



## IDENTIFICATION OF THE STATISTICALLY SIGNIFICANT AREAS PROTOCOL

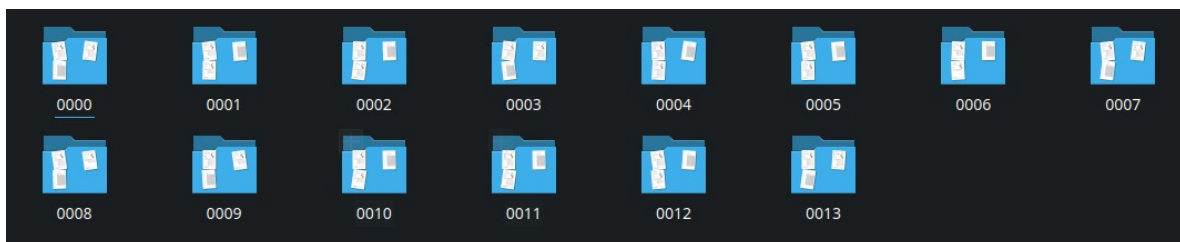
The aim of this protocol is to visualize the results of the Nonparametric statistic test performed on the cGICA data and extraction of ROI based on atlas. XjView toolbox will be used for this purpose (<https://www.alivelearn.net/xjview/>), the user manual can be downloaded from this link <https://www.alivelearn.net/xjview/documentation/>

### FILE STRUCTURE

The directory with the results of SnPM performed on the cGICA data is gonna have the distribution shown in Figure 1. Please name every folder with numbers like it is shown in Figure 1 where every number correspond to a RSN like this:

**0000:** Default Mode Network  
**0001:** Auditory Network  
**0002:** Cingulo Opercular  
**0003:** Dorsal Attention  
**0004:** Fronto Parietal  
**0005:** Medial Temporal Lobe  
**0006:** Parieto Medial

**0007:** Reward  
**0008:** Salience  
**0009:** Somatomotor Dorsal  
**0010:** Somatomotor Ventral  
**0011:** Unassigned  
**0012:** Ventral Attention  
**0013:** Visual Network

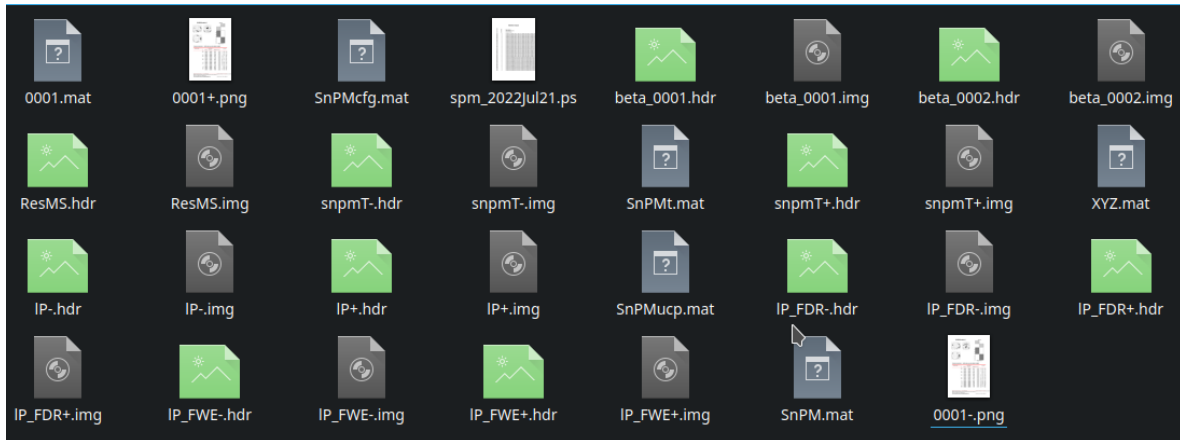


*Figure 1: SnPM file structure*

When you enter to a folder, you will see a content distribution as it is shown in Figure 2:

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Teléfono: [57+4] 219 6900 | Correo electrónico: [gruponeuropsicologia@udea.edu.co](mailto:gruponeuropsicologia@udea.edu.co)  
<http://www.udea.edu.co/neuropsicologiayconducta/> ▪ Medellín - Colombia

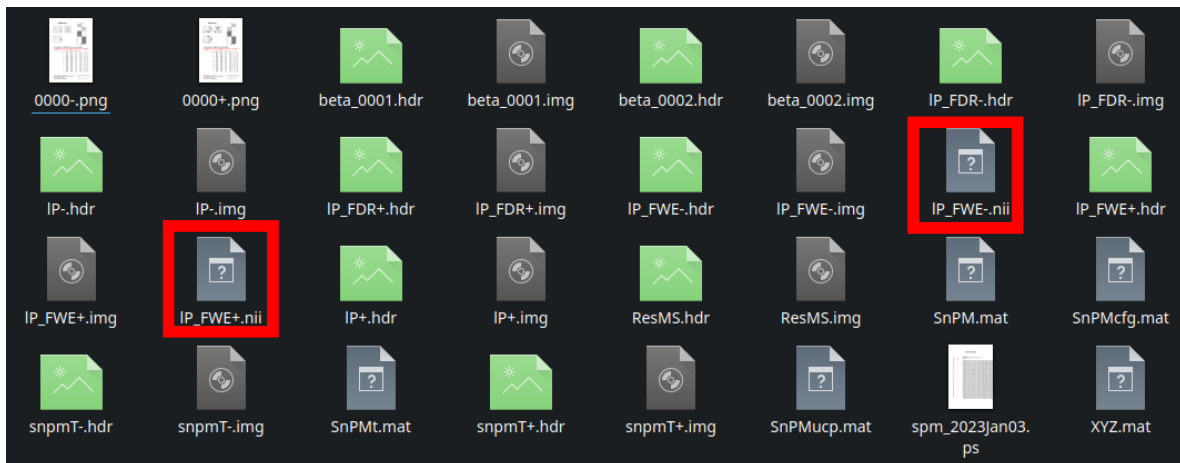


*Figure 2: SnPM Folder structure*

Inside every folder, the images with the Analyze format (.hdr y .img) will be converted to NifTI format (.nii) through FSL command:

```
»fslchfiletype NIFTI IP_FWE-.hdr IP_FWE-.nii
»fslchfiletype NIFTI IP_FWE+.hdr IP_FWE+.nii
```

The files you are gonna use are the NIfTI ones, these have the positive and negative results of SnPM (IP\_FWE-.nii and IP\_FWE+.nii). As it is shown in Figure 3.



*Figure 3: Positive and negative p-FWE statistics results of SnPM*

## INSTALLATION OF XjView TOOLBOX

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Go to <https://www.alivelearn.net/xjview/> and download the toolbox. Follow the steps that are indicated in the toolbox page.

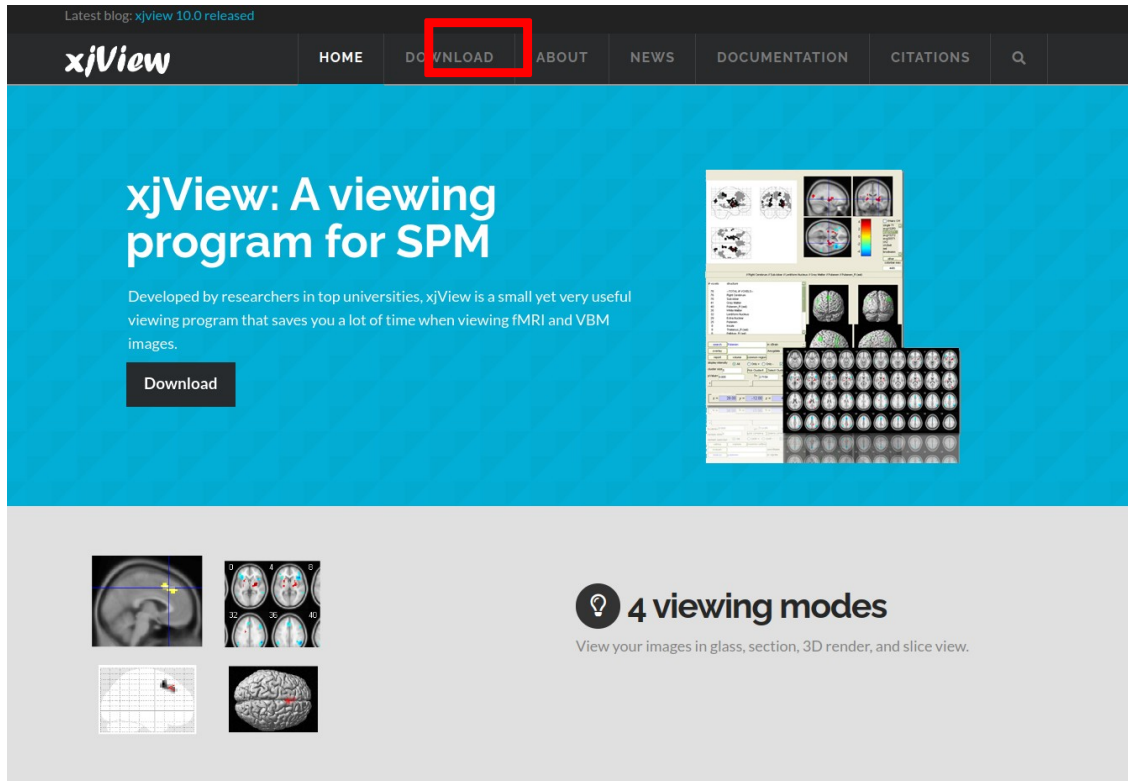


Figure 4: XjView toolbox website

## STEPS

The XjView folder will be added to Matlab through the option folder and subfolders. When you open the toolbox in Matlab, the following interface appears, Figure 5.

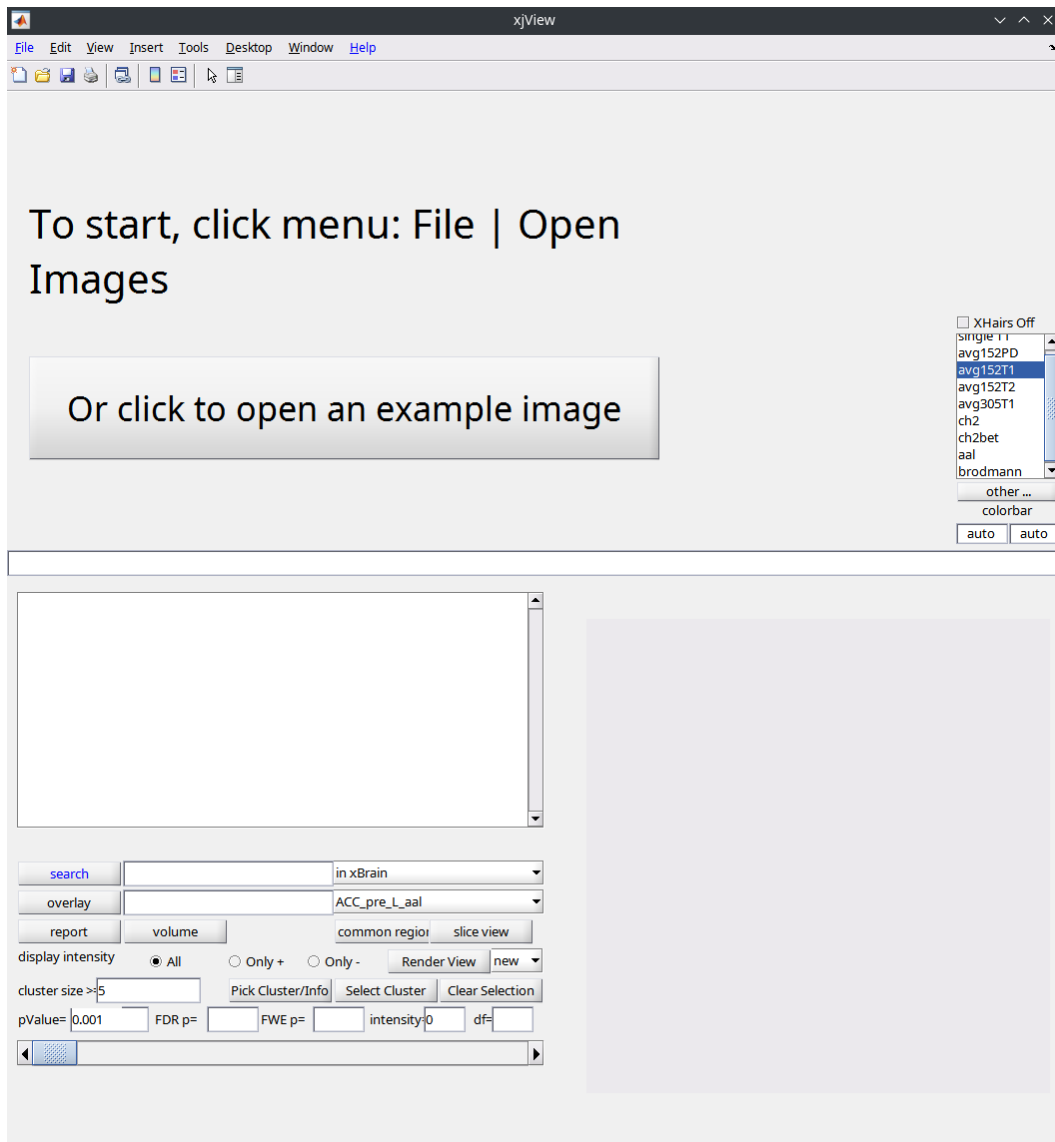
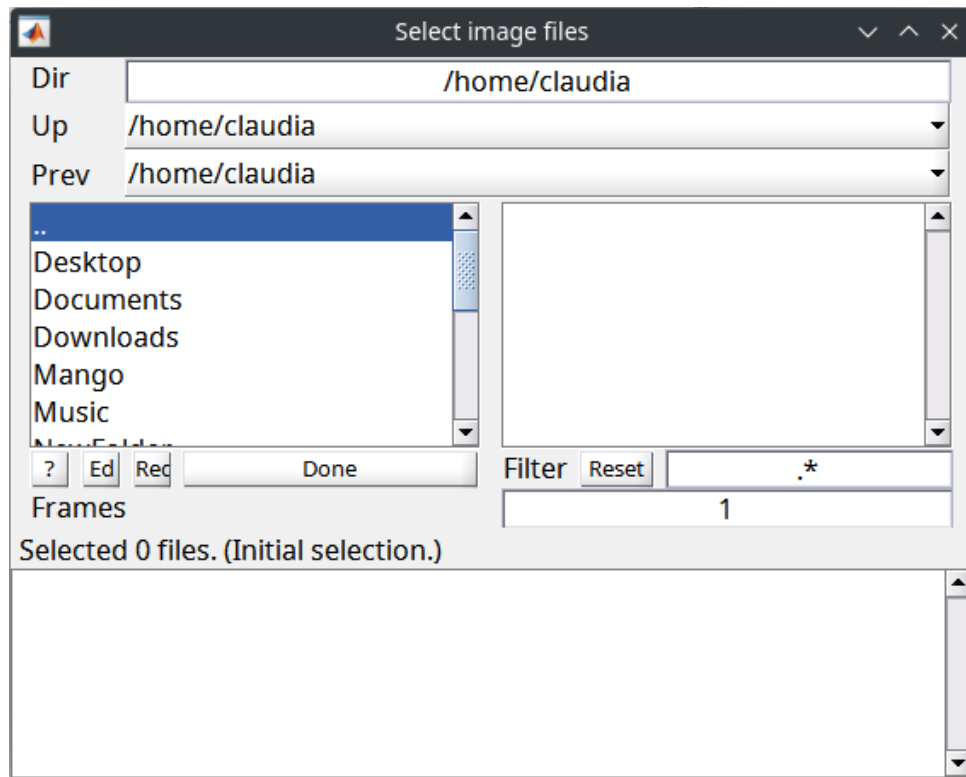


Figure 5: XjView interface

To select the image you are going to extract ROI descriptions, first go to the superior part of the toolbar and select “**File**”, next select “**Open images**” and the next window appears, Figure 6

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Teléfono: [57+4] 219 6900 | Correo electrónico: gruponeuropsicologia@udea.edu.co  
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*Figure 6: Selection of images to analyze*

On the left side of the window you can select the directory where the images are store. The images you are going to analyze are the results of SnPM performed on cGICA. Select the directory where those images are (como se observa en la Figure 1) and start with the first RSN you are going to extract the ROI from (0000 DMN).

When you are in the RSN folder, select the image IP\_FWE (+ / -).nii that is going to be analyzed in the toolbox. First the positive results and the same process is going to be repeated for the negative results Figure 7.

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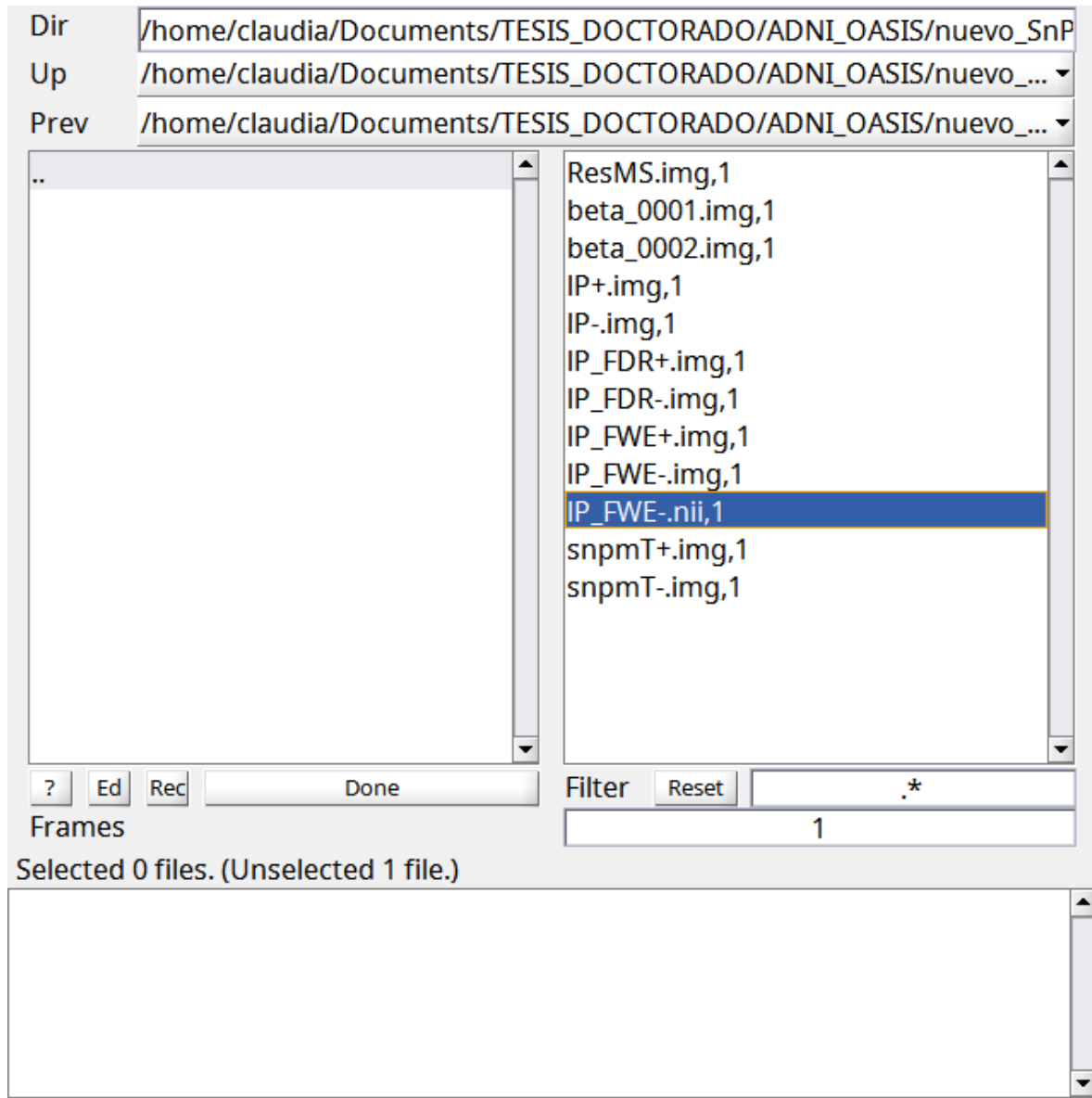


Figure 7: Positive and negative SnPM results

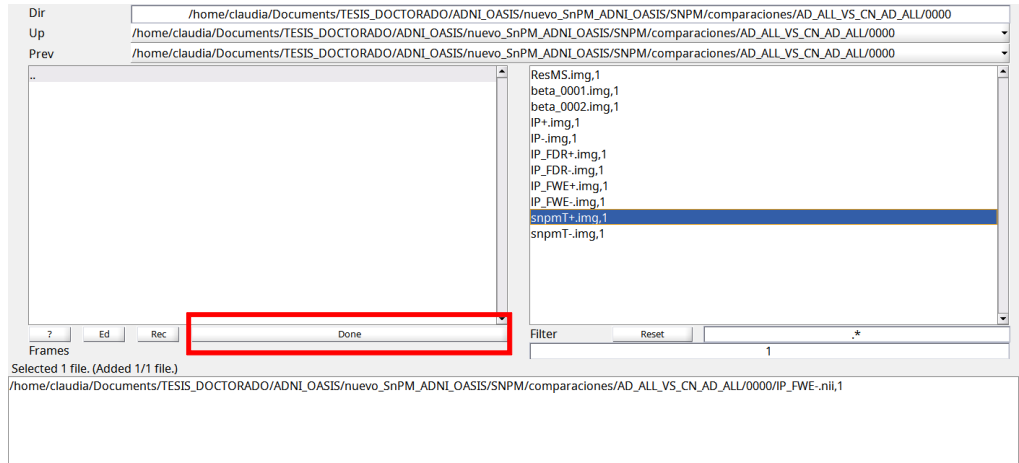
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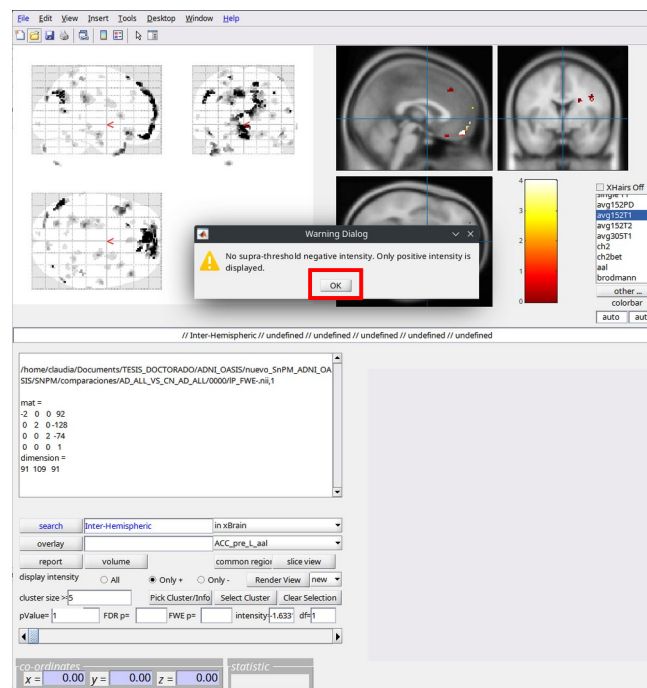
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Click on DONE to select the image you need to extract the ROI Figure 8.



*Figure 8: Selection of negative or positive image*

When you select the image a warning is going to appear Figure 9. Click on OK and you can continue.



*Figure 9: Warning message after image selection*

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Clusters that you will analyze are those with  $\geq 100$  voxels, write 100 in the part selected to cluster size Figure 10. Next, click **ENTER** on your keyboard in order to apply this change.

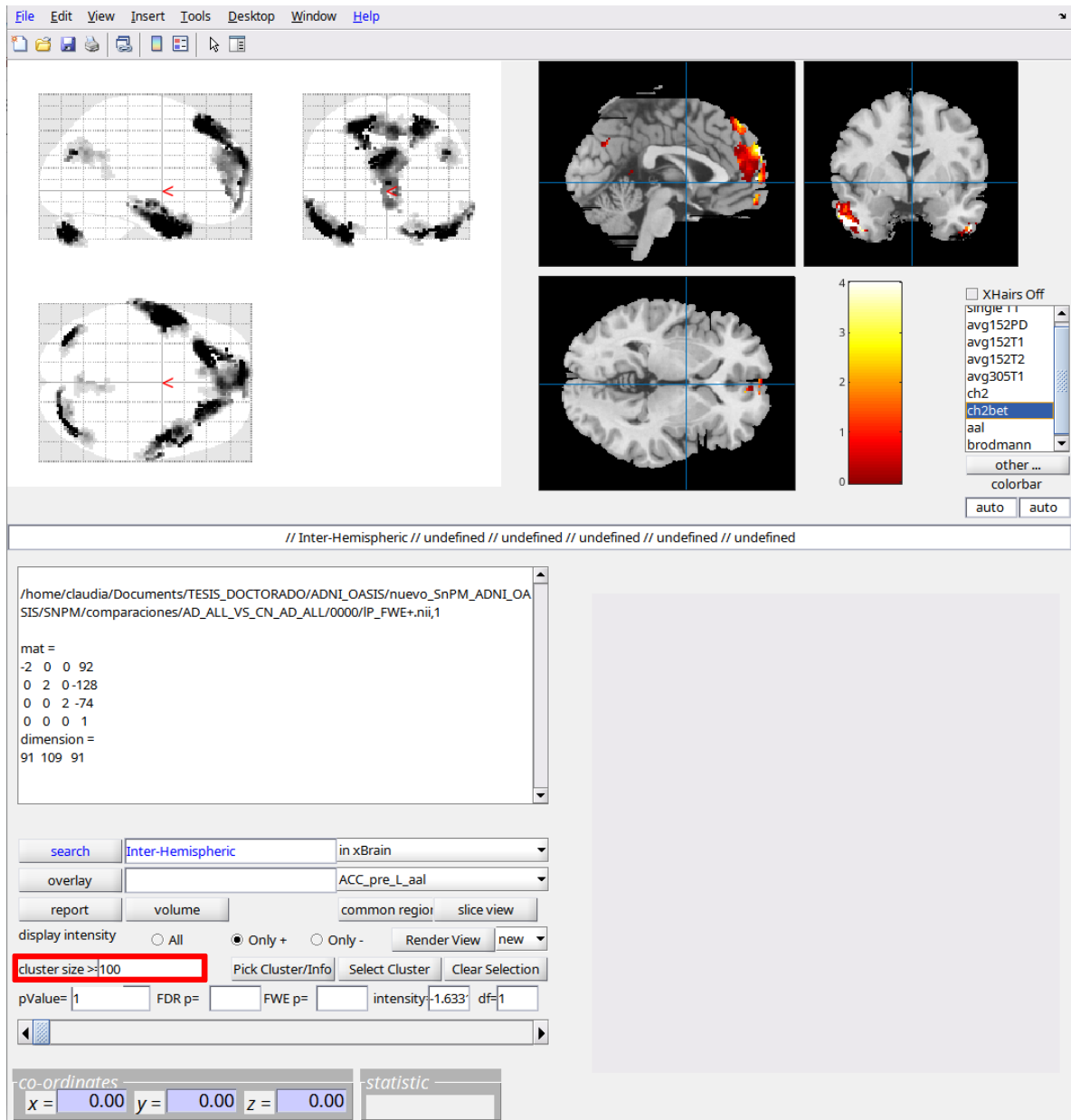


Figure 10: Selection of cluster size

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To extract the ROI you need to generate a REPORT. In the inferior toolbars you can find this option, click on it Figure 11.

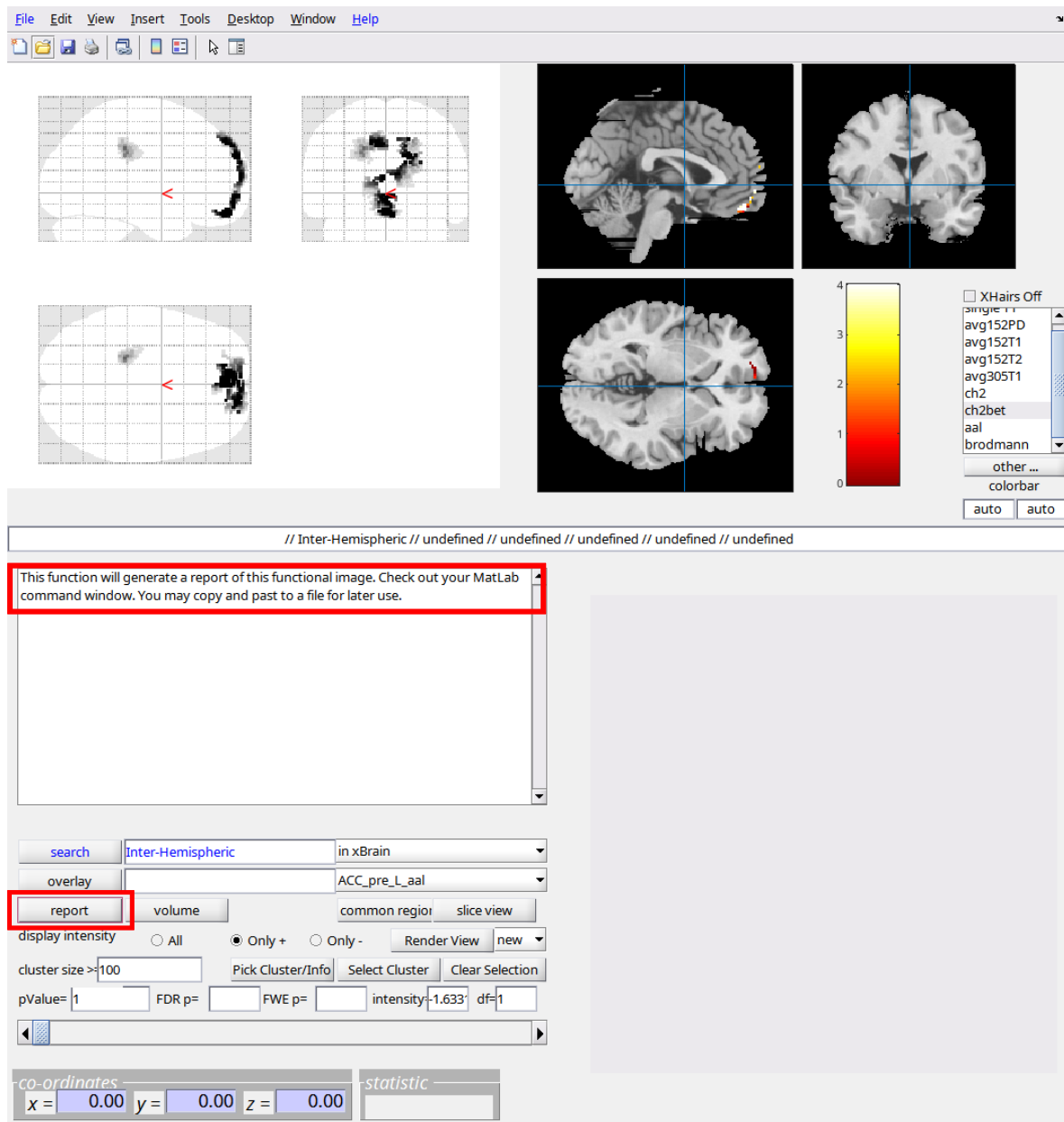


Figure 11: Report generation of the ROI

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After you generate the REPORT check Matlab bash to see the list and copy it Figure 12. You can select this list and copy it on a text editor and the name it.

```
Command Window
New to MATLAB? See resources for Getting Started.

3 Frontal_Sup_Medial_L (aal3v1)
2 Frontal_Mid_2_R (aal3v1)
1 brodmann area 8

-----
Cluster 3
Number of voxels: 208
Peak MNI coordinate: -20 -32 36
Peak MNI coordinate region: // Left Cerebrum // Frontal Lobe // Sub-Gyrus // White Matter // undefined // undefined
Peak intensity: 2.1192
Center of gravity MNI coordinate: -22 -29 34
Center of gravity MNI coordinate region: // Left Cerebrum // Frontal Lobe // Sub-Gyrus // White Matter // undefined // undefined
# voxels      structure
208 --TOTAL # VOXELS--
208 Left Cerebrum
195 White Matter
170 Sub-Gyrus
167 Frontal Lobe
34 Limbic Lobe
31 Cingulate Gyrus
10 brodmann area 31
10 Gray Matter
7 Sub-lobar
4 Extra-Nuclear
3 Lateral Ventricle
3 Cerebro-Spinal Fluid
1 Corpus Callosum
1 Cingulate_Mid_L (aal3v1)

-----
Cluster 4
Number of voxels: 100
Peak MNI coordinate: -6 54 38
Peak MNI coordinate region: // Left Cerebrum // Frontal Lobe // Superior Frontal Gyrus // Gray Matter // brodmann area 9 // Front
Peak intensity: 4
Center of gravity MNI coordinate: -11 53 41
Center of gravity MNI coordinate region: // Left Cerebrum // Frontal Lobe // Superior Frontal Gyrus // Gray Matter // brodmann ar
# voxels      structure
100 --TOTAL # VOXELS--
88 Left Cerebrum
88 Frontal Lobe
78 Superior Frontal Gyrus
63 Gray Matter
53 brodmann area 9
51 Frontal_Sup_2_L (aal3v1)
49 Frontal_Sup_Medial_L (aal3v1)
17 White Matter
10 Medial Frontal Gyrus
10 brodmann area 8
1 Inter-Hemispheric

fx >>
```

Figure 12: Report of RSN ROI in Matlab

The file name of every report must have the same name as the RSN you are analyzing and specify if it is a negative or positive result as shown in Figure 13 and save it in the same folder as the SnPM result for that RSN. The prefix of the file must be the group this file corresponds to, in the figure you see it is labeled as MCI, you should change it to G1 or G2 (group 1 or 2), with this format:

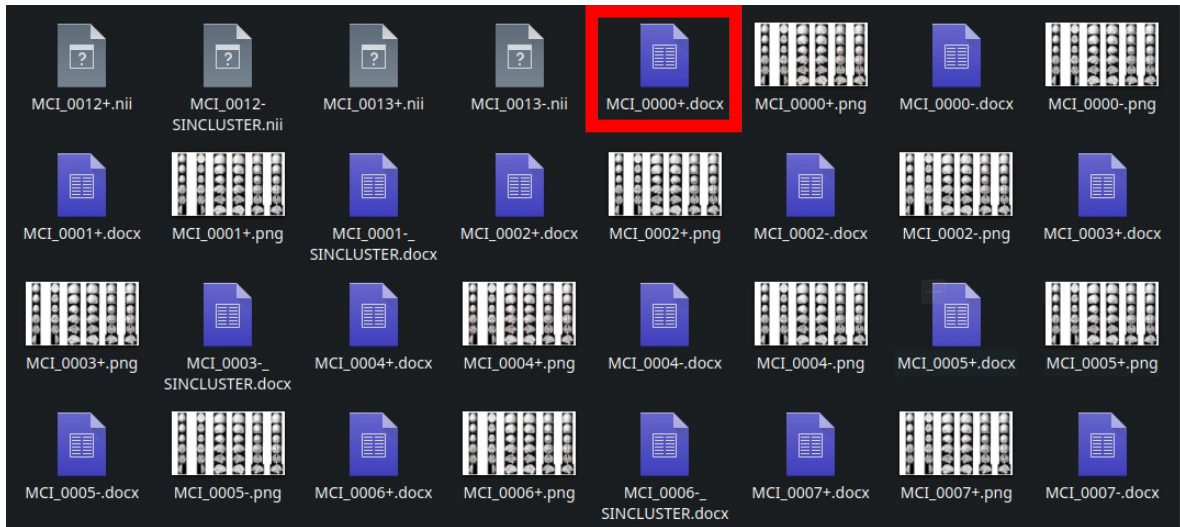
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*prefix\_XXXX+.txt*

Example:

*G1\_0000+.docx*



*Figure 13: SnPM folder structure with the ROI report file*

## RENDERIZATION OF THE IMAGE

After you create the report a rendered image must be saved of this process, in the inferior toolbar you can see a bottom named RENDER VIEW, click on it. Before, make sure it appears the option NEW, if not, choose it. Figure 14.

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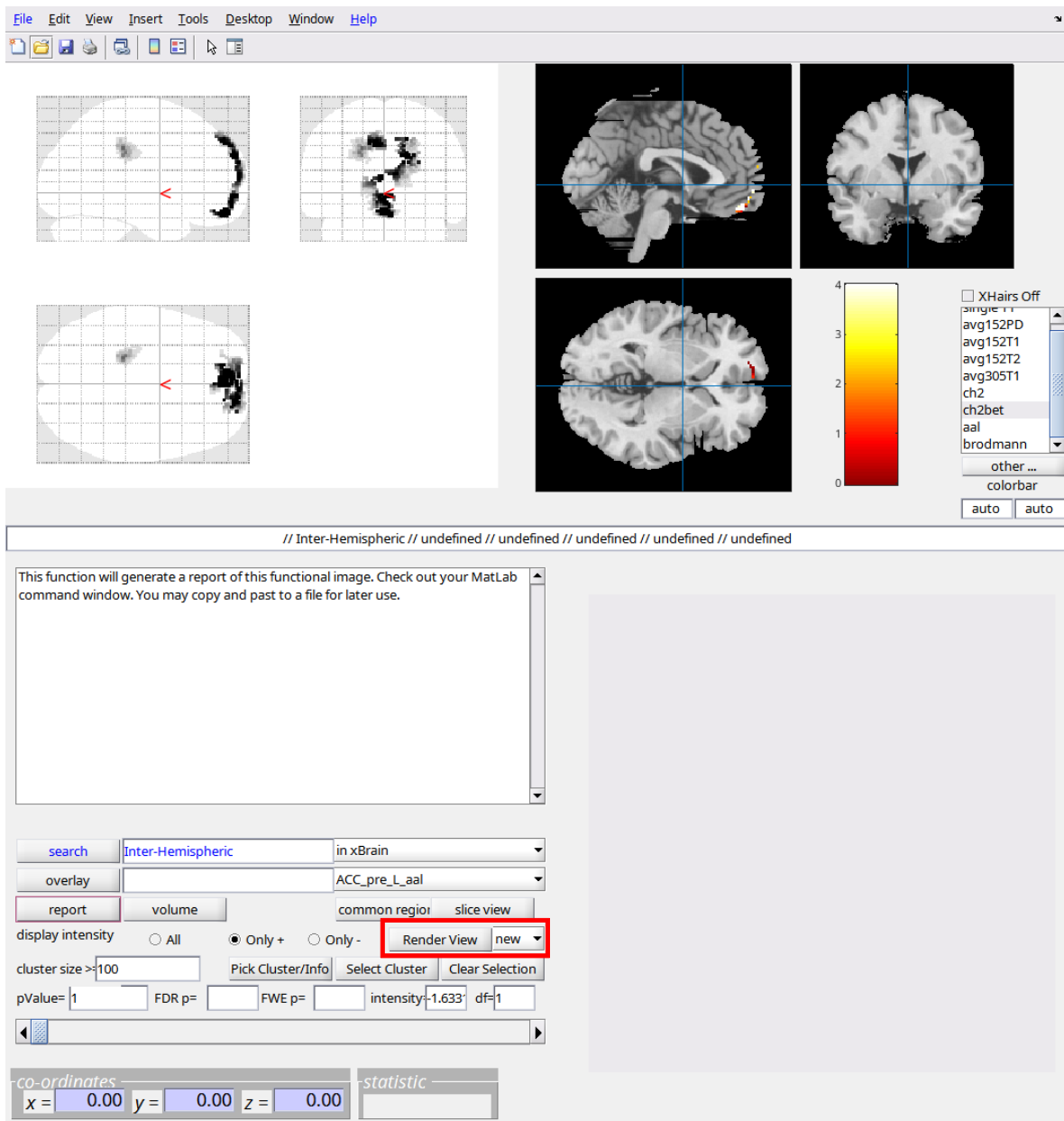


Figure 14: Render view of the reported clusters

When you click on RENDER VIEW a new window appears with the rendered image of the clusters found in the file (image) Figure 15. This images must be saved.

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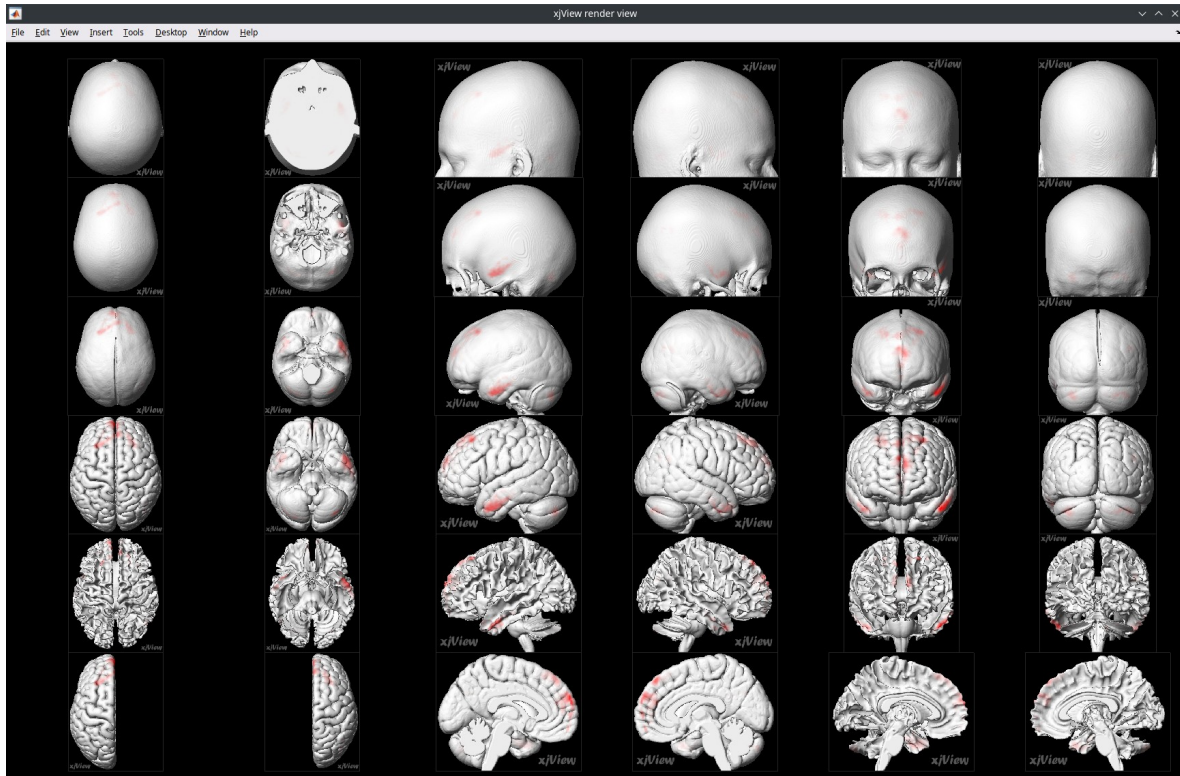
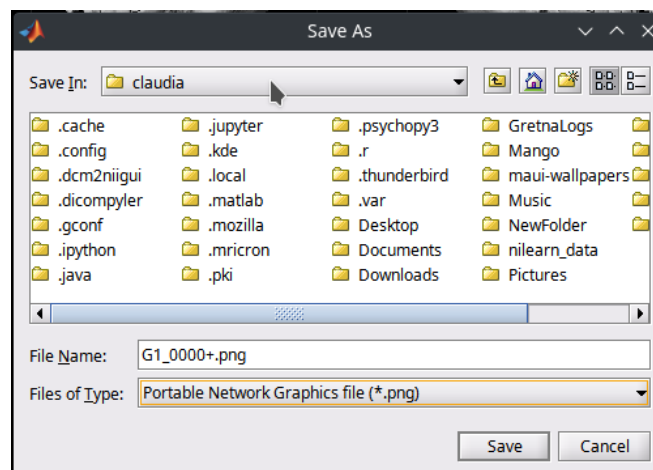


Figure 15: Render view of the clusters

As it is shown in Figure 16, the rendered image must be saved as **.jpg/.png** file in the same folder of the SnPM result for the specific RSN you are analyzing. Click on the left superior toolbar in FILE, next on SAVE AS, and a new window will open



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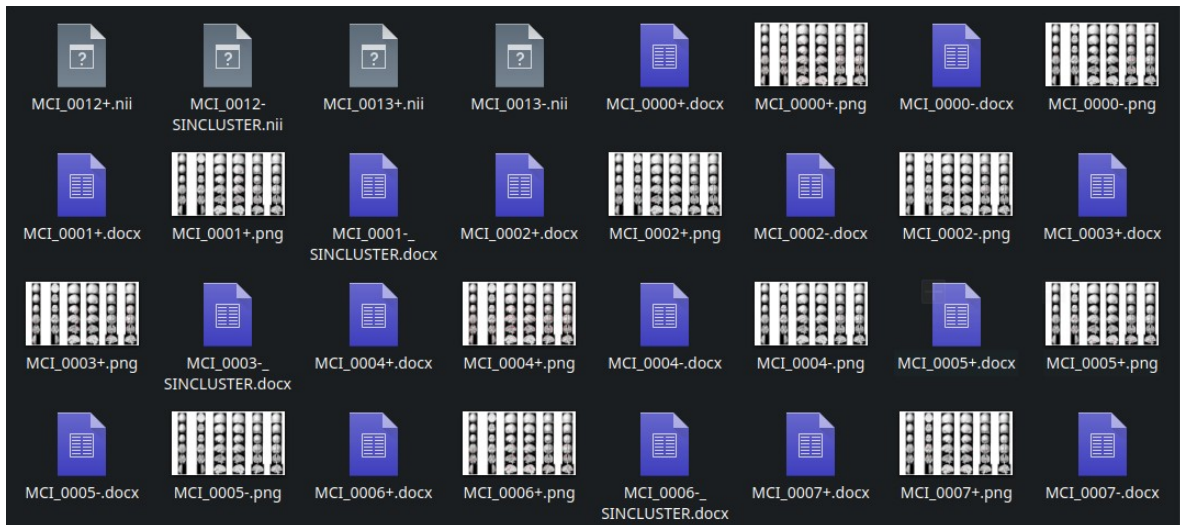


As the report, this file must have a prefix that is the group label and specify if it is a positive or negative report. with this format:

*prefix\_XXXX+.jpg*

Example:

*G1\_0000+.jpg*



*Figure 16: SnPM folder estructura with the rendered files*

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