Sharif University Of Technology

Neuroscience Lab

Introduction to fMRI (AFNI)

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Section 1: Brain Extraction

1.1 Removing the Skull and Surrounding Area of the Brain

By using the function 1, the skull is precisely separated from surrounding. The result show in figure 1.

$$3dSkullStrip \quad -inputsub-13\_T1w.nii.gz \quad -prefix \quad FT\_anat\_brain \tag{1}$$

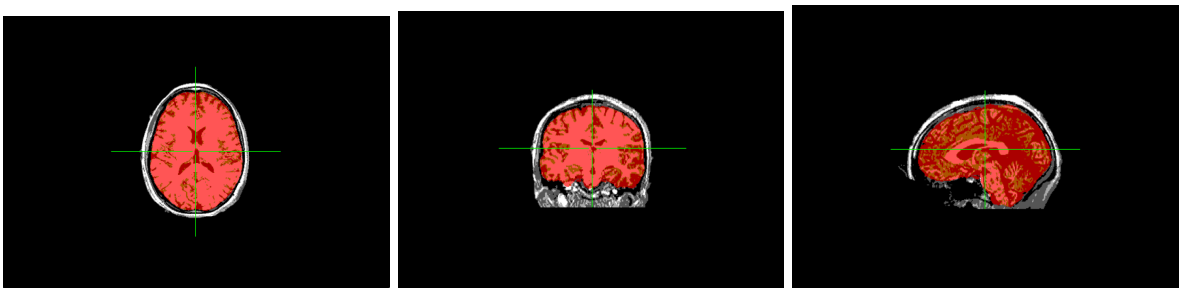

Figure 1: Skull- axial, coronal and sagittal view.

1.2 Making a Gray Matter Mask

By using the function 2 and the range is shown in figure 2, the gray matter mask is created.

$$3dcalc \quad -aFT\_anat\_brain+orig \quad -expr'within(a,600,2900)' \quad -prefix \quad anat\_3dcalc\_result \tag{2}$$

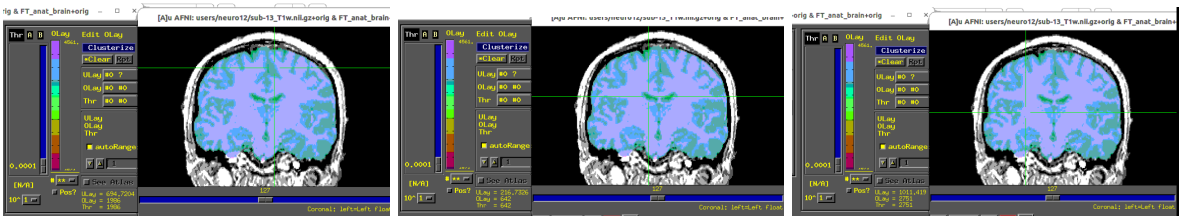

Figure 2: In order to: gray_matter,ventricle and white_matter.

Final mask:

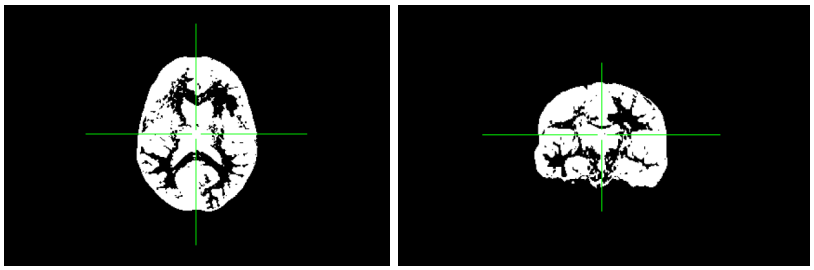

Figure 3: Gray Matter Mask.

Section 2: Pre-process Functional Image

I run the steps as below:

(About the slice time correction, we have the slice order, not time. So, I use the '3dinfo' function. This data has a time step equal $2s$ and the number of slice is 32. So dt equal $0.066s$. I save the slice time in a file and use 'tpattern' option in '3dTshift' function.)

step 1: slice time correction

$$3dTshift \quad -tpattern \quad '@time_slice.txt' \quad -prefix \quad sub-13_task_tshift \\ sub-13_task-visualoddballwithbuttonresponsetotargetstimuli_run-01_bold.nii.gz \quad (3)$$

step 2: motion correction

$$3dvolreg \quad -verbose \quad -zpad1 \quad -base \quad sub-13_task_tshift+orig \\ -1Dfile \quad dfile.FT1.1D \quad -prefix \quad sub-13_task.volreg \\ -cubic \quad -1Dmatrix_save mat.FT1.vr.aff12.1D \quad sub-13_task_tshift+orig \quad (4)$$

step 3: normalize to mean

$$3dTstat \quad -mean \quad -prefix \quad meanfunc1.nii.gz \quad sub-13_task.volreg+orig \\ 3dcalc \quad -a \quad sub-13_task.volreg+orig \quad -b \quad meanfunc1.nii.gz \\ -expr'(a-b)/(abs(b)+1)*astep(b,200)*100' \quad -prefix sub-13_task.scale \\ 3dAutomask \quad -clfrac \quad 0.4 \quad -prefix \quad clean_base.nii.gz meanfunc1.nii.gz \\ 3dBandpass \quad -input \quad sub-13_task.scale+orig \quad -mask \quad clean_base.nii.gz \quad -blur \quad 5 \\ -band \quad 0.01 \quad 0.1 \quad -prefix \quad sub-13_task.scale.smooth \quad (5)$$

In figure , you can see the functional image before and after pre-processing:

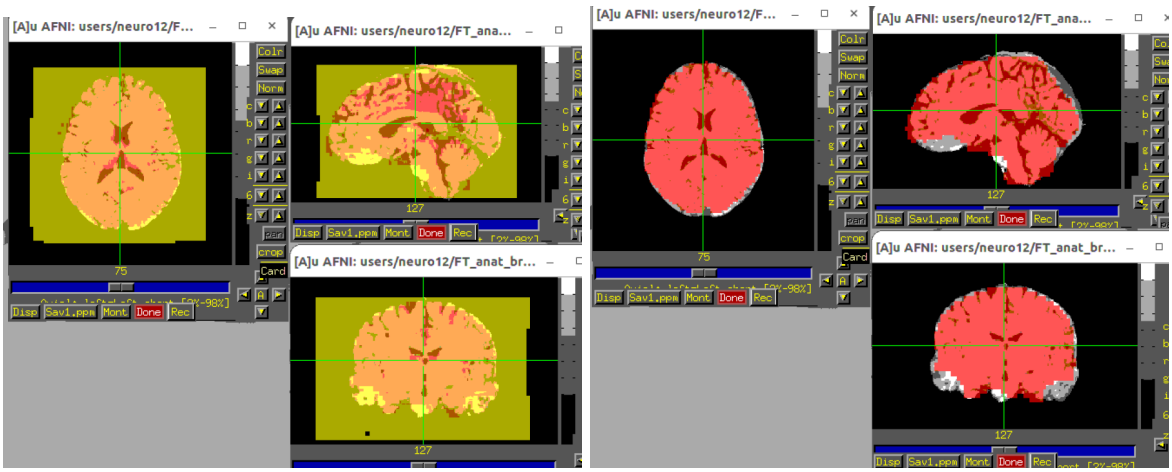

Figure 4: Pre-processing functional image; left: before, right: after pre-processing (clean_base)

Section 3: Align functional and structural image

Align EPI and anatomical datasets by using a below function:

$$\begin{aligned} &align\_epi\_anat.py \quad -anat2epi \quad -anat \quad FT_anat_brain + orig \\ &-anat_has_skull \quad no \quad -suffix_al_junk \\ &-epiclean_base.nii.gz \quad -epi_base0 \\ &-epi_strip \quad 3dAutomask \\ &-cost \quad nmi \quad -giant_move \quad -rigid_body \\ &-volreg \quad off \quad -tshift off \end{aligned} \tag{6}$$

Align anatomical to epi:

$$\begin{aligned} &cat_matvec \quad FT_anat_brain_al_junk_mat.aff12.1D \quad -I \quad > \quad func2mri_warp.1D \\ &3dAllineate \quad -base FT_anat_brain + orig \\ &-input \quad clean_base.nii.gz \\ &-1Dmatrix_apply \quad func2mri_warp.1D \\ &-prefix \quad epimask2anat.nii.gz \end{aligned} \tag{7}$$

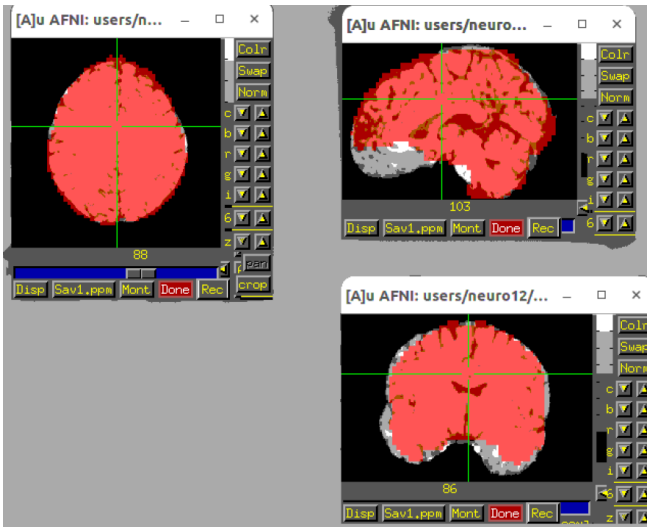

Figure 5: Align epi to anat; underlay: FT_anat_brain_al_junk, overlay: clean_base

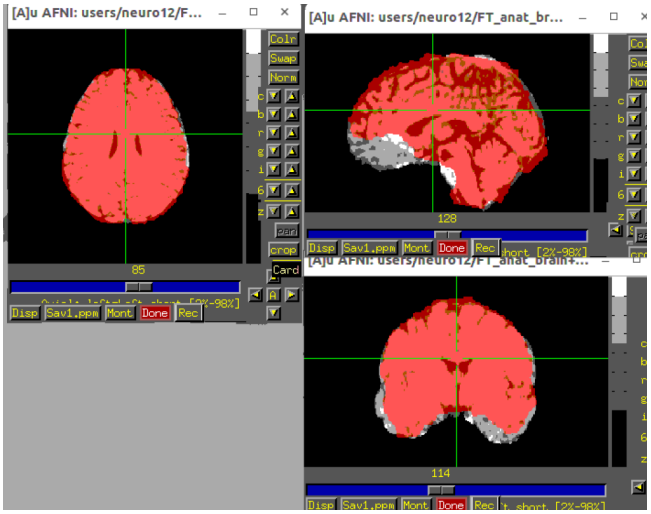

Figure 6: Align anat to epi; underlay: FT_anat_brain, overlay: epimask2anat

Section 4: Regressors & GLM

The onset time of each stimulus (usual and unusual), the subject response, the contrast and the mean of these two type of stimulus is considered as a regressors. I use the '3dDeconvolve' function as below:

$$\begin{aligned} &3dDeconvolve \quad -input \quad sub-13_task.scale.smooth+orig \\ &\quad -polort \quad 0 \\ &\quad -num_stimts \quad 3 \\ &\quad -stim_times \quad 1 \quad visual_time.txt \quad 'BLOCK(0.2,1)' \\ &\quad -stim_label \quad 1 \quad visual \\ &\quad -stim_times \quad 2 \quad oddball_time.txt \quad 'BLOCK(0.2,1)' \\ &\quad -stim_label \quad 2 \quad oddball \\ &\quad -stim_times_FSL \quad 3 \quad response_time.txt \quad 'dmBLOCK(1)' \\ &\quad -stim_label \quad 3 \quad response \\ &\quad -jobs \quad 2 \\ &\quad -gltsym \quad 'SYM: \quad visual \quad -oddball' \\ &\quad -glt_label \quad 1 \quad V-Odd \\ &\quad -gltsym \quad 'SYM: \quad 0.5*visual \quad +0.5*oddball' \\ &\quad -glt_label \quad 2 \quad mean.VOdd \\ &\quad -fout \quad -tout \quad -x1D \quad X.xmat.1D \quad -xjpeg \quad X.jpg \\ &\quad -errts \quad errts.sub-13 \\ &\quad -bucket \quad stats.sub-13 \end{aligned} \tag{8}$$

The GLM coefficient is mapped to anatomical image by using '3dAllineate' function:

$$\begin{aligned} &3dAllineate \quad -base \quad FT_anat_train+orig \\ &\quad -input \quad stats.sub-13+orig \\ &\quad -1Dmatrix_apply \quad func2mri_warp.1D \\ &\quad -prefix \quad GLM_stats2anat.nii.gz \end{aligned} \tag{9}$$

$$\begin{aligned} &3dAllineate \quad -baseFT_anat_train+orig \\ &\quad -input \quad errts.sub-13+orig \\ &\quad -1Dmatrix_apply \quad func2mri_warp.1D \\ &\quad -prefix \quad GLM_errts2anat.nii.gz \end{aligned} \tag{10}$$

Now, I show each regressors coefficient on the anatomical images. The region with higher value were more active for the task.

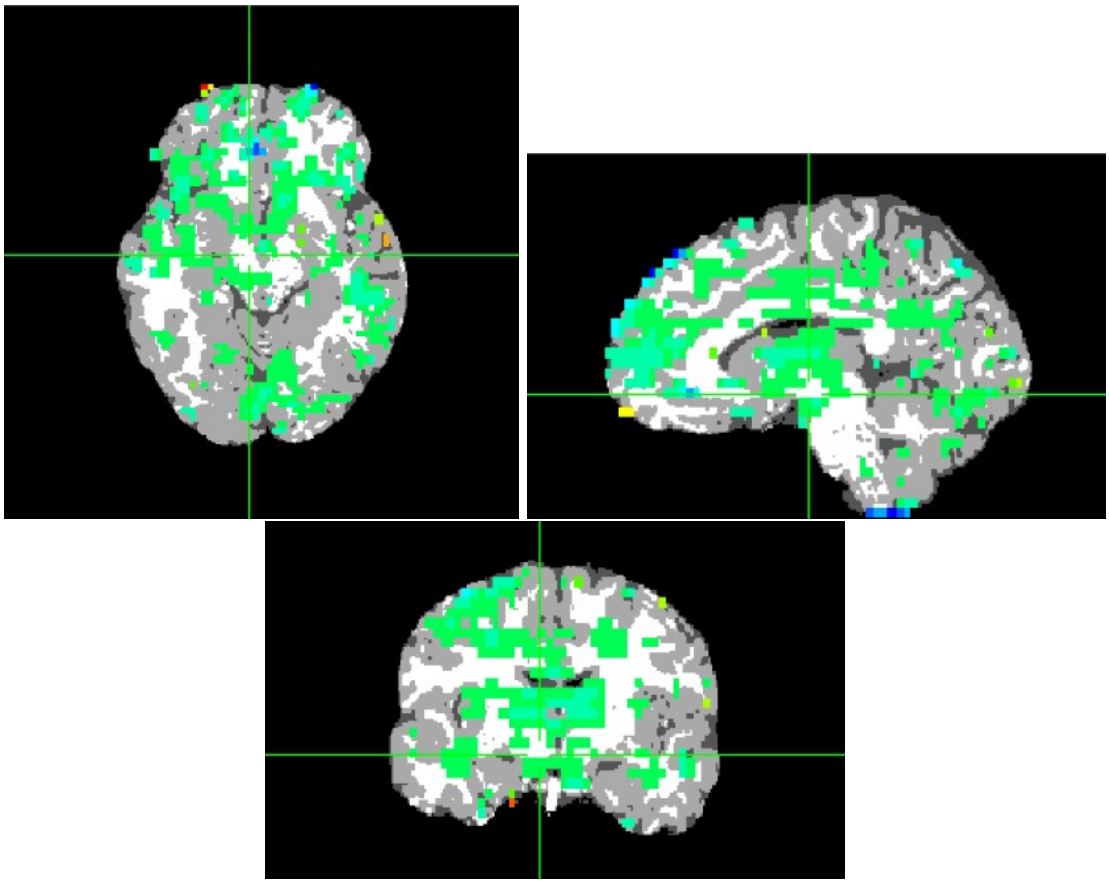

Figure 7: Active region when the normal stimulus is shown. ($(p < 0.05)$)

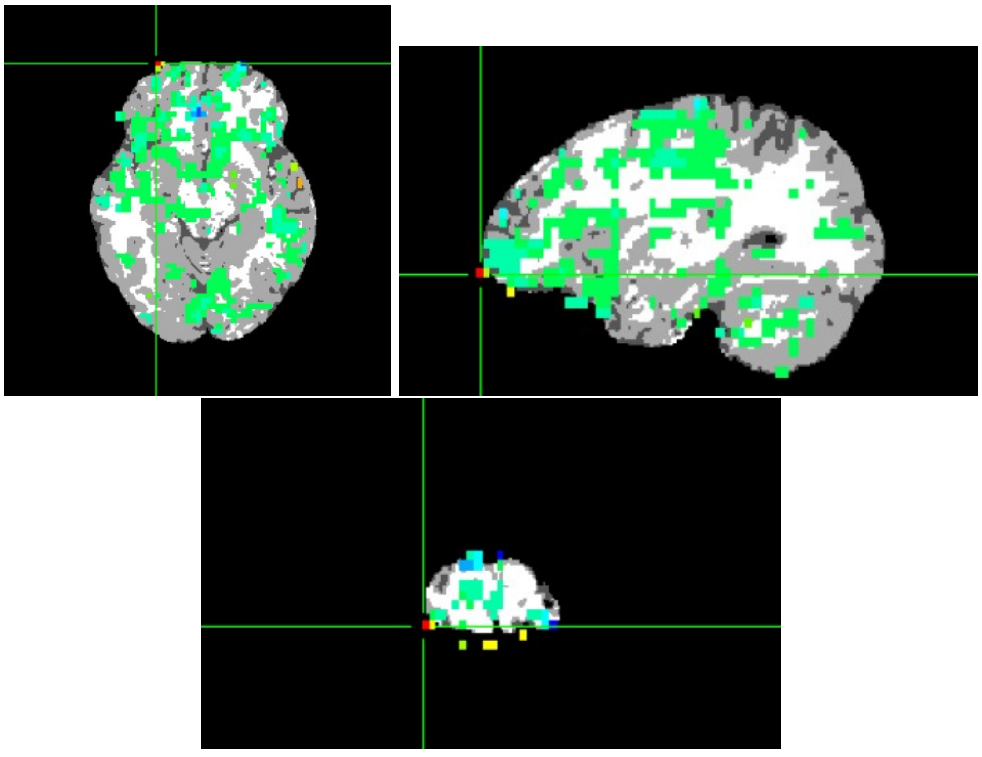

Figure 8: The most active region when the normal stimulus is shown. ($(p < 0.05)$)

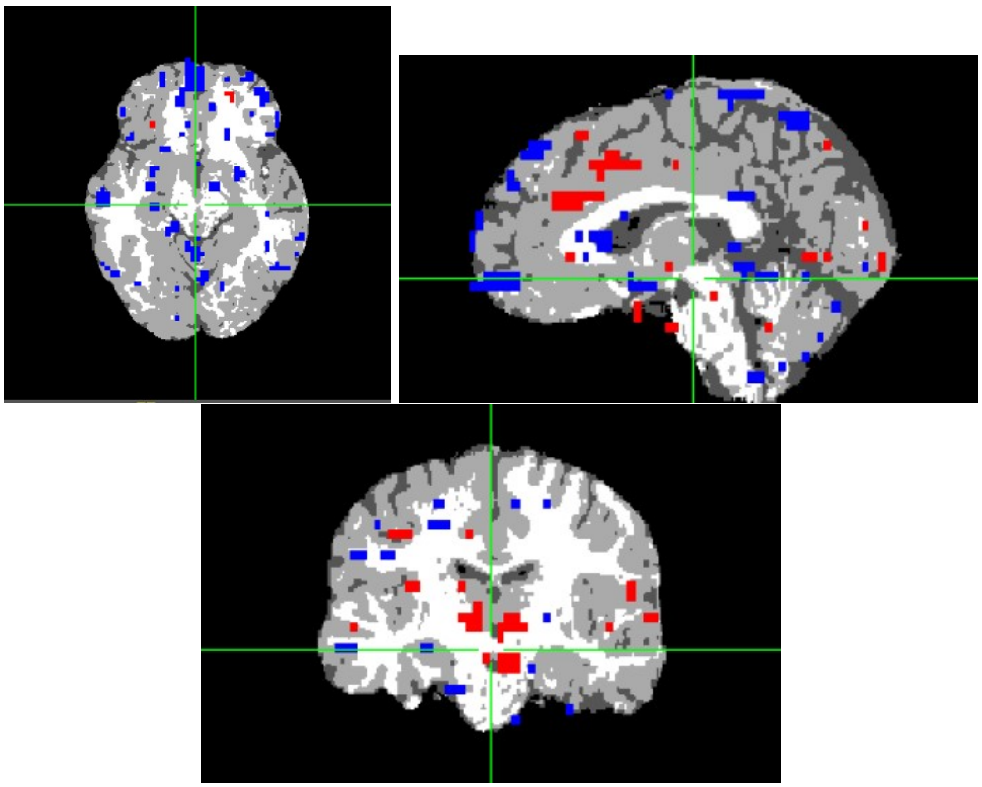

Figure 9: Active region when the oddball stimulus is shown. ($(p < 0.05)$)

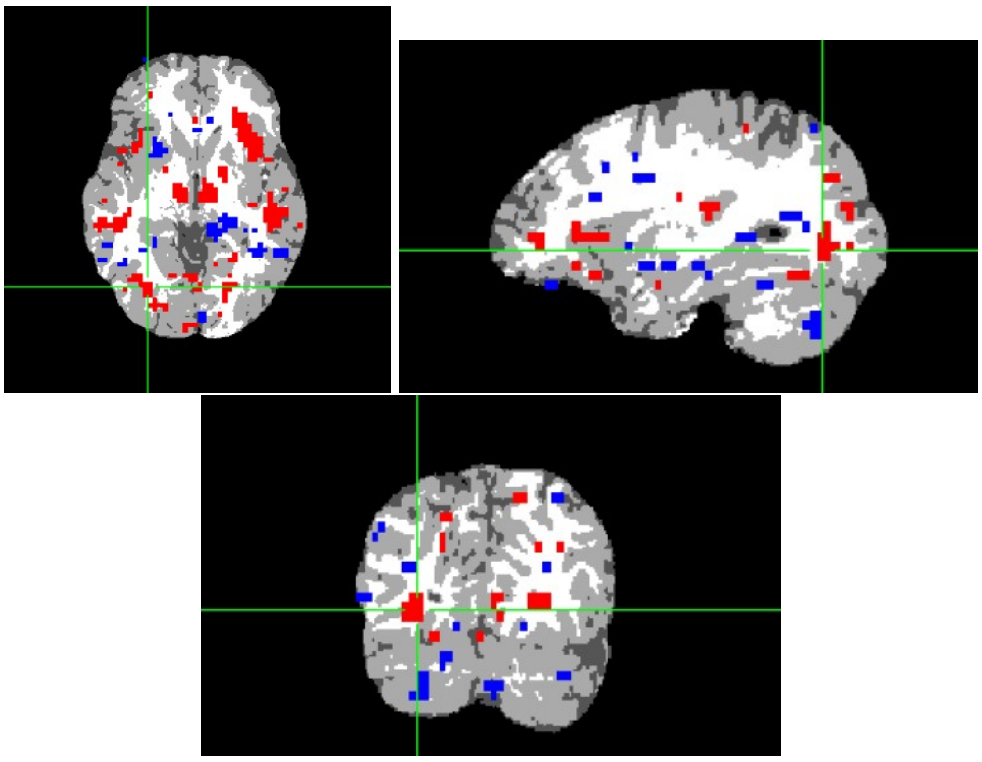

Figure 10: The most active region when the oddball stimulus is shown. ($(p < 0.05)$)

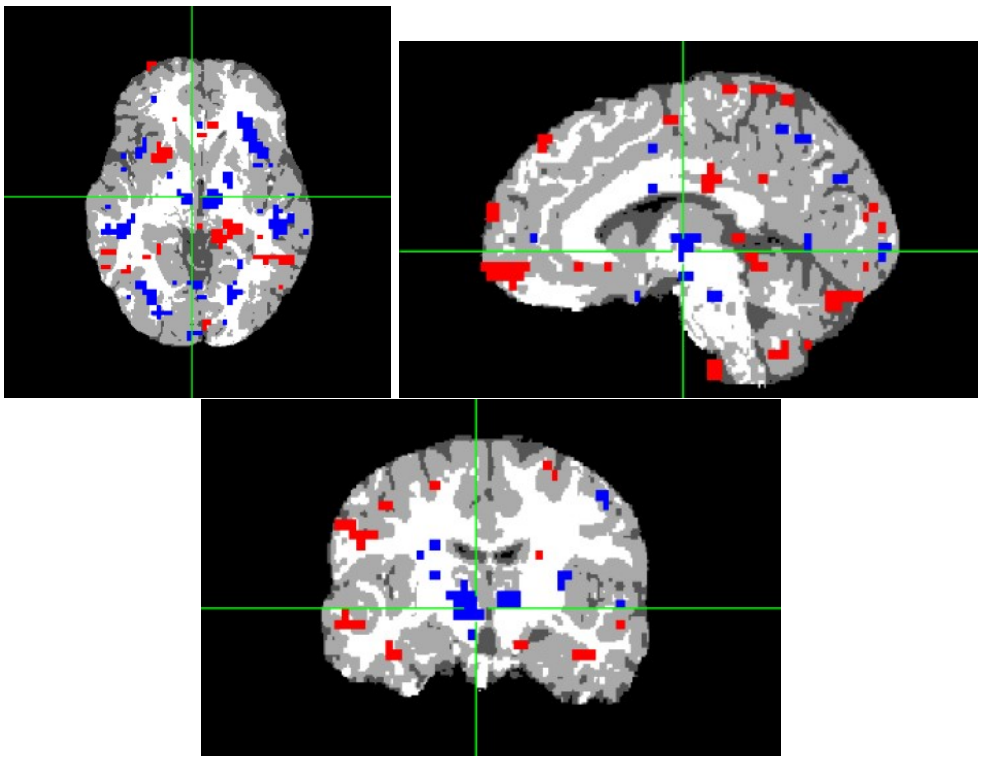

Figure 11: The most active region in the response time.($(p < 0.05)$)

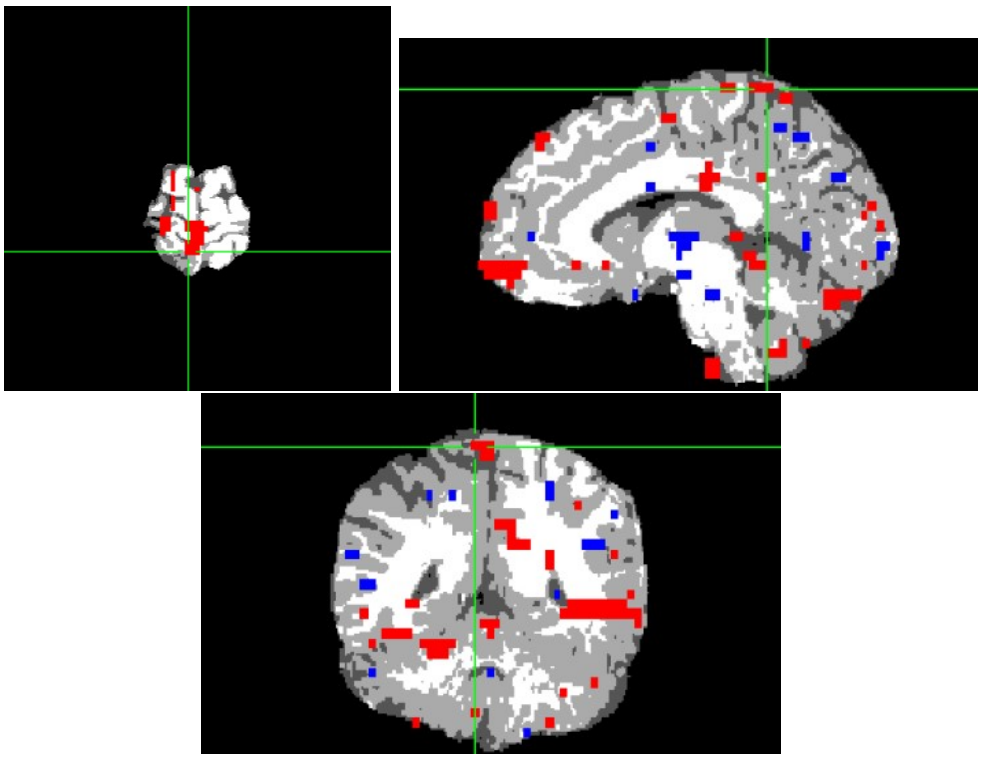

Figure 12: The most active region in the response time.($(p < 0.05)$)

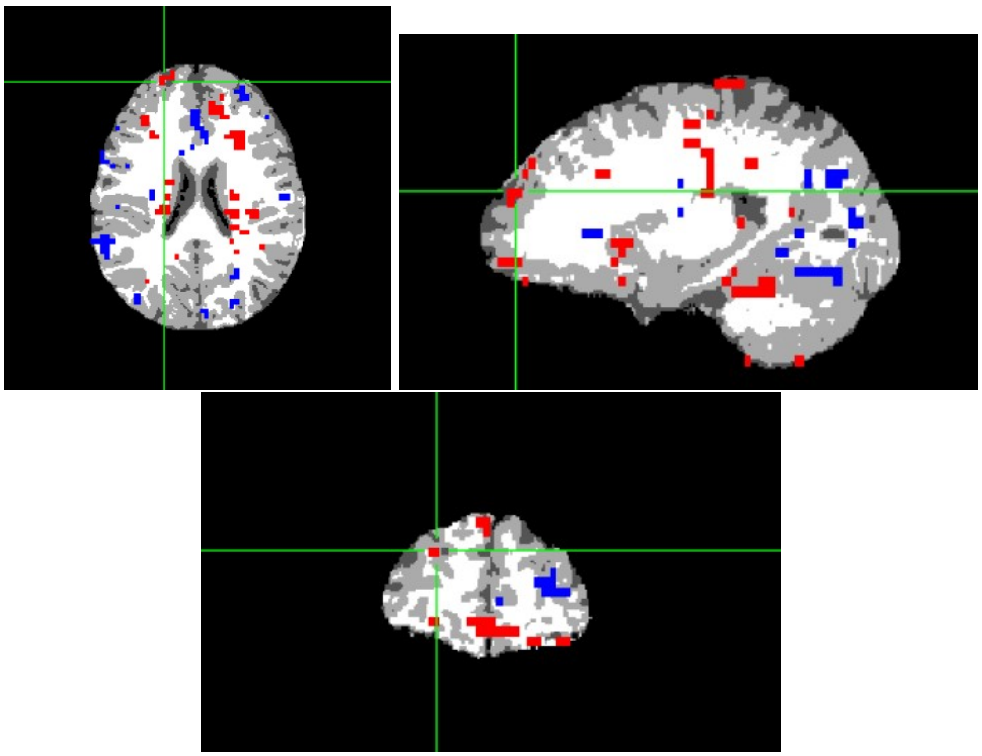

Figure 13: The difference regions' activities (normal - oddball). ($(p < 0.05)$)

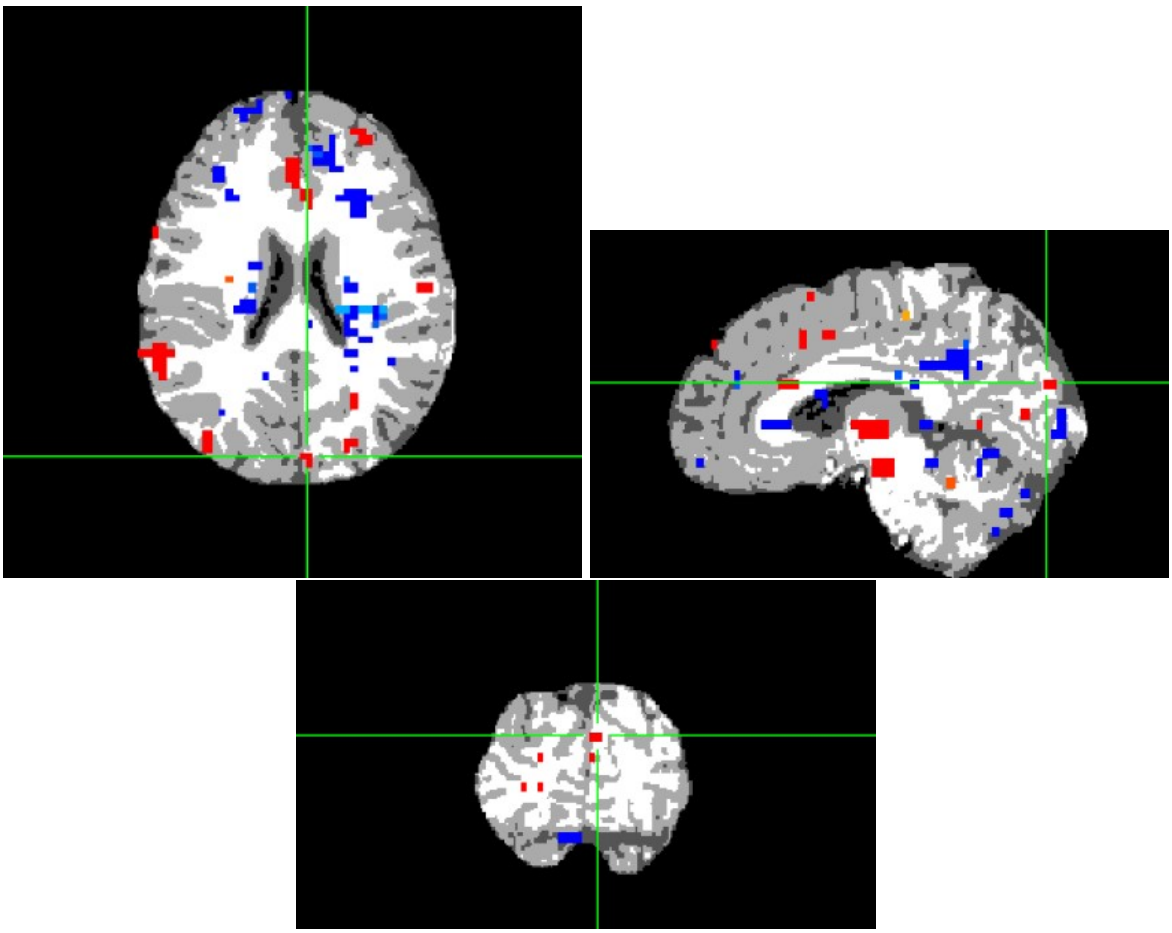

Figure 14: The mean of region activity ($(p < 0.05)$). It show the common regions where are be activated for both stimulus.