ROI Analysis Task

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Sec : 2
BN :25
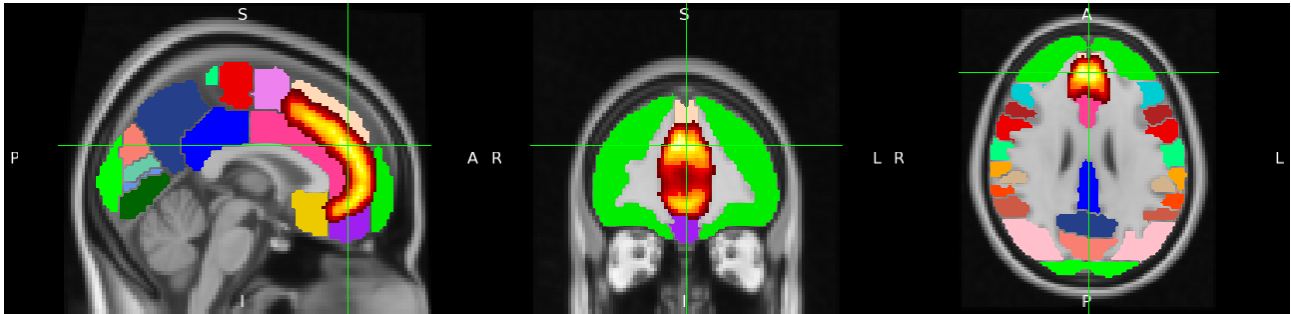**ID:9203396**

<mark>Anatomical ROI</mark>

<mark>Steps</mark>

To perform ROI -Whole brain- analysis, follow these steps:

1) Create your anatomical mask:
    - Open fsleyes and from standards open MNI152_T1_2mm.nii.gz
    - From settings ortho view, open atlases , harvard oxford cortical atlas
    - Choose paracingulate gyrus and save the template as PCG.nii.gz

2) Merge all zstats of Cope3 by running the following command in   cope3.feat/stats
<mark>fslmerge -t allZstats.nii.gz `ls zstat* | sort -V</mark>

3) Run the following command in order to get the means
<mark>fslmeants -i allZstats.nii.gz -m PCG.nii.gz</mark>

4) Now do one sample t-test using R language to obtain the results

```
1  #perform one sample t-test on cope3 means
2
3  my_data <- c(1.363002 ,0.222655 ,1.062275 ,-0.211897, 1.062275 ,
       -0.211897 , -0.101921 , 0.207988 , 0.720686 , 0.701019 ,
       0.265103 , 0.035617,-0.279518
4  ,0.256199 ,-0.076181,-0.131394 ,-0.107646 ,-0.393942,0.204620 ,
       -0.912633, -0.626931,-0.138006 ,-0.029543 ,0.363852 , 1.002289
       ,-0.366796 ,-0.546775 ,0.212949 )
5
6  t.test(my_data)
7
```

```
Rscript /tmp/VlTHIk00la.r
One Sample t-testdata:  my_data
t = 1.2174, df = 27, p-value = 0.234alternative hypothesis: true meanis
    not equal to095percent confidence interval:
 -0.08678481  0.34003117
sample estimates:
mean of x
0.1266232
```

```
1.363002
0.222655
1.062275
-0.211897
-0.101921
0.207988
0.720686
0.701019
0.265103
0.035617
-0.279518
0.256199
-0.076181
-0.131394
-0.107646
-0.393942
0.204620
-0.912633
-0.626931
-0.138006
-0.029543
0.363852
1.002289
-0.366796
-0.546775
0.212949
```

<mark>Drawbacks:</mark>

- insignificant Results

- Limited flexibility as Anatomical ROIs often have fixed shapes and sizes.

- Reduction of sensitivity for detecting functional activations due to the imperfect alignment

To perform a spherical ROI on voxel location [0,20,44] , do the following:

1- Open MNI template in fsleyes and get the voxel location.

2- In the terminal go to the FLANKER directory and type the following which shall give you a centroid of these voxel locations:

fslmaths $FSLDIR/data/standard/MNI152_T1_2mm.nii.gz -mul 0 -add 1 -roi 45 1 73 1 58 1 0 1 Jahn_ROI_dmPFC_0_20_44.nii.gz -odt float

3- Run the following command to expand this single voxel with specific raduis 5mm :

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

4- Run the following command to binarize the results :

fslmaths Jahn_Sphere_dmPFC_0_20_44.nii.gz -bin Jahn_Sphere_bin_dmPFC_0_20_44.nii.gz

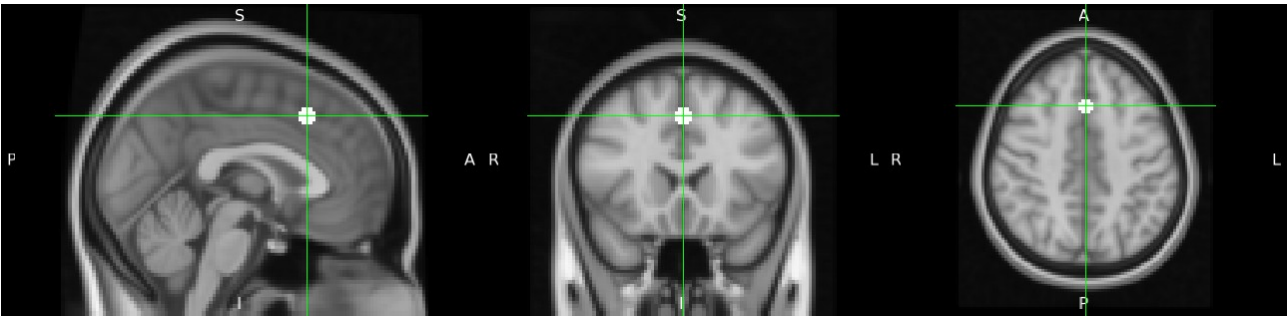5- Get the means of this voxel location by running the following command   :
 fslmeants -i allZstats.nii.gz -m Jahn_Sphere_bin_dmPFC_0_20_44.nii.gz

```
1.328597
0.747626
1.265742
0.513243
0.963755
1.420346
1.878770
2.210789
-0.084014
-0.179238
0.416731
1.368610
-0.378935
-0.218356
0.853670
0.429024
1.175458
0.153742
-0.740903
0.493883
0.637472
0.911115
1.552971
0.327688
-0.811581
0.991190
```
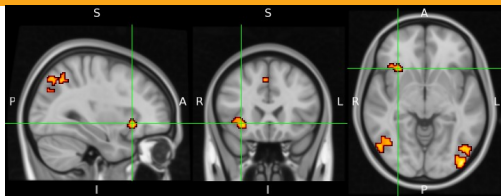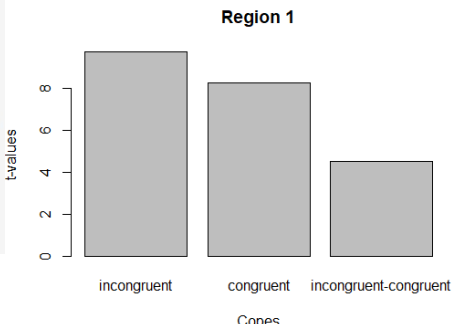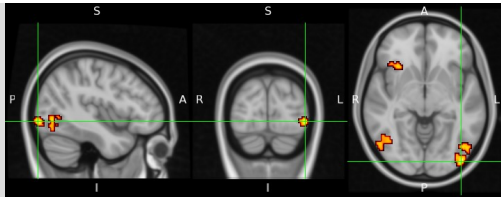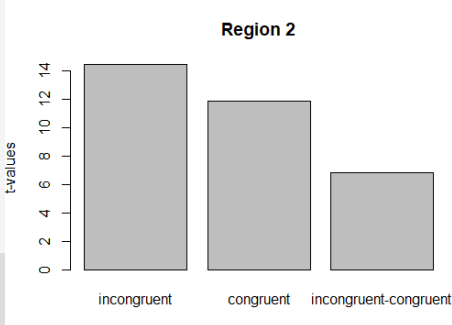
6- Finally , do one sample t-test using R to get your results

```
Rscript /tmp/VlTHIk00la.r
Read 26 items
One Sample t-test

data:  my_data
t = 4.3729, df = 25, p-value = 0.0001893
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 0.3505255 0.9746588
sample estimates:
mean of x
0.6625921
```
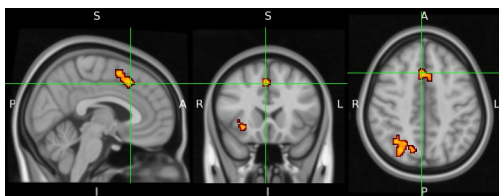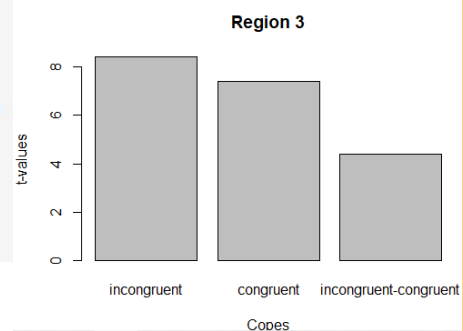

Cope-3 ROI:

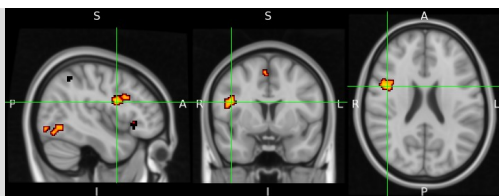| Region	Screenshot	t-test	Barchart
1		```Rscript /tmp/2U2X7CHesn.r``` Read 26 items One Sample t-test data: data t = 4.498, df = 25, p-value = 0.0001369 alternative hypothesis: true mean is not equal to 0 95 percent confidence interval: 0.3993701 1.0739842 sample estimates: mean of x 0.7366772	
2		```Rscript /tmp/2U2X7CHesn.r``` Read 26 items One Sample t-test data: data t = 6.8351, df = 25, p-value = 3.65e-07 alternative hypothesis: true mean is not equal to 0 95 percent confidence interval: 0.5375733 1.0012508 sample estimates: mean of x 0.769412	

3


```
Rscript /tmp/2U2X7CHesn.r
Read 26 items
One Sample t-test

data:  datat = 4.388, df = 25, p-value = 0.000182
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 0.3832853 1.0613159
sample estimates:
mean of x
0.7223006
```
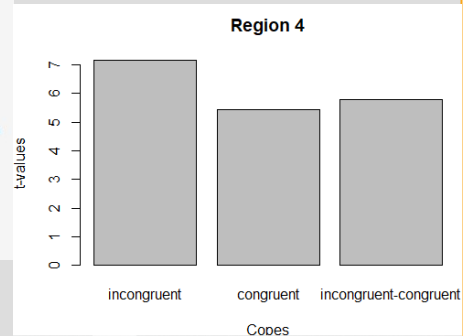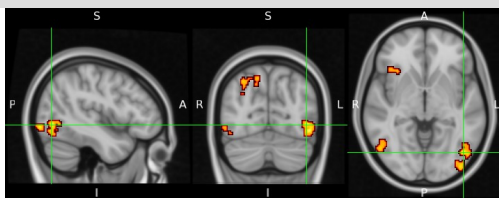

Region 3

4


```
Rscript /tmp/2U2X7CHesn.r
Read 26 items
One Sample t-test

data:  data
t = 5.7845, df = 25, p-value = 4.976e-06
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 0.514200 1.082799
sample estimates:
mean of x
0.7984997
```
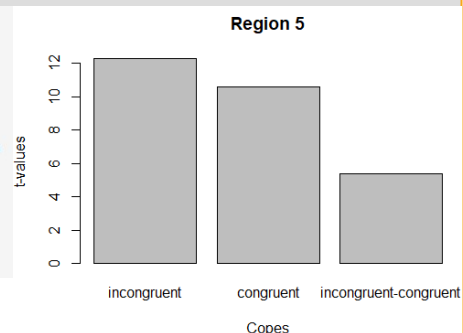

Region 4

5


```
Rscript /tmp/2U2X7CHesn.r
Read 26 items
One Sample t-test

data:  data
t = 5.3712, df = 25, p-value = 1.431e-05
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 0.4880618 1.0951192
sample estimates:
mean of x
0.7915905
```


Region 5

6


```
Rscript /tmp/2U2X7CHesn.r
Read 26 items
One Sample t-test

data:  data
t = 4.5252, df = 25, p-value = 0.0001276
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 0.3687835 0.9848763
sample estimates:
mean of x
0.6768299
```
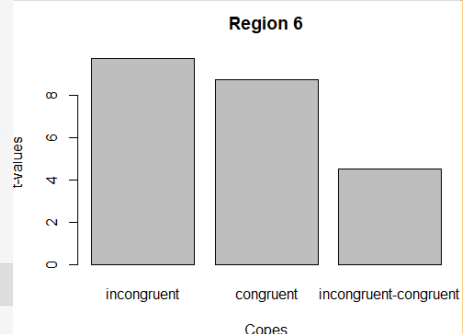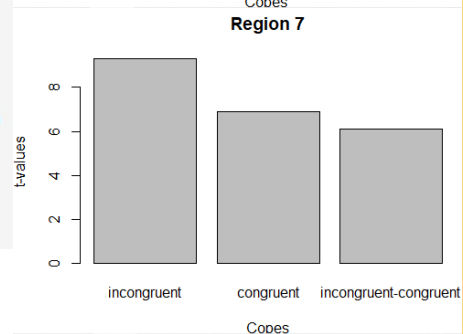

Region 6

7


```
Rscript /tmp/2U2X7CHesn.r
Read 26 items
One Sample t-test

data:  data
t = 6.1018, df = 25, p-value = 2.234e-06
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 0.5469379 1.1042694
sample estimates:
mean of x
0.8256037
```


Region 7

Exercises

Exercise1

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?

Non Binarized mask

Binarized mask

```
1.535599
0.410002
1.062533
-0.168917
0.051022
0.166877
0.865305
0.916918
0.242828
0.034246
-0.308607
0.405376
-0.148192
-0.346448
-0.081243
-0.430577
0.265449
-1.088206
-0.527704
-0.084251
0.029294
0.413119
1.065850
-0.465764
-0.594572
0.155415
```

The difference is considered small in the means and the results of one sample t-test.

```
1.363002
0.222655
1.062275
-0.211897
-0.101921
0.207988
0.720686
0.701019
0.265103
0.035617
-0.279518
0.256199
-0.076181
-0.131394
-0.107646
-0.393942
0.204620
-0.912633
-0.626931
-0.138006
-0.029543
0.363852
1.002289
-0.366796
-0.546775
0.212949
```

```
Rscript /tmp/2U2X7CHesn.r
Read 26 items
One Sample t-test

data:  data
t = 1.1056, df = 25, p-value = 0.2794
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -0.1120052  0.3716477
sample estimates:
mean of x
0.1298212
```

```
Rscript /tmp/V1THIk00Ja.r
One Sample t-testdata:  my_data
t = 1.2174, df = 27, p-value = 0.234alternative hypothesis: true meanis
    not equal to095percent confidence interval:
 -0.08678481  0.34003117
sample estimates:
mean of x
0.1266232
```

Exercise2

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.

Run the following commands:

```
fslmaths $FSLDIR/data/standard/MNI152_T1_2mm.nii.gz -mul 0 -add 1 -roi 36 1 -2 1 48  1 0 1 Jahn_ROI_dmPFC_36_-2_48.nii.gz -odt float

fslmaths Jahn_ROI_dmPFC_36_-2_48.nii.gz -kernel sphere 7 -fmean Jahn_Sphere_dmPFC_36_-2_48.nii.gz -odt float

fslmaths Jahn_Sphere_dmPFC_36_-2_48.nii.gz -bin Jahn_Sphere_bin_dmPFC_36_-2_48.nii.gz

fslmeants -i allZstats3.nii.gz -m Jahn_Sphere_bin_dmPFC_36_-2_48.nii.gz
```


Exercise3

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).

   1) Create your anatomical mask:
         -Open fsleyes and from standards open MNI152_T1_2mm.nii.gz
         - From settings ortho view, open atlases , harvard oxford subcortical atlas
         - Choose RightAmygdala and save the template as RightAmygdala.nii.gz
   2) Merge all zstats of Cope1 by running the following command in
   cope1.feat/stats   fslmerge -t allZstats.nii.gz `ls zstat* | sort -V

3) Run the following command in order to get the means
     fslmeants -i allZstats.nii.gz -m RightAmygdala.nii.gz

4) Now do one sample t-test using R language to obtain the results

```
Rscript /tmp/2U2X7CHesn.r
Read 26 items
One Sample t-testdata:  data
t = 2.954, df = 25, p-value = 0.006741
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 0.1278506 0.7165915
sample estimates:
mean of x
 0.422221
```

0.536840
0.885784
-0.350861
1.256197
0.712485
-0.271271
0.324466
0.355686
0.435731
0.859471
0.019151
0.432119
0.725281
-0.166431
1.774395
-0.015443
0.969244
-1.572548
0.736836
0.664731
1.980601
-0.517568
0.614159
0.632559
-0.289146

RightAmygdala Mask
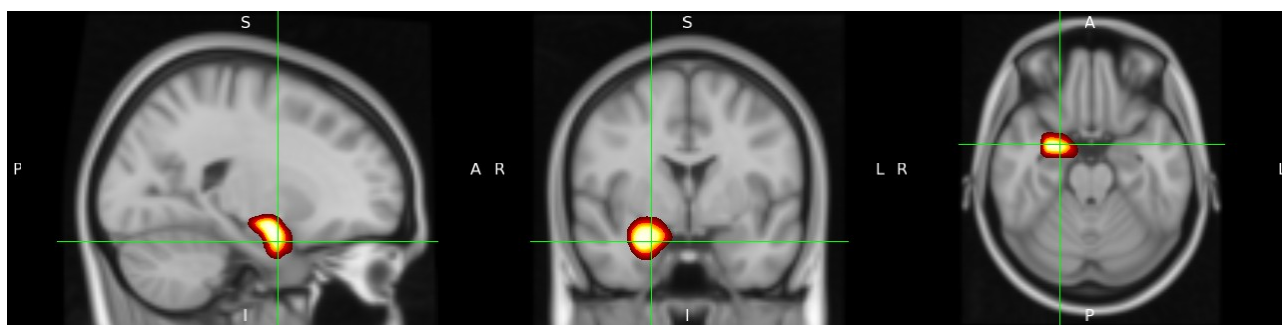
For a better quality images , see the attached files :)