Cognitive Control Related to the Flanker Task

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I. Introduction

Functional Magnetic Resonance Imaging (fMRI) has become an indispensable tool in neuroscience for mapping brain activity. This report outlines a comprehensive experiment utilizing the FMRIB Software Library (FSL) to process, analyze, and interpret fMRI data. I conducted first, second, and third level analyses to identify neural activation patterns, employing robust preprocessing techniques and statistical models. The analysis culminated in Receiver Operating Characteristic (ROC) analysis to evaluate the performance of the predictive models. This report presents a detailed account of the methods and findings, highlighting the steps taken to ensure the accuracy and reliability of the results.

The primary objective of analyzing the Flanker dataset is to understand the neural mechanisms underlying cognitive control and conflict resolution. The Flanker task is widely used in cognitive neuroscience to study how individuals manage and resolve conflicts between competing stimuli, providing insights into attention, executive function, and the brain regions involved in these processes. Through fMRI data analysis, we aim to identify the specific brain areas activated during different conditions of the Flanker task, elucidate the temporal dynamics of these activations, and explore how individual differences in performance are reflected in neural activity.

II. Brain Anatomy:

Before diving into this experiment we need to first achieve basic levels of knowledge about brain anatomy to be able to interpret the results of our search.

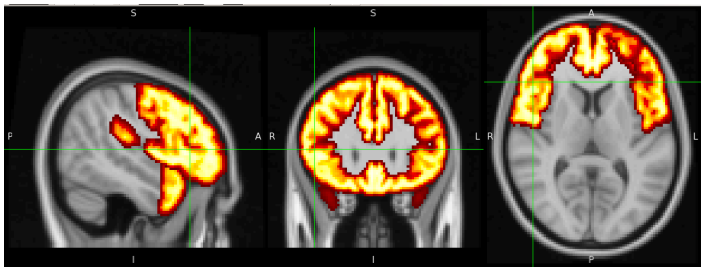
Lopes:

Cerebrum:

The largest part of the brain.
Controls voluntary muscle movement.
The centre of emotion, thought, memory, and language.
The cerebrum is made of the following regions:

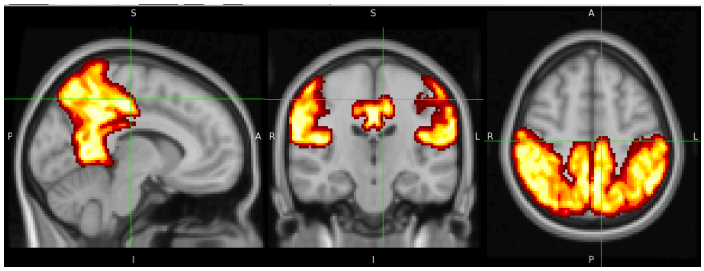
Frontal Lobe:

Located at the front of the brain, the frontal lobe is involved in higher cognitive functions such as reasoning, planning, decision-making, and voluntary movement. It also plays a role in personality and social behaviour.



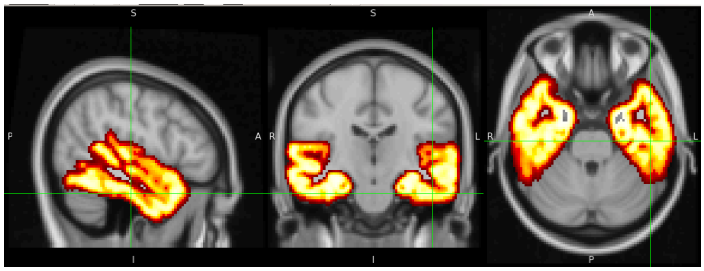
Parietal Lobe:

Positioned behind the frontal lobe, the parietal lobe is responsible for processing sensory information from the body, including touch, temperature, pain, and proprioception.



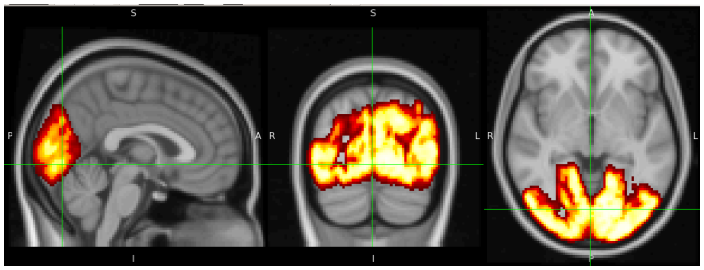
Temporal Lobe:

On the sides of the brain. Primarily associated with auditory processing and memory.



Occipital Lobe:

Found in the back of the brain.Primarily responsible for processing visual information.

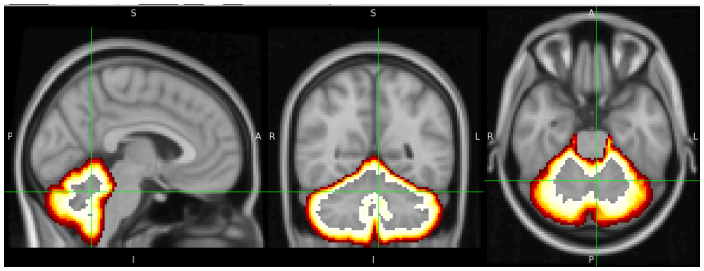


The old brain:

The term "old brain" typically refers to the structures of the brain that are evolutionarily older and are involved in basic survival function, like the cerebellum and the Brainstem.

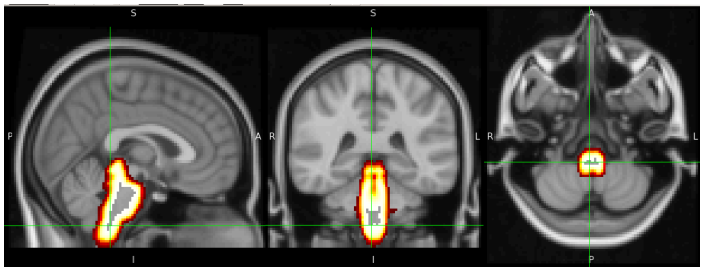
Cerebellum:

The cerebellum, often referred to as the "little brain" due to its appearance, is a distinct structure located at the back of the brain, beneath the cerebrum. One of the primary functions of the cerebellum is to coordinate voluntary movements and maintain smooth, precise motor control. It's also responsible for integrating sensory information related to balance and body posture. Plays a critical role in motor learning and skill acquisition, also is involved in timing and predictive control of movements, enabling precise timing of muscle contractions.



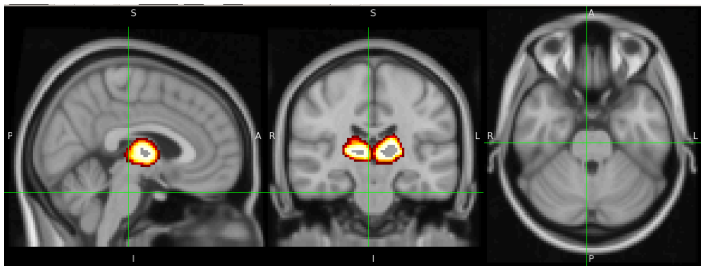
Brain Stem:

A critical structure located at the base of the brain, connecting the brain to the spinal cord. Essential for maintaining basic physiological functions and serves.



Thalums:

Located deep within the brain, situated between the cerebral cortex and the midbrain. It acts as a relay station for sensory information travelling to the cerebral cortex, playing a crucial role in sensory perception, motor control, and regulation of consciousness.



Pons:

Situated above the medulla, the pons serves as a bridge connecting different regions of the brain. Involved in regulating sleep, breathing, and certain aspects of facial movement

(Could not find clear highlight of the pons in the Atlas but it's located just above the brainstem)

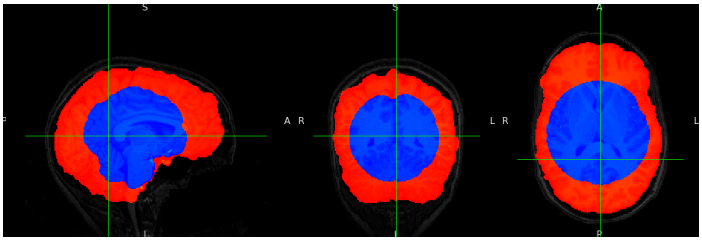
III. Preprocessing:

The preprocessing of fMRI data is essential for ensuring the accuracy and reliability of subsequent analyses. For the Flanker task dataset, preprocessing involved several key steps: motion correction to address head movements, slice timing correction to align acquisition times across slices, and spatial normalization to a standard anatomical template. Brain extraction was performed to isolate the brain from non-brain tissues, followed by spatial smoothing to enhance the signal-to-noise ratio. High-pass filtering was applied to remove low-frequency drifts, and precise registration aligned functional images with anatomical images and the standard template. These steps prepared the data for robust analysis, enabling accurate detection of neural activations related to cognitive control and conflict resolution..

BET:

BET, short for Brain Extraction Tool, a tool commonly used in neuroimaging to remove non-brain tissue from MRI images. The primary purpose of BET is to accurately delineate the brain region from surrounding non-brain structures, such as the skull and scalp. This process, also known as skull stripping or brain extraction, ensures that subsequent analyses focus solely on brain tissue, eliminating interference from other sources.

We are Doing skull striping on a subject with a high threshold value and a lower one and seeing the difference.



In the previous figure , the red colour corresponds to the fractional intensity threshold of 0.1, while the blue colour represents the threshold of 0.9. As anticipated, higher threshold values result in more brain tissue being excluded, whereas lower values retain more brain data. Therefore, selecting the appropriate threshold value is crucial to ensure minimal loss of relevant brain information. In this case, opting for the 0.1 threshold is preferable as it preserves more brain data compared to the 0.9 threshold.

Scripting:

The process of using the gui to calculate an image for each threshold value is quite time consuming, so I have made a script that iterates over all subjects and calculates the (0.1, 0.2 and 0.5) images for the same subject. That way it's faster to view the images and choose the proper value for the subject.

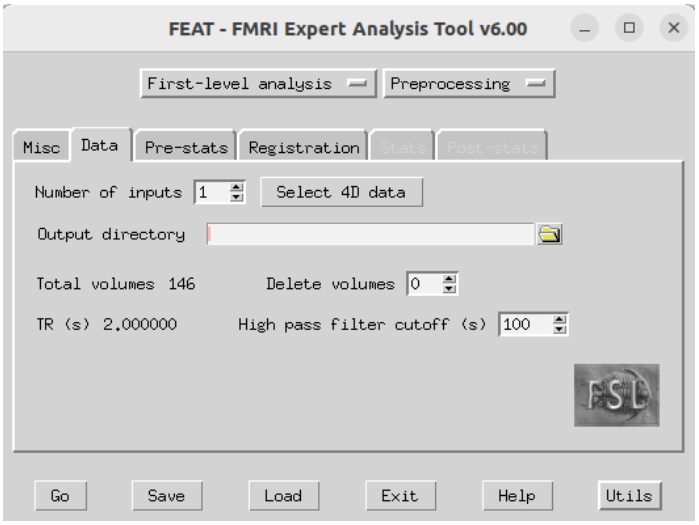
```
#!/bin/bash

# Define the path to the FSL bin directory
FSL_DIR="/usr/local/fsl/bin"

# Define the input and output directories
INPUT_DIR="/home/omar_nabil/Documents/flanker/Data"
OUTPUT_DIR="/home/omar_nabil/Documents/flanker/Data"

# Iterate over subjects
for (( sub_num = 3; sub_num <= 10; sub_num++ )); do
    # Define the subject ID
    subject="sub-$(printf '%02d' $sub_num)"

  # Apply to all three threshold values
    $FSL_DIR/bet $INPUT_DIR/$subject/anat/${subject}_T1w $OUTPUT_DIR/$subject/anat/${subject}
_T1w_brain_f0.5_g0 -f 0.5 -g 0
    $FSL_DIR/bet $INPUT_DIR/$subject/anat/${subject}_T1w $OUTPUT_DIR/$subject/anat/${subject}
_T1w_brain_f0.2_g0 -f 0.2 -g 0
    $FSL_DIR/bet $INPUT_DIR/$subject/anat/${subject}_T1w $OUTPUT_DIR/$subject/anat/${subject}
_T1w_brain_f0.1_g0 -f 0.1 -g 0

    echo "Processing $subject completed."
done
# Indicator to let me know that it's done
echo "All subjects processed."
```

FEAT / First level analysis Setup:

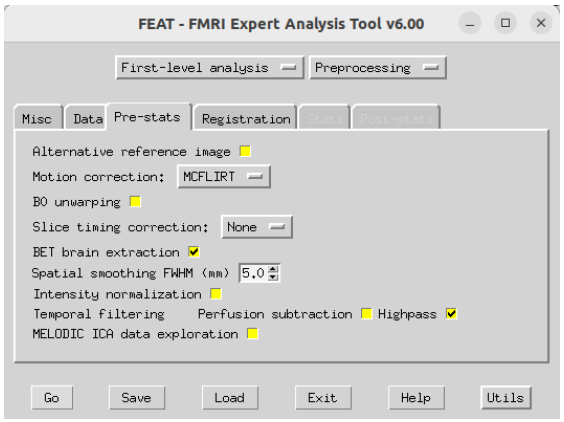
Working on the preprocessing on sub-08_task-flanker_run-2_bold.

Setup:

Firstly: reading the data from its header.



As we can see in the image the sample has 146 Volumes and has TR of 2.0. This data will be quite helpful further on with the other preprocessing techniques.



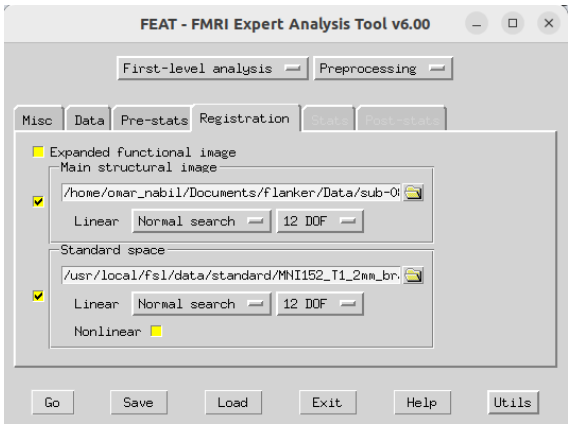


FIG_4 displays the parameters set for motion correction and the smoothing kernel applied during the preprocessing of RUN_1 for the subject under consideration.

FIG_5 illustrates the degrees of freedom selected for this report's preprocessing procedures.

Results:

Motion Correction:

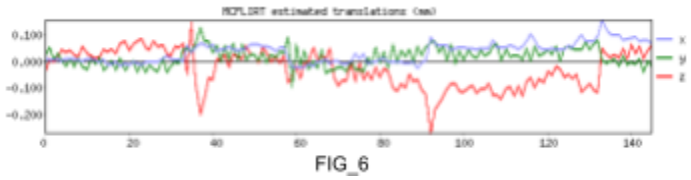


FIG_6

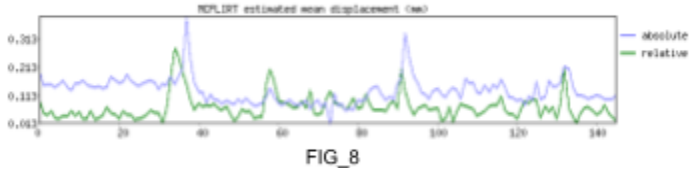


FIG_8

All the graphs depicted in FIG_6, FIG_7, and FIG_8 indicate the deviation of each volume from the reference volume. Notably, a spike is observed at the 35th volume, which is intriguing as it was not readily noticeable during manual data inspection. However, aside from this anomaly, the data appears to be within acceptable ranges. While the deviations are not significant enough to warrant concern regarding data integrity, further investigation into the cause of the spike may be warranted for thoroughness.

Slice timing correction:

As seen in the setup stage we had a TR of 2 seconds, so we do not need to do slice timing correction as it won't really result in better outcome.

Registration and Normalisation:

the pivotal steps in the entire preprocessing pipeline. These processes are the culmination of all preceding efforts, as they aim to align individual brain images with a standardized template, facilitating group-level analyses and comparisons across subjects.

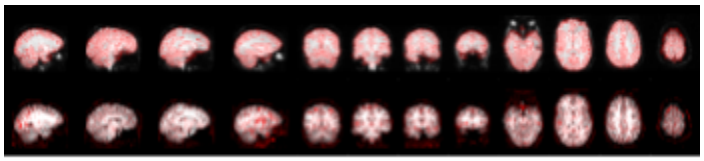


FIG_9

FIG_9 demonstrates examples on Registration. Shows the mapping of the functional data into the anatomical.

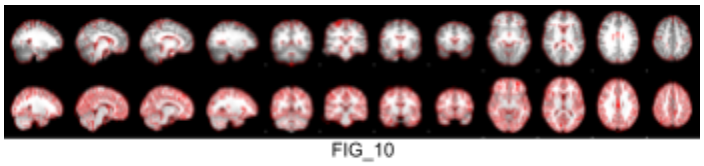


FIG_10

FIG_10 shows the mapping of anatomical into the standard brain (MINI).

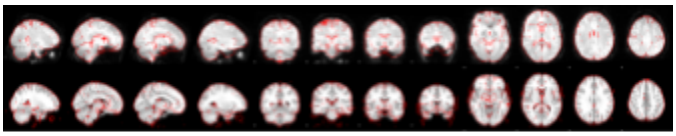


FIG_11

FIG_11 demonstrates the ultimate goal of our preprocessing: aligning functional data with a high-quality standard template. This step ensures consistency across subjects, enabling robust and generalizable analyses without concerns about individual variations in brain size.

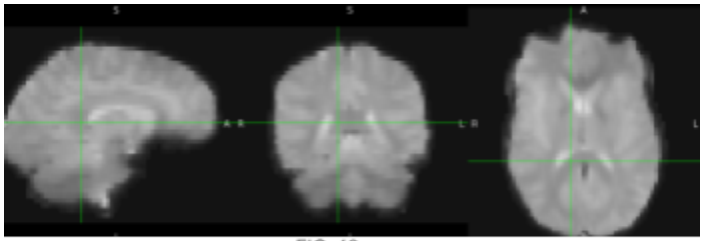


FIG_12

All aspects of the run appear normal and devoid of noticeable issues, as evidenced by the results depicted in FIG_12.

smoothing:

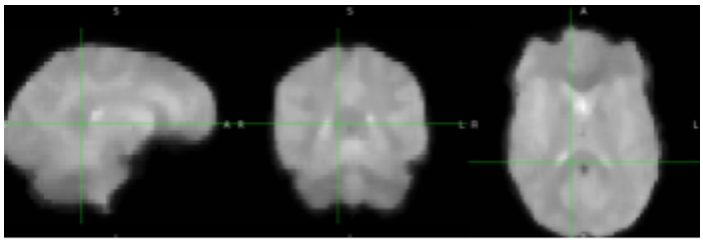


FIG_13 (3mm)

As seen from the results of FIG_13 it's quite obvious that the image seems good in comparison to previous images (a very little increase in resolution)

DIfferent DOF Comparison:

12 DOF

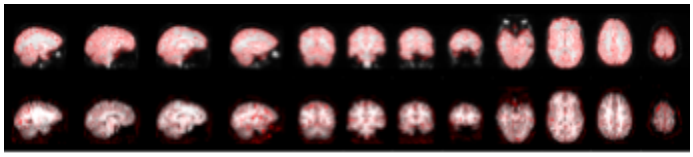


FIG_18

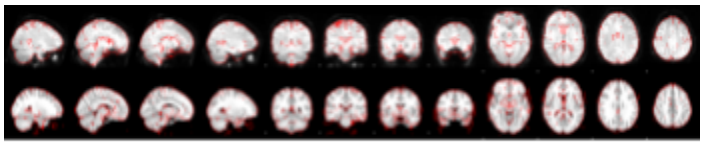


FIG_20

I think of it as the baseline of all of our experiments as it's most

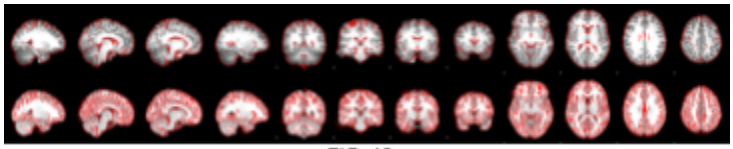


FIG_19

commonly used.

3 DOf:

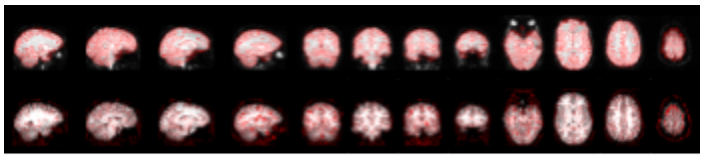


FIG_15

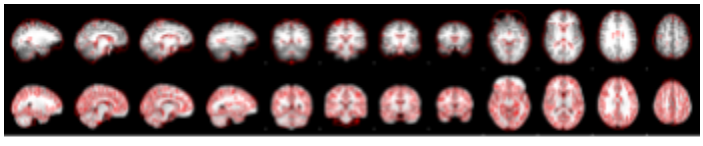


FIG_17

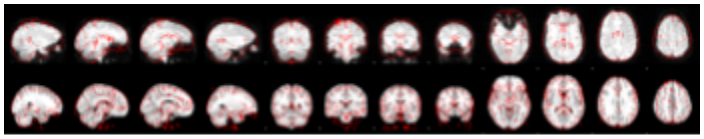


FIG_16

As can be clearly stated from the previous pictures that were done on the same subject but with only 3 DOF in both the regularisation and normalisation. The brain volume is not mapped properly, not terribly but you can clearly state the difference between the 3 and the 12 DOF .

Conclusion:

Losing the extra DOF may seem like a good idea for how much time and computational power it saves, but there are clear differences when it comes to mapping when you compare them to each other.

BBR:

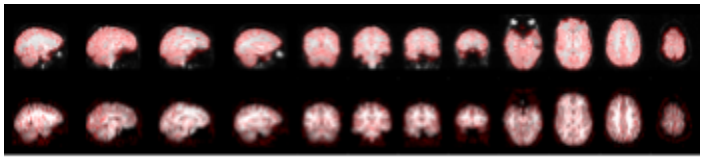


FIG_21

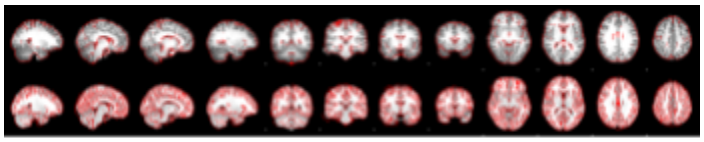


FIG_22

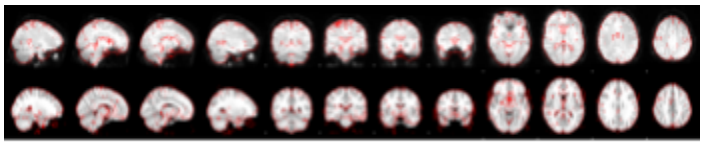


FIG_23

Although the results from the BBR registration may not exhibit significant improvements discernible to the naked eye, the considerable increase in computation time suggests underlying enhancements that may not be immediately apparent. The prolonged processing duration typically indicates that the algorithm has performed more intricate calculations to achieve finer adjustments, thereby potentially refining the alignment in subtle yet meaningful ways. Therefore, despite the lack of overt visual changes, the extended processing time implies that the BBR approach likely contributed to improved registration accuracy, warranting its consideration for preprocessing pipelines where meticulous alignment is essential.

The Case of Using it:

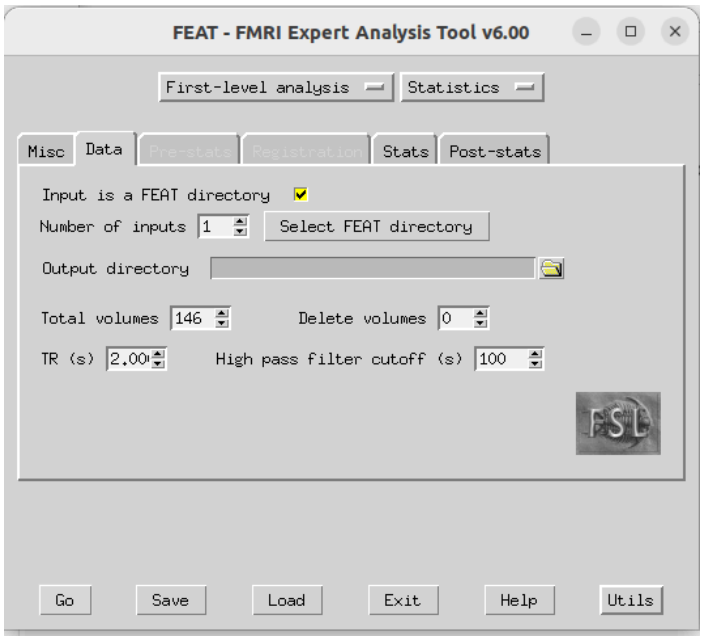
The case for using BBR over 12DOF registration could be strengthened by conducting a detailed comparative analysis between the two methods. This analysis could involve assessing the specific improvements achieved by BBR in alignment accuracy, potentially resulting in better accuracy in subsequent analyses. By presenting concrete evidence of enhanced alignment and its potential impact on overall accuracy, one could effectively advocate for the adoption of BBR in preprocessing pipelines.

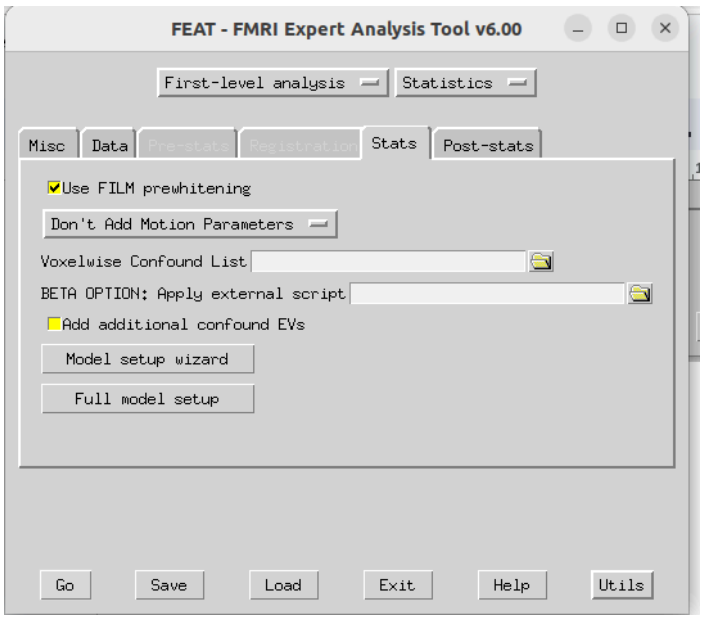
IV. Modeling

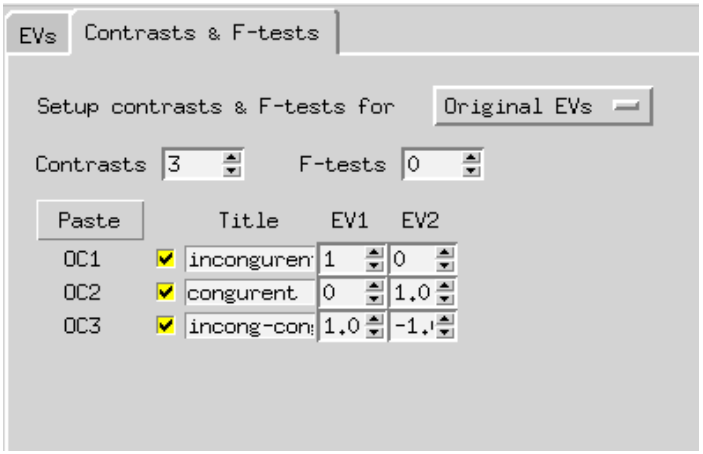
We continued the preprocessing process we did on subject_8 in the previous report. Now comes in the modelling part of the process. We will use the following equation for our model: $y = \boldsymbol{\beta}_1 X_1 + \boldsymbol{\beta}_2 X_2$. Where y is the time series data from each voxel, $\boldsymbol{\beta}_1$ and $\boldsymbol{\beta}_2$ are the parameter estimates. X_1 and X_2 are the regressors.

Setup:

1- Start with adding the FEAT data from the processed sub_8 data.

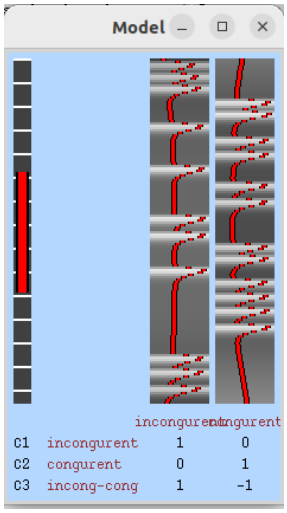




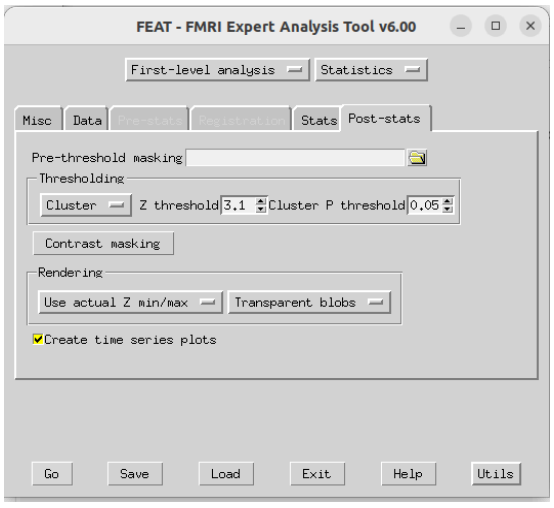


I added only 3 contrasts to see each EV separately and the difference between them .

3- observe the result and make sure that there is no overlap between the two EVs.

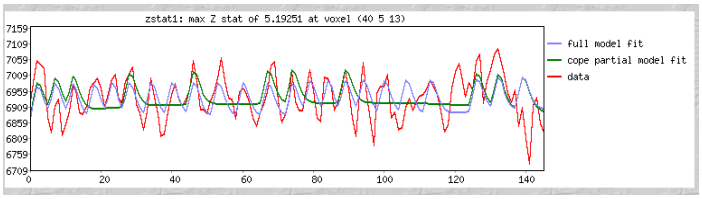


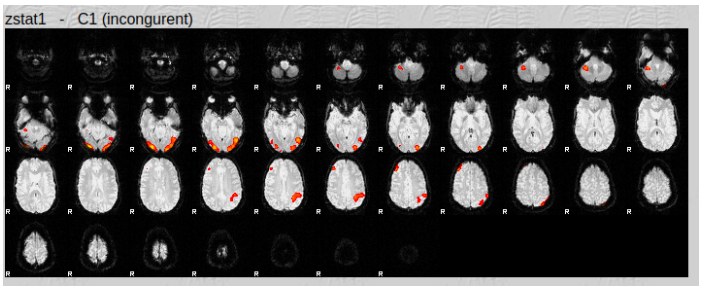
4- Then set up the thresholding factor (I left it at default but we can adjust it depending on our application).



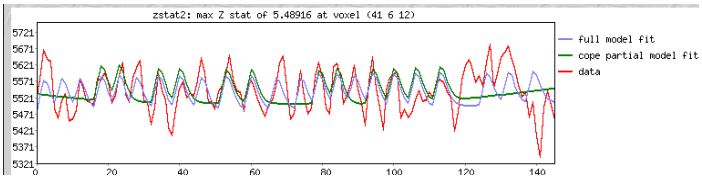
Results:

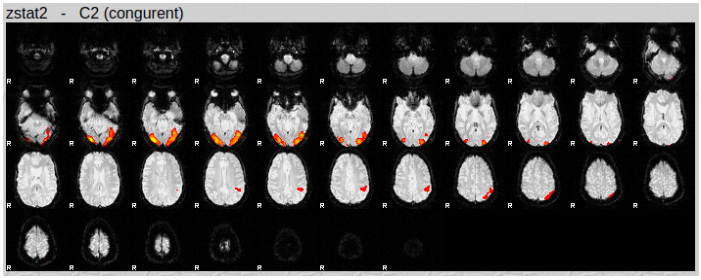
1- Incongruent:



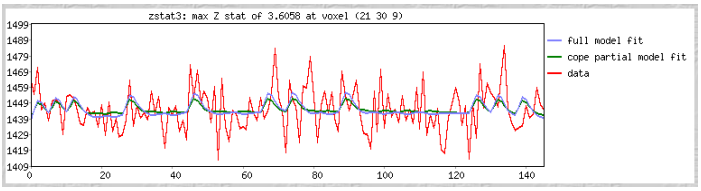


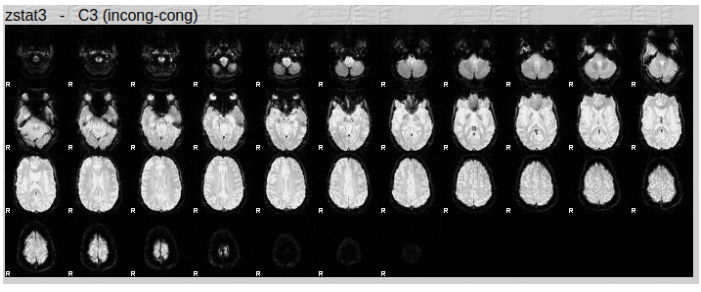
2- Congruent:





3- Incongruent - Congruent :





Observation:

We can clearly see that the contrast that represents the difference between the EVs, shows nothing. What I think this means is that for both functions they use the same region of the brain so when we subtract them it results in a blank graph as they cancel each other out. This or that there may be something wrong with the processing we did with the data.

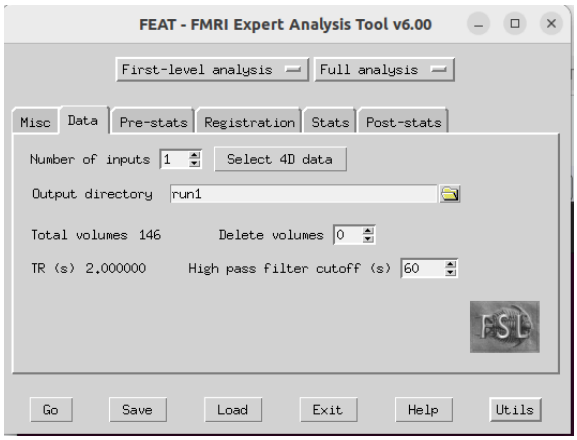
V. Scripting

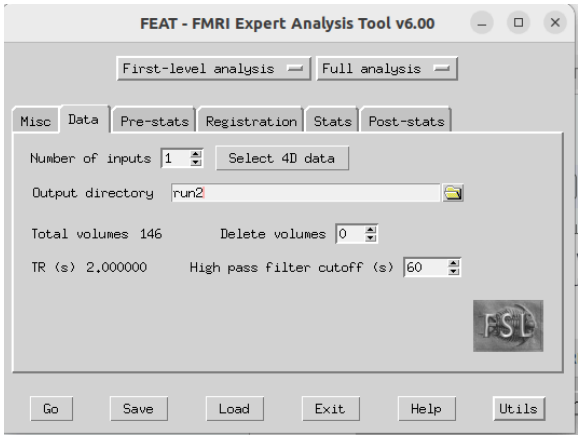
As we venture further into our analysis, we encounter an issue. Thus far, our methodologies have been applied to a select few subjects by manual processes. Extending these steps to encompass the entire dataset manually presents a challenge. Hence, the transition to scripting becomes imperative. It offers a seamless transition, allowing us to replicate previous tasks with precision and efficiency through automation, avoiding any human errors that may happen during the process.

Steps:

1- Reference:

We need to have a reference to what we are replicating and trying to do on the rest of the data set. So we have to do the full analysis on a run1 and run2 of a subject and keep the .fsf files so we can use them in our script.





After setting up both of these like our previous steps we press save so we can get hold of the .fsf file that contains the code to be executed by FSL.

We get a file that looks like this :

```
# FEAT version number
set fmri(version) 6.00

# Are we in MELODIC?
set fmri(inmelodic) 0

# Analysis level
# 1 : First-level analysis
# 2 : Higher-level analysis
set fmri(level) 1

# Which stages to run
# 0 : No first-level analysis (registration and/or group stats only)
# 7 : Full first-level analysis
# 1 : Pre-processing
# 2 : Statistics
set fmri(analysis) 7

# Use relative filenames
set fmri(relative_yn) 0

# Balloon help
set fmri(help_yn) 1

# Run Featwatcher
set fmri(featwatcher_yn) 1

# Cleanup first-level standard-space images
set fmri(sscleanup_yn) 0

# Output directory
set fmri(outputdir) "run1"

# TR(s)
```

2- Automation:

Now we want to use these files to apply on all of the subjects we have so we get a .feat file for each run. This is where scripting comes in place.
We start by creating a for loop that iterates over all the subjects:

```
for id in `seq -w 1 26` ; do
    subj="sub-$id"
    echo "===> Starting processing of $subj"
    echo
    cd $subj

```

Then check if the Skull-stripped brain image exists or not.

```
        if [ ! -f anat/${subj}_T1w_brain_f02.nii.gz ];
```

If it doesn't exist we go ahead and create it for this subject. We used a 0.2 threshold for all the data as it seems to work well with most of them (we can do this separately if we want to have a specific factor for each subject like we did at the beginning).

```
    bet2 anat/${subj}_T1w.nii.gz \
        anat/${subj}_T1w_brain_f02.nii.gz -f 0.2
fi
```

Then copy the design files into the subject directory we are working on:

```
cp ../design_run1.fsf .
cp ../design_run2.fsf .
```

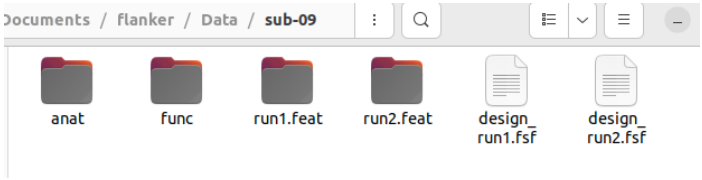
The replace the name of the original subject (sub-08) with the subject we are currently in and apply the feat script:

```
sed -i  "s|sub-08|${subj}|g" \
    design_run1.fsf
sed -i  "s|sub-08|${subj}|g" \
    design_run2.fsf
echo "===> Starting feat for run 1"
feat design_run1.fsf
echo "===> Starting feat for run 2"
feat design_run2.fsf
        echo
```

Then go back out of the original directory :

```
    cd ..
done
```

Applying this script on all the subjects will result in a feat file for each file for each subject.



VI. Second Level Analysis

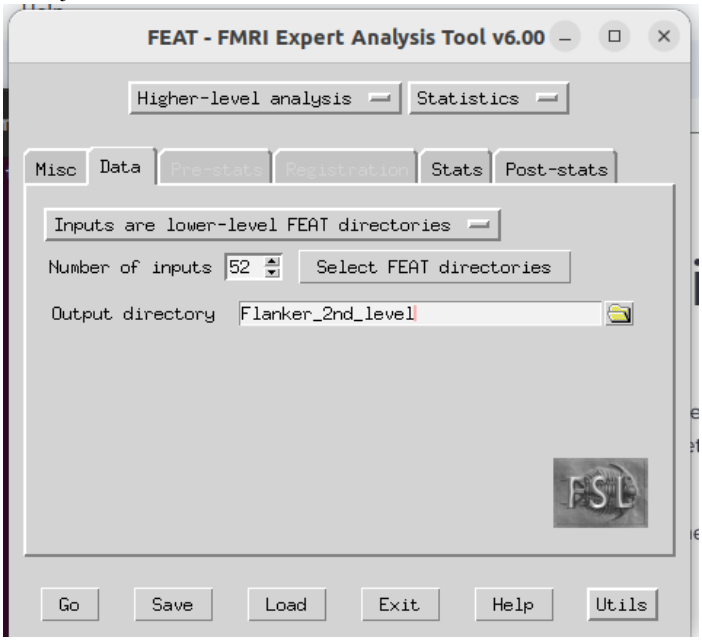
A second-level analysis, also known as a group analysis, involves combining the results of individual analyses from the first level. In FSL, this means averaging the parameter estimates and contrast estimates obtained from the first-level analyses for each subject.

So we need to combine the .feat files of each subject and average them together.

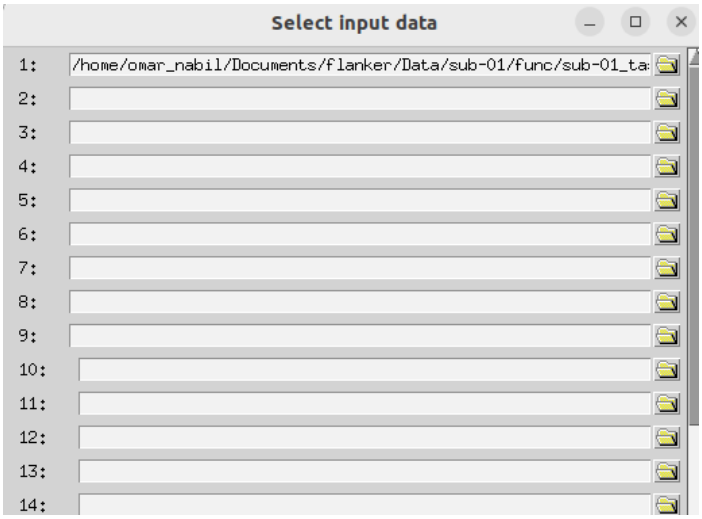
Steps:

1- Inputs

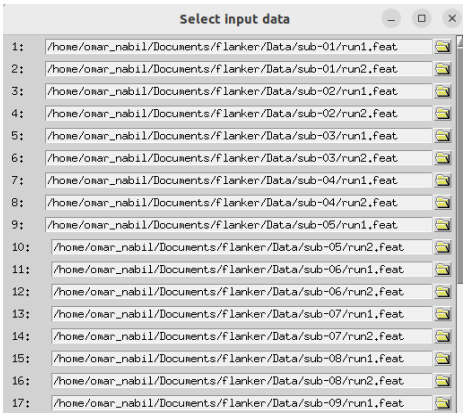
Set the number of inputs to be 52 so we can enter all 2 runs for all 26 subjects we have.

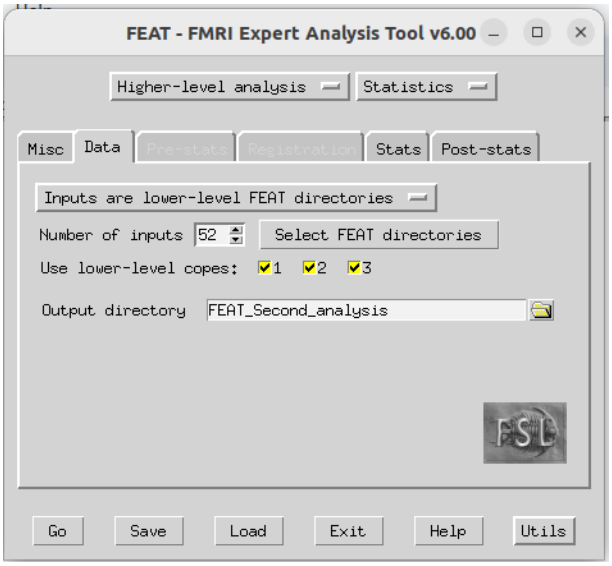


When it comes to applying to putting in all the paths we can do them manually or by using the paste option in the tap.



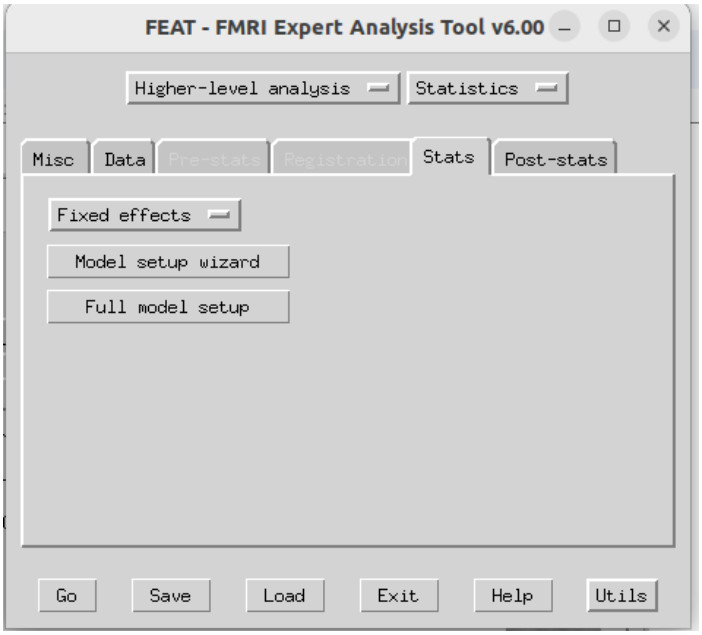
After adding the paths:



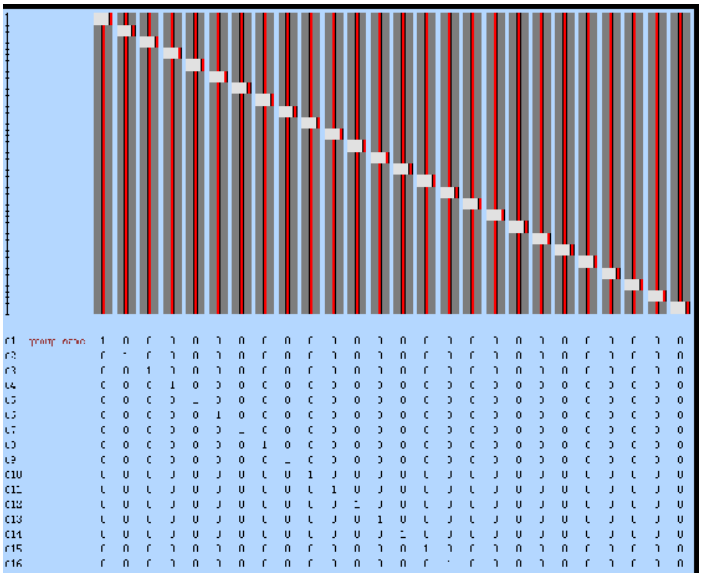


2- Design Matrix

Then we go into setting up the model. Basically tell FSL how to combine these files:



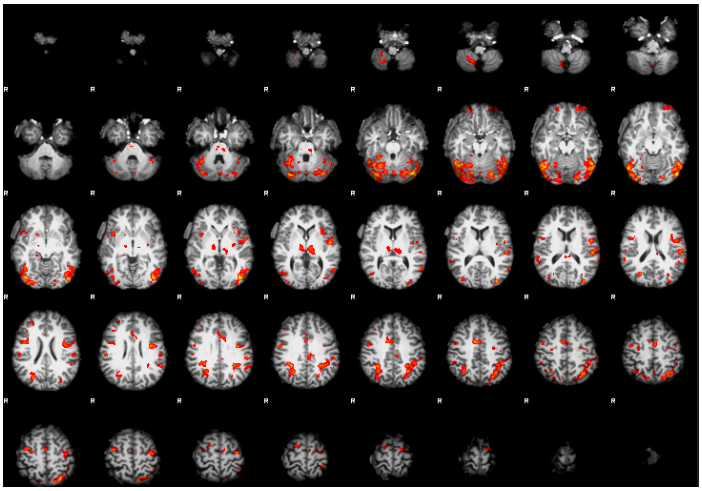
Then go ahead and make the design matrix(can's show the actual tap due to lagging issues):



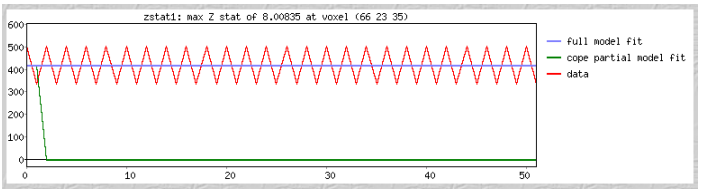
Now just go ahead and run the model.

Results:

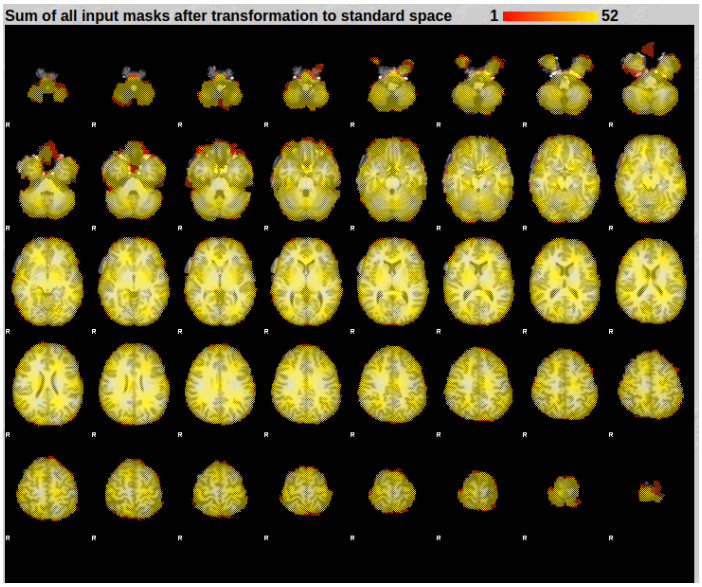
Sub-01 after the z threshold:



Sub-01 Time series:



Sum of all masks:



Summary:

Thus far we completed the second level analysis on our data set in which we averaged the values of each run1 and run2 of all the subjects, so now we have only one file that represents each subject we have. We can use these files down the line of our 3rd level analysis.

VII. Third Level Analysis

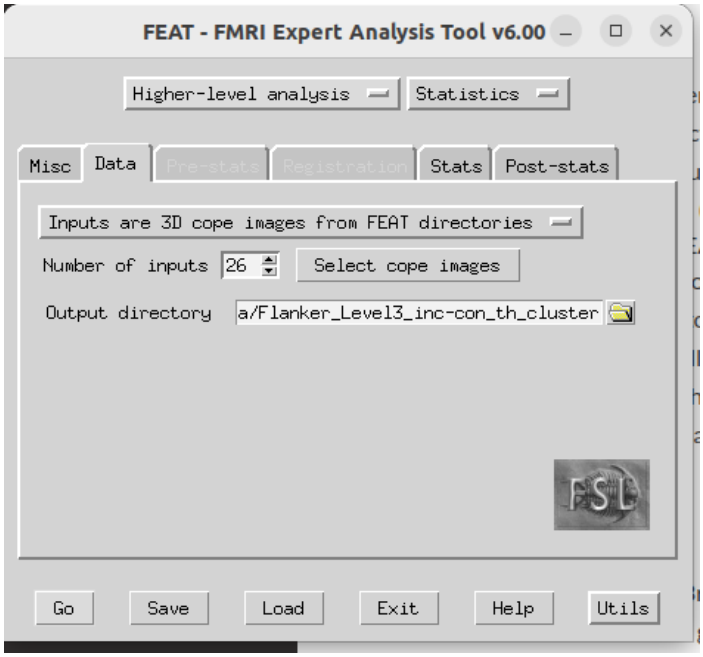
In this part we will be exploring the next step of our process which is third level analysis. Third level analysis is an analysis that is used to transition from individual subject analyses to group-level investigations. It serves to validate and generalise findings by confirming consistent activation patterns across subjects. By combining the data from multiple subjects, it provides an understanding of neural processes that takes place for the task that we have.This analysis employs statistical techniques to account for within-subject and between-subject variability, enabling researchers to draw meaningful conclusions about the whole population.

Steps:

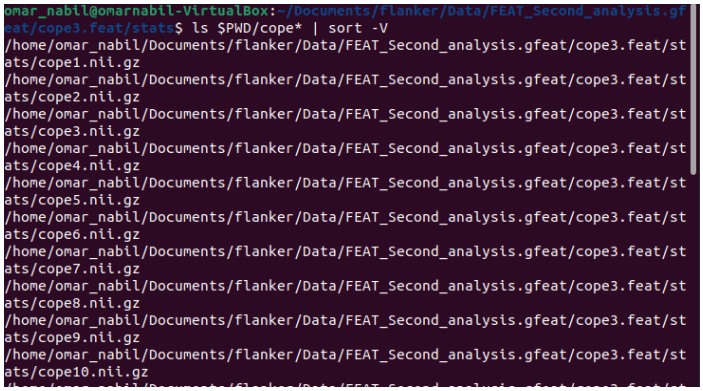
1- Inputs:

In the third level our inputs like the name indicates are the results of the second level analysis. We take as inputs the z-stats from the second level analysis which is a map from second level analysis that provides a quantitative representation of the strength and location of neural activations or differences across the group and depending on which cope we are dealing with we will choose the statistical map for all the subjects by doing the following:

1- select the number of subjects we have and the output directory



2- Add the path for all the FEAT directories for all the subjects. We collect them via the following command: (ls $PWD/cope* | sort -V).



Then past all of them in them in the select input data tap:

2- Modelling:

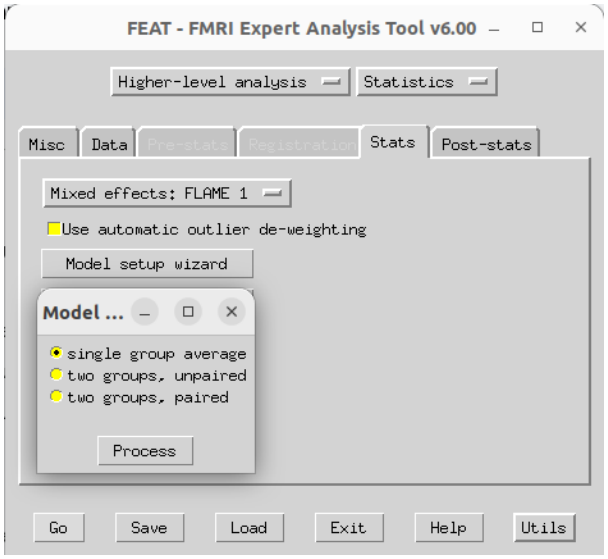
In the stats tap we can choose the model we are using and the type of effect we want. We choose to keep the Mixed effects to it's default value.
There are several statistical approaches available, each with its own strengths and considerations. Let's break down the options mentioned and why Mixed Effects FLAME 1 is often chosen as the best option:

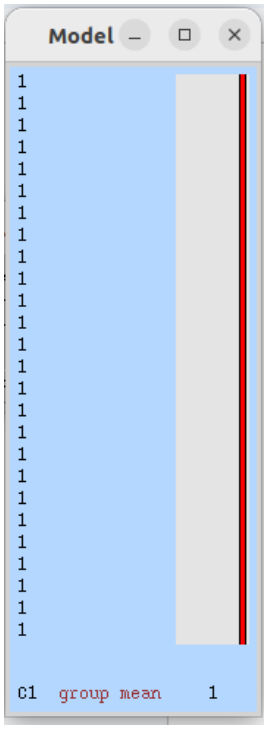
Statistical models:

1. **Mixed Effects Model (FLAME 1)**:
    - Strengths:
        - Models both within-subject and between-subject variability, providing more accurate parameter estimates.
        - Results are more generalizable to the population from which the sample was drawn.
        - Strikes a balance between accuracy and computational efficiency.
    - Considerations:
        - May not be suitable for extremely large datasets due to computational demands.
        - Assumes normality and homoscedasticity of data.
2. **Mixed Effects Model (FLAME 1+2)**:
    - Strengths:
        - Potentially slightly improved accuracy over FLAME 1.
    - Considerations:
        - Computational time is significantly longer compared to FLAME 1.
        - Minimal additional benefit in accuracy compared to FLAME 1.
3. **Randomise (Non-Parametric Approach)**:
    - Strengths:
        - Robust to violations of assumptions about normality and homoscedasticity.
        - Suitable for data that do not meet parametric assumptions.
    - Considerations:
        - Results may be less precise compared to parametric methods under certain conditions.
        - Computational demands can be high, especially for large datasets.
        - Limited ability to model within-subject variability explicitly.

Mixed Effects FLAME 1 is often considered the best option as it provides a good balance between accuracy and computational efficiency while effectively modelling both within-subject and between-subject variability.

We can also use the model setup wizard to create our design matrix as we are only averaging all the subjects equally.





3- Thresholding:

When it comes to the poststats tap it offers multiple different options for thresholding, each offering different and unique utilisation of statistics.

The techniques available:

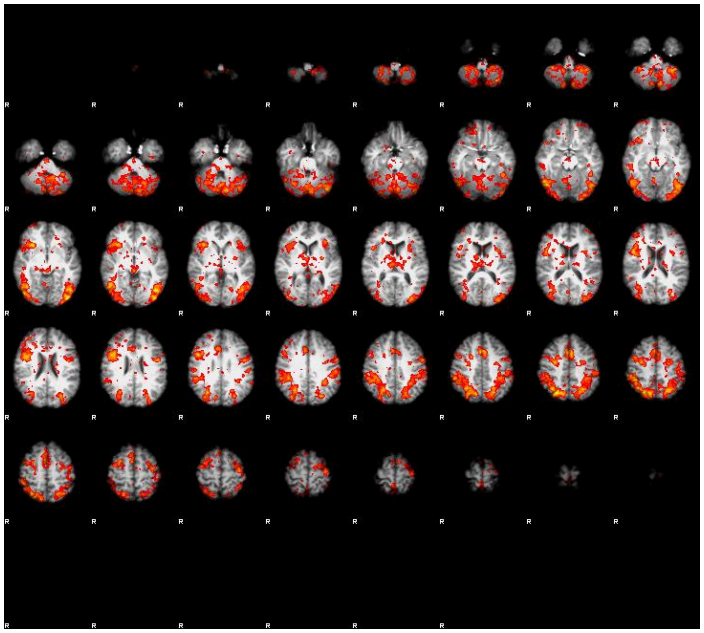
1. **None**:
    - This option displays the parameter estimate at every voxel without any thresholding, regardless of significance.
    - Useful for exploring the entire dataset without filtering out potentially relevant regions.
2. **Uncorrected**:
    - Allows individual voxels to pass a specified Z-threshold(usually set to 3.1), showing only voxels with values exceeding this threshold.
    - Offers a straightforward way to visualise regions of significant activation or differences without correction for multiple comparisons.
3. **Voxel**:
    - Implements maximum height thresholding based on Gaussian Random Field theory.
    - Less conservative than Bonferroni correction, this method considers the spatial smoothness of the data to identify clusters of significant voxels.
    - Useful for balancing sensitivity and specificity in identifying clusters while controlling the family-wise error rate.
4. **Cluster**:
    - Utilises cluster-defining thresholding to determine the significance of clusters of voxels.
    - Recognizes that neighbouring voxels are not independent and adjusts for reduced degrees of freedom.
    - This approach considers the size of clusters and their frequency in simulations to determine significance.
    - Helps identify clusters of activation or differences while controlling for false positives inherent in multiple comparisons.

The following are the results of applying all the mentioned techniques on the cope3 from the previous second level analysis:

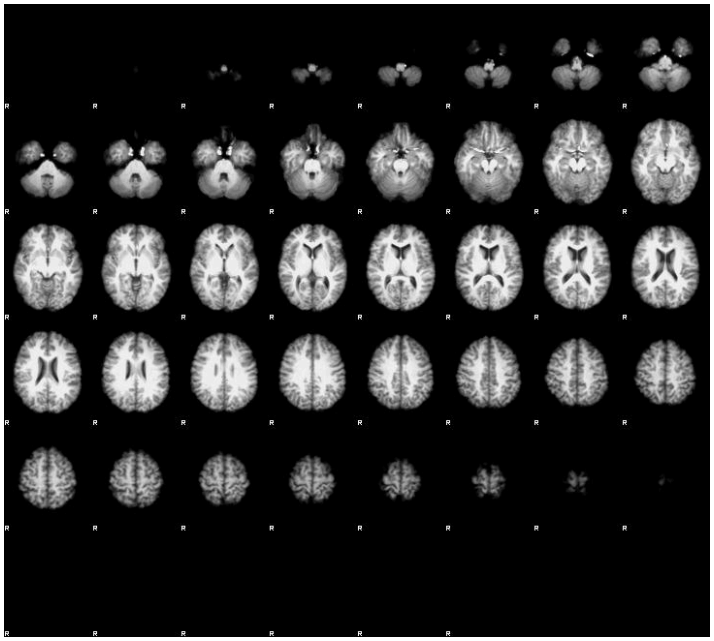
Results:

None: does nothing to the data so it does not output any results to show.

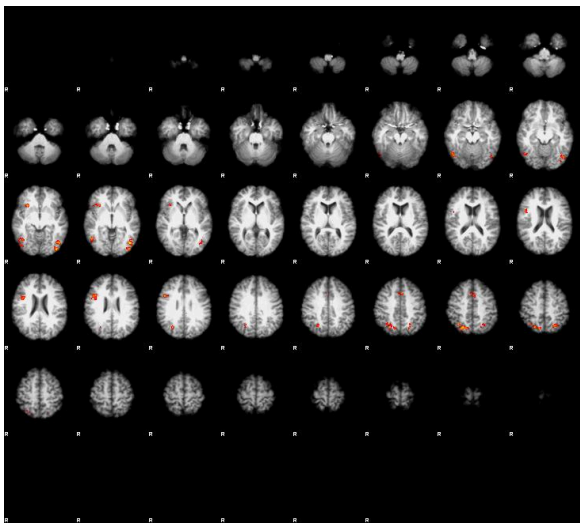
Uncorrected:



Voxel:



Cluster:



Regions that were active :

Paracingulate Gyrus:involved in a variety of cognitive functions, including decision-making, emotion regulation, and attention allocation.

The Inferior Frontal Gyrus (IFG): involved in various cognitive functions, particularly those related to language processing, speech production, and executive control.

Activation/Deactivation meaning:

We have been using the term activation very frequently recently and we need to make sure we know what it stands for, its changes in the level of neural activity in specific brain regions in response to certain stimuli or tasks. So if this region is more active that means that this part of the brain has something to do with the task that is being performed currently. So the body gives it more blood so in response we say that it's "More active".

Deactivation refers to a decrease in neural activity in a specific brain region during a particular task or stimulus. The brain does this to focus on what's important and filter out distractions. So, when you're doing a task, some parts quiet down to let other parts do their job better.

It's a constant rotation between activation and deactivation of regions of the brain because we have limited resources so we have to spread them properly .

VIII. ROI Analysis

In this part we dive deep into the process of ROI Analysis. What we are trying to do is see particular brain regions that we feel are relevant to the activity or cognitive process under study. These areas are frequently selected in accordance with theoretical concerns, anatomical landmarks, or prior study. Following the selection of the ROIs (Regions of interest), the data is examined to see the degree of response or activation in these areas during the relevant task or condition.

So in simple terms we are looking at a smaller part of the brain and focusing on it instead looking at the whole thing as we did before and we use statistical models to help us determine whether these regions can be considered to be active and it's not a result in misinterpretation of data (Like having a big difference in cope-3 due to different levels of deactivations and not activations)

ROI analysis findings can offer important new perspectives on the relative contributions of various brain areas to particular behaviours or cognitive processes.

Steps:

1- ROI:

This part has two approaches. We either pick a whole region of the brain and start our calculations based on that or choose one voxel (usually the one with the highest activation value) , create a sphere around it and keep going with our calculations using that mask.

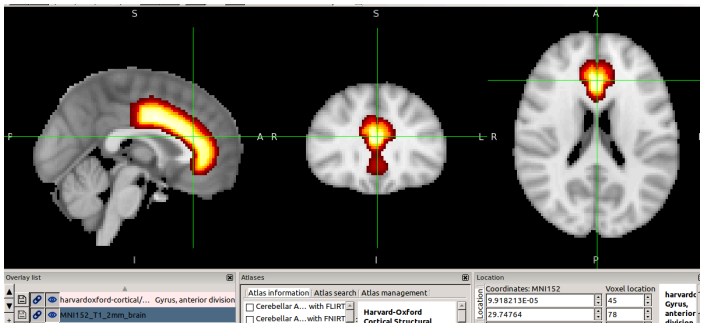
This part will be a bit out of convention in comparison with previous reports, I will explain each process till the end with it's observations and then do a comparison at the end

Atlas based ROI:

atlas-based approach to define regions of interest (ROIs) within the brain. Atlases serve as templates that highlight anatomical or functional regions, providing a systematic framework for investigating brain activity. W choose the region of which we are studying based on previous researches. In our case we choose the Paracingulate Gyrus based on previous knowledge.

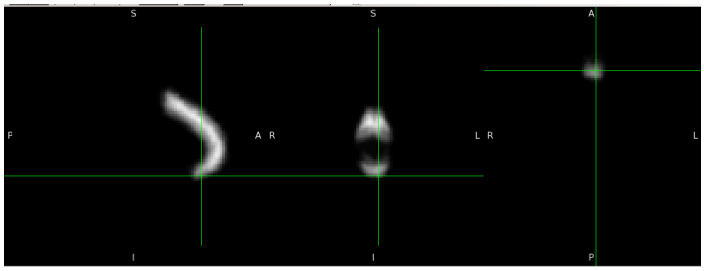
1- Creating the mask:

We will use the atlas to highlight the region that we want and extract the binary mask of the region that we will use down the line:



So we select the region and extract the mask by clicking on the save option next to it.

This will result in the following mask:



2- Data extraction:

With our masks in place, the next step involves retrieving pertinent data from the second-level analysis, which encapsulates activation patterns for each subject. Throughout the analysis, various data maps have been produced, such as t-statistic maps, cope images, and variance images. However we will opt to extract data from the z-statistic maps. These maps undergo conversion into a normally distributed format which is helpful for us.

For the sake of simplicity we will merge all the zstats data into one file using the following command:(fslmerge -t allZstats.nii.gz `ls zstat* | sort -V`). This command concatenates all z-statistic images into a unified dataset along the time dimension, denoted by the "-t" option, essentially putting all the volumes into a larger dataset. The output dataset is named "allZstats.nii.gz".

Then utilising the fslmeants command, we extract data from the PCG mask: (fslmeants -i allZstats.nii.gz -m PCG.nii.gz). This command will output 26 numbers, one per subject. Each number represents the contrast estimate for that subject, averaged across all voxels within the specified PCG mask.

```
omar_nabil@omarnabil-VirtualBox:~/Documents/flanker/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
```

The values can be positive values when there is greater activation during incongruent trials compared to congruent trials. However, it can also result in negative values when there is greater activation during congruent trials compared to incongruent trials as we are dealing with cope-3..

3- T-test:

We then take all of these numbers and apply a t-test on them to see if our hypothesis is rejected or not. Our hypothesis is that the region is not activated and based on the p value we get we can reject or approve the hypothesis. We use a t-test to evaluate whether the region shows significant activation. If the p-value is below 0.05, we reject the null hypothesis, indicating activation. If not, we fail to reject the null hypothesis, suggesting no significant activation.

```
main.r                                   Run        Output
 6  -0.087538                                      Rscript /tmp/rdkEevA8Ng.r
 7  0.228115                                       Read 26 items
 8  0.745255
 9  0.745922                                           One Sample t-test
10  0.267038
11  0.050253                                       data:  x
12  -0.272654                                      t = 0.97041, df = 25, p-value = 0.3411
13  0.265128                                       alternative hypothesis: true mean is not equal to 0
14  -0.084951                                      95 percent confidence interval:
15  -0.133633                                       -0.1162828  0.3234992
16  -0.114938                                      sample estimates:
17  -0.389024                                      mean of x
18  0.210950                                       0.1036082
19  -0.964052
20  -0.657895                                      === Session Ended. Please Run the code again ===
21  -0.192762
22  -0.039086
23  0.357768
24  0.997227
25  -0.360570
26  -0.546491
27  0.216187
28
29  t.test(x)
```

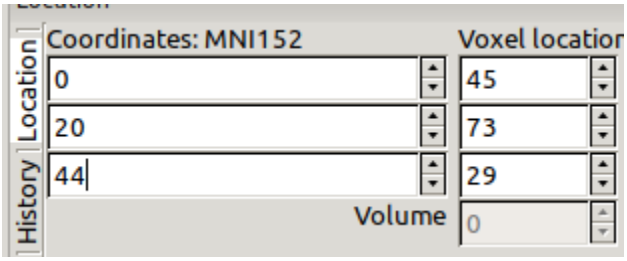
We see a p value of 0.34 which does not pass our threshold which means that we fail to reject the hypothesis. This may be due to the large size of the mask that we are using (Atlas based). The large size of the mask can cause some regions to cancel each other out so the best solution for this is to use a different approach for ROI creation.

Spherical mask:

When using a spherical mask approach, we define regions of interest around specific brain coordinates(usually we choose voxels with the highest activity values). First, we select coordinates of interest. Then, we create a spherical mask around these coordinates. This mask is applied to the fMRI data to extract activation patterns.

Voxel coordinates:

Wefirst get the mini coordinates for peak activation and we transform it into voxel coordinates:



Then we create the base for our sphere using the following command specifying the coordinates of the base voxel: (fslmaths $FSLDIR/data/standard/MNI152_T1_2mm.nii.gz -mul 0 -add 1 -roi 45 1 73 1 58 1 0 1 Jahn_ROI_dmPFC_0_20_44.nii.gz -odt float)

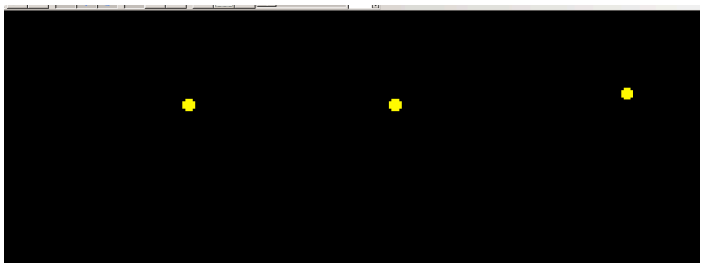
Then we need to create the sphere around our voxel so we will use the following command:

(fslmaths Jahn_ROI_dmPFC_0_20_44.nii.gz -kernel sphere 5 -fmean Jahn_Sphere_dmPFC_0_20_44.nii.gz -odt float)

And then binarize the mask.

```
omar_nabil@omarnabil-VirtualBox:~/Documents/flanker/Data$ fslmaths $FSLDIR/data/
standard/MNI152_T1_2mm.nii.gz -mul 0 -add 1 -roi 45 1 73 1 58 1 0 1 Jahn_ROI_dmP
FC_0_20_44.nii.gz -odt float
omar_nabil@omarnabil-VirtualBox:~/Documents/flanker/Data$ fslmaths Jahn_ROI_dmPF
C_0_20_44.nii.gz -kernel sphere 5 -fmean Jahn_Sphere_dmPFC_0_20_44.nii.gz -odt f
loat
omar_nabil@omarnabil-VirtualBox:~/Documents/flanker/Data$ fslmaths Jahn_Sphere_d
mPFC_0_20_44.nii.gz -bin Jahn_Sphere_bin_dmPFC_0_20_44.nii.gz
omar_nabil@omarnabil-VirtualBox:~/Documents/flanker/Data$
```

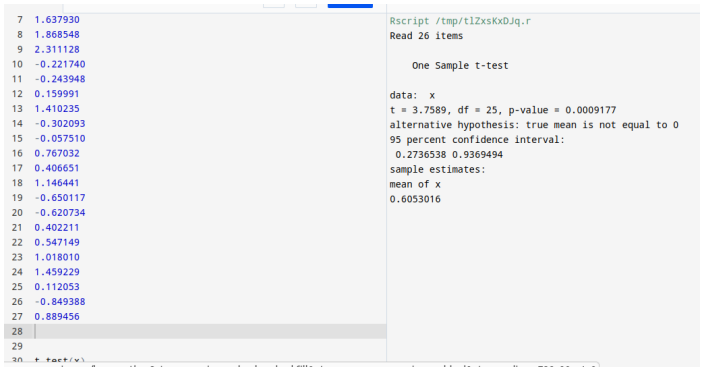
This is the results mask:



Then we apply the same steps that we did previously to calculate the p value and check our hypothesis.

```
omar_nabil@omarnabil-VirtualBox:~/Documents/flanker/Data$ fslmeants -i allZsta
.nii.gz -m Jahn_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
```

Then apply the t-test:

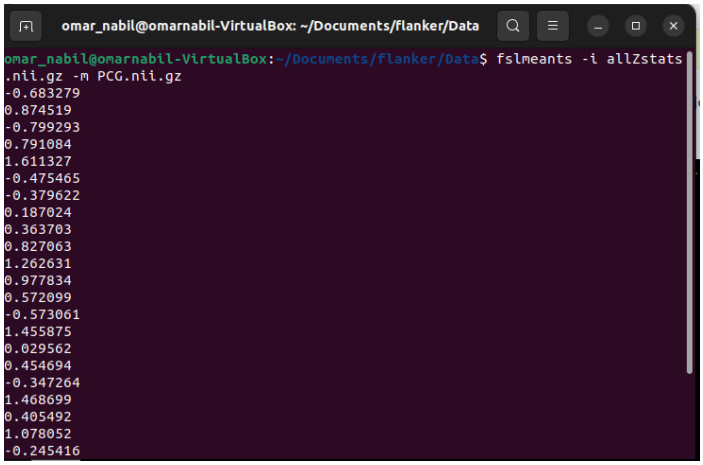


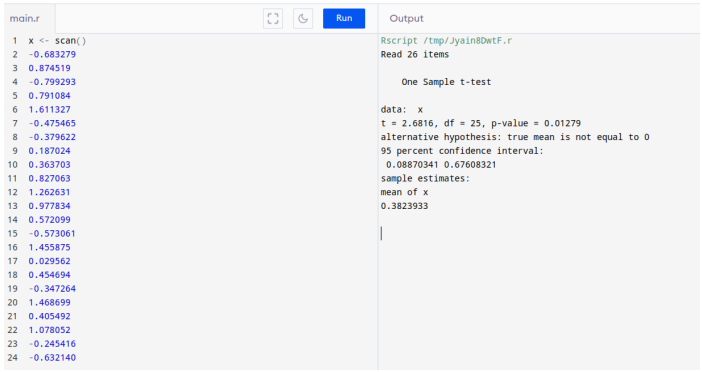
The obtained p-value is notably small and falls below our predetermined threshold, indicating statistical significance. Consequently, we can confidently reject our hypothesis, as the data provides compelling evidence to the opposite.

Results:

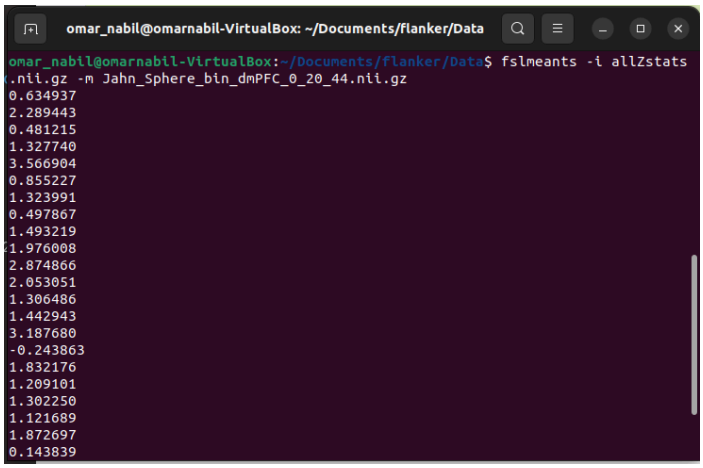
The following will be the results of applying the same processes on the other two copes.

Cope-2_Atlas based mask:





Cope-2_spherical based mask:



```
main.r                                                    Run        Output
1  x <- scan()                                                       Rscript /tmp/MAK8iZeELO.r
2  0.634937                                                          Read 26 items
3  2.289443
4  0.481215                                                             One Sample t-test
5  1.327740
6  3.566904                                                          data:  x
7  0.855227                                                          t = 7.9607, df = 25, p-value = 2.57e-08
8  1.323991                                                          alternative hypothesis: true mean is not equal to 0
9  0.497867                                                          95 percent confidence interval:
10 1.493219                                                           1.035874 1.758925
11 1.976008                                                          sample estimates:
12 2.874866                                                          mean of x
13 2.053051                                                           1.397399
14 1.306486
15 1.442943
16 3.187680
17 -0.243863
18 1.832176
19 1.209101
20 1.302250
21 1.121689
22 1.872697
23 0.143839
```

Cope-1_Atlas based mask:

```
omar_nabil@omarnabil-VirtualBox: ~/Documents/flanker/Data
omar_nabil@omarnabil-VirtualBox:~/Documents/flanker/Data$ fslmeants -i 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
```

```
main.r                                                    Run        Output
6  1.378904                                                          Rscript /tmp/mEJtk424aR.r
7  -0.276878                                                         Read 26 items
8  0.284840
9  0.937007                                                             One Sample t-test
10 0.621358
11 0.880154                                                          data:  x
12 0.985694                                                          t = 3.9377, df = 25, p-value = 0.0005812
13 1.167754                                                          alternative hypothesis: true mean is not equal to 0
14 0.496890                                                          95 percent confidence interval:
15 -0.737808                                                          0.2319975 0.7407886
16 1.346424                                                          sample estimates:
17 -0.330895                                                         mean of x
18 0.637774                                                           0.486393
19 -1.253987
20 0.788773
21 0.217294
22 1.066111
23 0.169197
24 0.492838
25 0.465999
26 -0.047969
27 0.536678
28
```

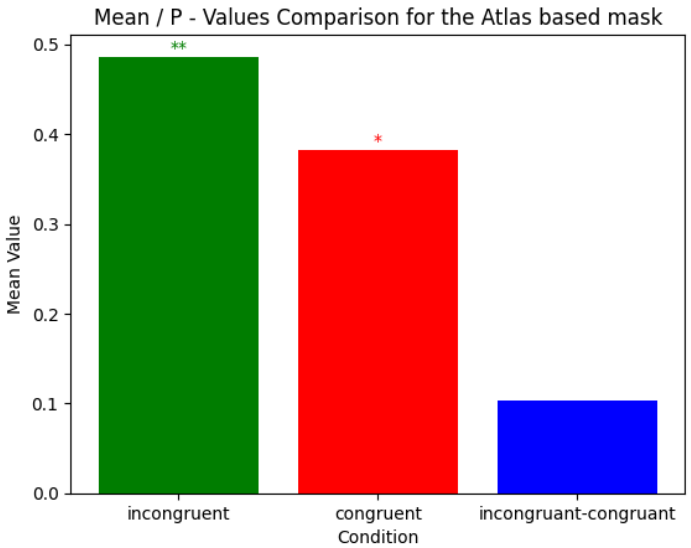
Cope-1_spherical based mask:

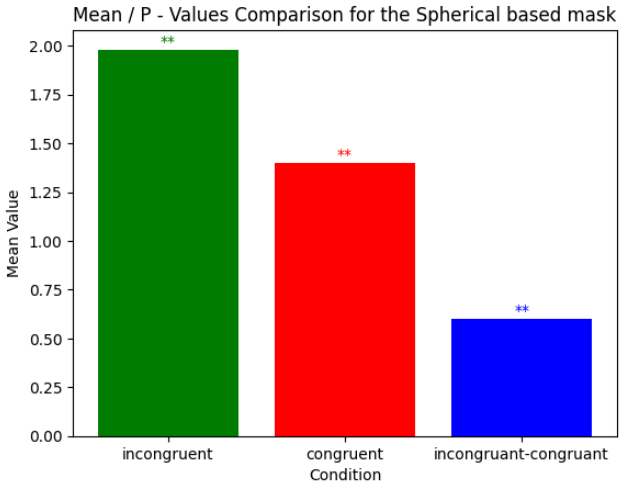
```
omar_nabil@omarnabil-VirtualBox: ~/Documents/flanker/Data
omar_nabil@omarnabil-VirtualBox:~/Documents/flanker/Data$ fslmeants -i allZstats
.nii.gz -m Jahn_Sphere_bin_dmPFC_0_20_44.nii.gz
1.901615
3.118286
1.668114
1.828725
4.212729
2.510646
3.018982
2.917934
1.246839
1.719434
2.984716
3.300570
1.027082
1.401403
3.857215
0.199767
2.867935
0.466228
0.595518
1.437114
2.610784
1.234587
```

```
main.r                                                    Run        Output
1  x <- scan()                                                       Rscript /tmp/Do5uK5ywWD.r
2  1.901615                                                          Read 26 items
3  3.118286
4  1.668114                                                             One Sample t-test
5  1.828725
6  4.212729                                                          data:  x
7  2.510646                                                          t = 8.865, df = 25, p-value = 3.44e-09
8  3.018982                                                          alternative hypothesis: true mean is not equal to 0
9  2.917934                                                          95 percent confidence interval:
10 1.246839                                                           1.520563 2.440901
11 1.719434                                                          sample estimates:
12 2.984716                                                          mean of x
13 3.300570                                                           1.980732
14 1.027082
15 1.401403
16 3.857215
17 0.199767
18 2.867935
19 0.466228
20 0.595518
21 1.437114
22 2.610784
23 1.234587
24 2.733579
```

As we saw in all the previous results with the two other copes they all show significance to our data.

Bar-Plots





The bar charts generated with Matplotlib offer a clear depiction of activation levels across various conditions, highlighting significant activations with (*)

Conclusion:

In our analysis, we explored two methods for ROI selection: atlas-based and spherical masks. The atlas-based approach relies on predefined anatomical or functional regions, while the spherical mask approach targets high-activation voxels and creates a region around them. Our findings illustrate that the choice of mask significantly impacts the results. The atlas-based mask, due to its larger size, may obscure significant activations by averaging out the activity, leading to non-significant p-values, as seen with a p-value of 0.34 in the Paracingulate Gyrus analysis. Conversely, the spherical mask approach, which focuses on peak activation voxels, yielded statistically significant results, allowing us to reject the null hypothesis.

IX. Final Conclusion:

Do we use the same regions of the brain for both congruent and incongruent tasks?

While there is overlap in activation between conditions, differences in activation patterns as we have seen with cope-3 which showed us the difference between the activation of both of them, while it's small but it's still significant and shows that there is a difference in the brain functionality that reflects a varying cognitive demands of congruent versus incongruent trials, with incongruent trials typically requiring more pronounced engagement of regions involved in conflict resolution. Individual differences may also influence activation patterns, highlighting the complexity of cognitive control processes and their neural underpinnings in tasks involving attention and response inhibition.

X. References

1- A. Jahn, "Andy's Brain Book," Accessed: Jan. 09, 2024. [Online]. Available: https://andysbrainbook.readthedocs.io/en/latest/