ReStNeuMap v0.1
A tool for automatic extraction of resting state fMRI networks in neurosurgical practice

Based on:

Tutorial

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I. Getting Started

For installation steps, see the README.txt file.

Please consider that in order to run ReStNeuMap, at least 4GB free space are needed.

I.I Data structure

In order to run ReStNeuMap, each patient's anatomical and resting-state DICOM data <u>need</u> to be stored in two different folders, one for anatomical files and the other for resting-state files containing only their respective DICOM files from the same subject.

- As an example, in our sample dataset you can find DICOM files from a demonstrative subject organized as follows:
  - **anatomy_dicom** folder, containing the patient's T1 DICOM
  - **rsfmri_dicom** folder, containing the patient's rs-fMRI DICOM

I.II Path Check

In matlab, check that the spm12 folders and subfolders and ReStNeuMap_files folders and subfolders are added to matlab path.
If not, add them as described in the README.txt file at point II of the Installation section.

II. Running ReStNeuMap

On matlab command line, simply run:

```
ReStNeuMap_main
```

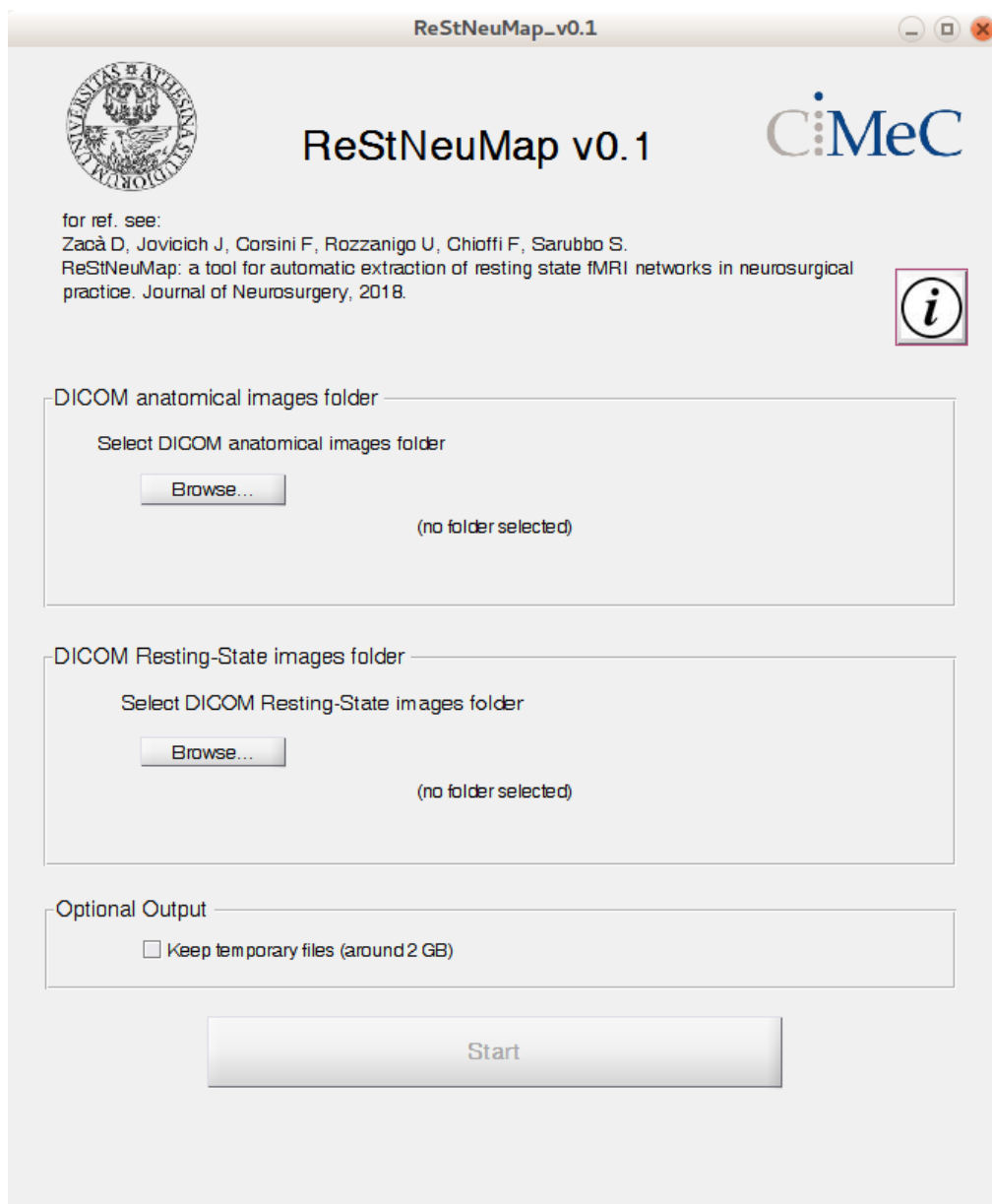A GUI (Graphic User Interface) will open (fig. 1):

Figure 1: ReStNeuMap GUI will open when you launch ReStNeuMap.

Click on each Browse button for selecting respectively:
- the folder where the patient's anatomical dicom files are saved
- the folder where the patient's resting-state dicom files are saved

If you want to keep temporary files created by ReStNeuMap for debugging purposes, check the Optional Output box (temporary files takes ~2GB). ReStNeuMap does not need that you keep temporary files to run, and we suggest to not keep them for saving hard disk space. However, for inspecting temporary files this might be useful.

Once all the folders listed above are selected, the Start button will turn red (fig.2):
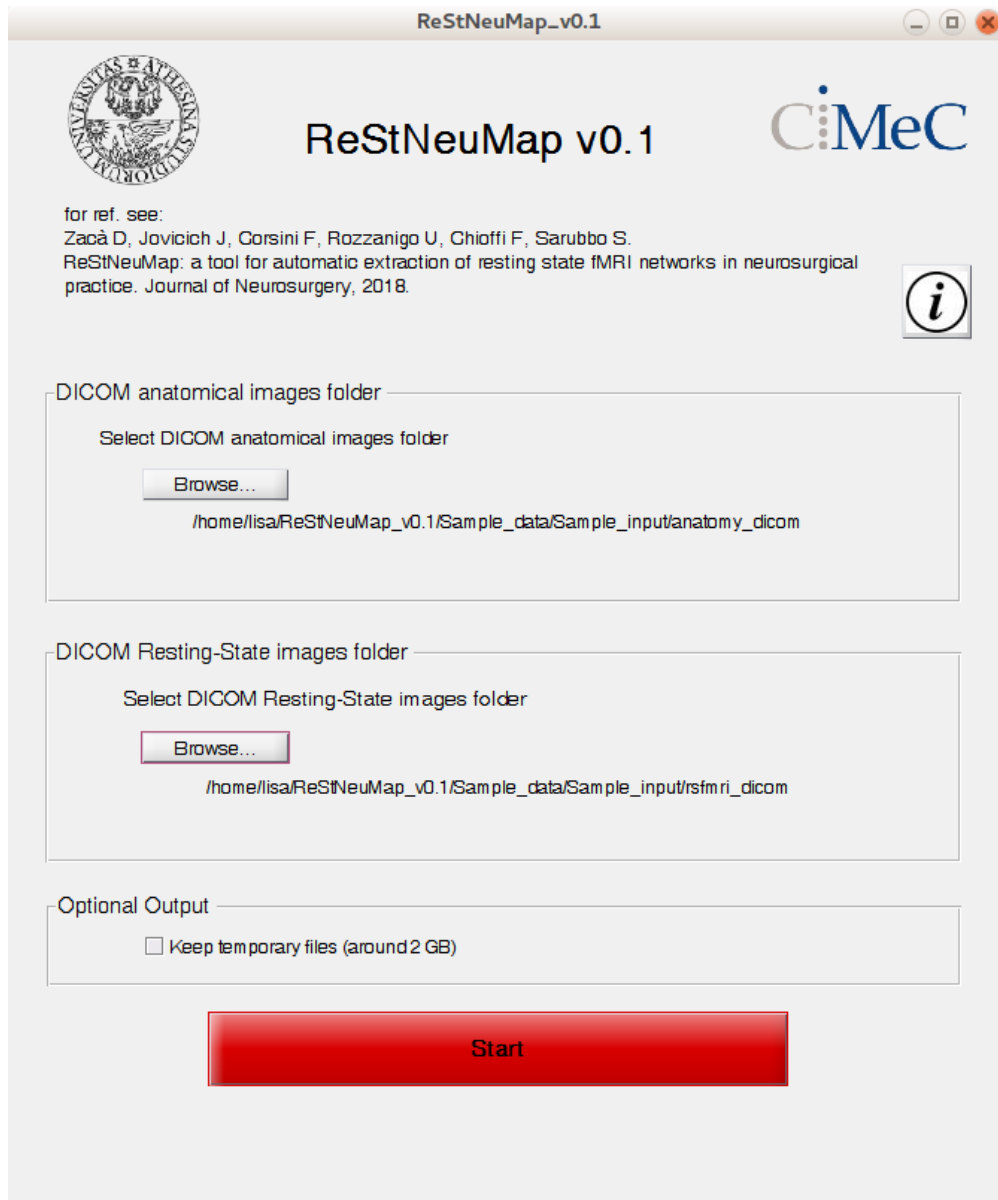

Figure 2: ReStNeuMap GUI's "Start" button will become red when you select the paths.

Simply click on the red Start button to launch ReStNeuMap processing.
Please note that It takes around 35' to run in a Dell XPS9560 i7700HQ 16GB RAM on Linux Ubuntu 16.04.
During the processing, you will be informed by ReStNeuMap advancement status by the progress bar shown in fig. 3. Please do not close it.
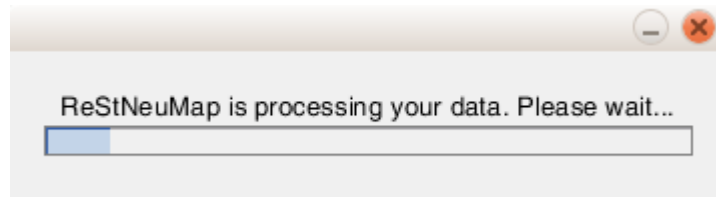
Figure 3: ReStNeuMap's progress bar.

Moreover, a window will open showing reoriented T1 and rs-fMRI slices for visual inspection. You can close it at any time (fig. 4).
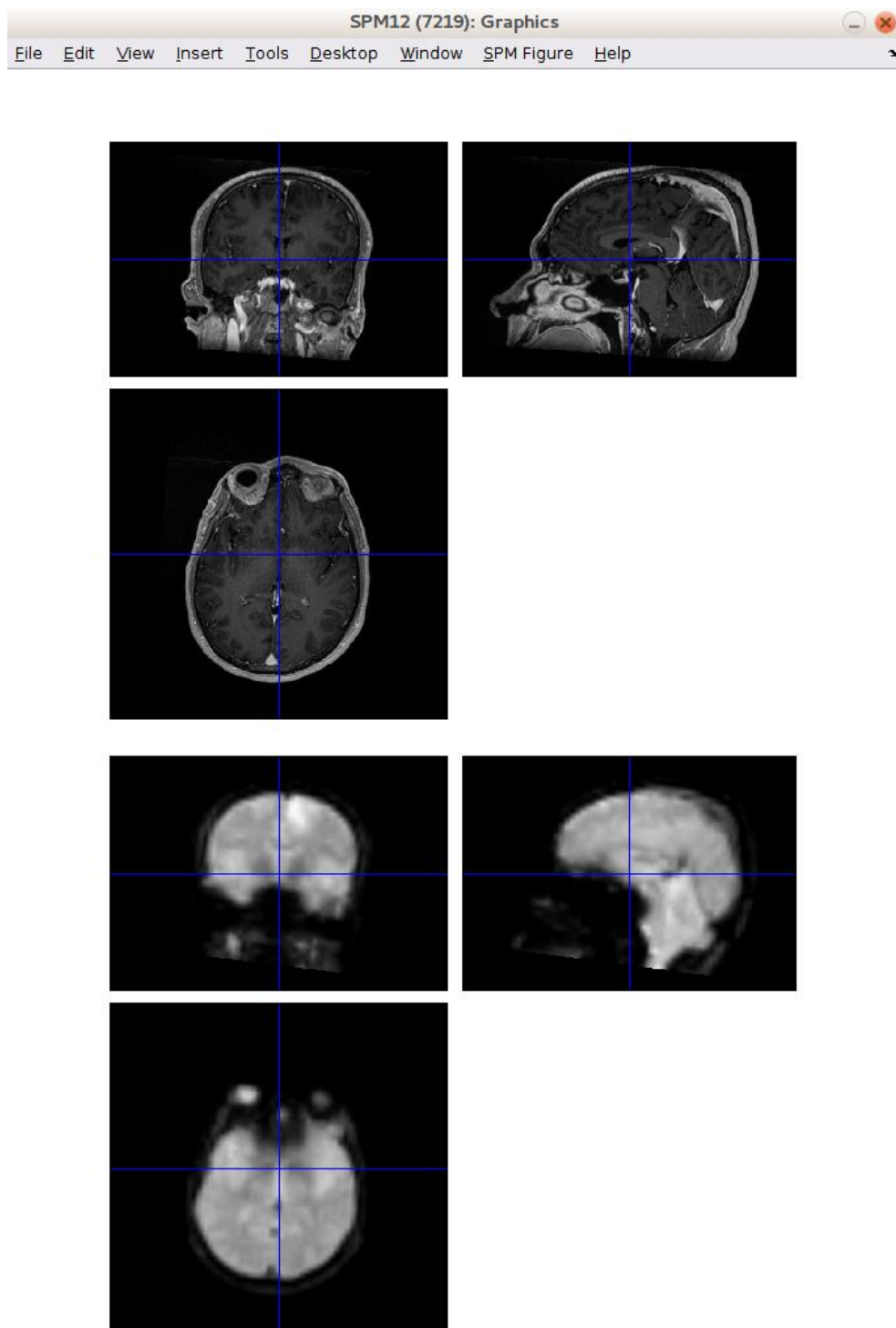

Figure 4: reoriented T1 and rs-fMRI slices visual inspection display.

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When the ReStNeuMap processing is complete, you will be shown the following pop-up window (fig. 5):
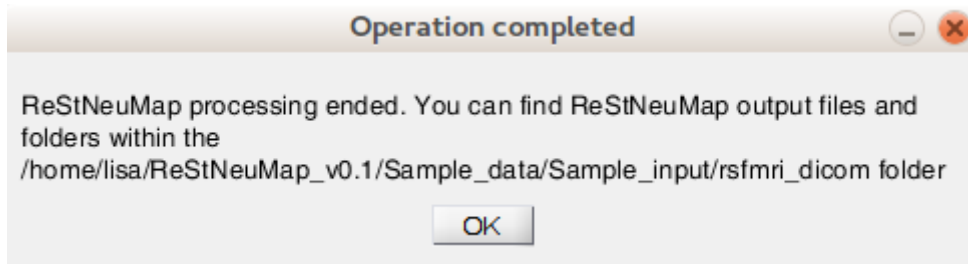

Figure 5: Operation completed popup-window.

Then close it: ReStNeuMap has ended.

Please note that if for any reason ReStNeuMap processing is fully interrupted before its completion (not just 'paused' in matlab), you need to eliminate all the temporary files it generates and reconfigure the initial folder setup (each patient's anatomical and resting-state DICOM data in two different folders, one for anatomical files and the other for resting-state files containing only their respective DICOM files from the same subject).

III. Output files
Once ReStNeuMap processing ends, within the original (raw) dicom resting-state folder you will find the following folders:
- rawdata
- ProcessDir
- QualityAssuranceMetrics
- (TemporaryFiles, if the Optional Output box is checked)

III.I rawdata folder
The rawdata folder will contain the original resting-state dicom files. ReStNeuMap simply moves them into this newly created rawdata folder.

III.II ProcessDir folder
ProcessDir will contain patient's rs-networks extracted by ReStNeuMap (fig. 6).
The following files and folders will be created within the ProcessDir folder:
- folders:
  - vmasksm4D_mask.ica
  - vmasksm4D_mask.ica+
  - vmasksm4D_mask.ica++

◦ vmasksm4D_mask.ica+++

containing each the output files of each melodic run.

- files:

file name	description
sm4D_mask.nii	preprocessing output without outliers substitution
s*T1-T1.nii	patient's reoriented T1
vmasksm4D_mask.mat and vmasksm4D_mask.nii	preprocessing output with outliers substitution
rwLanguage.nii	language network template in patient's space at resting-state image resolution
rwprim_Visual.nii	visual network template in patient's space at resting-state image resolution
rwSensorimotor.nii	sensorimotor network template in patient's space at resting-state image resolution
wLanguage.nii	language network template in patient's space at T1 resolution
wSensorimotor.nii	sensorimotor network template in patient's space at T1 resolution
wprim_Visual.nii	visual network template in patient's space at T1 resolution
lang.nii	patient's language network without any applied threshold
lang_25.nii	patient's language network for z>2.5 threshold
lang_30.nii	patient's language network for z>3 threshold
lang_35.nii	patient's language network for z>3.5 threshold
lang_mean_zscores.txt	text file containing mean connectivity values (z-score) for respectively: lang_25.nii lang_30.nii lang_35.nii
motor.nii	patient's motor network without any applied threshold
motor_25.nii	patient's motor network for z>2.5 threshold
motor_30.nii	patient's motor network for z>3 threshold
motor_35.nii	patient's motor network for z>3.5 threshold
motor_mean_zscores.txt	text file containing mean connectivity values (z-score) for respectively: motor_25.nii motor_30.nii motor_35.nii
vis.nii	patient's visual network without any applied

	threshold
vis_25.nii	patient's visual network for z>2.5 threshold
vis_30.nii	patient's visual network for z>3 threshold
vis_35.nii	patient's visual network for z>3.5 threshold
visual_mean_zscores.txt	text file containing mean connectivity values (z-score) for respectively: vis_25.nii vis_30.nii vis_35.nii
vInputDetFiltReg_4D.nii	whole time series after outliers volume substitution (substitution through interpolation of preceding and following volumes). Outliers estimation is calculated on time series after head motion correction. Spatial smoothing on brain mask (merging of grey matter, white matter, CSF from SPM segmentation) is applied
output_files_list.txt	list of expected output files with brief description
ReStNeuMap_melodicrun.sh	ReStNeuMap shell script run through matlab
ReStNeuMap_fslstatsrun.sh	ReStNeuMap shell script run through matlab

Here follow some examples of rs-networks extracted through ReStNeuMap (fig. 6):

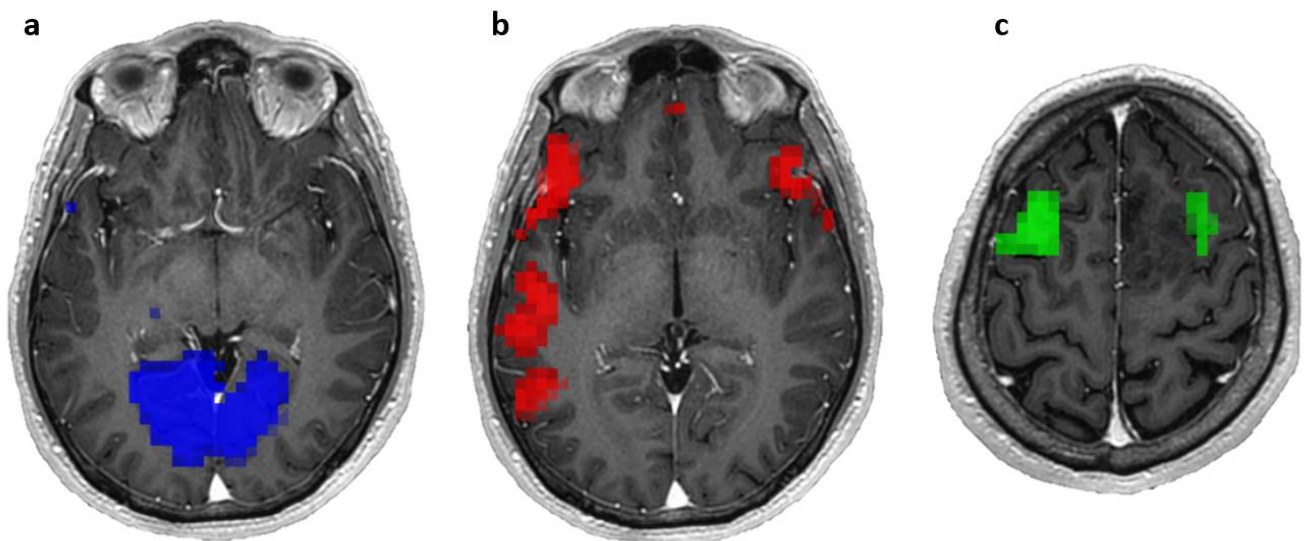*Figure 6: rs-networks extracted by ReStNeuMap (MRIcroGL display) overlaid on patient's reoriented T1 image. a) patient's visual network for z>3 (vis_30.nii); b) patient's language network for z>3 (lang_30.nii); c) patient's motor network for z>3 (motor_30.nii).*

III.III QualityAssuranceMetrics folder
The following files will be created within the QualityAssuranceMetrics folder:

- ○ art_deweighted.txt and art_repaired.txt: text files reporting the outliers volume replaced
- ○ artglobalXX.jpg (where XX is the name of the folder initially containing rs-fMRI dicom files): ArtRepair summary

III.IV TemporaryFiles folder (only created if Optional Output box is checked)

The following files will be created within the TemporaryFiles folder if the Optional Output box is checked:

file name	description
4D_*.nii	3D volume output of matlab dicom import on raw data
4D.nii	4D volume obtained joining along time the 4D_*** volumes
a4D.nii	time series after slice timing correction
ua4D_*.nii	time series after head motion correction (with the SPM unwarp option)
craOutBrick.nii	time series after head motion correction (with the SPM unwarp option) with the first 4 volumes cut
InputDetFiltReg_*.nii	3D volumes after filtering operation (median, detrending and butterworth)
smInputDetFiltReg_*.nii	3D volumes after filtering operation (median, detrending and butterworth) after spatial gaussian smoothing (kernel twice the voxel size)
masksmInputDetFiltReg_*.nii	same volumes as above after brain masking
vInputDetFiltReg_*.nii	3D volumes after filtering operation (median, butterworth) with outliers volume replaced
vmasksmInputDetFiltReg_*.nii	same volumes as above after brain masking
c1XXX,c2XXX,c3XX, c4XX, c5XX	gray, white matter, csf, bone and any other soft tissue probability maps obtained with the SPM segmentation tool
rc1XXX, rc2XXX, rc3XXX	same maps as above coregistered to rs-fMRI data
rp_a4D.txt	text file including rigid body head motion correction parameters
s*T1.nii	Patient's T1 images
s*T1_seg8.mat	Matlab file including information about the segmentation process
y_*T1.nii	deformation field and its inverse (iy_*T1) used to normalize images from subject to MNI space and

	backward (e.g. motor network template to subject space at T1 image resolution)
meanua4D.nii	mean rs-fMRI volume after slice timing and head motion correction
raOutBrick.nii	slice timing and motion corrected time series
ArtifactMask.nii	brain mask where outliers investigation is performed

.mat files with prefix identical to the corresponding NIfTI file include header information. The type of information included depends on the type of image. You can consult https://www.fil.ion.ucl.ac.uk/spm/software/spm12/ for further information.

IV. Credits

This software was written by Domenico Zacà, Lisa Novello, and Jorge Jovicich, at the Center for Mind/Brain Sciences, University of Trento, Italy.
Please send any bug reports or questions to jorge.jovicich@unitn.it

An accompanying manuscript has been published in the Journal of Neurosurgery. If you use our tool, please cite this work as:
Zacà D., Jovicich J., Corsini F., Rozzanigo U., Chioffi F., and Sarubbo S., ReStNeuMap: a tool for automatic extraction of resting state fMRI networks in neurosurgical practice. Journal of Neurosurgery, 2018.

Our software uses and provides functions from the following freely available tools:
- ArtRepair: http://cibsr.stanford.edu/tools/human-brain-project/artrepair-software.html
- AFNI functions: https://afni.nimh.nih.gov/

This software is made available to promote use of resting-state fMRI data for research. This software is supplied as is. No formal quality assurance checks were made on the software other than those described in the original publication (Zacà et al., JNS, 2018), and no formal support or maintenance is provided or implied.