



دانشگاه تهران

پردیس دانشکده‌های فنی

دانشکده‌ی مهندسی برق و کامپیوتر

تمرین چهارم درس مبانی علوم شناختی

نام و نام خانوادگی:

سینا پیرمرادیان

شماره دانشجویی:

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استاد:

دکتر محمدرضا ابوالقاسمی دهاقانی

Introduction:

The first part of the exercise is related to the preprocessing and FMRI analysis using the SPM toolbox.

Functional Magnetic Resonance Imaging (fMRI) is a non-invasive imaging technique that uses magnetic fields and radio waves to measure changes in blood flow in the brain. These changes are associated with brain activity, and fMRI can be used to track brain activity in real time.

FMRI has become an essential tool in neuroscience research, and it is also used in clinical settings to diagnose and treat brain disorders.

In this report, we will discuss the preprocessing steps involved in analyzing FMRI data using the SPM toolbox and also for surveying the connectivity between some sections of the brain we use CONN toolbox.

The steps include data importing, slice timing, realignment and re-slicing, apply VDM, and artifact removal techniques, co-registration, normalization and smoothing.

1. FMRI Preprocessing Steps

In this section, we intend to preprocess the FMRI data. We know that it is crucial for improving the quality, interpretability, and reliability of the results. The following steps were performed on the FMRI data using the SPM toolbox:

1. Data Preparation:

The data set consists of 4 files, we have two types of data, anatomical and functional, and first we check the structural data. These data are three-dimensional and show the structure of the brain with high resolution, then we will examine the functional data. These data are 4D, the fourth dimension of which is time and shows the blood oxygen in each Voxel in each TR.

Structural data shows different scans of the brain in a unit of time, when the resolution of the structural data is reduced. It makes us unable to see the structure of the brain well in functional images. Therefore, the goal is to use structural data and put these two functional and structural data on top of each other.

When the person is in the machine and the machine is mapping his brain, the person may shake his head, which will cause our information mapping in the time series to be disturbed. Therefore, another goal is to remove unwanted movements of the subject.

1.1. Make a directory:

First, we determine where the data is located and introduce the data path to the SPM toolbox. The specified path is shown in Figure 1.

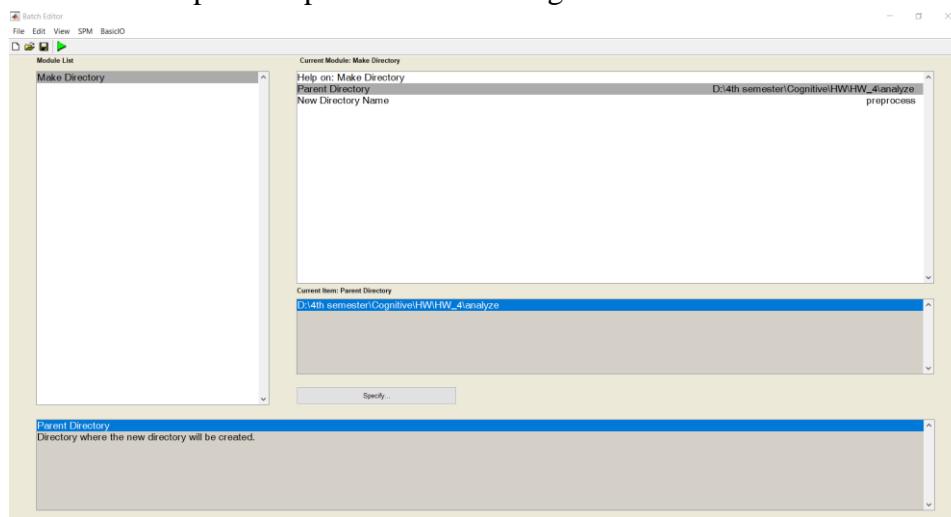


Figure 1

1.2. Slice Timing:

By using Slice Timing, the time difference and distance between different parts of the brain that were mapped can be eliminated. In other words, the mapping of different levels of the brain faces a time difference, so we use Slice Timing to eliminate this time difference. The process is that we eliminate this time difference by using the number of levels and mapping repetition time that is set during the test in the device.

The parameters that were provided to us for Slicing Time in the Json files were as follows: there were 36 Slices and TR, which is Time Repetition, was equal to 2. Simens method has also been used to arrange the slices, first the even slices and then the odd slices. The settings are shown in Figure 2.

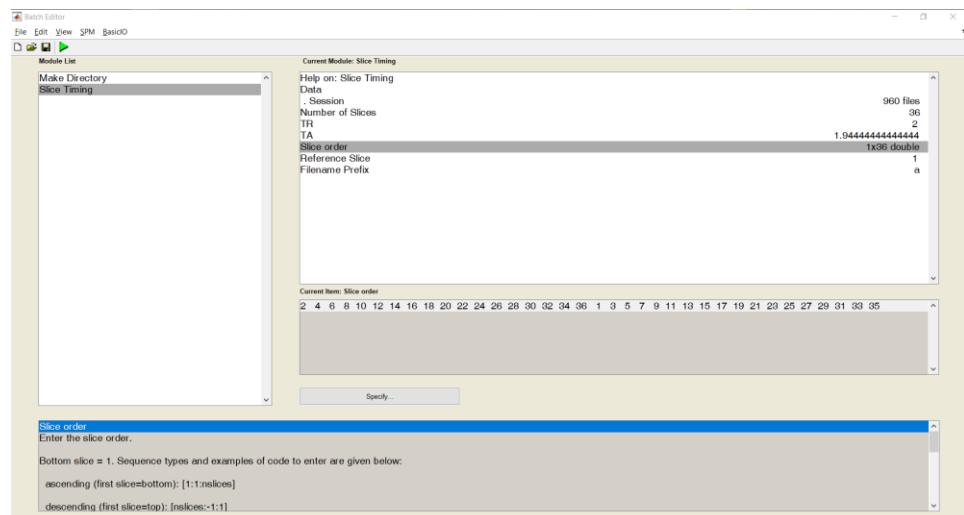


Figure 2

1.3. Realignment, Estimate and Reslice:

In this section, The Estimate part refers to estimating the amount that each volume is out of alignment with a reference volume, and Reslice indicates that these estimates will be used to nudge each of the volumes into alignment with the reference volume. At this step, the types of head movements of the Subject are estimated and we standardize the data accordingly.

The settings of this part are shown in Figure 3 and the summary and output of this part is shown in Figure 4.

As can be seen in output figure, the types of movements the head rotation in the direction of the side and height as well as the location compared to the first slice, which is actually reference, is given.

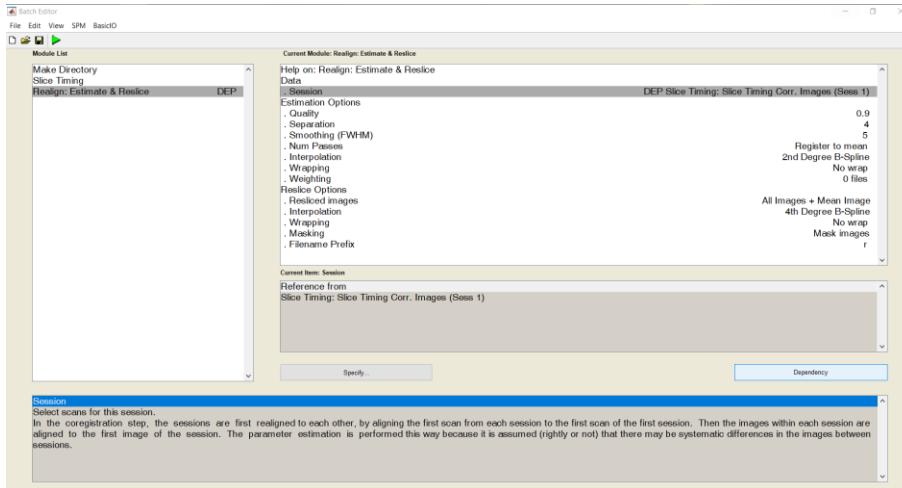


Figure 3

Image realignment

```

1 D:\4th semester\Cognitive\HWHW_4\analyze\data\sub-01\func\asub-01_task-Facetask_run-01_bold.nii,1
2 D:\4th semester\Cognitive\HWHW_4\analyze\data\sub-01\func\asub-01_task-Facetask_run-01_bold.nii,2
3 D:\4th semester\Cognitive\HWHW_4\analyze\data\sub-01\func\asub-01_task-Facetask_run-01_bold.nii,3
4 D:\4th semester\Cognitive\HWHW_4\analyze\data\sub-01\func\asub-01_task-Facetask_run-01_bold.nii,4
5 D:\4th semester\Cognitive\HWHW_4\analyze\data\sub-01\func\asub-01_task-Facetask_run-01_bold.nii,5
6 D:\4th semester\Cognitive\HWHW_4\analyze\data\sub-01\func\asub-01_task-Facetask_run-01_bold.nii,6
7 D:\4th semester\Cognitive\HWHW_4\analyze\data\sub-01\func\asub-01_task-Facetask_run-01_bold.nii,7
8 D:\4th semester\Cognitive\HWHW_4\analyze\data\sub-01\func\asub-01_task-Facetask_run-01_bold.nii,8
9 D:\4th semester\Cognitive\HWHW_4\analyze\data\sub-01\func\asub-01_task-Facetask_run-01_bold.nii,9
10 D:\4th semester\Cognitive\HWHW_4\analyze\data\sub-01\func\asub-01_task-Facetask_run-01_bold.nii,10
11 D:\4th semester\Cognitive\HWHW_4\analyze\data\sub-01\func\asub-01_task-Facetask_run-01_bold.nii,11
12 D:\4th semester\Cognitive\HWHW_4\analyze\data\sub-01\func\asub-01_task-Facetask_run-01_bold.nii,12
..... etc

```

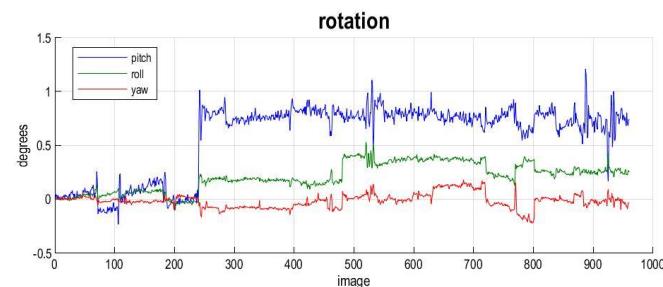
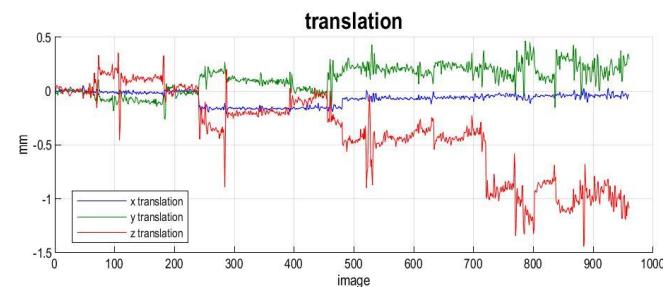


Figure 4

1.4. Calculate VDM:

It has been tried to create brain location maps based on the first brain image taken from the person, and we get VDM or brain location map. In the following, we tried to map other images based on this obtained map.

In this step, we must calculate the value of the range and phase of the functional data and apply it to the entire data. The phase and amplitude data are available in the fmap folder. VDM settings are shown in Figure 5.

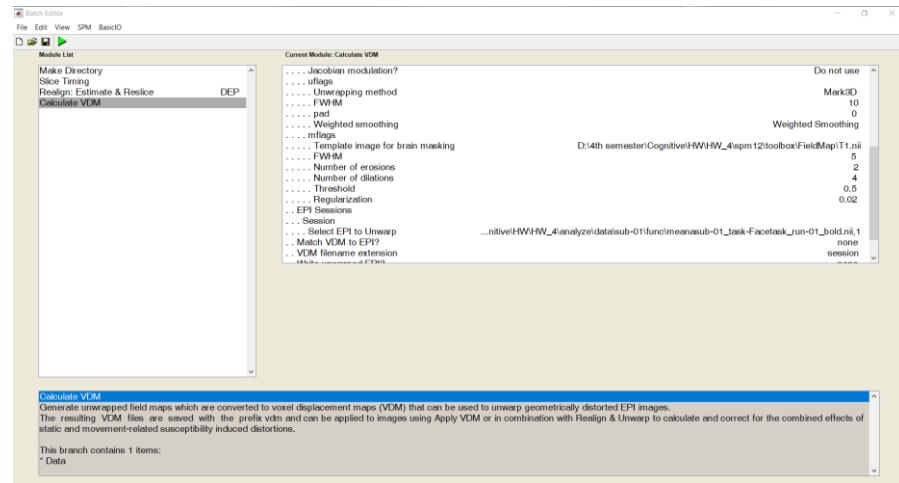


Figure 5

1.5. Apply VDM

After applying VDM, the angle changes relative to different axes disappear and all images become more uniform. The setting of this part is shown in Figure 6 and the VDM output is shown in Figure 7.

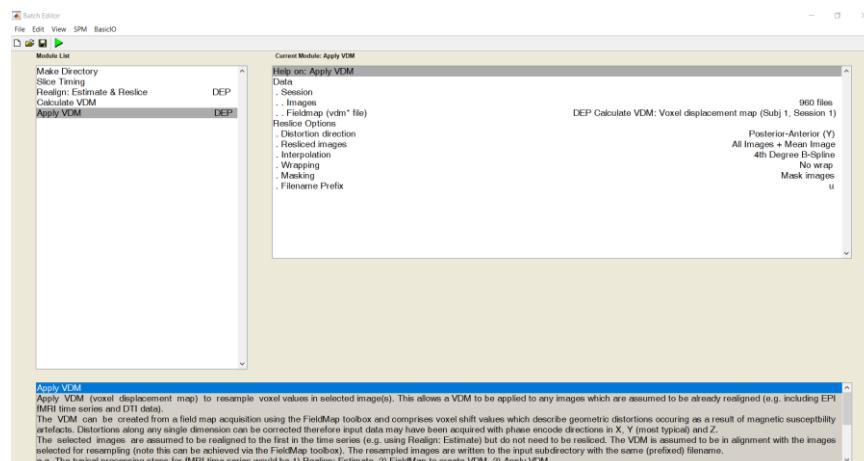


Figure 6

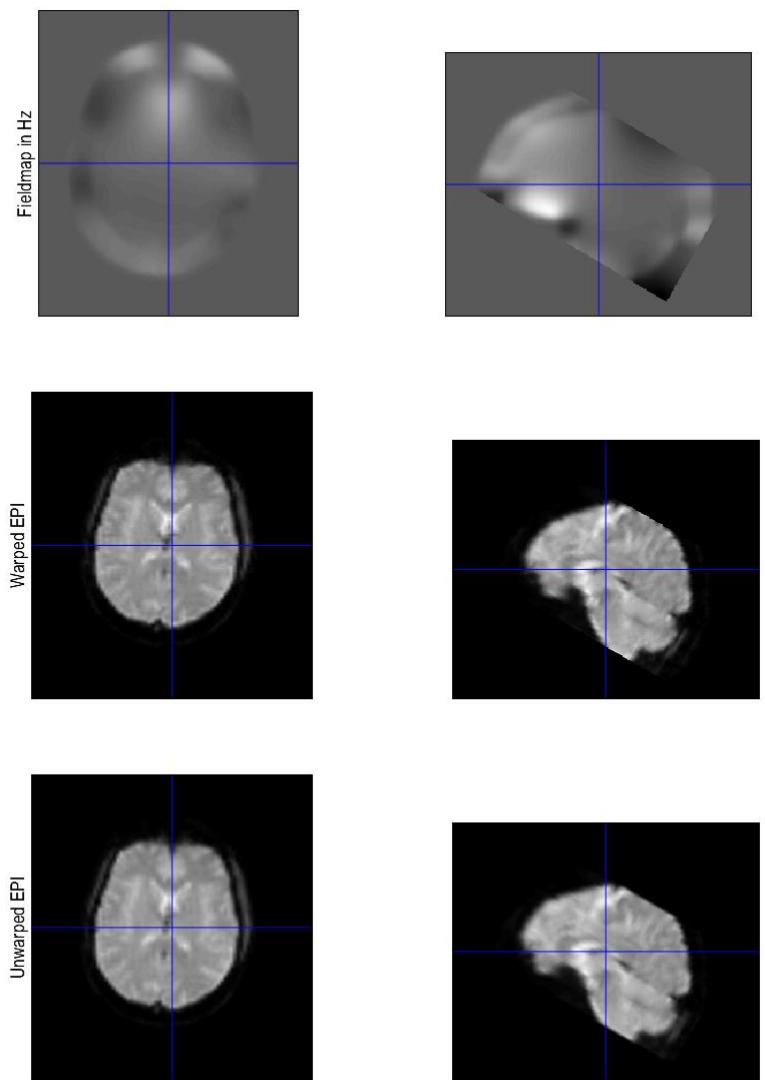


Figure 7

1.6 Co-registration:

In this step, we try to calculate the transformation matrix of structural data on functional data.

At the end of co-registration, the voxel-to-voxel affine transformation matrix is displayed, along with the histograms for the images in the original orientations, and the final orientations. The setting part is shown s Figure 8.

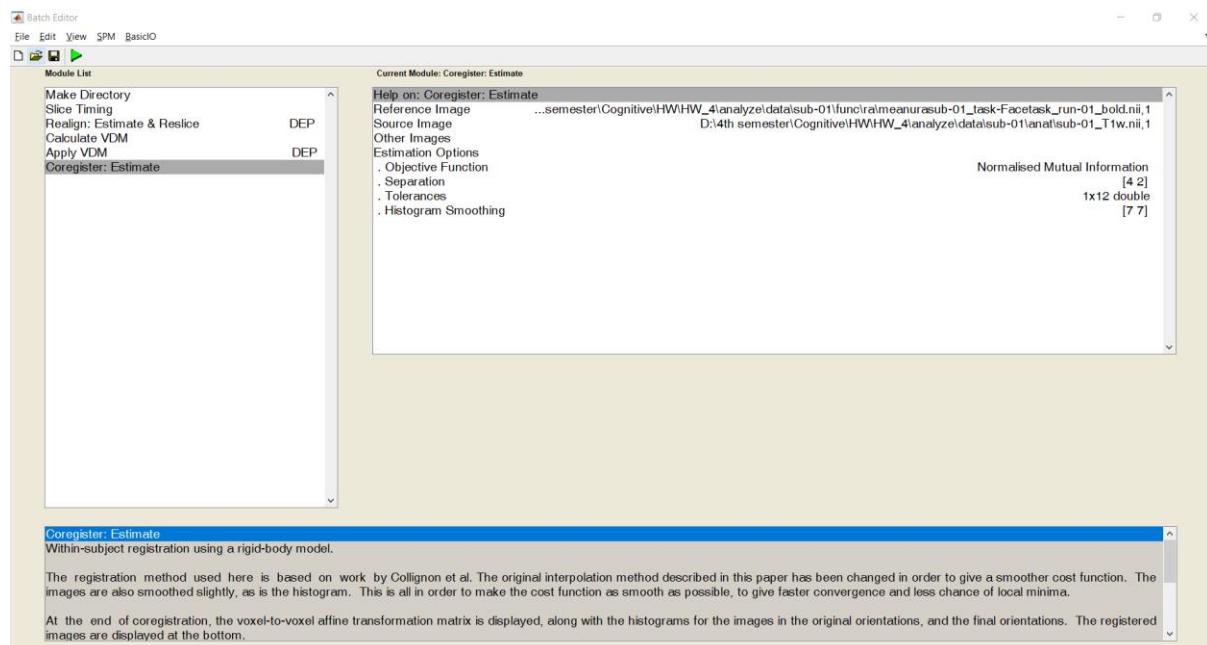


Figure 8

1.7. Normalization-estimation and write

After the anatomical image has been segmented, we can use those segmentations to normalize the image.

Select the Deformation Field that you created in the anat directory during Segmentation, and for Images to Write select all of the realigned and slice-time corrected images.

The settings related to estimation and writing are shown in Figure 9 and 10, respectively.

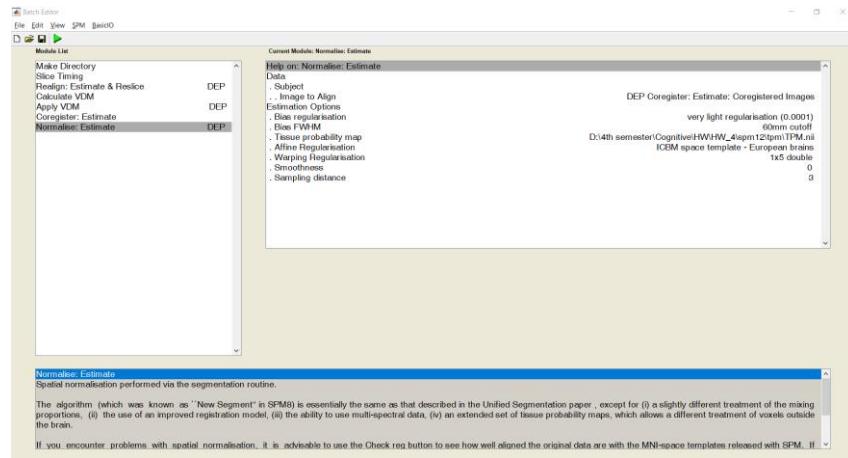


Figure 9

1.8. Normalization- write 1

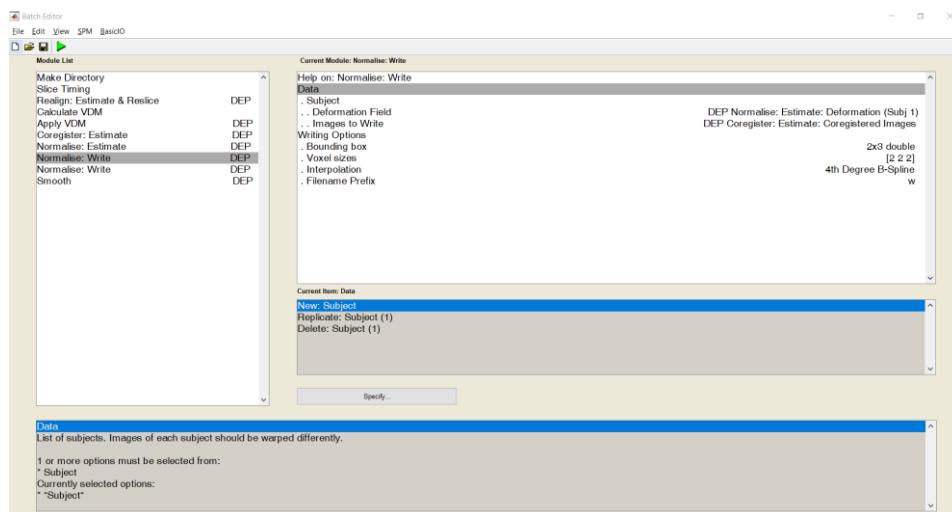


Figure 10

The output related to normalization, joint histogram before and after dropping the anatomical data on the functional data can be seen in Figure 11.

Normalised Mutual Information Coregistration

$$X_1 = -0.328X -0.031Y -0.022Z +76.125$$

$$Y_1 = -0.038X +0.292Y +0.150Z -15.707$$

$$Z_1 = -0.005X -0.139Y +0.269Z -9.535$$

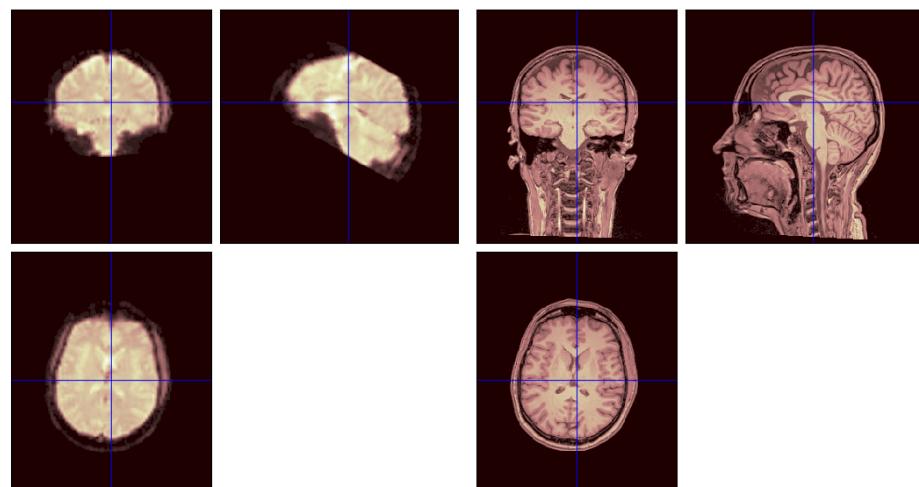
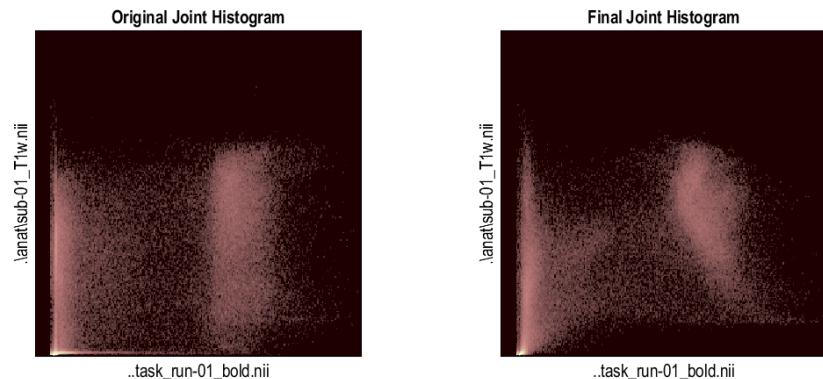


Figure 11

Here in Figure 12, we check to make sure that both the outlines of the brains and the internal structures are well-aligned.

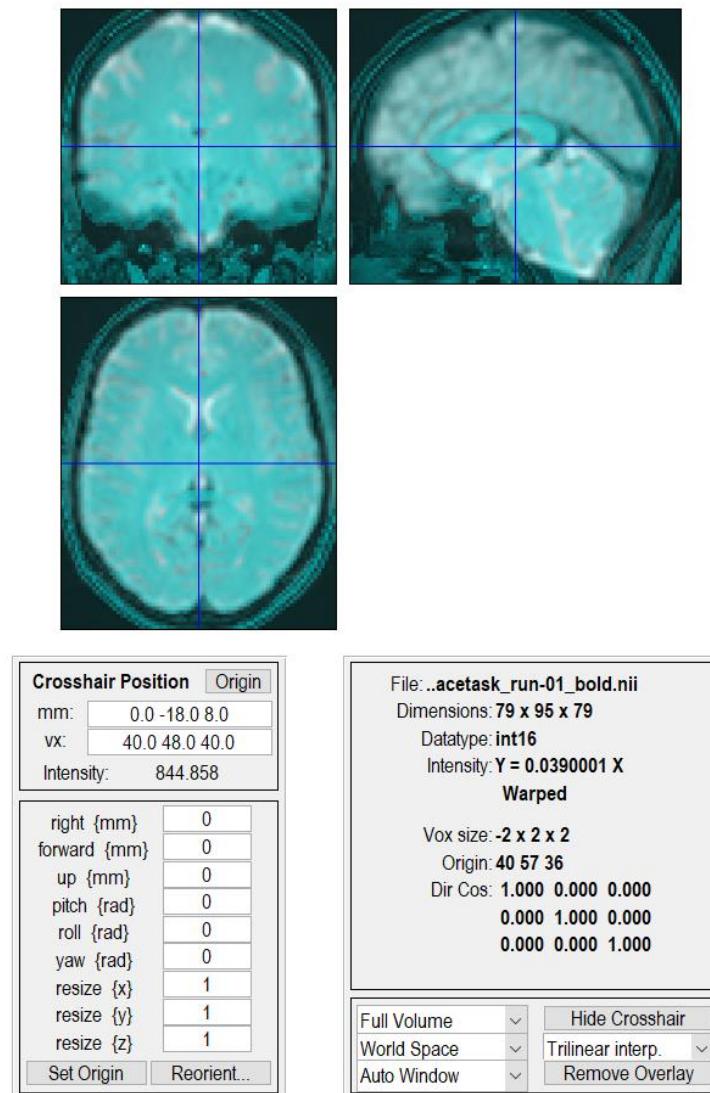


Figure 12

1.9. Normalization- write 2

Select the Deformation Field that you created in the anat directory during Segmentation, and for Images to Write select all of the output of apply VDM images.

The settings related to estimation and writing are shown in Figure 9 and 13, respectively.

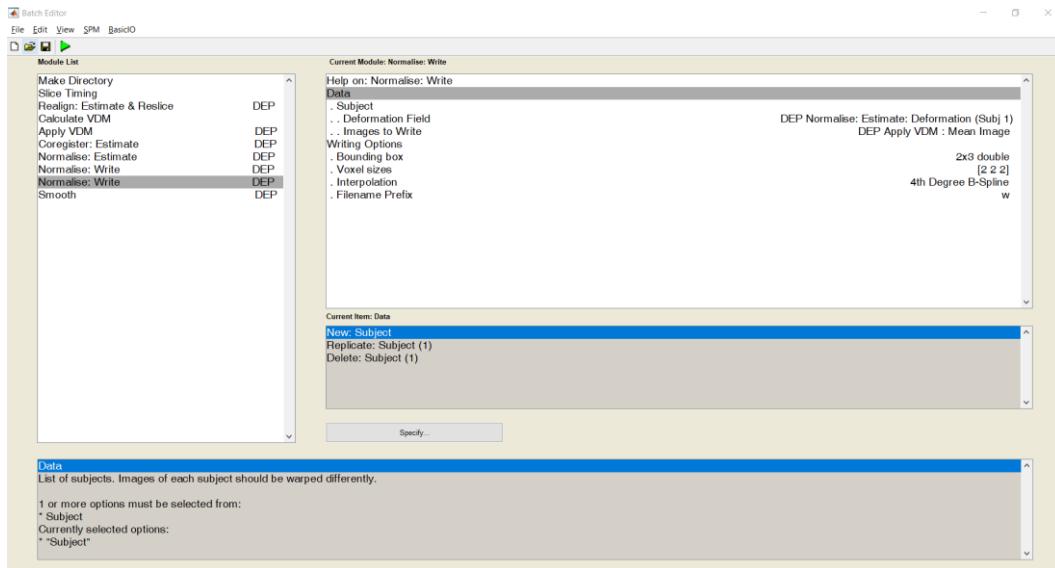


Figure 13

The output related to normalization, joint histogram before and after dropping the anatomical data on the functional data can be seen in Figure 14.

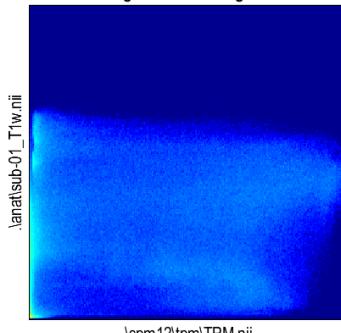
Normalised Mutual Information Coregistration

$$X_1 = -0.666X + 0.005Y - 0.015Z + 121.124$$

$$Y_1 = 0.002X + 0.656Y + 0.117Z - 20.179$$

$$Z_1 = -0.015X - 0.117Y + 0.656Z - 38.154$$

Original Joint Histogram



Final Joint Histogram

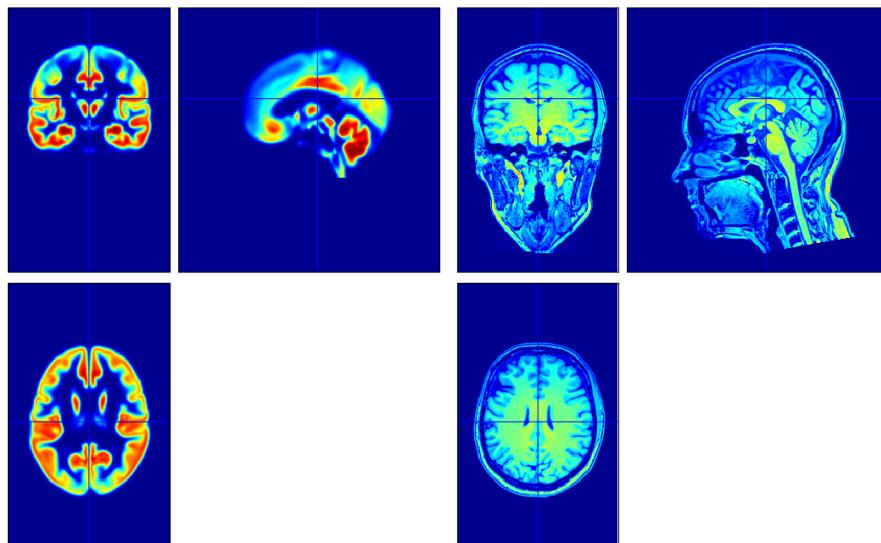
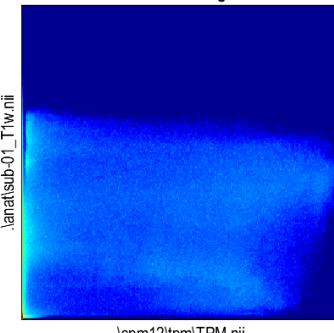
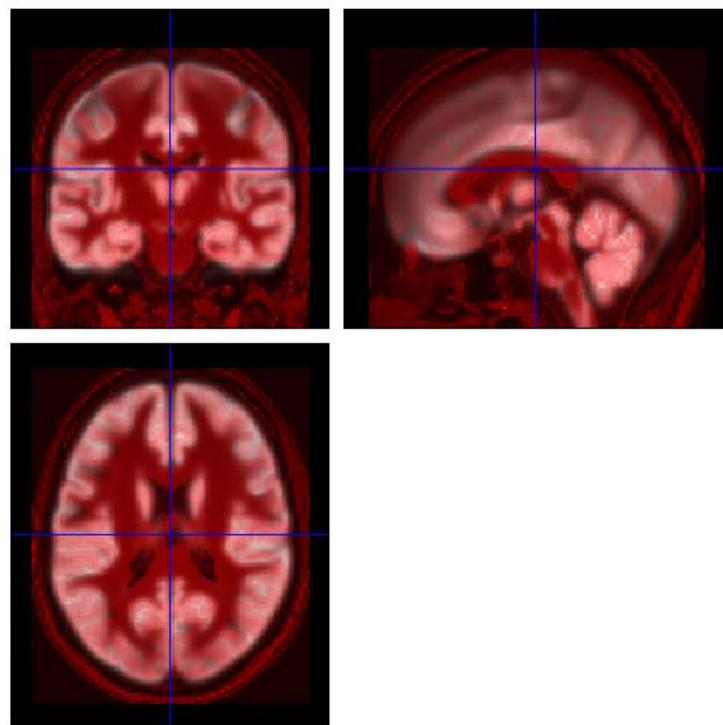


Figure 14

Here in Figure 15, we check to make sure that both the template of the brains and the internal structures are well-aligned.



Crosshair Position		Origin
mm:	0.0 -18.0 18.0	
vx:	61.0 73.0 61.0	
Intensity:	0.0296865	
right {mm}	0	
forward {mm}	0	
up {mm}	0	
pitch {rad}	0	
roll {rad}	0	
yaw {rad}	0	
resize {x}	1	
resize {y}	1	
resize {z}	1	
<input type="button" value="Set Origin"/>		<input type="button" value="Reorient..."/>

File: \HW_4\spm12\tpm\TPM.nii
 Dimensions: 121 x 145 x 121
 Datatype: float32
 Intensity: Y = 1 X
tissue probability map
 Vox size: -1.5 x 1.5 x 1.5
 Origin: 61 85 49
 Dir Cos:
 1.000 0.000 0.000
 0.000 1.000 0.000
 0.000 0.000 1.000

<input type="button" value="Full Volume"/>	<input type="button" value="Hide Crosshair"/>
<input type="button" value="World Space"/>	<input type="button" value="Trilinear interp."/>
<input type="button" value="Auto Window"/>	<input type="button" value="Remove Overlay"/>

Figure 15

As can be seen in Figure 10, the signal in channels A1 and A2 has a strong distortion and has no similarity with brain signals.

1.10. Smoothing

The spatial smoothing is performed with a spatially stationary Gaussian filter. The settings related to smoothing are shown in Figure 16.

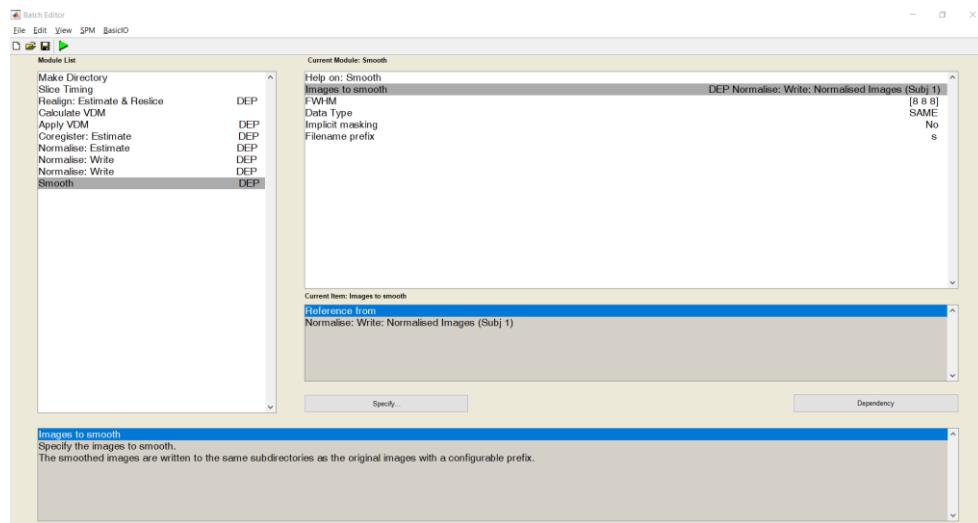


Figure 16

Here in Figure 17, we check to make sure that both the outlines of the brains and the internal smooth structures are well-aligned.

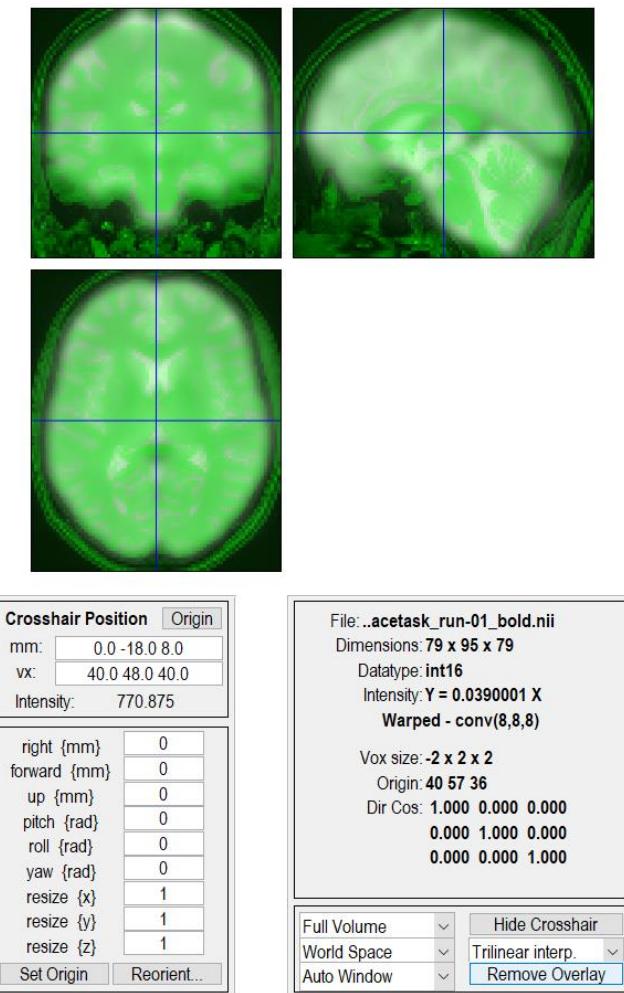


Figure 17

At the end of smoothing, the fMRI data is pre-processed and we can use it for the processing steps and design matrix extraction.

2. Using statistical analyze to separate and estimate face and non-face

2.1. Implement the last part of the task paradigm

To separate the face and house trials and generate two β values with fMRI statistical analysis. The aim is creating the design matrix at the end of this Question.

In this section, we intend to extract the design matrix using the output of the pre-processing section, and using statistical analysis, we want to show the effect of each face and house in oxygenating different parts of the brain.

First, we need to extract the exact indices related to Face and Non-face trials from each of our 4 Subjects. The MATLAB code for this part is in the separation file.

Also, the settings of this section will be such that we will have a session for Face and also a Session for Non-face data, in each of which we have all 960 Scans, which is the total number of our 4 Subject Slices. The settings of this part are in Specifi 1st-level in the SPM software in the fmri model *separation.mat* file, and the settings related to statistical analysis for Face and non-Face are shown in Figure 18 and 19 respectively, and the output design matrix is shown in Figure 20.

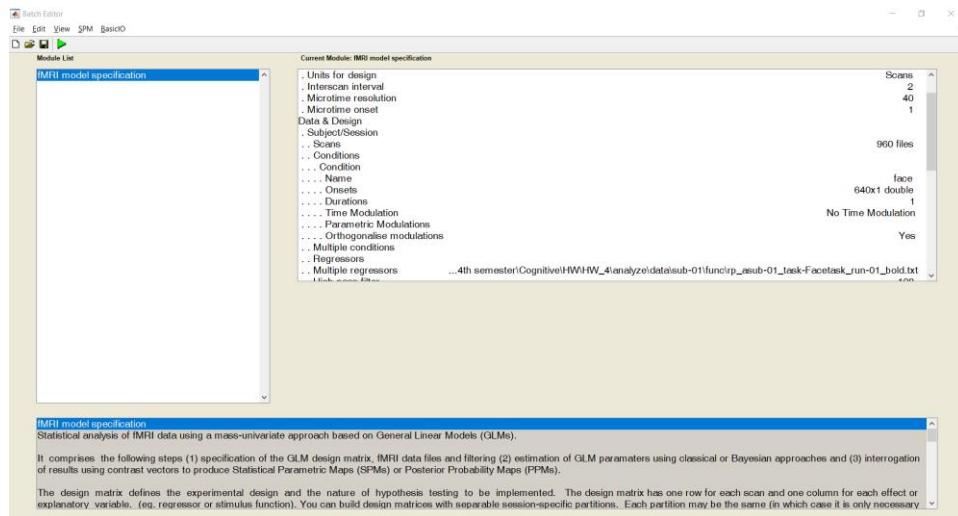


Figure 18

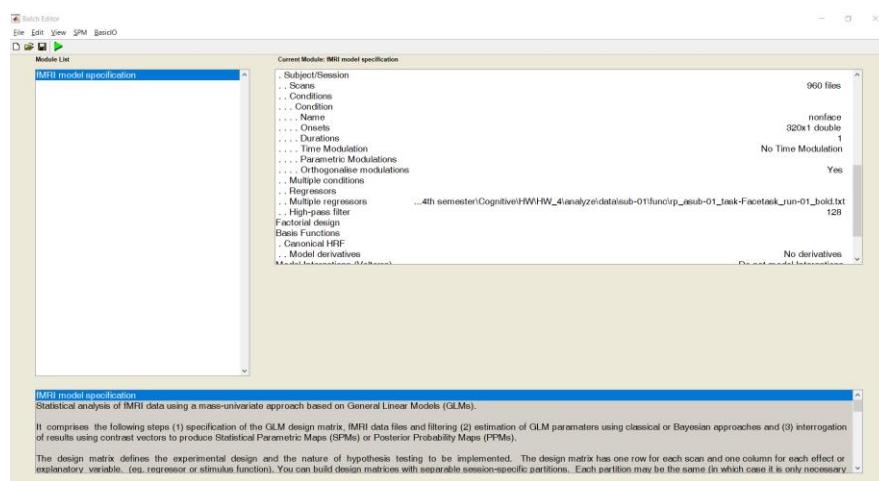


Figure 19

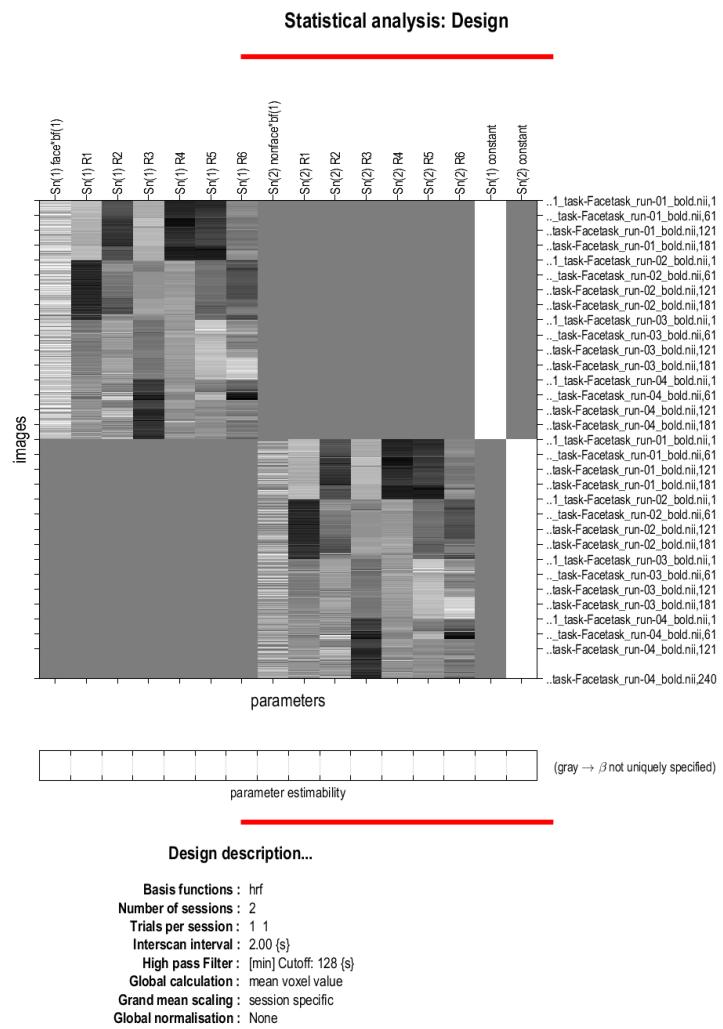


Figure 20

To estimate the value of repressors or beta coefficient, we select the *Estimation button* and try to estimate the values of the coefficients, and then use the *Result button* to create contrasts.

In Figure 21 shows the estimate setting.

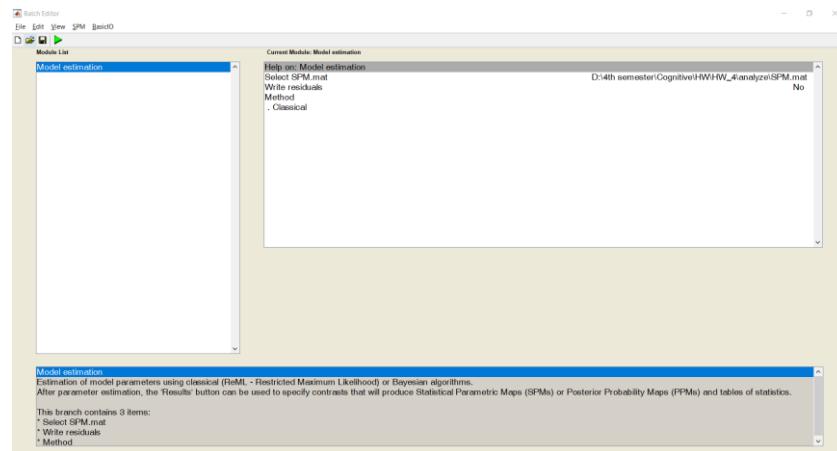


Figure 21

In Figure 22 shows the settings for creating 2 contrasts, face and non-face.



Figure 22

2.2. Face

As shown in Figures 23 and 24, many areas of the brain are involved, and the blood supply is far greater in the FFa region when the subject sees the facial data.

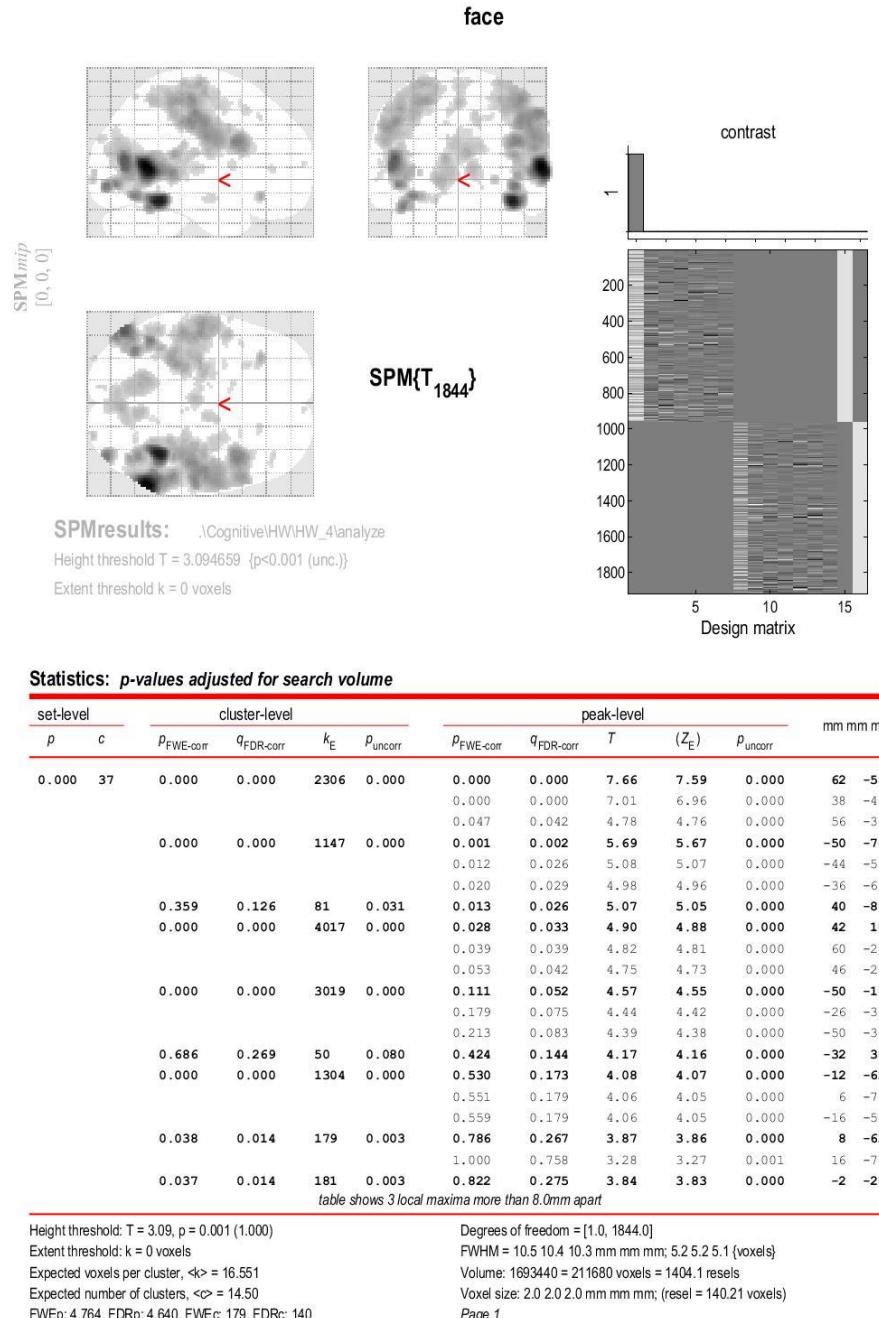


Figure 23

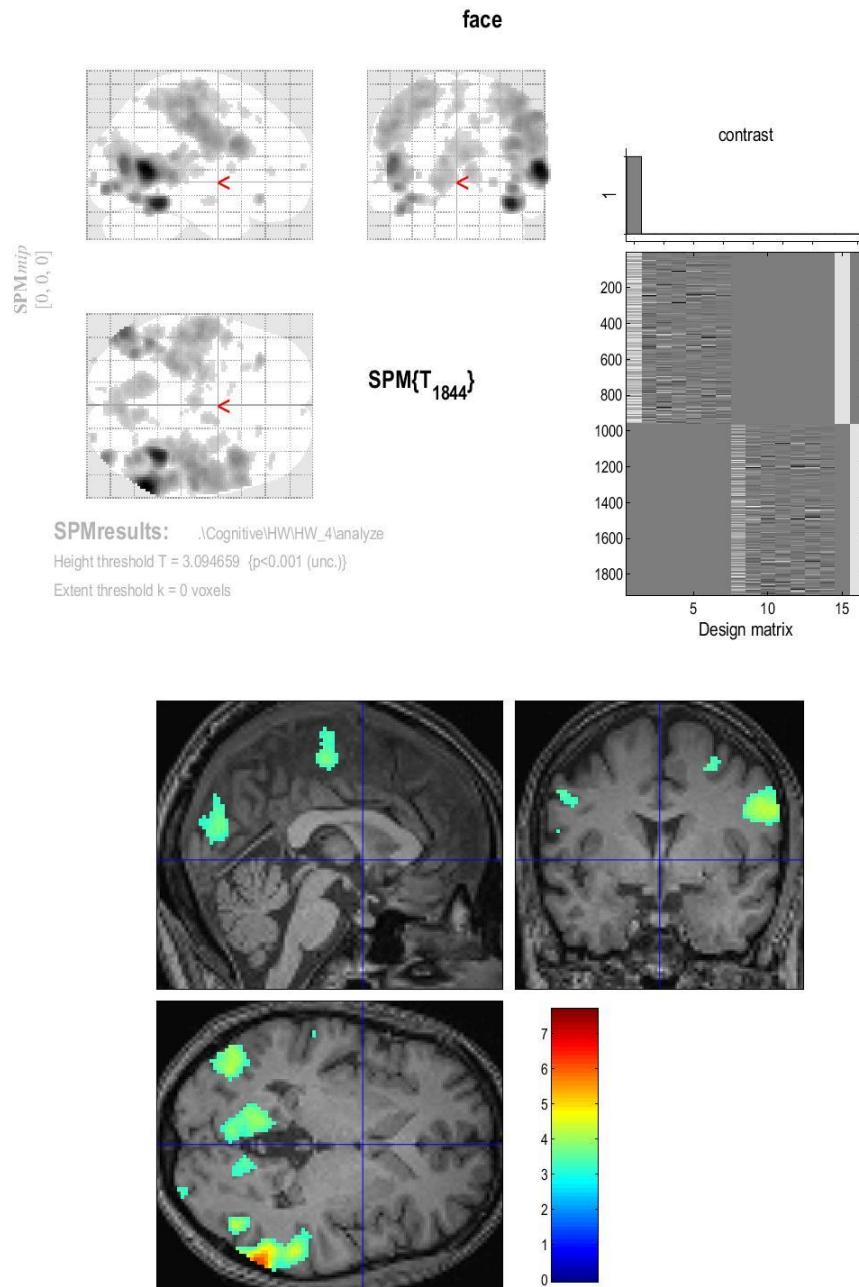


Figure 24

2.3. Non-Face

As shown in Figures 25 and 26, there are fewer areas of the brain involved and less blood supply in the FFA region when we view the home data. We

expect the PPA area to be activated when we view home images, as mentioned in section 2.3.

The same settings have been made for Non face data in figures 25 and 26.

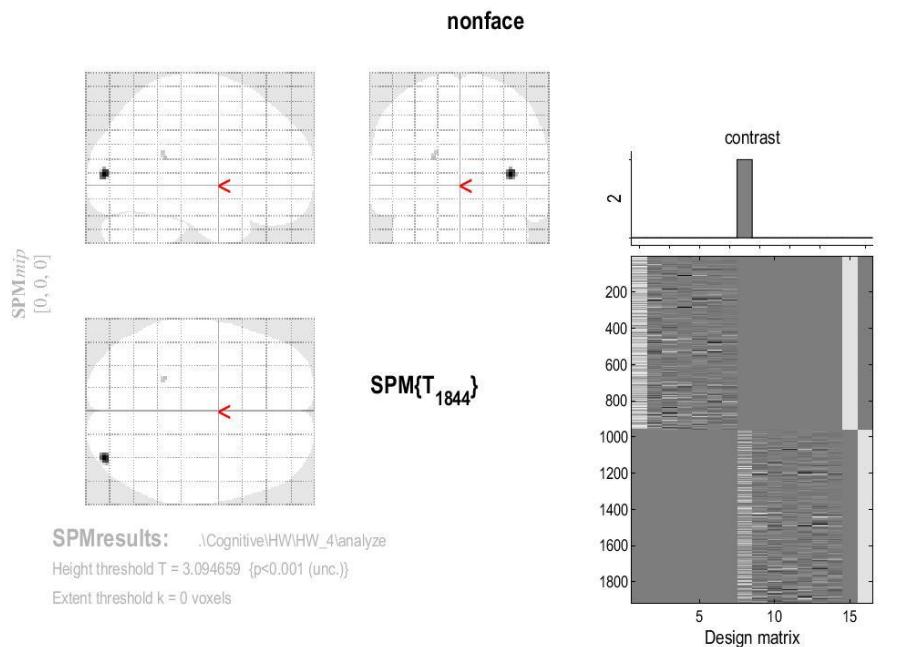
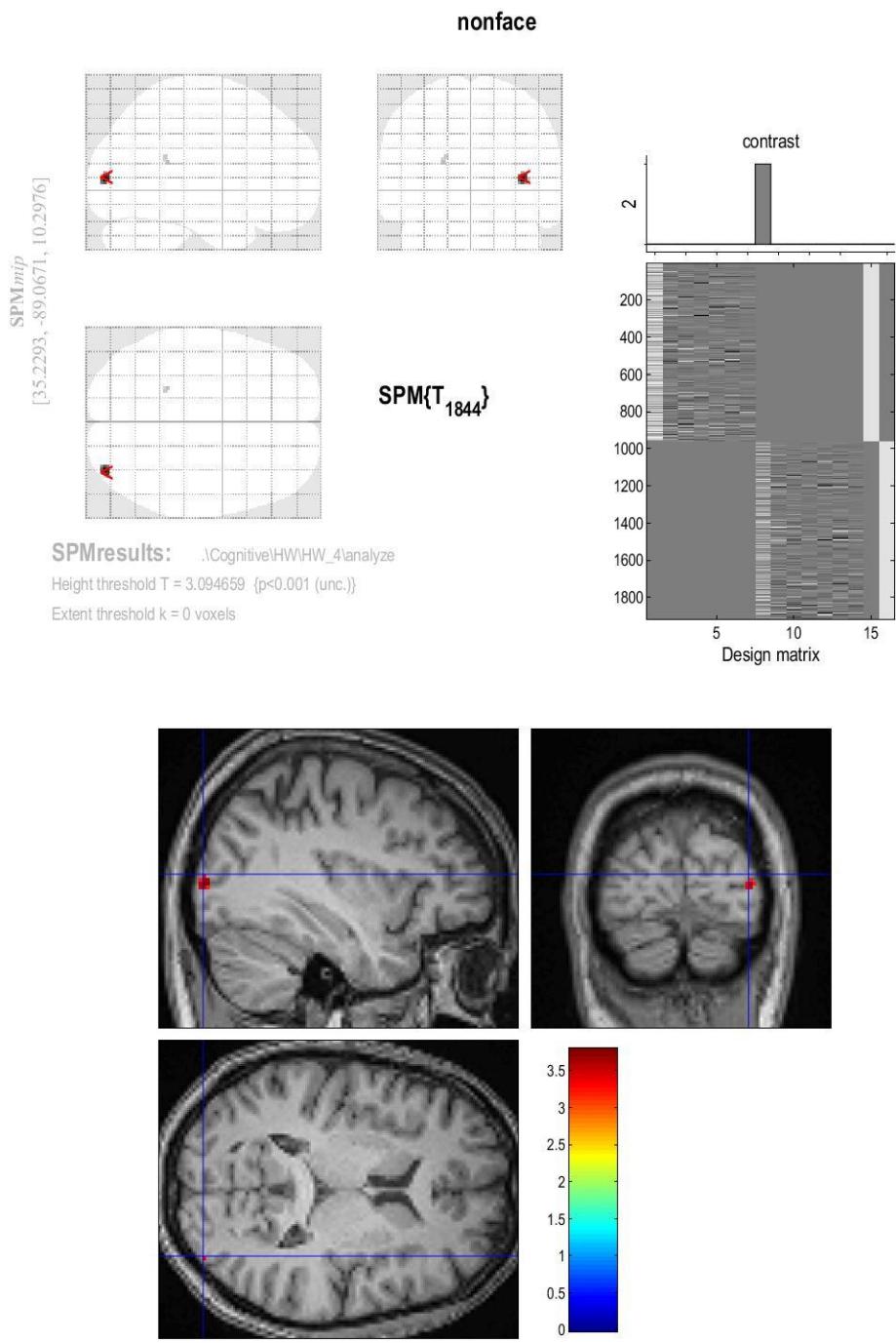


table shows 3 local maxima more than 8.0mm apart

Height threshold: T = 3.09, p = 0.001 (1.000)
Extent threshold: k = 0 voxels
Expected voxels per cluster, $\langle k \rangle = 16.551$
Expected number of clusters, $\langle c \rangle = 14.50$
FWEp: 4.764, FDRp: Inf, FWEc: Inf, FDRc: Inf

Degrees of freedom = [1.0, 1844.0]
FWHM = 10.5 10.4 10.3 mm mm mm; 5.2 5.2 5.1 (voxels)
Volume: 1693440 = 211680 voxels = 1404.1 resels
Voxel size: 2.0 2.0 2.0 mm mm mm; (resel = 140.21 voxels)

Figure 25



3. Using AAL atlas to analyze FFA and PPA

3.1. Choosing best mask for PPA and FFA

Question 2 is done in Section 1. We use the AAL atlas to analyze and compare the FFA and PPA data, because exactly these two areas are defined in the AAL atlas.

To use the ALL atlas, we first add the WFU_pickatlas toolbox to SPM. Then we try to find a suitable mask for both PPA and FFA areas, meaning we choose the largest mask.

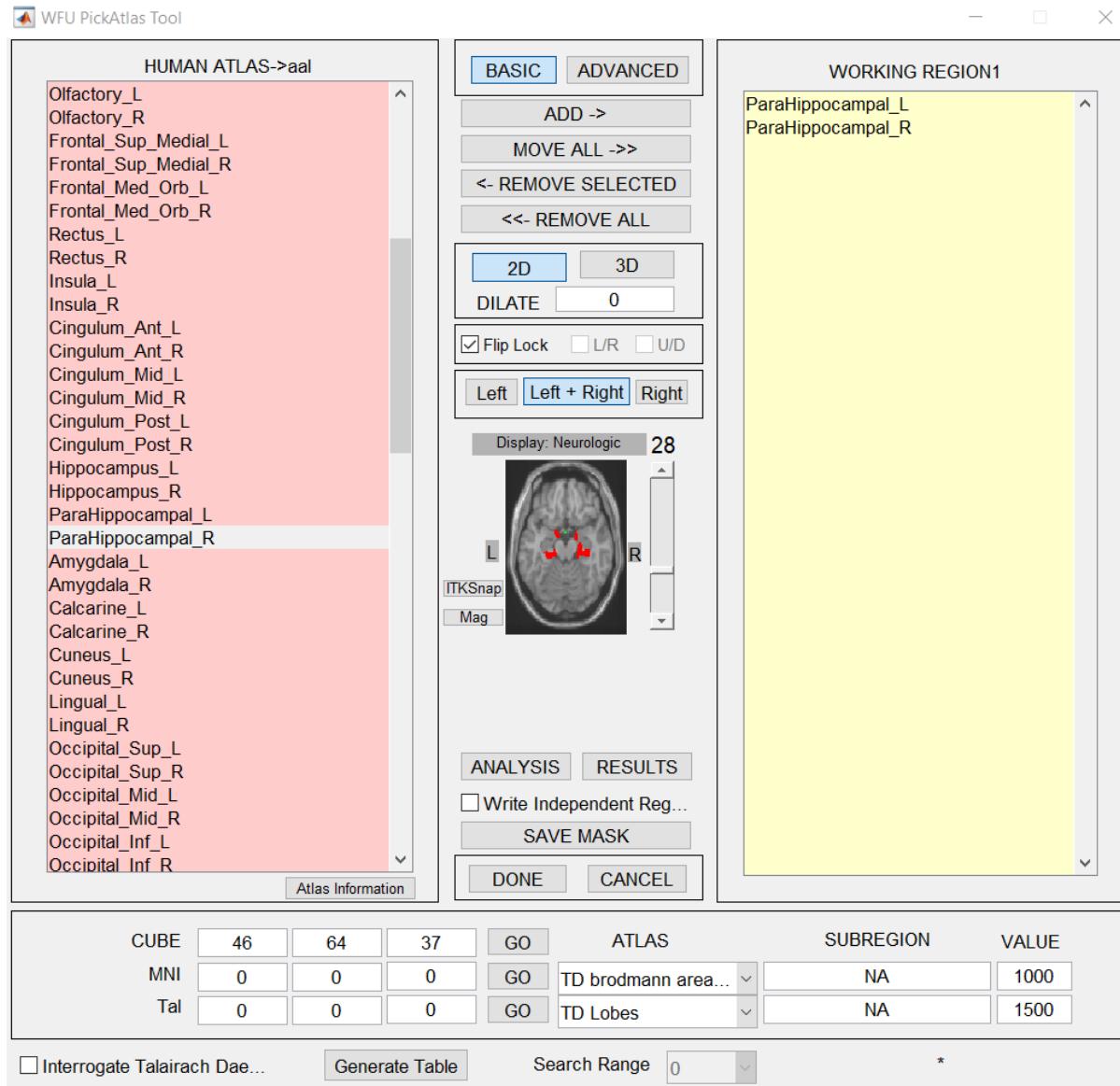


Figure 27

As seen in Figure 27, we want to analyze the areas between the two hemispheres of the brain, we select the left and right paraHippocampal areas, and after

selecting the largest mask, we save the mask corresponding to this area under the name ppa.

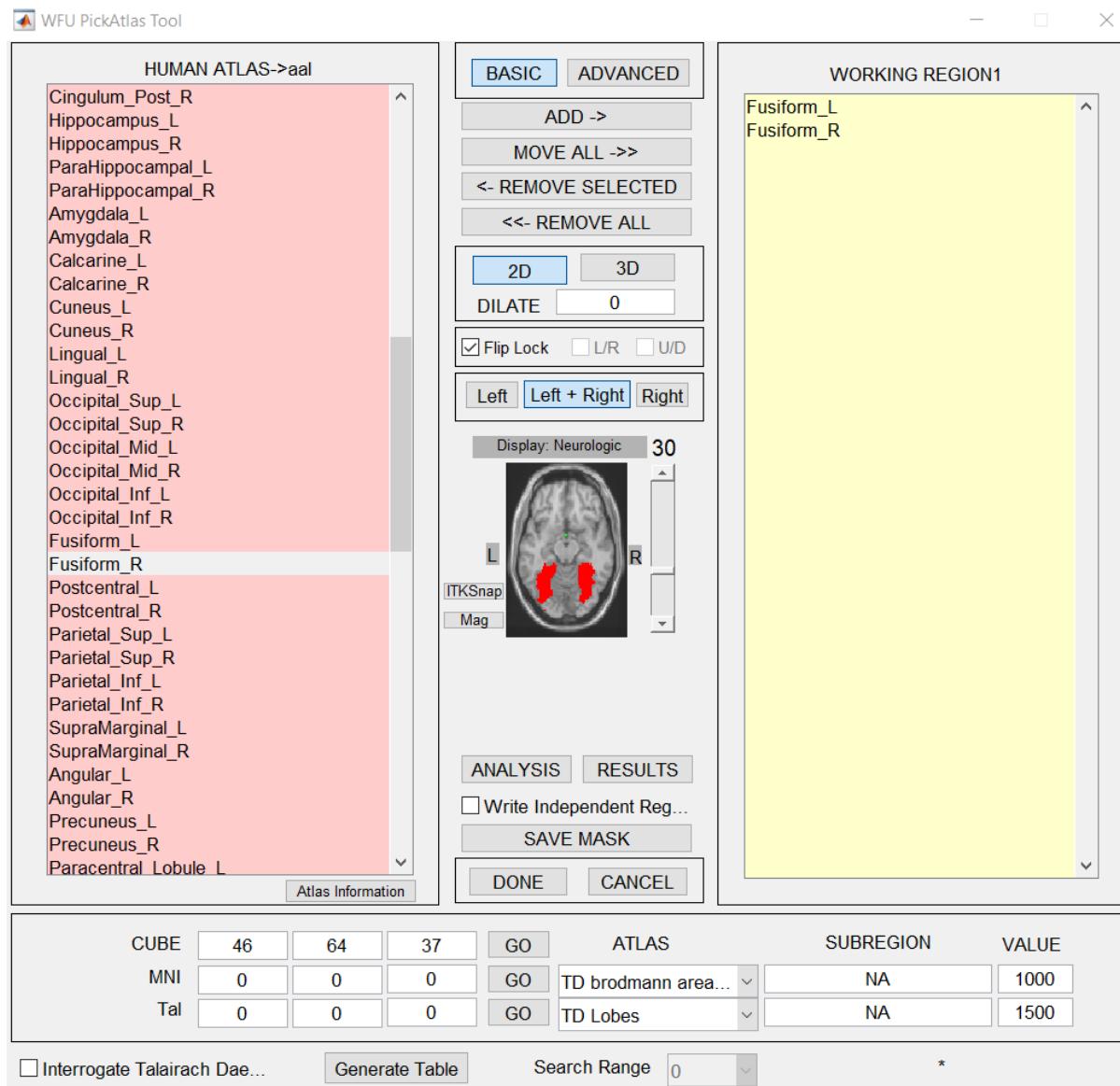


Figure 28

As seen in Figure 28, we want to analyze the areas between the two hemispheres of the brain, we choose the two Fusiform areas, left and right, and after selecting the largest mask, we save the mask corresponding to this area under the name ffa.

3.2. PPA:

3.2.1 Face:

In Figure 29, we see the p-value for half of the sphere. As shown in the figure and the p-value, the left and right ppa regions are not related to each other when the subject sees the face image.

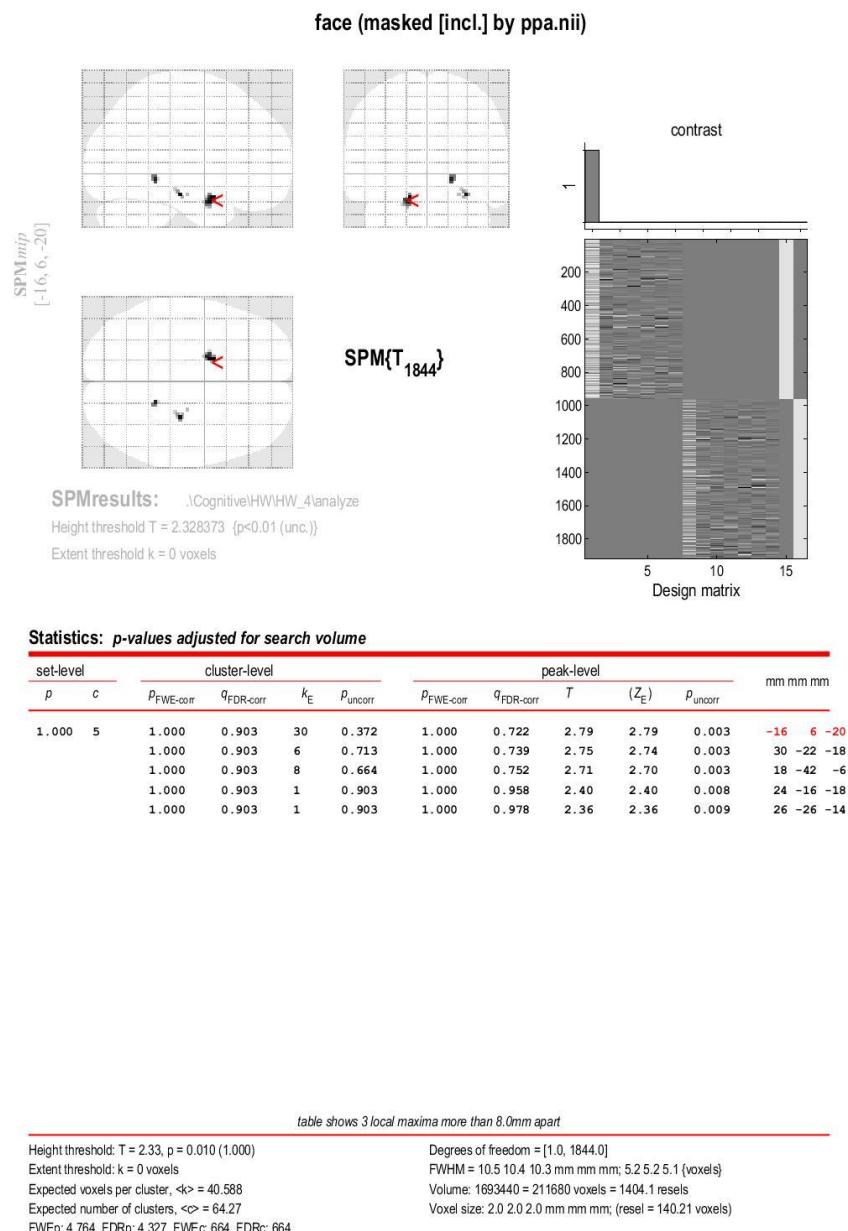


Figure 29

For the ppa mask, when the subject sees the face image, we expect this area to have very little activity, as we can see in Figure 30, the sectional view of the brain, the oxygenation to these areas is minimal.

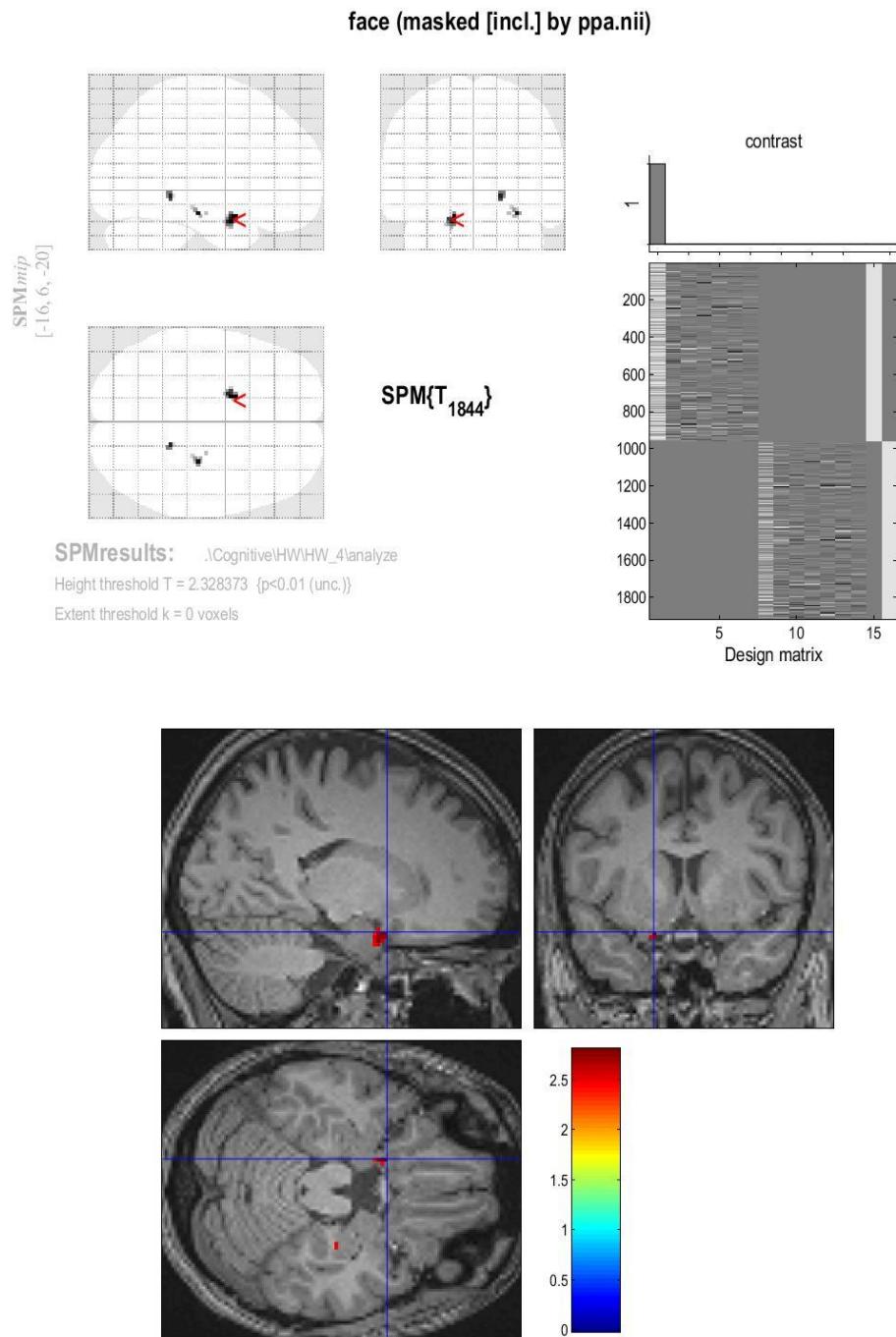
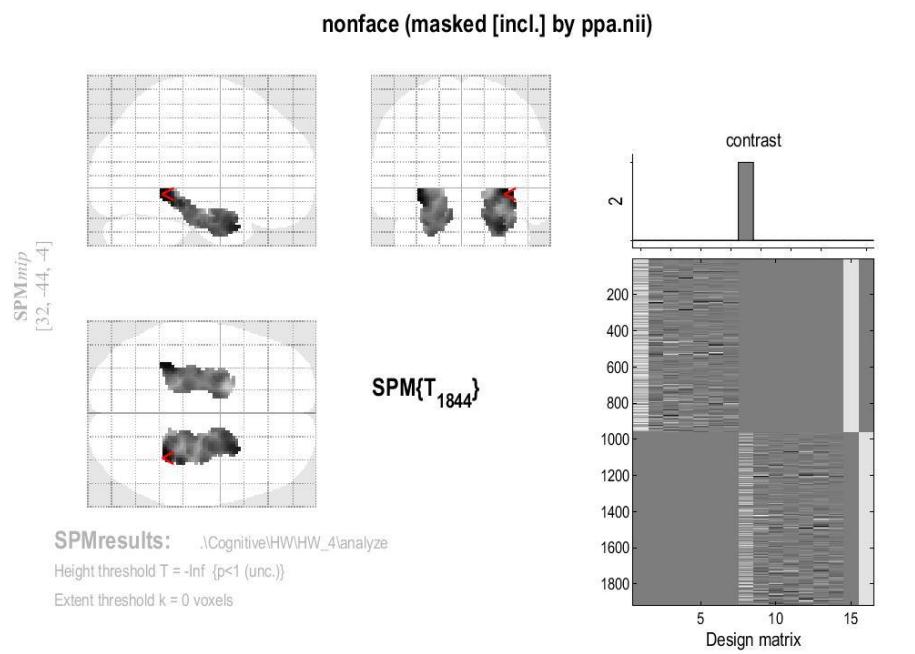


Figure 30

3.2.2. Non-Face:

In Figure 31, we see the p-value for half of the sphere. As shown in the figure and the p-value, the left and right ppa regions are related to each other when the subject sees the non-face image.



Statistics: p-values adjusted for search volume

set-level		cluster-level				peak-level				mm mm mm			
p	c	$p_{FWE\text{-corr}}$	$q_{FDR\text{-corr}}$	k_E	p_{uncorr}	$p_{FWE\text{-corr}}$	$q_{FDR\text{-corr}}$	T	(Z_E)	p_{uncorr}	mm	mm	mm
0.801	2	0.950	1.000	1034	1.000	1.000	39.134	1.78	1.79	0.037	32	-44	-4
						1.000	30.106	1.04	1.09	0.139	28	10	-30
0.950		1.000		857	1.000	1.000	39.409	1.58	1.59	0.055	-34	-40	-10
						1.000	39.409	1.40	1.42	0.078	-34	-46	-4
						1.000	26.463	0.07	0.32	0.376	-10	-4	-24

table shows 3 local maxima more than 8.0mm apart

Height threshold: T = -Inf, p = 0.632 (0.950)
Extent threshold: k = 0 voxels
Expected voxels per cluster, $\langle k \rangle = 631440696914548736.000$
Expected number of clusters, $\langle c \rangle = 3.00$
FWEp: 4.764, FDRp: Inf, FWEc: Inf, FDRc: Inf
Degrees of freedom = [1, 1844.0]
FWHM = 10.5 10.4 10.3 mm mm mm; 5.2 5.2 5.1 (voxels)
Volume: 1693440 = 211680 voxels = 1404.1 resels
Voxel size: 2.0 2.0 2.0 mm mm mm; (resel = 140.21 voxels)

Figure 31

For the ppa mask, when the subject sees the non-face image, we expect this area to have relatively much activity, as we can see in Figure 32, the sectional view of the brain, the oxygenation to these areas is relatively maximal.

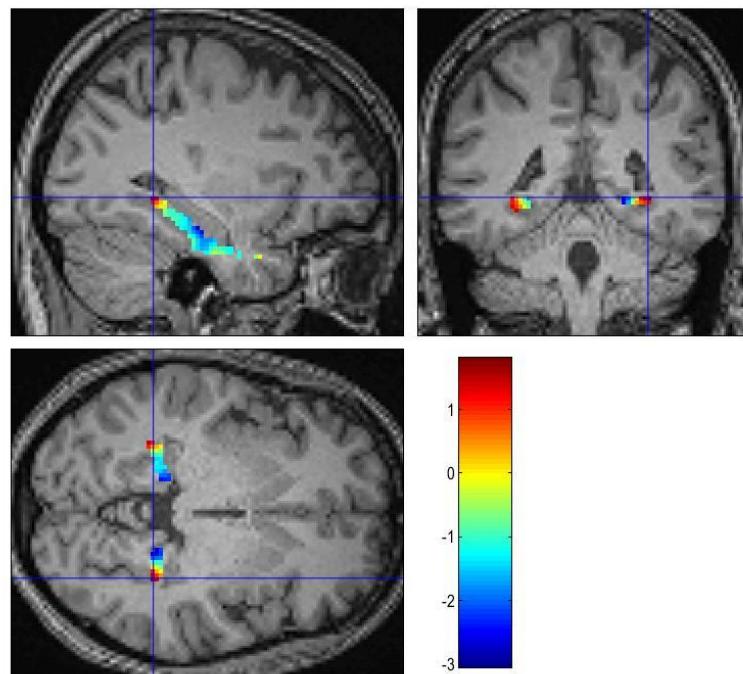
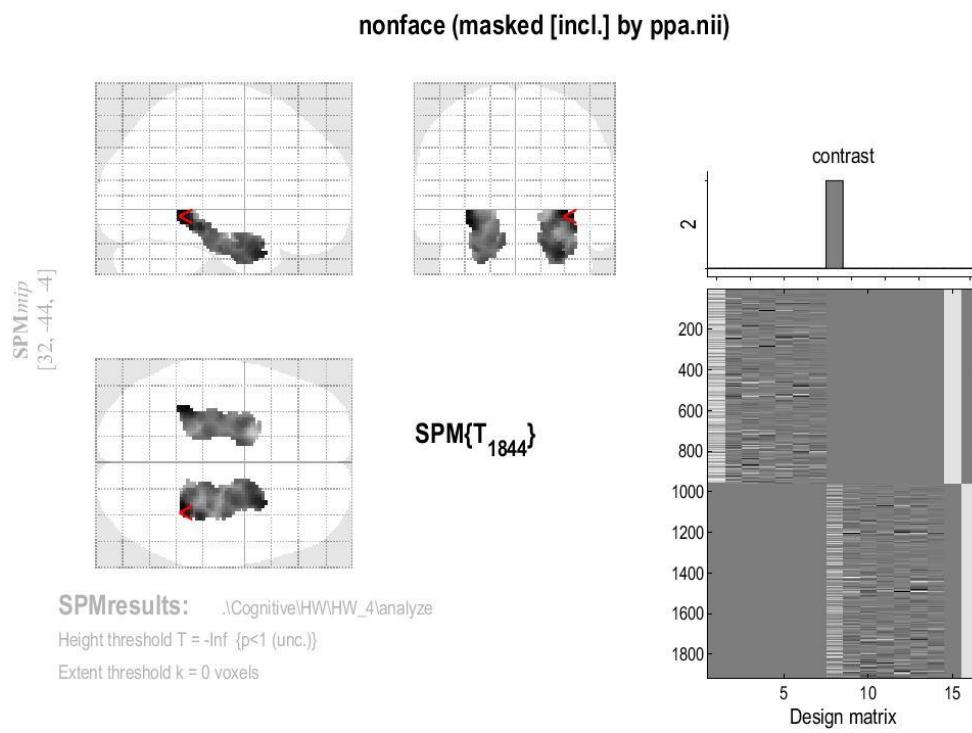
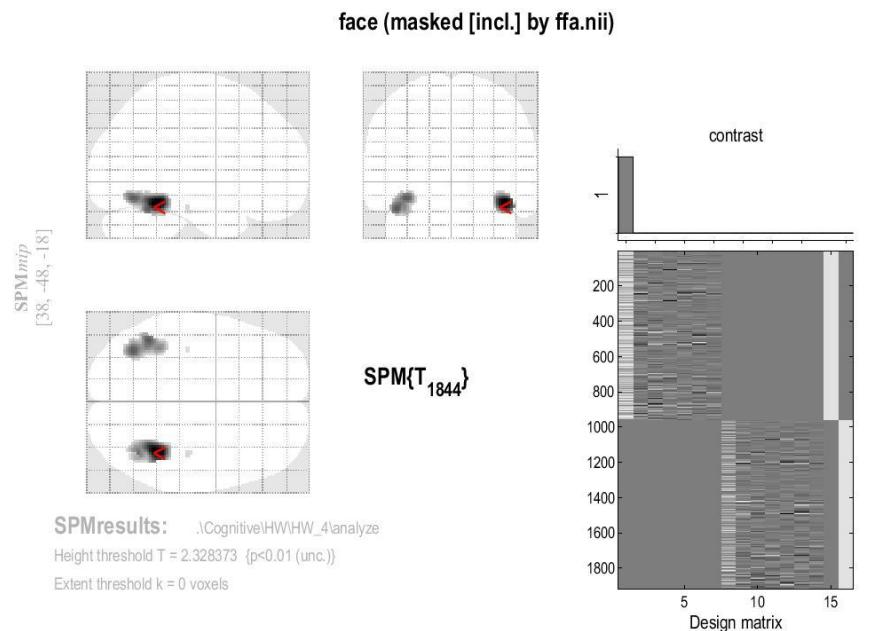


Figure 32

3.3.FFA:

3.3.1. Face:

In Figure 33, we see the p-value for half of the sphere. As shown in the figure and the p-value, the left and right ffa regions are related to each other when the subject sees the face image.



Statistics: p-values adjusted for search volume

set-level		cluster-level				peak-level					mm mm mm		
p	c	$p_{FWE\text{-corr}}$	$q_{FDR\text{-corr}}$	k_E	p_{uncorr}	$p_{FWE\text{-corr}}$	$q_{FDR\text{-corr}}$	T	(Z_E)	p_{uncorr}	38 -48 -18	40 -62 -14	-44 -54 -22
1.000	4	0.147	0.343	449	0.002	0.000	0.000	7.01	6.96	0.000	38 -48 -18		
		0.227	0.343	396	0.004	0.121	0.030	4.54	4.53	0.000	40 -62 -14		
				0.012	0.013	5.08	5.07	0.000	-44 -54 -22				
				0.020	0.014	4.98	4.96	0.000	-36 -66 -14				
				0.511	0.085	4.09	4.08	0.000	-38 -46 -20				
		1.000	0.903	6	0.713	1.000	0.909	2.50	2.50	0.006	42 -24 -20		
		1.000	0.903	3	0.808	1.000	0.958	2.39	2.39	0.009	-38 -24 -20		

table shows 3 local maxima more than 8.0mm apart

Height threshold: $T = 2.33$, $p = 0.010$ (1.000)

Degrees of freedom = [1.0, 1844.0]

Extent threshold: $k = 0$ voxels

FWHM = 10.5 10.4 10.3 mm mm mm; 5.2 5.2 5.1 (voxels)

Expected voxels per cluster, $\langle k \rangle = 40.588$

Volume: 1693440 = 211680 voxels = 1404.1 resels

Expected number of clusters, $\langle c \rangle = 64.27$

Voxel size: 2.0 2.0 2.0 mm mm mm; (resel = 140.21 voxels)

FWEp: 4.764, FDRp: 4.327, FWEc: 664, FDRc: 664

Figure 33

For the ffa mask, when the subject sees the face image, we expect this area to have relatively much activity, as we can see in Figure 34, the sectional view of the brain, the oxygenation to these areas is maximal.

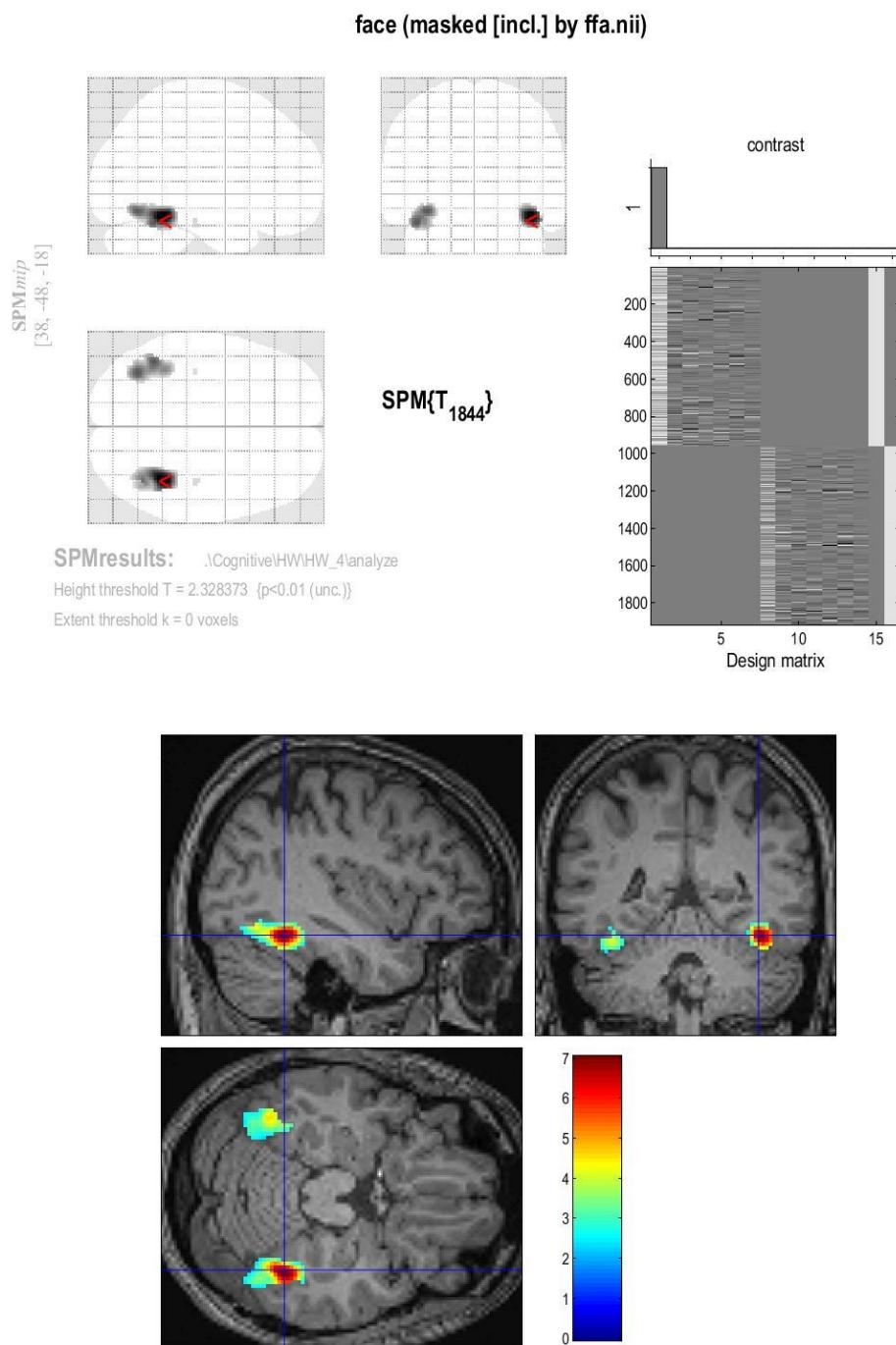


Figure 34

3.3.2. Non-Face:

In Figure 35, we see the p-value for half of the sphere. As shown in the figure and the p-value, the left and right ffa regions are not related to each other when the subject sees the non-face image.

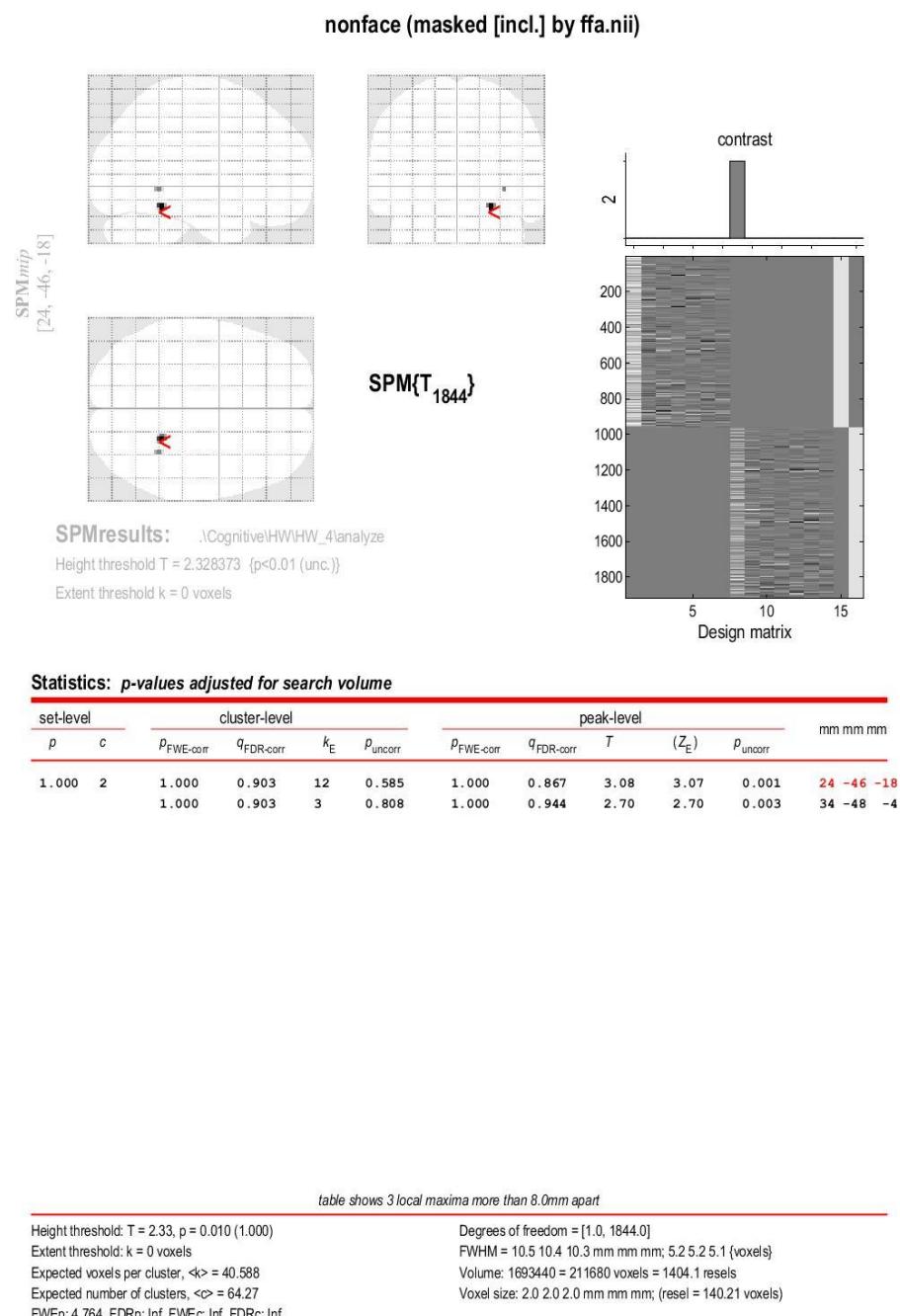


Figure 35

For the ffa mask, when the subject sees the non-face image, we expect this area to have very little activity, as we can see in Figure 36, the sectional view of the brain, the oxygenation to these areas is minimal.

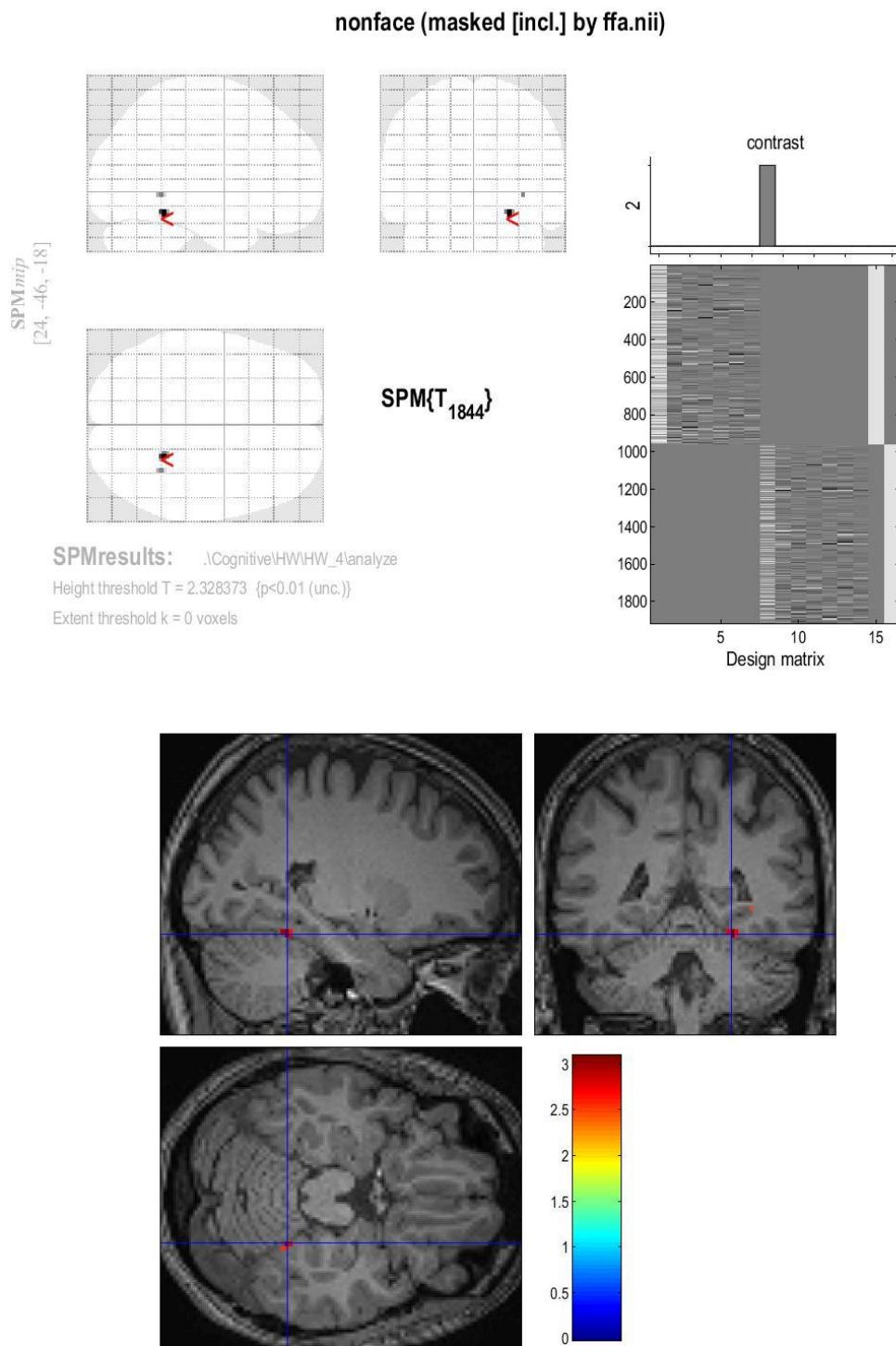


Figure 36

4. Compare the Dynamic Functional Connectivity:

4.1. Connectivity matrix:

Also, by using the conn tool in the SPM software, we are going to get the brain connectivity for the subjects, the steps using this tool are shown in figure 37 to 42.

The connectivity matrix for all atlases and regions can be seen in the Figure37.

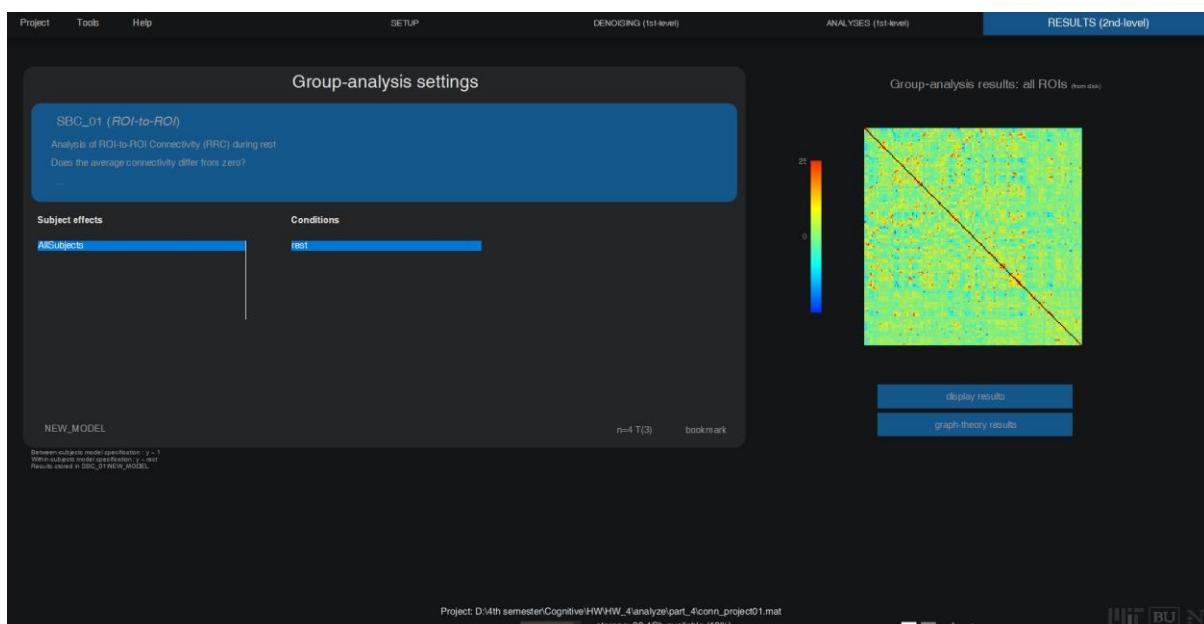


Figure 37

The graphical model of the relationship between all of the atlases and regions is shown in the Figure38.

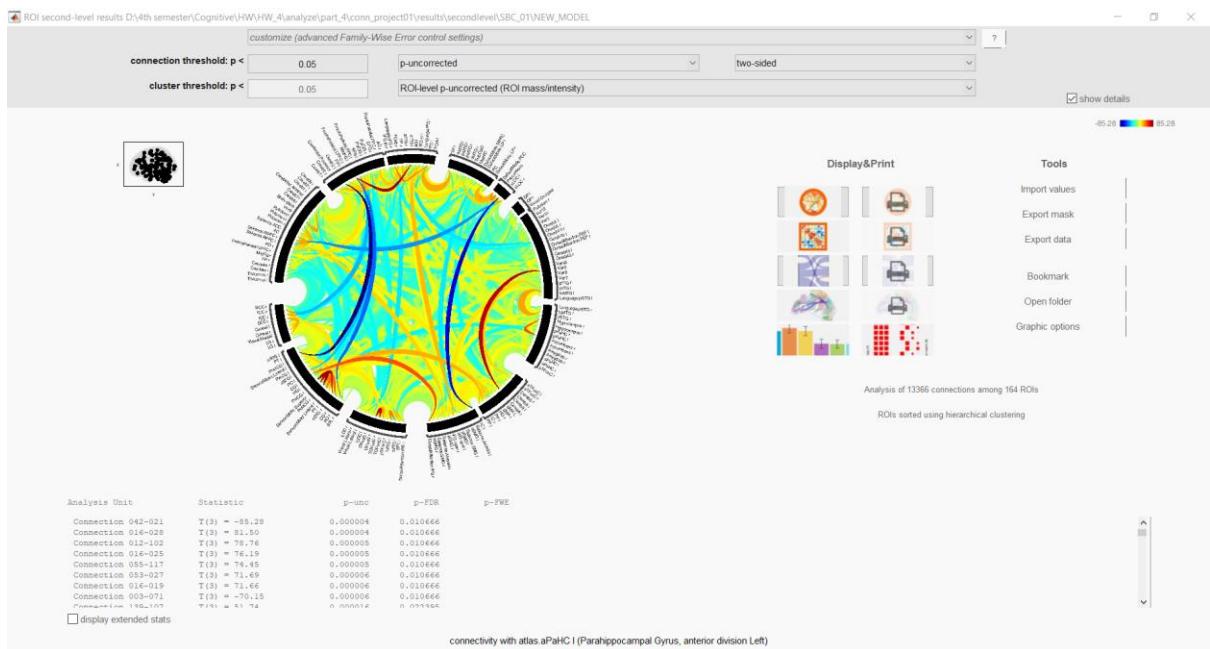


Figure 38

The connectivity matrix for the all of the atlases and regions can be seen in the Figure39.



Figure 39

The required atlases can be seen in Figure 40.

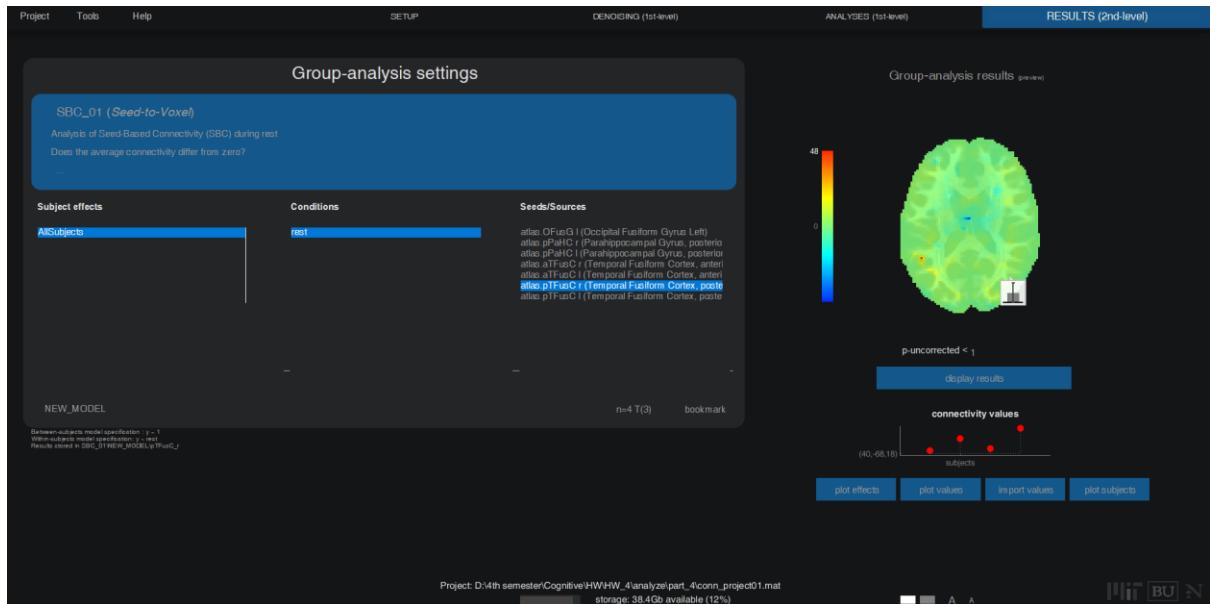


Figure 40

The graphical model of the relationship between the atlases and the desired regions is shown in the Figure 41.

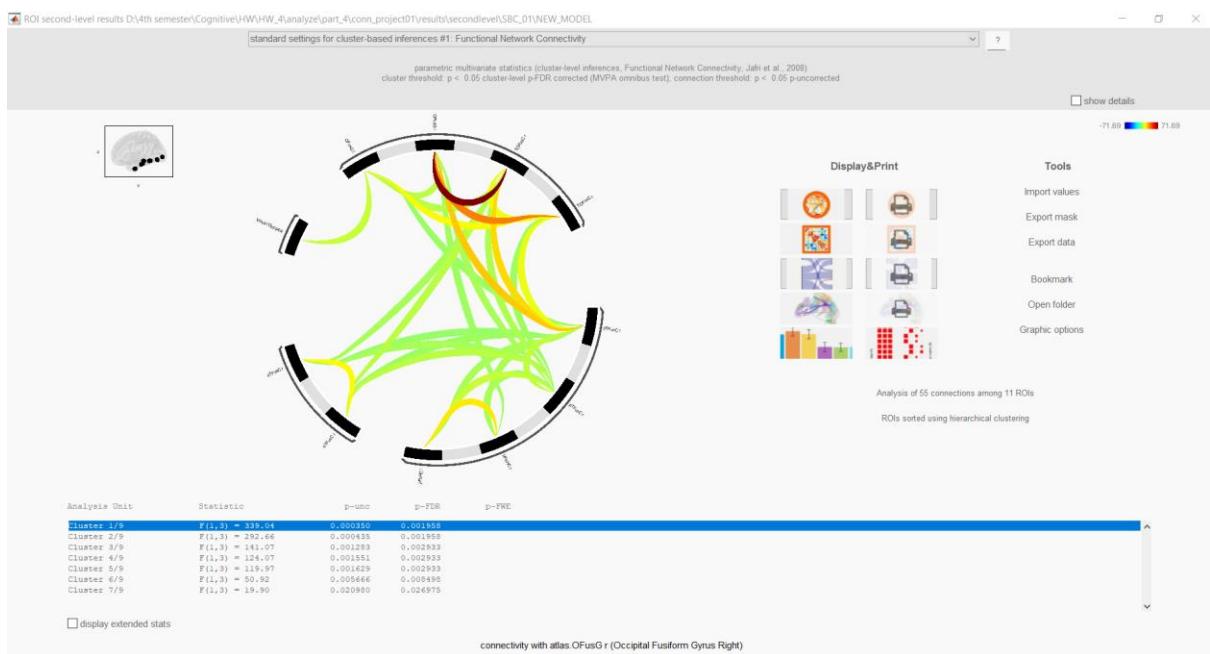


Figure 41

The connectivity matrix for the desired atlases and regions (ffa, ppa, visual cortex areas-V1 to V4) can be seen in the Figure 42.

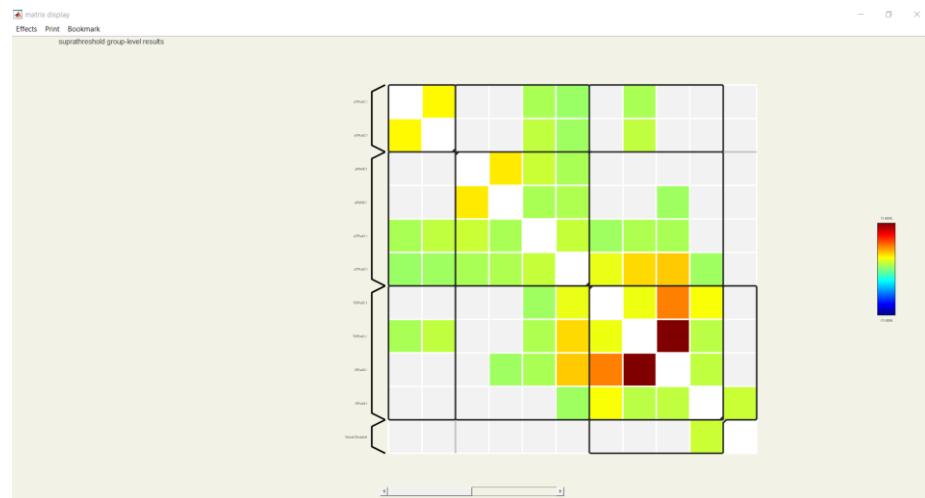


Figure 42