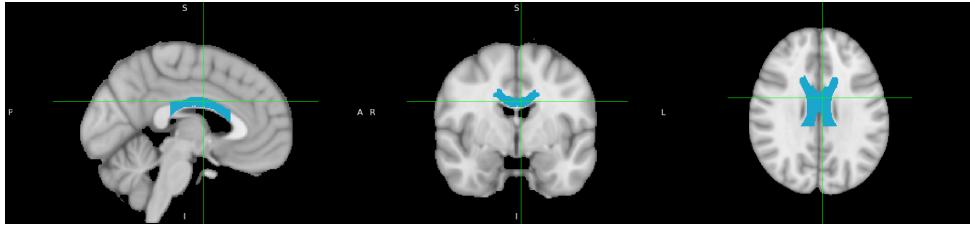


Figure 39: The corpus callosum

5 Statistics and Modeling

5.1 First Level Analysis

In this stage, we are ready to statistically model the activation of brain regions as well as describe such regions anatomically for each run of each subject. This would help us to highlight the regions that are likely to be involved in the task of interest. Towards that end, we would employ the general linear model (GLM). Since we are dealing with two-task-based experiment, namely congruent and incongruent, we would have 2 parameters to be estimated for each voxel, we could think of that as the probabilistic contribution of each task in the voxel activation.

$$Y = \beta_1 x_1 + \beta_2 x_2 + \text{error} \quad (1)$$

The GLM used in our case is shown in 1. The equation consists of several terms we need to investigate each of which. Firstly, the (Y), which represents the time-series signal detected at specific voxel. Secondly, the ($\beta_1 \& \beta_2$), which represent the weights or parameter estimates of the linear model for task (1 & 2). Thirdly ($x_1 \& x_2$), which represent the regressors of the model, phrased differently the expected hemodynamic response. Lastly, the residual term which regresses out all the other irrelevant activations.

The (Y) term is already measured, which again represents the signal intensity over the entire run at specific voxel. The ($\beta_1 \& \beta_2$) are the target values, which we need to estimate. The ($x_1 \& x_2$) are the hemodynamic responses that are expected from each task. In order to evaluate such responses, we make use of BOLD Response, which stands for blood-oxygen-level-dependent response or rather signal. This is similar to the impulse response of a linear system. The BOLD response is represented as gamma distribution function, with a peak close to the beginning of the time axis (i.e., the x-axis) and a long tail to the right [40].

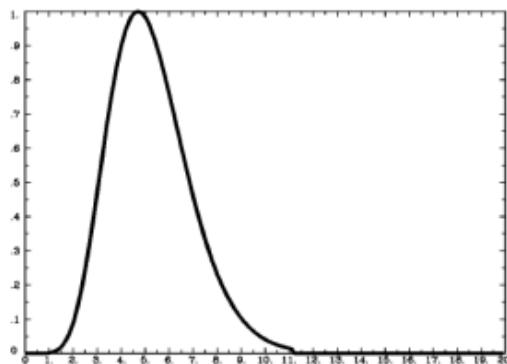


Figure 40: BOLD response



Figure 41: Sequence of stimuli

Since we have in the run multiple stimuli, for congruent and incongruent, like that depicted in [41]. Therefore, we need to get the accumulative response of the BOLD, which in turn give rise to the hemodynamic response of each task. This could be achieved by convolving the BOLD response with the sequence of stimuli of each task in each run [42].



Figure 42: Accumulative BOLD response

Before evaluating such responses, we need to separate the sequence of stimuli of each task in the run. The timing and duration of the the stimuli as well as the corresponding task is recorded in the events tsv file of each run file. We have used a script to perform this task, which you could find the script in the appendix.

Now, we have got a clue of how the statistical analysis is being done as well as we have separated the stimuli sequence of each task in each run. we could now run the statistical analysis to come up with the parameter estimates (pe's) and the contrast between them, which is known as contrast of parameter estimates (cope's).

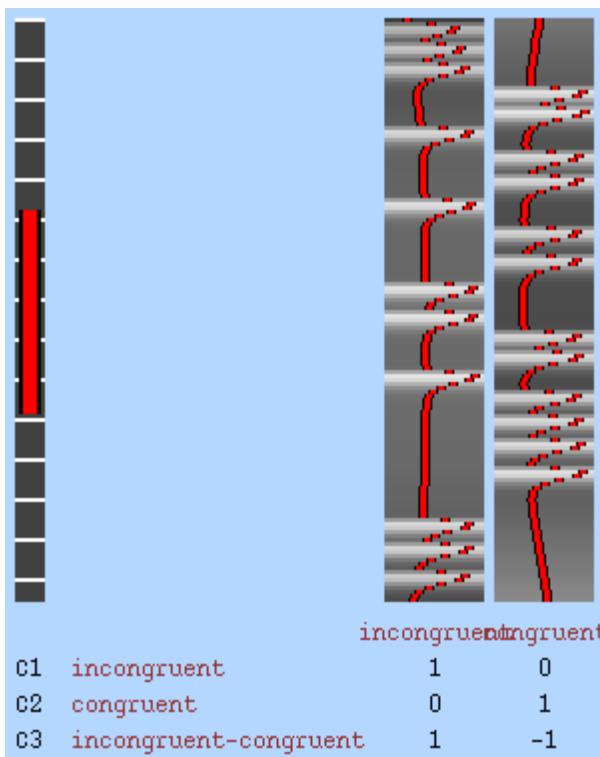


Figure 43: Design matrix for run 1

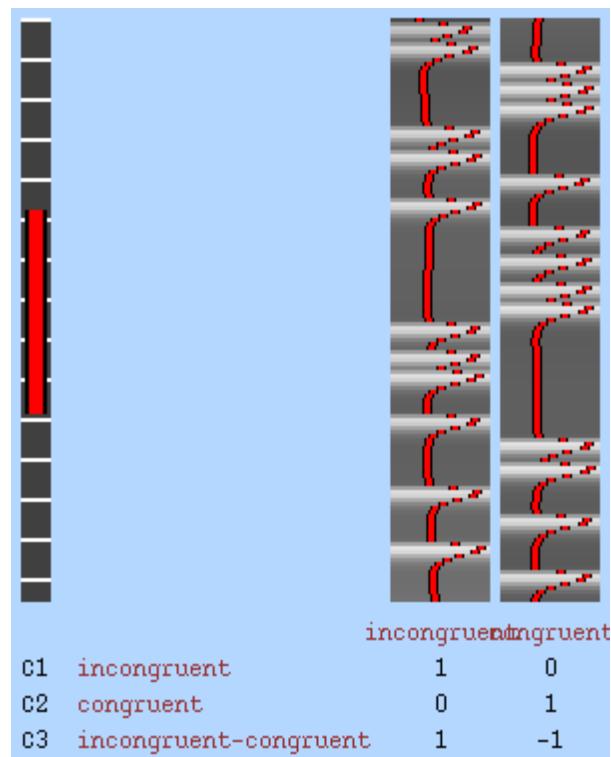


Figure 44: Design matrix for run 2

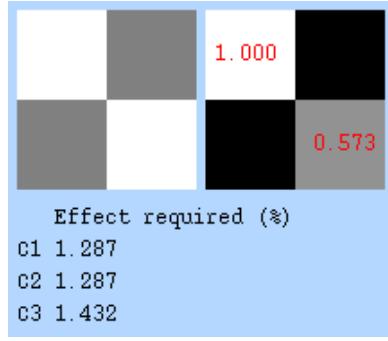


Figure 45: Covariance matrix and design efficiency for run 1

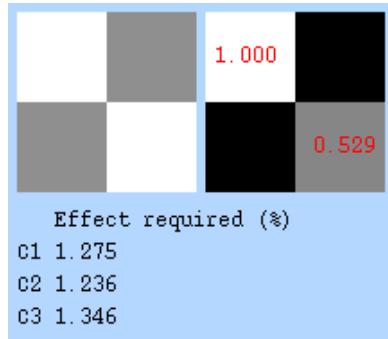


Figure 46: Covariance matrix and design efficiency for run 2

If we have looked at design matrices, we could deduce that there isn't any overlapping between stimuli, which signifies a well conducted experiment. If we notice, we could see a red bar in the left most side of the design matrix, This is a low pass filter, which prevents the high frequencies in the typical HDR, which is typically a noise.

In the above, we can see a covariance matrix as well as a design efficiency. Understanding the covariance matrix and design efficiency helps you set up and interpret our fMRI study better.

The covariance matrix shows how much the estimated brain activity levels (parameters) for different conditions (congruent vs. incongruent stimuli) vary together. This shows if there are any strong relationships (correlations) between These conditions that might affect our results as well as it helps us to get a sense of how precise our estimates are.

On the other hand, the design efficiency measures how well the experimental setup (like the timing and order of stimuli) can detect differences in brain activity between conditions. This could reflect on the accuracy of the GLM.

Let's consider the modeling results and statistical results we come up with up to this point. The time series figures [47, 49, 51] depict the full fitted model compared to the data (signal measured) as well as partial fitted model due to one of three copes, namely (incongruent), (congruent) or (incongruent - congruent), as being the only regressor. This helps us to get a sense of how each cope contributes to the full measured signal.

On the other hand, the map images for each cope shows the statistically significant regions due to each cope, in other words, the candidate activation regions for each cope.

To conduct the 1st Level analysis on the entire subjects, we have saved a template settings

for run1 and run2 for subject (8). Then, replaced all the namings that is related to subject 8 to each subject and run the analysis. The replacement and running commands have been considered in the bash script in the Appendix.

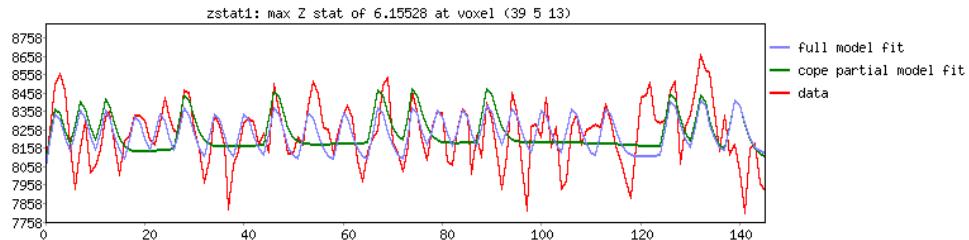


Figure 47: The cope 1 (incongruent) partial model fit in time series for run 1

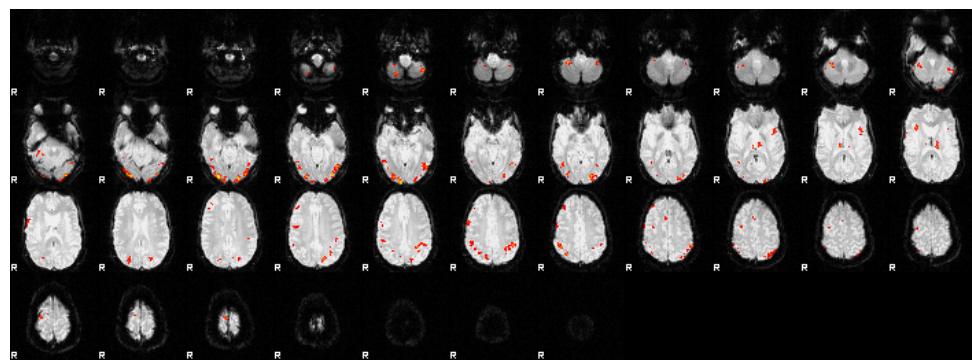


Figure 48: The rendered z-stats of cope 1 (incongruent) for run 1

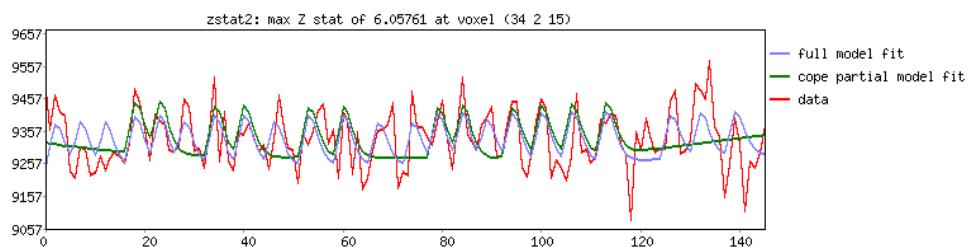


Figure 49: The cope 2 (congruent) partial model fit in time series for run 1

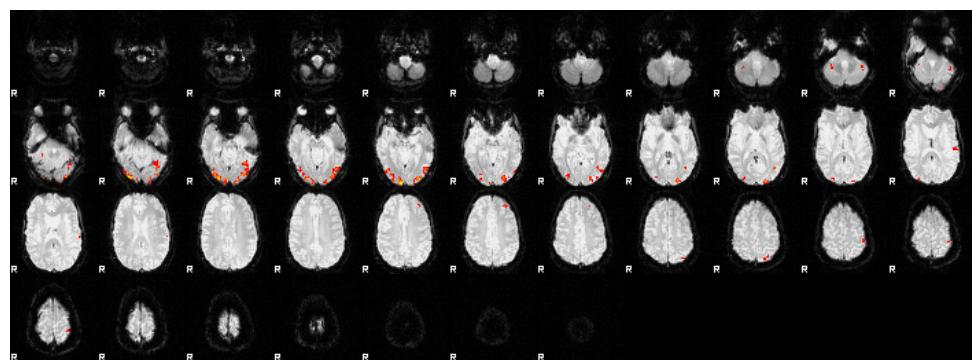


Figure 50: The rendered z-stats of cope 2 (congruent) for run 1

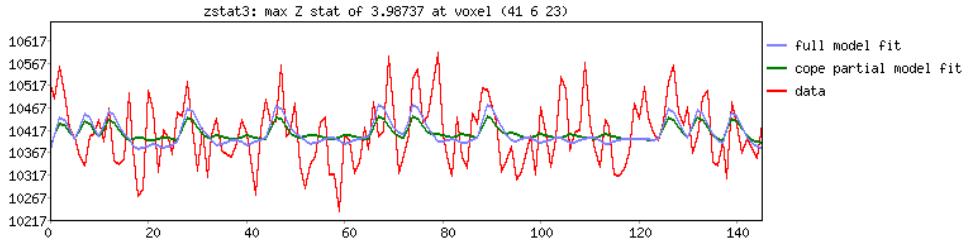


Figure 51: The cope 3 (incongruent - congruent) partial model fit in time series for run 1

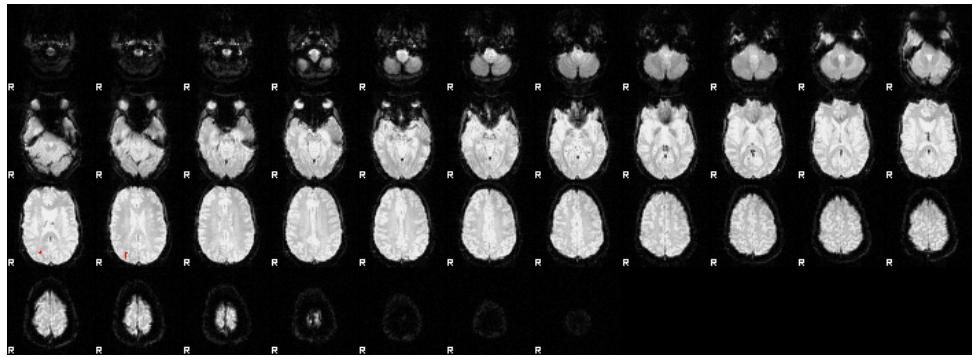


Figure 52: The rendered z-stats of cope 3 (incongruent - congruent) for run 1

5.2 Second Level Analysis

Once we have preprocessed and analyzed all of the runs for all of the subjects in the Flanker dataset, we are ready to run a 2nd-level analysis. In the second level analysis, we make use of the copes we have computed in the first level analysis and average them out per each subject while applying some thresholding [53]. This step is paving the way for the group analysis, or in other word the 3rd level analysis.

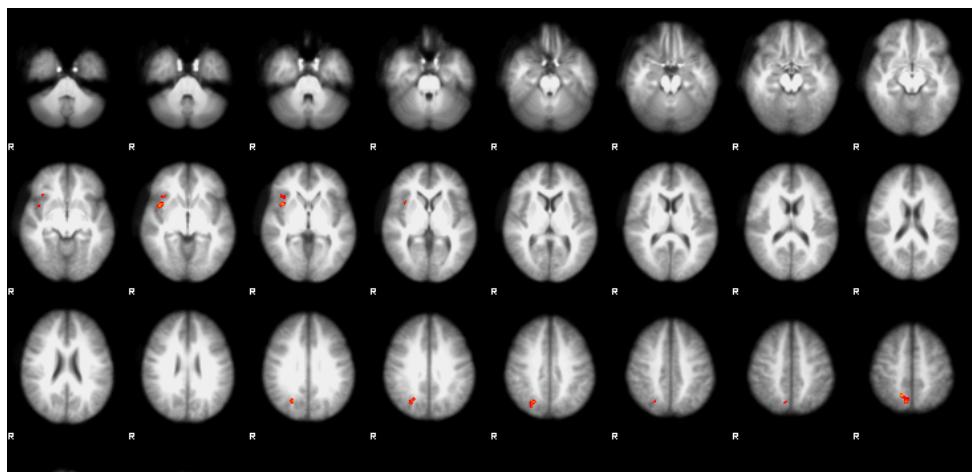


Figure 53: The rendered thresholded z-stats for subject 8

5.3 Third Level Analysis

Our goal in analyzing this dataset is to generalize the results to the population that the sample was drawn from. In other words, if we see changes in brain activity in our sample, can we say that these changes would likely be seen in the population as well?

To test this, we will run a 3rd-level analysis. In FSL, a 3rd-level analysis is a group-level analysis - we calculate the standard error and the mean for a contrast estimate, and then test whether the average estimate is statistically significant [54,]55].

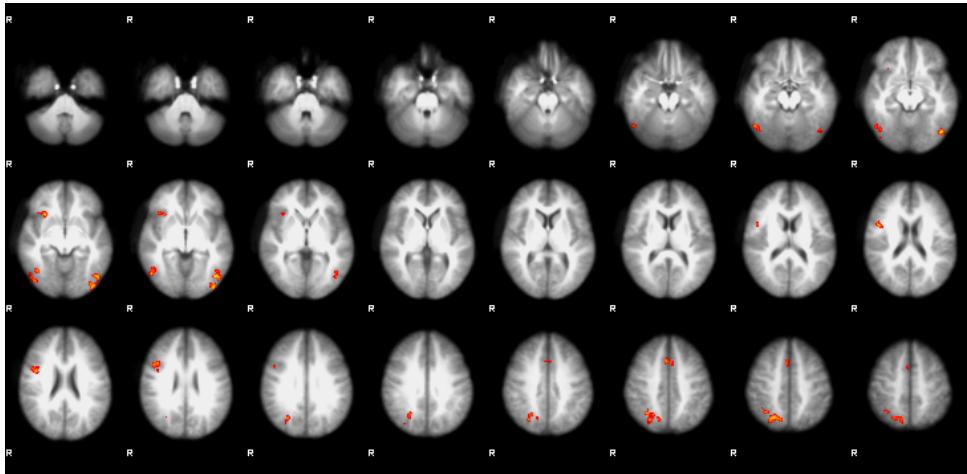


Figure 54: The rendered thresholded z-stats for entire dataset



Figure 55: The statistically significant regions

6 ROI Analysis

After conducting the group analysis, we came up with 6 different Regions, which might be involved in the cognitive task of interest. These regions show high statistical significance for one task over the other. To conclude which task is the more significant, we would take a mask of specific size, in our case $5mm$. Then, extract the average z-stats for each cope of the three. After that, we would apply a t-test to know which one of two task contribute the most.

6.1 Region 1

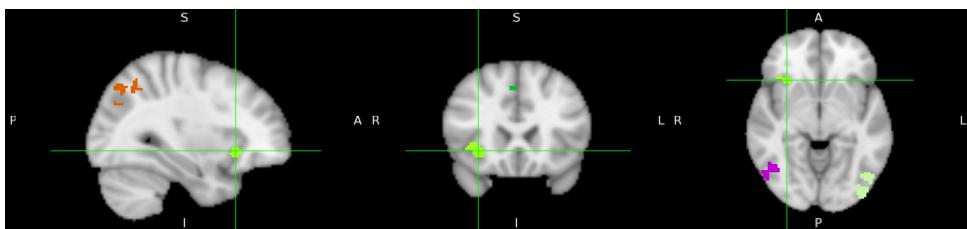


Figure 56: Cluster 1, highlighted with the cursor

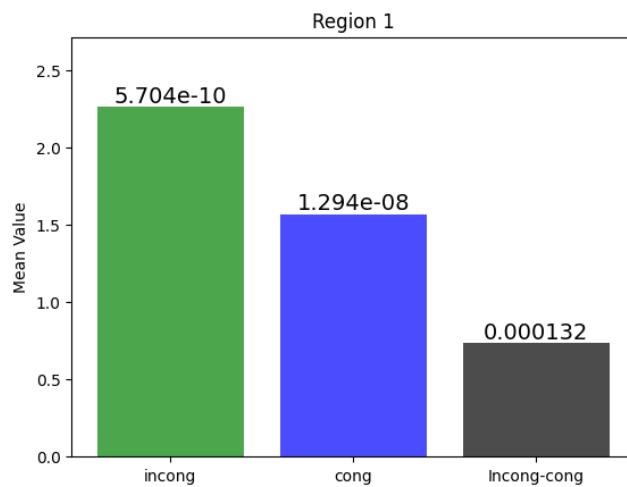


Figure 57: the average of z-stats for each cope with the statistical significance of each

6.2 Region 2

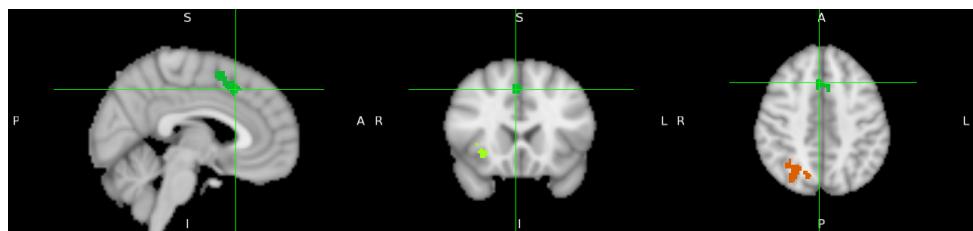


Figure 58: Cluster 2, highlighted with the cursor

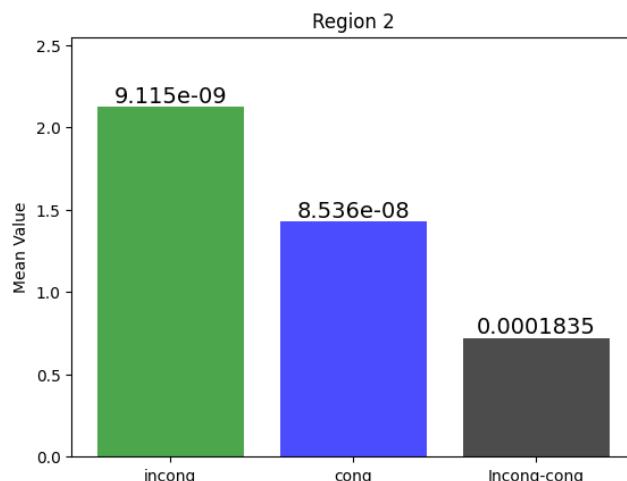


Figure 59: the average of z-stats for each cope with the statistical significance of each

6.3 Region 3

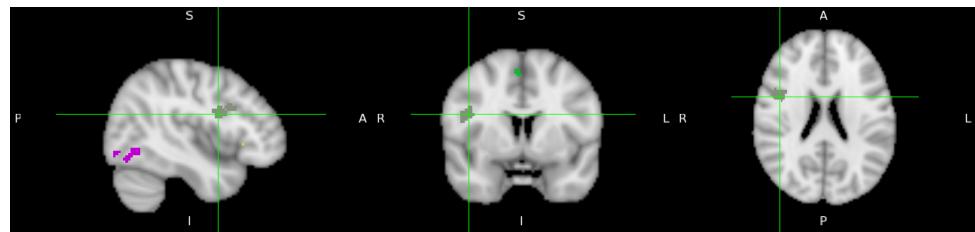


Figure 60: Cluster 3, highlighted with the cursor

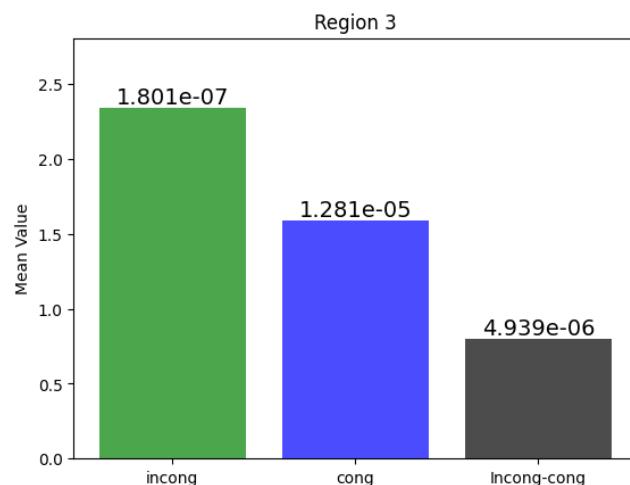


Figure 61: the average of z-stats for each cope with the statistical significance of each

6.4 Region 4

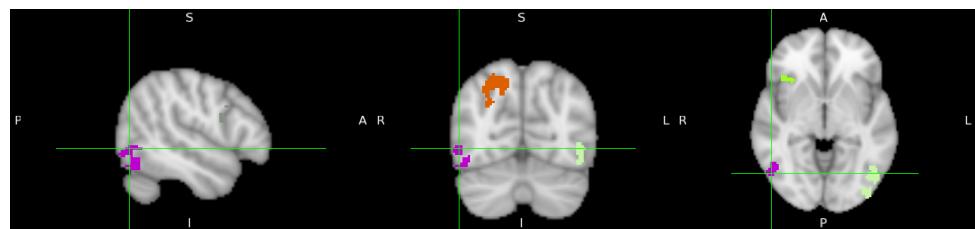


Figure 62: Cluster 4, highlighted with the cursor

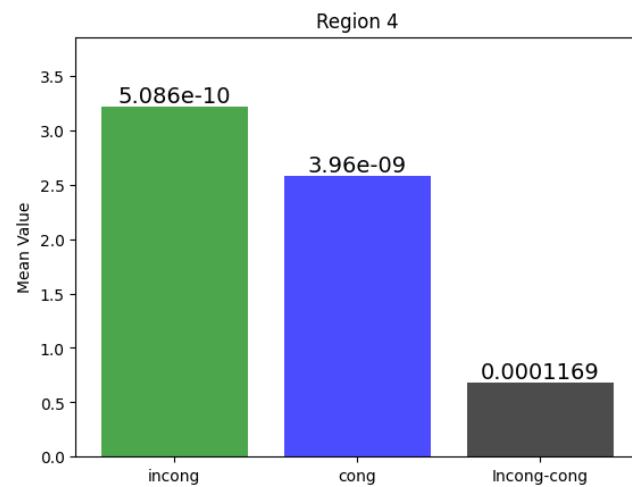


Figure 63: the average of z-stats for each cope with the statistical significance of each

6.5 Region 5

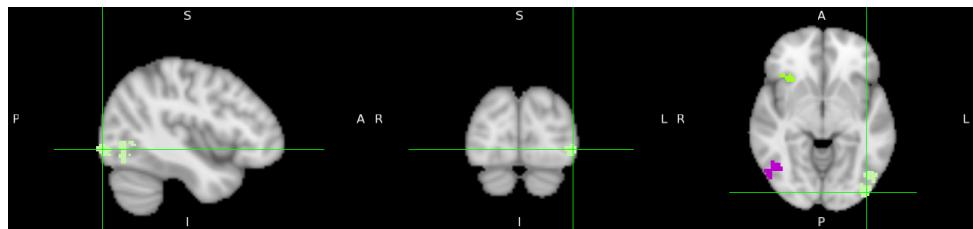


Figure 64: Cluster 5, highlighted with the cursor

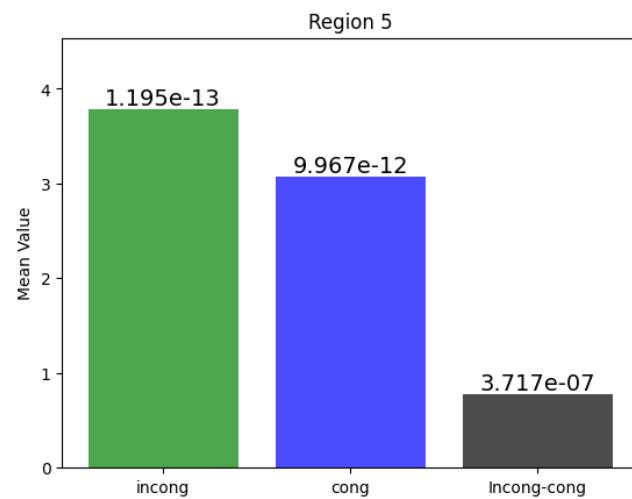


Figure 65: the average of z-stats for each cope with the statistical significance of each

6.6 Region 6

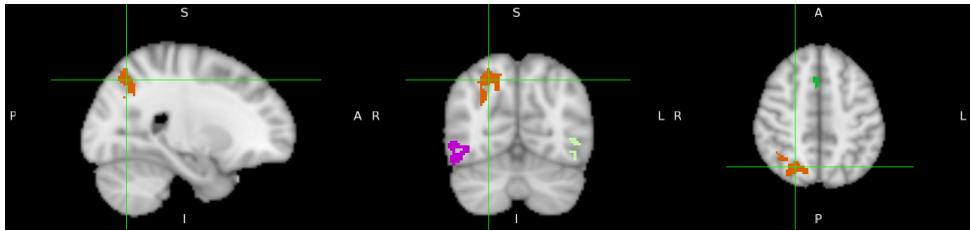


Figure 66: Cluster 6, highlighted with the cursor

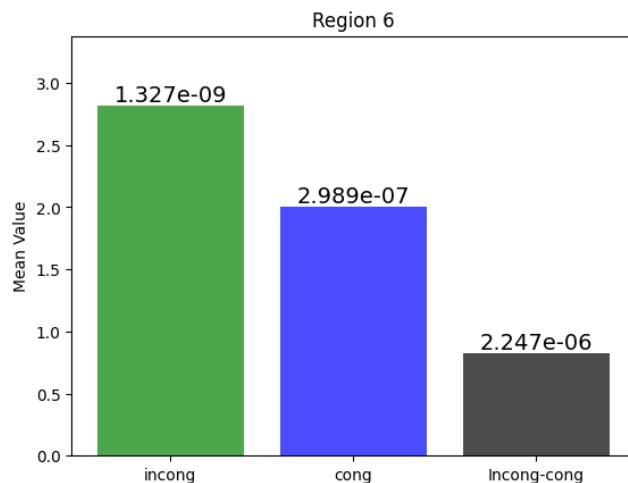


Figure 67: the average of z-stats for each cope with the statistical significance of each

6.7 Observations

The results across Figures 57 through 67 strongly indicate that these brain regions are significantly involved in processing incongruent tasks, as evidenced by the low p-values and elevated mean responses. This suggests a key role for these areas in cognitive processes related to conflict monitoring, attention, or inhibitory control. Future research could help clarify the precise nature of their involvement and whether these regions are part of a broader neural network responsible for handling cognitive demands associated with incongruency.

7 Conclusion

In conclusion, the analysis of the Flanker dataset reveals significant insights into the cognitive mechanisms underlying task performance. The consistent patterns observed in the visualization results highlight the critical role of specific brain regions in processing incongruent tasks, evidenced by their lower p-values and higher mean values. These findings suggest that the regions examined are not only statistically significant but also functionally relevant, likely contributing to essential cognitive processes such as conflict resolution and cognitive control.

The strong activation of these areas during incongruent task performance underscores their importance in managing attentional resources and navigating cognitive challenges. While these results provide compelling evidence for the involvement of these regions, further research is necessary to delineate their precise roles within a broader neural network. Investigating the causal relationships and exploring connectivity dynamics among these areas will enhance our understanding of the neural basis of cognitive control.

Overall, this analysis enriches our comprehension of the intricate interplay between brain function and cognitive demands, paving the way for future studies aimed at unraveling the complexities of executive functioning in both healthy and clinical populations.

References

- [1] OpenNeuro. (n.d.). Dataset: ds000102. Retrieved from
<https://openneuro.org/datasets/ds000102/versions/00001>
- [2] Analysis of imaging artifacts in MR brain images. (2012). Retrieved from
<https://www.researchgate.net/publication/272238318>

Appendix

Skull Stripping Bash Script

```
1 # Check if the correct number of arguments is provided
2 if [ "$#" -lt 2 ]; then
3     echo "Usage: $0 <threshold> <subject_list or 'all'>" # all option allows
4         ↪ for applying skull stripping to all subjects in the directory in
5         ↪ which the script exists.
6     exit 1
7 fi
8 # Extract threshold value from the first argument
9 threshold=$1
10 # Shift arguments to get the list of subjects or 'all'
11 shift
12 # Function to check if skull stripping file exists with the same threshold
13 skull_stripped_exists() {
14     local subject_dir="$1"
15     local threshold="$2"
16     local skull_stripped_file="${subject_dir}/anat/${subject}_T1w_brain_${threshold}.nii.gz"
17     [ -f "$skull_stripped_file" ] # check if the target file already exists
18         ↪ in the subject directory.
19 }
20 # Loop through subject numbers provided as arguments or process all
21     ↪ directories
22 if [ "$1" = "all" ]; then
23     for subject_dir in */; do # iterating over the entire folders in the
24         ↪ current folder
25     subject="${subject_dir%/}" # Remove trailing slash
26     if ! skull_stripped_exists "$subject_dir" "$threshold"; then
27         input_file="/home/joyou159/Downloads/Data/${subject}/anat/${subject}_T1w"
28         output_file="${input_file}_brain_${threshold}"
29         bet "$input_file" "$output_file" -f "$threshold" -g 0
30     else
31         echo "Skipping ${subject_dir}: skull stripping file already exists
32             ↪ with the same threshold."
33     fi
34 done
35 else
36     # Loop through subject numbers provided as arguments
37     for subject in "$@"; do
38         input_file="/home/joyou159/Downloads/Data/${subject}/anat/${subject}_T1w"
39         output_file="${input_file}_brain_${threshold}"
40         if ! skull_stripped_exists "/home/joyou159/Downloads/Data/${subject}"/"$threshold"; then
41             bet "$input_file" "$output_file" -f "$threshold" -g 0
42         else
43             echo "Skipping ${subject}: skull stripping file already exists
44                 ↪ with the same threshold."
45         fi
46     done
47 fi
```

Customize the paths in the code as needed to match your directory structure. Please note that the provided code assumes that the data is located in the same directory. Adjust the paths accordingly to match the actual location of your data files.

Making FSL's Timings

```
1 #Check whether the file subjList.txt exists; if not, create it
2 if [ ! -f subjList.txt ]; then
3     ls -d sub-?? > subjList.txt
4 fi
5 #Loop over all subjects and format timing files into FSL format
6 for subj in `cat subjList.txt` ; do
7     cd ${subj}/func #Navigate to the subject's func directory, which
8         ↪ contains the timing files
9     #Extract the onset times for the incongruent and congruent trials
10        ↪ for each run.
11     cat ${subj}_task-flanker_run-1_events.tsv | awk '{if ($3==""
12         ↪ incongruent_correct") {print $1, $2, "1"} }' > incongruent_run1
13         ↪ .txt
14     cat ${subj}_task-flanker_run-1_events.tsv | awk '{if ($3==""
15         ↪ congruent_correct") {print $1, $2, "1"} }' > congruent_run1.txt
16     cat ${subj}_task-flanker_run-2_events.tsv | awk '{if ($3==""
17         ↪ incongruent_correct") {print $1, $2, "1"} }' > incongruent_run2
18         ↪ .txt
19     cat ${subj}_task-flanker_run-2_events.tsv | awk '{if ($3==""
20         ↪ congruent_correct") {print $1, $2, "1"} }' > congruent_run2.txt
21     cd ../..
22 done
```

This script only extracts the trials in which the subject made a correct response. Accuracy is nearly 100% for all subjects.

Conducting 1st Level Analysis on Entire Subjects using Templates

```
1 #!/bin/bash
2 # Generate the subject list to make modifying this script to run just a
3 # subset of subjects easier.
4 for id in `seq -w 1 26`; do
5     subj="sub-$id"
6     echo "====> Starting processing of $subj"
7     cd $subj
8     # Copy the design files into the subject directory, and then change
9     # sub -08 to the current subject number
10    cp ./design_run1.fsf .
11    cp ./design_run2.fsf .
12    # Note that we are using the | character to delimit the patterns instead
13    # of the usual / character because there are / characters in the
14    # pattern.
15    sed -i "s|sub-08|${subj}|g" design_run1.fsf
16    sed -i "s|sub-08|${subj}|g" design_run2.fsf
17    # Now everything is set up to run feat
18    echo "====> Starting feat for run 1"
19    feat design_run1.fsf
20    echo "====> Starting feat for run 2"
21    feat design_run2.fsf
22    echo
23    # Go back to the directory containing all of the subjects, and repeat
24    # the loop
25    cd ..
26 done
27 echo
```