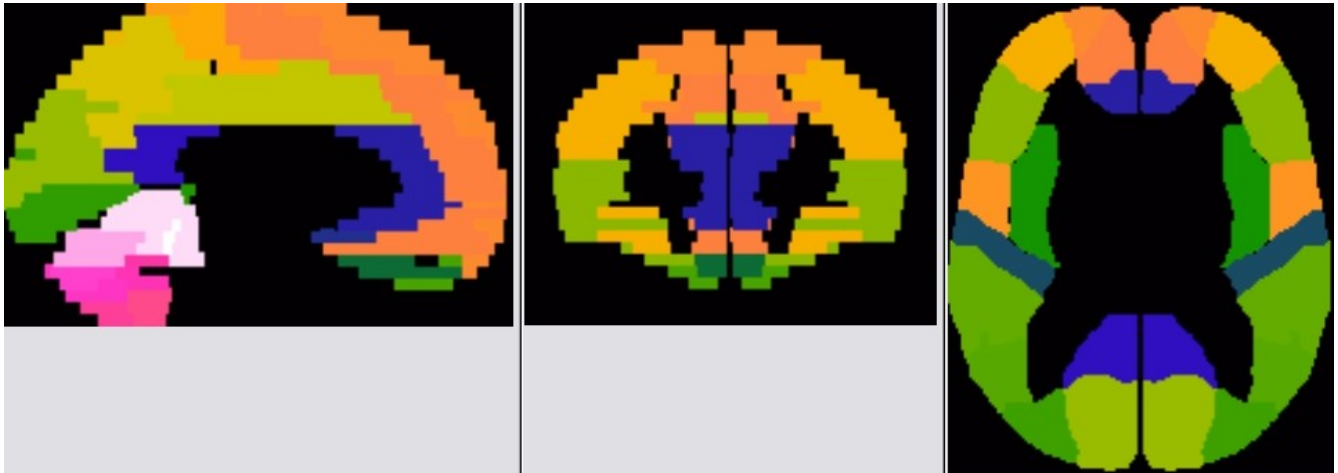


ClassTAL.m Script

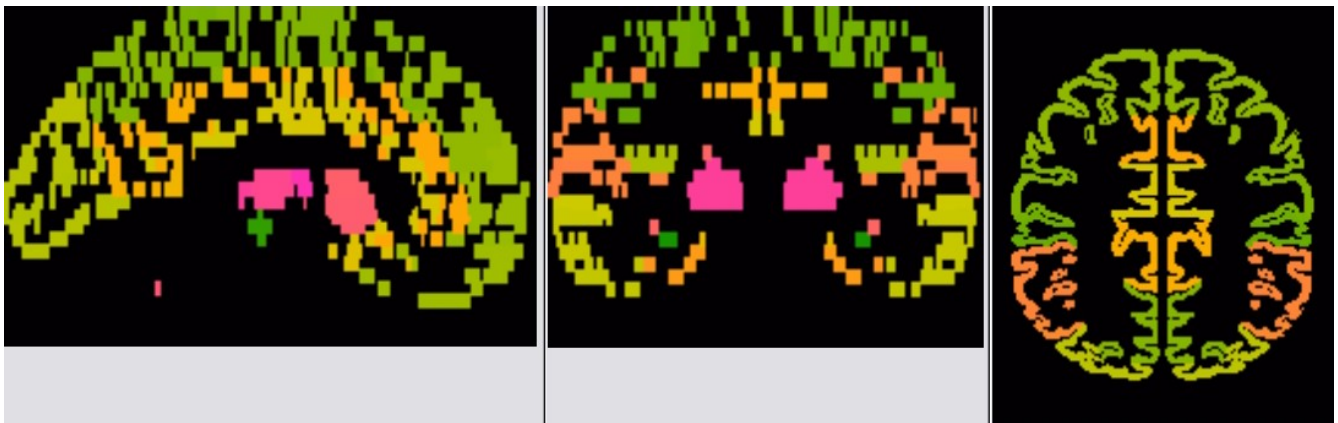
We realized a Matlab® script (version 7.0) for voxel of interest (VOI) analysis. Using the AFNI data collection (<http://afni.nimh.nih.gov>), we saved two atlas in .mat format, the atlas are arrays of 140x172x120 voxels with a 1x1x1 mm³ resolution. The first has been created for Gyrus classification of the normalized brain in the Talairach space (fig. 1) and the second for Brodmann Areas (BA, fig. 2).

Figure 1 Gyrus AFNI Template



Three orthogonal slices of the template showing different Gyrus in different color

Figure 2 Brodmann Areas AFNI Template



Three orthogonal slices of the template showing different BA in different color

Next we created other atlases forcing the classification of null voxels on the basis of a simple algorithm: if the absolute majority (>50%) of nearest voxels (see fig. 3 bottom left) belong to a category we assigned that voxel to it. Using iteratively the algorithm we saved eight more atlases (called R1, R2, R3, R4) with an increasing numbers of classified voxels, but also with some image degradation (see fig. 3).

The inputs of the script were .voi files saved from Brain Voyager QX© (<http://www.brainvoyager.com>) volume maps. This files contained samples of statistically significant voxels, divided in clusters. The script can compare them with the selected atlases to produce some outputs described in the following paragraphs.

Figure 3 Brodmann Area AFNI R1 Template



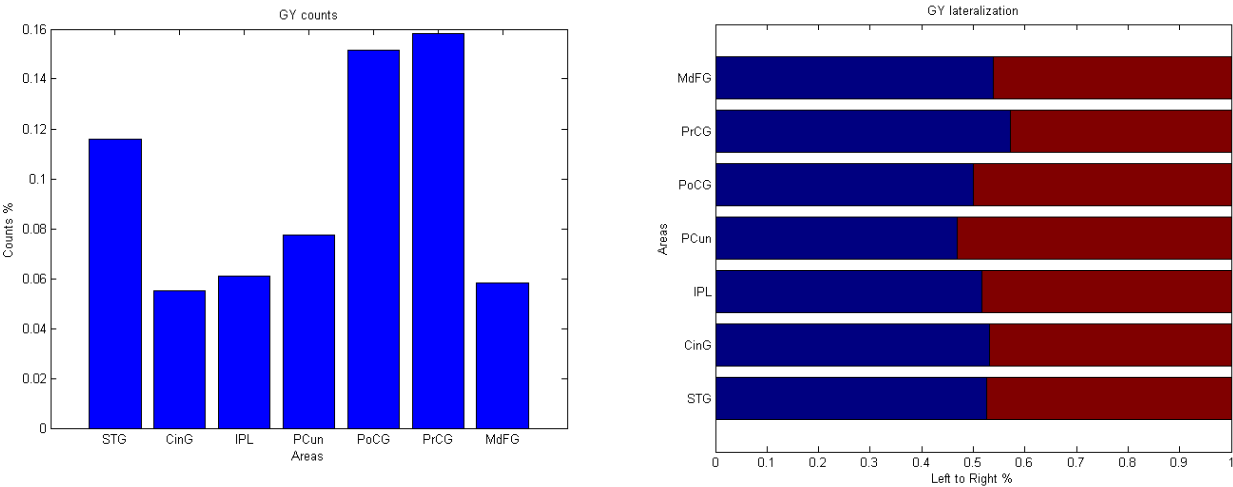
Three orthogonal slices of the template showing different BA in different color after near voxel forced classification

Gyrus Output

In the Gyrus output mode the script produces three graphs using the selected AFNI Gyrus atlas:

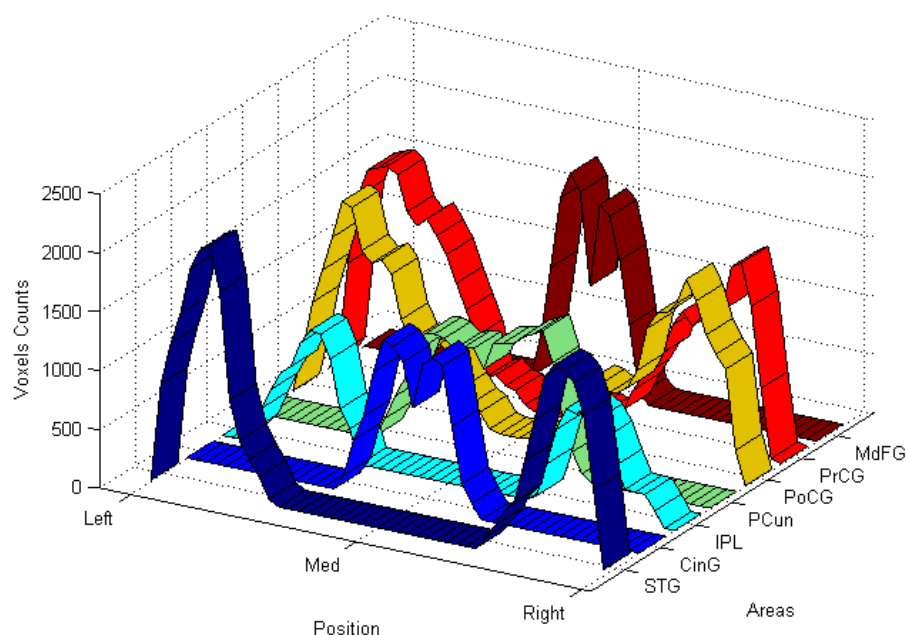
- the percentage of active voxels divided by the cerebral gyri (see fig. 4 on the left), the procedure stops at a fixed threshold of the total number of voxels (p.e. with a 5% threshold the script graphs the gyri that contains a number of active voxel greater than 5% of total active voxel, see fig. 4);
- the lateralization percent of the gyri that overcome the threshold (see fig. 4 on the right);
- the number of active voxels of the supra-threshold areas as a function of the gyrus and of the Talairach coordinate X (left to right, see fig. 5).

Figure 4 Gyrus Output 1 & 2



Gyrus counts percent (left) and gyrus lateralization (right)

Figure 5 Gyrus Output 3



Gyrus counts in function of areas and lateralization

The possible abbreviations of the output figures are: PCC = Posterior Cingulate; ACC = Anterior Cingulate; SbCG = Subcallosal Gyrus; TTG = Transverse Temporal Gyrus; Unc = Uncus; RG = Rectal Gyrus; FG = Fusiform Gyrus; IOG = Inferior Occipital Gyrus; ITG = Inferior Temporal Gyrus; Ins = Insula; PaHG = Parahippocampal Gyrus; LG = Lingual Gyrus; MOG = Middle Occipital Gyrus; OrG = Orbital Gyrus; MTG = Middle Temporal Gyrus; STG = Superior Temporal Gyrus; SOG = Superior Occipital Gyrus; IFG = Inferior Frontal Gyrus; Cun = Cuneus; Ang = Angular Gyrus; SMG = Supramarginal Gyrus; CinG = Cingulate Gyrus; IPL = Inferior Parietal Lobule; Pcun = Precuneus; SPL = Superior Parietal Lobule; MFG = Middle Frontal Gyrus; PaCL = Paracentral Lobule; PoCG = Postcentral Gyrus; PrCG = Precentral Gyrus; SFG = Superior Frontal Gyrus; MdFG = Medial Frontal Gyrus; vUv = Uvula of Vermis; vPyr = Pyramis of Vermis; vTub = Tuber of Vermis; vDec = Declive of Vermis; vCul = Culmen of Vermis; Cton = Cerebellar Tonsil; SLun = Inferior Semi-Lunar Lobule; Fast = Fastigium; Dent = Dentate; Nod = Nodule; Uvu = Uvula; Pyr = Pyramis; Tub = Tuber; Dec = Declive; Cul = Culmen; Clin = Cerebellar Lingual.

Brodman Areas Output

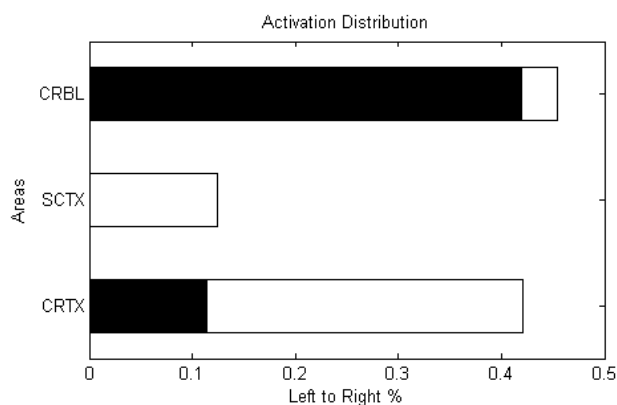
The Brodmann Areas mode produces the same three graphs described above using a BA AFNI atlas. The possible abbreviations are: Hippo = Hippocampus; Amg = Amygdala; HyTH = Hypothalamus; SN = Substantia Nigra; CauTa = Caudate Tail; CauBo = Caudate Body; CauHd = Caudate Head; VAN = Ventral Anterior Nucleus; VPMN = Ventral Posterior Medial Nucleus; VPLN = Ventral Posterior Lateral Nucleus; MDN = Medial Dorsal Nucleus; LDN = Lateral Dorsal Nucleus; Pulv = Pulvinar; LPN = Lateral Posterior Nucleus; VLN = Ventral Lateral Nucleus; MN = Midline Nucleus; AN = Anterior Nucleus; MaBo = Mammillary Body; Md GP = Medial Globus Pallidus; Lt GP = Lateral Globus Pallidus; Put = Putamen; NAcc = Nucleus Accumbens; MGB = Medial Geniculus Body; LGB

= Lateral Geniculum Body; SuTH = Subthalamic Nucleus; BA 1-47 = Brodmann Area 1-47.

Activation Output

In the Activation mode the voxels are assigned to one of three groups: cerebellar voxels (CRBL), subcortical voxels (SCTX) and cortical voxels (CRTX). The relative percents of the groups are graphed together with their lateralization (see fig. 6, black for left and white for right). The classification proceeds in a serial fashion starting with the AFNI Gyrus atlas (CRTX and CRBL) and finishing the remaining voxels with the AFNI BA atlas. The unclassifiable voxels are excluded from the graph (i.e. sum of the three groups = 100%).

Figure 6 Activation Output

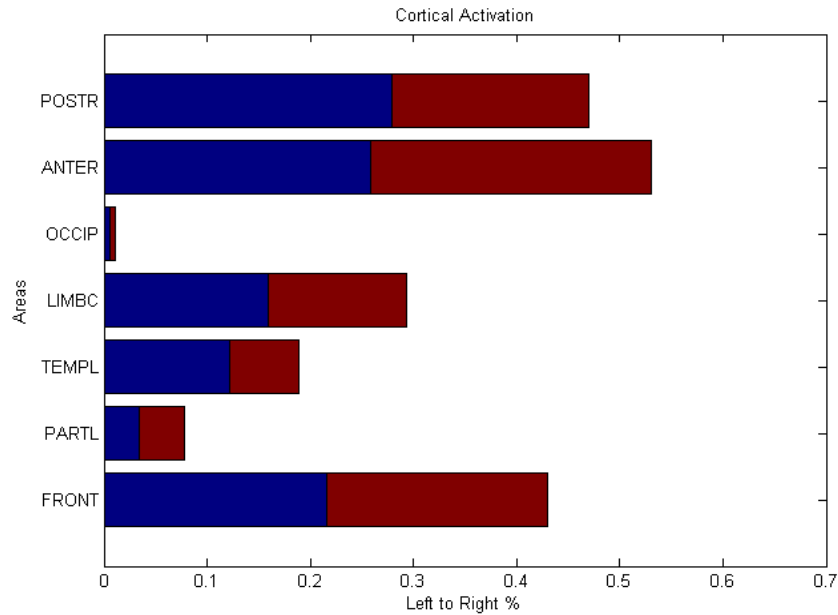


Percentages of cortical, subcortical and cerebellar total activation

Lobes Output

In the Lobes mode the cortical voxels are assigned to one of brain's lobes using a AFNI Gyrus atlas. The relative percents are graphed together with lateralization (see fig. 7, blue for left and red for right).

Figure 7 Lobes Output



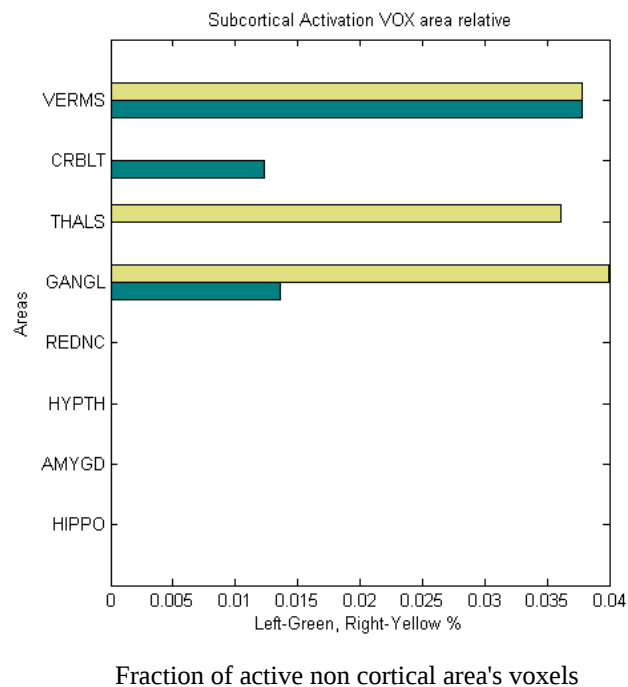
Lobes relative activation

Abbreviations: POSTR = Posterior Brain (behind Central Gyrus); ANTER = Anterior Brain (); OCCIP = Occipital Lobe; LIMBC = Limbic Lobe; TEMPL = Temporal Lobe; PARTL = Parietal Lobe; FRONT = Frontal Lobe.

Subcortical Output

In the Subcortical mode the output is a graph of the left (in green) and right (in yellow) fraction of the voxels that are active (i.e 100% = all area's voxels are activated) in some important non cortical areas (see fig. 8). The classification uses a BA AFNI atlas.

Figure 8 Subcortical Output

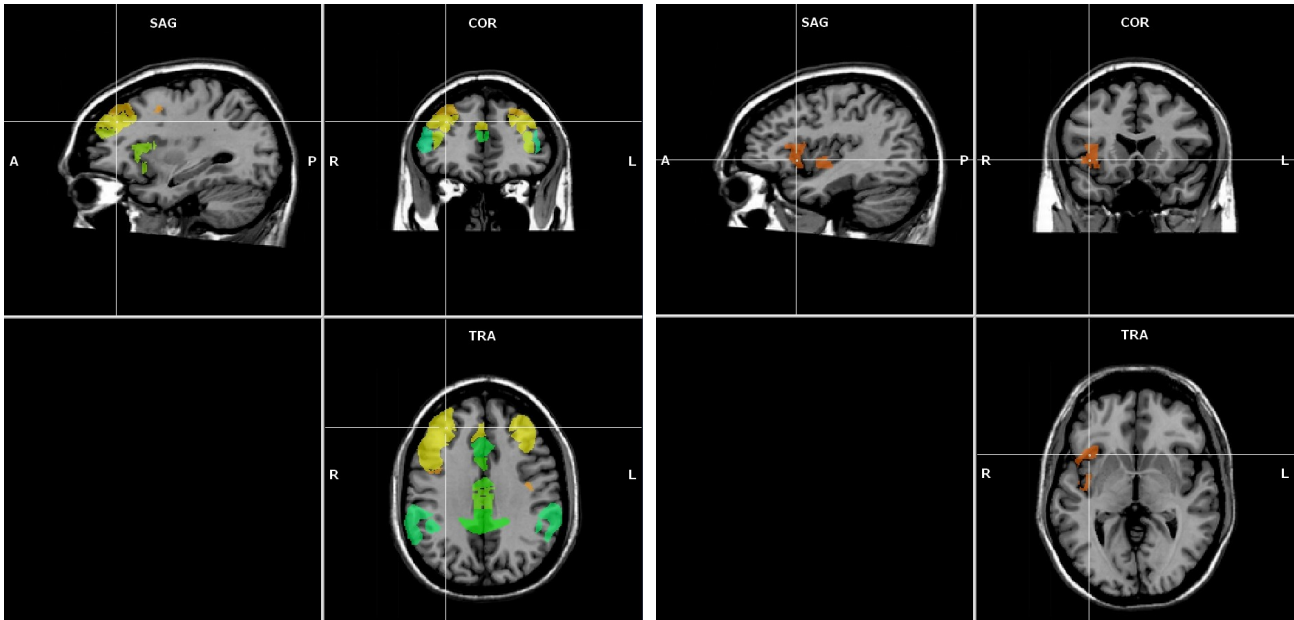


Abbreviations: VERMS = Vermis; CRBLT = Lateral Cerebellum; THALS = Thalamus; GANGL = Basal Ganglia; REDNC = Red Nucleus; HYPTH = Hypothalamus; AMYGD = Amygdala; HIPPO = Hippocampus.

Segmentation Output

In the Segmentation mode the voxels of the BA or Gyrus mode are saved in .voi or .img (analyze) format files (see fig. 9).

Figure 9 Segmentation Output



In different color voxels from different BA (left) and insular active voxels subsample (right) displayed by Brain Voyager©

Table Output

In Table Mode the outputs is a .txt file with many rows (see tab. 1). Every row represents an area that meet some criteria: the number of active voxels included in the area surpasses a fixed fraction of total activation voxels (default = 5%) or the number of active voxels surpasses a fixed fraction of the total voxels of that area (default = 25%) or the number of active voxels surpasses a fixed absolute number of voxels in subcortical areas (default = 125) or the number of active voxels surpasses a minimum fixed absolute number of voxels (default = 100).

Every row contains the following data: name of the gyrus preceded by the left, right or bilateral attribute, number of active voxels, lateralization, Brodmann areas of the voxels group in decrescent order.

The maximum number of Brodmann Areas written in the table is fixed (default = 4) to not obscure the output readability.

The output can be of the total activation voxels or cluster by cluster with also the Tailarach's coordinates of the peak's activations including their gyrus and Brodmann area specification.

Table 1 Activations Summary

Area	Voxels	L/R%	Left BA	Right BA
Bilat Middle Frontal Gyrus	27529	35/65%	9 8 10 46	9 8 10 46
Bilat Cingulate Gyrus	26379	51/49%	31 24 32 23	31 24 32 23
Bilat Out of Gyrus	16444	49/51%	23 6 31 9	23 13 6 31

Bilat Inferior Parietal Lobule	13035	39/61%	40 13 22 39	40 13 22
Bilat Superior Frontal Gyrus	8078	48/52%	9 10 6 8	9 10 6 8
Bilat Supramarginal Gyrus	7561	33/67%	40 39	40 39
Bilat Inferior Frontal Gyrus	4514	7/93%	46 10	47 46 45 9
Bilat Insula	3279	1/99%	13 40	13 47 22 21
Bilat Precuneus	3200	40/60%	7 31 39 19	7 31 5
Bilat Medial Frontal Gyrus	2642	33/67%	6 9 32 8	6 9 32 8
Bilat Superior Temporal Gyrus	2539	12/88%	22 13 42 40	22 39 13 42
Bilat Precentral Gyrus	2503	24/76%	9 6 4 8	9 6 44
Bilat Paracentral Lobule	1105	52/48%	31 24	31 24
Bilat Angular Gyrus	833	42/58%	39 40	39 40
Bilat Posterior Cingulate	724	50/50%	23	23
Bilat Anterior Cingulate	698	65/35%	32 24	32 24
Right Cuneus	360	0/100%		7 18 19 31
Right Ventral Lateral Nucleus	319	0/100%		
Bilat Postcentral Gyrus	306	87/13%	40 2 42	40 2
Right Middle Temporal Gyrus	214	0/100%		21 20 39
Right Medial Dorsal Nucleus	159	0/100%		
Right Ventral Posterior Lateral Nucleus	137	0/100%		

Table of the total activation

Download

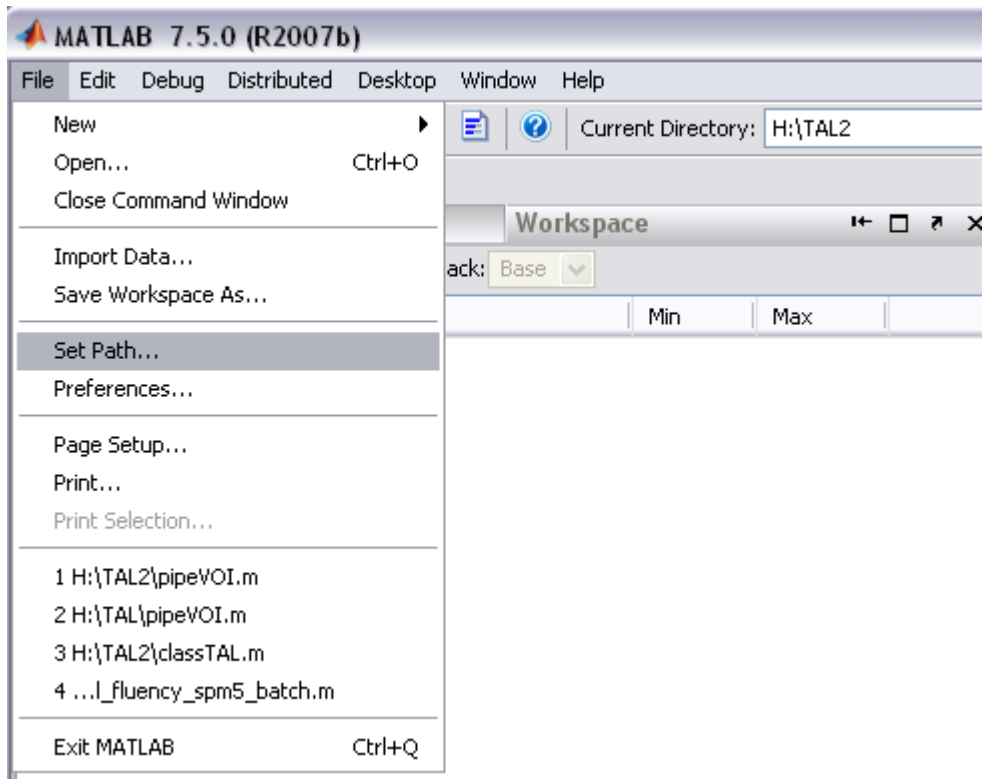
The script and the atlases (both in .mat or .img format) are available to anyone for examination or use at the Nature Preceding site (<http://precedings.nature.com>). For help or support send an e-mail at federico.dagata@unito.it.

Installation

To install the script download the .zip file, extract all the files in the same directory and add the

directory to the paths of matlab (Menu – File – Set Path... – Add Folder..., see fig. 10).

Figure 10 Installation



Video Capture of the Set Path installation

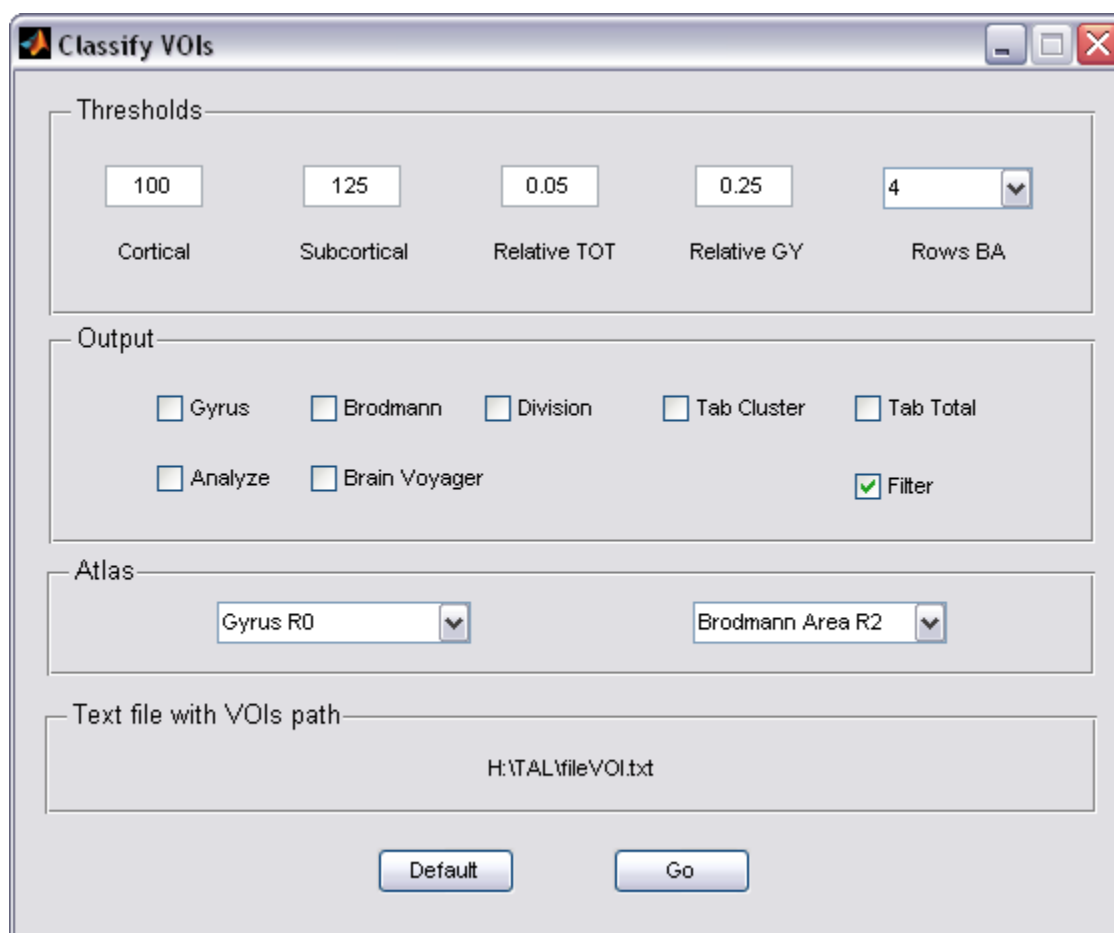
How to use

From the Matlab® Command window write “classTAL” and press <CR> key. It will appear a GUI window like that of fig. 11. Inside the window there are 4 panels: “Thresholds”, “Output”, “Atlas”, “Text file” and two buttons: “Default”, “Go”.

Inside “Thresholds” there are 4 input boxes and a popup menu in which it is possible to set the thresholds of all the script’s outputs. “Cortical” input represents the absolute minimum number of voxels needed to insert a cortical gyrus in the script’s output. “Subcortical” input represents the absolute minimum number of voxels needed to insert a subcortical area in the script’s output. “Relative TOT” input represents the number of voxels (computed as a percent of the total number of voxels, 5% in fig. 11) needed to insert an area in the script’s output. “Relative GY” input represents the number of voxels inside every gyrus (computed as a percent of the total number of the gyrus, 25% in fig. 11) needed to insert that cortical gyrus in the script’s output. The thresholds are applied with a logical OR, so to be excluded from the output an area should have less voxels than all the set voxels thresholds.

“Rows BA” menu represents the number of BA reported in the Table Output for every table rows (see tab. 1, with the 4 “Rows BA” setting in the Left and Right BA columns were reported the 4 most represented BA).

Figure 11 Script GUI



Video Capture of the Graphical User Interface

Inside “Output” there are 8 check boxes that can be set on or of to select the required outputs (see output section above). With the “Filter” check box on the areas under the thresholds are deleted from the output saved, but same text is always written in the Matlab® Command Window, the areas that will be deleted from the saved file are highlighted with an asterisk “*” (see fig. 20 in the Example below).

Inside “Atlas” there are 2 popup menus with the Atlases (Gyrus R0, R1, R2, R3, R4; Brodmann Area R0, R1, R2, R3, R4) used for the classification of the voxels (see above for the description of the Atlases).

Inside “Text file” there is the complete file’s path of the fileVOI.txt. This file is a text file that the script uses to find the VOIs’ files. FileVOI.txt should be edited with any file editor (e.g. edit command of Matlab® or notepad of Windows as in fig. 12), then the script searches the listed BrainVoyager© VOIs’ files and analyzes them. The VOIs’ files could be as much as one need, they must be one for one text row and they must not have the file format specification (i.e. the final .voi). If one wants the Cluster table output in the same directory of the .voi file there must be the file with the peaks coordinates table (a BrainVoyager© .txt file that must have the same name of the .voi file, but with a .pk.txt file file format as in fig. 16).

Pressing “Default” button the setting of the GUI are changed back to the defaults (Cortical=100, Subcortical=125, Relative TOT=0.05, Relative GY=0.25, Rows BA=4, no checked into Output saving Filter, Gyrus R0 and Brodmann Area R2 for the Atlas).

Pressing “Go” button the script will be executed, the output will be shown in the Matlab® Command window and saved in the same directory of the VOIs files. The output will be multiple on the basis of the color of voxels in the .voi file: orange (i.e. RGB 255, 75, 0 in the Select Color window of the menu

Analysis – Region-of-Interest Analysis – Edit; see fig. 17) would be activation voxels, blue (i.e. RGB 0, 75, 255; see fig. 17) deactivation voxels and everything else would be not specified or other. All the output will have a “_Activ”, “_Deact” or “_Other” suffix on the basis of the color.

The Gyrus output produces 3 .bmp files named as the original VOI file (multiplied for _Activ, _Deact and _Other subsamples) with a “GY”, “GY3D” and “GYlat” at the end (output 1, 2 and 3, fig. 4, 5).

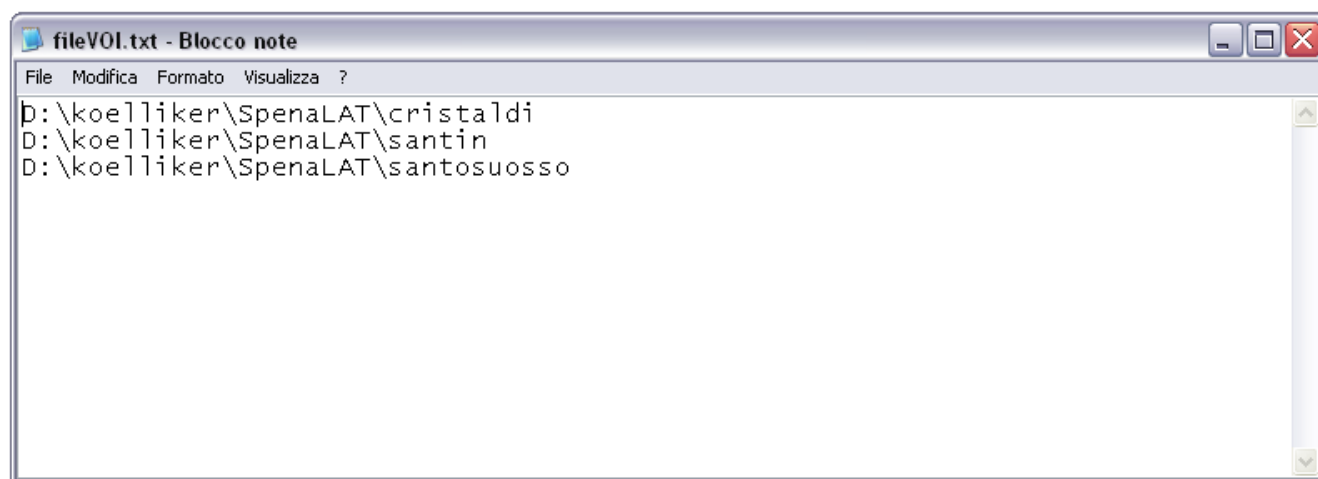
The Brodmann output produces 3 .bmp files (multiplied for _Activ, _Deact and _Other subsamples) with a “BA”, “BA3D” and “BALat” at the end (same as output 1, 2 and 3, fig. 4, 5, but with the BA atlas instead of the Gyrus Atlas; fig. 4 and 5).

The Division output produce 3 .bmp files (multiplied for _Activ, _Deact and _Other subsamples) with a “PART”, “LOBE” and “SUB” at the end (fig. 6, 7, 8).

The Tab Cluster and Tab Total outputs produce 1 .txt file (multiplied for _Activ, _Deact and _Other subsamples) each (with a final “_Clust” for the first) with a table like tab. 1 (with the peaks voxels classification and in separated clusters for Tab Cluster).

The Analyze and Brain Voyager outputs produce 2 kind of files each (1 for Gyrus and 1 for BA) with the Segmentation output maps (see fig. 9). The 4 Analyze files (.hdr plus .img) will be named “_GYtot” and “BATot”, the 2 Brain Voyager files (.voi) will be named “_bvq_gy” and “_bvq_ba”.

Figure 12 Editing VOIs paths



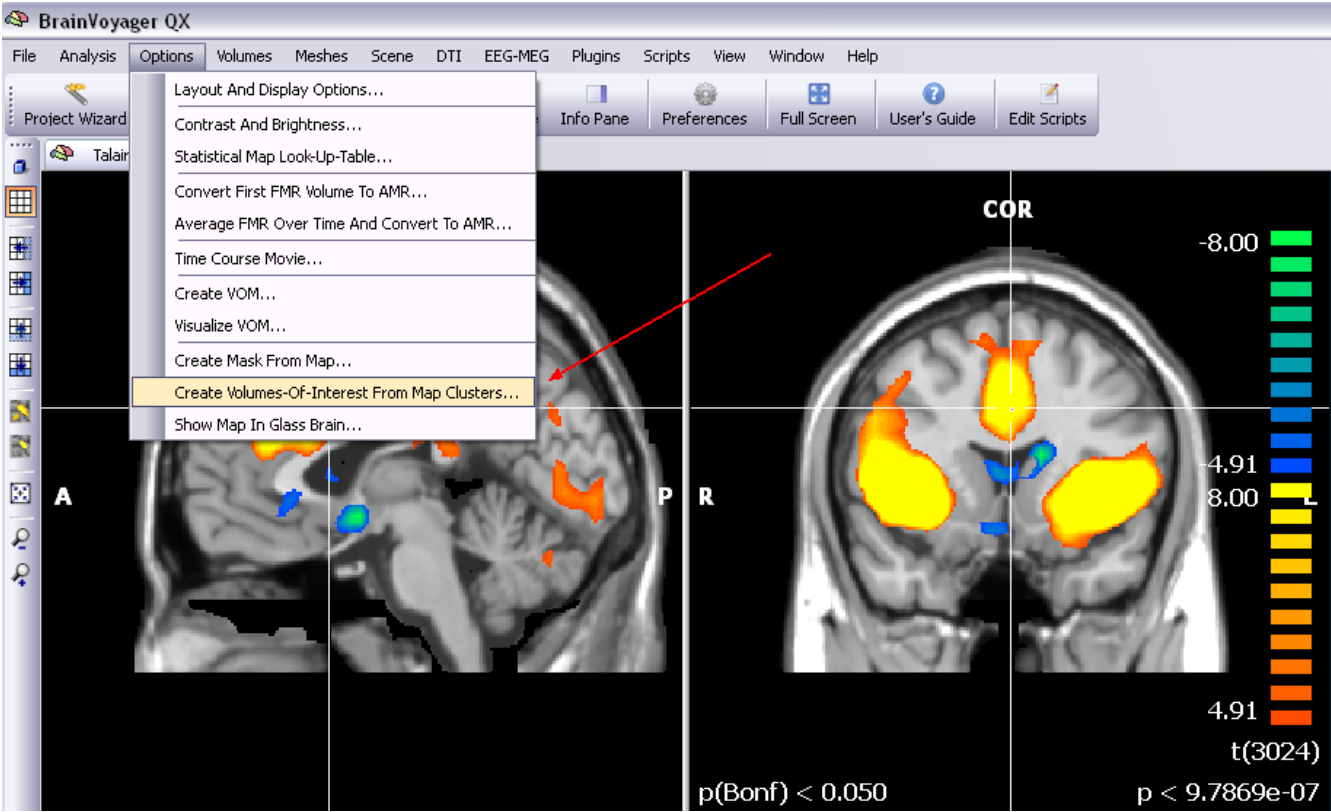
Video Capture of the fileVOI.txt content

Example

Here is a step by step example on the way to use the script.

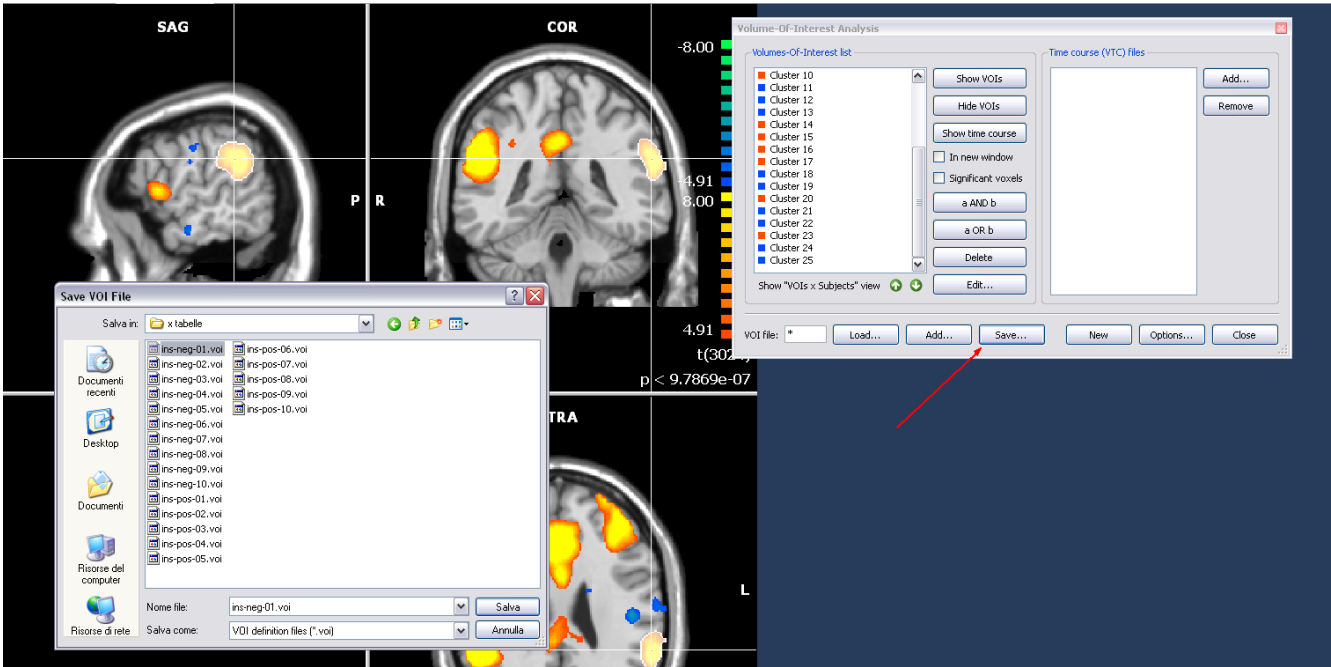
1. Open a .vmp of interest in BrainVoyager© with a map of an experimental contrast.
2. Use the Option – Create Volume-Of-Interest From Map Cluster command (fig. 13) to create clusters VOI (fig. 14).

Figure 13 From .vmp to .voi



Video Capture of the conversion of a statistical parametric map into a VOI file

Figure 14 Saving the VOI file

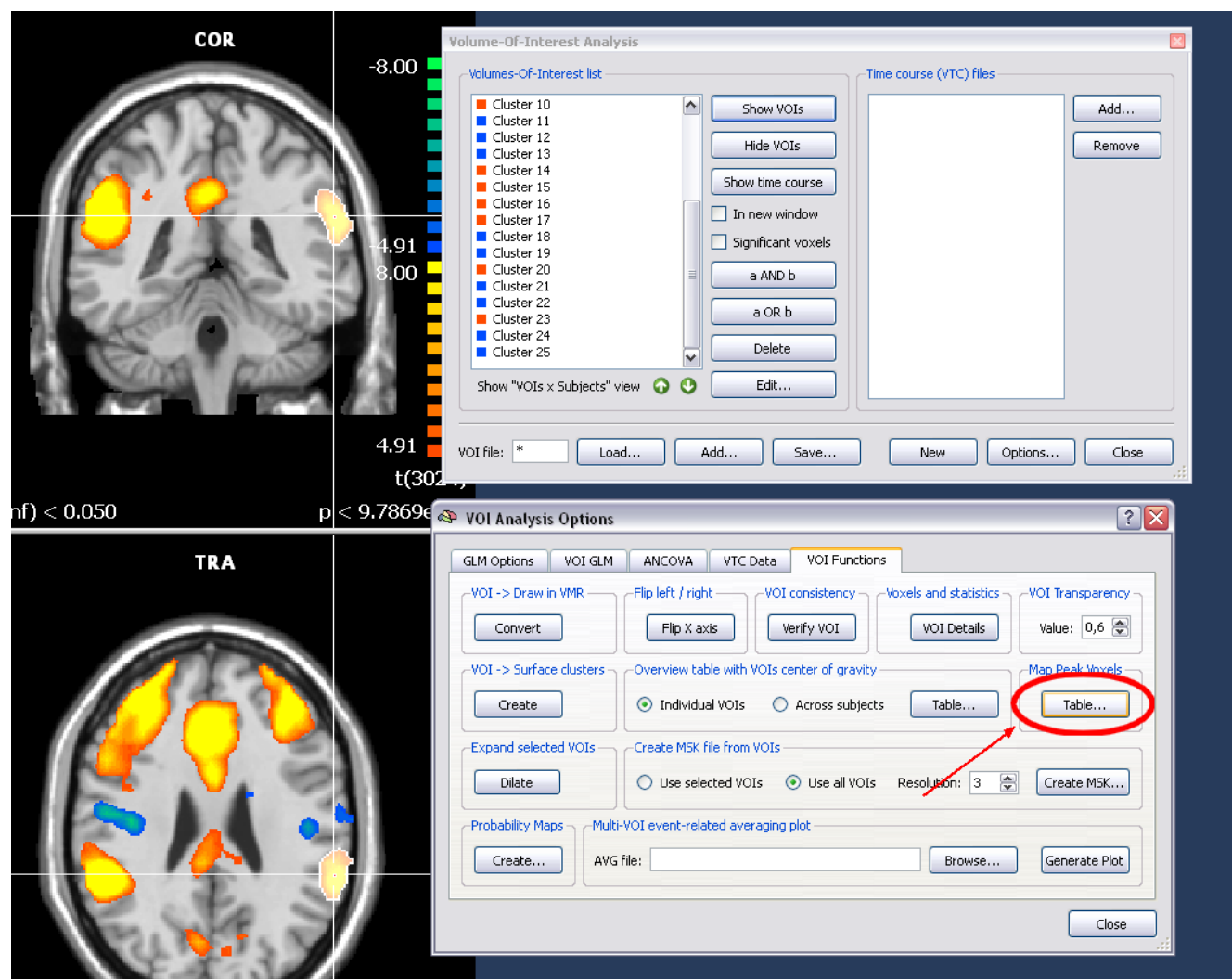


Video Capture of the VOI saving

3. Save the file .voi in a directory (fig. 14). Use the notepad (fig. 12) to modify the file VOI.txt to point to the .voi file.

4. If you want also the Tab Cluster output you must save the .pk.txt file in the same directory of the .voi file. To do so use the Option – VOI Functions – Table button in the Analysis – Volume-Of-Interest panel (fig. 15, 16).

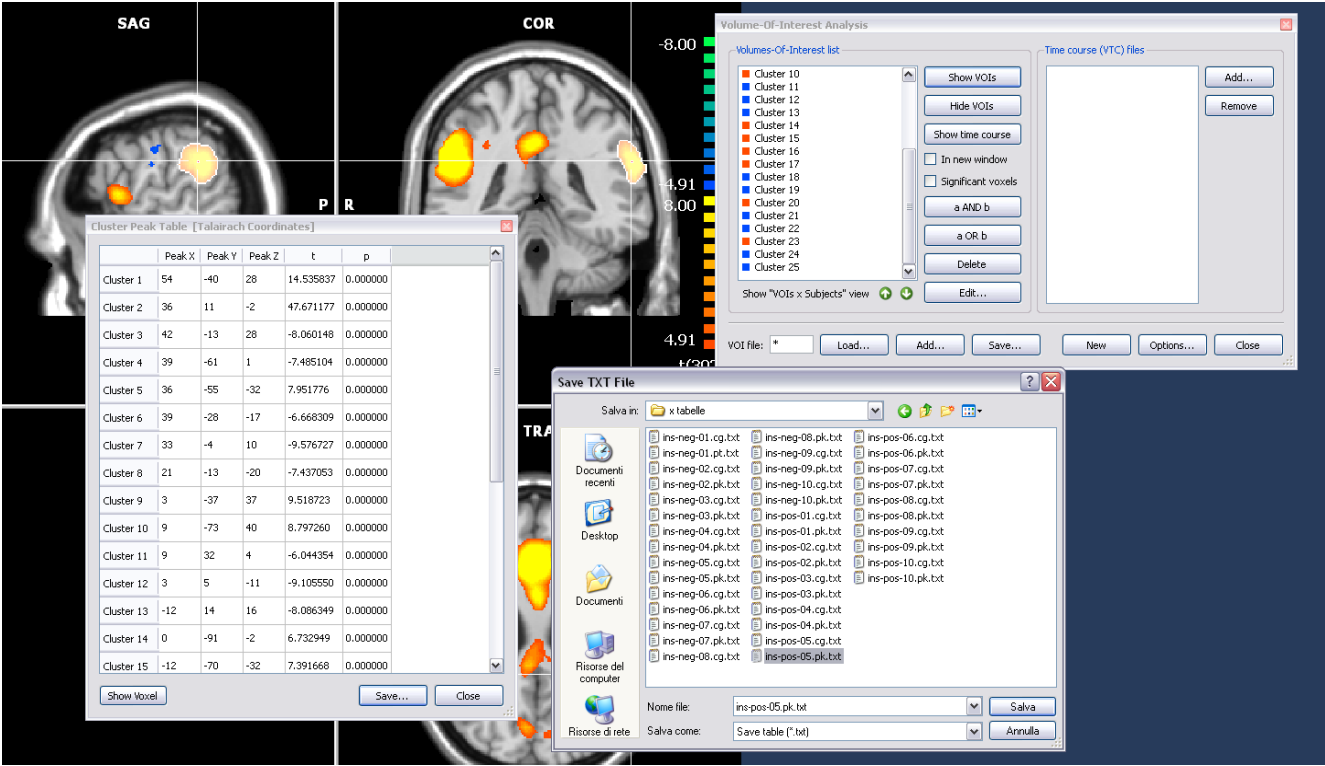
Figure 15 Opening Peaks Table



Video Capture of the opening of the Peaks Table .pk.txt file

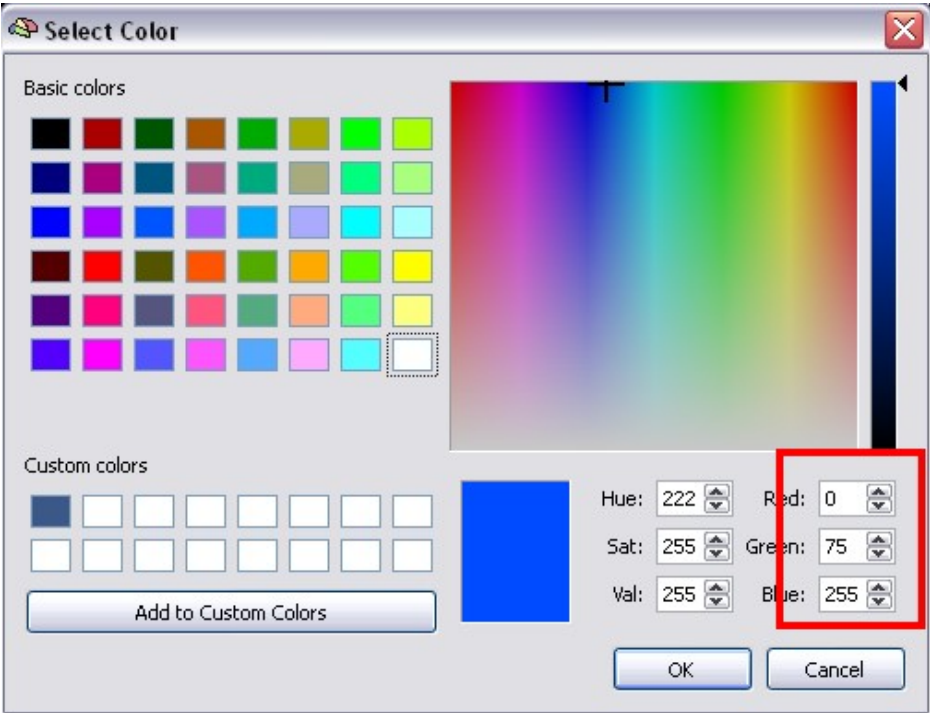
5. If necessary edit the clusters (Select Color window of the menu Analysis – Region-of-Interest Analysis – Edit; see fig. 17) to be sure that activated voxels are in orange color (RGB 255, 75, 0) and deactivated voxels are in blue color (RGB 0, 75, 255).
6. Set the thresholds, the atlas and the output you want (fig. 11)
7. Press the Go button to execute the script.
8. You can look at the output in the Command window and if you want you can copy and paste the textual output.
9. The script saves the selected outputs in files inside the directory of VOIs files.
10. You can run again the script with other settings overwriting the files.

Figure 16 Saving Peak Table



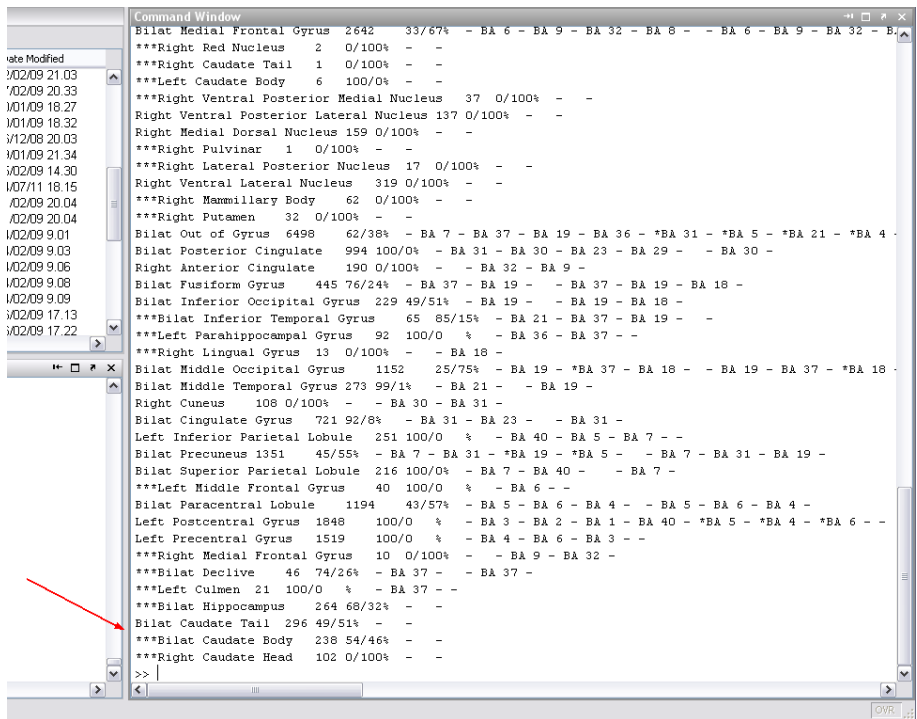
Video Capture of the of the creation of the Peaks Table .pk.txt file

Figure 17 Color Editing



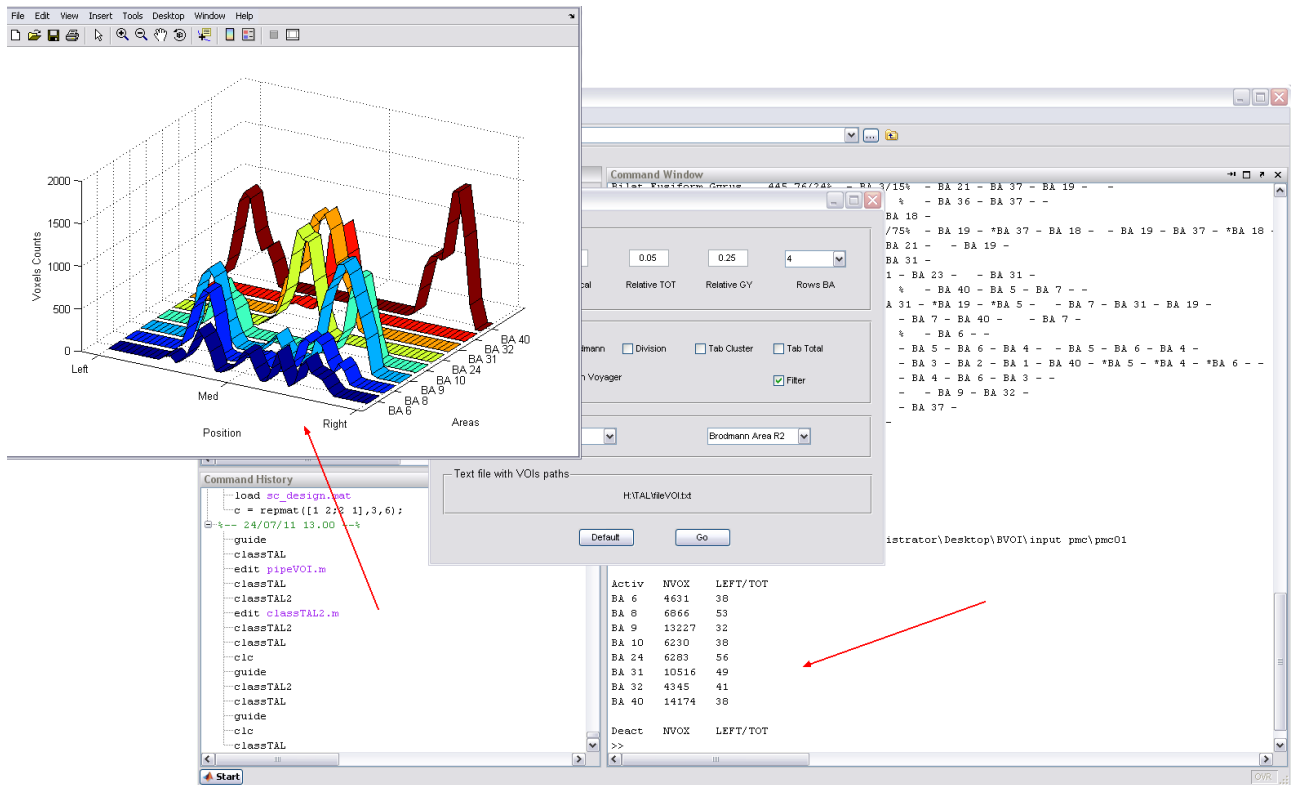
Video Capture of the Select Color panel

Figure 18 Command Window Output



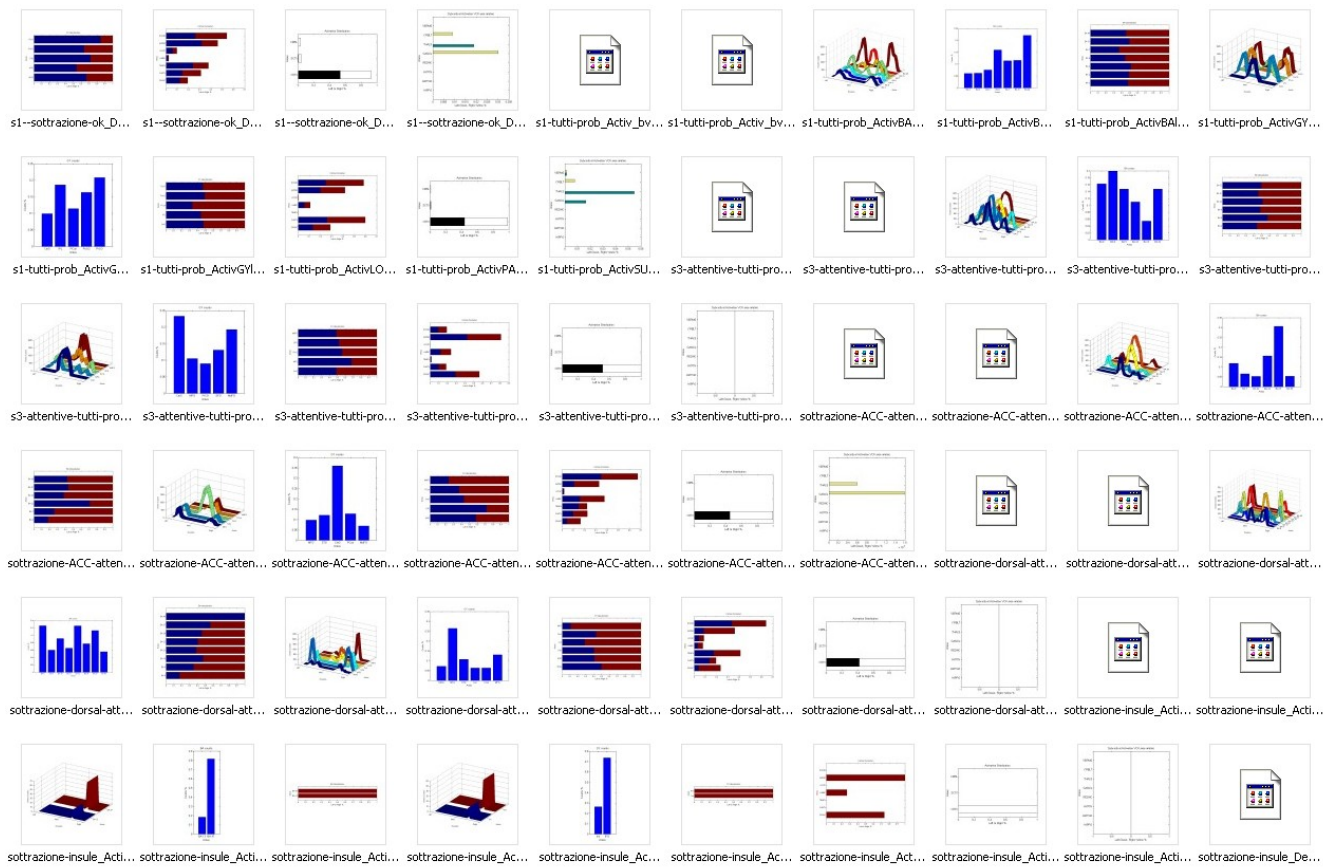
Video Capture of the Matlab® textual output

Figure 19 Script Running



Video Capture of the script running and saving output files

Figure 20 Output Files



Video Capture of the directory with the saved outputs

Compatibility

The script was tested with Matlab® 7.x.x and Brain Voyager QX© 1.x.x 2.x.x without any problems. We do not guarantee for its functioning with other versions and we are not responsible for any possible malfunctioning or subsequent inconvenient.