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SBME 3038
Medical Equipment Design

Functional MRI Task Report

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1. Quality Control Assessment:

1.1 Introduction:

- Utilized FSL tool to conduct rigorous quality control on T1 and T2* images and volumes.
- Established an Excel sheet as a comprehensive record, detailing observations, and analyses.
- Executed meticulous evaluations encompassing:
 - Comprehensive assessment of image quality.
 - Thorough examination of subject motion artifacts.
 - Precise scrutiny of facial feature extraction accuracy.
 - In-depth analysis of volume metrics, accompanied by insightful annotations and visual representations.



Quality control	
Sub_1	Run_1 the subject moved a little move in the volume 145
Sub_1	Run_2 the subject don't move while the run and the eye is removed from the volumes well
Sub_1	T1 High quality image and the face is hidden perfectly
Sub_1	Notes X-rain [Brain colors] show a better details and quality
Sub_2	Run_1 A very small movement from volume 60 to almost 90
Sub_2	Run_2 the subject move his/her a noticeable move
Sub_2	T1 The image quality is very high, but the mouse of the subject don't removed well
Sub_2	Notes There is no specific note for this subject
Sub_3	Run_1 From volume 65 : 75 the subject moved a strong move
Sub_3	Run_2 the subject moved a lot
Sub_3	T1 There is other thing expect of the skull of the subject in the scanned image, but the quality is very good and the face removed well
Sub_3	Notes A small head compared to the other subjects
Sub_4	Run_1 the subject moved a little move from volume 50: volume 90
Sub_4	Run_2 almost the subject didn't move
Sub_4	T1 The image quality is very high, but the mouse of the subject don't removed well
Sub_4	Notes A small head compared to the other subjects and the quality of the scanned volume is very poor compared to the other subjects
Sub_5	Run_1 the subject move in volume 80 a little move
Sub_5	Run_2 the subject eye blink too much
Sub_5	T1 High quality image and the face is masked perfectly
Sub_5	Notes There is no specific note for this subject
Sub_6	Run_1 almost the subject didn't move or blinking
Sub_6	Run_2 The subject move in the start of the run from volume 0:15 but after that didn't move again
Sub_6	T1 High quality image and the face is masked perfectly
Sub_6	Notes There is other thing expect of the skull of the subject in the scanned image.
Sub_6	Run_1 the subject move a normal move of any human, there is eye blinking in many volumes like 17, 20, 33 and others
Sub_6	Run_2 the subject don't move while the run but the eye blinking with a stronger way than run 1

1.2 Motion Artifact:

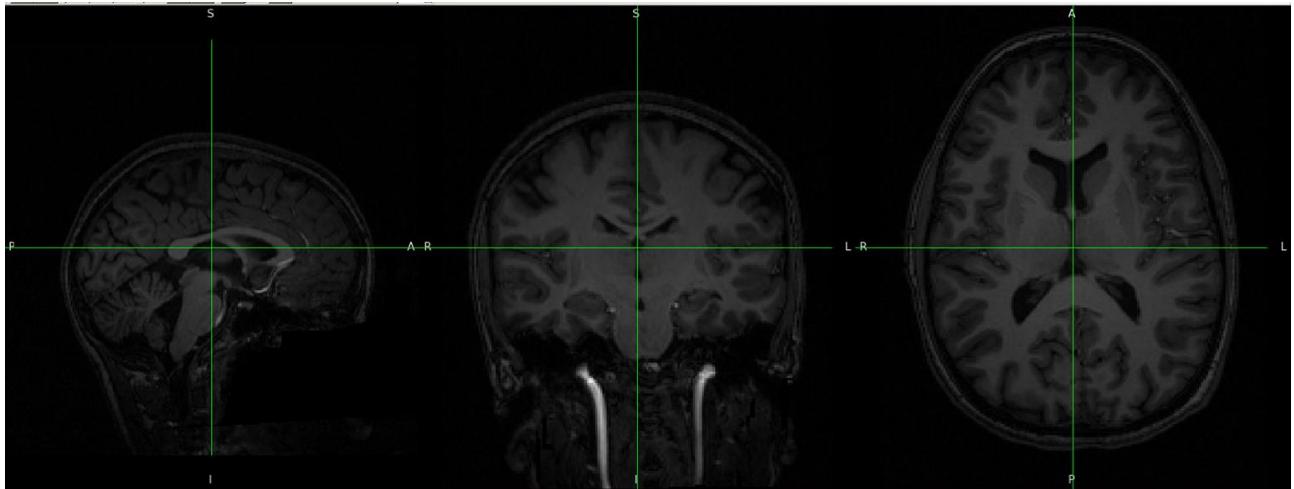
Patient motion such as respiration, cardiac motion, eye movements, swallowing and minor subject movement is the largest physiological effect that causes artifacts. Movement of the object being imaged during the sequence results in inconsistencies in phase and amplitude, which lead to blurring and ghosting.

The nature of the motion artifact depends on the timing of the motion with respect to the acquisition.

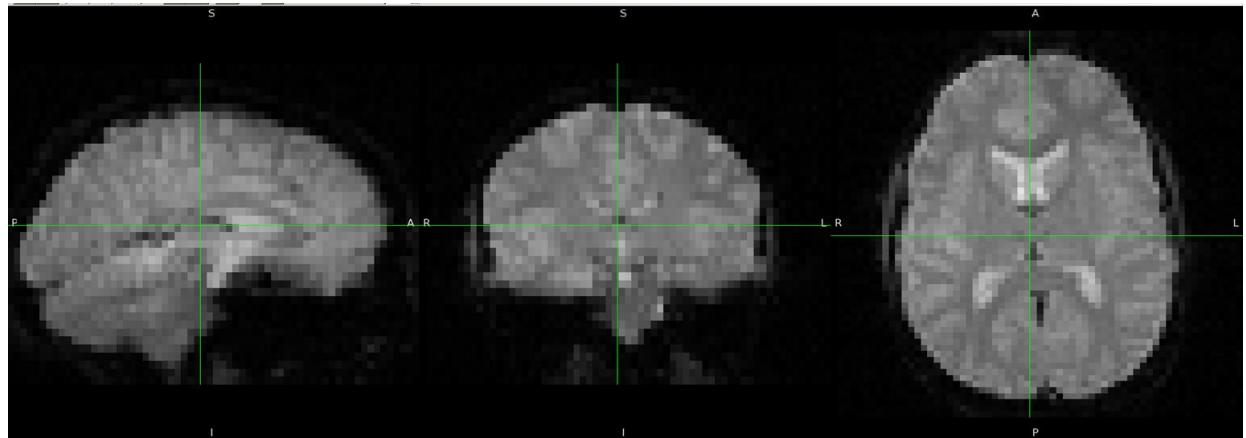
1.3 QC Table:

Subject Name	Quality control			
	T1	Run 1	Run 2	Notes on T1
Sub_1	High quality image and the face is hidden perfectly	the subject moved a little move in the volume 145	the subject don't move while the run and the eye is removed from the volumes well	X-rain [Brain colors] show a better details and quality
Sub_4	The image quality is very high, but the mouse of the subject don't removed well	the subject moved a little move from volume 50: volume 90	almost the subject didn't move	A small head compared to the other subjects and the quality of the scanned volume is very poor compared to the other subjects.
Sub_8	very high quality image and the face is removed in a good way	the movement is almost zero the subject don't move, we can detect the eye blinking and the blood reaches the eye from volume 85:115	the subject move a very small move from volume 0 to volume 90	the gray/white matters is looking more detailed and explained when the color image is (NH-new[brain colors])
Sub_14	A high quality image and good face remove	The subject didn't move at all	The subject start to move from volume 140 until the end of the run	Open the image in Render1t and coordinates x = -105.1201, y = 22.07359, z = -22.29812
Sub_17	A small head compared to the other subjects and the quality is very high but the mouse are not masked	The subject move in the last 2 or 3 volumes	The subject moved in volume 30:40	There is no specific note for this subject

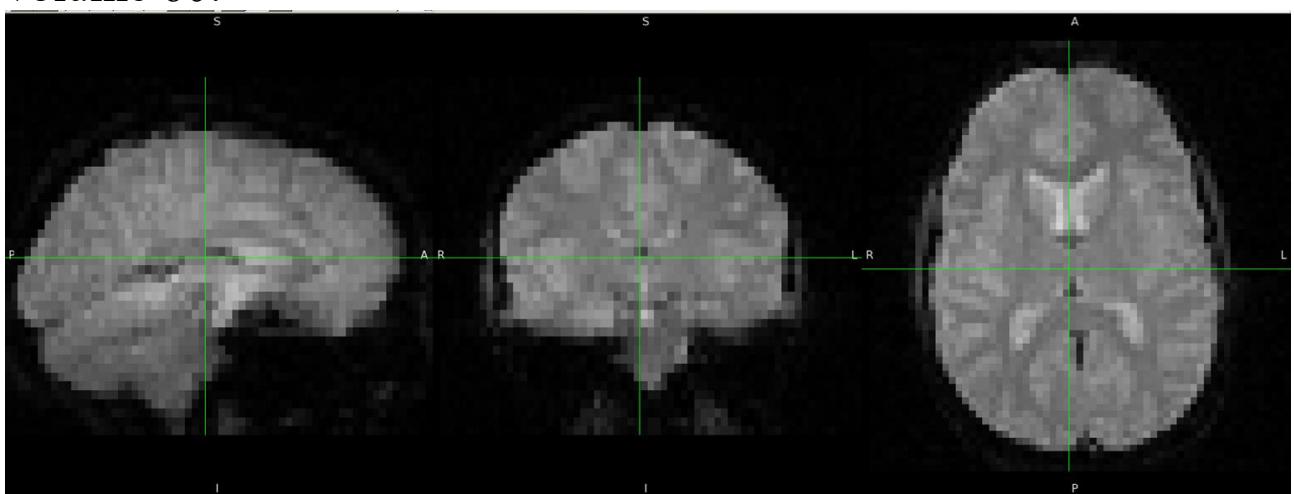
1.4 Sample of images from the QC: sub1 T1:



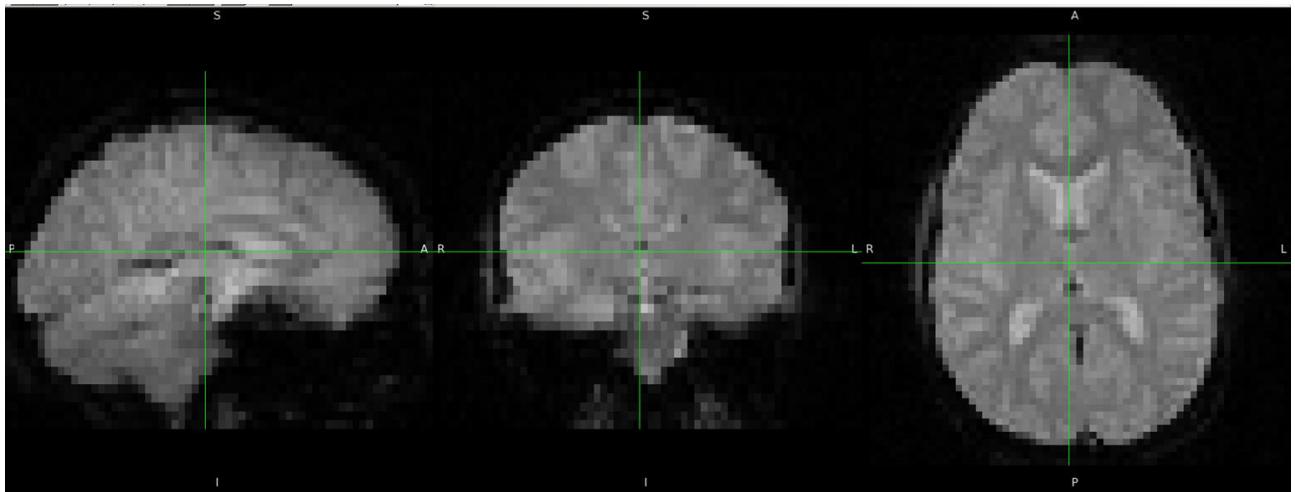
Sub1 Run1:
Volume 0:



volume 60:



Volume 145:

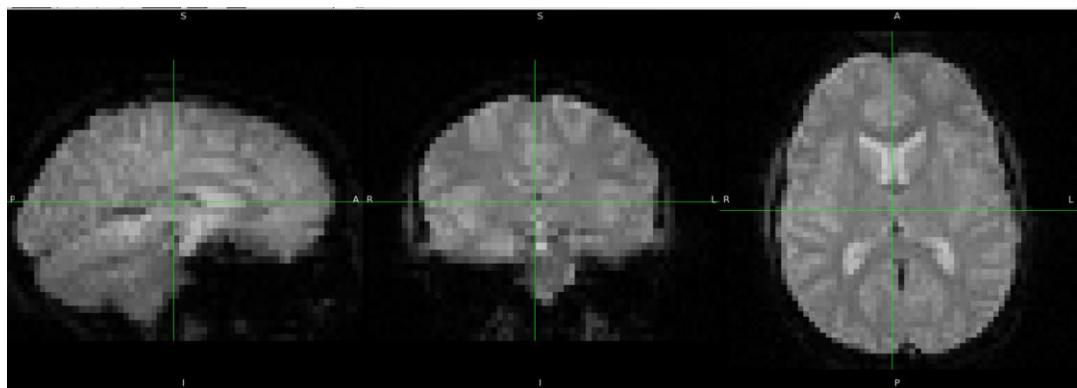


Note:

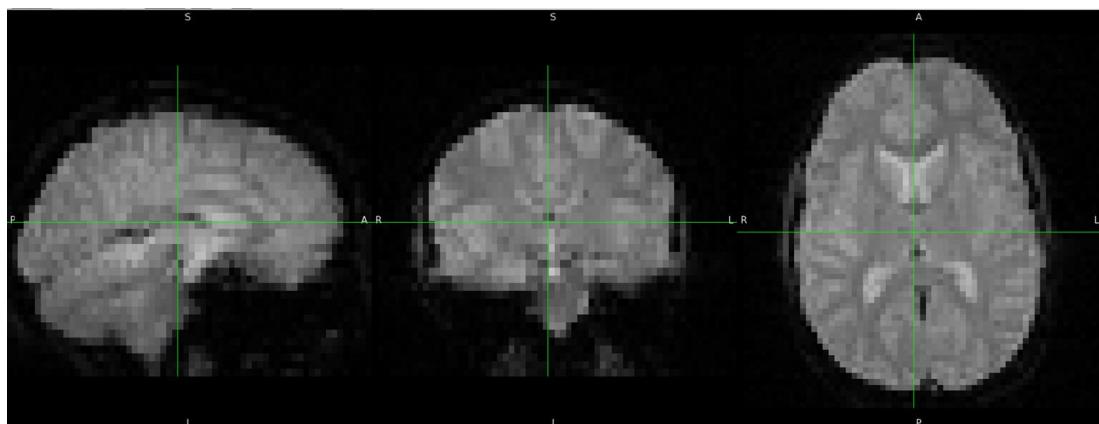
by applying the volumes as video we can detect that the subject move in the run 1 in he last two volumes but in run 2 the subject don't move at all.

Sub1 Run2:

Volume 0:



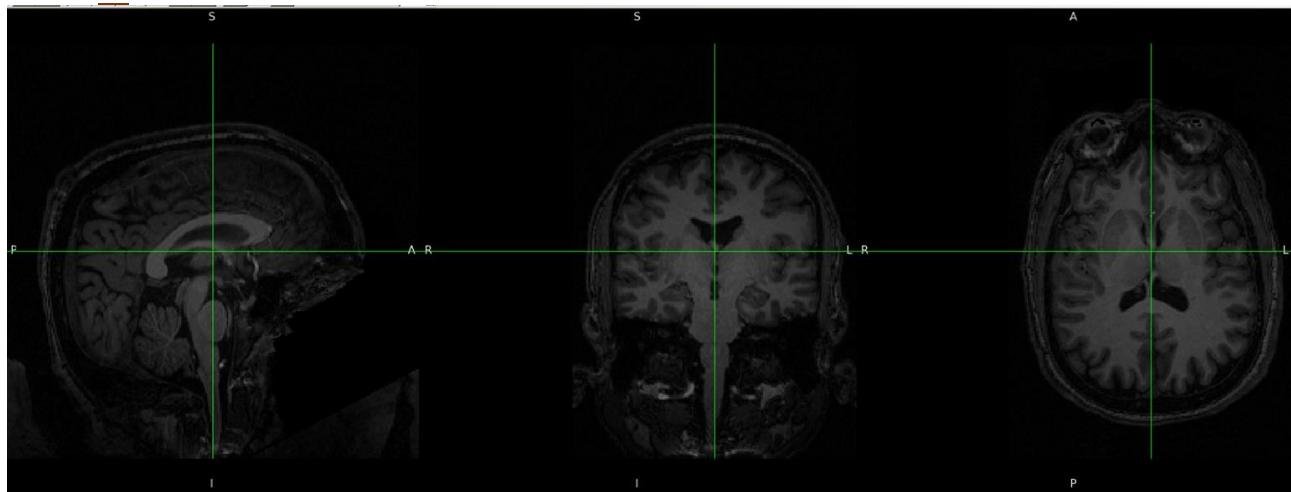
Volume 145:



Note:

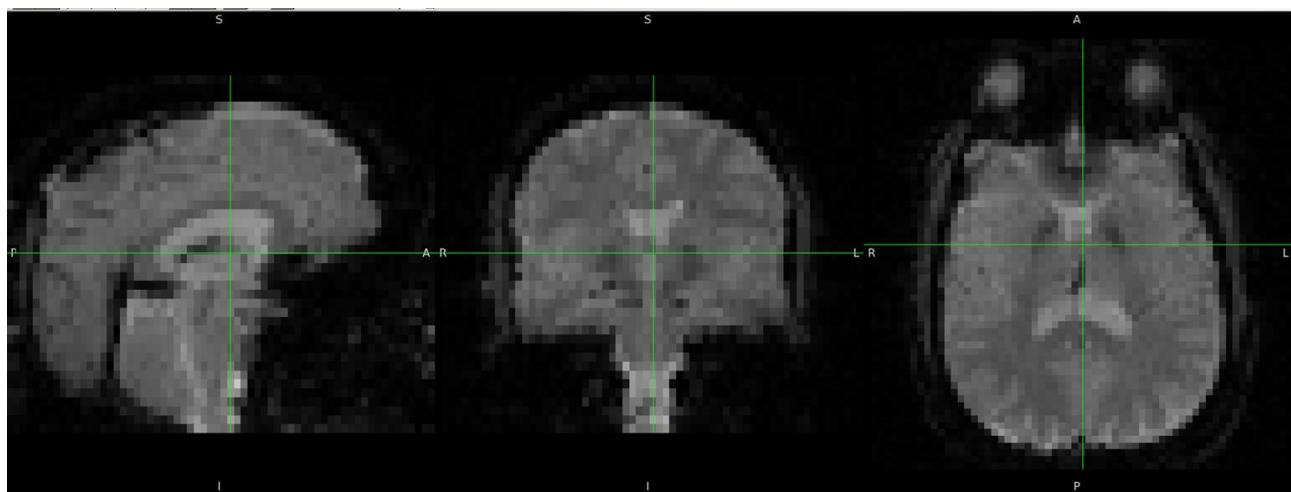
we can see that the brain shape and size is different from one to another and we can see that by comparing the size and shape of subject 1 brain and subject 20 brain

Sub_20 T1:

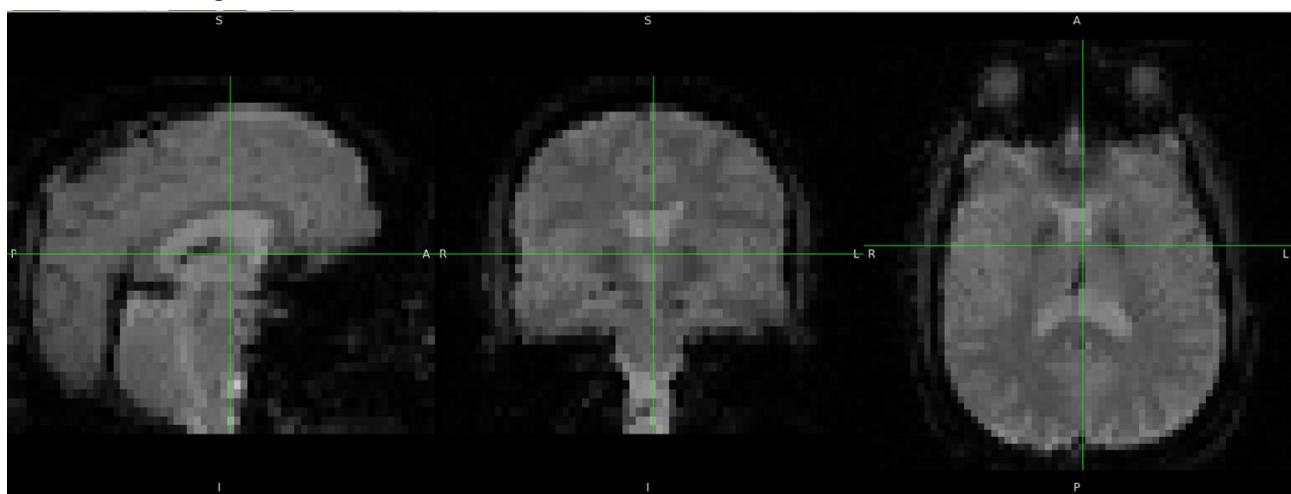


sub20 Run 1:

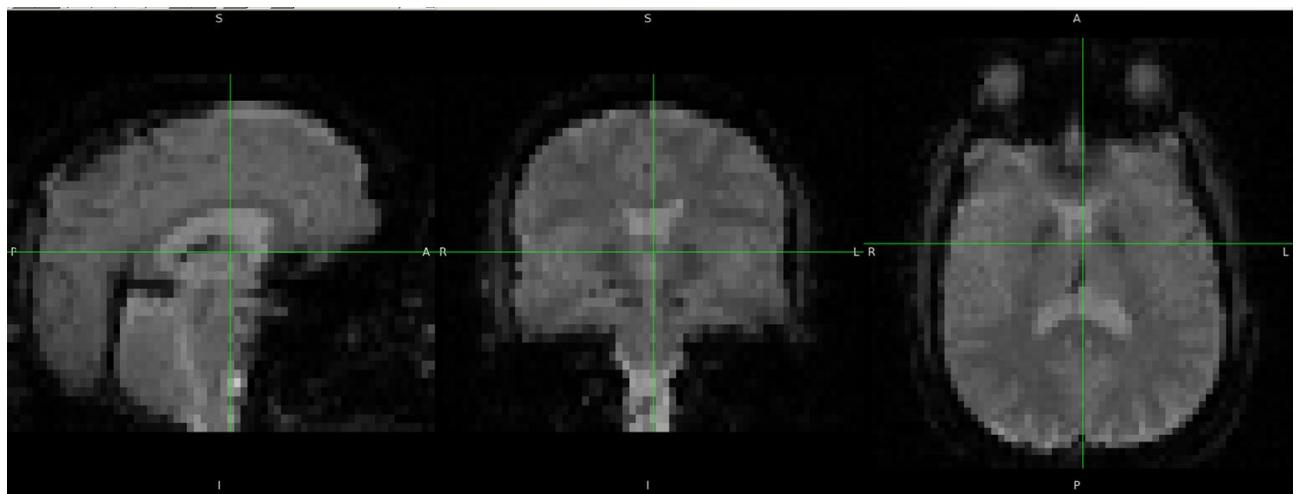
volume 0:



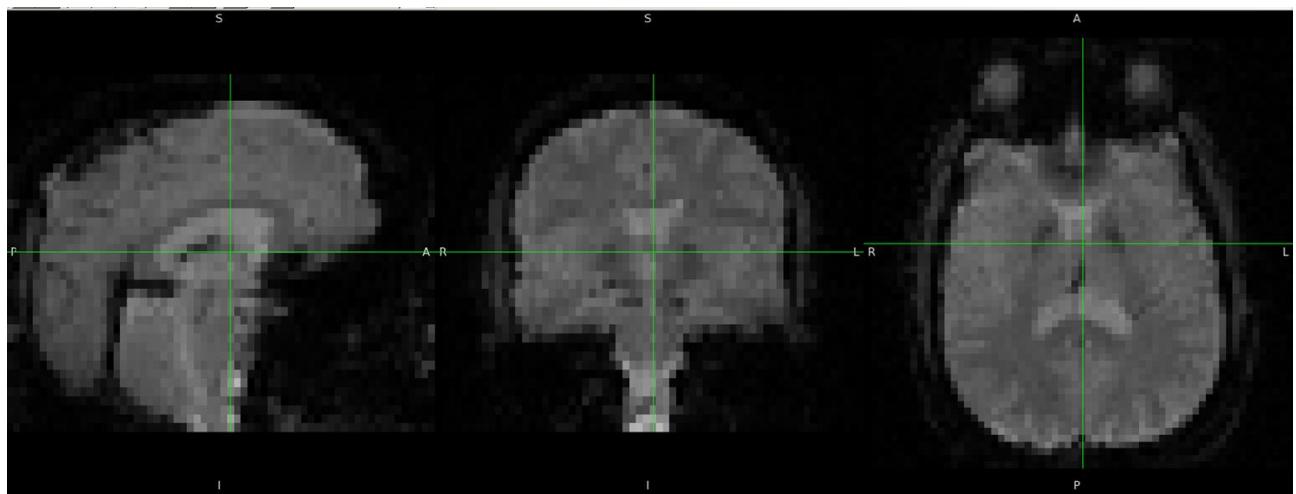
volume 145:



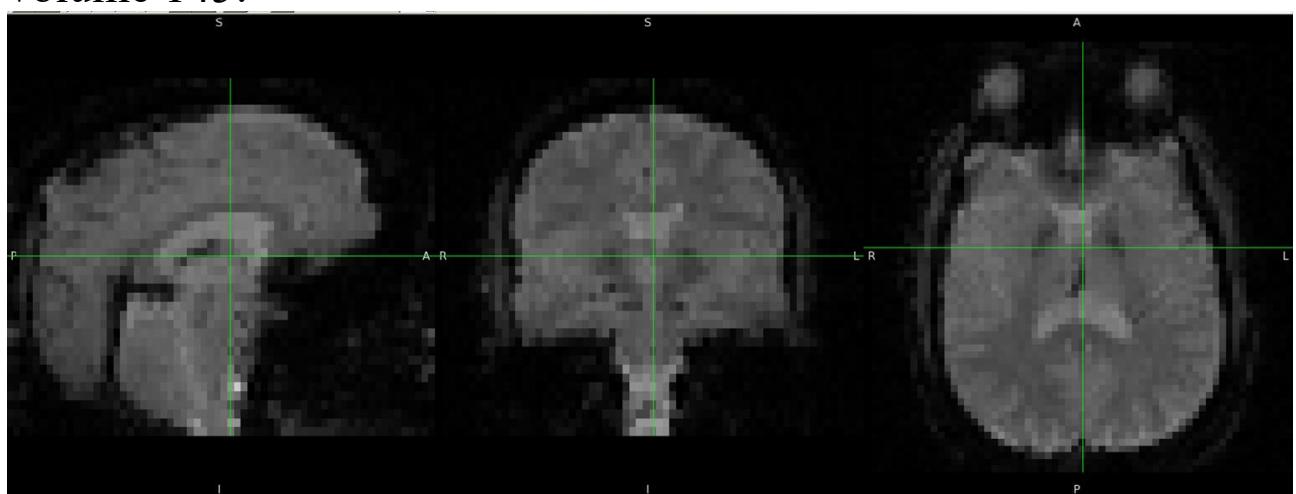
Sub20 Run 2:
volume 0:



volume 140:



volume 145:



the excel sheet has the detailed QC with some notes of how I see the subject's structural images and which volume the subject moved in.

2. Neuroanatomy:

This is some of brain regions from the slides and some of them I get it from searching

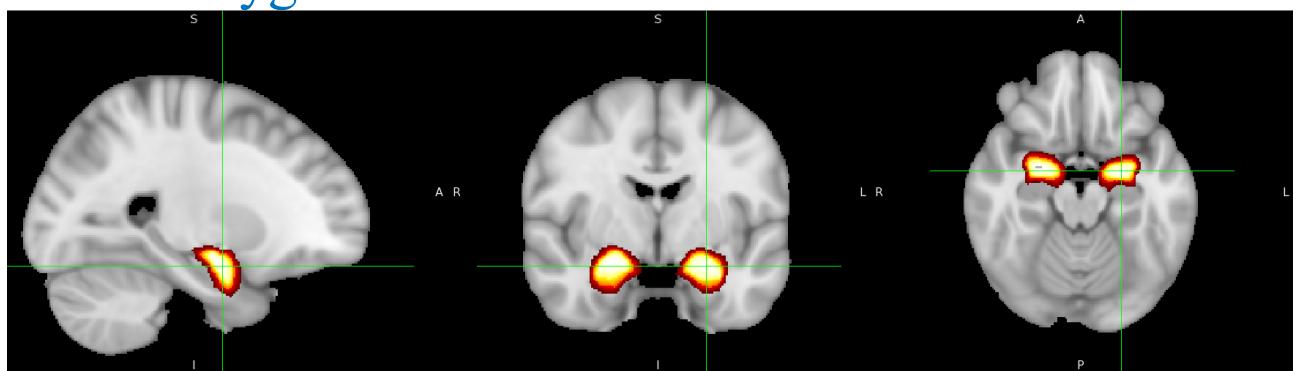
System / divisions	Region / subdivisions	Brain part / Subcortical components	Function
Forebrain	Limbic system	Amygdala	<ul style="list-style-type: none"> • Memory Formation • Social Behavior • Emotional Processing • Stress Response
		Olfactory bulb	<ul style="list-style-type: none"> • Sense of Smell • Modulation of Behavior and Physiology
		Hippocampus	<ul style="list-style-type: none"> • hold short-term memories and transfer them to long-term storage in our brains • emotional processing
		Cingulate gyrus	<ul style="list-style-type: none"> • Communication • Regulates Aggressive Behavior • Language Expression • Decision Making
		Fornix	<ul style="list-style-type: none"> • Memory Consolidation • Hypothalamic Regulation • Reciprocal Connections
Diencephalon		The hypothalamus	<ul style="list-style-type: none"> • produce hormones • plays a role growth, thirst, weight control, etc. • Thermoregulation
		Thalamus	<ul style="list-style-type: none"> • Prioritizing attention • Relaying sensory information • Relaying motor (movement) information • Regulation of Sleep and Circadian Rhythms
		Epithalamus	<ul style="list-style-type: none"> • connect the limbic system to other parts of the brain
The basal ganglia	Striatum		
			<ul style="list-style-type: none"> • motor control • habit formation • Cognition

	“Telencephalon “	Globus pallidus	<ul style="list-style-type: none"> • Reward Processing • Motor Inhibition • Output Nucleus of Basal Ganglia • proprioceptive movements
		Subthalamic nucleus	<ul style="list-style-type: none"> • Motor Control • Movement Disorders
		putamen	<ul style="list-style-type: none"> • Motor Learning and Habit Formation • Action Selection and Inhibition • speech articulation • language functions
the central nervous system	The brainstem	Midbrain	<ul style="list-style-type: none"> • Pain Modulation • Auditory Reflexes • Motor Control • Regulation of Arousal and Consciousness
		Pons	<ul style="list-style-type: none"> • Relay Center for Motor and Sensory Pathways • manages pain signals • It influences sleep cycle
		Medulla oblongata	<ul style="list-style-type: none"> • Manages heart, circulation and breathing • Nerve connections • Coughing and Sneezing Reflexes
spinocerebellar system	The cerebellum	Anterior lobe	<ul style="list-style-type: none"> • Balance and Coordination • Motor Control • Sensorimotor Integration • fine tuning of body movements
		Posterior lobe	<ul style="list-style-type: none"> • Assists in premotor planning • Coordinates fine, distal volitional movements • Ability to judge time intervals and produce accurate rhythm
		Flocculonodular lobe	<ul style="list-style-type: none"> • Eye Movement Control • Vertigo and Motion Sickness • Spatial Orientation

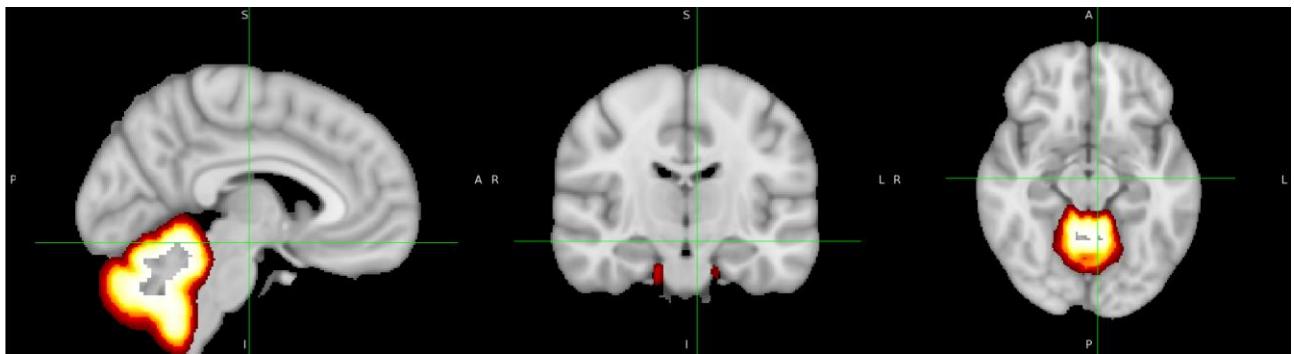
Cortex	Parieto-occipital fissure	<ul style="list-style-type: none"> • Spatial Awareness • Attention • Sensorimotor Integration • Visual Processing • Visual Memory
	Calcarine fissure	<ul style="list-style-type: none"> • Primary Visual Processing • Retinotopic Organization • Visual Perception
	Lingual gyrus	<ul style="list-style-type: none"> • Object recognition • Processing of complex visual stimuli
	cuneus	<ul style="list-style-type: none"> • receives visual information from the same-sided superior quadrantic retina • visual processing
	insula	<ul style="list-style-type: none"> • Emotion Regulation • Interoception • Sensory Processing • Social Cognition • Language Processing • Decision-Making

Some images from FSL from the atlases overlayed on MNI_brain_1mm:

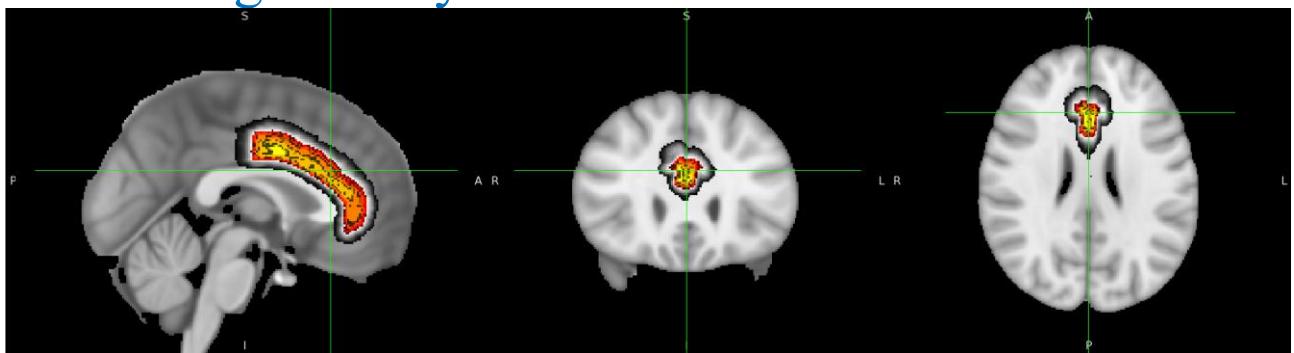
1- Amygdala:



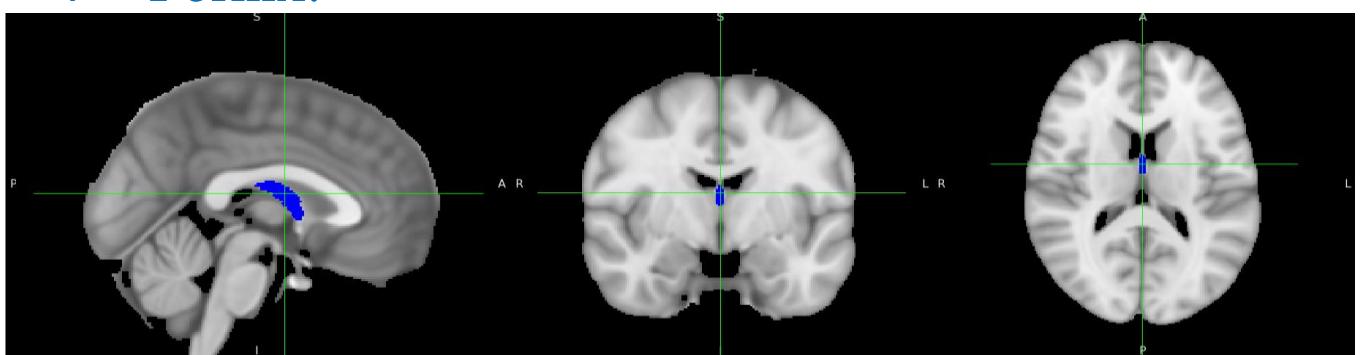
2- Cerebellum:



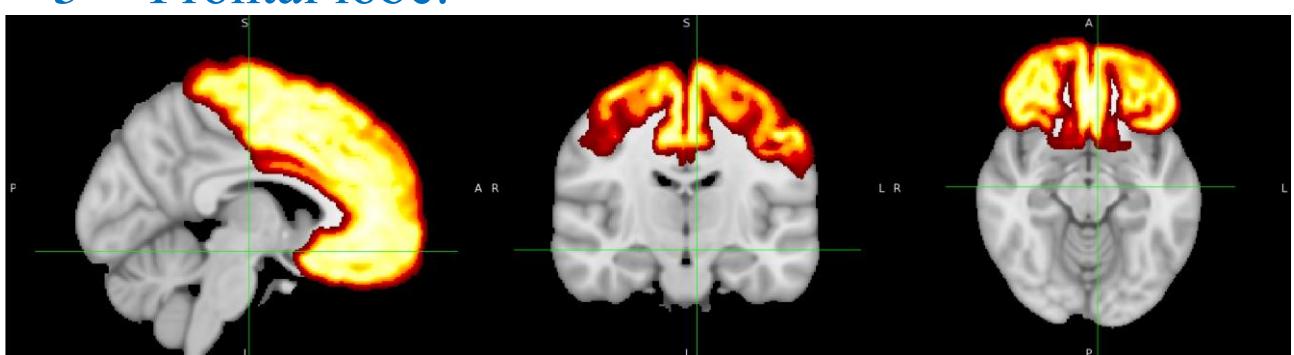
3- Cingulate Gyrus:



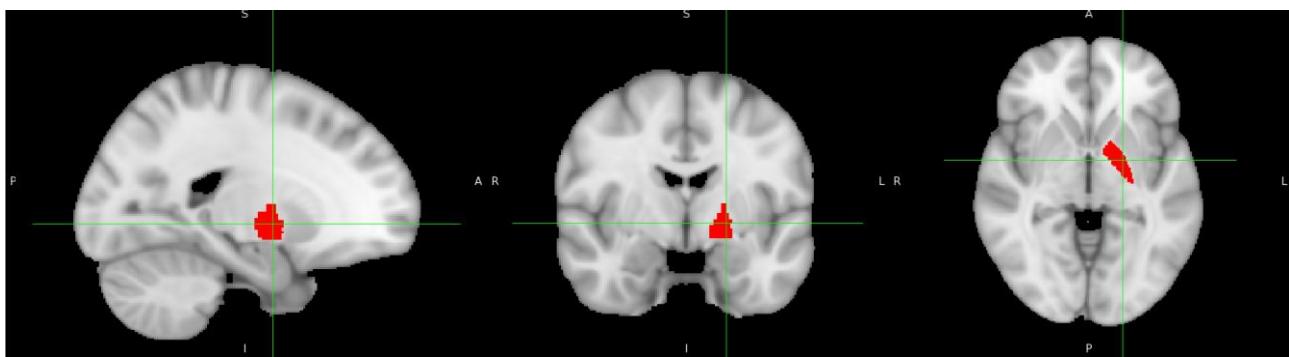
4- Fornix:



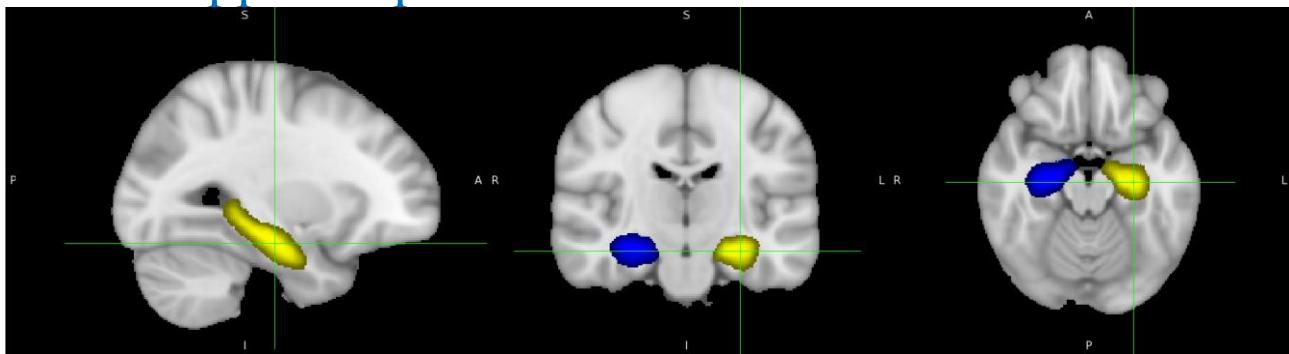
5- Frontal lobe:



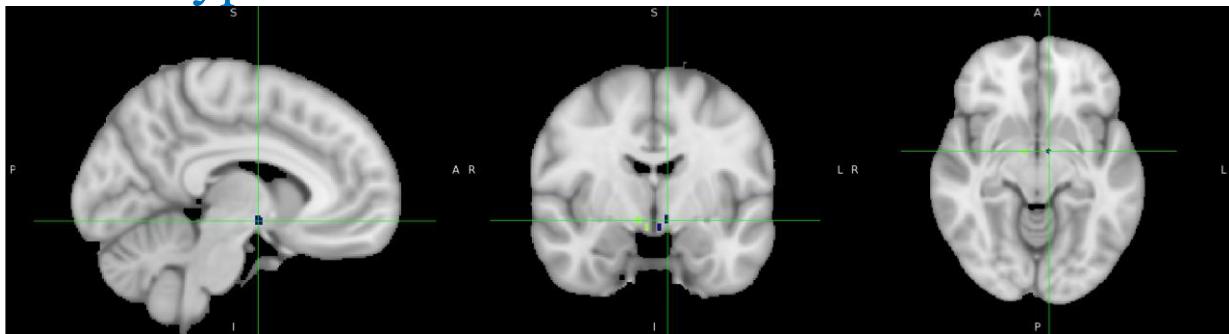
6- Globus Pallidus:



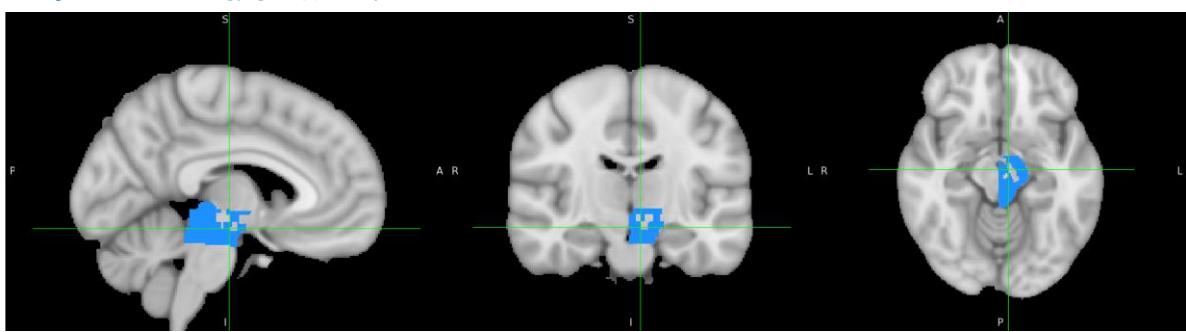
7- Hippocampus:



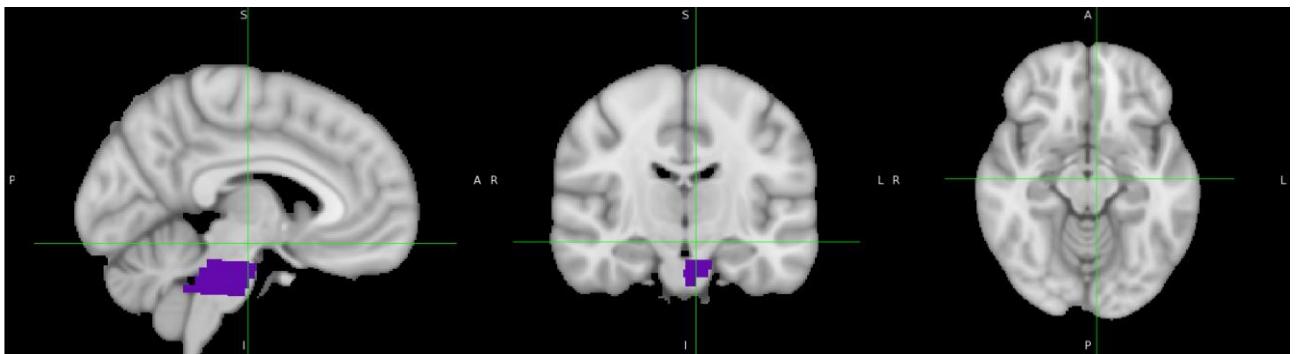
8- Hypothalamus:



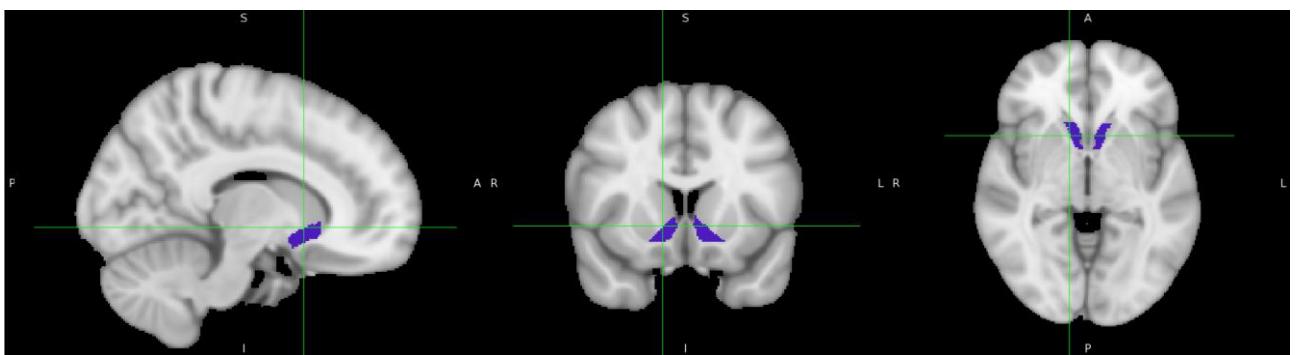
9- Midbrain:



10- Pons:



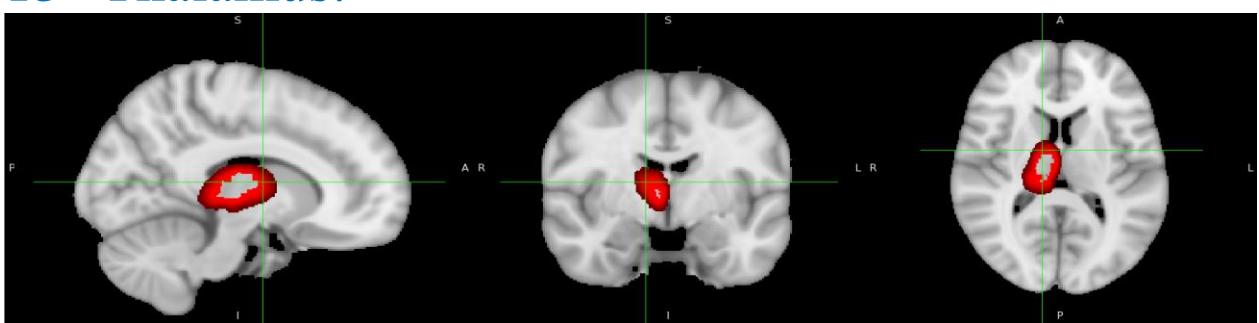
11- Striatum:



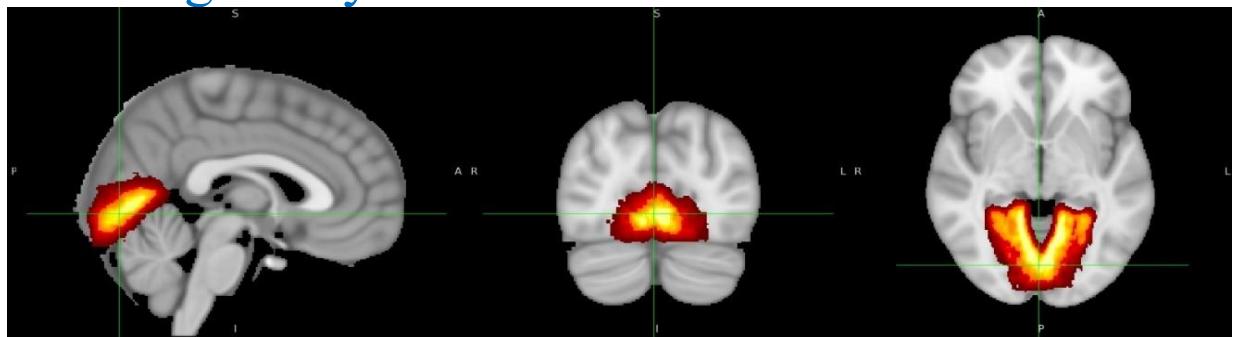
12- Putamen:



13- Thalamus:

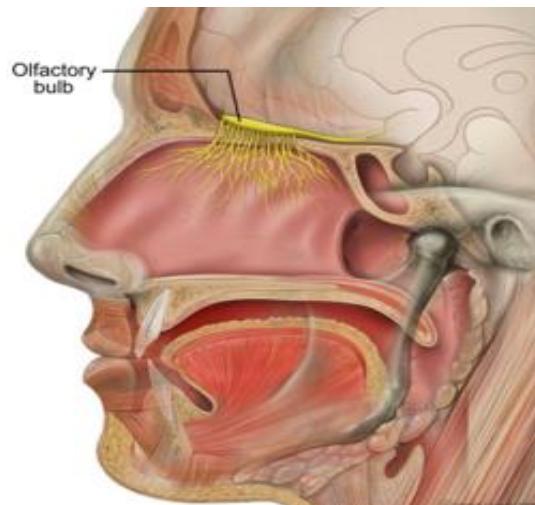


14- Lingual Gyrus:

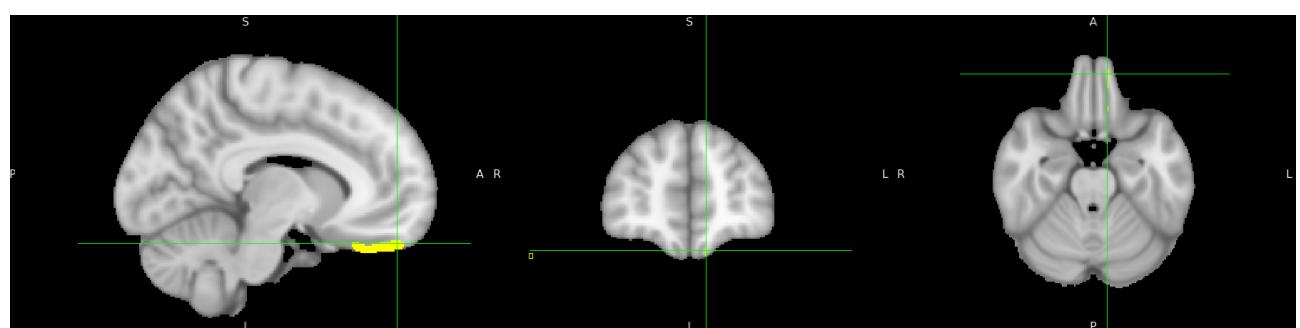


15- Olfactory bulb:

I didn't see it in any atlas so I search for the location in google and get this image



So by Edit mode in FSL I select ROI and draw the location in the MNI standard space:



3. Preprocessing:

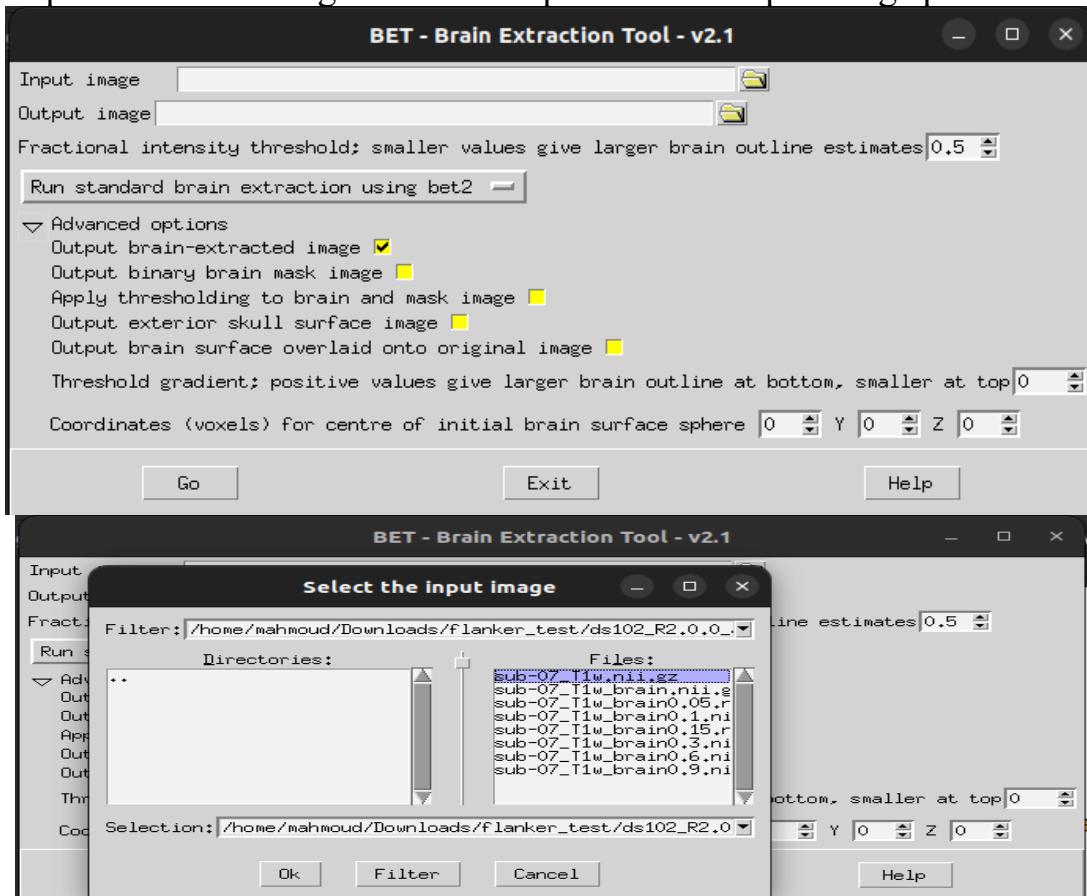
3.1 Skull Extraction with BET:

- Employed Brain Extraction Tool (BET) within FSL to execute precise skull extraction procedures.
- Applied sophisticated threshold algorithms to delineate brain structures accurately.
- Methodically compared multiple threshold settings against original structural images to optimize extraction efficacy.
- Ensured the integrity of brain extraction through meticulous comparison of masked images, effectively mitigating any instances of brain fragmentation or loss.

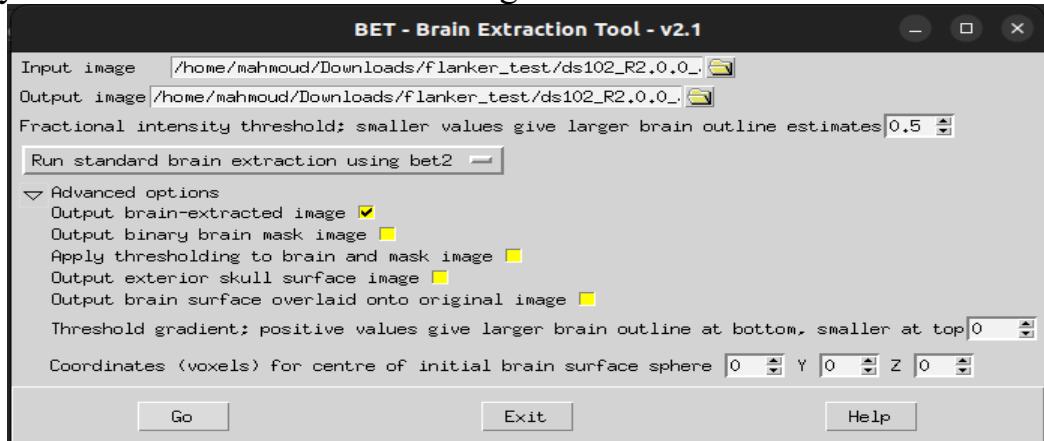
3.1.1 Steps to apply the threshold on the images:

1) open fsl and choose BET brain extraction.

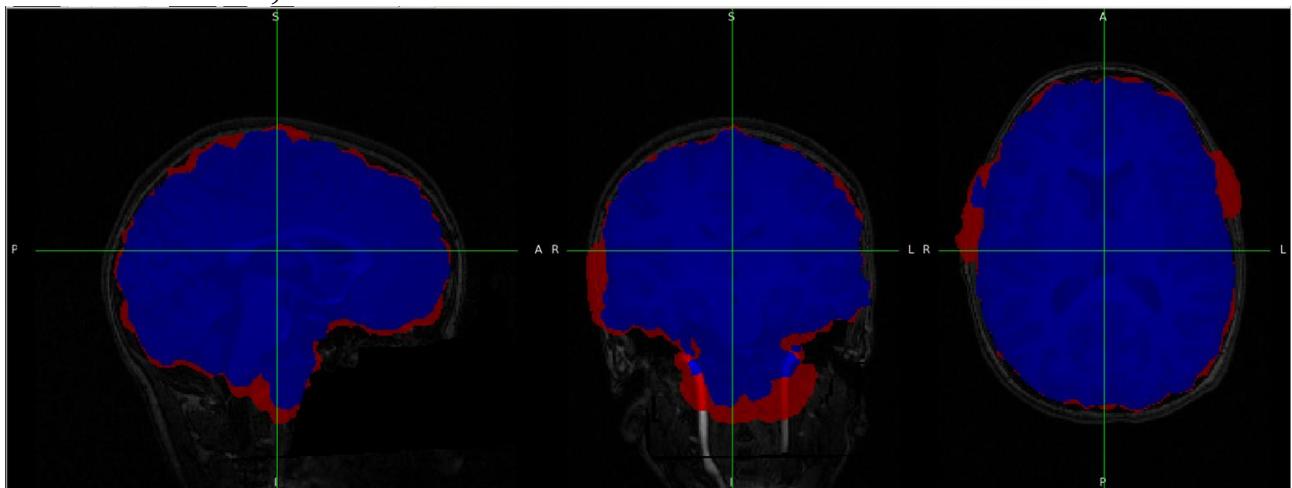
2) after open the BET dialog choose the input and the output image path.



3) Apply the suitable threshold and click go:



Sub1 comparison between the original structural image, threshold = 0.1 “in red”, and threshold = 0.5 “in blue”

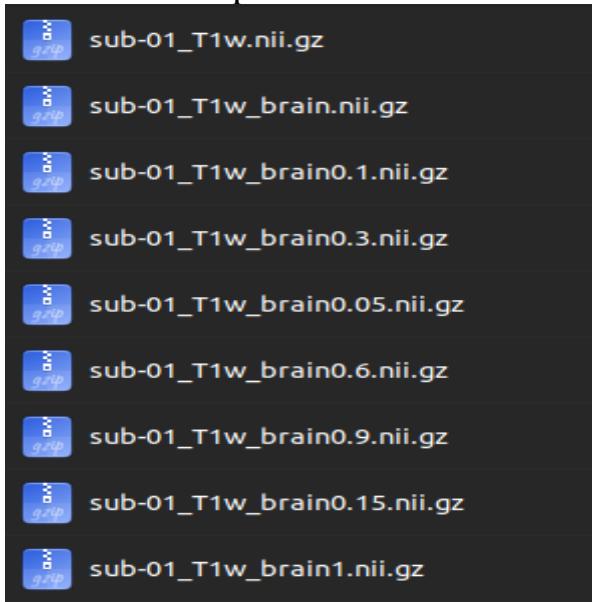


3.1.2 Bash script to automate the operation:

I applied many threshold value for all the subjects and almost compare all the value with each other and choose the best one and put it in the excel sheet of pre-processing

```
1 #!/bin/bash
2
3 # Define the base path and variables
4 base_path="/home/mahmoud/Downloads/flanker_test/ds102_R2.0.0_all_data/ds102_R2.0.0"
5 prefix="sub-"
6 suffix="_T1w"
7 brain_suffix="_T1w_brain0.1"
8 f_value=0.1
9
10 # Loop through subjects from 1 to 26
11 for ((i=1; i<=26; i++))
12 do
13     subject=$(printf "%02d" $i) # Zero-padding for subject number
14     input_file="$base_path/${prefix}${subject}/anat/${prefix}${subject}${suffix}"
15     output_file="$base_path/${prefix}${subject}/anat/${prefix}${subject}${brain_suffix}"
16
17     # Execute the command with current variables
18     /home/mahmoud/fsl/bin/bet "$input_file" "$output_file" -f "$f_value" -g 0
19 done
```

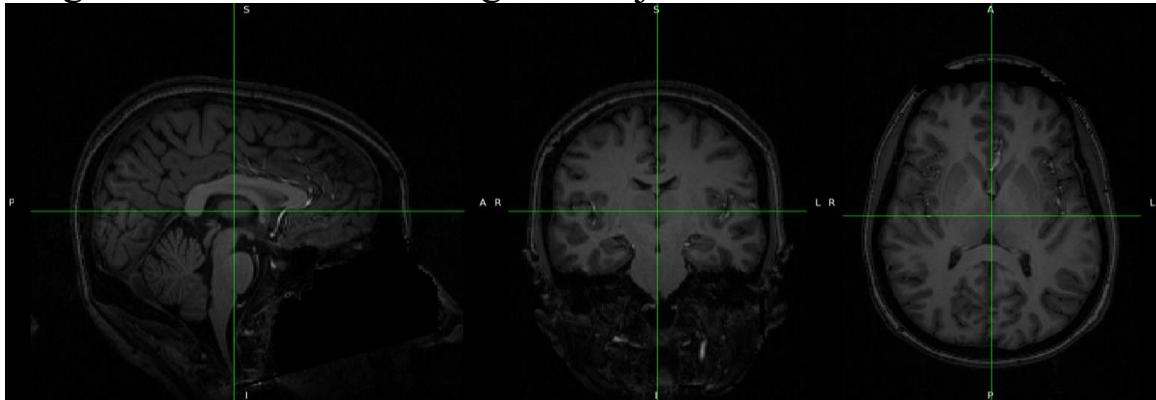
the threshold values I tried and compared:



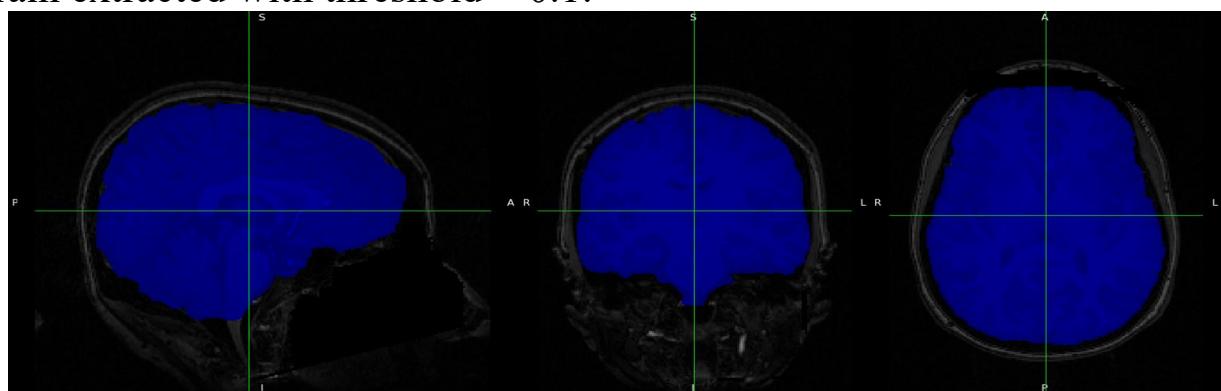
3.1.3 Exercises

- 1) Change the fractional intensity threshold to 0.1 and rerun BET, making sure to choose an appropriate output name to keep your files organized. View the result in FSLeyes. Repeat these steps with a fractional intensity threshold of 0.9. What do you notice? What seems to be a good threshold?

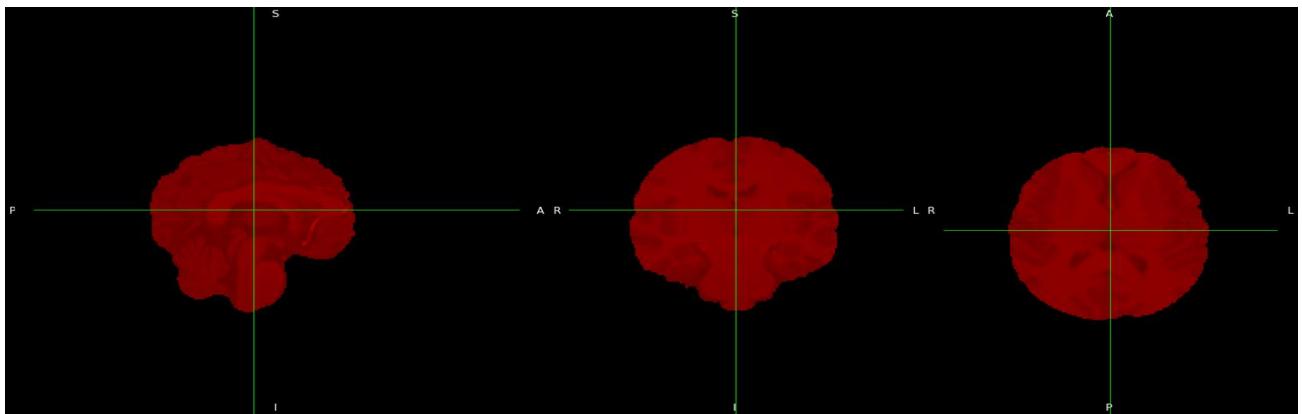
The original brain structure image of subject 7:



brain extracted with threshold = 0.1:



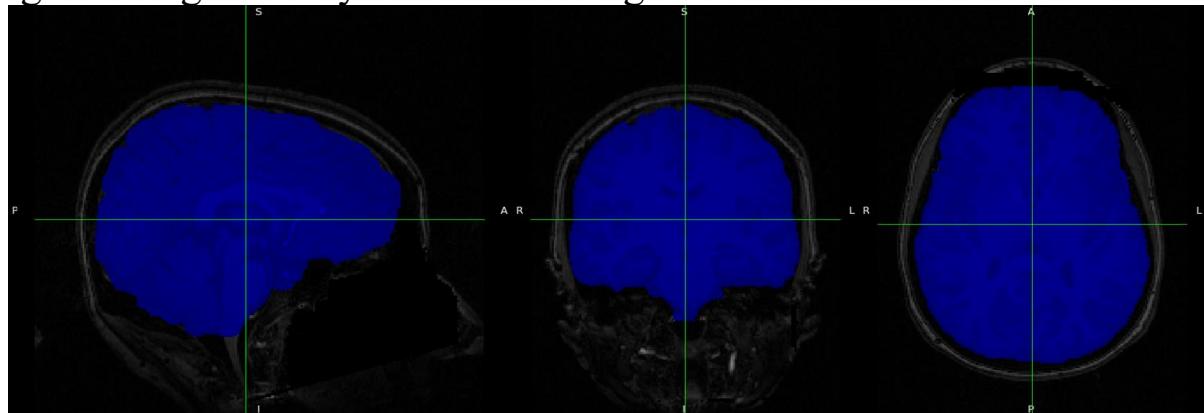
brain extracted with threshold = 0.9:



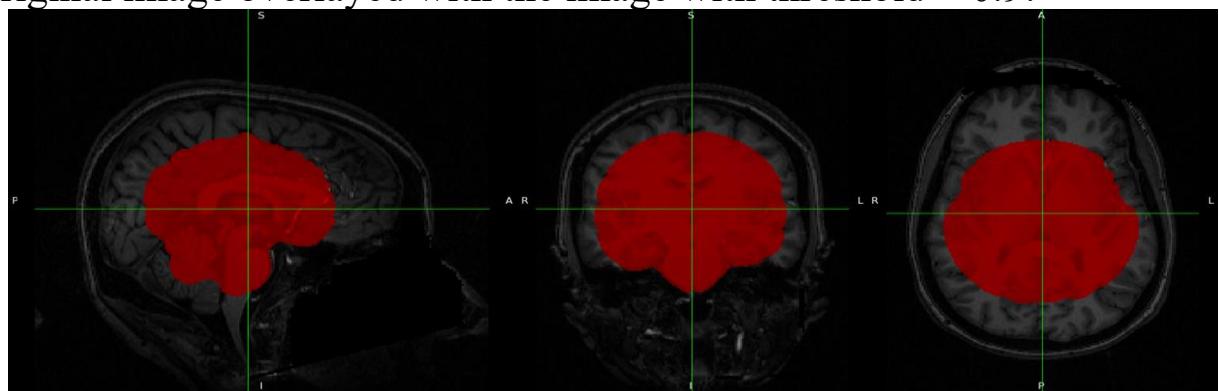
I notice that the low threshold make parts of skull to extracted with the brain, but in high threshold mask there is a lot of parts in the brain are removed which is very bad for our experiment.

2) Experiment with different contrast colors for the overlay image in FSLeys to see which one you like the best. Use the Zoom slider to focus on a region you think hasn't been stripped well. Take a photo of the montage

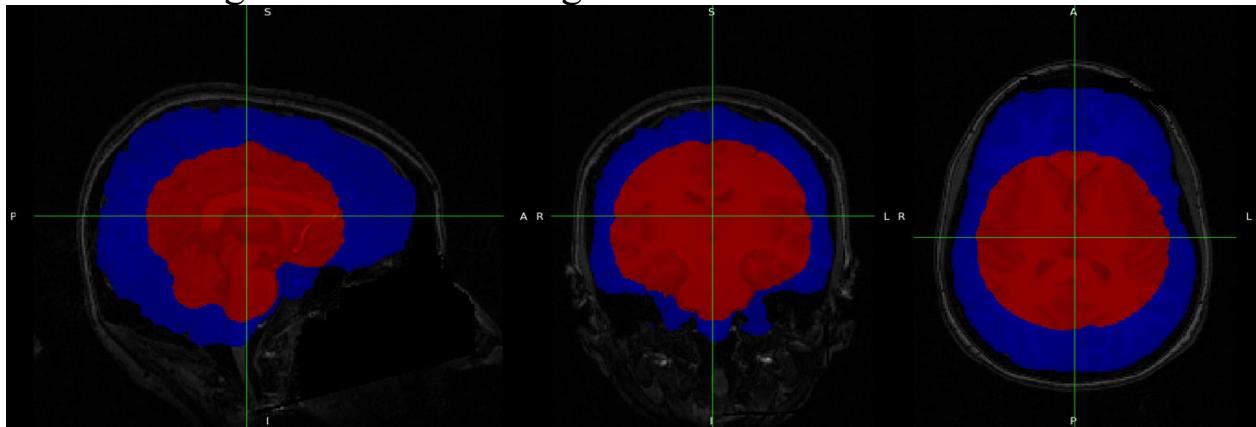
Original image overlayed with the image with threshold = 0.1:



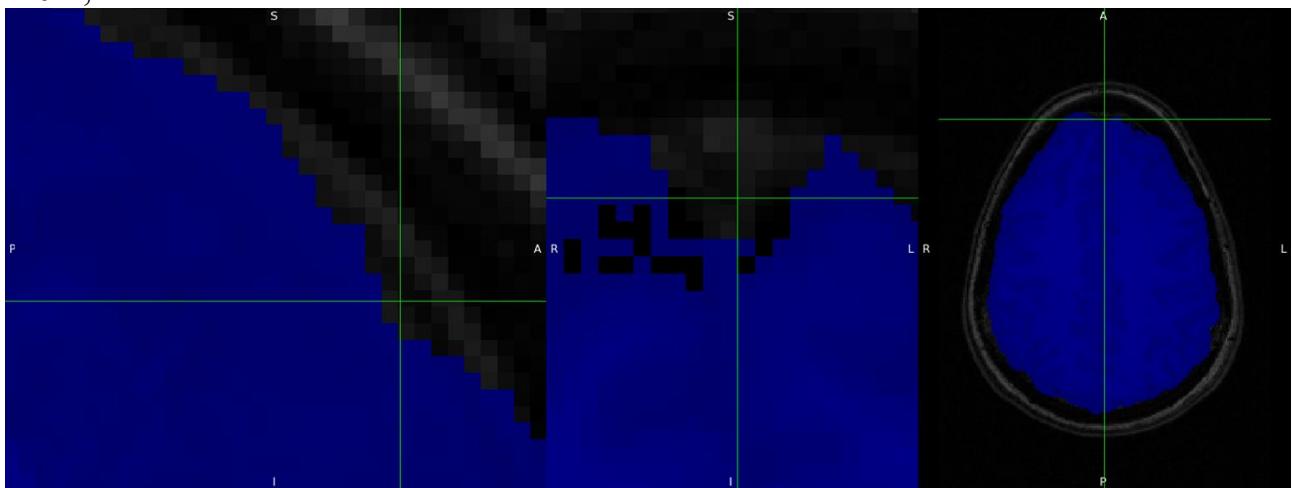
Original image overlayed with the image with threshold = 0.9:



The three images in the same image:



but there is also some regions in the brain are out of the mask in the case of threshold = 0.1, I will show on case for this:



3.2 FEAT fMRI Analysis:

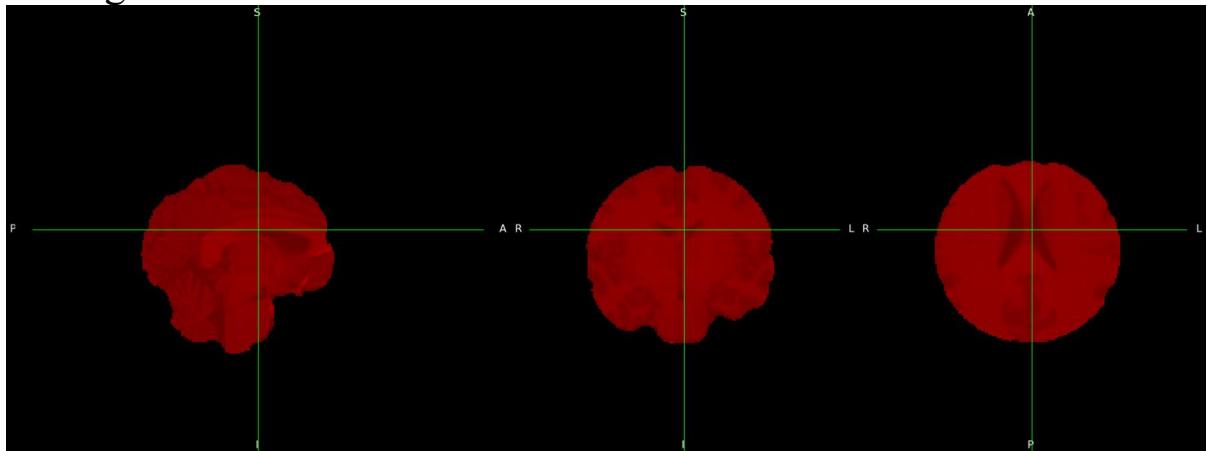
3.1 Introduction:

- Seamlessly integrated FEAT fMRI analysis for robust normalization and registration processes.
- Facilitated seamless alignment of T1 images with functional MRI data by leveraging standard templates.
- Capitalized on the versatility of FSL's standard templates, specifically MNI152_T1_2mm_brain and MNI152_T1_1mm_brain, to discern nuanced differences in registration outcomes and optimize analysis accuracy.

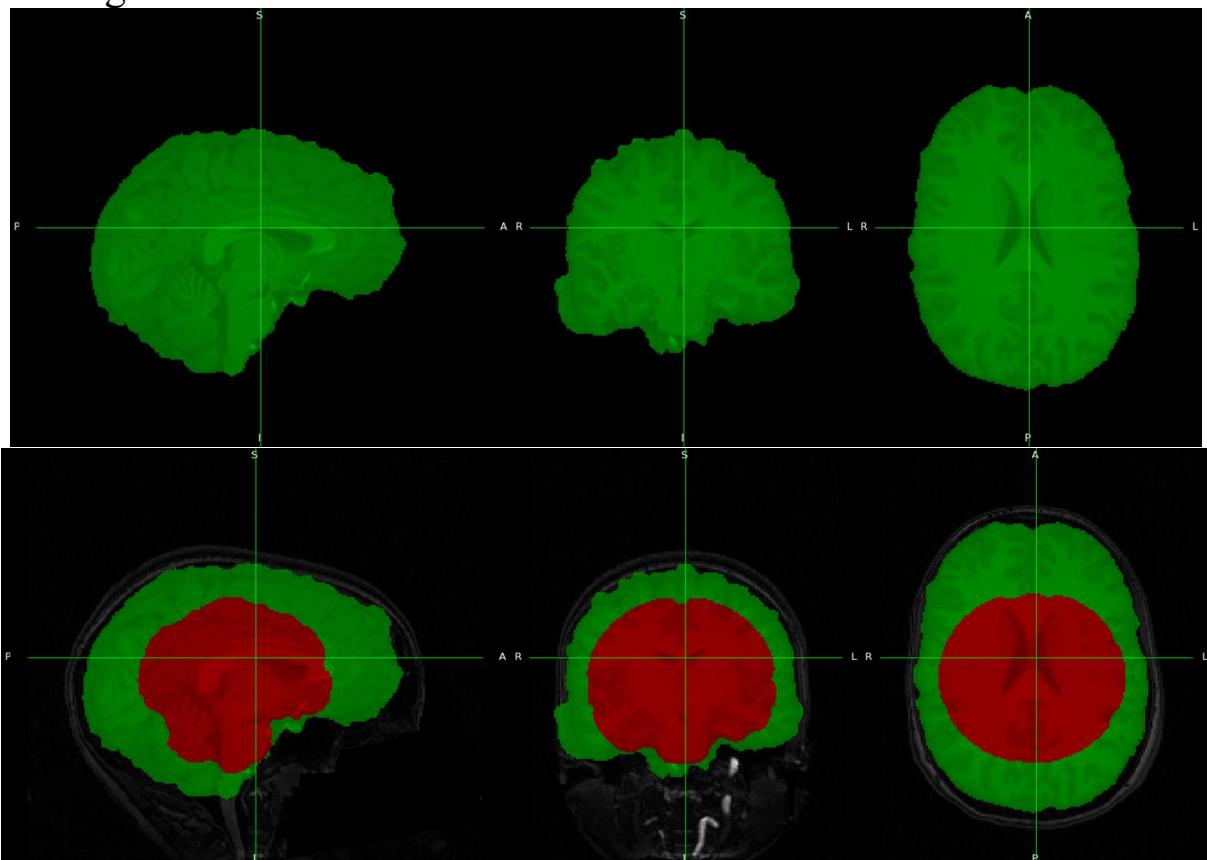
3.2 Exercises

- 1) Run BET on the anatomical image sub-08_T1w.nii.gz with two separate fractional intensity thresholds: 0.1 and 0.9. Take a snapshot of each output image with FSLeyes using the camera button. Note the differences between the two. Is the output what you expected? If you had to use one image or the other, which one would you choose?

The image with threshold = 0.9:



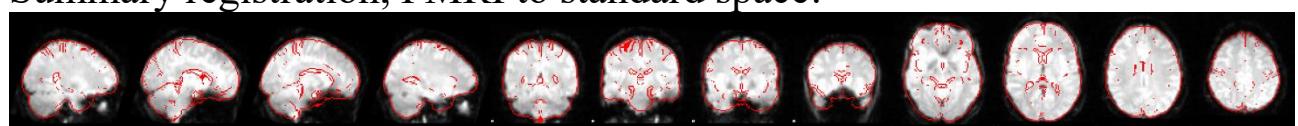
The image with threshold = 0.1:



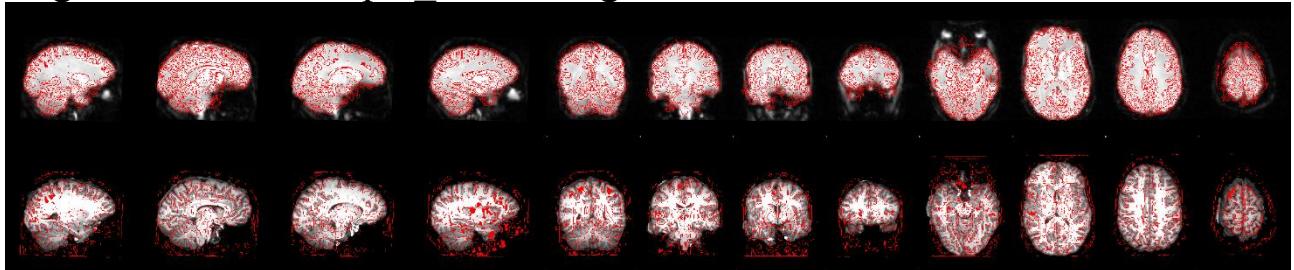
2) Preprocess run 2 of the functional data using the FEAT GUI. To do this, select sub-08_task-flanker_run2.nii.gz from the func directory, change the output directory to run2, and make sure Preprocessing is selected from the dropdown menu. Keep the other settings the same as when you analyzed run 1. Do the same quality checks that you did for run 1.

Run1:

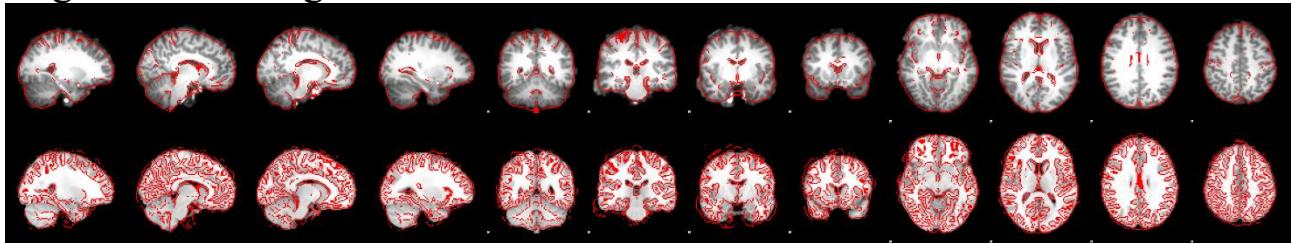
Summary registration, FMRI to standard space:



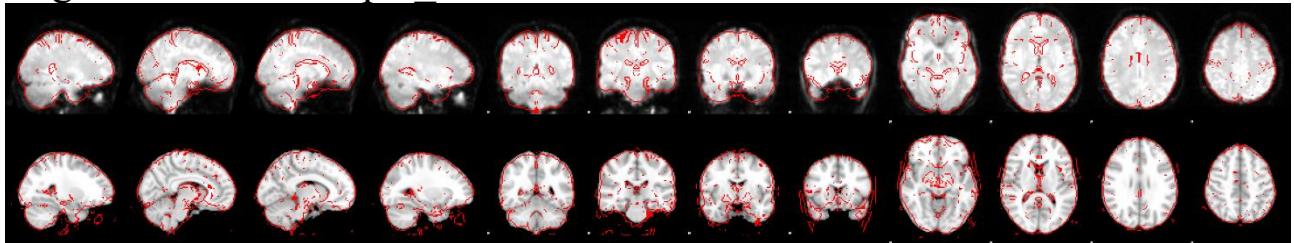
Registration of example_func to highres:



Registration of highres to standard:

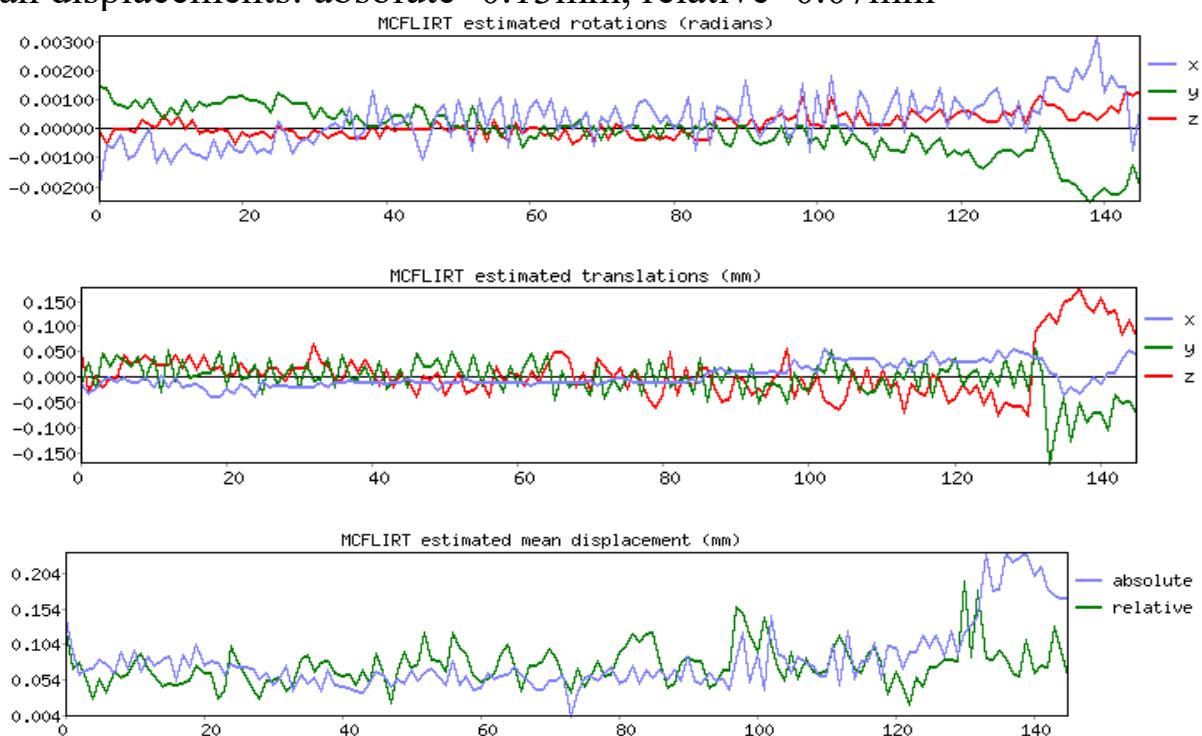


Registration of example_func to standard:



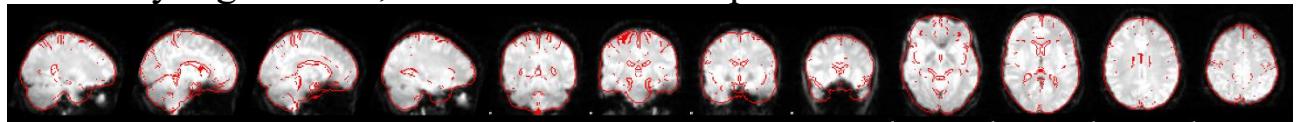
MCFLIRT Motion correction:

Mean displacements: absolute=0.13mm, relative=0.07mm

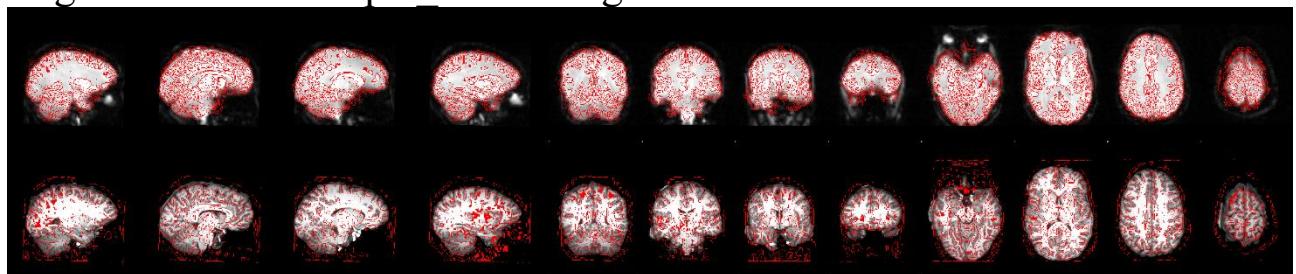


Run2:

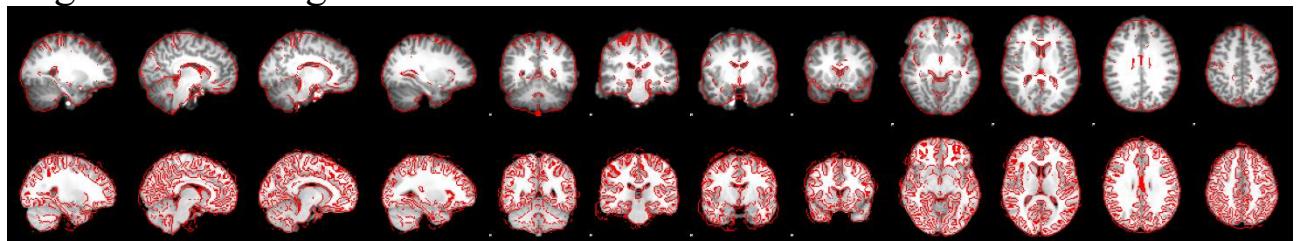
Summary registration, FMRI to standard space:



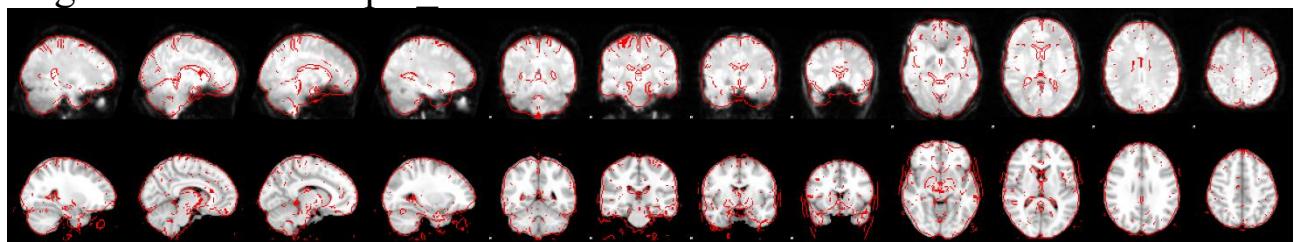
Registration of example func to highres:



Registration of highres to standard:

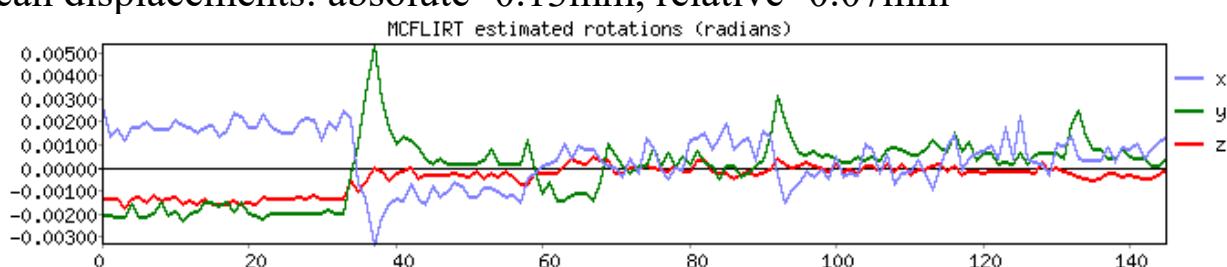


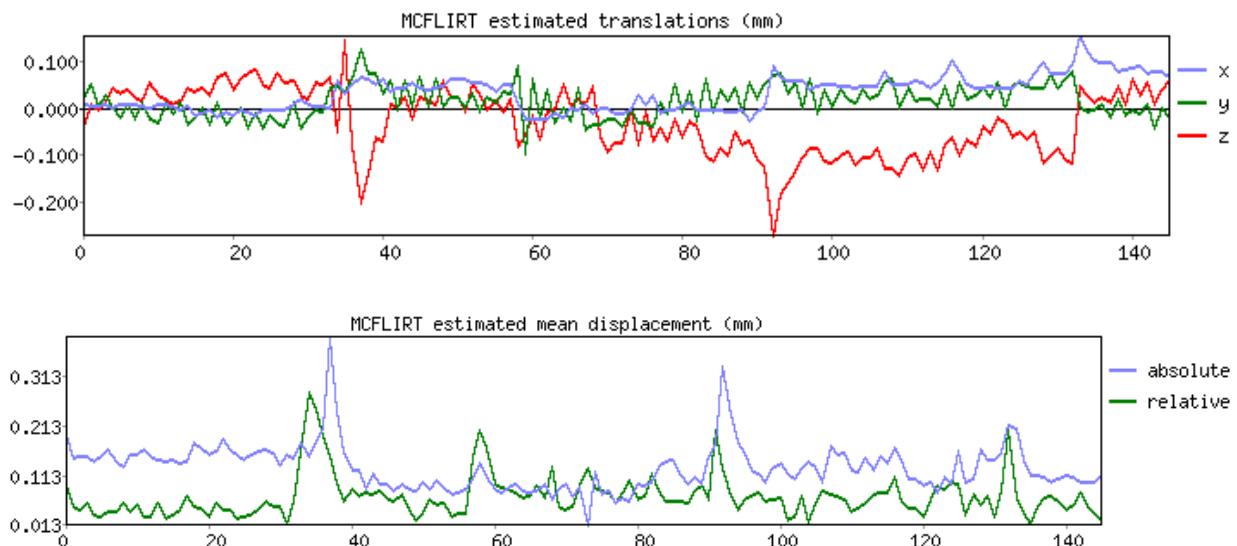
Registration of example func to standard:



MCFLIRT Motion correction

Mean displacements: absolute=0.13mm, relative=0.07mm





3) Preprocess run 1 using a 3mm smoothing kernel, keeping the other preprocessing options the same. Before you look at the output, run another analysis with a 12mm smoothing kernel. Think about what you would expect the preprocessed functional data to look like, and then load the filtered_func_data.nii.gz images from each analysis into FSLeyes. How do they compare to your predictions?

3mm Smoothing Kernel:

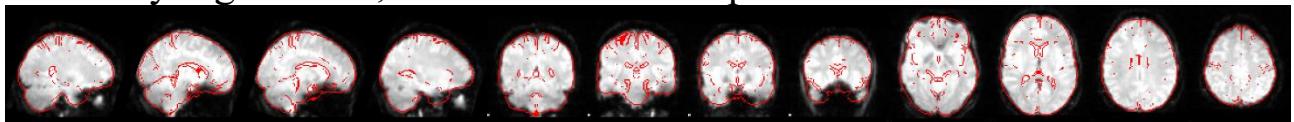
- With a 3mm smoothing kernel, I would expect to see moderate blurring of the functional images compared to the original data.
- The activation patterns might appear more diffuse and less sharp due to the smoothing process.
- Signal-to-noise ratio could potentially improve slightly as noise is reduced through spatial averaging.
- Fine-scale details in the activation maps may become less pronounced.

12mm Smoothing Kernel:

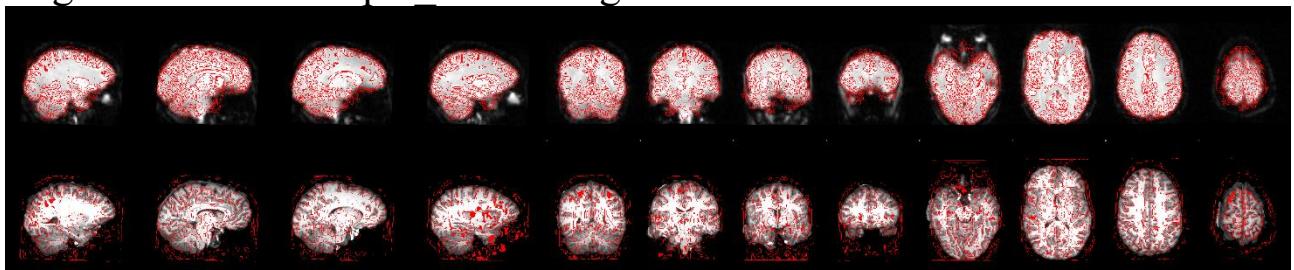
- Using a larger 12mm smoothing kernel, I anticipate more pronounced blurring compared to the 3mm kernel.
- Activation patterns are likely to appear even more diffuse and smoothed out.
- The signal-to-noise ratio might further improve as more spatial averaging is applied.
- Fine details and small-scale activations could be significantly attenuated or obscured by the stronger smoothing.

Run1 with kernel = 3mm:

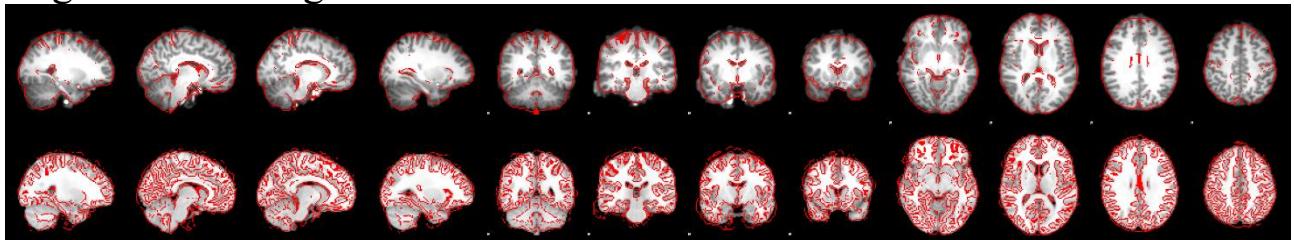
Summary registration, FMRI to standard space:



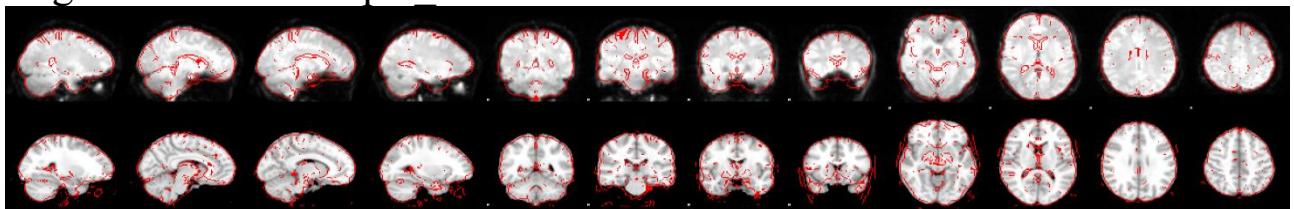
Registration of example func to highres:



Registration of highres to standard:

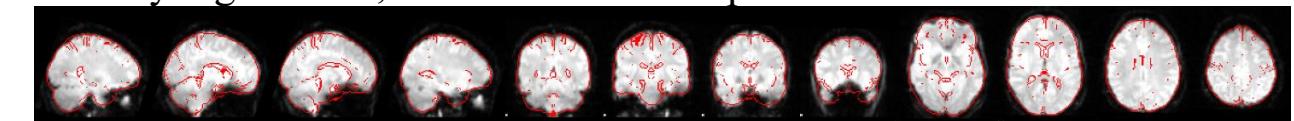


Registration of example func to standard:

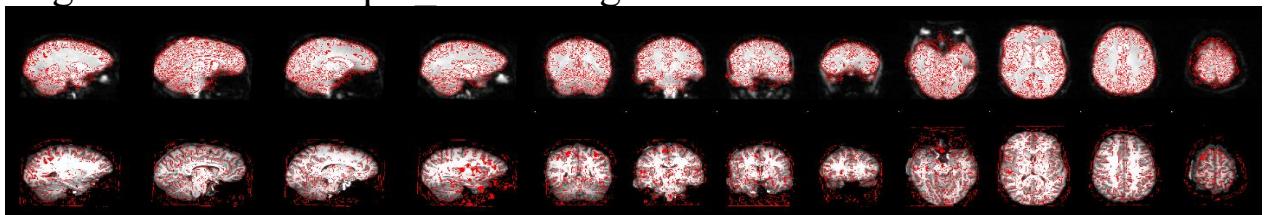


Run1 with kernel = 12mm:

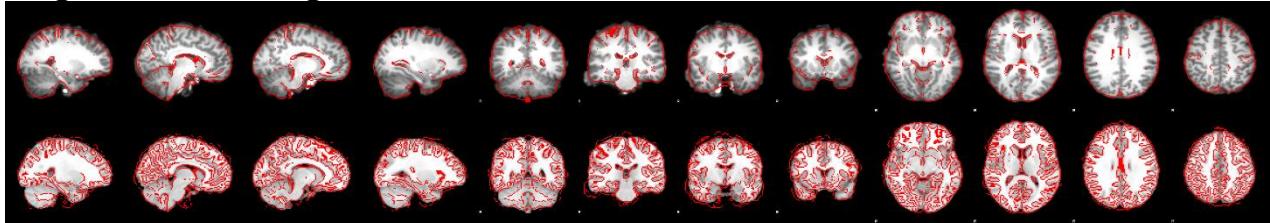
Summary registration, FMRI to standard space:



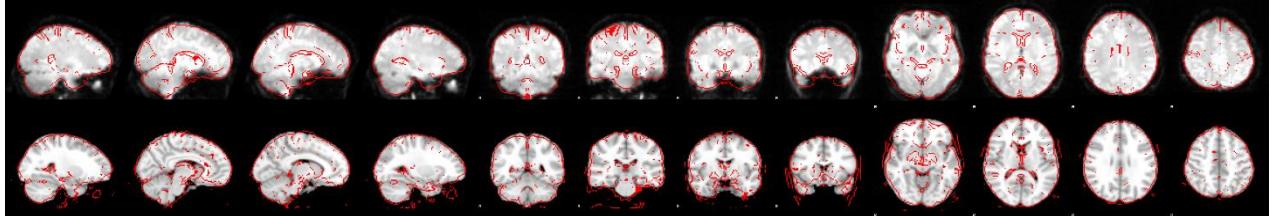
Registration of example func to highres:



Registration of highres to standard:

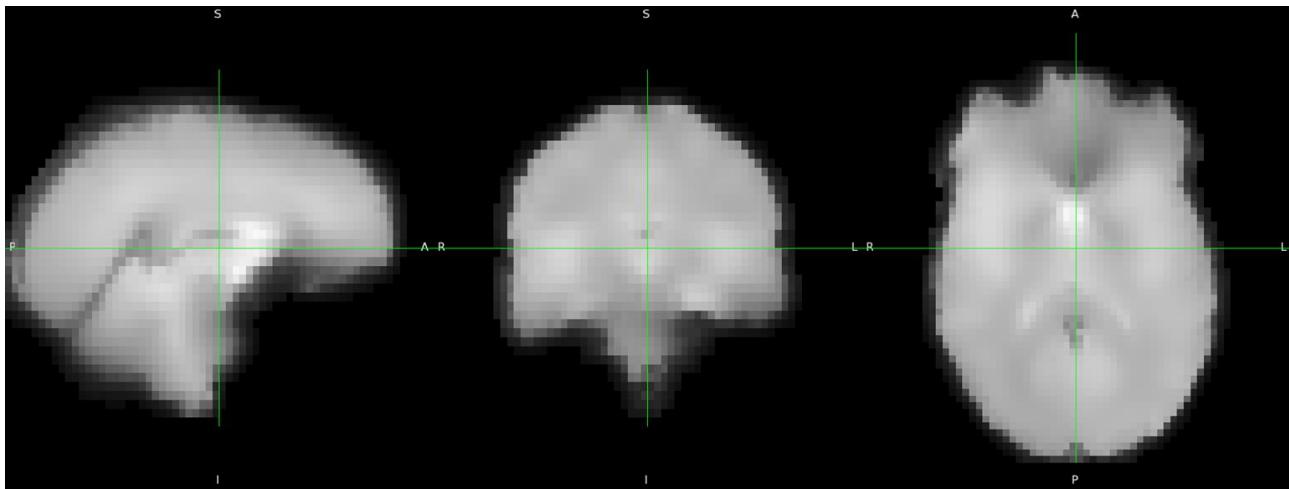


Registration of example func to standard:

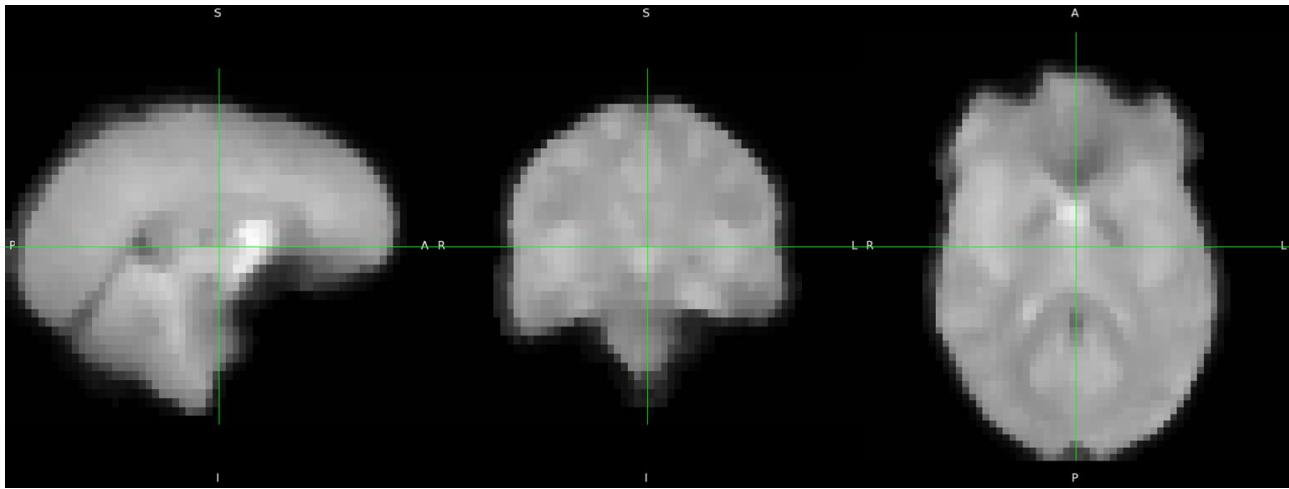


by add the filtered images in the FSLeyes:

kernel = 12mm:



Kernel = 3mm:

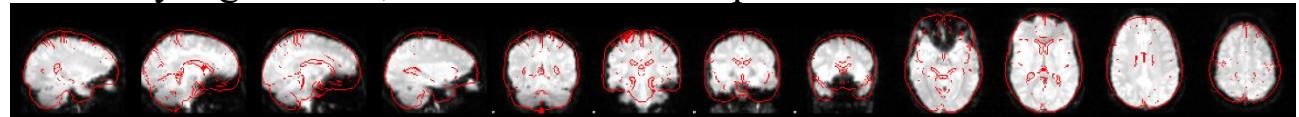


The results aligned with my predictions very accurately.

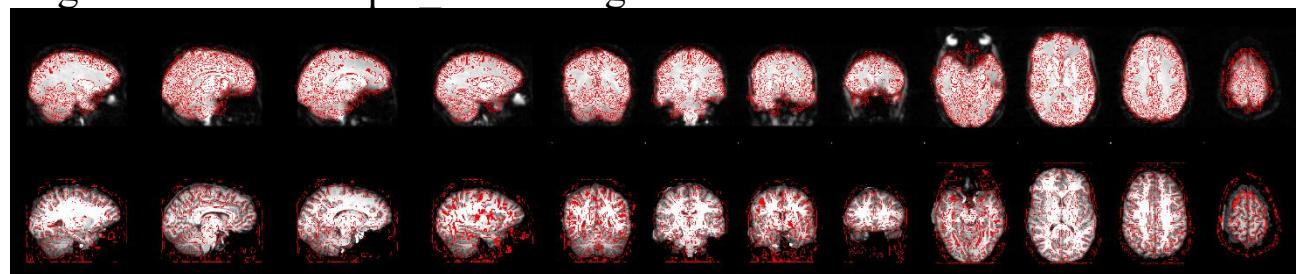
4. Preprocess run 1 using 3DOF for registration and normalization. How is the output different from what you saw when you ran the preprocessing with 12DOF? Why?

Run1 with 3DOF:

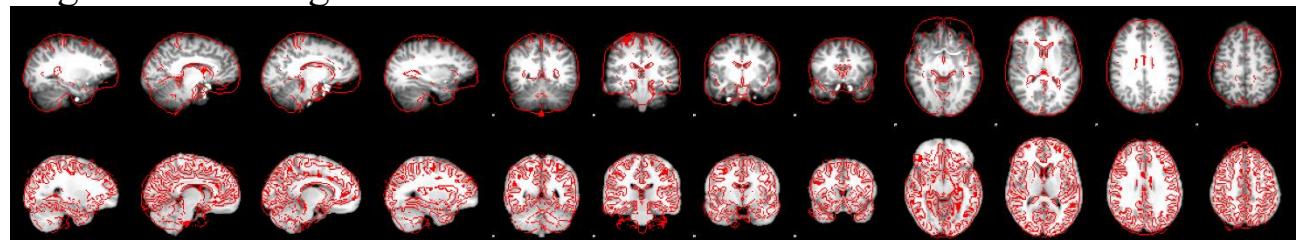
Summary registration, FMRI to standard space:



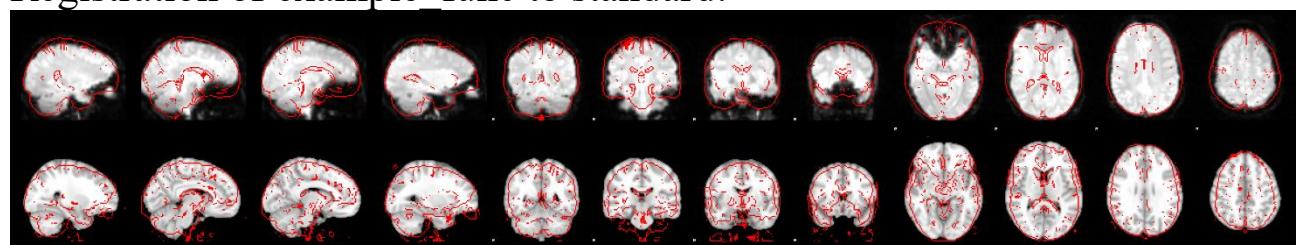
Registration of example func to highres:



Registration of highres to standard:



Registration of example func to standard:



Registration Precision:

3DOF: Limited to translation and rotation (x, y, z) only; no scaling or deformation considered.

12DOF: Offers flexibility with scaling and deformation alongside translation and rotation, potentially leading to a more precise alignment.

Normalization Accuracy:

3DOF: May result in less accurate normalization due to neglect of scaling and deformation, causing residual distortions, especially in complex anatomical regions.

12DOF: Provides better normalization accuracy by accounting for complex anatomical variability through additional degrees of freedom, enhancing alignment to standard templates.

Effects on Statistical Analyses:

3DOF: Potential for introducing biases or inaccuracies in spatial normalization, impacting statistical analyses such as group-level comparisons or region-of-interest analyses.

12DOF: Facilitates a more accurate alignment of functional data, leading to more reliable and reproducible statistical outcomes in subsequent analyses.

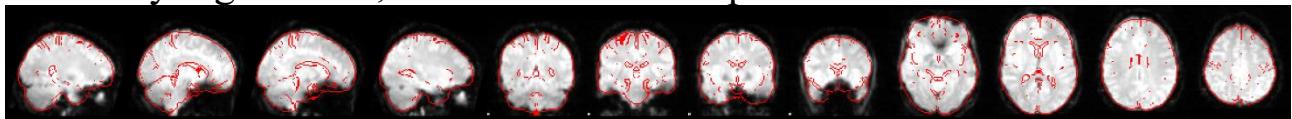
5) Rerun registration for run 1 using BBR instead of 12DOF. What difference does it make? How would you make a case to someone that you should use one instead of the other?

BBR, or Boundary-Based Registration, zooms in on the boundary between gray and white matter during registration. This targeted approach often results in more accurate alignment, especially in tricky areas.

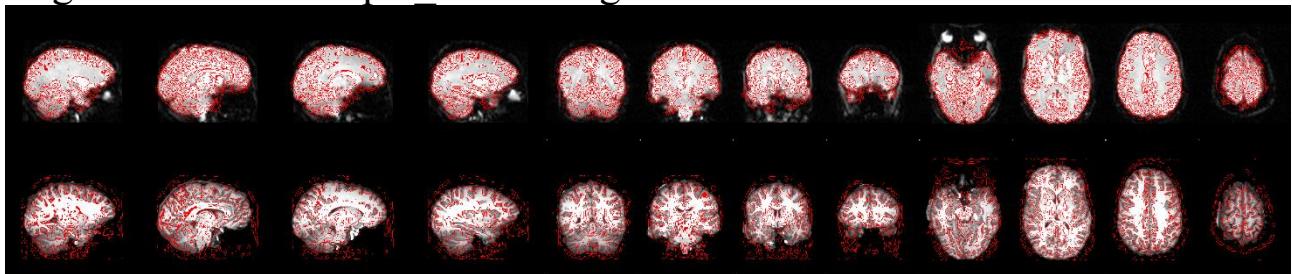
If anyone ask me I will recommend the 12DOF if the time of the experiment is important because the BBR take a very long time, but according to the quality the BBR results is more accurate and have more details

BBR:

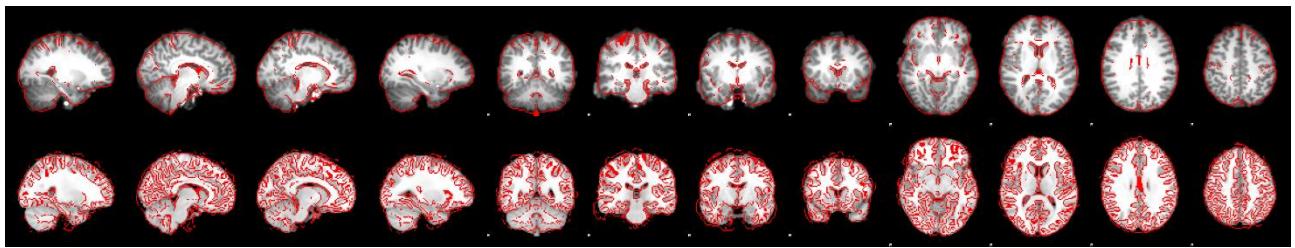
Summary registration, FMRI to standard space:



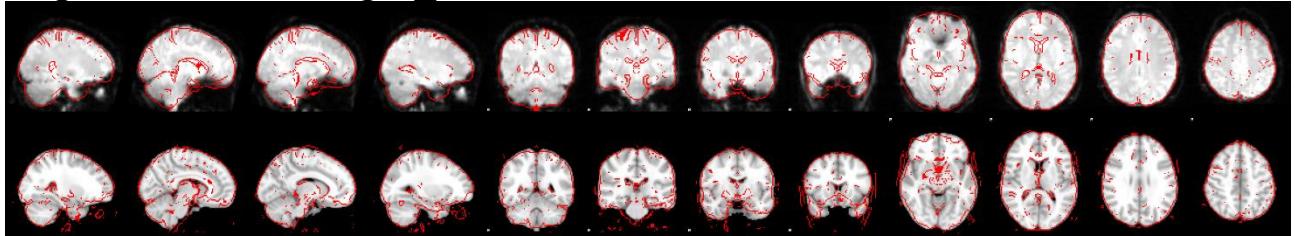
Registration of example func to highres:



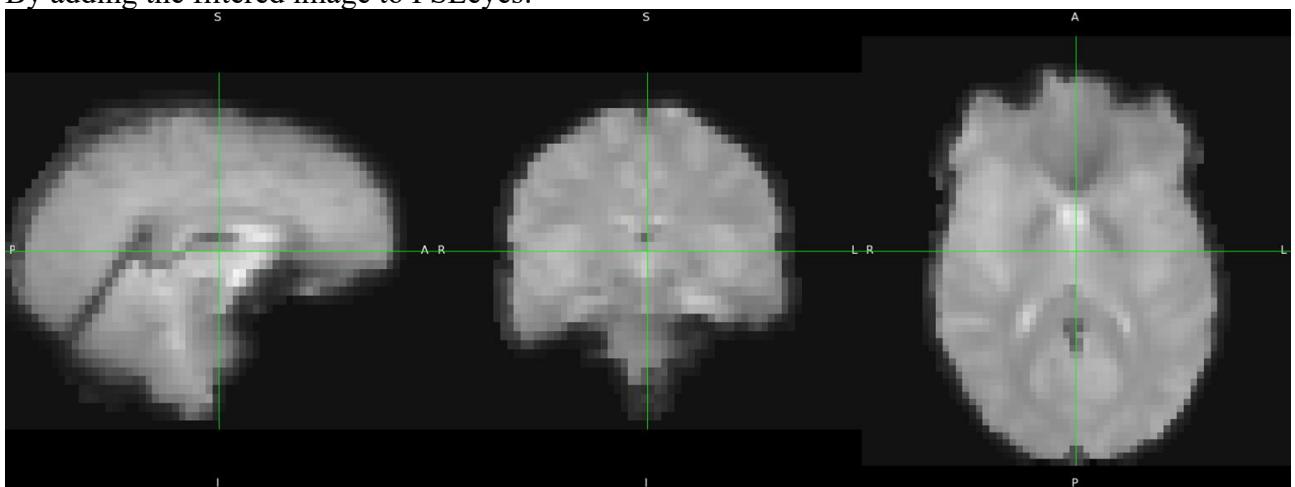
Registration of highres to standard:



Registration of example_func to standard:

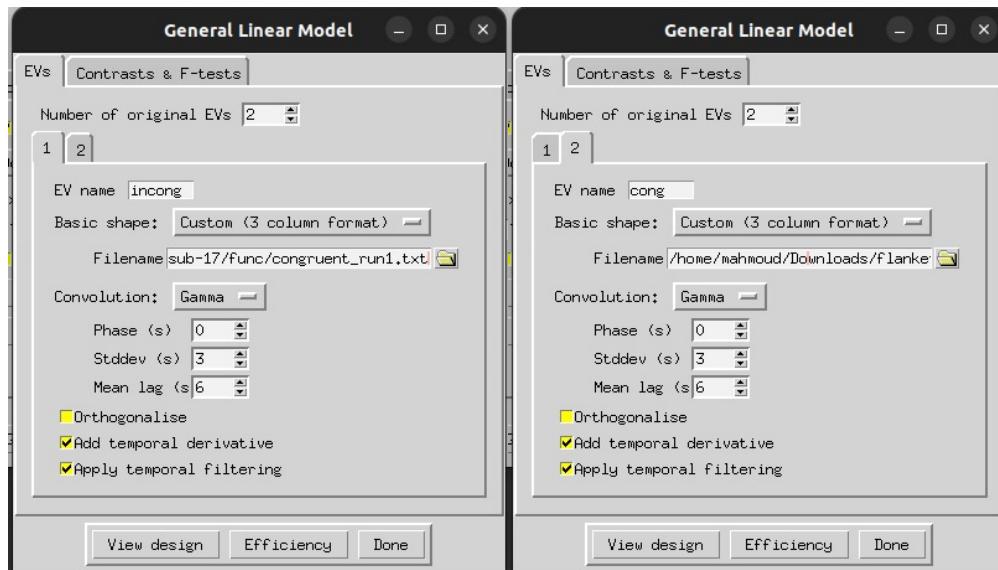


By adding the filtered image to FSLeyes:

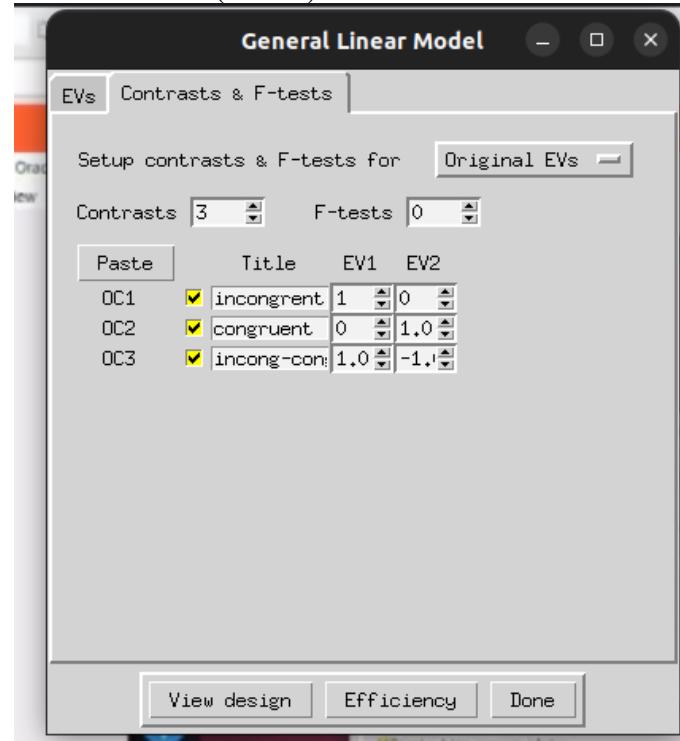


4. Statistics:

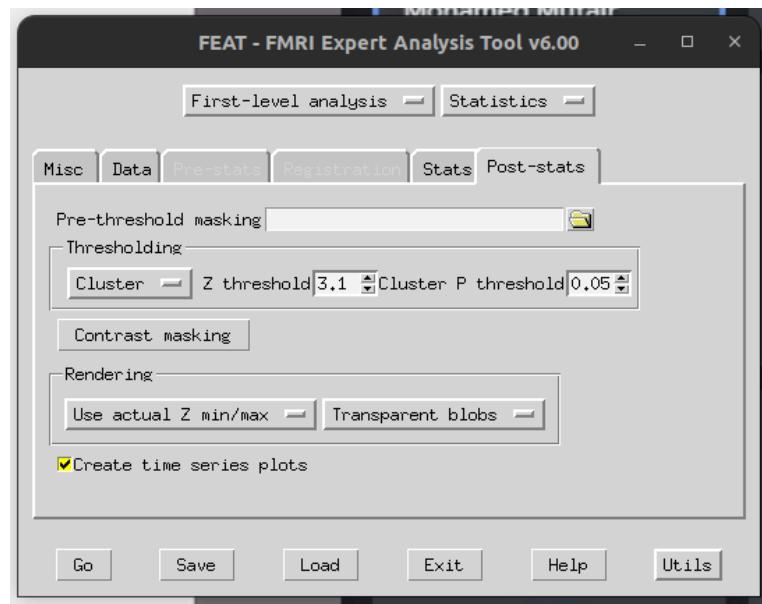
In flanker data set we have 2 events(regressors) that we need to get the parameters estimate for them by using FSL and FEAT analysis on sub17 that I already do the pre processing analysis on it. The choice of sub17 because the subject head is has a different shape compared to other subject and motion artifacts is very high. by setting the settings as :



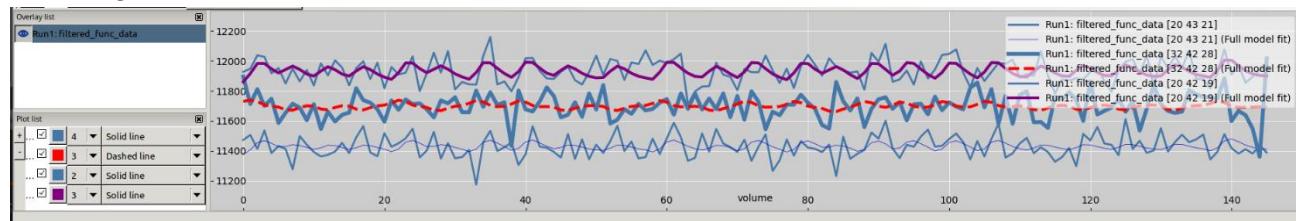
And the contrast of parameter estimate (COPE) is



And set the z-threshold value by 3.1 to see which voxel is related to the task by neglect any voxel has the threshold value less than 3.1:

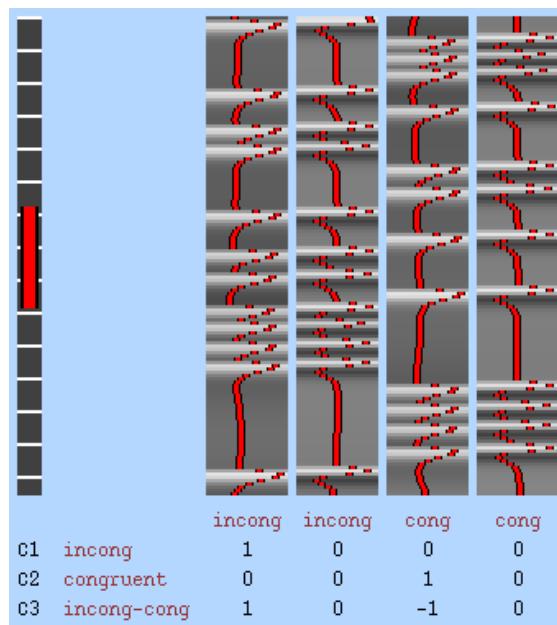


Time series of sub 17 after and before preprocessing analysis and before statistics analysis for a random 3 voxels:



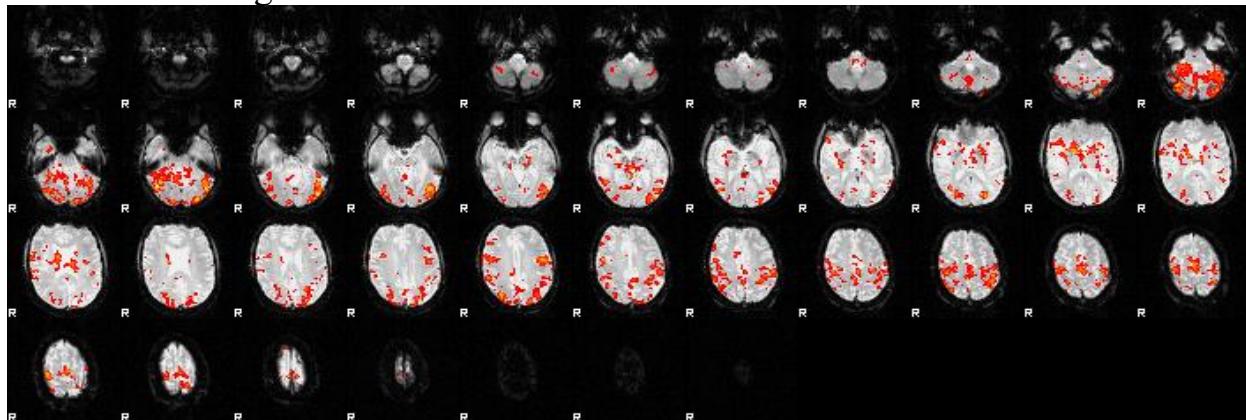
The result of the analysis:

- Design matrices run1:



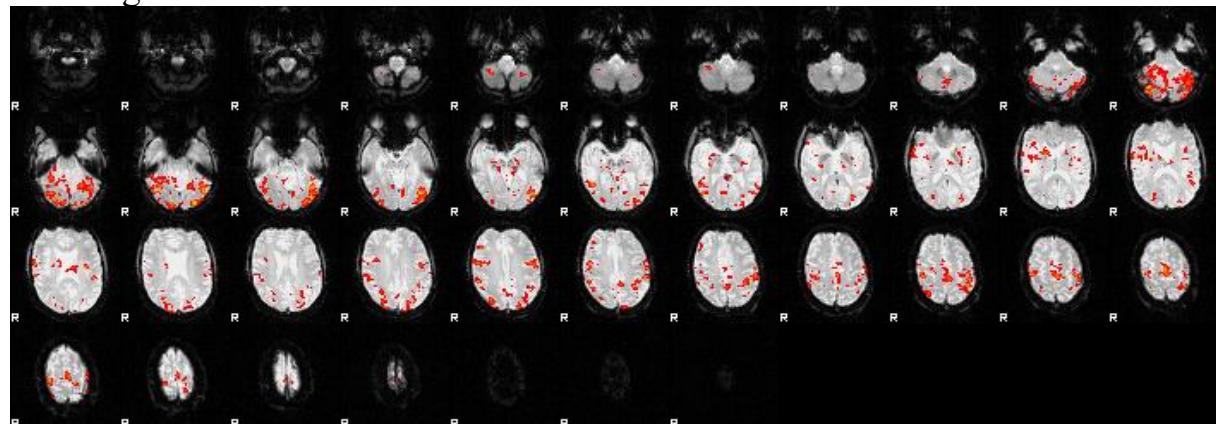
- Rendered threshold zstat1 run1:

Is for incongruent task we can notice that the voxels works is more than the voxels in congruent task



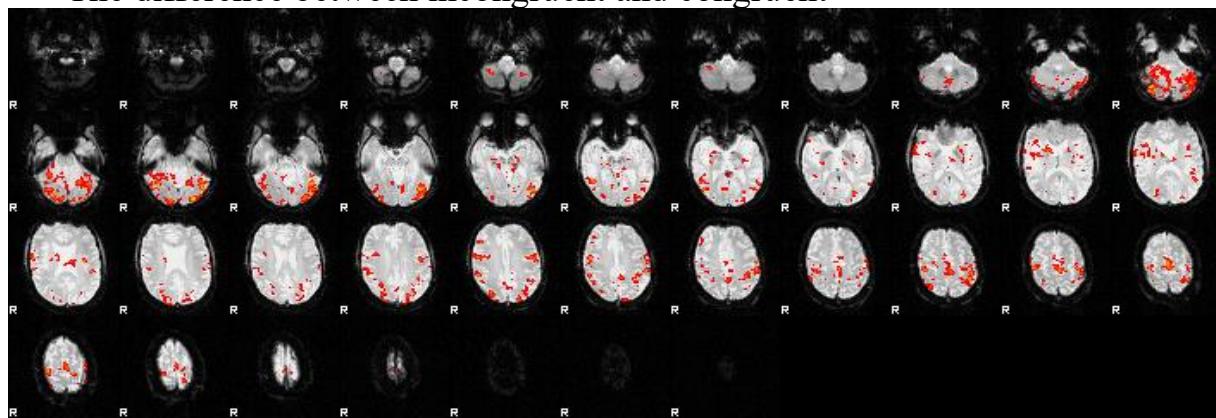
- Rendered threshold zstat2 run1:

Is for congruent task and we can notice the intensity of the voxels related to the congruent



- Rendered threshold zstat3 run1:

The difference between incongruent and congruent



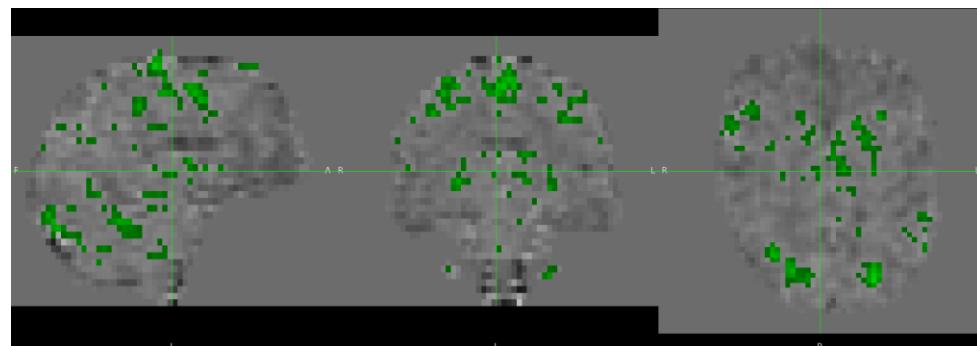
Results from FSL: PE and COPE of random voxel run1:

```
cope3  
[32 31 19]: 39.0511360168457  
cope2  
[32 31 19]: 236.3956756591797  
cope1  
[32 31 19]: 275.4468078613281  
pe2  
[32 31 19]: 57.9863395690918  
pe1  
[32 31 19]: 275.4468078613281
```

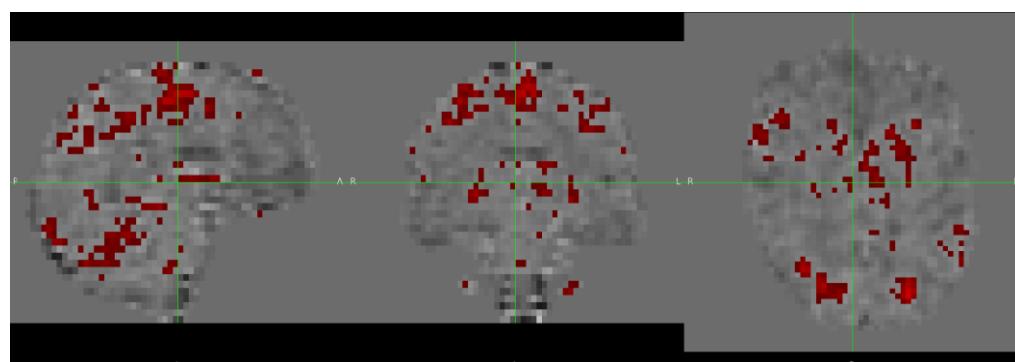
PE and COPE of random voxel run1:

```
cope3  
[31 31 19]: 85.59854888916016  
cope2  
[31 31 19]: 81.57654571533203  
cope1  
[31 31 19]: 167.1750946044922  
pe2  
[31 31 19]: 216.22080993652344  
pe1  
[31 31 19]: 167.1750946044922
```

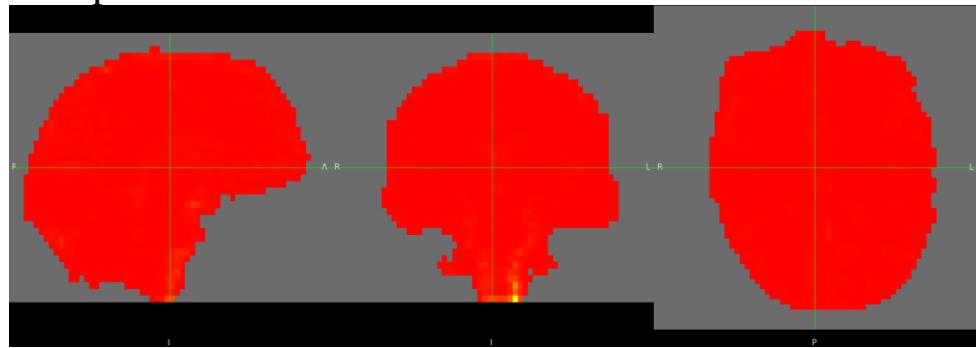
COPE1 with zstat1 in green for run1:



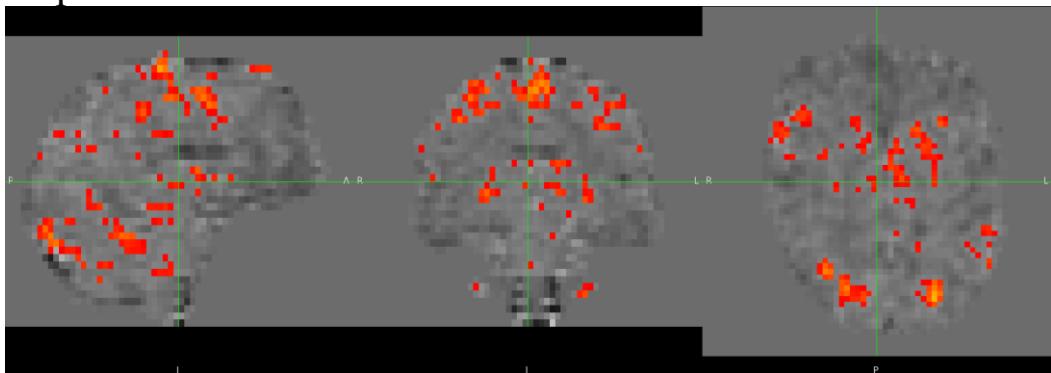
Pe1 with tstat1:



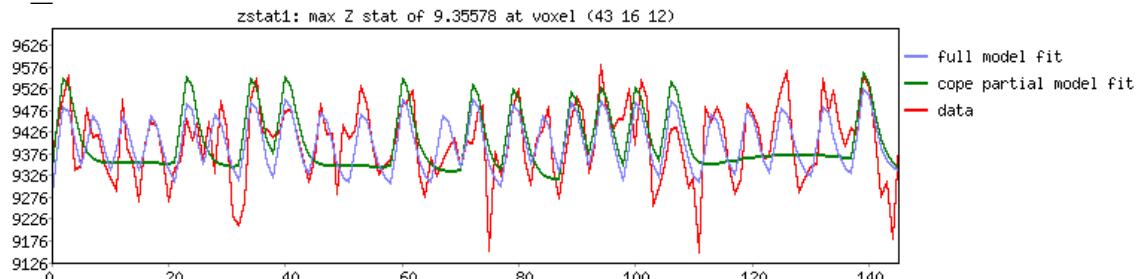
variance of cope1:



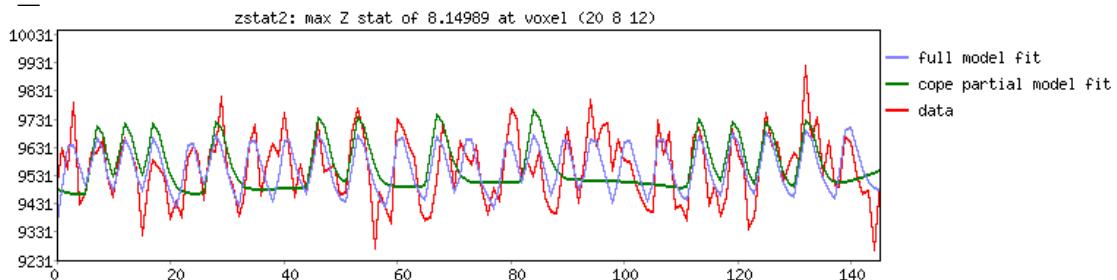
zstat1 for pe1 and threshold 3.1:



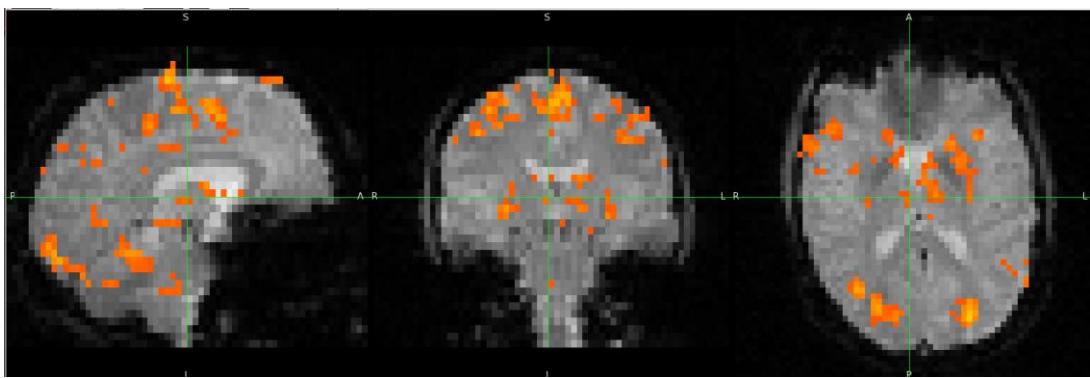
tsplot_zstat1:



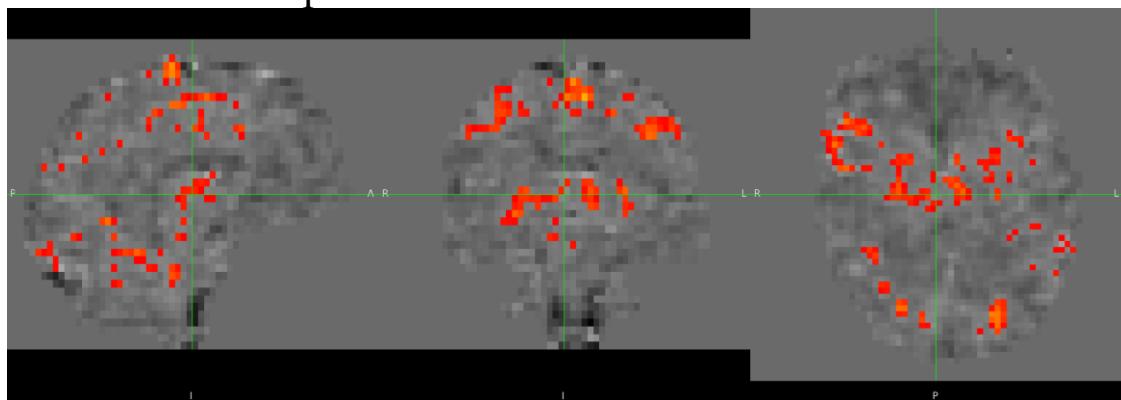
tsplot_zstat3:



examplefunction_threshold_zstat1 for run2:



Threshold zstat2 with pe12 for run 2:



5. Scripting for full level analysis

```
#!/bin/bash

# Generate the subject list to make modifying this script
# to run just a subset of subjects easier.

# Starting subject ID
start_id=1

for id in ${seq ${start_id} }; do
    subj="sub-${id}"
    echo "====> Starting processing of ${subj}"
    echo

    # Navigate to the subject directory
    cd "${subj}"

    # If the brain mask doesn't exist, create it
    if [ ! -f anat/${subj}_T1w_brain0.15.nii.gz ]; then
        echo "Skull-stripped brain not found, using bet with a fractional intensity
threshold of 0.15"
        # Note: This fractional intensity appears to work well for most of the subjects in
the
        # Flanker dataset. You may want to change it if you modify this script for your
own study.
        bet2 anat/${subj}_T1w.nii.gz
        anat/${subj}_T1w_brain0.15.nii.gz -f 0.15
    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 .

    # Note that we are using the | character to delimit the patterns
    # instead of the usual / character because there are / characters
    # in the pattern.
    sed -i "s|sub-01|${subj}|g" design_run1.fsf
    sed -i "s|sub-01|${subj}|g" design_run2.fsf

    # Create output directory for run1 and run2
    mkdir -p ${subj}_run1_FEAT
    mkdir -p ${subj}_run2_FEAT

    # Move to the output directories
    cd ${subj}_run1_FEAT

    # Now everything is set up to run feat for run1
    echo "====> Starting feat for run 1"
    feat ./design_run1.fsf

    # Move back to the subject directory
    cd ..

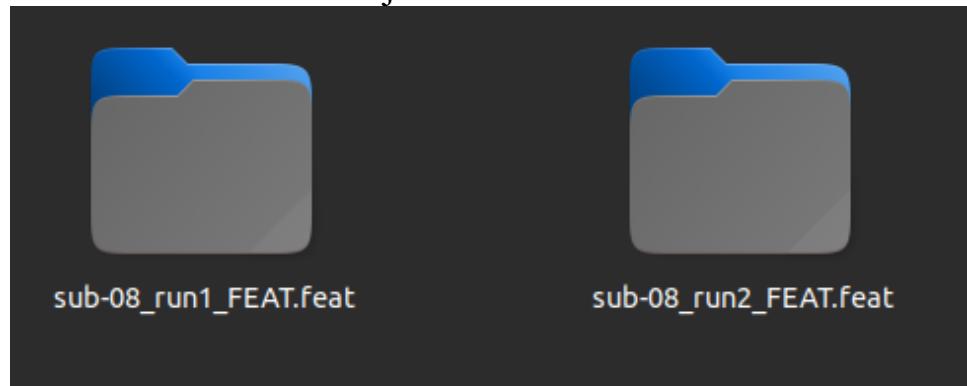
    # Move to the output directories for run2
    cd ${subj}_run2_FEAT

    # Now everything is set up to run feat for run2
    echo "====> Starting feat for run 2"
    feat ./design_run2.fsf

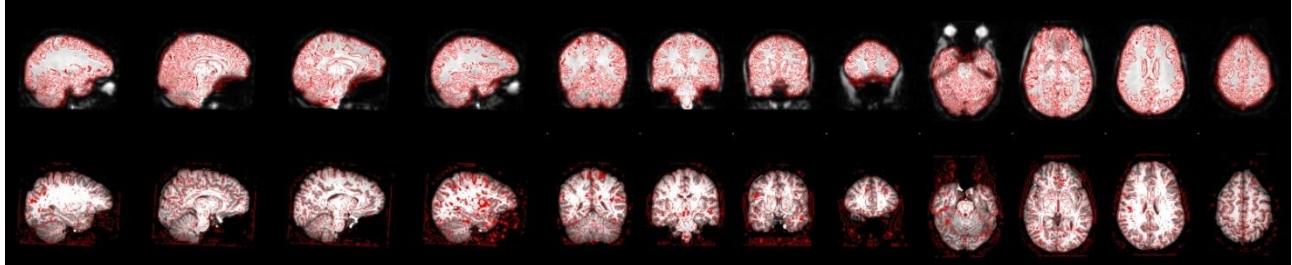
    # Move back to the subject directory
    cd ..

    # Go back to the directory containing all of the subjects, and repeat the loop
    cd ..
done
```

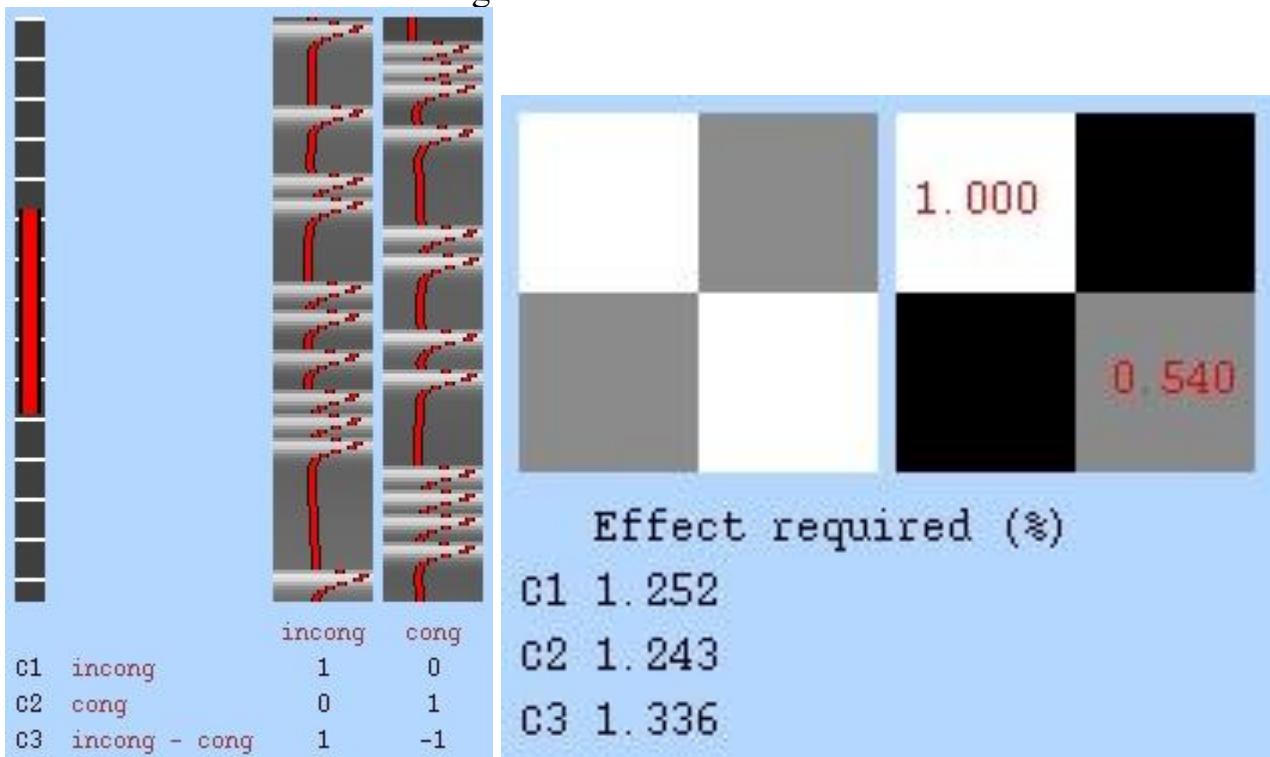
The result is 2 folders in each subject one for run1.feat and the other for run2.feat



Sample of the results in the subject 07 run1 feat analysis:



and the time series and the design matrix is:

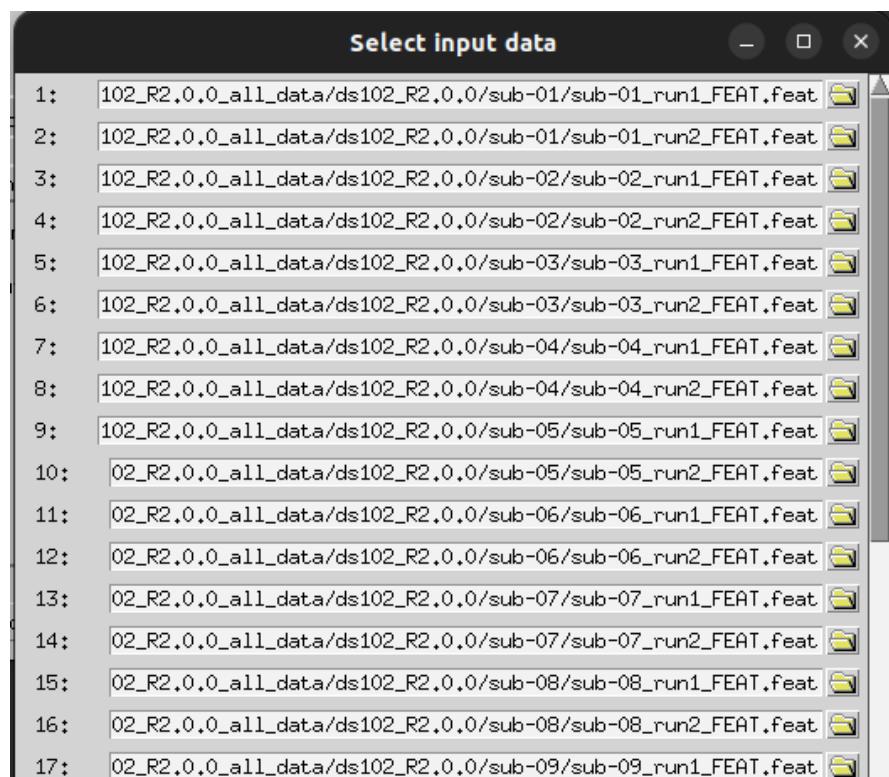


6. 2nd level analysis:

I use the terminal to get the list of the subjects and runs and copy the results.

```
mahmoud@Mahmoud:~/Downloads/flanker_test/ds102_R2.0.0_all_data/ds102_R2.0.0$ ls -d $PWD/sub-??/sub-??_run*_FEAT.feat
/home/nahmoud/Downloads/flanker_test/ds102_R2.0.0_all_data/ds102_R2.0.0/sub-01/sub-01_run1_FEAT.feat
/home/nahmoud/Downloads/flanker_test/ds102_R2.0.0_all_data/ds102_R2.0.0/sub-01/sub-01_run2_FEAT.feat
/home/nahmoud/Downloads/flanker_test/ds102_R2.0.0_all_data/ds102_R2.0.0/sub-02/sub-02_run1_FEAT.feat
/home/nahmoud/Downloads/flanker_test/ds102_R2.0.0_all_data/ds102_R2.0.0/sub-02/sub-02_run2_FEAT.feat
/home/nahmoud/Downloads/flanker_test/ds102_R2.0.0_all_data/ds102_R2.0.0/sub-03/sub-03_run1_FEAT.feat
/home/nahmoud/Downloads/flanker_test/ds102_R2.0.0_all_data/ds102_R2.0.0/sub-03/sub-03_run2_FEAT.feat
/home/nahmoud/Downloads/flanker_test/ds102_R2.0.0_all_data/ds102_R2.0.0/sub-04/sub-04_run1_FEAT.feat
/home/nahmoud/Downloads/flanker_test/ds102_R2.0.0_all_data/ds102_R2.0.0/sub-04/sub-04_run2_FEAT.feat
/home/nahmoud/Downloads/flanker_test/ds102_R2.0.0_all_data/ds102_R2.0.0/sub-05/sub-05_run1_FEAT.feat
/home/nahmoud/Downloads/flanker_test/ds102_R2.0.0_all_data/ds102_R2.0.0/sub-05/sub-05_run2_FEAT.feat
/home/nahmoud/Downloads/flanker_test/ds102_R2.0.0_all_data/ds102_R2.0.0/sub-06/sub-06_run1_FEAT.feat
/home/nahmoud/Downloads/flanker_test/ds102_R2.0.0_all_data/ds102_R2.0.0/sub-06/sub-06_run2_FEAT.feat
/home/nahmoud/Downloads/flanker_test/ds102_R2.0.0_all_data/ds102_R2.0.0/sub-07/sub-07_run1_FEAT.feat
/home/nahmoud/Downloads/flanker_test/ds102_R2.0.0_all_data/ds102_R2.0.0/sub-07/sub-07_run2_FEAT.feat
/home/nahmoud/Downloads/flanker_test/ds102_R2.0.0_all_data/ds102_R2.0.0/sub-08/sub-08_run1_FEAT.feat
/home/nahmoud/Downloads/flanker_test/ds102_R2.0.0_all_data/ds102_R2.0.0/sub-08/sub-08_run2_FEAT.feat
/home/nahmoud/Downloads/flanker_test/ds102_R2.0.0_all_data/ds102_R2.0.0/sub-09/sub-09_run1_FEAT.feat
/home/nahmoud/Downloads/flanker_test/ds102_R2.0.0_all_data/ds102_R2.0.0/sub-09/sub-09_run2_FEAT.feat
/home/nahmoud/Downloads/flanker_test/ds102_R2.0.0_all_data/ds102_R2.0.0/sub-10/sub-10_run1_FEAT.feat
/home/nahmoud/Downloads/flanker_test/ds102_R2.0.0_all_data/ds102_R2.0.0/sub-10/sub-10_run2_FEAT.feat
/home/nahmoud/Downloads/flanker_test/ds102_R2.0.0_all_data/ds102_R2.0.0/sub-11/sub-11_run1_FEAT.feat
/home/nahmoud/Downloads/flanker_test/ds102_R2.0.0_all_data/ds102_R2.0.0/sub-11/sub-11_run2_FEAT.feat
/home/nahmoud/Downloads/flanker_test/ds102_R2.0.0_all_data/ds102_R2.0.0/sub-12/sub-12_run1_FEAT.feat
/home/nahmoud/Downloads/flanker_test/ds102_R2.0.0_all_data/ds102_R2.0.0/sub-12/sub-12_run2_FEAT.feat
/home/nahmoud/Downloads/flanker_test/ds102_R2.0.0_all_data/ds102_R2.0.0/sub-13/sub-13_run1_FEAT.feat
/home/nahmoud/Downloads/flanker_test/ds102_R2.0.0_all_data/ds102_R2.0.0/sub-13/sub-13_run2_FEAT.feat
/home/nahmoud/Downloads/flanker_test/ds102_R2.0.0_all_data/ds102_R2.0.0/sub-14/sub-14_run1_FEAT.feat
/home/nahmoud/Downloads/flanker_test/ds102_R2.0.0_all_data/ds102_R2.0.0/sub-14/sub-14_run2_FEAT.feat
/home/nahmoud/Downloads/flanker_test/ds102_R2.0.0_all_data/ds102_R2.0.0/sub-15/sub-15_run1_FEAT.feat
/home/nahmoud/Downloads/flanker_test/ds102_R2.0.0_all_data/ds102_R2.0.0/sub-15/sub-15_run2_FEAT.feat
```

Then in the FEAT gui in the higher level analysis I set the directories of the runs for every subjects.



The next step is to fill the EVs and Contrast values in the stats page.

in this step I make two approaches the first one is by try scripting so I write this script to fill the values automatically by make the template that have the directories of the runs and set for loop to iterate on the columns of the EVs and by this equation set the value by 1 or 0

```
# Set EV values for each input
for (( inputnum=1; inputnum<=$EVs; inputnum++ )); do
    evg_input="evg$EVnum.$inputnum"
    if [ $EVnum -eq $inputnum ]; then
        fmri_evg_input="set fmri($evg_input) 1"
    else
        fmri_evg_input="set fmri($evg_input) 0"
    fi
    echo "$fmri_evg_input"
done
```

And the contrast to be in a diagonal shape by:

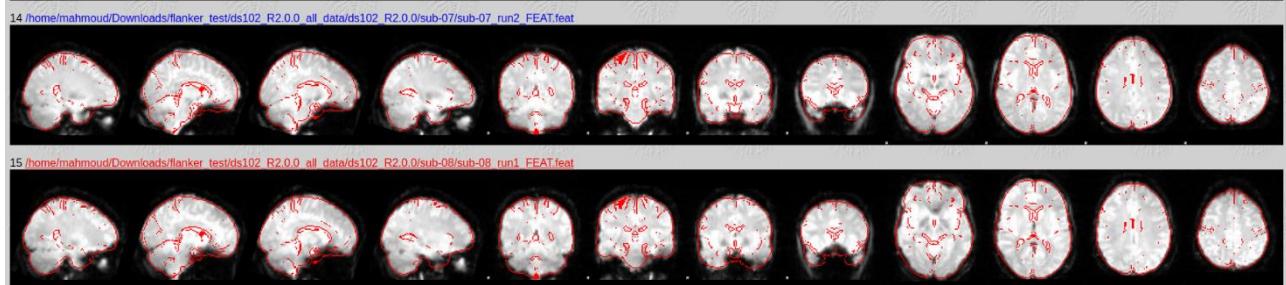
```
# Set up contrasts
for (( connum=1; connum<=$EVs; connum++ )); do
    conname="C$conum"
    fmri_connname="set fmri(conname$conum) \"\$conname\""
    fmri_con_real="set fmri(con_real.$conum.$conum) 1"

    # Print the commands
    echo "$fmri_connname"
    echo "$fmri_con_real"
done
```

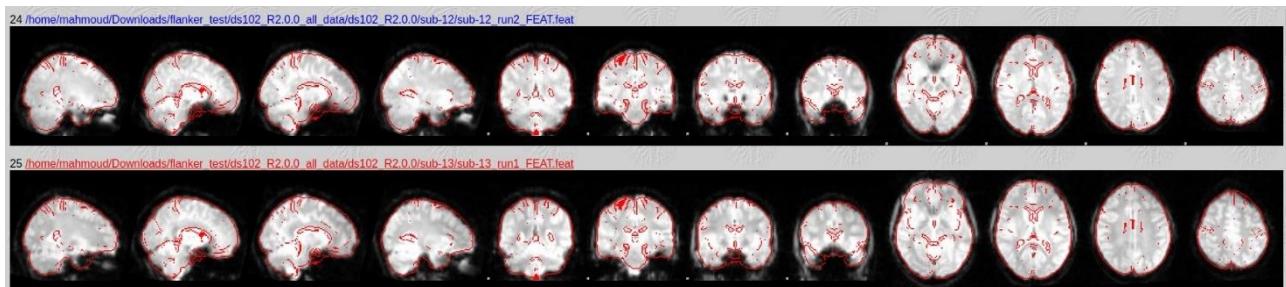

Then the design matrix appears:

And about 2 hours the results of the higher-level analysis is done and this is sample of the results:

I see that in the regression the two subject 7 and 8 have some differences and by looking at the QC table I see that the two subjects has a different shape of structure image and moves in a different volumes.



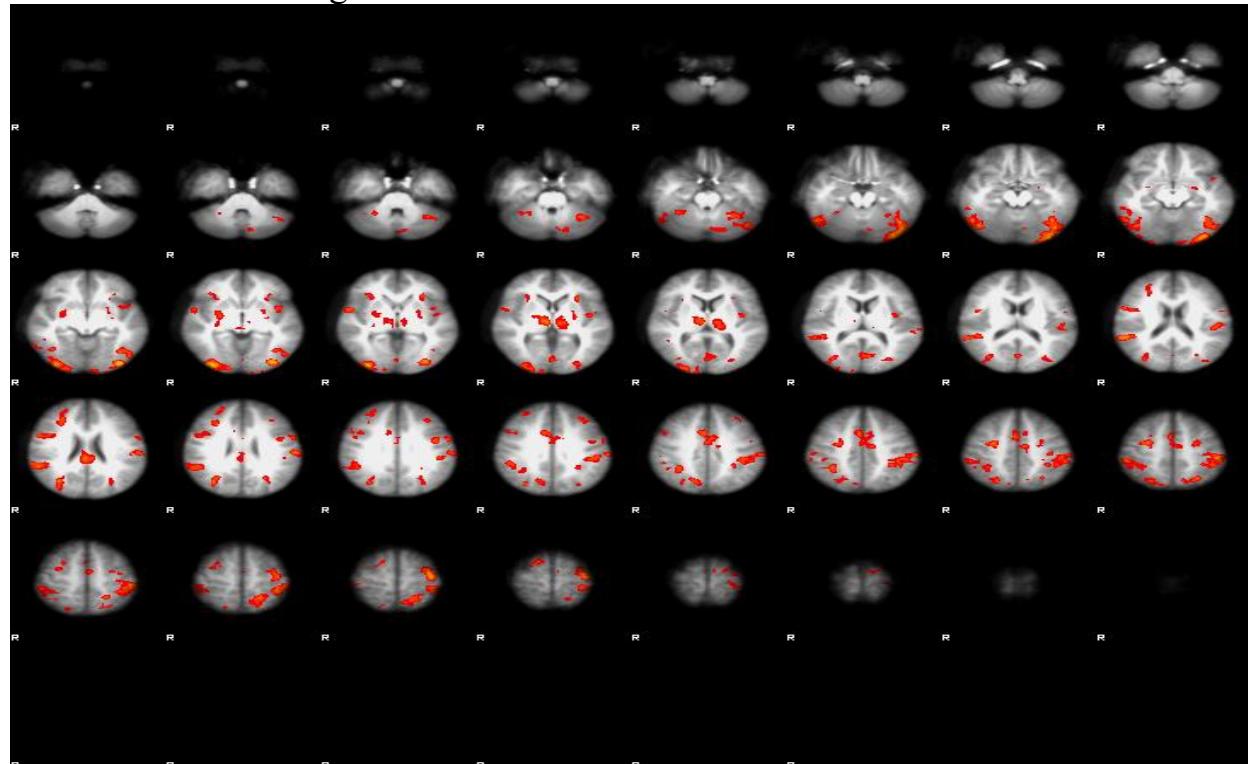
Other sample of results between sub-12 and sub-13:



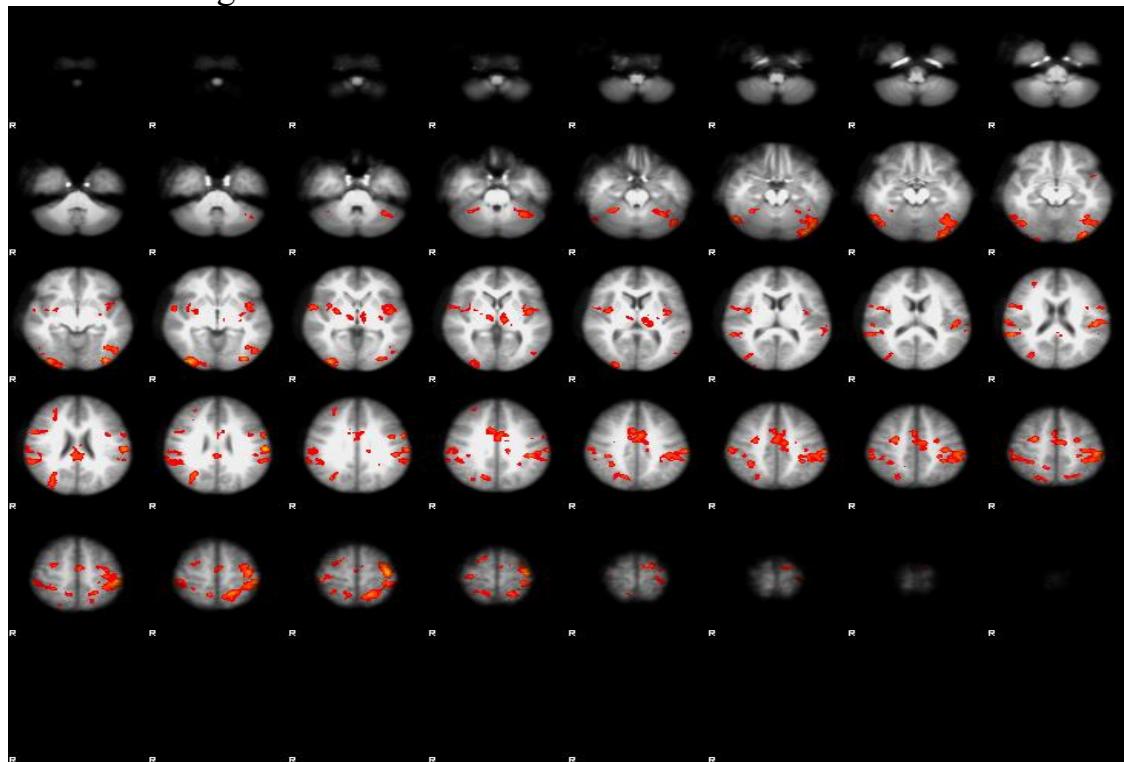
This is some of the results of stat for the higher-level analysis:

And we can detect the regions of brain that have activate at each task from these two results images.

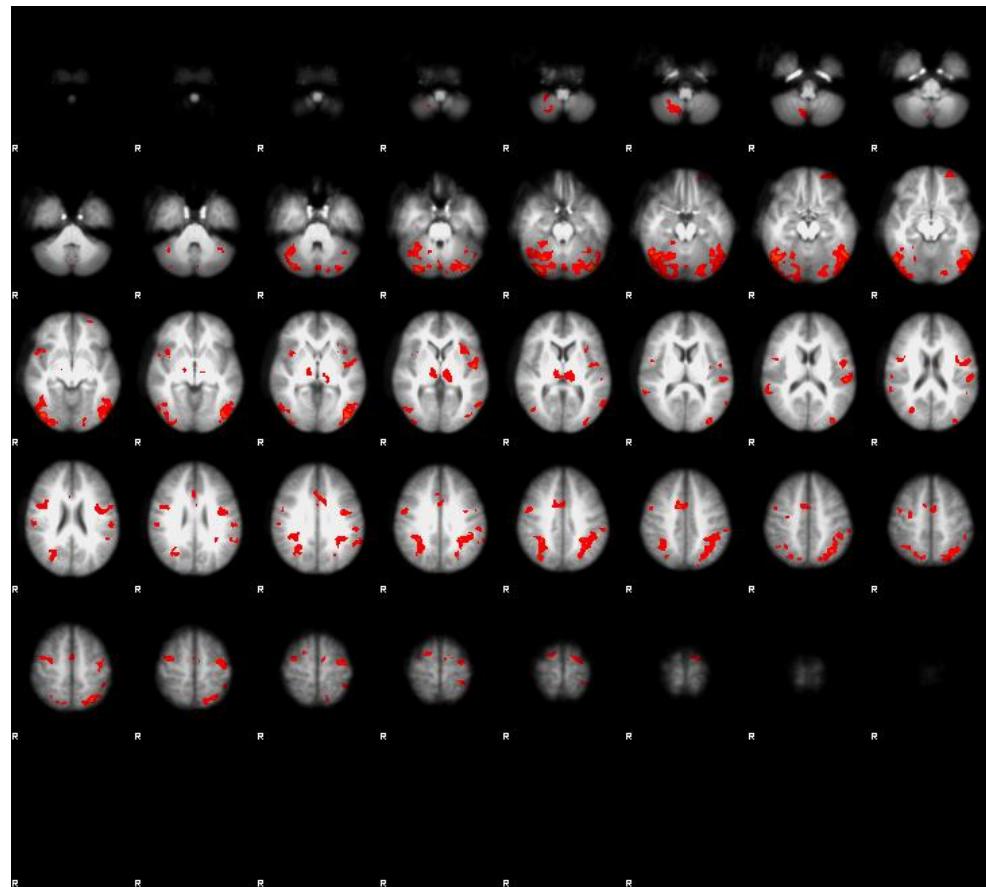
Zstat4 – C4 for incongruent task:



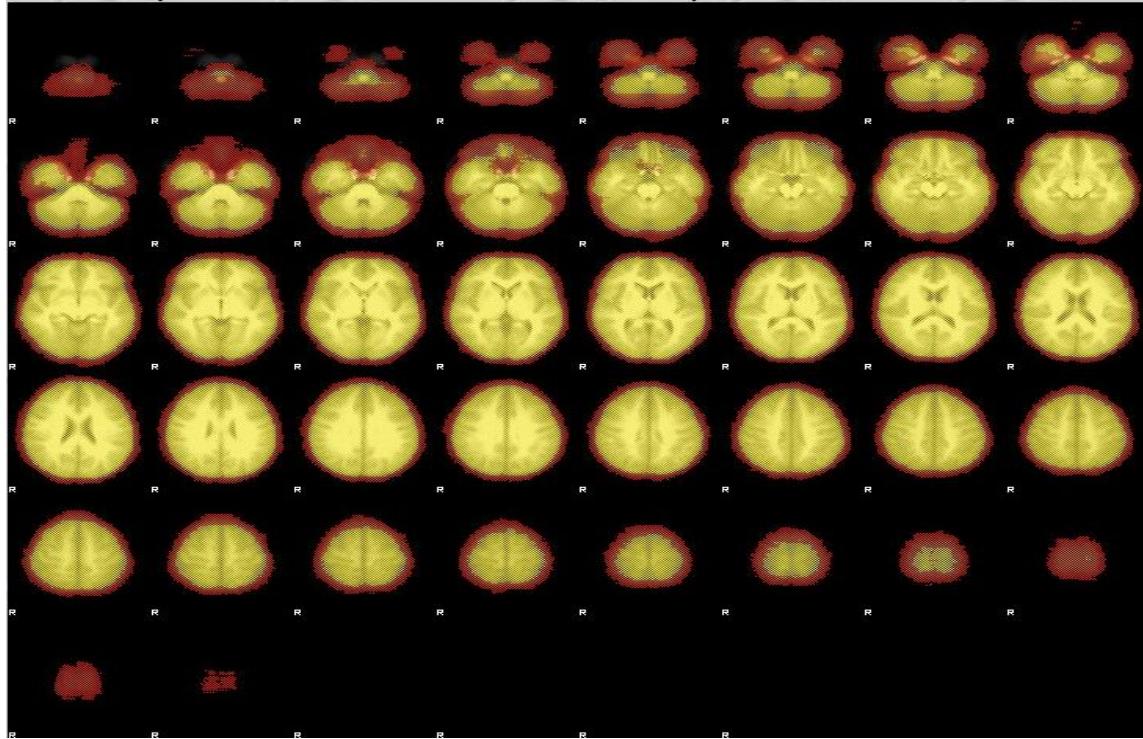
Zstat4 – C4 for congruent task:



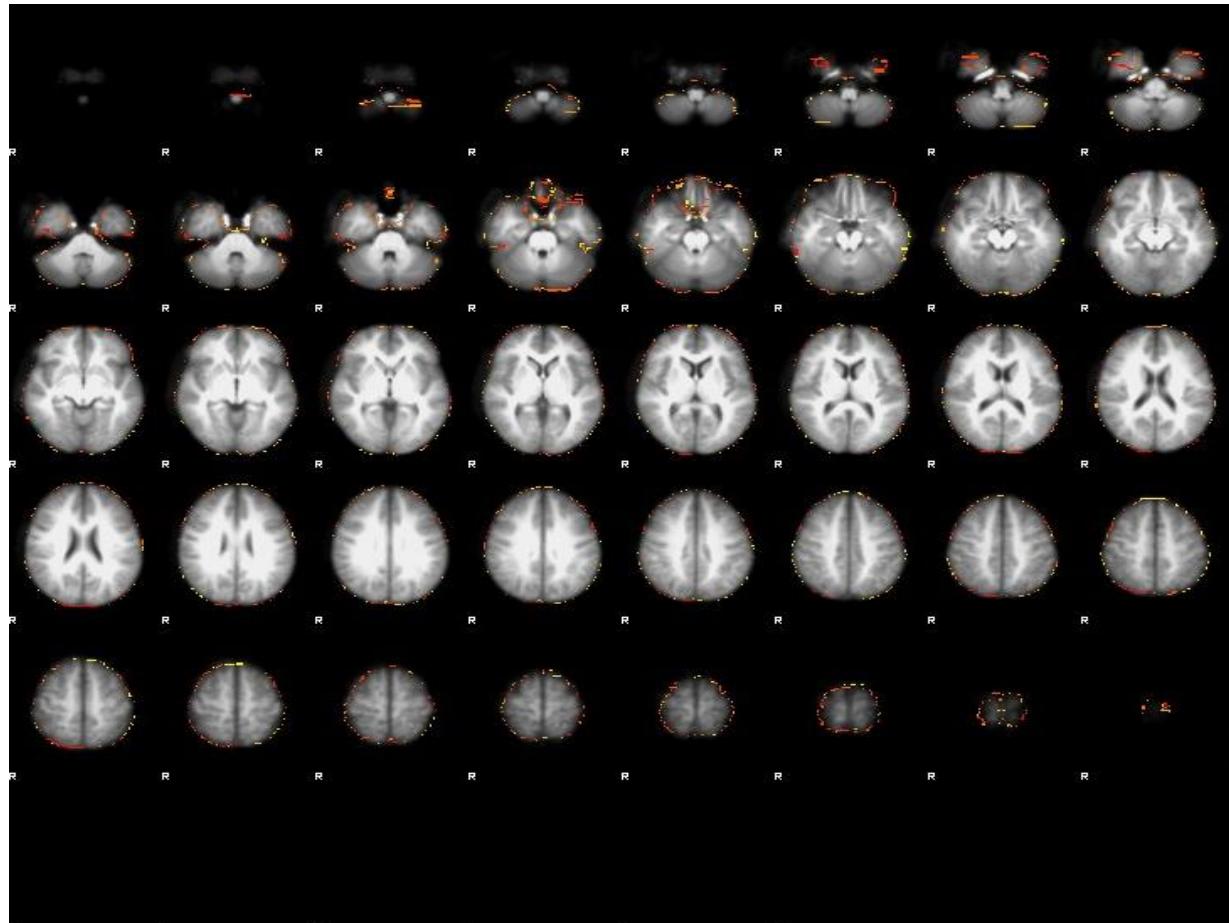
zStat1 – C1 (group mean):



And this is the sum of all input masks after transformation to standard space:

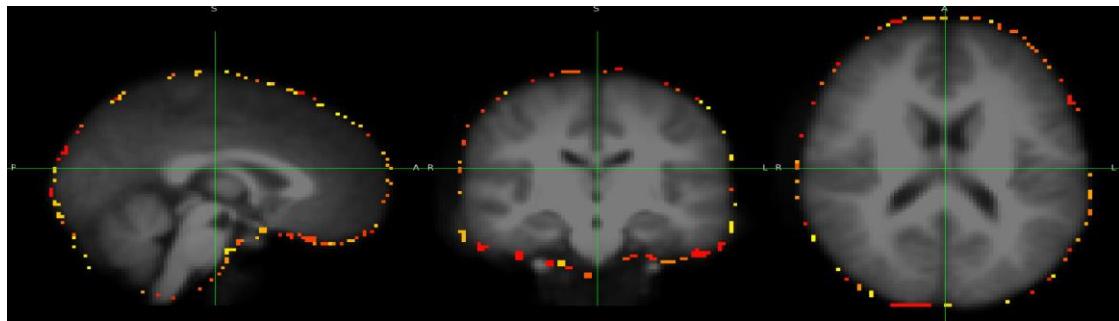


Unique missing-mask voxels:

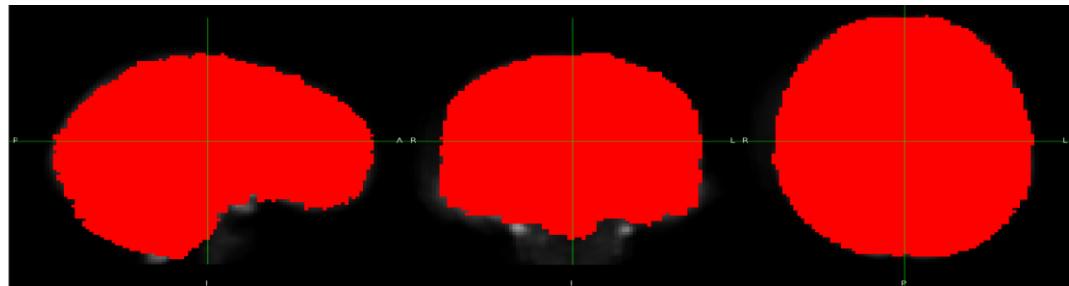


And from the FSLeyes I check some of the zstat results and masked images and this is sample of the outputs I check:

MaskUnique overlayed by mask Unique ovelayed:

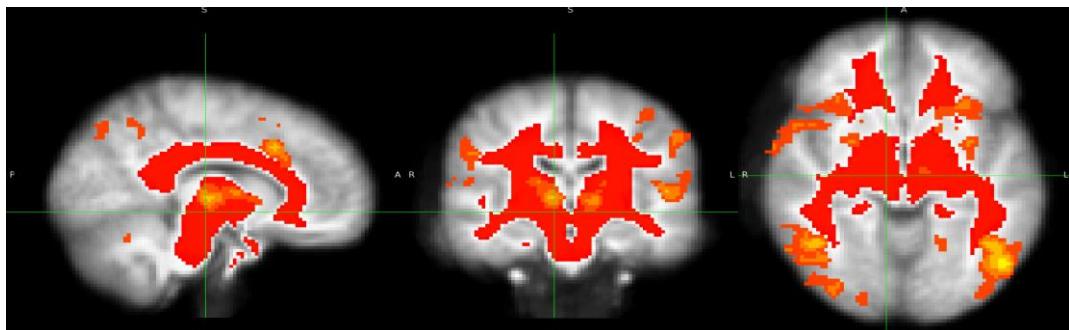


The rendered structure image and the mask:

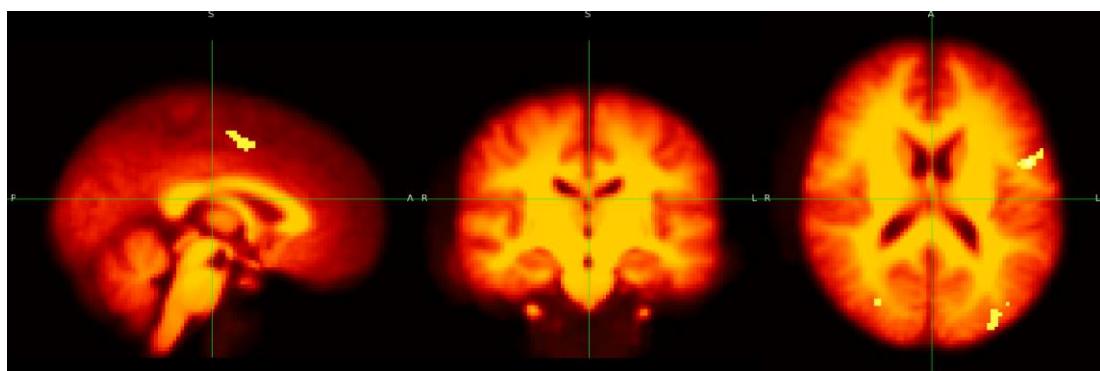


The results of statistical analysis for the group level analysis:

Rendered zstat5:

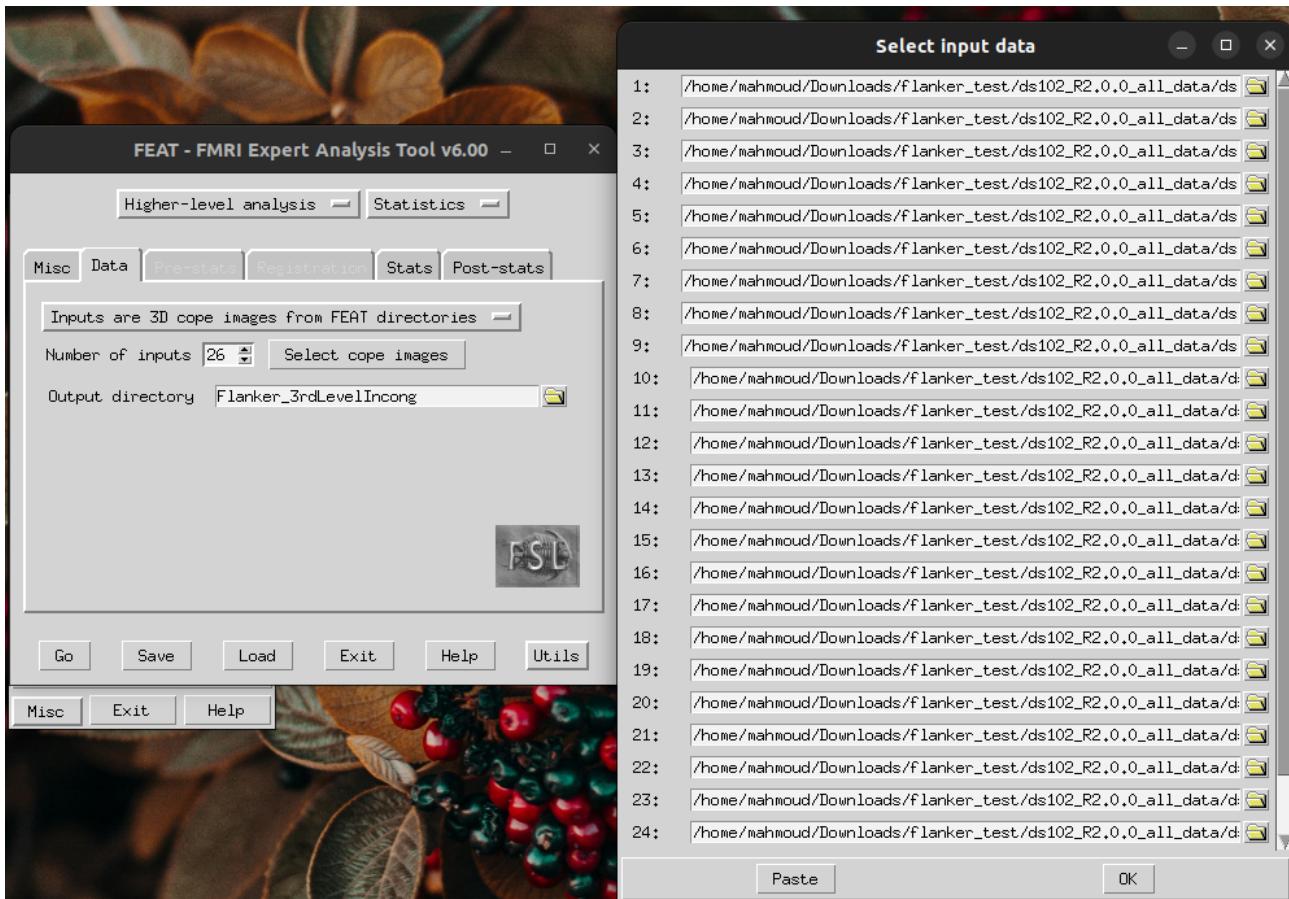


Rendered zstat26:



7. 3rd Level analysis:

The FEAT gui settings:



Bash script

first I define a design template for each cope and save the design template and using script I change the model

the **Fixed Effects model** assumes all variability is within subjects, ignoring any random effects due to different subjects. This approach is particularly useful when combining multiple sessions or runs from the same subject, as it treats the data as a single entity without considering between-subject variability. Consequently, the results from a Fixed Effects model apply strictly to the specific subjects included in the analysis and cannot be generalized to a larger population.

The **Mixed Effects: Simple OLS model** introduces both within-subject and between-subject variability, acknowledging that there is variability between different subjects. However, it does not partition these variances correctly, which can lead to an underestimation of variance at the group level. As a result, this model may produce overly optimistic statistical inferences. While it offers an improvement over Fixed Effects by considering more variability sources, it is still not fully accurate for robust group-level analysis.

Mixed Effects: FLAME 1 (FMRIB's Local Analysis of Mixed Effects) advances the accuracy by effectively separating within-subject and between-subject variability. This separation allows for a more precise estimation of group-level effects. FLAME 1 is suitable for most standard group analyses in fMRI, providing a reliable balance between accuracy and computational demand. The results obtained from FLAME 1 can be generalized to the population level, making it a robust choice for higher-level fMRI analysis.

Finally, **Mixed Effects: FLAME 1+2** further refines the FLAME 1 approach by using an iterative Bayesian technique to more accurately model higher-level variance components. This method is more computationally intensive but delivers the most reliable and precise inferences. FLAME 1+2 accounts for all sources of variability robustly, providing the highest accuracy and generalizability for complex group-level analyses. This model is ideal for researchers needing the most detailed and reliable results in their fMRI studies.

```

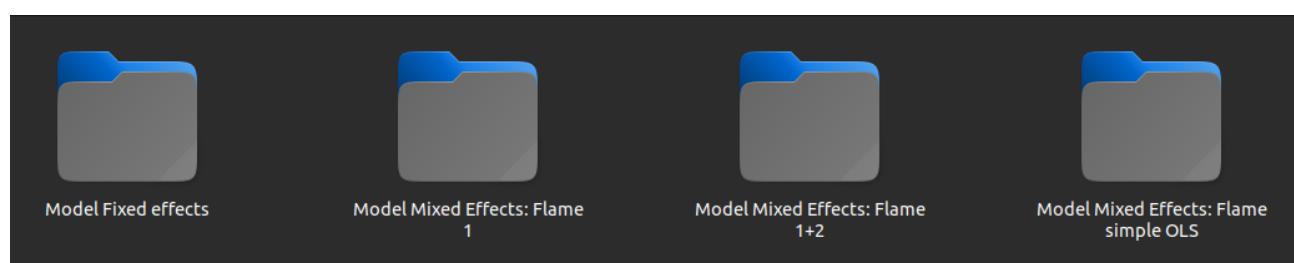
145# Higher-level modelling
146# 3 : Fixed effects
147# 0 : Mixed Effects: Simple OLS
148# 2 : Mixed Effects: FLAME 1
149# 1 : Mixed Effects: FLAME 1+2
150set fmri(mixed_yn) 3
---
```

The script:

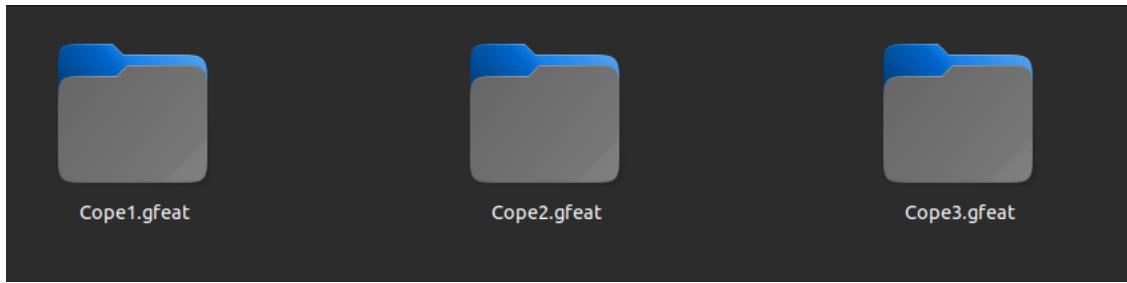
```

1#!/bin/bash
2
3
4template_file="thirdLevelModelCope3.fsf"
5
6output_directory="Flanker_3rdLevelCope3"
7
8# Loop through four times
9for i in {0..3}; do
10    # Increment the value of fmri(mixed_yn)
11    mixed_value=$((i % 4))
12
13    sed -i "s/set fmri(mixed_yn) [0-9]/set fmri(mixed_yn) $mixed_value/" "$template_file"
14
15    |
16    sed -i "s|set fmri(outputdir) \".*\"|set fmri(outputdir) \"$output_directory\"|"
17    "$template_file"
18
19    # Run FEAT
20    feat "$template_file"
21done
22
```

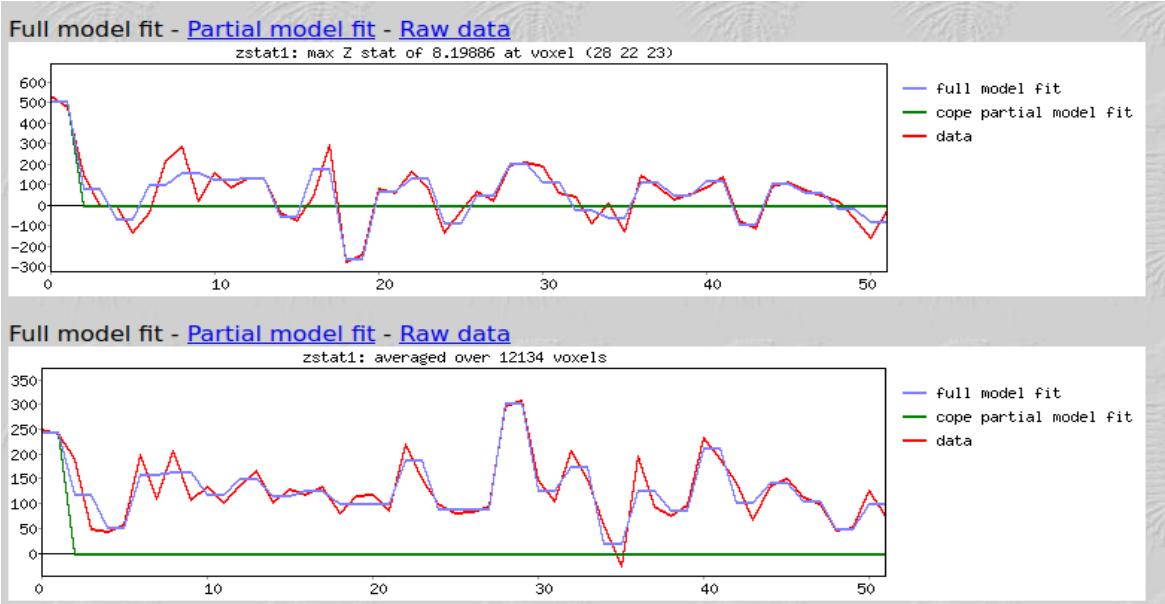
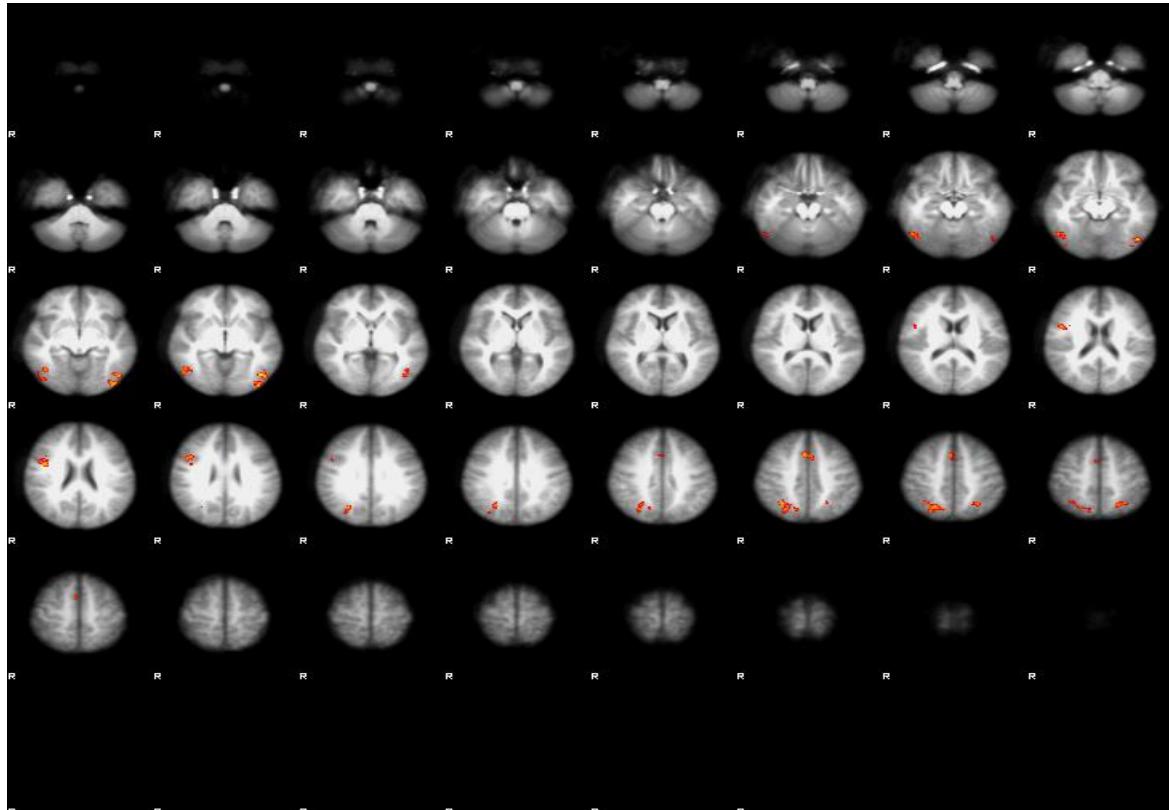
The output folders:



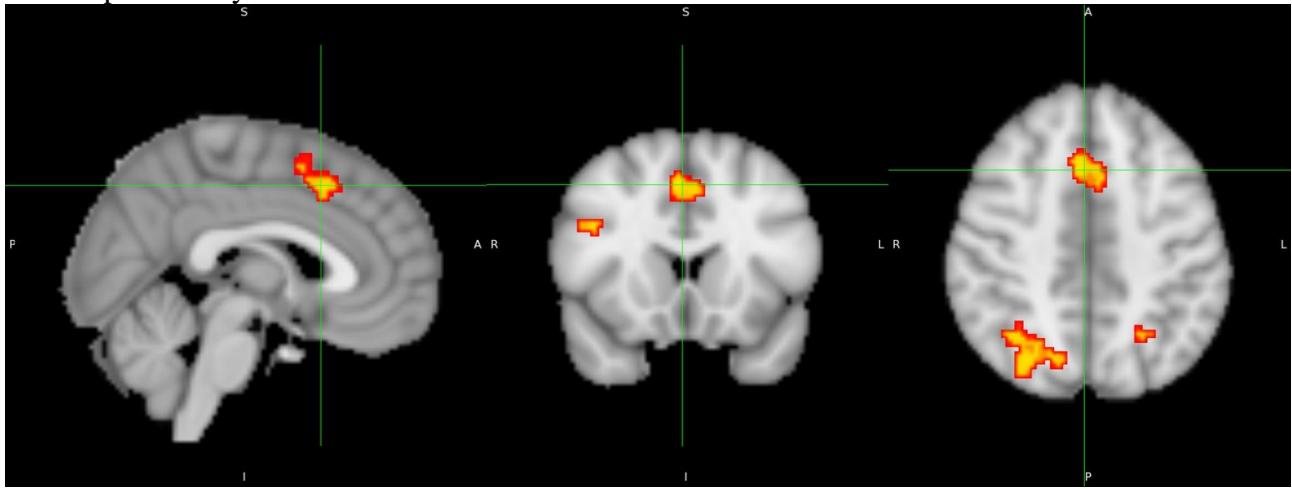
And for each model folder:



The output for model mixed effects: Flame 1:



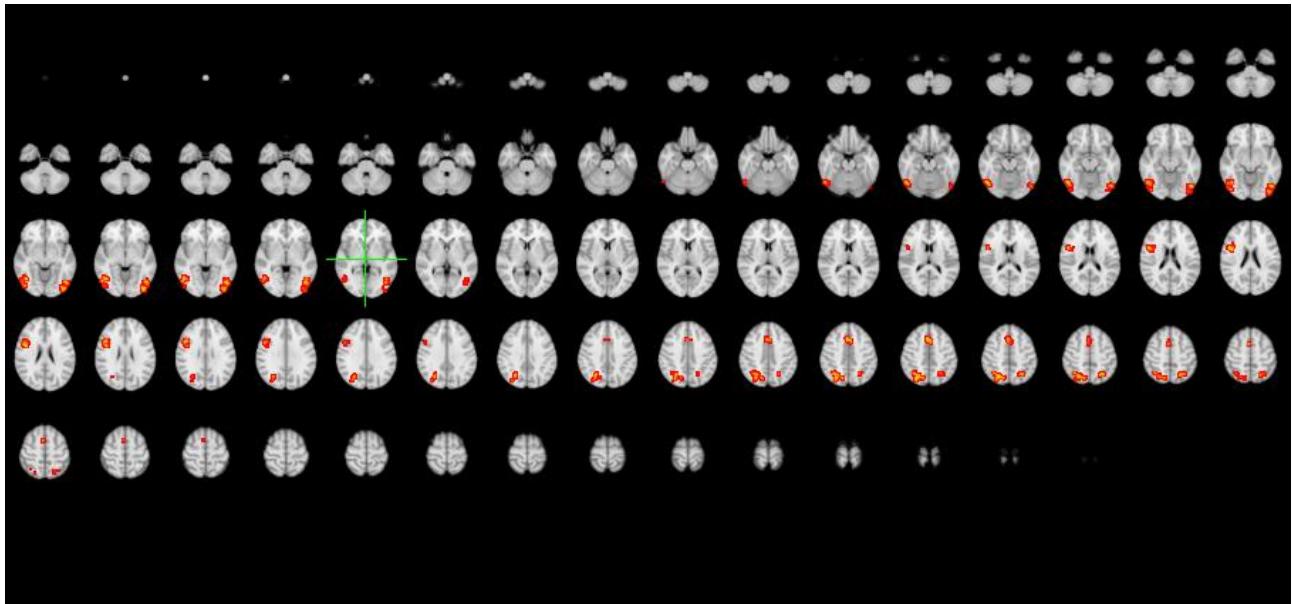
The output in fsleyes:



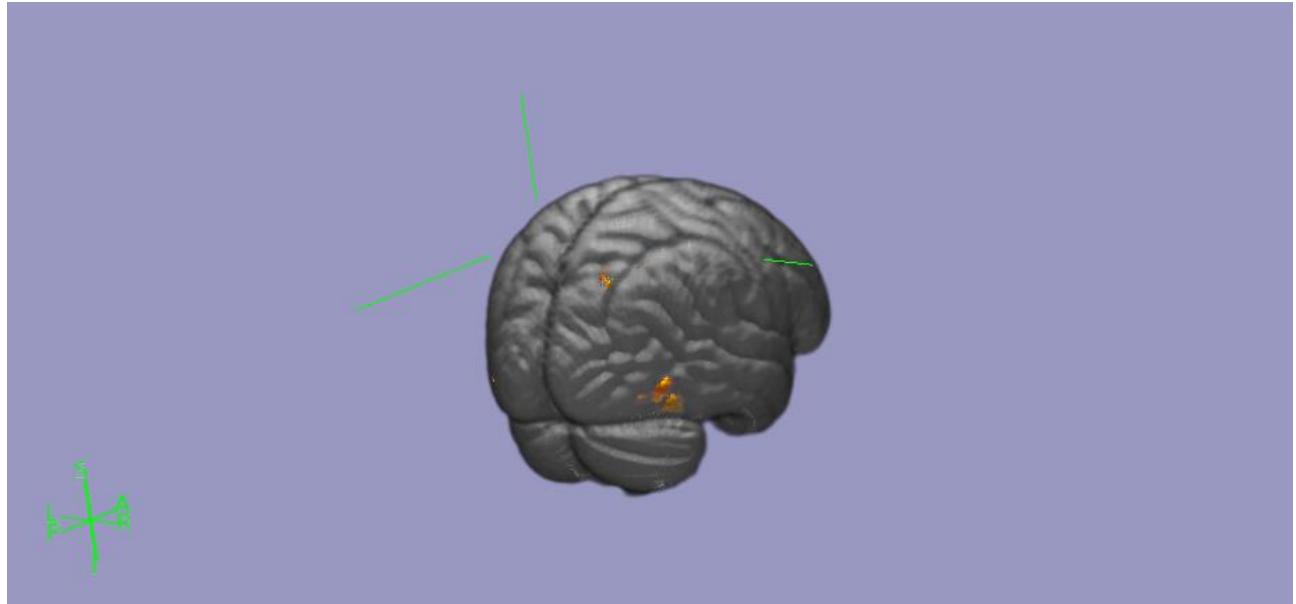
The clusters of the experiment:

Cluster browser							
cope1:filtered_func_data							
Z statistics for COPE1 (group mean)				Add Z statistics		Add cluster mask	
Cluster index	Size (voxels)	P	-log10(P)	Z Max	Z Max location	COPE Max	COPE Max location
7.0	392.0	4.77e-07	6.32	4.03	[33.0 30.0 60.0]	→ [31.7 29.9 50.0]	→ [30.0 26.0 59.0]
6.0	259.0	3.73e-05	4.43	3.82	[24.0 31.0 33.0]	→ [20.7 30.1 30.8]	→ [18.0 32.0 26.0]
5.0	185.0	0.000589	3.23	4.07	[23.0 65.0 48.0]	→ [22.1 66.9 25.48.0]	→ [20.0 69.0 51.0]
4.0	184.0	0.000613	3.21	4.26	[67.0 28.0 35.0]	→ [68.1 27.6 32.595]	→ [69.0 27.0 30.0]
3.0	140.0	0.00379	2.42	3.93	[43.0 71.0 59.0]	→ [43.98 70.3 59.4]	→ [44.0 71.0 58.0]
2.0	102.0	0.0213	1.67	4.12	[66.0 20.0 33.0]	→ [65.35 20.45 32.665]	→ [66.0 19.0 33.0]
1.0	89.0	0.04	1.4	3.74	[59.0 33.0 61.0]	→ [57.8 32.5 60.85]	→ [60.0 32.0 61.0]

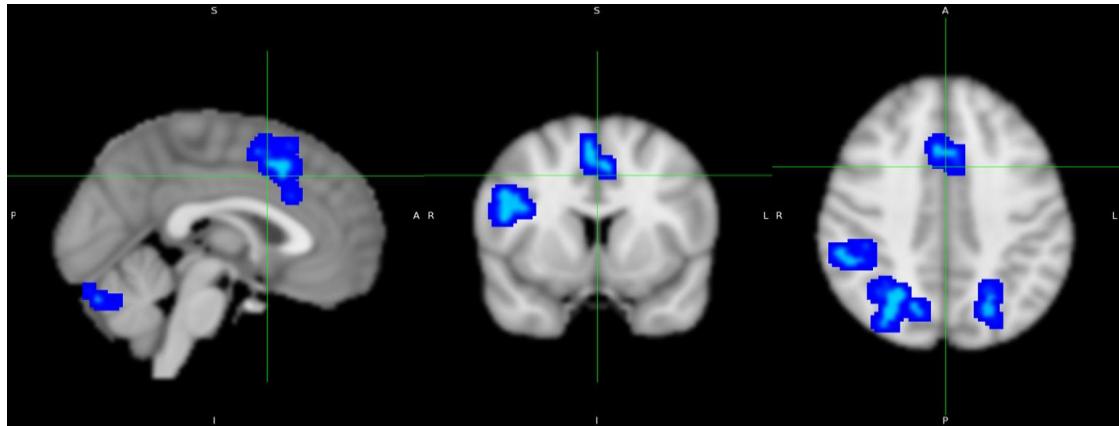
The light box view to see the change in the region clearly:



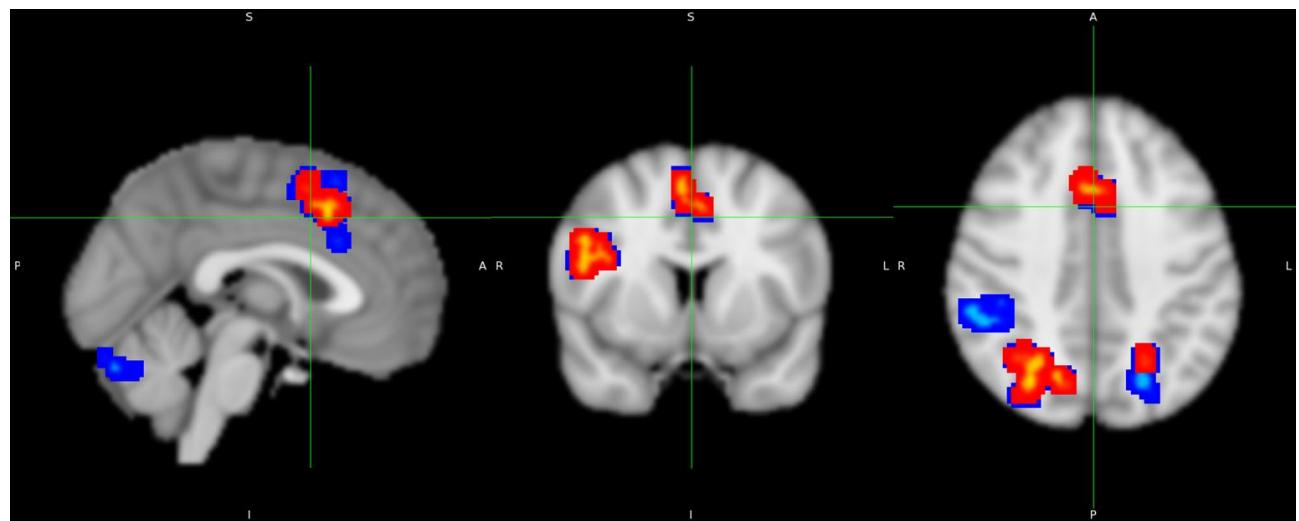
The 3D view of the clusters:



The output for model mixed effects: Flame 1 + 2:



The difference between Flame 1 and Flame 1 + 2 in fsleyes:



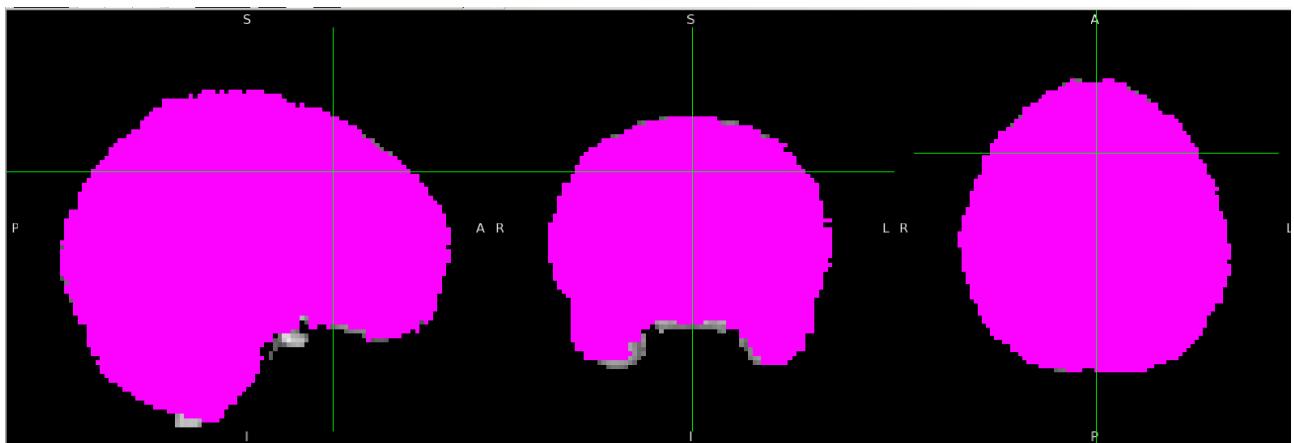
Exercises:

1 - In the Post-stats tab, set the Thresholding to None, and re-run the analysis (changing the output directory to something that indicates that no threshold is being used). Examine the results in fsleyes. How do they compare to the cluster-corrected results?

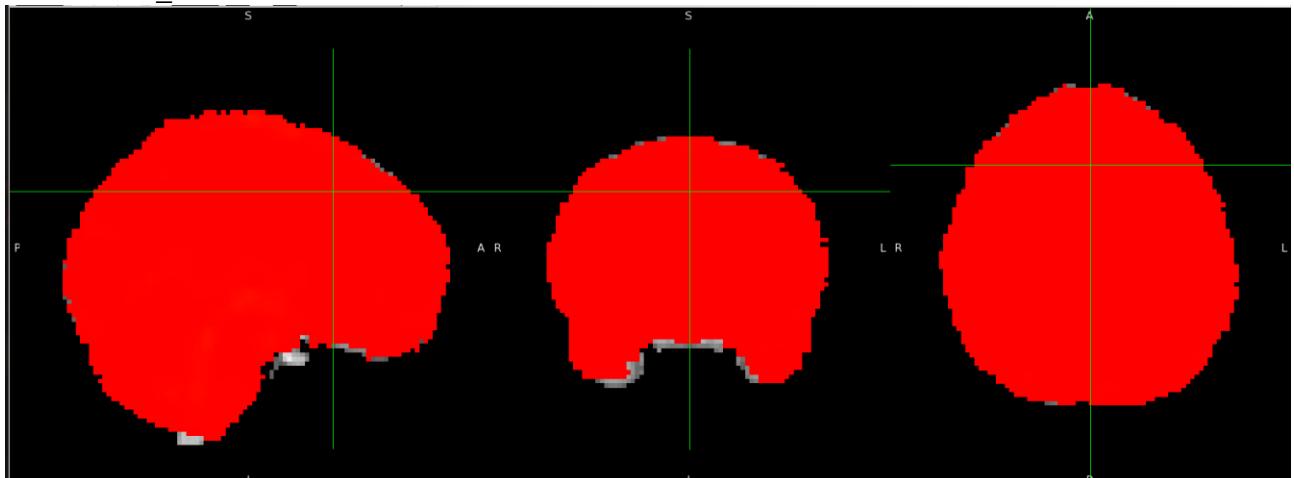
After re-running the analysis with the thresholding set to "None" and examining the results in fsleyes, I observed a significant difference compared to the cluster-corrected results. Without any thresholding applied, almost all the voxels in the brain image appear highlighted. This lack of filtering means that voxels with both high and low statistical significance are displayed, resulting in a densely populated image. It becomes challenging to distinguish which areas are genuinely significant, as the image is cluttered with numerous activations.

In contrast, the cluster-corrected results are much more refined and interpretable. The cluster correction method only shows clusters of voxels that exceed a certain size and significance level, effectively filtering out noise and highlighting regions more likely to represent true activations. These results display a sparse and focused pattern of activations, making it easier to identify meaningful regions in the brain.

By opening the fsleyes to see the output and open the todf_filtered_func:



And the var_filtered function:

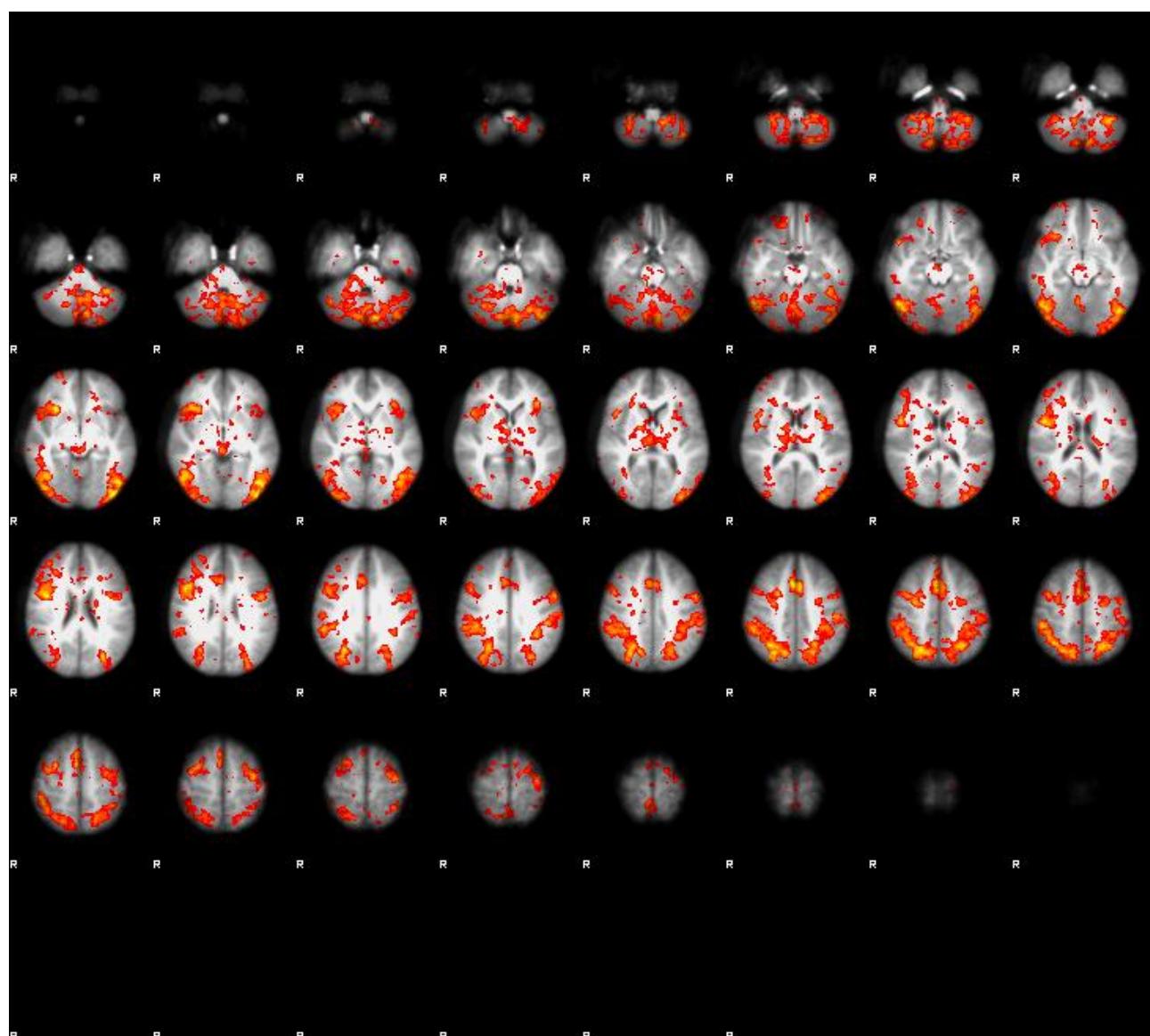


- Do the same procedure in the previous exercise, this time using an Uncorrected threshold. Then, repeat the procedure with a Voxel threshold. Note any differences between these results and what you generated with the cluster-corrected results. In your own words, describe why the results are different.

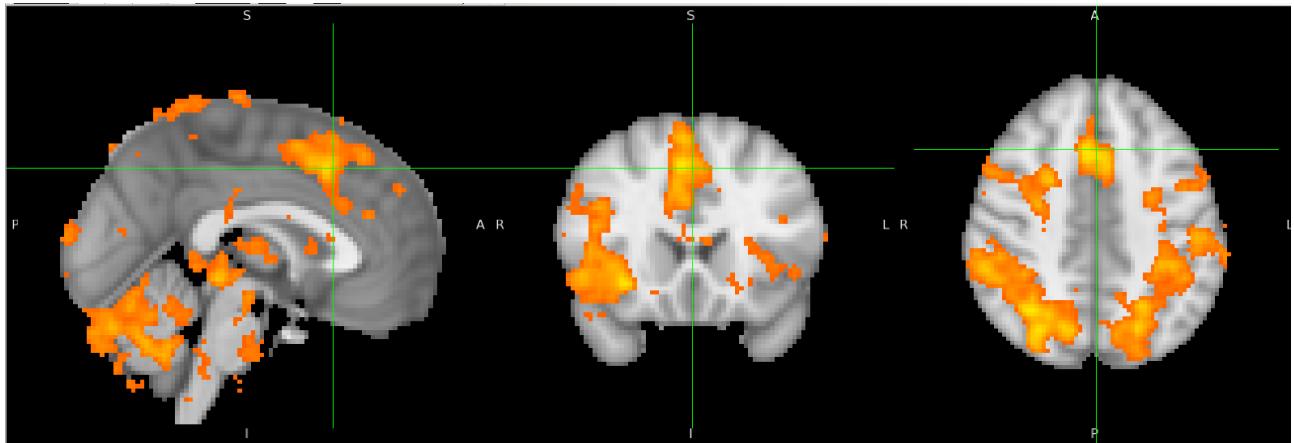
I conducted a neuroimaging analysis using three different thresholding methods: uncorrected, voxel threshold, and cluster-corrected. Here's a summary of the observations and differences:

Uncorrected Threshold

- **Observation:** The results displayed a large number of highlighted voxels, similar to having no threshold at all. Many of these voxels might not be genuinely significant.
- **Explanation:** This method does not account for multiple comparisons, leading to a higher likelihood of false positives. Every voxel is tested independently, which can result in many voxels appearing significant by chance.

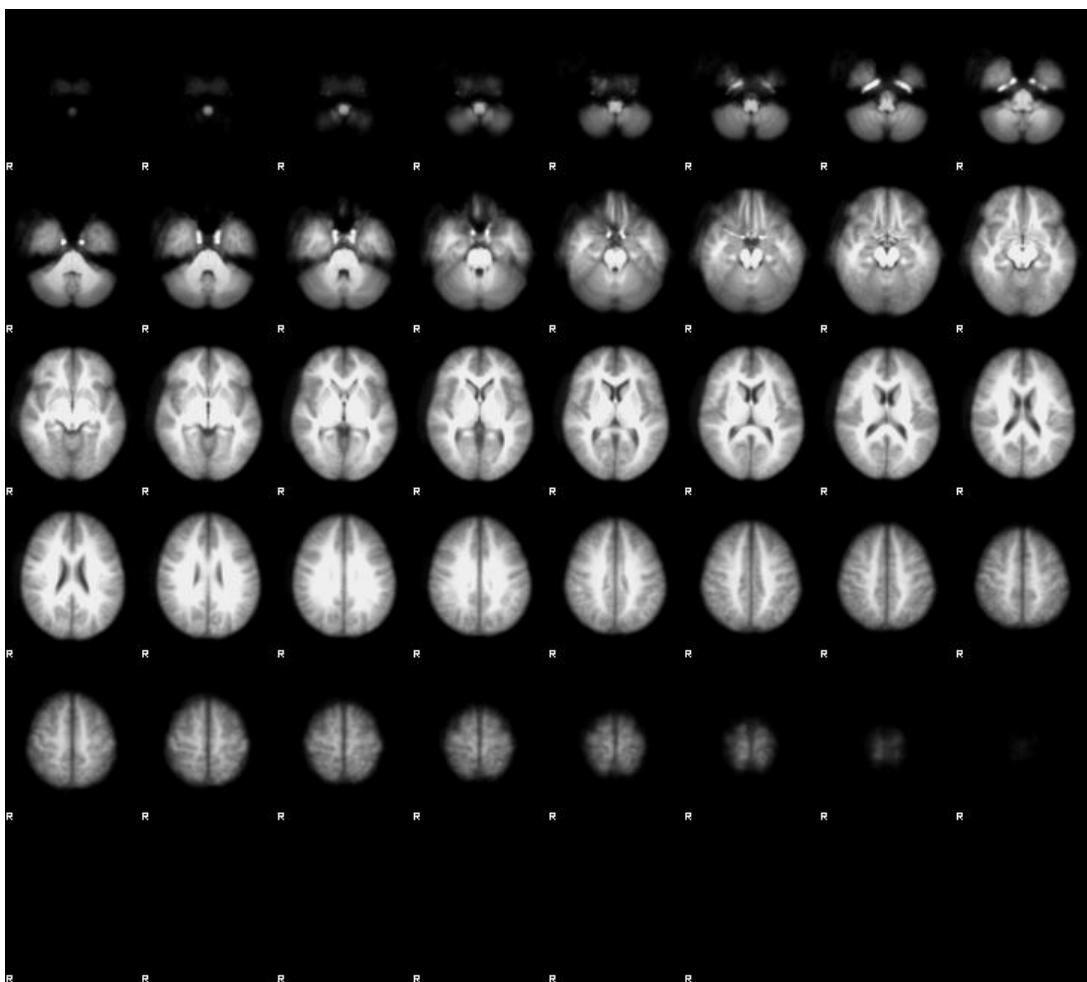


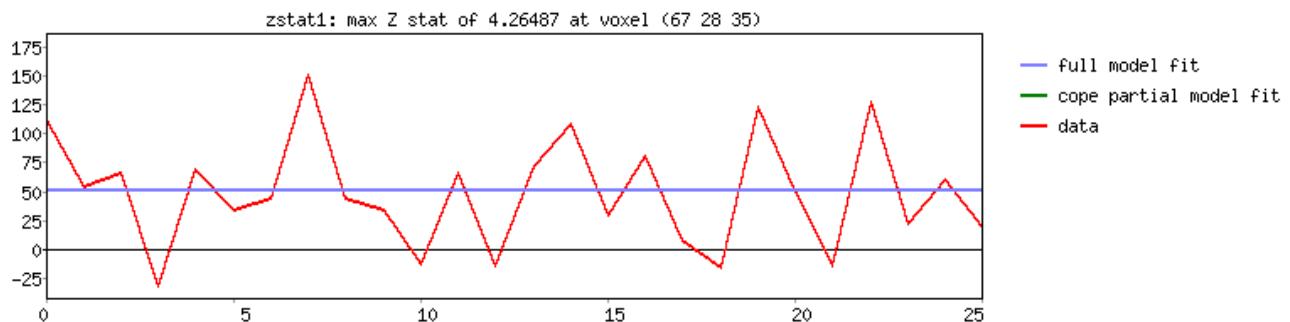
Opening the output in fsleyes:



Voxel Threshold

- **Observation:** The results were more refined than the uncorrected method but still showed more voxels than the cluster-corrected results. This method applied a significance threshold at the voxel level.
- **Explanation:** While this reduces the number of false positives compared to the uncorrected method, it doesn't consider the spatial extent of activations. This can lead to significant activations being small and scattered without context.





Cluster-Corrected Threshold

- **Observation:** This method provided the most refined and interpretable results, showing only clusters of voxels that passed both size and significance criteria.
- **Explanation:** Cluster correction controls for multiple comparisons and considers the spatial relationship between voxels. This reduces false positives and highlights regions of true activations, making the results clearer and more reliable.

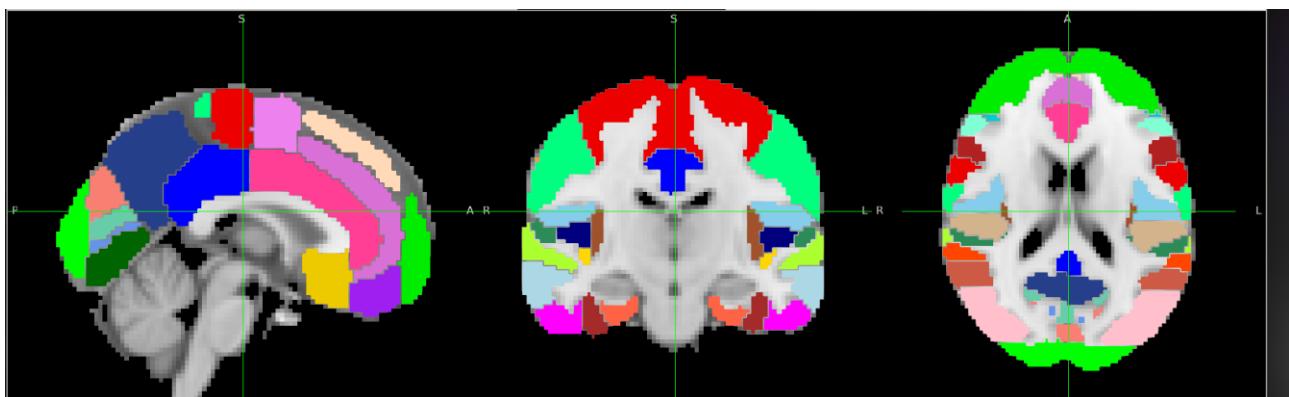
Why the Results Differ

The differences arise because each method handles statistical significance and spatial relationships differently. The uncorrected threshold tests each voxel independently, leading to many false positives. The voxel threshold applies a significance cutoff but still misses the broader spatial context. The cluster-corrected method, however, combines statistical significance with spatial extent, ensuring that only meaningful clusters of activations are highlighted.

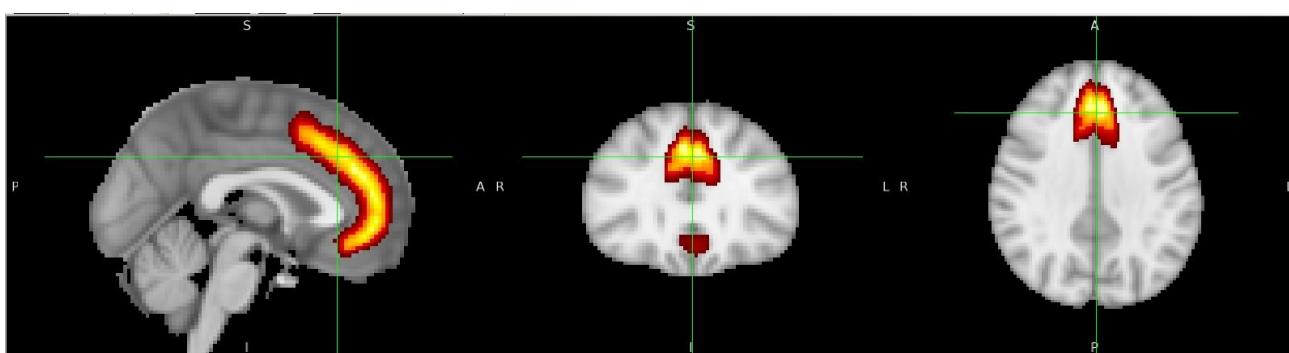
8. ROI analysis ‘Whole brain analysis’:

8.1 Atlas based ROI:

Using Harvard – oxford cortical structure atlas : is a probabilistic atlas which means that the voxels at the center of the crosshairs in the viewing window is assigned a probability of belonging to a brain structure.



The paracingulate gyrus in the atlas:



Using scripts of bash combined with FSL scripts to get the stats of COPE3 with the paracingulate gyrus ROI, and using Rstudio the results is

```
> t.test(x)

One Sample t-test

data: x
t = 0.97116, df = 25, p-value = 0.3408
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
-0.1143325  0.3183702
sample estimates:
mean of x
0.1020188
```

The contrast estimates are significantly different from zero “ $P = 0.3408$ ” this results aren’t statistically significant. This may be because the anatomical mask is so large that encompasses several distinct functional regions so we go for the spherical ROI that minimize the region of interest.

8.2 Spherical based ROI:

This ROI is more localized so we have more power to detect the cognitive control effect.

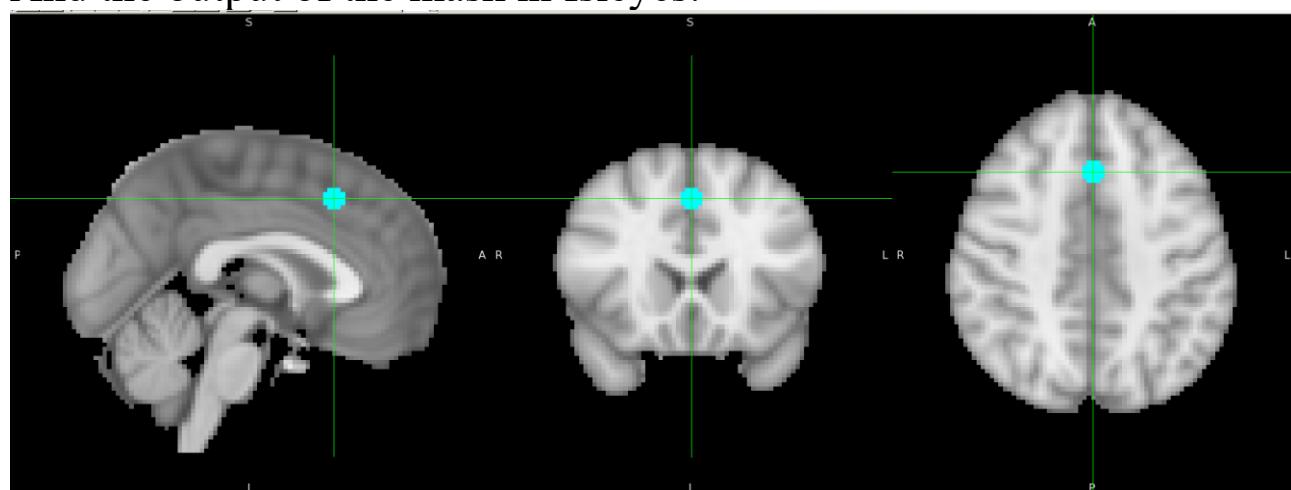
We can apply the ROI for the coordinates (0, 20, 44) on the MNI standard image and the stats will be:

```
> t.test(y)

One Sample t-test

data: y
t = 4.5339, df = 25, p-value = 0.0001247
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
0.3578045 0.9534369
sample estimates:
mean of x
0.6556207
```

And the output of the mask in fsleyes:



Exercise:

1- The mask used with fslmeants is binarized, meaning that any voxel containing a numerical value greater than zero will be converted to a “1”, and then data will be extracted only from those voxels labeled with a “1”. You will recall that the mask created with fsleyes is probabilistic. If you want to weight the extracted contrast estimates by the probability weight, you can do this by using the -w option with fslmeants. Try typing: fslmeants -i allZstats.nii.gz -m PCG.nii.gz -w

And observe how the numbers are different from the previous method that used a binarized mask. Is the difference small? Large? Is it what you would expect?

Binarized Mask Results:

- The mean value of the extracted data was 0.6556.
- The t-test showed a highly significant result ($p=0.0001247$), indicating that the mean is significantly different from zero.
- The confidence interval did not include zero (0.3578 to 0.9534).

Weighted Mask Results:

- The mean value of the extracted data was 0.1020.
- The t-test showed a non-significant result ($p=0.3408$), suggesting that the mean is not significantly different from zero.
- The confidence interval included zero (-0.1143 to 0.3184).

Observations and Interpretation:

- **Difference in Results:** The difference between the two methods is quite noticeable. The binarized mask results showed a higher mean and a significant difference from zero, while the weighted mask results did not show a significant difference.
- **Explanation:** This difference is expected. A binarized mask treats all included voxels equally, potentially inflating the mean by including voxels with lower probability values. In contrast, a weighted mask takes into account the probability of each voxel, providing a more accurate representation of the data. This reduces the influence of voxels with low probabilities, leading to a lower mean and potentially non-significant results.

Conclusion: Using a binarized mask can overestimate the mean and increase the risk of false positives because it treats all voxels equally. The weighted mask method, although potentially less sensitive, offers a more accurate reflection of the data by considering the probability weights of each voxel. This results in more reliable and interpretable findings.

Expectations for a Flanker Test Data Set: If applied to a flanker test data set, similar differences would be expected. The binarized mask might show more significant activations, potentially including spurious results, while the weighted mask would likely show fewer but more reliable activations. This method reduces noise and provides a clearer picture of the brain regions genuinely involved in the task.

2- Use the code given in the section on spherical ROI analysis to create a sphere with a 7mm radius located at MNI coordinates 36, -2, 48.

Expectation:

Mean Value: Likely to be closer to the true underlying activity. For the weighted mask, the mean might be lower than the binarized mask mean because lower-probability voxels are down-weighted.

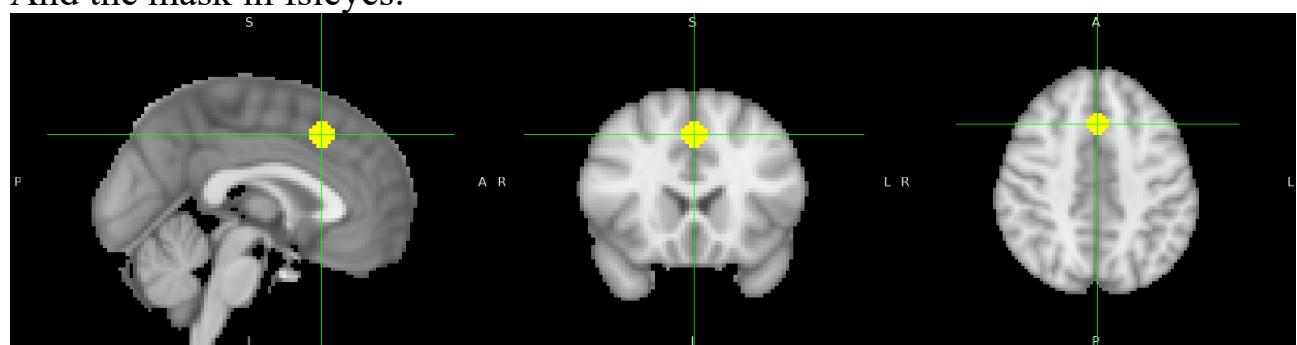
- **Confidence Interval:** May shift to reflect the more accurate weighting of voxel contributions.
- **Statistical Significance:** Could change depending on how the weighting affects the overall distribution of the data. The weighted mask is likely to provide a more conservative estimate, potentially leading to a less significant result if the noise is reduced.

```
> t.test(w)
```

```
One Sample t-test

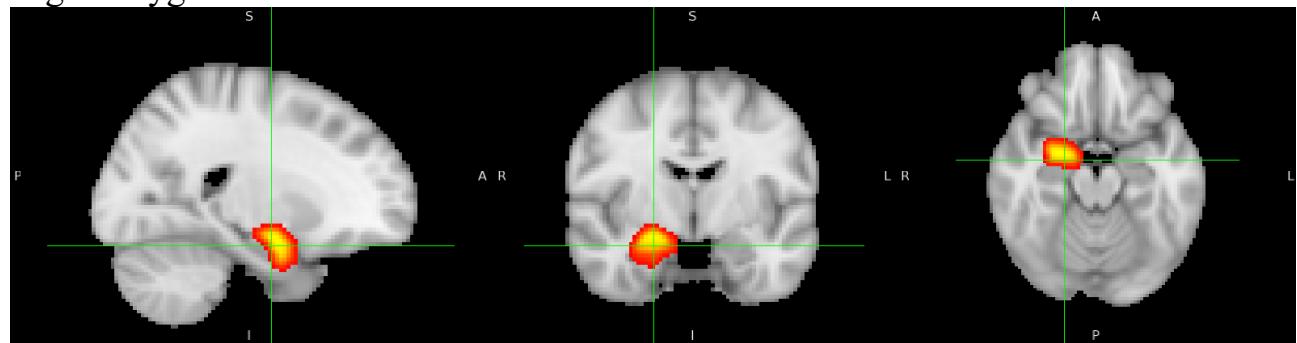
data: w
t = 4.34, df = 25, p-value = 0.0002061
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
0.3214165 0.9019720
sample estimates:
mean of x
0.6116943
```

And the mask in fsleyes:



3- Use the Harvard-Oxford subcortical atlas to create an anatomical mask of the right amygdala. Label it whatever you want. Then, extract the z-statistics from cope1 (i.e., the contrast estimates for Incongruent compared to baseline).

Right amygdala in Harvard-Oxford subcortical atlas:



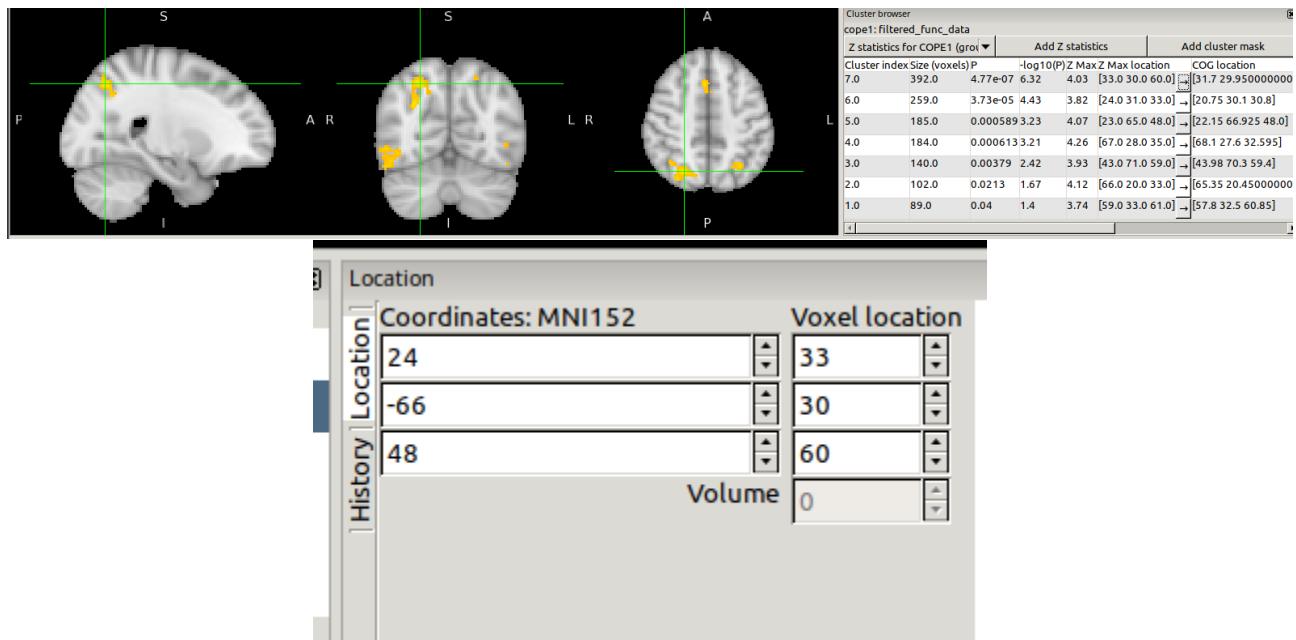
The results of extracting the zstats from COPE1 “incongruent task” and get the p-value and mean using Rstudio:

```
> t.test(m)
```

One Sample t-test

```
data: m
t = 2.9828, df = 25, p-value = 0.006293
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 0.1314132 0.7177278
sample estimates:
mean of x
0.4245705
```

8.3 The ROI using the coordinates of the max cluster from the 3rd level analysis.



So we go to make the script that make a binarized mask in this coordinates:

```
mahmoud@Mahmoud:~$ fslmaths $FSLDIR/data/standard/MNI152_T1_2mm.nii.gz -mul 0 -add 1 -roi 33 1 30 1 60 1 0 1 Degla_ROI_dmPFC_0_20_44.nii.gz -odt float
```

The statistical output for this cluster:

```
> t.test(s)
```

One Sample t-test

```
data: s
t = 5.8416, df = 25, p-value = 4.305e-06
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 0.5175547 1.0812259
sample estimates:
mean of x
0.7993903
```

We see that the P-value is almost zero that mean that the results are statistically significant.

9. Plotting the means and P-values for the COPEs:

- The code:

```
# Calculate means and p-values
mean_dif = np.mean(incong_cong)
mean_incong = np.mean(incong)
mean_cong = np.mean(cong)
p_value_dif = 0.3408
p_value_incong = 0.006293
P_value_cong = 0.01726

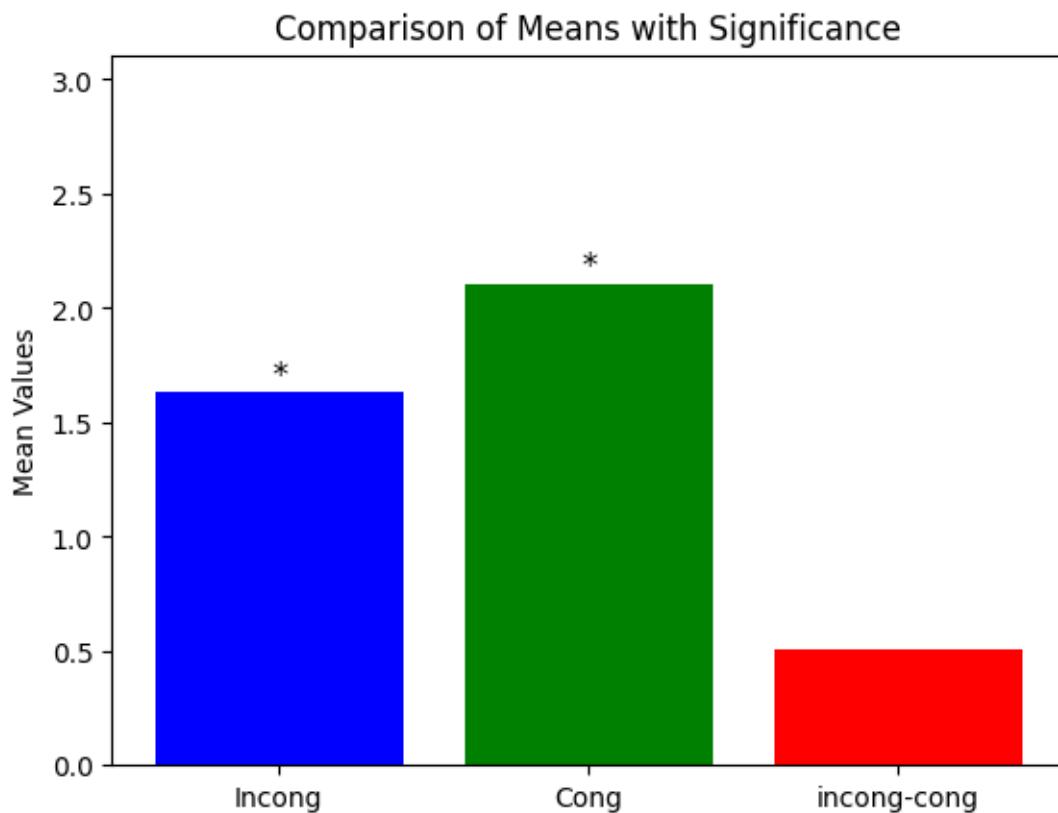
# Plotting
labels = ['Incong', 'Cong', 'incong-cong']
means = [mean_incong, mean_cong, mean_dif]
p_values = [p_value_incong, P_value_cong, p_value_dif]

fig, ax = plt.subplots()

bars = ax.bar(labels, means, color=['blue', 'green', 'red'])

# Adding stars based on p-values
for i, bar in enumerate(bars):
    yval = bar.get_height()
    if p_values[i] < 0.001:
        plt.text(bar.get_x() + bar.get_width()/2.0, yval, '**', ha='center', va='bottom', fontsize=12)
    elif p_values[i] < 0.05:
        plt.text(bar.get_x() + bar.get_width()/2.0, yval, '*', ha='center', va='bottom', fontsize=12)
```

- The results:



10. Expectations vs. Observations:

In the beginning of the experiment analysis, I expect some regions of the brain to activate according to study the neuroanatomy and study the Flanker event and dataset very well and be reading some of the research papers that related to this test events like this two papers:

Behavioral/Cognitive

Distinct Regions within Medial Prefrontal Cortex Process Pain and Cognition

¹Andrew Jahn,¹ ^{1,2}Derek Evan Nee,² William H. Alexander,³ and Joshua W. Brown⁴

¹Haskins Laboratories, New Haven, Connecticut 06511, ²Department of Psychology, Florida State University, Tallahassee, Florida 32312-4301, ³Department of Experimental Psychology, Ghent University, B-9000 Ghent, Belgium, and ⁴Department of Psychological and Brain Sciences, Indiana University, Bloomington, Indiana 47405

This paper give some regions and coordinates that activate after some events one of this events is very similar to the flanker “incongruent” event and this regions are:

Table 1. Whole-brain activations at $p < 0.001$ uncorrected, $p < 0.05$ cluster-corrected

Brain region	x	y	z	Zscore	Cluster-corrected <i>p</i> value	Cluster size (voxels)
Pain						
Right somatosensory cortex	38	-24	54	5.91	< 0.001	762
Right insula	40	-18	12	5.76	< 0.001	902
Left cerebellum	-28	-56	-24	5.43	< 0.001	832
Left cingulate gyrus	-2	30	14	5.17	< 0.001	788
Right cerebellum	2	-72	-14	4.26	< 0.001	524
Right parieto-occipital sulcus	8	-84	40	3.85	< 0.001	335

And the other paper is more related to the flanker test:

Competition between functional brain networks mediates behavioral variability

A.M. Clare Kelly,^a Lucina Q. Uddin,^a Bharat B. Biswal,^b
F. Xavier Castellanos,^a and Michael P. Milham^{a,*}

^aThe Phyllis Green and Randolph Cöwen Institute for Pediatric Neuroscience, NYU Child Study Center, New York, NY 10016, USA

^bDepartment of Radiology, University of Medicine and Dentistry of New Jersey, Newark, NJ 07101, USA

Received 2 April 2007; revised 24 July 2007; accepted 6 August 2007

Available online 23 August 2007

And that is the table of coordinates and regions:

	Cluster	x	y	z	Anatomical region
RSN 1	1	6	-78	-3	Lingual gyrus
	2	24	-78	-10	Lingual gyrus
	3	-30	-89	20	Middle occipital gyrus
RSN 2	1	-2	-51	27	Cingulate gyrus
	2	53	-57	23	Superior temporal gyrus
	3	2	54	-3	Middle frontal gyrus
	4	-20	-19	-18	Hippocampus
	5	6	-19	6	Thalamus
	6	-4	-6	40	Cingulate gyrus
RSN 3	1	-51	-7	8	Precentral gyrus
	2	-55	-18	8	Superior temporal gyrus
	3	57	-5	20	Precentral gyrus
	4	12	-17	0	Thalamus
	5	22	-16	-13	Hippocampus
	6	-2	-21	42	Paracentral lobule
RSN 4	1	46	6	34	Middle frontal gyrus
	2	44	-48	46	Inferior parietal lobule
	3	-38	-46	48	Superior parietal lobule
	4	-55	-58	-9	Inferior temporal gyrus
	5	62	-37	-3	Middle temporal gyrus
RSN 5	1	52	26	-4	Inferior frontal gyrus
	2	6	46	18	Medial frontal gyrus
	3	8	-47	41	Cingulate gyrus
	4	8	-16	40	Cingulate gyrus

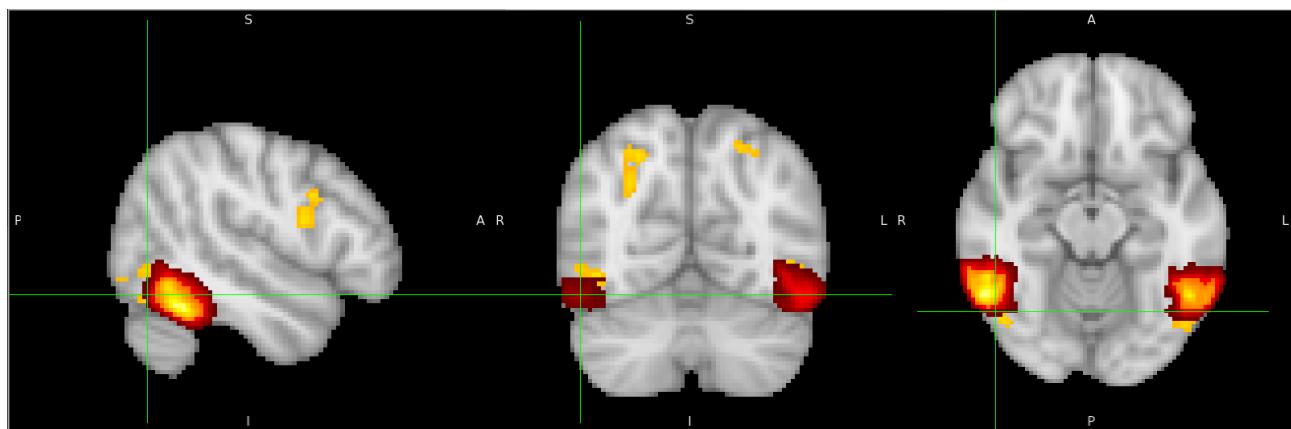
And me own expectations that this regions will lighting up:

- the **Dorsolateral Prefrontal Cortex** (DLPFC), would be lighting up. That's because it's crucial for keeping attention focused on the right thing and blocking out distractions.
- The **Anterior Cingulate Cortex** (ACC) would also be active. It's like a brain's referee, stepping in to resolve conflicts and make sure you're staying on track.
- **Inferior Parietal Lobule** (IPL) would be working hard too. It helps to shift attention where it's needed most, filtering out the noise and homing in on the important stuff.
- The **Dorsal Anterior Insula** would also be active. It's all about integrating different kinds of information in your brain, helping you make smart decisions even when things get tough.
- The **Superior Temporal Gyrus** might join in as well. It's usually involved in understanding language and sorting through different meanings, which could help in untangle conflicting messages in the task.
- The **Superior Parietal Lobule (SPL)** is another critical region of the brain involved in attentional processes and spatial awareness. It's responsible for integrating sensory information from various modalities, such as touch, vision, and proprioception, to create a coherent representation of the body and its surroundings in space.

The results and observations that these regions are firing during the incongruent condition:

temporal gyrus:

During the incongruent condition of the Flanker task, activation in the temporal gyrus might reflect its role in processing and integrating contextual information, including the semantic and spatial relationships between stimuli. Additionally, the temporal gyrus is involved in higher-order perceptual processing, such as detecting changes in sensory input and making fine-grained discriminations between stimuli.



Superior Parietal Lobule:

During the incongruent condition of the Flanker task, where there is conflict between the target and distractor stimuli, the SPL is expected to show increased activation. This activation likely reflects the role of the SPL in directing spatial attention and coordinating the selection of relevant information while suppressing interference from irrelevant stimuli.

The SPL is particularly involved in visuospatial processing and the manipulation of spatial representations in working memory. Activation in this region during the incongruent condition of the Flanker task may therefore indicate its contribution to resolving conflict by enhancing selective attention to the target stimulus and facilitating the inhibition of distracting information.

