



Cairo University
Faculty of Engineering
Systems and Biomedical Department



SBME 3048

FMRI Report

Student Name : Ali Sherif Badran

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Bench Number : 40

Submitted to : Dr. Meena M. Makary

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FMRI Task 1

Brain Extraction Tool (BET)

The Brain Extraction Tool (BET) is a software tool extensively used in neuroimaging research, specifically within the FMRIB Software Library (FSL) suite. The main objective of BET is to precisely define the borders of the brain in MRI images, effectively distinguishing brain tissue from non-brain structures like the skull, scalp, and other tissues outside the cranium. This process is of utmost importance in numerous neuroimaging analyses.

Skull Stripping on subject 20 structural image:

In this analysis I will try to remove the skull and non-brain areas from the structural image of subject 20 using FSL's brain extraction tool. I will be trying two fractional intensity thresholds 0.1 and 0.9, Where smaller fractional intensity thresholds values give larger brain outlines estimates. We shall then observe the results and choose the appropriate fractional intensity threshold to move on with it.

Fractional intensity threshold = 0.1

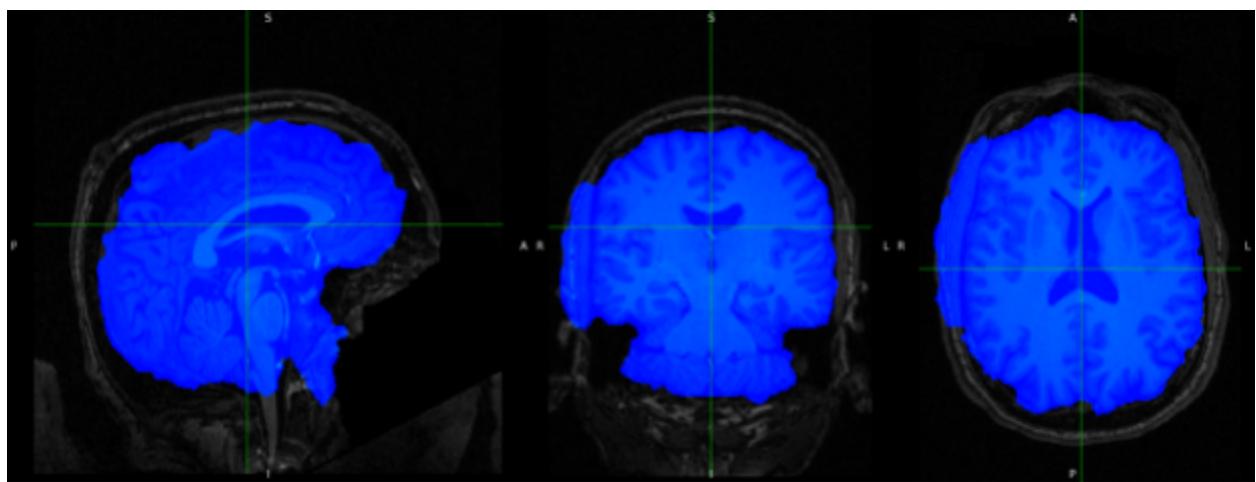


Fig. 1

We see in Fig. 1 that at fractional intensity threshold 0.1 the BET did not successfully remove all non-brain parts as we see in the left sides of the coronal and axial views.

Fractional intensity threshold = 0.9

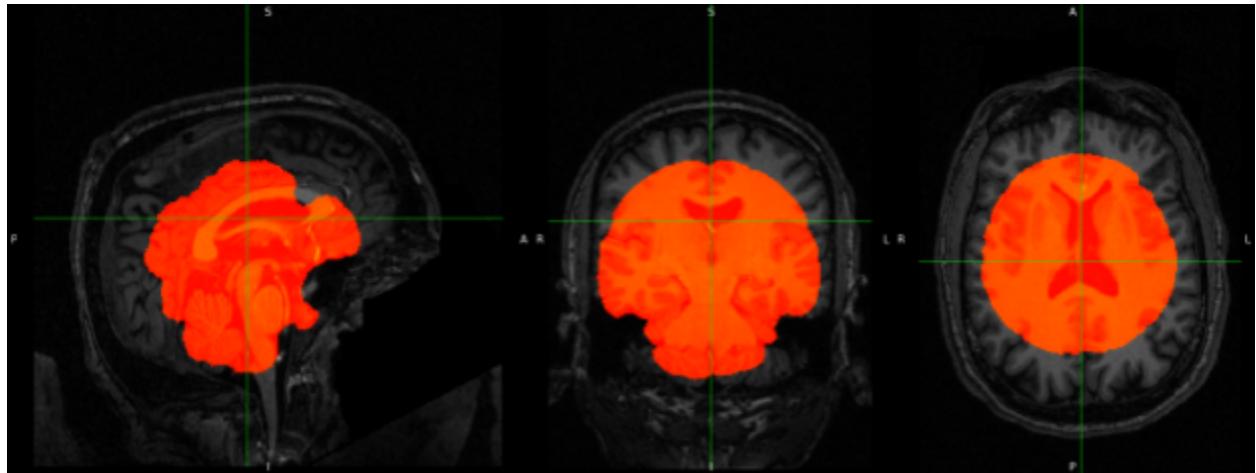


Fig. 2

We see in Fig. 2 that at fractional intensity threshold 0.9 the BET successfully removed all non-brain parts but it also removed parts of the brain.

In conclusion:

To conclude, the selection of the fraction intensity threshold holds significant importance in the examination of functional MRI (fMRI) data. The appropriate threshold value must be chosen in order to reach a balance between the sensitivity and specificity of the analysis outcomes.

Opting for a lower threshold can heighten sensitivity by encompassing a greater number of voxels in the analysis, potentially capturing subtle effects. However, this also increases the risk of false positives, where signals are detected erroneously. On the other hand, a higher threshold can enhance specificity by reducing the likelihood of false positives. Nevertheless, this approach may result in missed signals, cutting some parts of the brain and reduced sensitivity.

Hence, the value of the fractional intensity threshold that will be most appropriate between these two values is 0.1 because although it has some extra parts of the skull and non-brain images which can lead to extra processing, it doesn't remove nor cut off any part of the brain which may carry crucial data.

FMRIB's Expert Analysis Tool (FEAT)

FEAT is an advanced software application included in the FMRIB Software Library (FSL) that is specifically created for the thorough examination of functional magnetic resonance imaging (fMRI) data.

- FEAT offers robust preprocessing capabilities, allowing users to perform essential steps such as motion correction, spatial smoothing, slice-timing correction, and high-pass filtering. These preprocessing steps are crucial for ensuring the quality and reliability of subsequent fMRI analyses.
- FEAT enables users to conduct a variety of statistical analyses on preprocessed fMRI data, including general linear modeling (GLM) and analysis of variance (ANOVA). This allows for the identification of brain regions exhibiting task-related activation or connectivity changes.
- FEAT supports the specification and analysis of predefined ROIs, enabling targeted investigations of specific brain regions or networks implicated in particular cognitive tasks or experimental conditions.
- FEAT provides intuitive visualization tools for exploring and interpreting fMRI results, including statistical parametric maps, activation clusters, and time course plots. These visualization aids facilitate the communication of findings and insights to stakeholders and collaborators.

Preprocessing on subject 20 run 2 functional image:

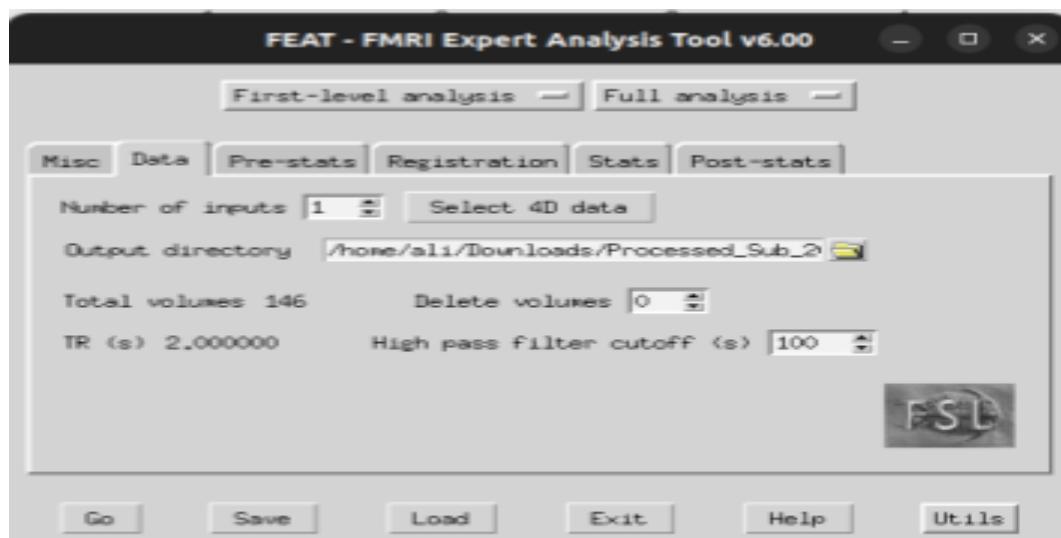


Fig. 3

Firstly, I Start with selecting the 4D data of subject 20 and specifying the output directory to run2. Then the tool shows me that the imaging was done using 146 volumes with TR equal to 2 seconds.

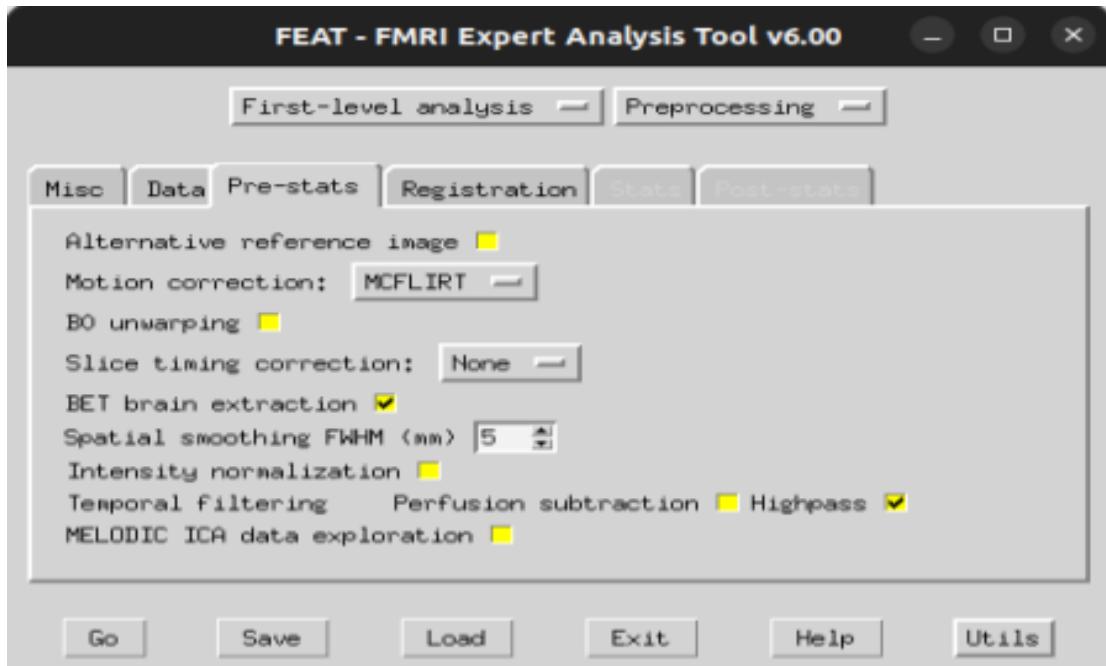


Fig. 4

In order to maintain consistency with run 1, Pre-Stats were specified while opting for MCFLIRT as the motion correction technique.

Due to the short repetition time (TR) of the dataset, slice timing correction was considered unnecessary, simplifying the preprocessing process.

Furthermore, a smoothing kernel size of 5 was chosen to aid in spatial smoothing, which helps in reducing noise and improving the statistical sensitivity in later stages of analysis.

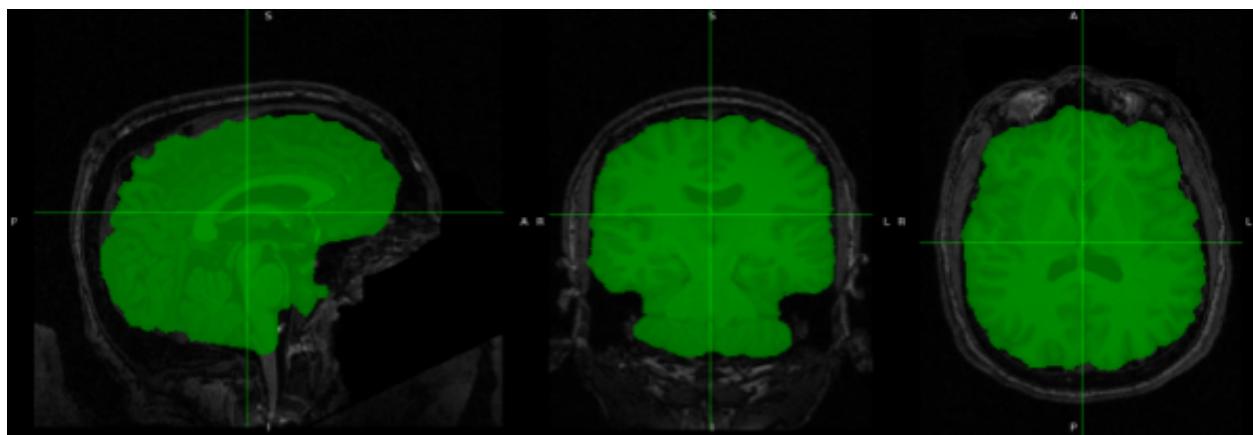


Fig. 5

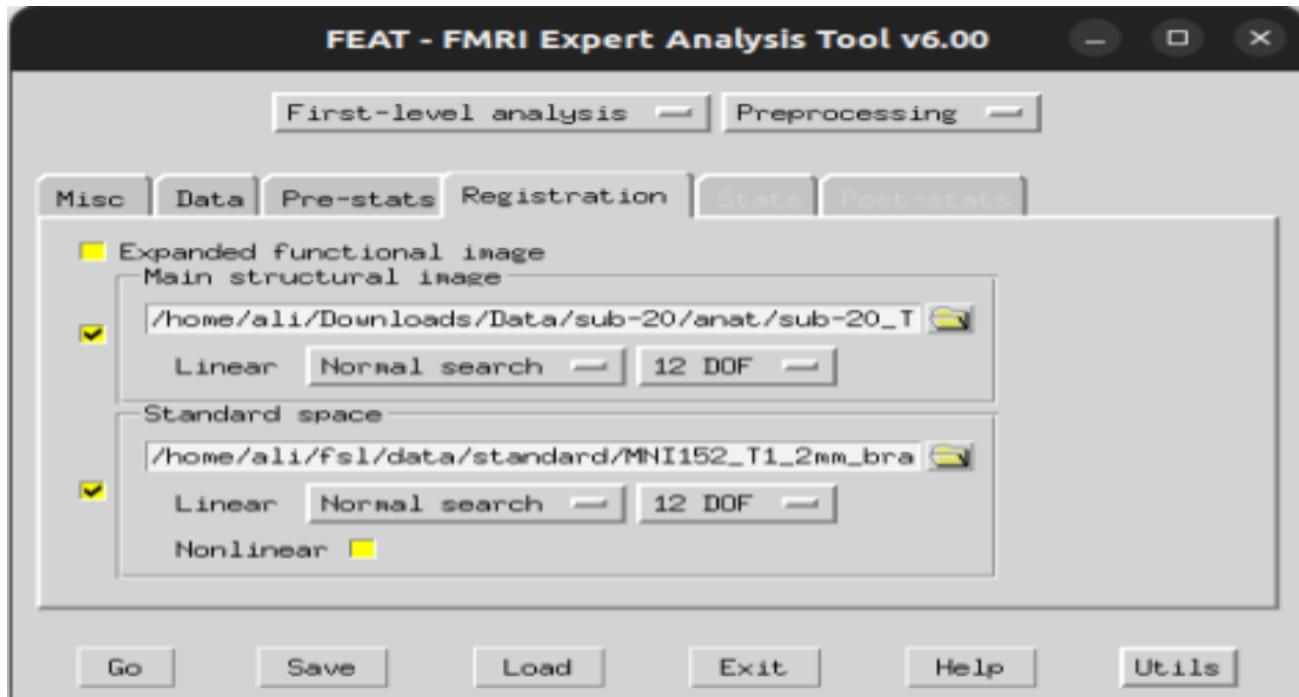


Fig. 6

Within Fig. 6, I specified the main structural image of subject 20 with fractional intensity threshold equal 0.3 as shown in Fig. 5, I found it to be the one with the perfect balance between the sensitivity and specificity for the analysis. The process initiates with the alignment of structural images specific to the subject with the MNI space, where the MNI152 2mm template was identified as the destination space. To streamline this alignment process a 12-degree-of-freedom affine transformation was specified to accommodate any potential differences in global scaling, rotation, and translation between the two spatial domains.

The results of the preprocessing:

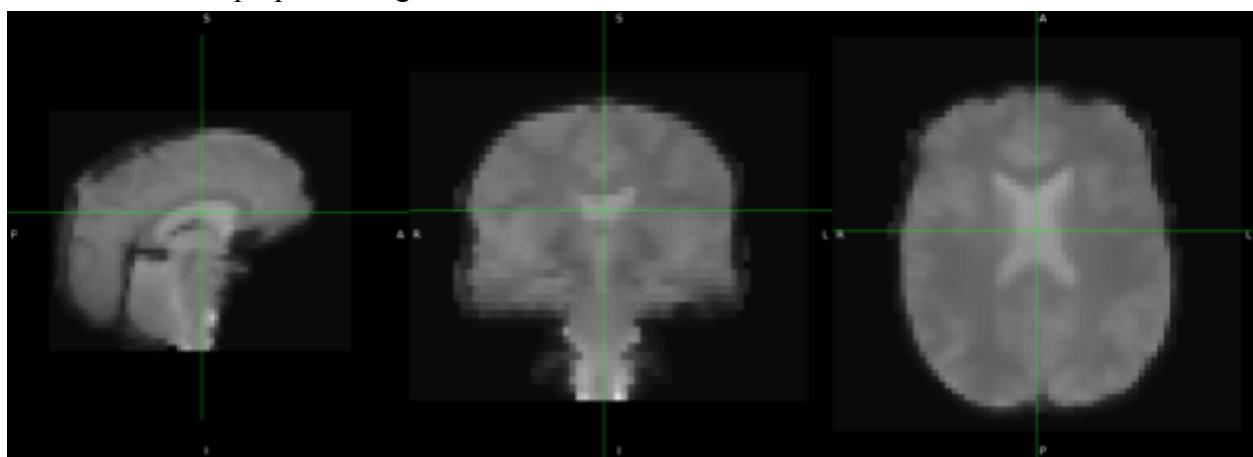


Fig. 7

Checking Registration and Normalization:

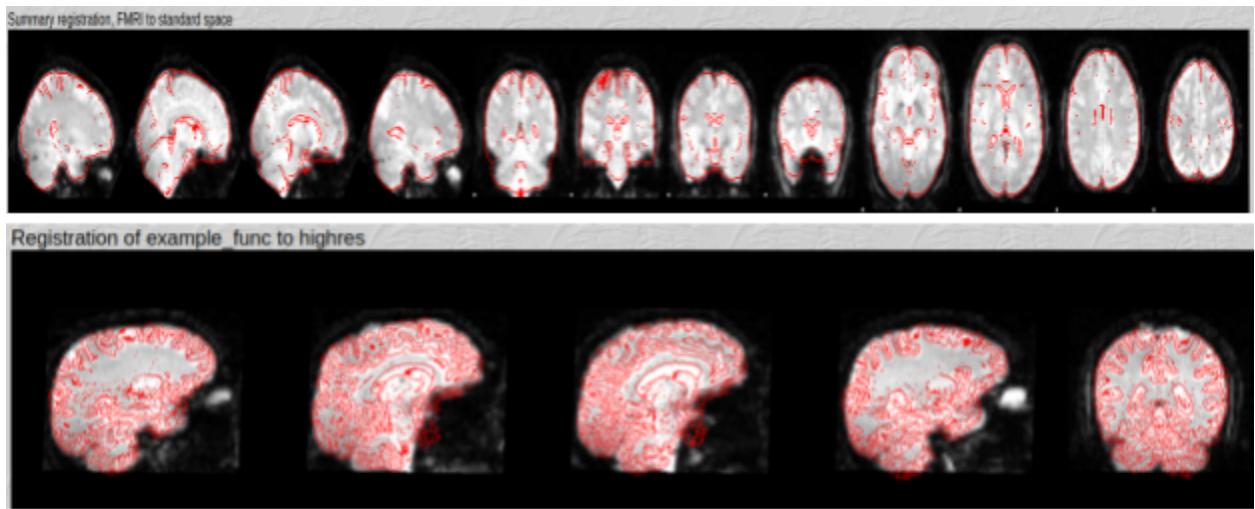


Fig. 8

Each image overlays the red outline of a brain onto a greyscale image of another brain. The first montage in Fig.8, Summary Registration, shows a representative functional image - in this case, the median image in the fMRI time-series - as the underlay, and the template brain as the red lines. This image is shown first, because if there were any problems in any of the previous registration or normalization steps, there would be obvious errors in this image, such as the image being skewed or largely outside of the red outline.

Checking Motion:

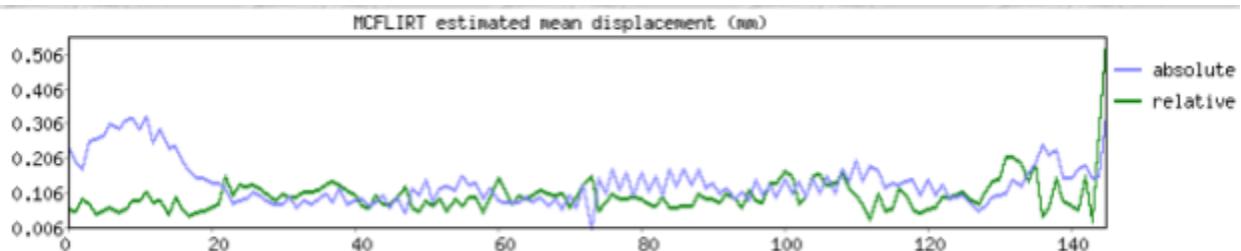


Fig. 9

In Fig. 9 we see that run 2 of subject 20 didn't have many motion artifacts.

Smoothing with 3mm kernel size vs 12 mm kernel size:

In this analysis, we performed preprocessing on the functional data of subject 20 run 1 using two different smoothing kernels: 3mm and 12mm. The aim was to observe how varying the smoothing kernel size affects the preprocessed functional data and to compare the results with our expectations.

Expectations:

Before examining the outputs, I anticipated the following:

- 3mm Smoothing Kernel: I anticipated that the information would show some gentle smoothing effects, making the signal stronger compared to the background noise without making the actual brain activity blurry. This would help keep the detailed features of brain activation intact.
- 12mm Smoothing Kernel: I anticipated that using the bigger 12mm smoothing kernel would make the data more blurry, which could result in losing some of the specific details and patterns of brain activation. However, I also believe that it would help reduce noise and make the overall signal clearer.

Results:

3mm Smoothing kernel

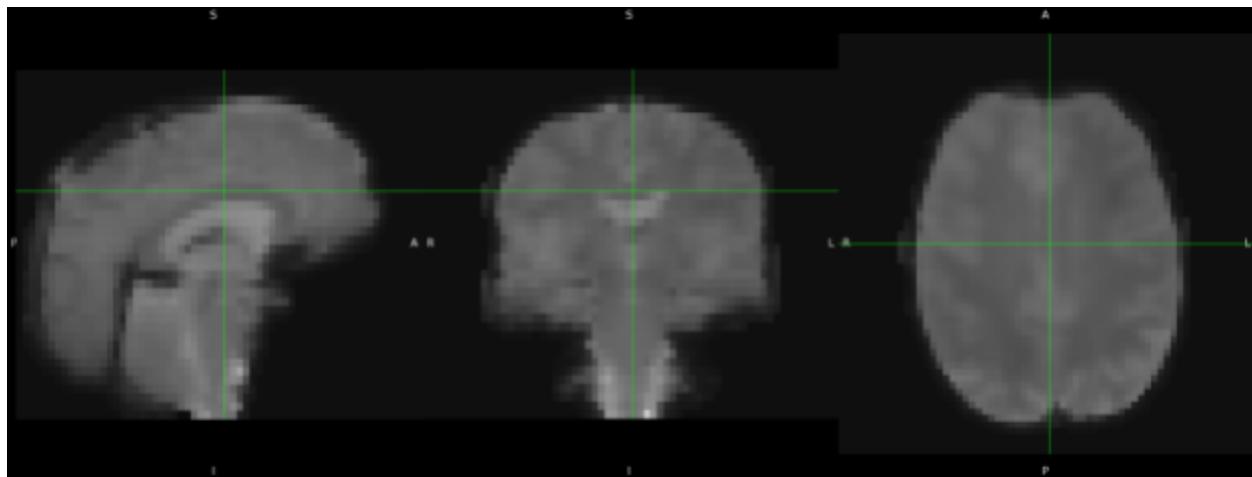


Fig. 10

From Fig. 10, we can see that the data maintained relatively sharp details without much blurring. The smoothing effects were subtle, improving the signal quality without losing spatial accuracy.

12mm Smoothing kernel

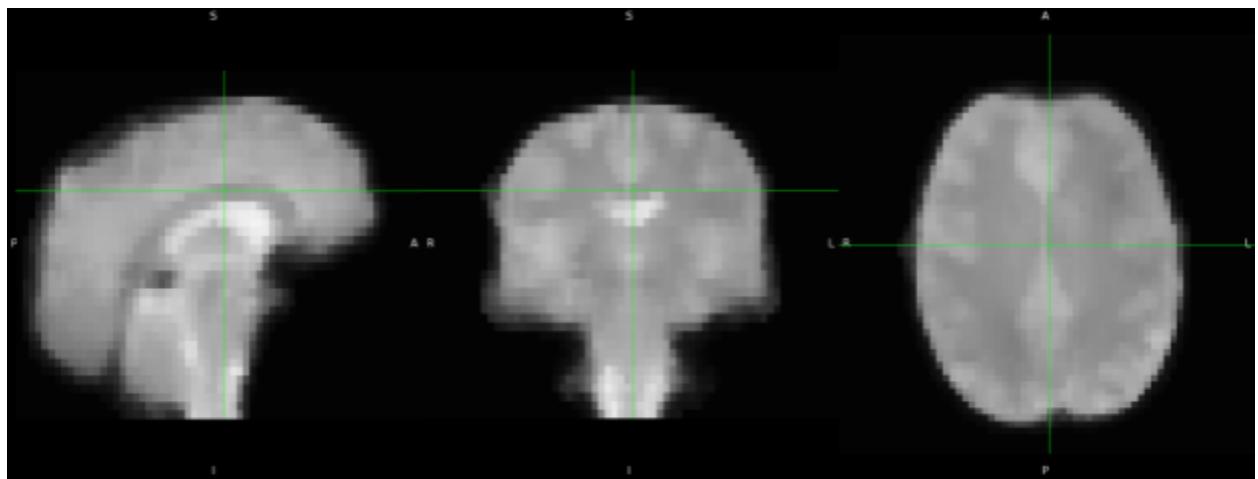


Fig. 11

On the other hand, from Fig. 11 the information analyzed using the 12mm smoothing kernel showed significant blurriness. Even though the main signal was still visible, the smaller details became harder to see. However, the bigger smoothing kernel successfully decreased the amount of noise, leading to a more even and consistent signal spread throughout the brain.

Registration with 3 DOF vs. 12 DOF:

In this analysis, we conducted preprocessing on the functional data of subject 20 run 1 using two different degrees of freedom (DOF) for registration and normalization: 3DOF and 12DOF. The aim was to evaluate how the choice of DOF affects the registration and normalization outcomes and to understand the differences observed in the preprocessed data.

Expectations:

Before examining the outputs, I anticipated the following:

- 3 DOF Registration: I expected that the 3DOF registration would give a more limited transformation, mainly showing the overall differences in position and orientation between the functional and structural images. As a result, I was expecting there to be possible misalignments or distortions in areas with complicated anatomical features or major nonlinear changes.
- 12 DOF Registration: With 12 DOF registration, I expected a more flexible transformation that could better accommodate local variations in brain anatomy and account for non-linear distortions. This should result in improved alignment accuracy.

Results:

3 DOF Registration

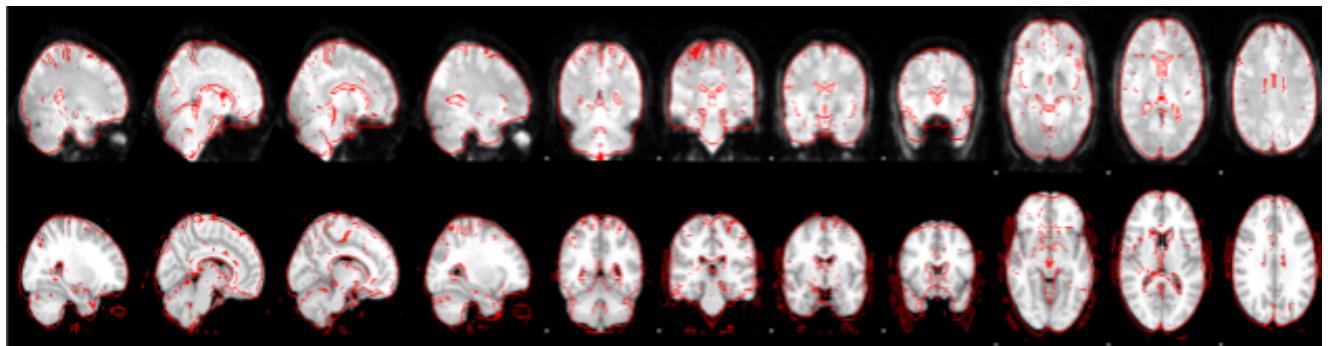


Fig. 12

Upon examining Fig. 10, It is clear that using 3 degrees of freedom for registration caused some misalignments and distortions, especially in areas with intricate anatomical details or non-linear deformations. Although the general alignment was okay, there were noticeable differences between the functional and structural images, which affected the registration results negatively.

12 DOF Registration

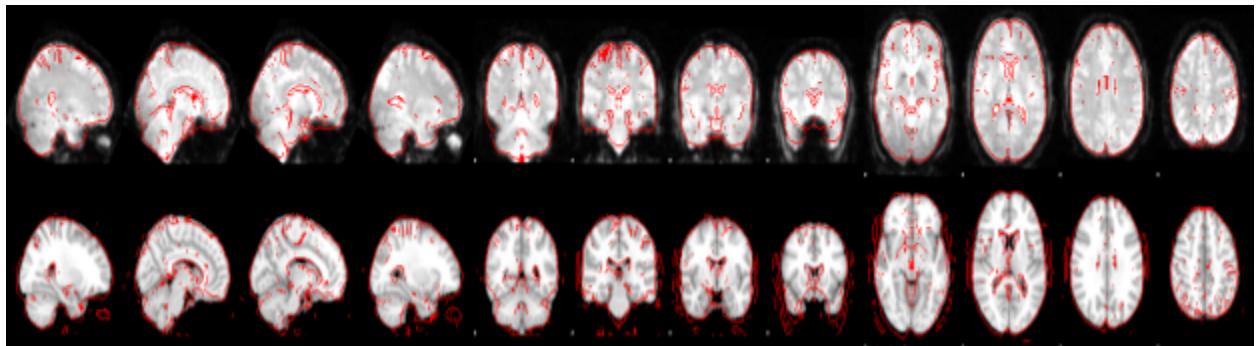


Fig. 13

On the other hand, when we look at Fig. 13, we can see that the preprocessing done with 12 DOF registration had a much better alignment accuracy and spatial coherence between the functional and structural images. This transformation was able to capture even the smallest details of the brain's anatomy and handle local differences more efficiently, leading to a more accurate registration result.

Registration with BBR vs. 12 DOF:

In this analysis, we conducted preprocessing on the functional data of subject 20 run 1 using two different registration methods: Boundary-Based Registration (BBR) and 12 degrees of freedom (12 DOF). The aim was to evaluate how the choice of registration method affects the alignment accuracy and spatial coherence between functional and structural images.

Expectations:

Before examining the outputs, I anticipated the following:

- **BBR Registration:** I expected that BBR would offer better alignment accuracy than 12 DOF registration because it can use boundary information to optimize the process. This should lead to a more accurate alignment, especially in areas with intricate anatomical features or non-linear distortions.
- **12 DOF Registration:** With 12 DOF registration, I expected that the transformation would be more flexible but less accurate, making it difficult to capture the small details of the anatomy. However, it should still align the functional and structural images reasonably well.

Results:

BBR Registration

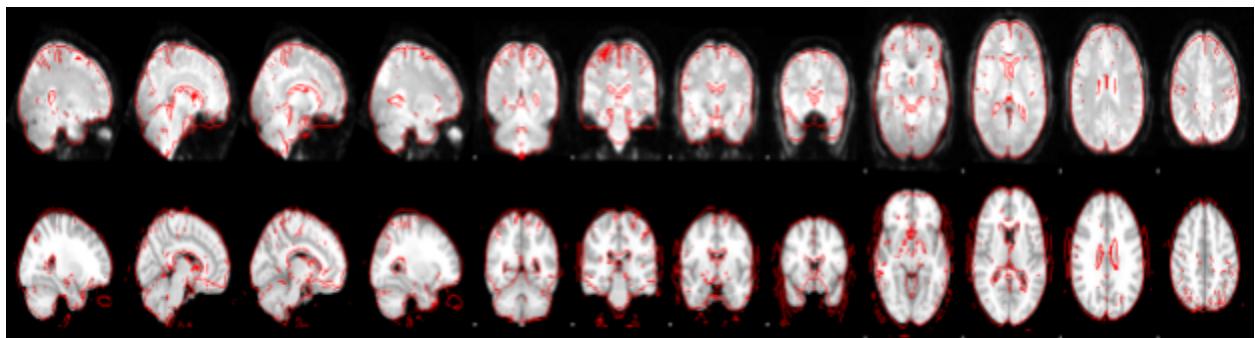


Fig. 14

Upon examining the output (Fig. 14), it is evident that BBR registration resulted in significantly improved alignment accuracy and spatial coherence between the functional and structural images. The transformation captured finer details of brain anatomy and exhibited better spatial correspondence, particularly in regions with complex anatomical features or non-linear distortions.

12 DOF Registration

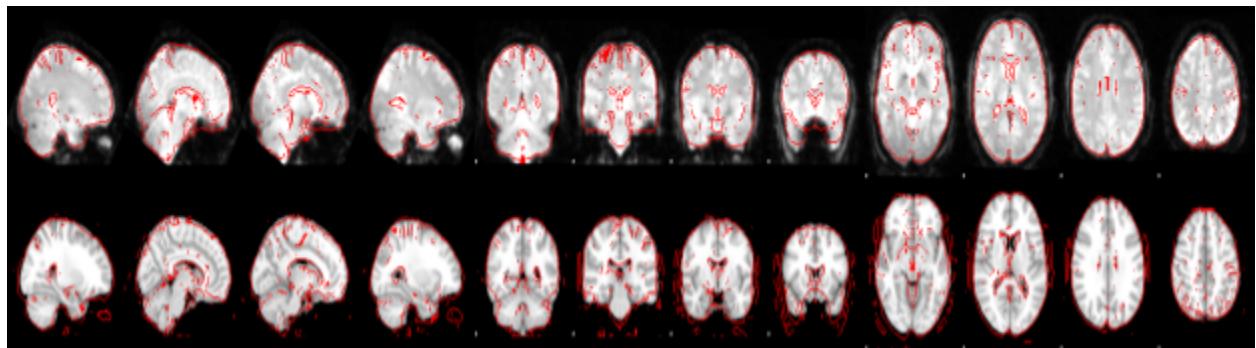


Fig. 15

In contrast, 12 DOF registration (Fig. 15) resulted in less precise alignment and spatial coherence between the functional and structural images compared to BBR. While the overall alignment was acceptable, there were noticeable differences between the registered images, with less accurate capture of fine anatomical details and increased susceptibility to misalignments or distortions.

Conclusion:

In conclusion, the choice of registration method significantly impacts the alignment accuracy and spatial coherence between functional and structural images. BBR registration offers superior performance, particularly in handling complex anatomical features and non-linear distortions, making it a more reliable choice for ensuring accurate registration outcomes in fMRI analysis.

General Conclusion:

In this series of exercises, I explored various preprocessing and analysis techniques using FSL (FMRIB Software Library) in the context of functional magnetic resonance imaging (fMRI) data. Through the execution of each task, I gained valuable insights into the impact of different methodological choices on the quality and interpretability of neuroimaging results.

1. **Brain Extraction with BET:** My examination of BET highlighted the importance of fractional intensity thresholding in extracting brain tissue from anatomical images. By comparing the outputs generated with different thresholds, we were able to discern the trade-offs between conservativeness and aggressiveness in brain extraction, aiding in informed decision-making for subsequent analyses.
2. **Preprocessing with FEAT GUI:** Utilizing the FEAT GUI, I conducted preprocessing on functional data, maintaining consistency in analysis settings while processing multiple

runs. This approach ensured standardization and reproducibility in our preprocessing pipeline, facilitating reliable data preparation for subsequent statistical analyses.

3. **Impact of Smoothing Kernels:** By varying the size of smoothing kernels during preprocessing, I observed distinct differences in the appearance of preprocessed functional data. Our comparison between 3mm and 12mm smoothing kernels underscored the importance of balancing spatial smoothing effects with the preservation of fine-grained anatomical features, thus influencing subsequent analyses and interpretation of results.
4. **Effect of Registration Degrees of Freedom:** My investigation into registration degrees of freedom revealed significant differences in alignment accuracy and spatial coherence between 3 DOF and 12 DOF methods. While 12 DOF registration provided greater flexibility, 3 DOF registration exhibited limitations in capturing fine anatomical details accurately, highlighting the importance of selecting an appropriate registration strategy based on the specific requirements of the study.
5. **Advantages of BBR Registration:** Finally, our comparison between BBR and 12 DOF registration methods demonstrated the superior alignment accuracy and robustness of BBR, particularly in handling complex anatomical features and non-linear distortions. This underscores the importance of leveraging advanced registration techniques to optimize the quality and reliability of neuroimaging analyses.

In conclusion, My exploration of various preprocessing and analysis techniques in fMRI data processing has provided valuable insights into the methodological considerations and their implications for neuroimaging research. By understanding the strengths and limitations of different approaches, researchers can make informed decisions to ensure the integrity and validity of their findings in the study of brain function and connectivity.

FMRI Task 2

Neuroanatomy: Structure of the Brain

Neuroanatomy is a field of anatomy that focuses on studying the structure and arrangement of the nervous system, specifically the brain and spinal cord. It is really important to grasp neuroanatomy in order to understand how the brain works and its connection to behavior, thinking, and different neurological conditions.

Major Brain Regions:

1. Cerebral Cortex:

- The brain's outermost layer is called the cerebral cortex, and it plays a crucial role in important mental processes like thinking, understanding, and moving voluntarily.
- This layer is further divided into four lobes: frontal, parietal, temporal, and occipital. Each lobe has its own unique functions and specific areas that handle different tasks.

2. Basal Ganglia:

- The basal ganglia are a group of nuclei located deep within the cerebral hemispheres.
- They are involved in motor control, procedural learning, and habit formation. Dysfunction of the basal ganglia can lead to movement disorders such as Parkinson's disease and Huntington's disease.

3. Limbic System:

- The limbic system is a collection of structures located on both sides of the thalamus beneath the cerebrum.
- It is primarily associated with emotions, motivation, learning, and memory. Key structures include the hippocampus, amygdala, and hypothalamus.

4. Thalamus:

- The thalamus is a small structure located at the top of the brainstem.
- It serves as a relay station for sensory information, relaying signals from sensory organs to the cerebral cortex and regulating consciousness, sleep, and alertness.

5. Hypothalamus:

- The hypothalamus is a region located below the thalamus and above the brainstem.
- It plays a crucial role in maintaining homeostasis by regulating functions such as hunger, thirst, body temperature, and sleep. It also controls the release of hormones from the pituitary gland.

6. Brainstem:

- The brainstem is the lower part of the brain that connects the cerebrum with the spinal cord.
- It regulates basic physiological functions such as breathing, heart rate, and consciousness. The brainstem consists of the midbrain, pons, and medulla oblongata.

7. Cerebellum:

- The cerebellum is located at the back of the brainstem, beneath the cerebrum.
- It is primarily involved in coordinating voluntary movements, balance, and posture. It also plays a role in motor learning and cognitive functions.

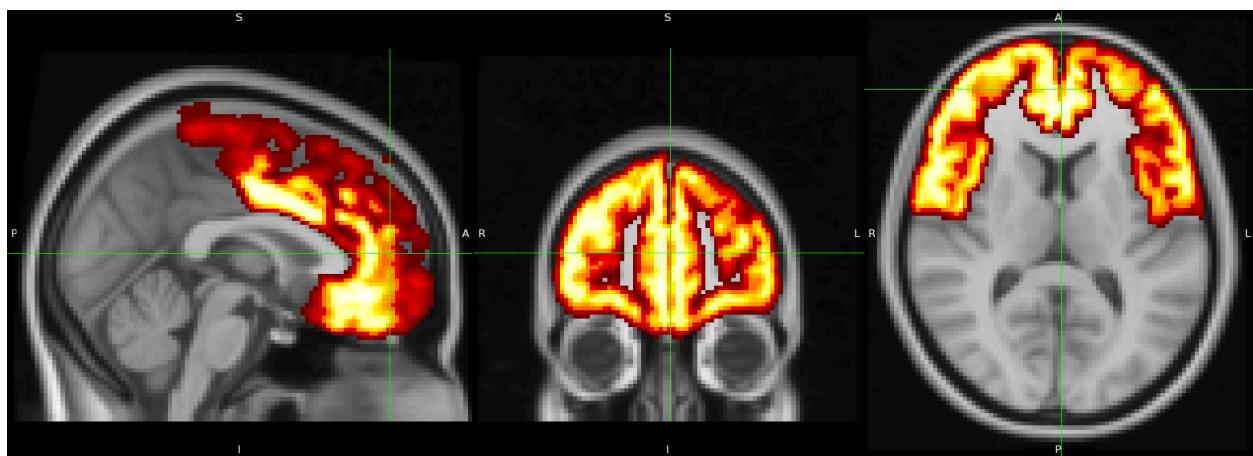
Detailed Anatomical Features and Functions of Each Region:

Each brain region has distinct anatomical features and functions that contribute to the overall functioning of the nervous system. Understanding these features is essential for understanding brain structure and its relationship to behavior and cognition.

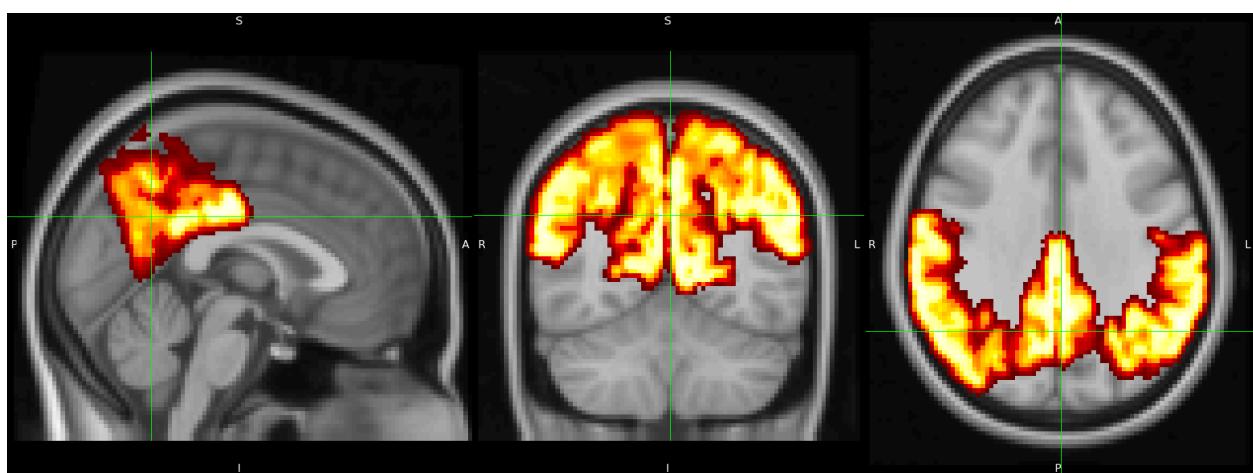
Cerebral Cortex:

The cerebral cortex is highly folded, increasing its surface area and allowing for more extensive neural connections. Different regions of the cortex are responsible for specific functions, such as the frontal lobe for executive functions and motor control, the parietal lobe for sensory processing, the temporal lobe for auditory processing and memory, and the occipital lobe for visual processing.

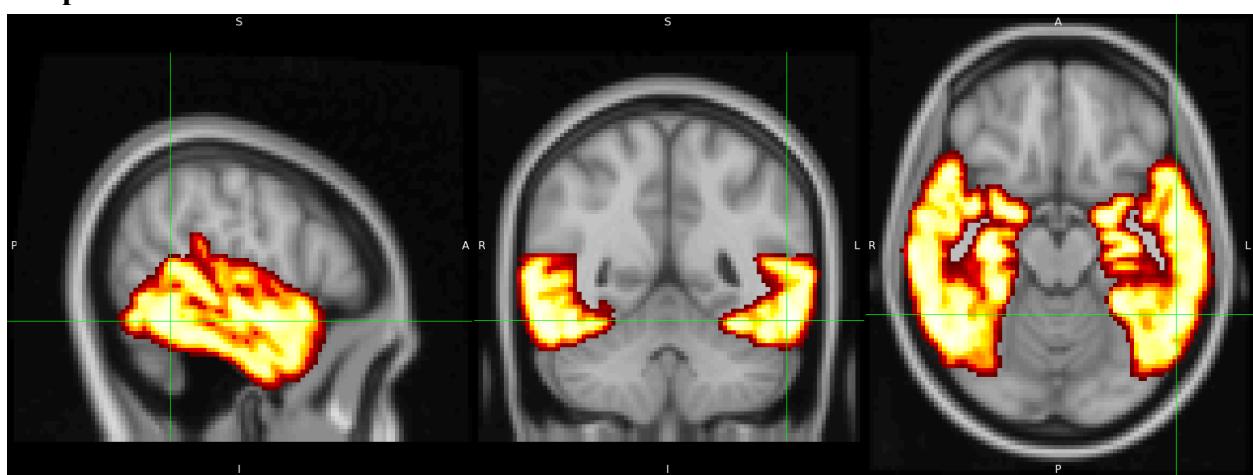
Frontal Lobe:



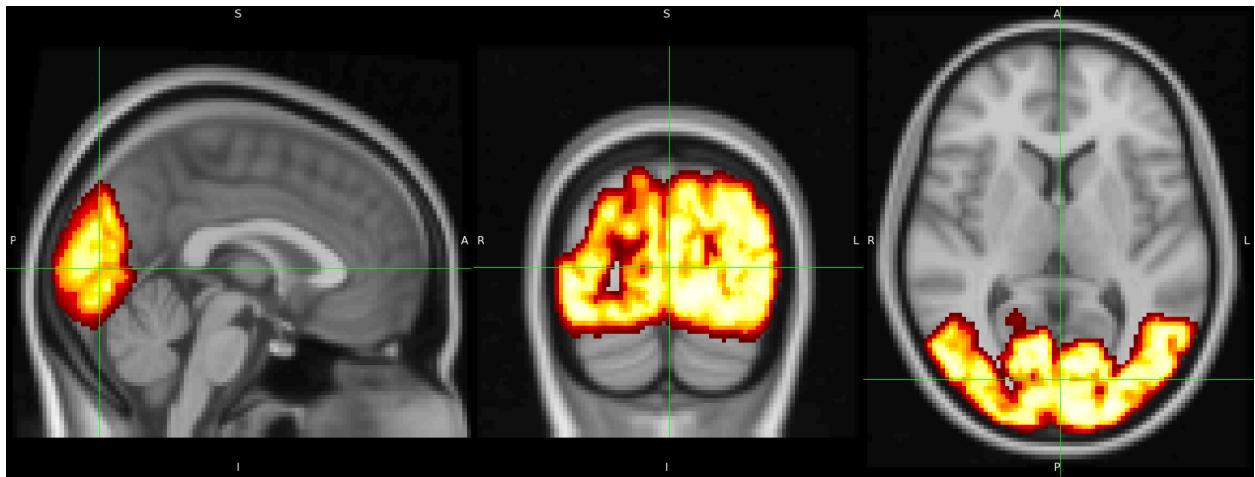
Parietal Lobe:



Temporal Lobe:



Occipital Lobe:



Basal Ganglia:

The basal ganglia consist of several nuclei, including the striatum, globus pallidus, and substantia nigra. These nuclei form circuits with the cerebral cortex and thalamus, modulating motor control and facilitating procedural learning and habit formation.

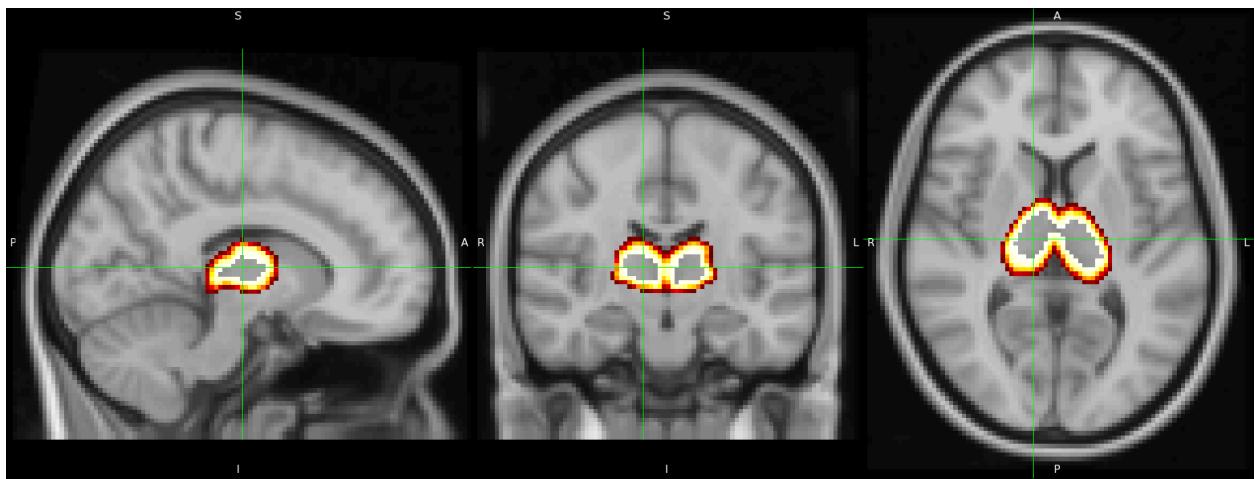
Limbic System:

The limbic system comprises interconnected structures involved in emotion, memory, and motivation. The hippocampus is essential for the formation and consolidation of long-term memories, while the amygdala plays a central role in processing emotions, particularly fear and aggression. The hypothalamus regulates various physiological processes and links the nervous system to the endocrine system via the pituitary gland.

Thalamus:

The thalamus consists of numerous nuclei that relay sensory information to the cerebral cortex. Different nuclei relay specific sensory modalities, such as vision, hearing, touch, and taste. Additionally, the thalamus regulates consciousness, alertness, and sleep-wake cycles.

Thalamus:



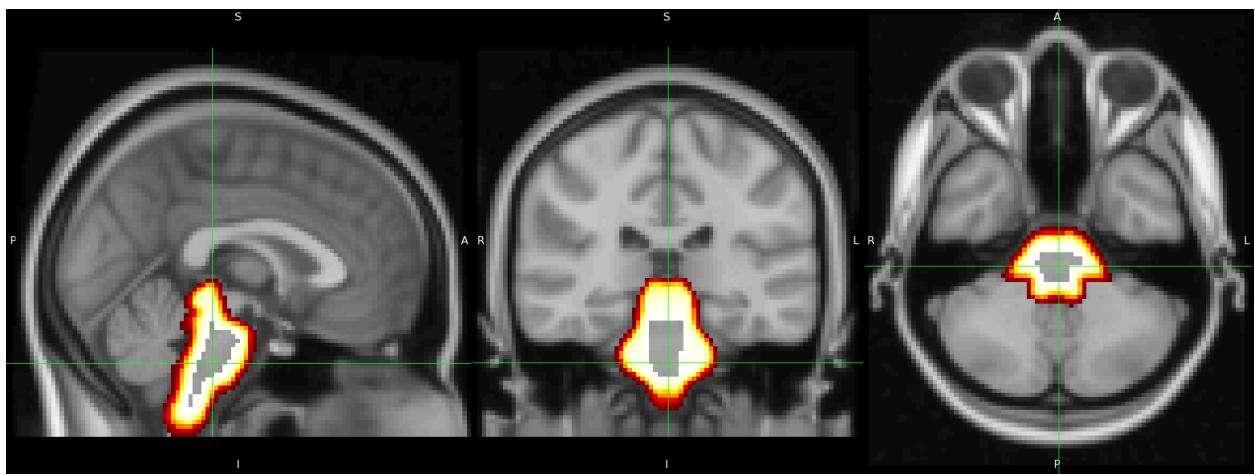
Hypothalamus:

The hypothalamus contains nuclei that control autonomic functions, endocrine regulation, and basic survival behaviors such as eating, drinking, and reproduction. It also regulates the body's response to stress and plays a role in circadian rhythms.

Brainstem:

The brainstem contains vital nuclei responsible for controlling essential functions such as breathing, heart rate, and blood pressure. The midbrain contains nuclei involved in visual and auditory reflexes, while the pons and medulla oblongata regulate autonomic functions and serve as relay centers for sensory and motor pathways.

Brainstem:



Cerebellum:

The cerebellum consists of highly organized layers of neurons called the cerebellar cortex. It receives input from the cerebral cortex and spinal cord and integrates this information to coordinate voluntary movements, maintain balance, and refine motor skills.

In conclusion, the brain is a complex organ composed of various interconnected regions, each with distinct anatomical features and functions. Understanding the neuroanatomy of the brain is essential for comprehending its role in behavior, cognition, and neurological disorders.

FMRI Task 3

Statistics and Modeling

In this report, we will delve into the significance of first-level analysis using FSL FEAT in studying brain activity with fMRI. This crucial step allows us to gain a deeper understanding of how the brain reacts to various tasks or stimuli in different individuals.

Once we have prepared the data (what we have done in task 1), we employ statistical techniques to examine how brain activity is connected to the experimental conditions. This typically entails creating a model using the General Linear Model (GLM), which takes into account factors such as the timing of stimuli and any variables that may interfere (such as head motion). By conducting this analysis, we can produce maps that highlight specific regions of the brain that display noteworthy activity in relation to the experimental conditions.

We will be working on subject 15 (sub-15).

Steps for the first-level analysis:

1. Creating timing files:

We want to make the fitted time-series to help us with the group analysis by using the beta weights we calculated. Let's examine the Flanker dataset. In the func directory of each subject, we will find files called events.tsv. These files hold three important details that we require to make our timing files, also known as onset files:

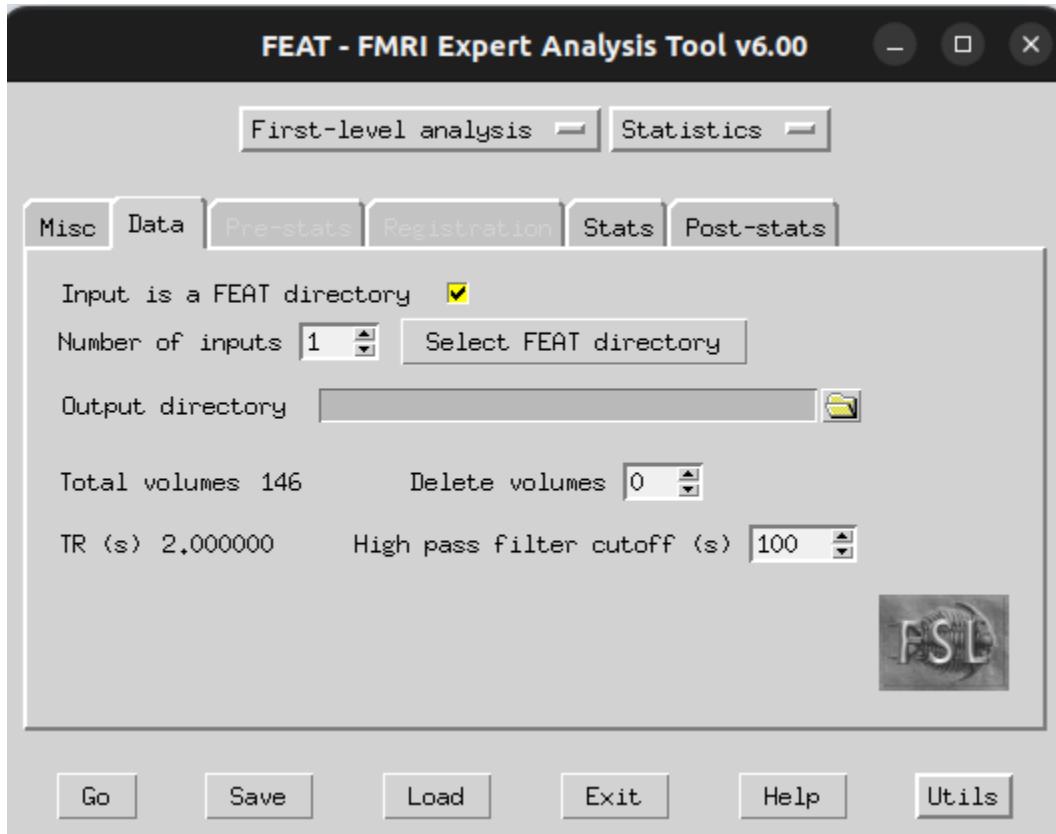
1. The condition's name.
2. The time, in seconds, when each trial of the condition took place, relative to the beginning of the scan.
3. The duration of each trial.

The information must be taken out of the events.tsv documents and organized in a format that can be understood by the FSL software.

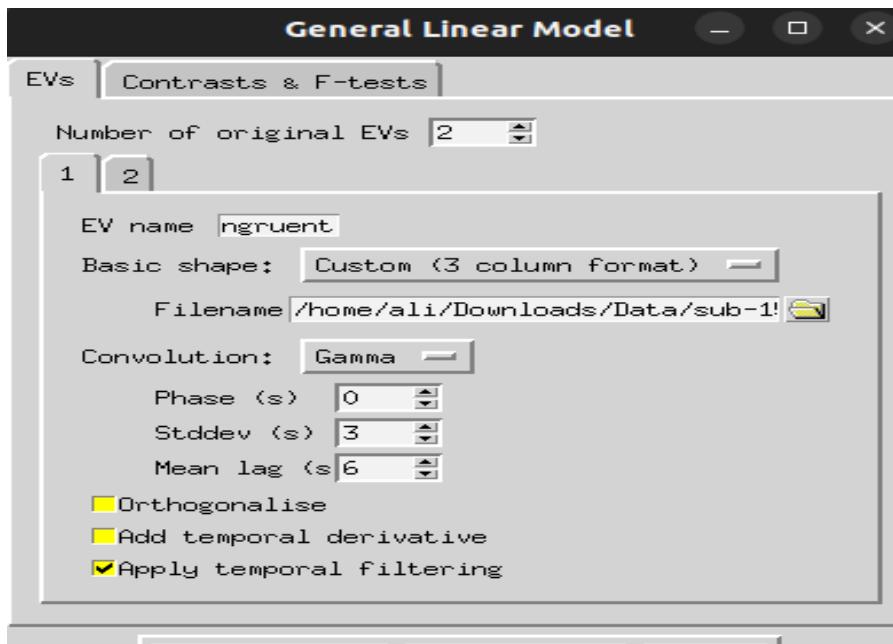
So we will run this script:

```
1#!/bin/bash
2
3 #Check whether the file subjList.txt exists; if not, create it
4 if [ ! -f subjList.txt ]; then
5   ls -d sub-?? > subjList.txt
6 fi
7
8 #Loop over all subjects and format timing files into FSL format
9 for subj in `cat subjList.txt` ; do
10   cd ${subj}/func #navigate to the subject's func directory, which contains the timing files
11
12   #Extract the onset times for the incongruent and congruent trials for each run. NOTE: This script only extracts the trials in which the subject made a correct response. Accuracy is nearly 100% for all subjects, but as an exercise the student can modify this to extract the incorrect trials as well.
13   cat ${subj}_task-flanker_run-1_events.tsv | awk '{if ($3=="incongruent_correct") {print $1, $2, "1"}' > incongruent_run1.txt
14   cat ${subj}_task-flanker_run-1_events.tsv | awk '{if ($3=="congruent_correct") {print $1, $2, "1"}' > congruent_run1.txt
15
16   cat ${subj}_task-flanker_run-2_events.tsv | awk '{if ($3=="incongruent_correct") {print $1, $2, "1"}' > incongruent_run2.txt
17   cat ${subj}_task-flanker_run-2_events.tsv | awk '{if ($3=="congruent_correct") {print $1, $2, "1"}' > congruent_run2.txt
18
19   cd ..
20 done
```

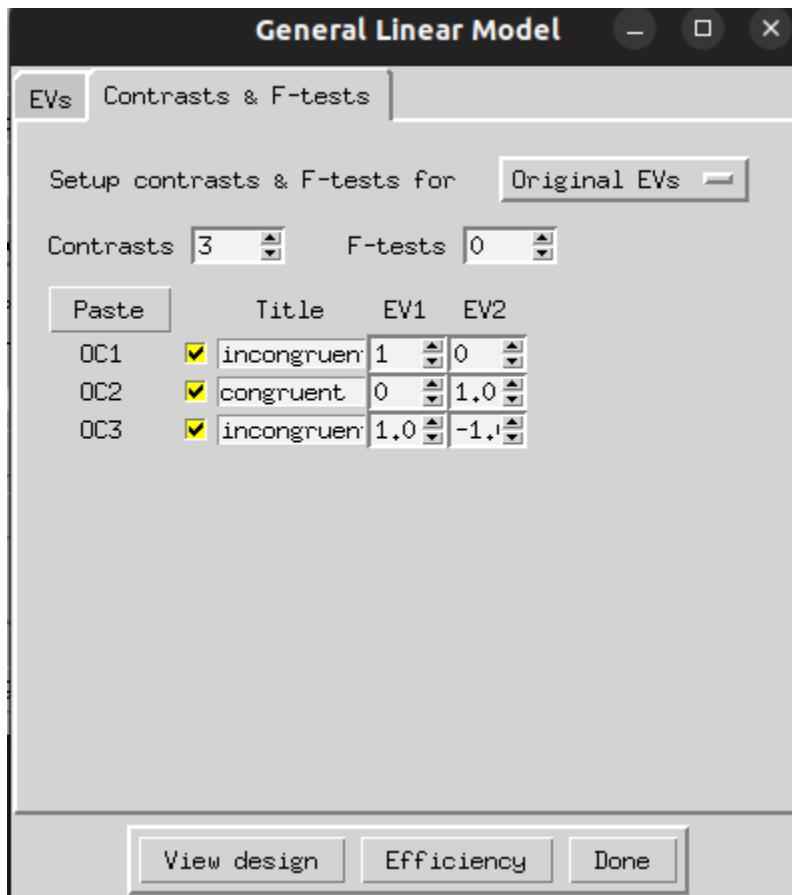
2. Open FEAT GUI then select Statistics instead of Full-analysis, go to data check the Input is a FEAT directory check box then load subject 15 run 1 feat directory:



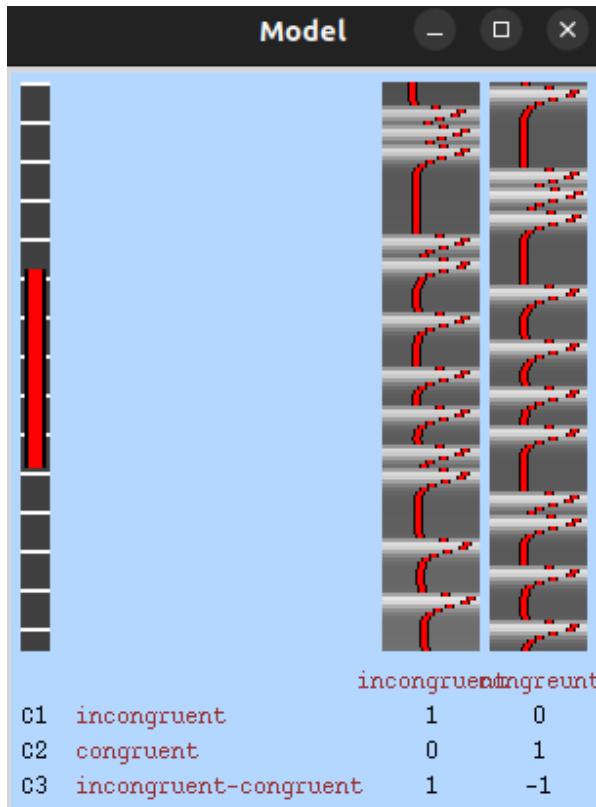
3. Go to full model setup add another EV name each incongruent and congruent select the shape (3 column format) then select their files uncheck the add temporal derivative checkbox



4. Go to contrasts and f-tests tab, add 3 contrast which are the incongruent(1,0), congruent(0,1) and incongruent-congruent(-1,1) then press done.



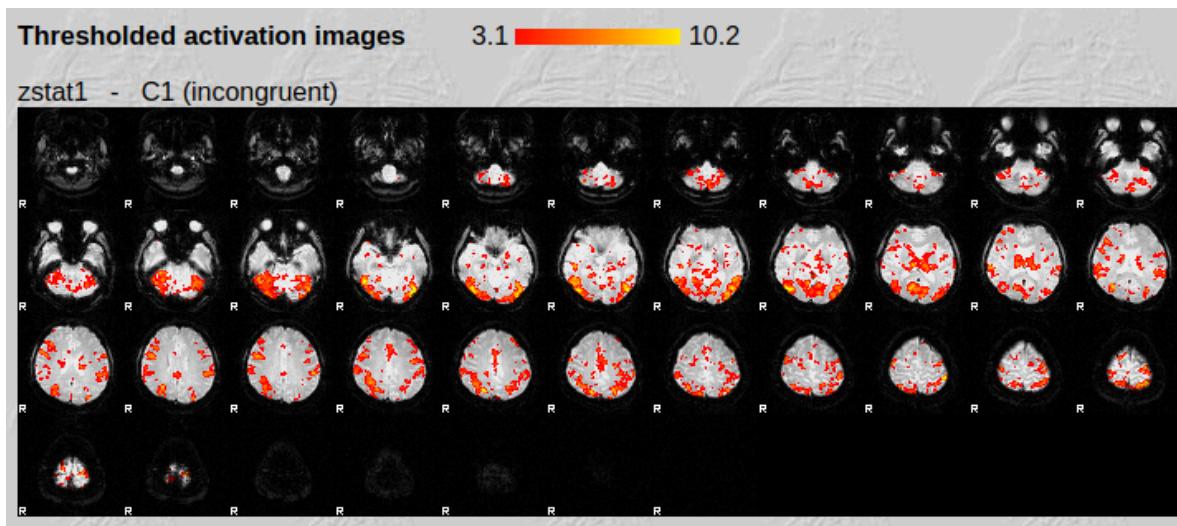
What we see now is the Design Matrix (regressors) of the two tasks (incongruent & congruent), we can see that there is no overlapping between them which is what we want.



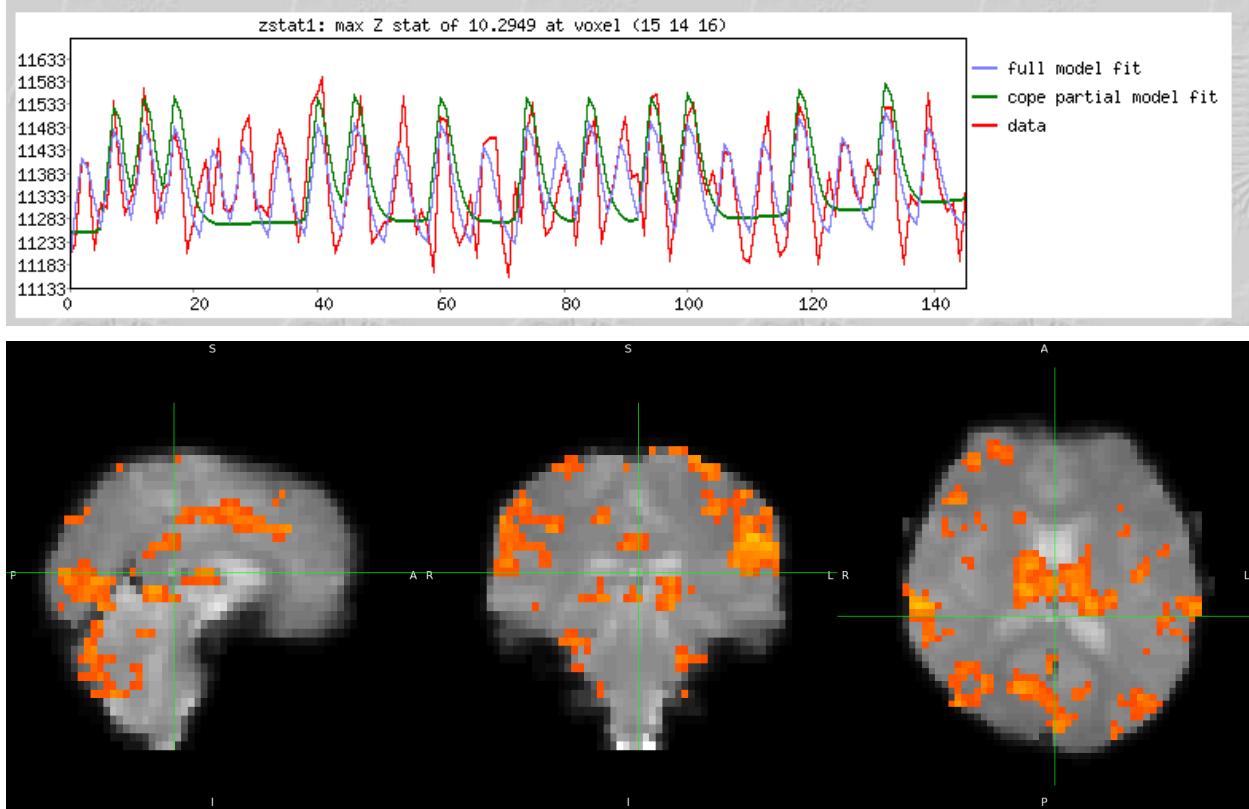
5. Repeat the same steps for congruent then for run 2 and rest of subject's run 1 and 2

Results and Observations

This image shows the activated regions of the brain during the incongruent task

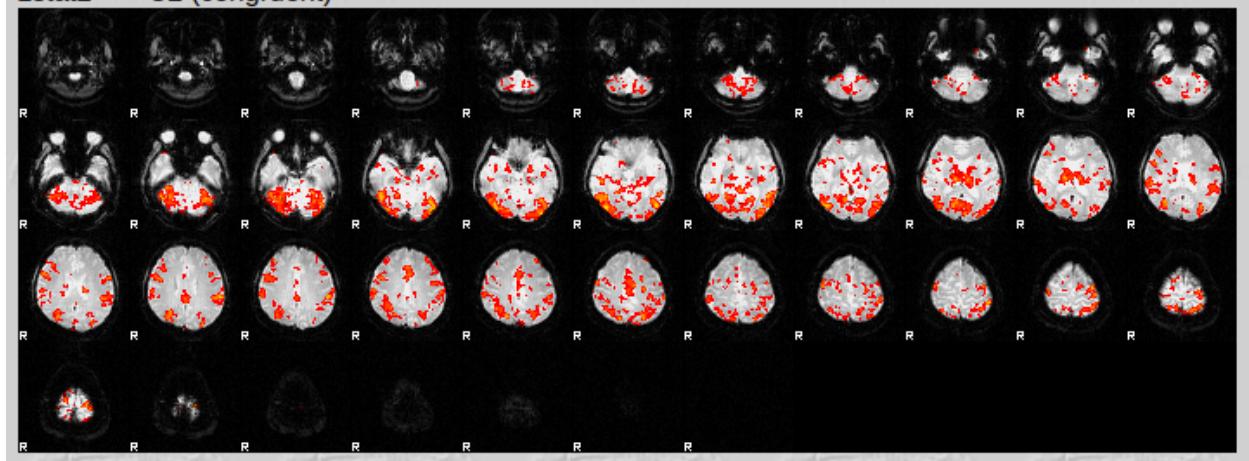


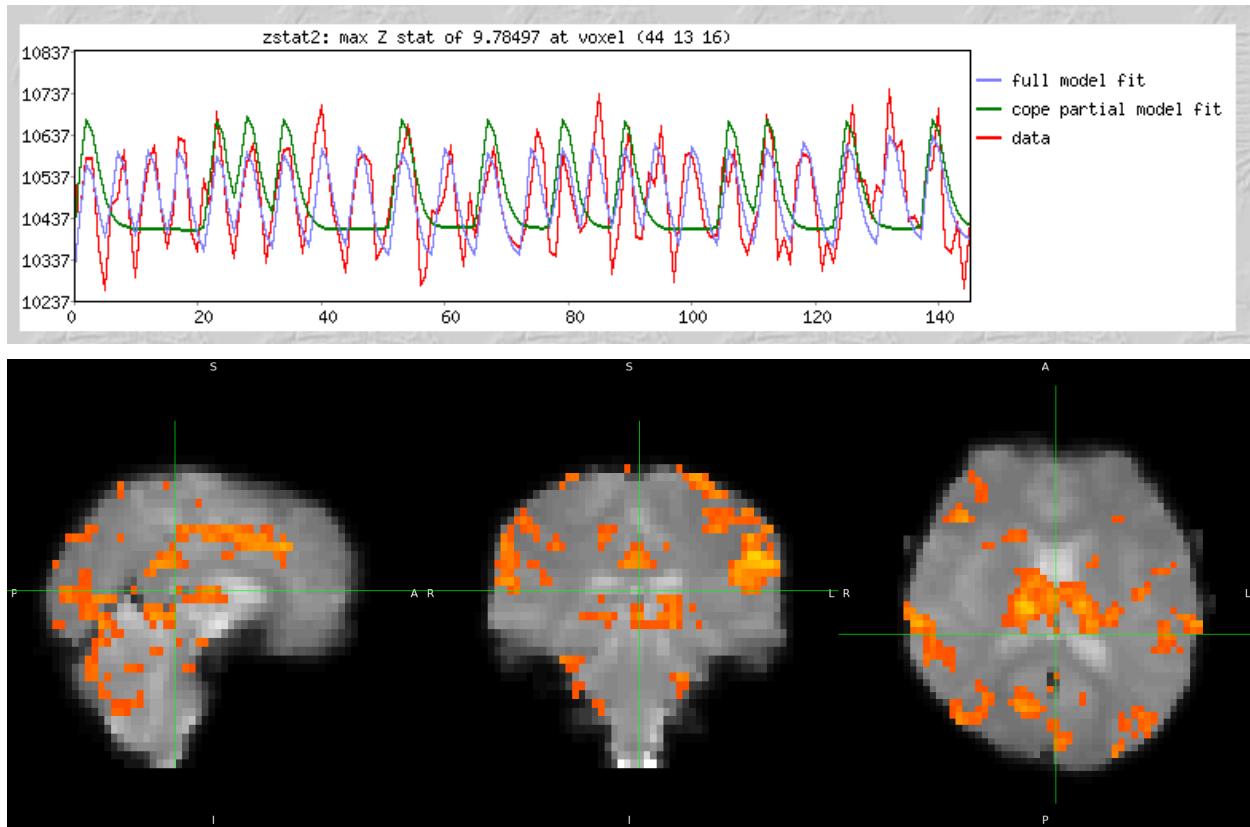
Time series plots



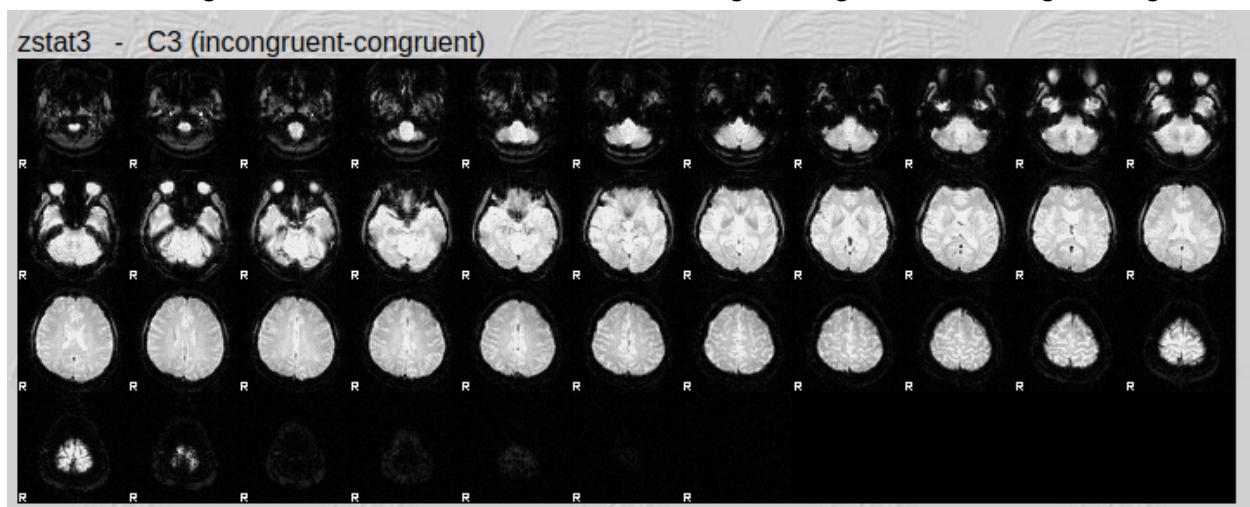
This image shows activated regions of the brain during the congruent task

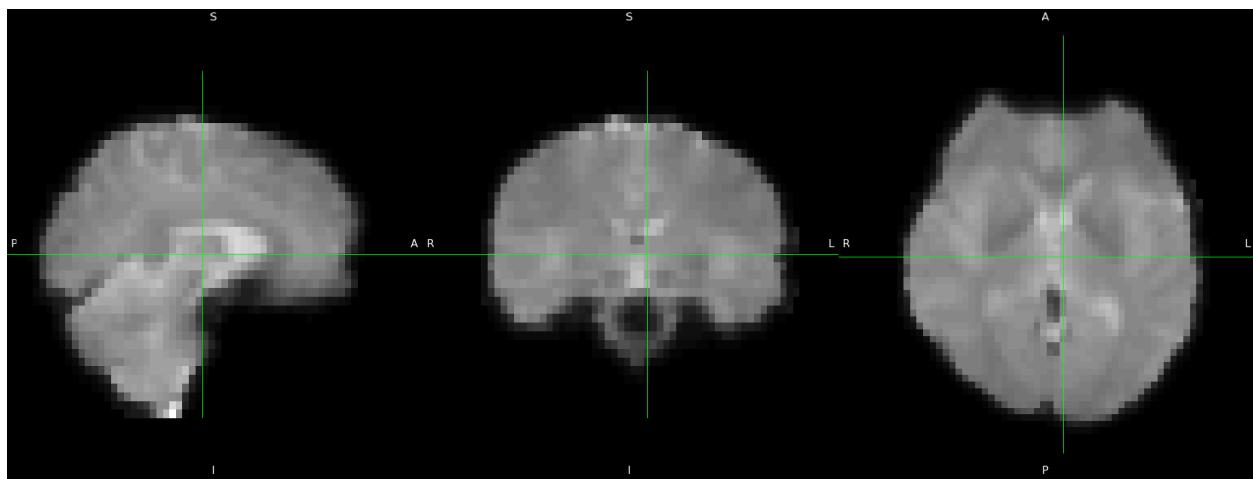
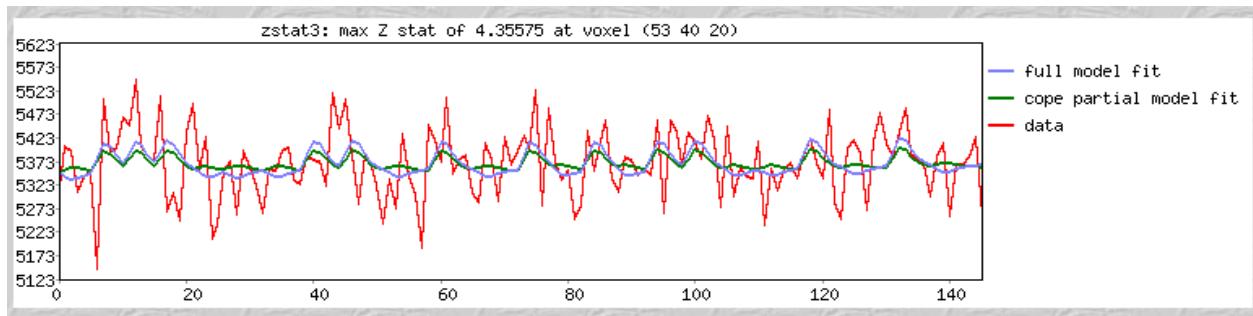
zstat2 - C2 (congruent)





This image shows the difference in between the incongruent regions and the congruent regions





FMRI Task 4 1.1

Introduction to scripting

Automation is extremely important in modern scientific research because it helps make things more efficient. Scripting, which is the art of writing code that can do tasks automatically, is now necessary in many different fields. Whether it's processing data or analyzing statistics, scripting allows researchers to automate tasks that they would otherwise have to do by hand. This not only saves time, but also reduces the chance of making mistakes. Additionally, scripting makes it possible to analyze large amounts of data quickly and effectively.

Challenges in Manual Analysis

Analyzing data manually works fine for small studies, but it gets really hard and mistake-prone when dealing with big datasets. When it comes to analyzing complex neuroimaging data, the chances of making mistakes go up, which can mess up the results. Plus, it takes too much time and effort to do manual analysis on large datasets, slowing down scientific research. Imagine doing the steps done in Task 3 **52 times** for both runs of the 26 subjects that's why now we try to script this process.

Creating Analysis Templates

One important technique in using scripting for neuroimaging analysis is to make analysis templates. These templates contain the whole analysis process, from preparing the data to creating statistical models, in a format that can be used again. By adjusting subject-specific variables, like subject IDs, analysis templates can be used consistently for many subjects and sessions, removing the need for manual adjustments.

Repeat the steps from Task 3 but instead of pressing Go at the end press Save.



Implementation: Scripting for Automated Analysis

In our research, we used scripting to automate the examination of brain imaging data from twenty-six subjects, each with two runs. We created a script called run_1stLevel_Analysis.sh to manage the analysis process for each subject and run. This script makes use of analysis templates created with FSL's FEAT GUI to carry out preprocessing, model fitting, and statistical analysis in a consistent way.



```
#!/bin/bash

# Loop through subjects from 01 to 26
for id in `seq -w 1 26` ; do
    subj="sub-$id"
    echo "====> Starting processing of $subj"
    echo

    # Change directory to current subject
    cd $subj

    # If the brain mask (BET) doesn't exist, create it
    if [ ! -f anat/${subj}_T1w_brain.nii.gz ]; then
        echo "Skull-stripped brain not found, using bet with a fractional intensity threshold of 0.2"

        # Skull-strip the T1-weighted image using bet2
        bet2 anat/${subj}_T1w.nii.gz \
              anat/${subj}_T1w_brain_f02.nii.gz -f 0.2
    fi

    # Copy the design files into the subject directory, and then
    # change "sub-01" to the current subject number
    cp ./design_run1.fsf .
    cp ./design_run2.fsf .

    # Replace subject ID in design files
    sed -i "s|sub-01|${subj}|g" design_run1.fsf
    sed -i "s|sub-01|${subj}|g" design_run2.fsf

    # Run FEAT analysis for run 1
    echo "====> Starting feat for run 1"
    feat design_run1.fsf

    # Run FEAT analysis for run 2
    echo "====> Starting feat for run 2"
    feat design_run2.fsf

    echo

    # Go back to the directory containing all of the subjects
    cd ..

done

echo "Script execution completed."
```

Conclusion

In summary, scripting plays a crucial role in today's neuroimaging research, allowing researchers to handle intricate analyses quickly and accurately. Through automating analysis processes and utilizing pre-made templates, researchers can speed up data analysis, reduce mistakes, and discover fresh perspectives from extensive neuroimaging datasets.

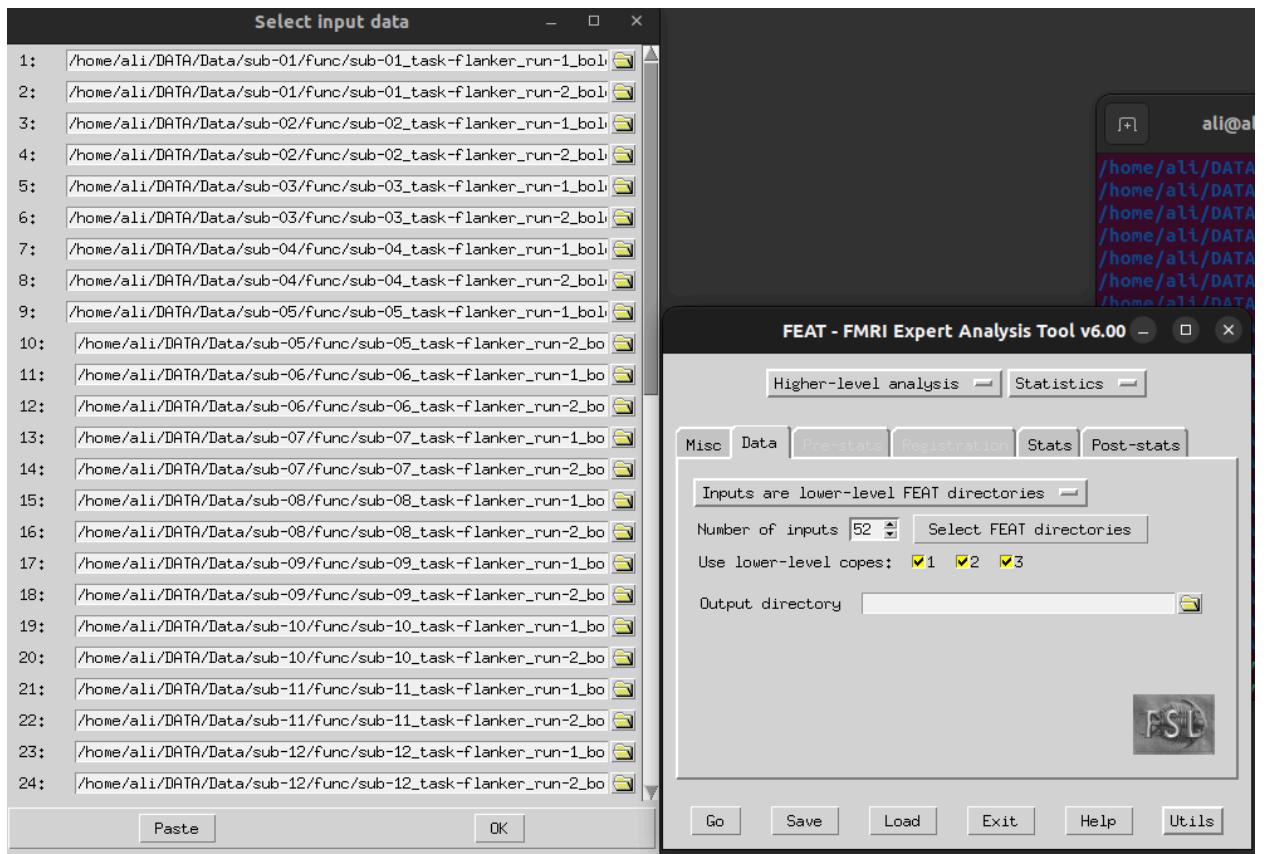
FMRI Task 4 1.2

Introduction to Second-Level Analysis

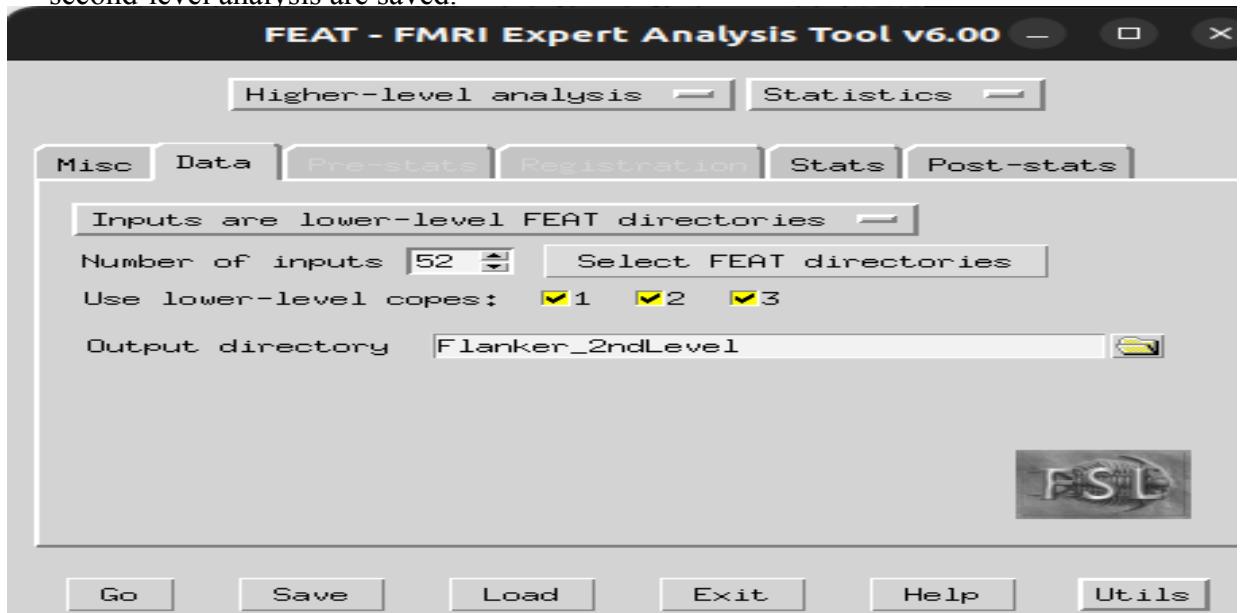
Once the individual runs for each subject in the Flanker dataset have been preprocessed and analyzed, the next stage is to perform a second-level analysis. In FSL (FMRIB Software Library), a second-level analysis that involves taking the average of the parameter estimates and contrast estimates obtained from the first-level analyses for each subject. The purpose of this process is to combine the results from different subjects and runs in order to gain a deeper understanding at a higher level.

Steps for the Second-level analysis

1. Selecting FEAT Directories:

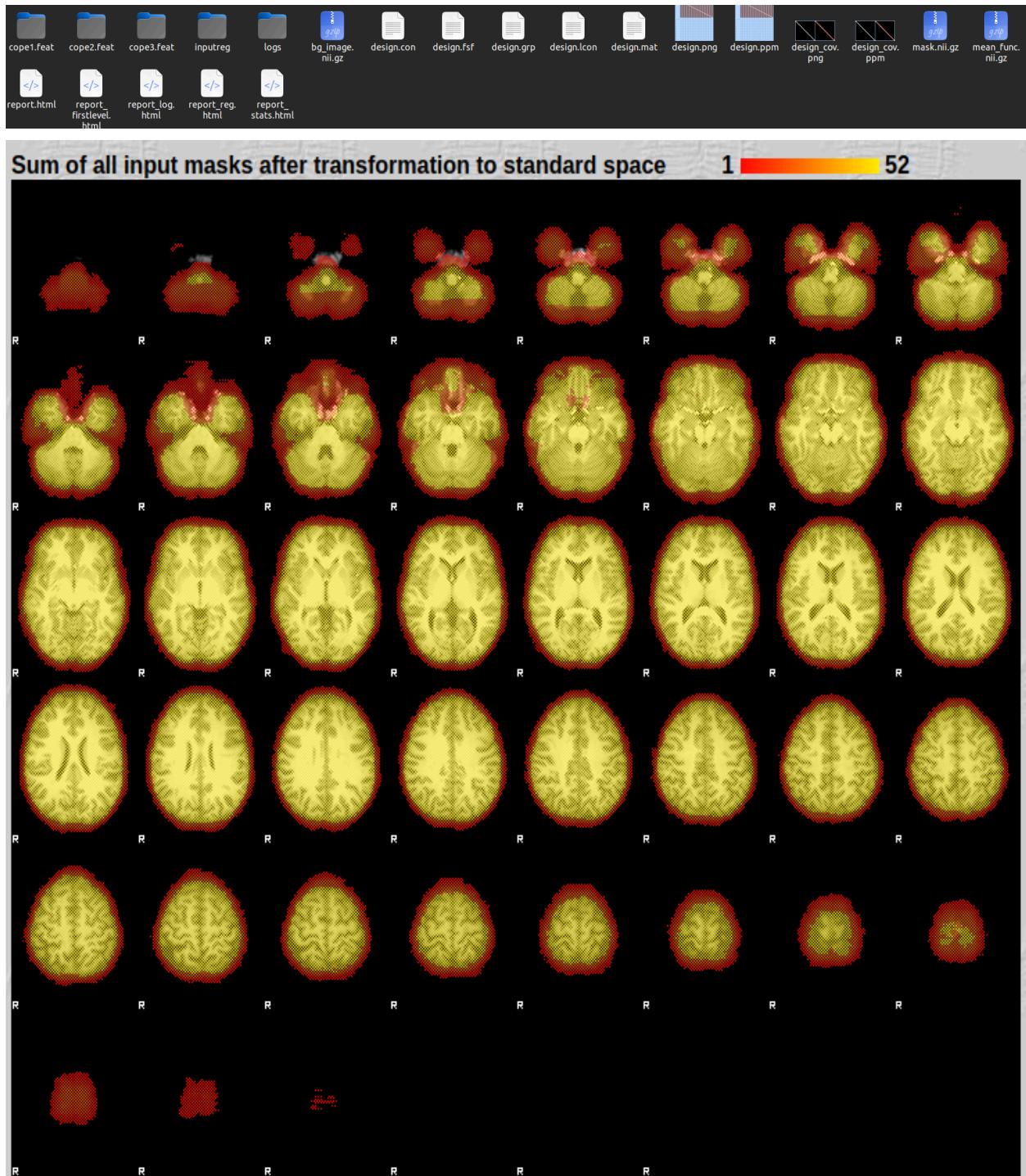


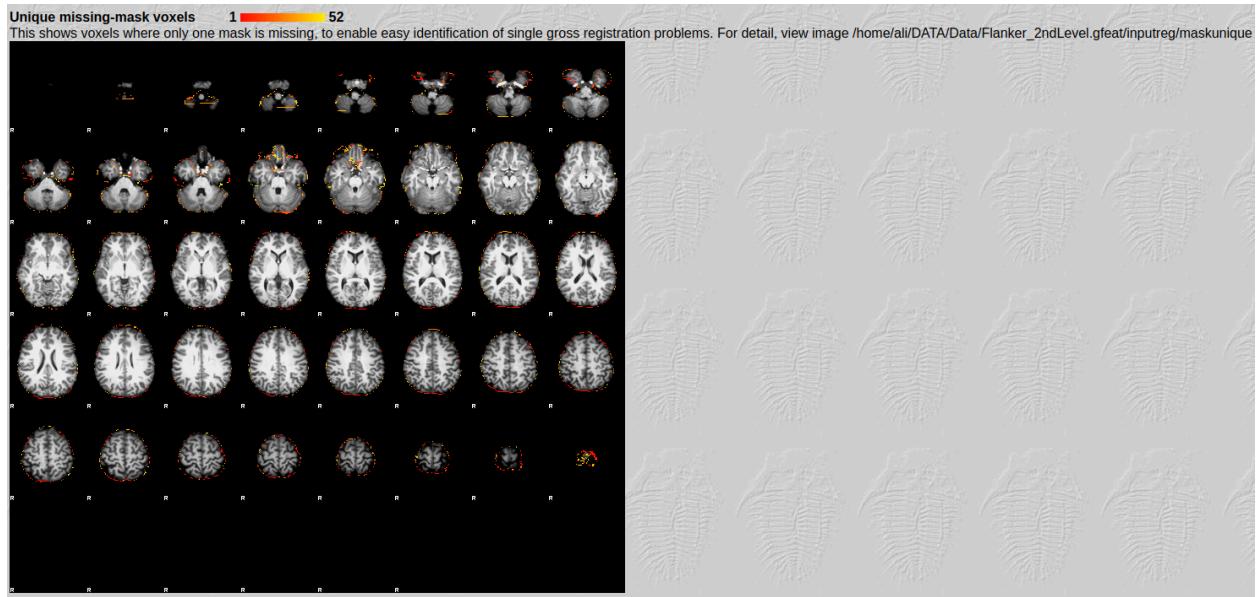
2. Defining Inputs and Outputs: In the FEAT GUI, users can select how many inputs they want, which matches the total number of FEAT directories. For example, in the Flanker dataset with 26 subjects and 2 runs each, there are 52 FEAT directories. Users have the option to analyze various lower-level contrasts, like incongruent and congruent conditions, as well as their variances. The output directory is where the results of the second-level analysis are saved.



3. Creating the General Linear Model (GLM): In the "Statistics" section of the FEAT Graphical User Interface, users set up the General Linear Model for analyzing data at the second level. They can choose between Fixed Effects, Mixed Effects (simple OLS, FLAME 1, FLAME 1+2), and Randomise. For the Flanker dataset, which focuses on averaging parameter estimates within each subject across runs, the Fixed Effects option is selected. Setting up the GLM includes specifying the number of subjects and determining which parameter estimates to average for each subject.
 4. Configuring Contrasts: In the "Contrasts & F-tests" section, users can set up contrasts for second-level analysis. For the Flanker dataset with 26 subjects, 26 contrasts are made, each showing the average parameter estimates for one subject. When all diagonal elements are set to 1, a unique contrast estimate is produced for each subject, showing the average of their parameter estimates throughout the runs.

Results





Conclusion

Neuroimaging researchers can gain a broader understanding of brain activity by conducting a second-level analysis. This analysis combines data from multiple subjects and runs, giving a more comprehensive view of the findings. By utilizing tools like FSL and GLM configuration, researchers can simplify the second-level analysis process and extract valuable insights from their data.

FMRI Task 5

Introduction to Third-Level Analysis

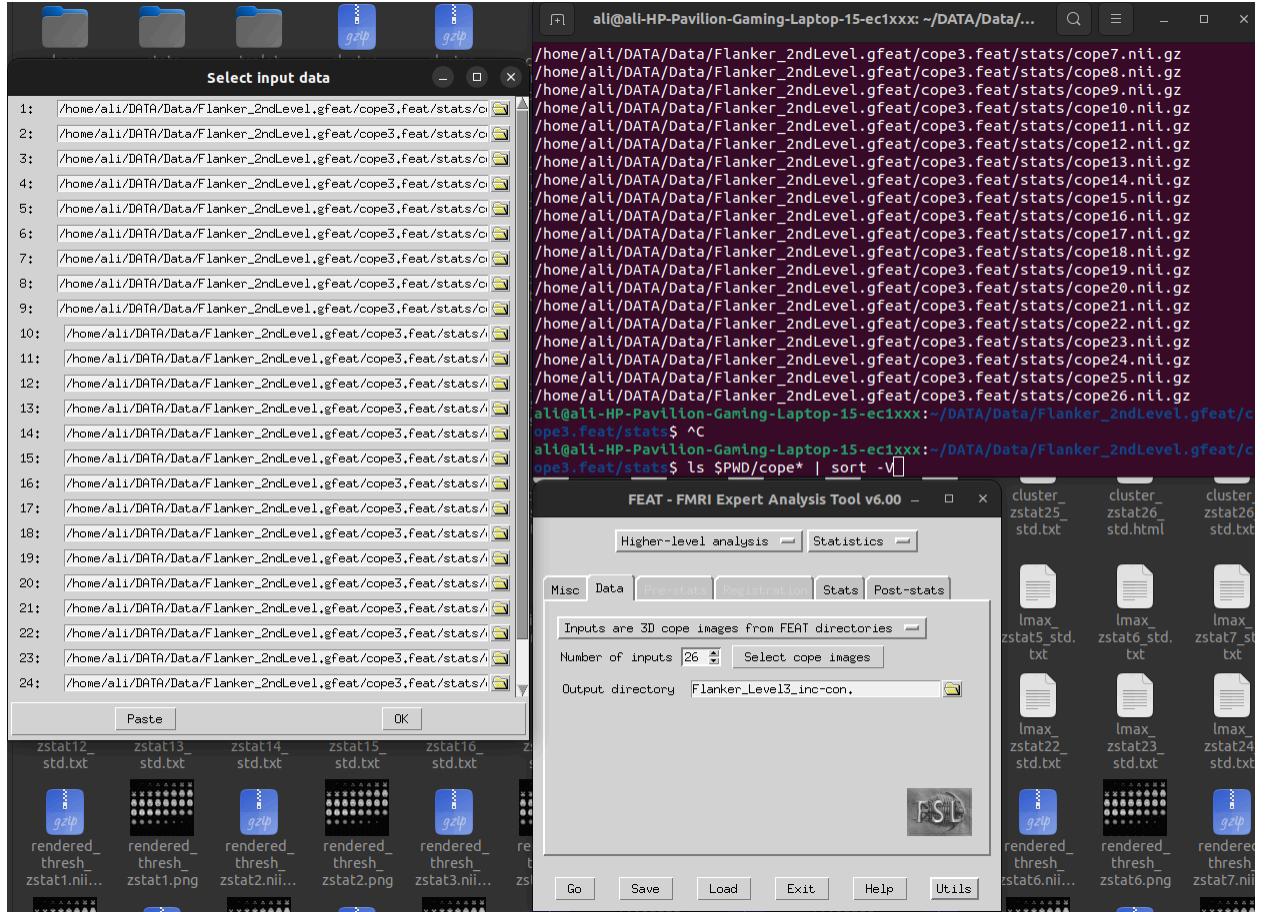
The journey in fMRI analysis progresses from understanding individual subject responses (first-level analysis) to aggregating these insights across subjects (second-level analysis). However, to comprehend broader trends and group effects, researchers often turn to third-level analysis. In this report, we elucidate the significance and methodology of third-level analysis within the context of fMRI research, particularly utilizing FSL (FMRIB Software Library).

Purpose and Significance

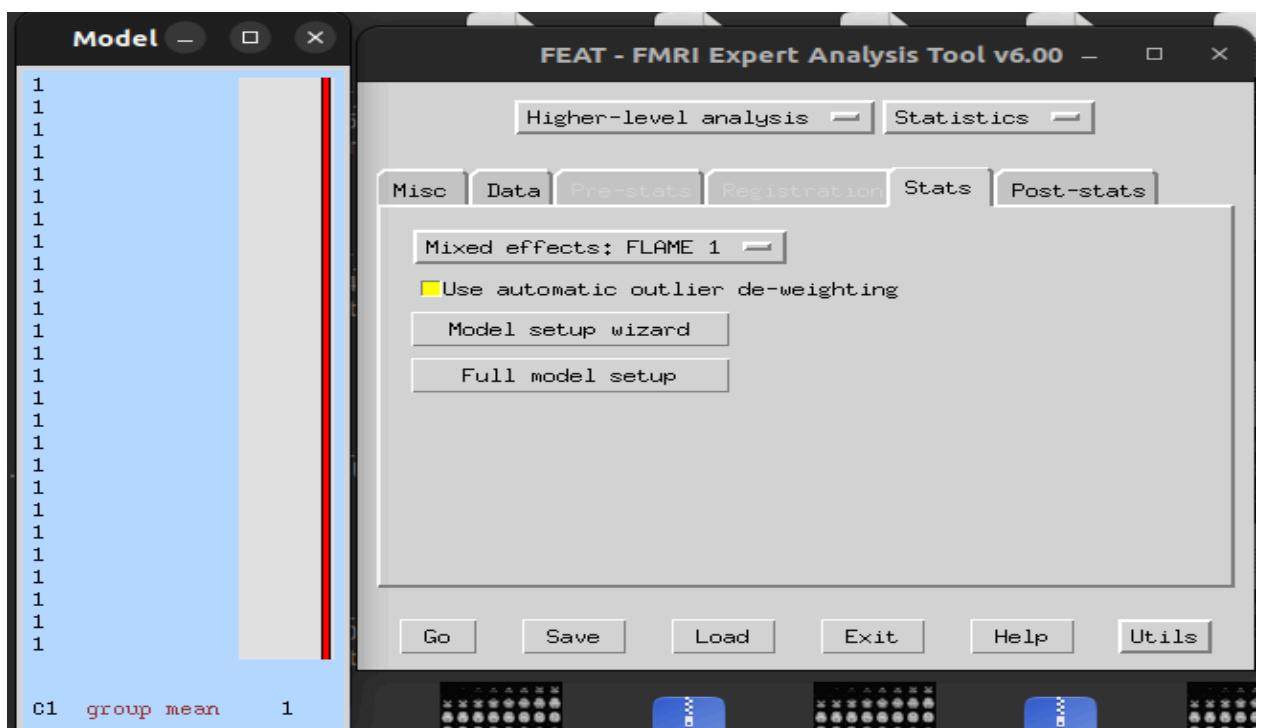
Third-level analysis builds upon second-level analysis by expanding the amalgamation of data across subjects to investigate broader trends or effects within larger populations or experimental conditions. This enables researchers to uncover patterns that may not be immediately evident at lower levels of analysis, thereby enhancing their comprehension of neural processes and behavior.

Steps for Third-Level Analysis

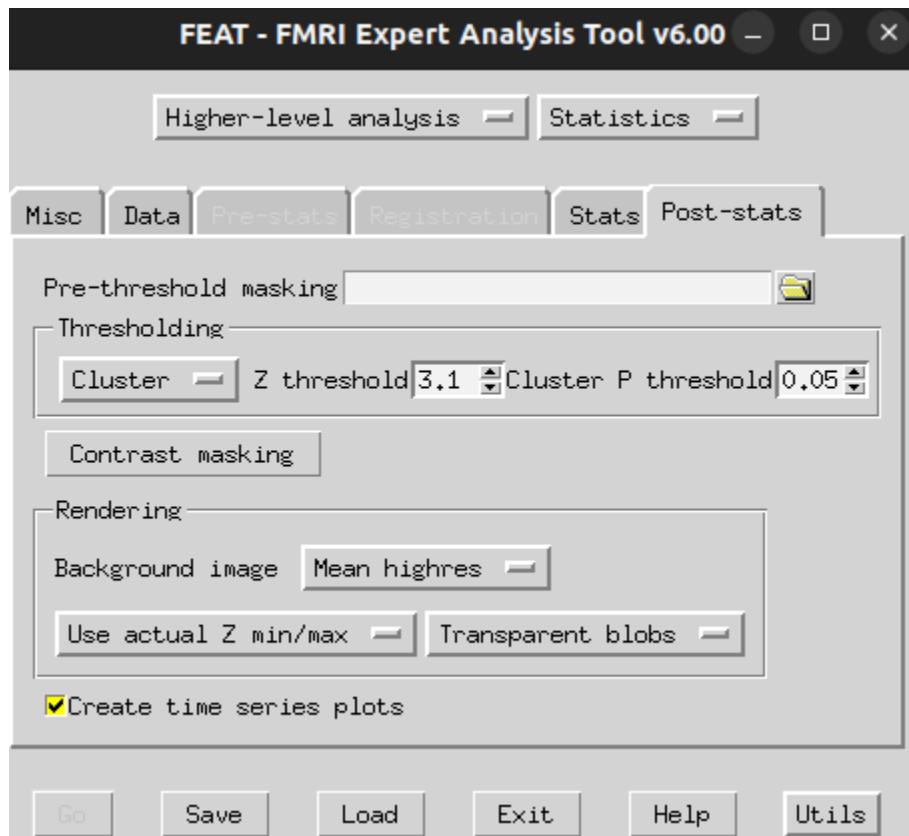
1. Data Selection: Comparable to the second-level analysis, the initial step involves the selection of suitable datasets, usually consisting of aggregated outcomes from second-level analyses. These datasets could include differences, parameter estimations, or statistical maps obtained from different experimental conditions or groups of subjects.



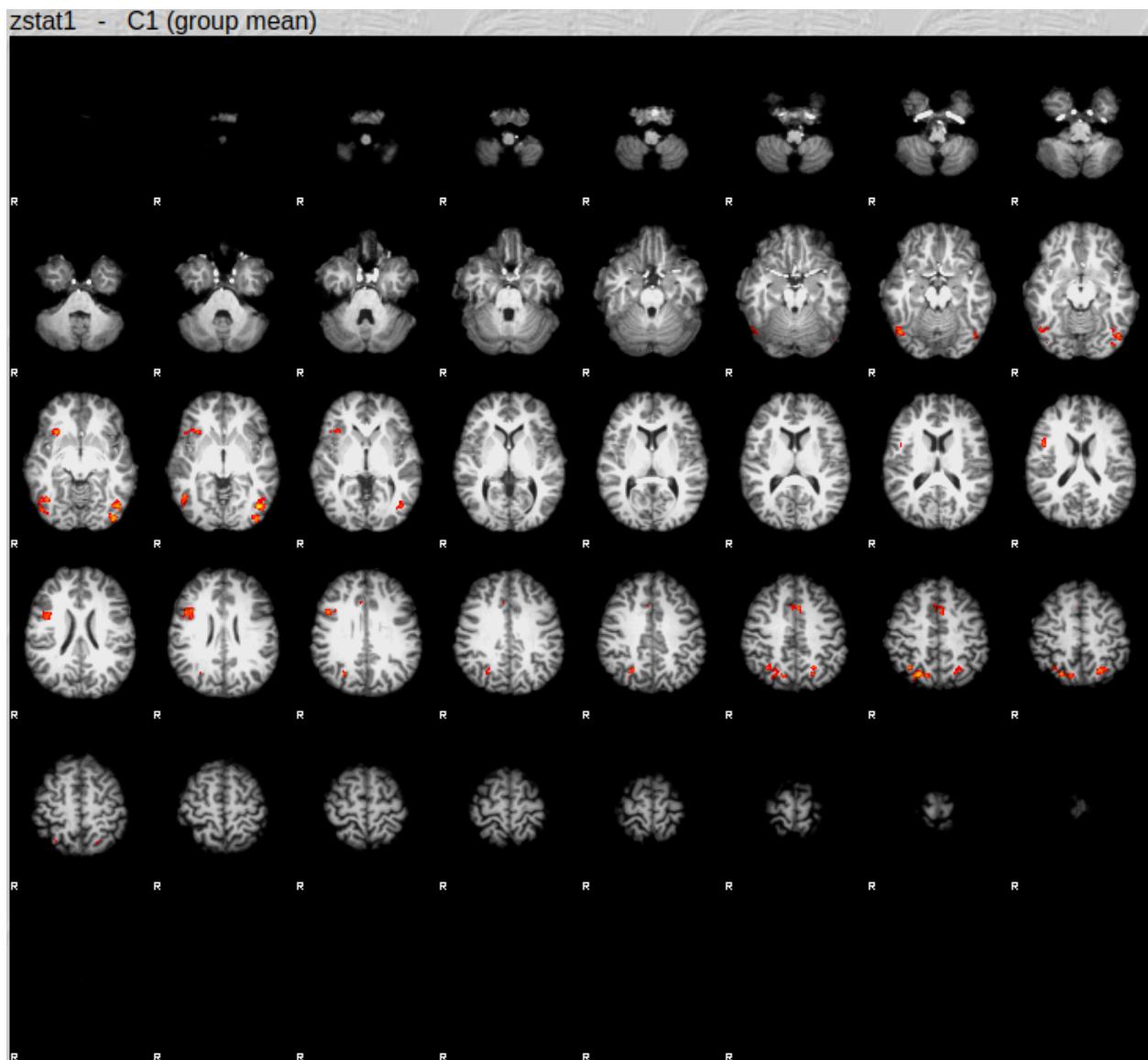
2. Grouping and Aggregation: In FSL, third-level analysis involves combining data from multiple second-level analyses, often organized based on experimental conditions, subject demographics, or clinical characteristics. This aggregation forms the basis for group-level inferences.



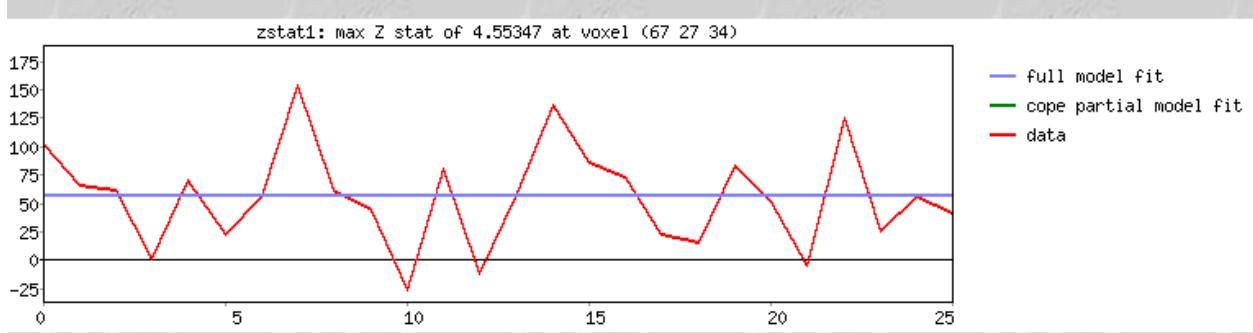
3. Statistical Analysis: Researchers employ sophisticated statistical models like mixed-effects or Bayesian frameworks to conduct a comprehensive analysis. By accounting for potential confounding factors and covariates, they aim to evaluate group-level effects. This crucial step enables the identification of noteworthy distinctions or resemblances among various groups or conditions, thereby shedding light on the underlying neural mechanisms.

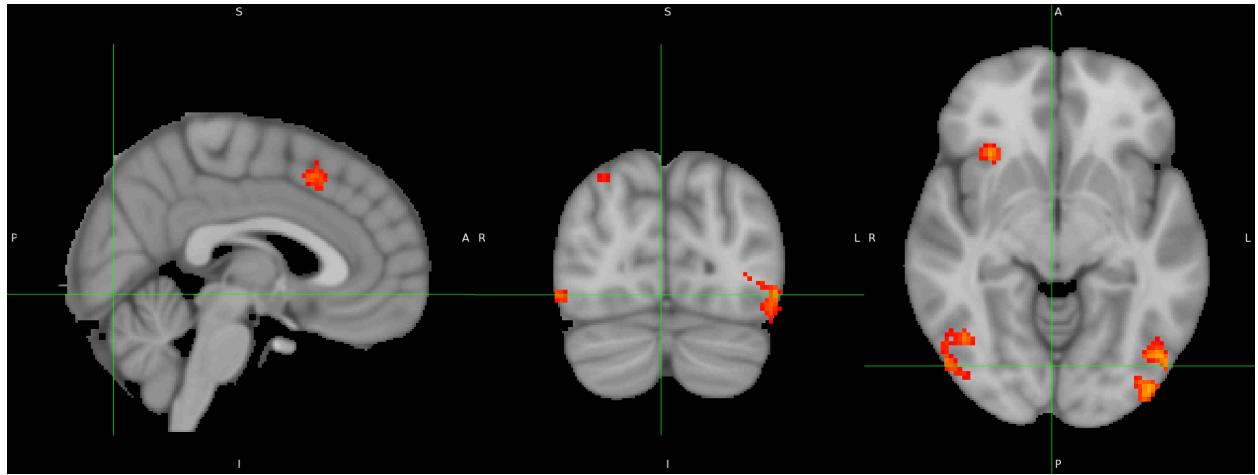


Results



Time series plots





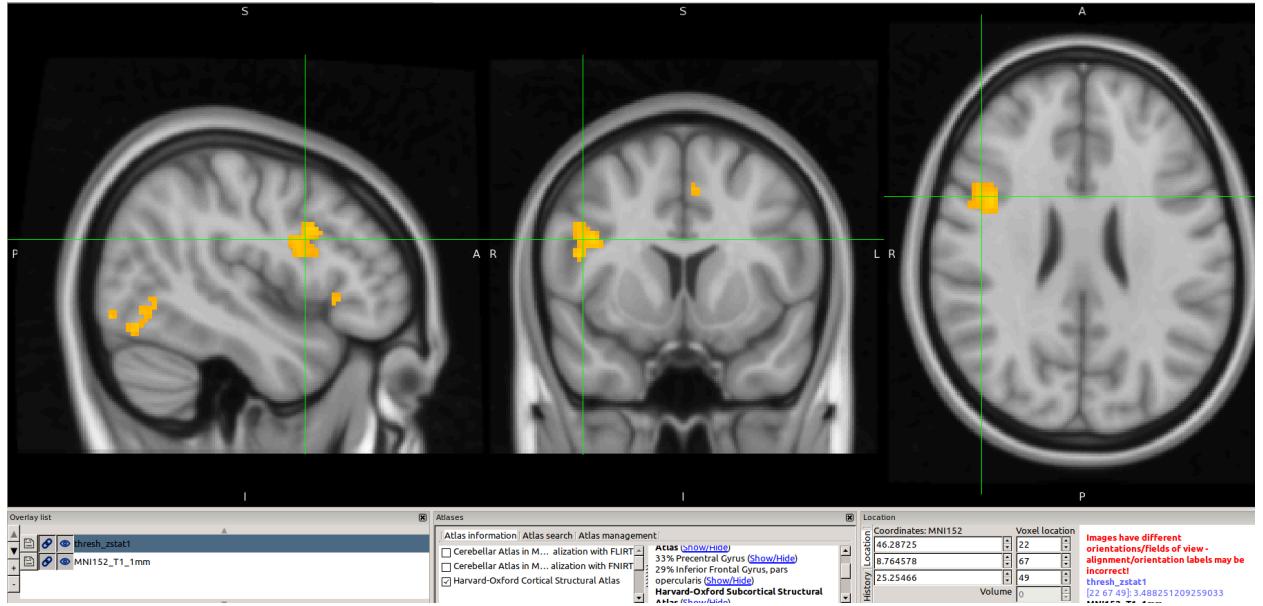
Conclusion

The activated parts found in cope3 (incongruent-congruent) was:

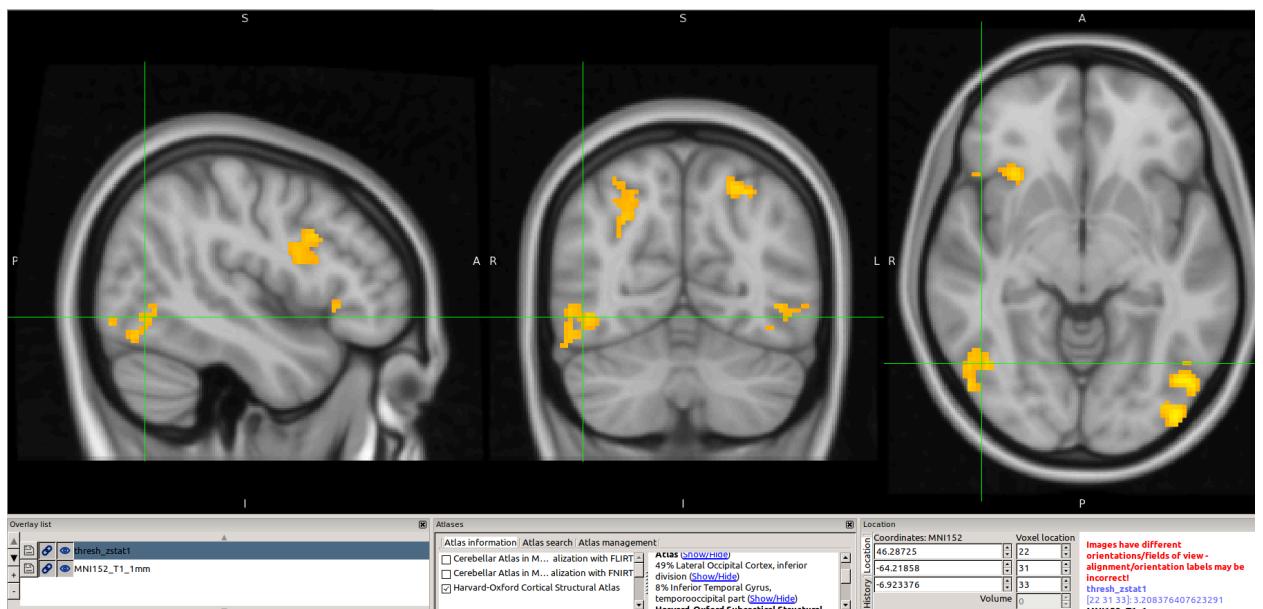
1. Paracingulate Gyrus: It is associated with cognitive control, decision-making, and error processing. It plays a critical role in tasks requiring conflict monitoring and resolution, such as the Flanker task we used.



2. Inferior Frontal Gyrus, pars opercularis: This region is implicated in language processing, including syntactic processing and phonological processing. Additionally, it is involved in broader executive functions such as inhibition and cognitive control, essential for managing incongruent stimuli in the Flanker task.



3. Lateral Occipital Cortex, inferior division: This part of the occipital lobe is primarily involved in visual processing, including object recognition and spatial attention. Its activation during the Flanker task indicates the increased visual processing load required to distinguish incongruent stimuli.



Deactivated Regions

Understanding Deactivation in fMRI

Deactivation in fMRI means that certain parts of the brain become less active when we perform a specific task or are in a certain condition, compared to when we are in a normal state. This can be seen as a decrease in the involvement of certain mental or sensory processes that are not as important or helpful for the task we are focusing on.

Significance of Deactivation

- Cognitive Efficiency: Deactivation helps the brain allocate its resources more efficiently by suppressing non-essential activities.
- Focus and Control: It supports enhanced focus on the task by reducing interference from other cognitive or sensory processes.
- Indicator of Engagement: The pattern of deactivation can indicate how demanding the task is and which regions are being downregulated to support task performance.

Example of Deactivated Regions

1. Deactivation in the Default Mode Network (DMN): It consists of a collection of brain regions that are commonly engaged during periods of rest and activities that involve internal focus, such as daydreaming and mind-wandering. Conversely, when individuals are engaged in tasks that require external focus, like the Flanker task, the DMN tends to exhibit deactivation.
2. Task-Irrelevant Sensory Areas: During the execution of a task, it is possible for sensory regions that are not directly engaged in the task to exhibit deactivation. For instance, when performing a visual task, it is plausible for auditory or somatosensory areas to undergo deactivation in order to minimize any potential interference.
3. Regions Involved in Suppressed Cognitive Processes: Regions associated with processes requiring inhibition, such as those involved in impulsive reactions or irrelevant memories, may exhibit deactivation. This deactivation aids in sustaining concentration and precision in task execution.

FMRI Task 6

Introduction to ROI Analysis

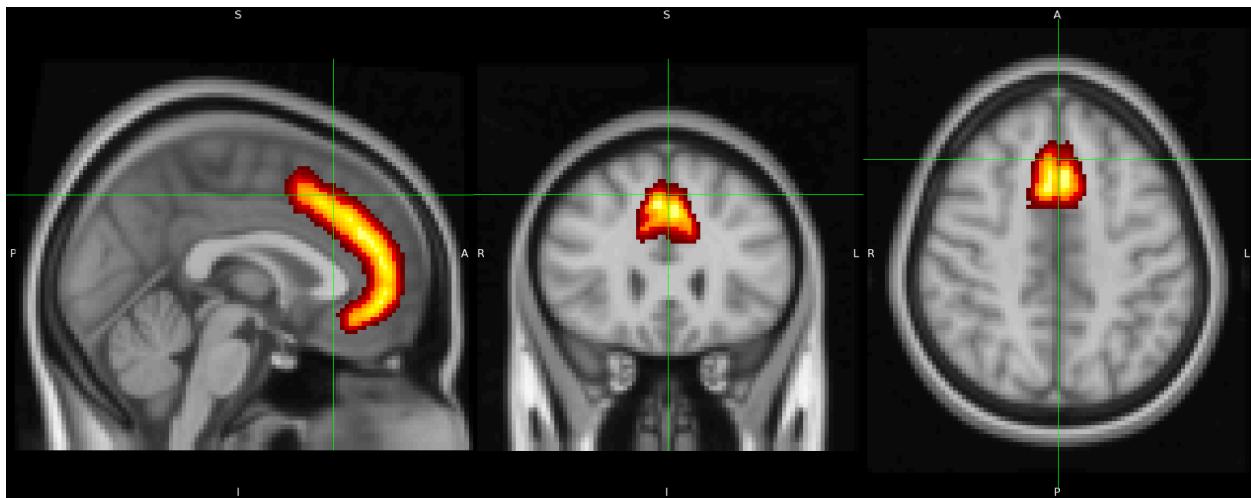
ROI analysis in fMRI is a method that researchers use to concentrate on specific areas of the brain that they believe are connected to the cognitive processes or behaviors they are studying. This approach is different from analyzing the entire brain because it gives more detailed information about the functional activity within predetermined regions. In this report, we delve into the importance and techniques of ROI analysis in fMRI research.

Purpose and Significance

ROI analysis provides numerous benefits, such as enhanced statistical strength and the opportunity to examine specific theories about brain activity. By focusing on predetermined areas derived from previous studies or anatomical references, scientists can gain deeper understanding of the neural processes involved in specific tasks or conditions.

Steps for ROI Analysis

1. Defining Regions of Interest (ROIs): To start, researchers need to choose specific brain regions of interest using existing knowledge, brain maps, or functional information. ROIs can be outlined manually or by utilizing standard brain templates and atlases found in FSL. In our task we will use two ways for selecting the regions. The first method is using an atlas we will select the Paracingulate Gyrus as a mask.



2. Data Extraction: After identifying the ROIs, the next step is to extract the BOLD signal data from these areas. This process includes using FSL tools to separate the time-series data that corresponds to the ROIs from the preprocessed fMRI data.

For the Incongruent-Congruent contrast estimate, The data maps have been computed in various ways, such as t-statistic maps, cope images, and variance images. It is preferred to extract data from the z-statistic maps because they have been transformed into a format that follows a normal distribution. In my view, this makes it simpler to graph and understand the data. We will merge all of the z-statistic maps into a single dataset to make our ROI easier. To do that we will run this code in the terminal:

```
fslmerge -t allZstats.nii.gz `ls zstat* | sort -V`
```

To extract the data from the PCG mask(multiply the PCG mask by the extracted data from the zstats) use this code:

```
fslmeants -i allZstats.nii.gz -m PCG.nii.gz
```

This will print the contrast estimate for each subject averaged across all of the voxels in the mask.

```
ali@ali-HP-Pavillion-Gaming-Laptop-15-ec1xxx:~/DATA/Data$ fslmeants -i allZstats.nii.gz -m PCG.nii.gz
1.363013
0.245036
1.051421
-0.205906
-0.087538
0.228115
0.745255
0.745922
0.267038
0.050253
-0.272654
0.265128
-0.084951
-0.133633
-0.114938
-0.389024
0.210950
-0.964052
-0.657895
-0.192762
-0.039086
0.357768
0.997227
-0.360570
-0.546491
0.216187
```

These numbers can be negative if the contrast estimate of the congruent is higher than that of the incongruent.

3. Analysis of Data: Statistical analyses are then conducted on the extracted ROI data to evaluate the significance of the neural activity observed. We will run a t-test on these values, Our assumption in the beginning is that the Paracingulate Gyrus is not activated during our task.

```
n> data <- c(1.363013, 0.245036, 1.051421, -0.205906, -0.087538, 0.228115, 0.7452
55,
      0.745922, 0.267038, 0.050253, -0.272654, 0.265128, -0.084951, -0.13363
3,
      -0.114938, -0.389024, 0.210950, -0.964052, -0.657895, -0.192762,
      -0.039086, 0.357768, 0.997227, -0.360570, -0.546491, 0.216187)
> result <- t.test(data)
> print(result)

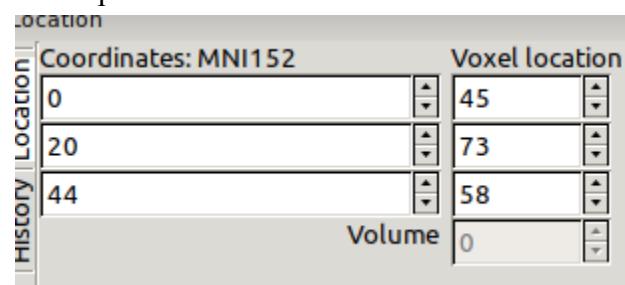
  One Sample t-test

data: data
t = 0.97041, df = 25, p-value = 0.3411
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
-0.1162828 0.3234992
sample estimates:
mean of x
0.1036082
```

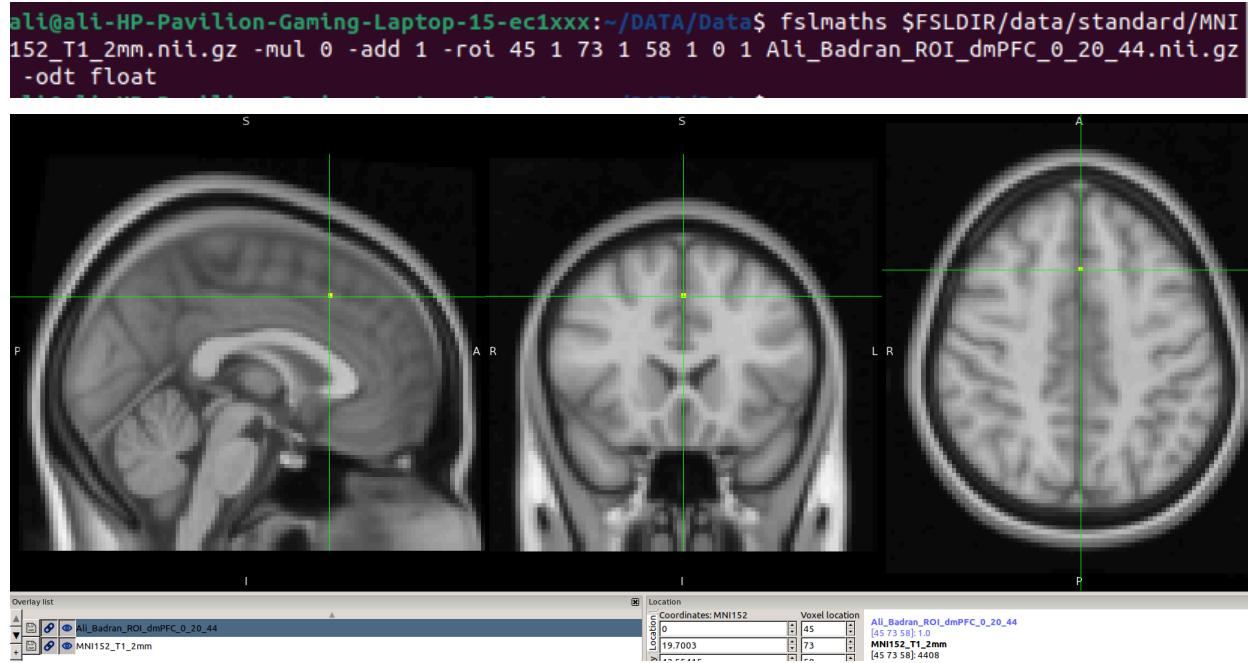
After running the t-test we found that the p-value was equal 0.3411 which is Greater than 0.05 this mean that the hypothesis we assumed was true and the Paracingulate Gyrus is not activated and this happened because although there was activated region the mask we chose was very big that the inactive voxel dominated over the active ones so will try another test but we will change the mask.

4. Extracting Data from a Sphere: We will create a spherical ROI and extract data from it using coordinates derived from an independent study or using coordinates of voxels with high activation derived from the Third Level Analysis we did in the previous report.

After loading the MNI152_T1_2mm standard into fsleyes we will go to MNI coordinates (0, 20, 44) which we got from a related experimental design also intended to tap into cognitive control - with a peak t-statistic at these coordinates.

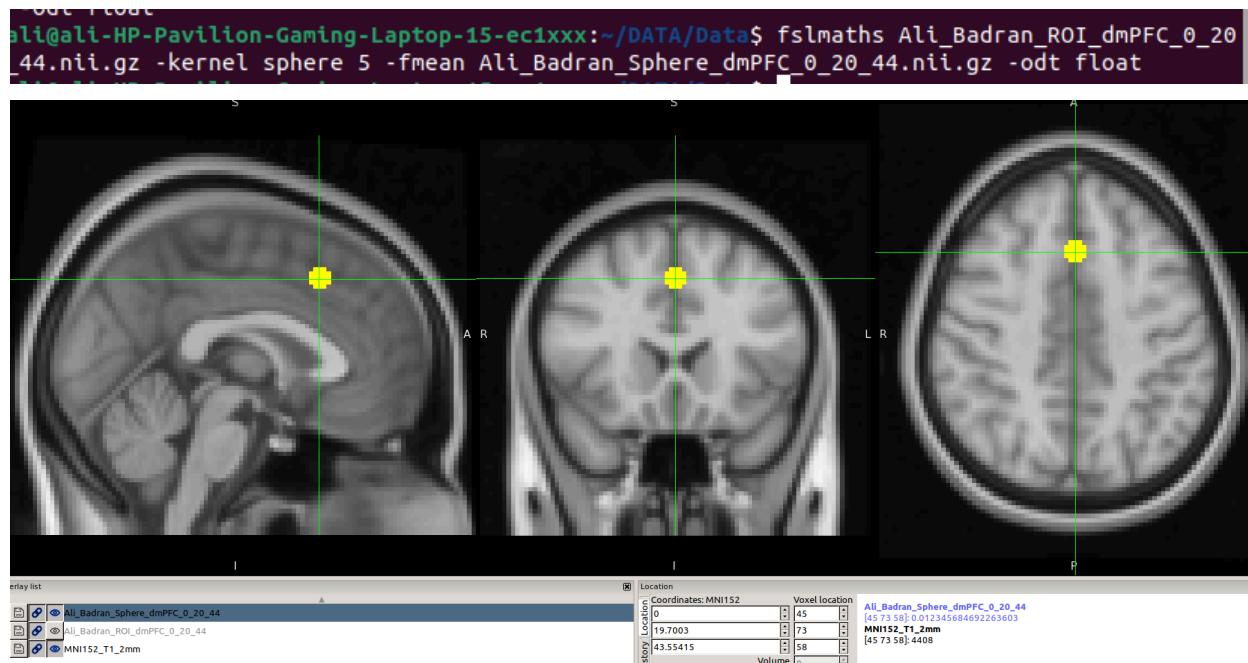


After getting the voxel coordinates we will run a command that marks the voxel coordinates we pass to it

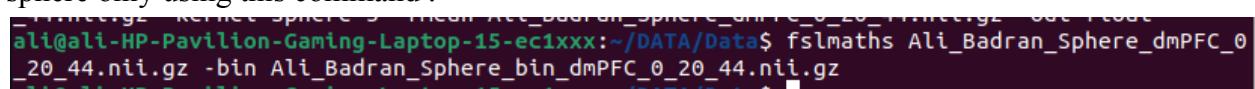


We can see here the marked voxel highlighted in fsleyes.

Now we will run another command that expands the single voxel into a sphere with a radius of 5mm.



We can see here the sphere generated around the chosen voxel, now we have to binarize the sphere only using this command .



Last step is to extract data from this sphere by multiplying it with the data we got from the stat files. We will use this command:

```
ali@ali-HP-Pavilion-Gaming-Laptop-15-ec1xxx:~/DATA/Data$ fslmeants -i allZstats.nii.gz -m A
li_Badran_Sphere_bin_dmPFC_0_20_44.nii.gz
1.327972
0.741809
1.075685
0.412434
0.989408
1.637930
1.868548
2.311128
-0.221740
-0.243948
0.159991
1.410235
-0.302093
-0.057510
0.767032
0.406651
1.146441
-0.650117
-0.620734
0.402211
0.547149
1.018010
1.459229
0.112053
-0.849388
0.889456
```

Now let's apply t-test to these value to identify whether this mask is activated in the incongruent-congruent or not

```
> # Enter the data
data <- c(1.327972, 0.741809, 1.075685, 0.412434, 0.989408, 1.637930, 1.868548,
       2.311128, -0.221740, -0.243948, 0.159991, 1.410235, -0.302093, -0.057510,
       0.767032, 0.406651, 1.146441, -0.650117, -0.620734, 0.402211, 0.547149,
       1.018010, 1.459229, 0.112053, -0.849388, 0.889456)

# Perform a one-sample t-test
result <- t.test(data)

# Print the results
print(result)

One Sample t-test

data: data
t = 3.7589, df = 25, p-value = 0.0009177
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 0.2736538 0.9369494
sample estimates:
mean of x
0.6053016
```

Since the p-value now is 0.0009177 which is less than 0.05 this means that the assumption is false and the selected region mask is activated at the incongruent-congruent.

Incongruent cope1

- Paracingulate Gyrus Mask

```
ali@ali-HP-Pavilion-Gaming-Laptop-15-ec1xxx:~/DATA/Data$ fslmeants -i incongruent_allZstats.nii.gz -m PCG.nii.gz
0.707171
1.177101
0.337838
0.597957
1.378904
-0.276878
0.284840
0.937007
0.621358
0.880154
0.985694
1.167754
0.496890
-0.737808
1.346424
-0.330895
0.637774
-1.253987
0.788773
0.217294
1.066111
0.169197
0.492838
0.465999
-0.047969
0.536678
```

```
> # Enter the data
data <- c(0.707171, 1.177101, 0.337838, 0.597957, 1.378904, -0.276878, 0.284840,
       0.937007, 0.621358, 0.880154, 0.985694, 1.167754, 0.496890, -0.737808,
       1.346424, -0.330895, 0.637774, -1.253987, 0.788773, 0.217294, 1.066111,
       0.169197, 0.492838, 0.465999, -0.047969, 0.536678)

# Perform a one-sample t-test
result <- t.test(data)

# Print the results
print(result)

One Sample t-test

data: data
t = 3.9377, df = 25, p-value = 0.0005812
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 0.2319975 0.7407886
sample estimates:
mean of x
 0.486393
```

- Spherical mask

```
ali@ali-HP-Pavilion-Gaming-Laptop-15-ec1xxx:~/DATA/Data$ fslmeants -i incongruent_allzstats
.nii.gz -m Ali_Badran_Sphere_bin_dmPFC_0_20_44.nii.gz
1.901615
3.118286
1.668114
1.828725
4.212729
2.510646
3.018982
2.917934
1.246839
1.719434
2.984716
3.300570
1.027082
1.401403
3.857215
0.199767
2.867935
0.466228
0.595518
1.437114
2.610784
1.234587
2.733579
0.729099
-0.051981
1.962108

> # Enter the data
data <- c(1.901615, 3.118286, 1.668114, 1.828725, 4.212729, 2.510646, 3.018982,
       2.917934, 1.246839, 1.719434, 2.984716, 3.300570, 1.027082, 1.401403,
       3.857215, 0.199767, 2.867935, 0.466228, 0.595518, 1.437114, 2.610784,
       1.234587, 2.733579, 0.729099, -0.051981, 1.962108)

# Perform a one-sample t-test
result <- t.test(data)

# Print the results
print(result)

      One Sample t-test

data:  data
t = 8.865, df = 25, p-value = 3.44e-09
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 1.520563 2.440901
sample estimates:
mean of x
 1.980732
```

Congruent Cope 2

- Paracingulate Gyrus Mask

```
ali@ali-HP-Pavilion-Gaming-Laptop-15-ec1xxx:~/DATA/Data$ fslmeants -i congruent_allZstats.nii.gz -m PCG.nii.gz
-0.683279
0.874519
-0.799293
0.791084
1.611327
-0.475465
-0.379622
0.187024
0.363703
0.827063
1.262631
0.977834
0.572099
-0.573061
1.455875
0.029562
0.454694
-0.347264
1.468699
0.405492
1.078052
-0.245416
-0.632140
0.835044
0.543075
0.339989

> # Enter the data
data <- c(-0.683279, 0.874519, -0.799293, 0.791084, 1.611327, -0.475465, -0.379622,
       0.187024, 0.363703, 0.827063, 1.262631, 0.977834, 0.572099, -0.573061,
       1.455875, 0.029562, 0.454694, -0.347264, 1.468699, 0.405492, 1.078052,
       -0.245416, -0.632140, 0.835044, 0.543075, 0.339989)

# Perform a one-sample t-test
result <- t.test(data)

# Print the results
print(result)

One Sample t-test

data: data
t = 2.6816, df = 25, p-value = 0.01279
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 0.08870341 0.67608321
sample estimates:
mean of x
0.3823933
```

- Spherical

```
ali@ali-HP-Pavilion-Gaming-Laptop-15-ec1xxx:~/DATA/Data$ fslmeants -i congruent_allZstats.nii.gz -m Ali_Badran_Sphere_bin_dmPFC_0_20_44.nii.gz
0.634937
2.289443
0.481215
1.327740
3.566904
0.855227
1.323991
0.497867
1.493219
1.976008
2.874866
2.053051
1.306486
1.442943
3.187680
-0.243863
1.832176
1.209101
1.302250
1.121689
1.872697
0.143839
1.139664
0.598753
0.892869
1.151631

> # Enter the data
data <- c(0.634937, 2.289443, 0.481215, 1.327740, 3.566904, 0.855227, 1.323991,
       0.497867, 1.493219, 1.976008, 2.874866, 2.053051, 1.306486, 1.442943,
       3.187680, -0.243863, 1.832176, 1.209101, 1.302250, 1.121689, 1.872697,
       0.143839, 1.139664, 0.598753, 0.892869, 1.151631)

# Perform a one-sample t-test
result <- t.test(data)

# Print the results
print(result)

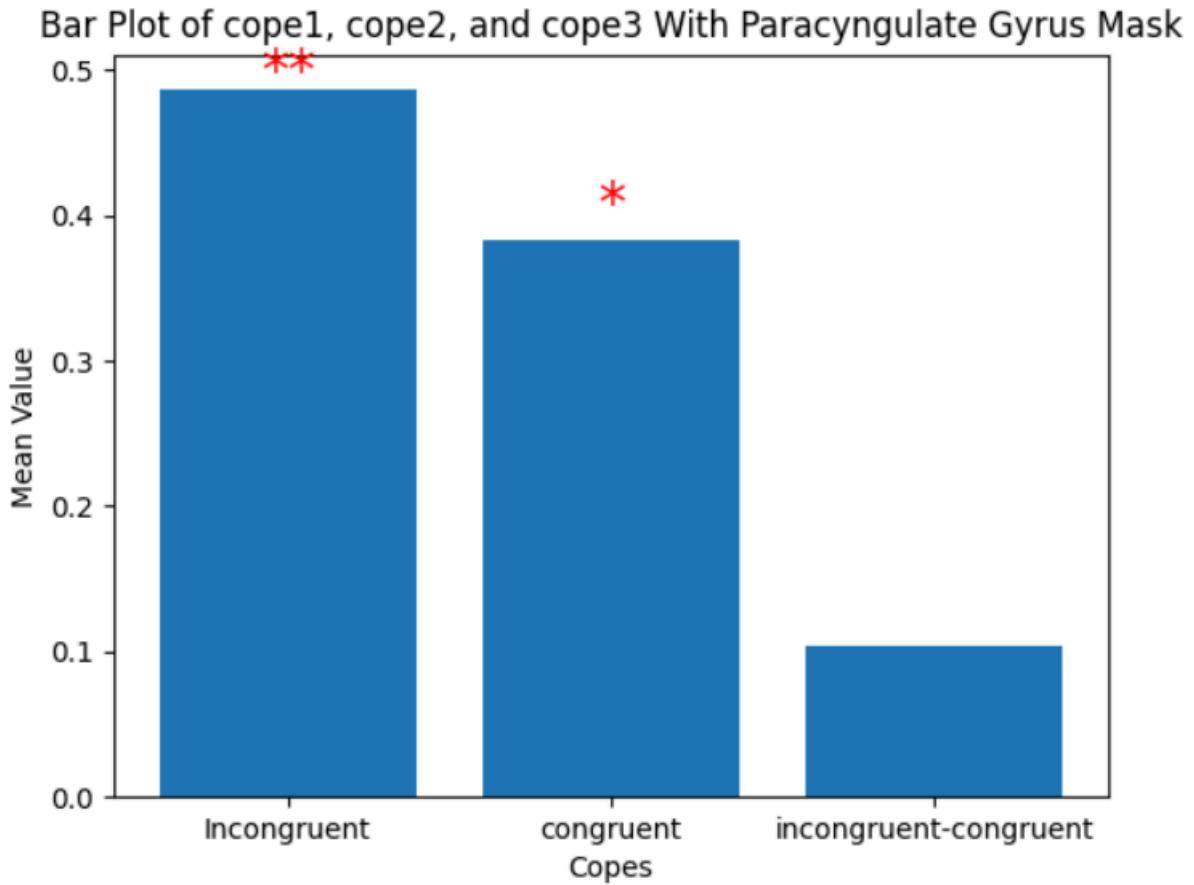
      One Sample t-test

data:  data
t = 7.9607, df = 25, p-value = 2.57e-08
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 1.035874 1.758925
sample estimates:
mean of x
 1.397399
```

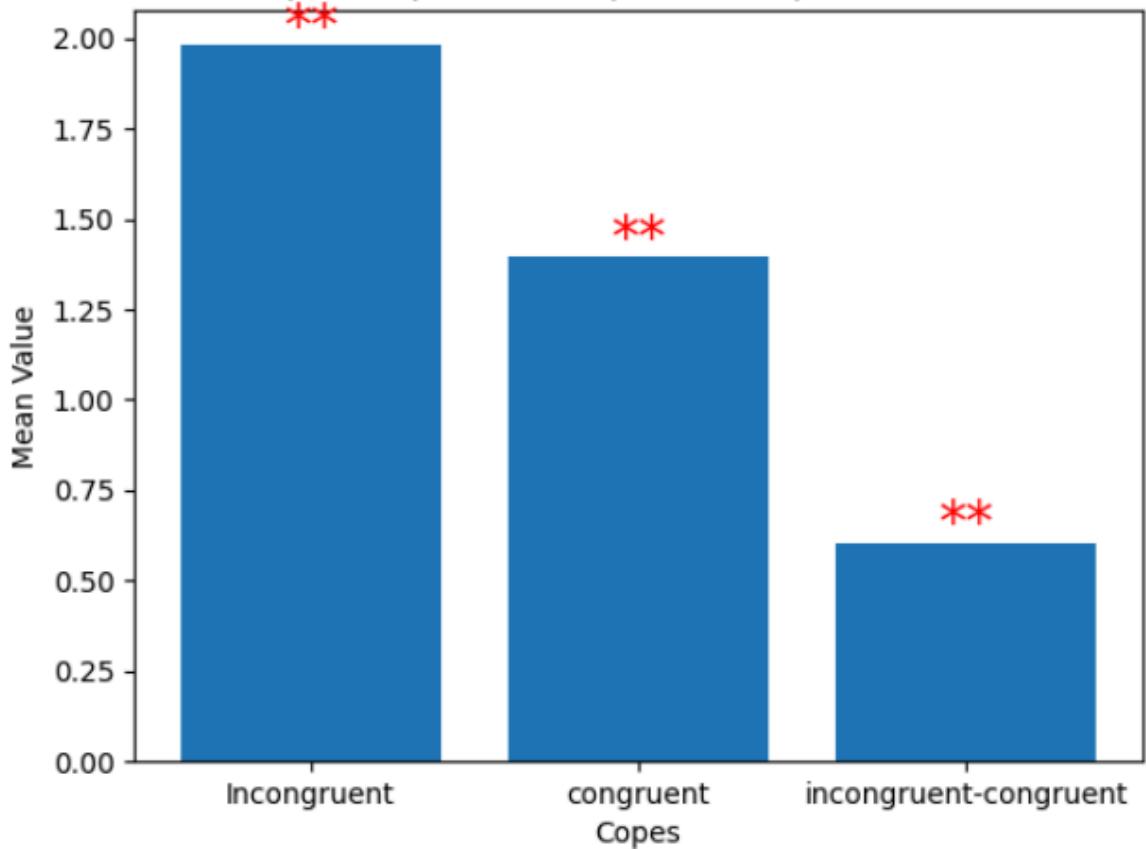
From the above we conclude that Incongruent and congruent data extracted from both PCG and the spherical both fail the hypothesis which means they are all activated.

B-Plots

Using Matplot.lib



Bar Plot of cope1, cope2, and cope3 With Sphere with radius 5 Mask



The bar plots created using Matplotlib provide a clear visual representation of the activation levels across different conditions, with significant activations marked appropriately. These visual aids complement the statistical findings and help in conveying the results effectively.

Conclusion

The examination of ROI using anatomical and spherical masks offered important information regarding the neural basis of cognitive control tasks. Despite the lack of significant findings with the anatomical mask, the spherical ROI method revealed notable activation in the Paracingulate Gyrus, emphasizing the necessity of accurate and specific ROI selection in fMRI research. These results emphasize the significance of the Paracingulate Gyrus and other identified brain regions in conflict monitoring and cognitive control, enhancing our comprehension of the neural processes associated with these functions.