ReStNeuMap v0.3: TUTORIAL

A tool for automatic extraction of resting state fMRI networks
(tested in neurosurgical practice)

Based on:

- Moretto M, Luciani BF, Zigiotto L, Saviola F, Tambalo S, Cabalo DG, Annicchiarico L, Venturini M, Jovicich J, and Sarubbo S. R*esting state functional networks in gliomas: validation with Direct Electric Stimulation of a new tool for planning brain resections.* Neurosurgery, 2024.
  DOI: 10.1227/neu.0000000000003012

- Zacà D, Jovicich J, Corsini F, Rozzanigo U, Chioffi F, Sarubbo S. *ReStNeuMap: a tool for automatic extraction of resting state fMRI networks in neurosurgical practice*. Journal of Neurosurgery, 2018.
  DOI: 10.3171/2018.4.JNS18474.

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1. Getting Started

For installation steps, see the README.txt file.
Please consider that in order to run ReStNeuMap, at least 4GB free space is needed.

1.1 Data structure

In order to run ReStNeuMap, each patient's anatomical and resting-state DICOM data need 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.

1.2 Path check

In matlab, check that the spm12 folders and subfolders and ReStNeuMap_files folders and subfolders are added to the matlab path.
If not, add them as described in the README.txt file at point 2.2 of the Installation section.

2. Running ReStNeuMap

On matlab command line, simply run:

```
ReStNeuMap_main
```

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

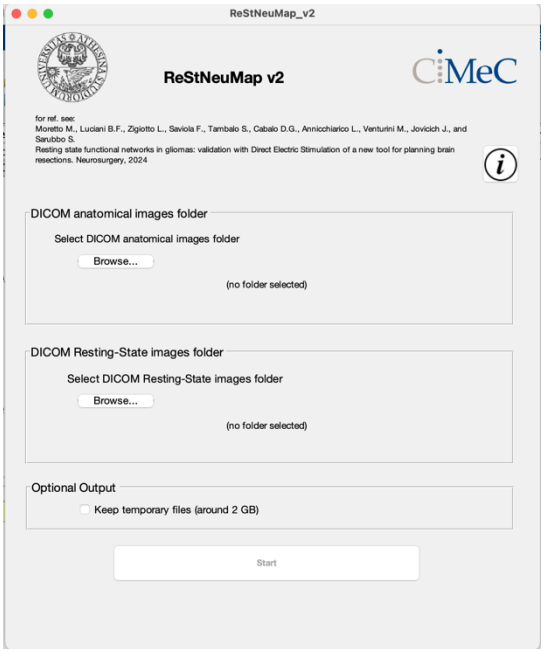

Figure 1 : ReStNeuMap GUI will open when you launch ReStNeuMap.

If you want to keep temporary files created by ReStNeuMap for debugging purposes, check the Optional Output box (temporary files take ~2GB). ReStNeuMap does not need you to keep temporary files to run, and we suggest not keeping 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):

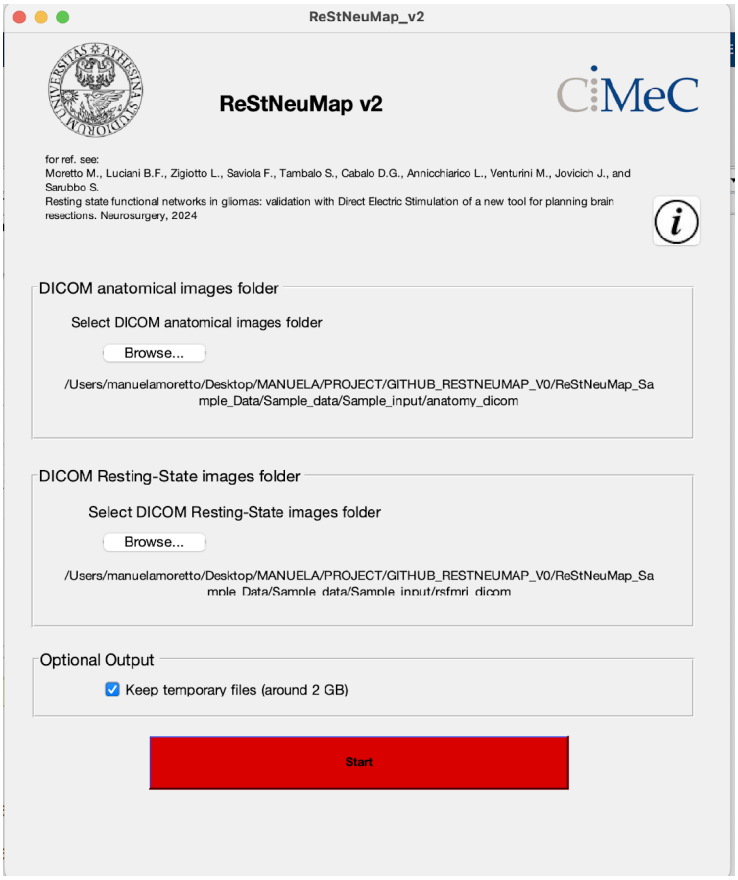

Figure 2 : ReStNeuMap GUI's "Start" button will become red when you select the paths.

Simply click on the red Start button to launch ReStNeuMap processing.
Please note that It takes around 35' to run on 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.

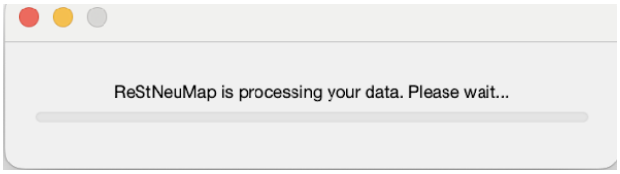

Figure 3 : ReStNeuMap's progress bar.

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

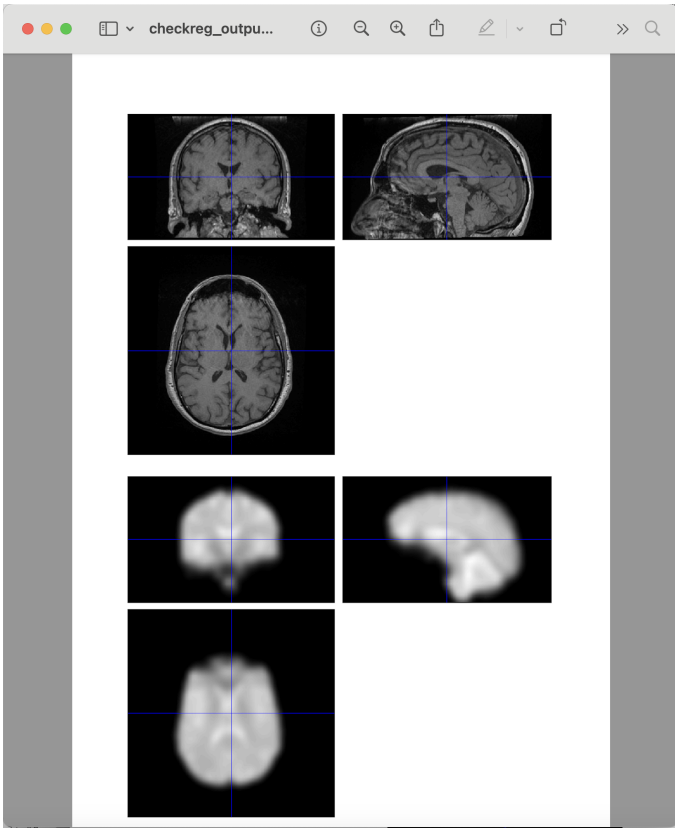

Figure 4 : reoriented T1 and rs-fMRI slices visual inspection display.

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

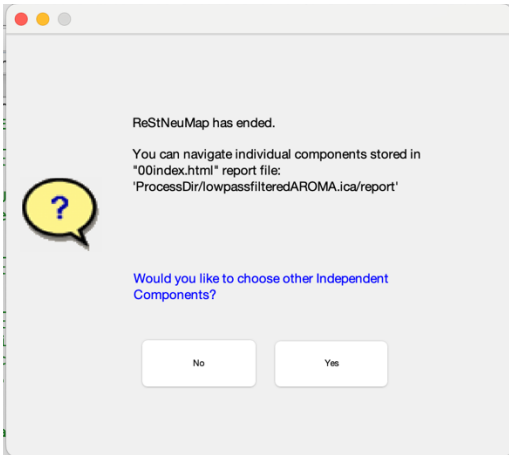

Figure 5 : Operation completed popup-window.

If you are satisfied with the automatic selection of the three ICs for each network, you can press “No” and ReStNeuMap will end. Otherwise, if you are not satisfied with ReStNeuMap’s automatic selection, you can insert the index of the ICs you want to visualise.

After this step 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).

2.1 Output files

Once ReStNeuMap processing ends, within the original (raw) dicom resting-state folder you will find the following folders:

- ICA-AROMA
- rawdata
- ProcessDir
- QualityAssuranceMetrics

2.1.1 ICA-AROMA folder

The ICA-AROMA folder (fig. 6) will contain the outputs after running ICA-AROMA in the rs-fMRI preprocessing pipeline.

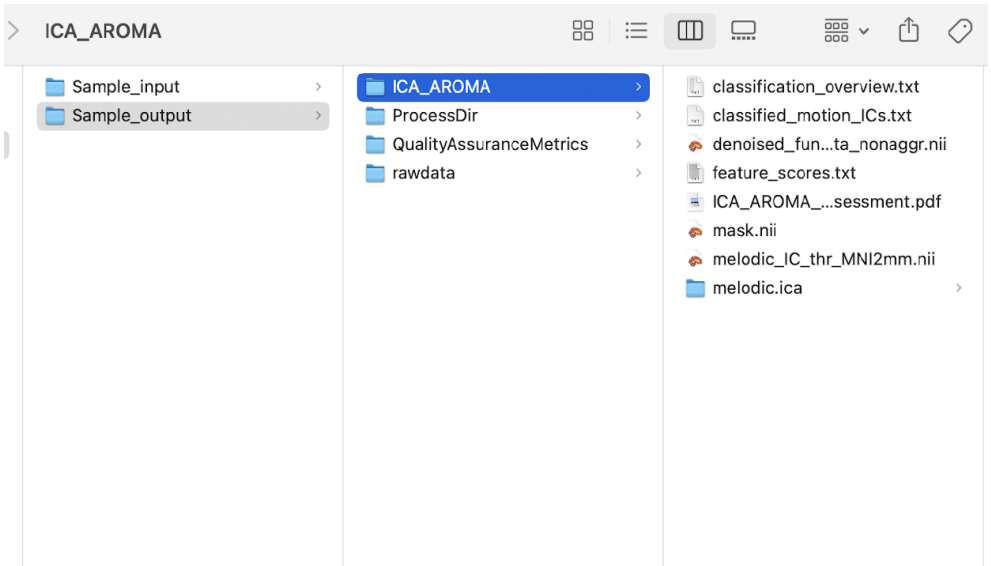

Figure 6 : Structure of the ICA-AROMA folder.

2.1.2 rawdata folder

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

2.1.3 ProcessDir folder

The ProcessDir folder will contain the outputs displayed in fig. 7.

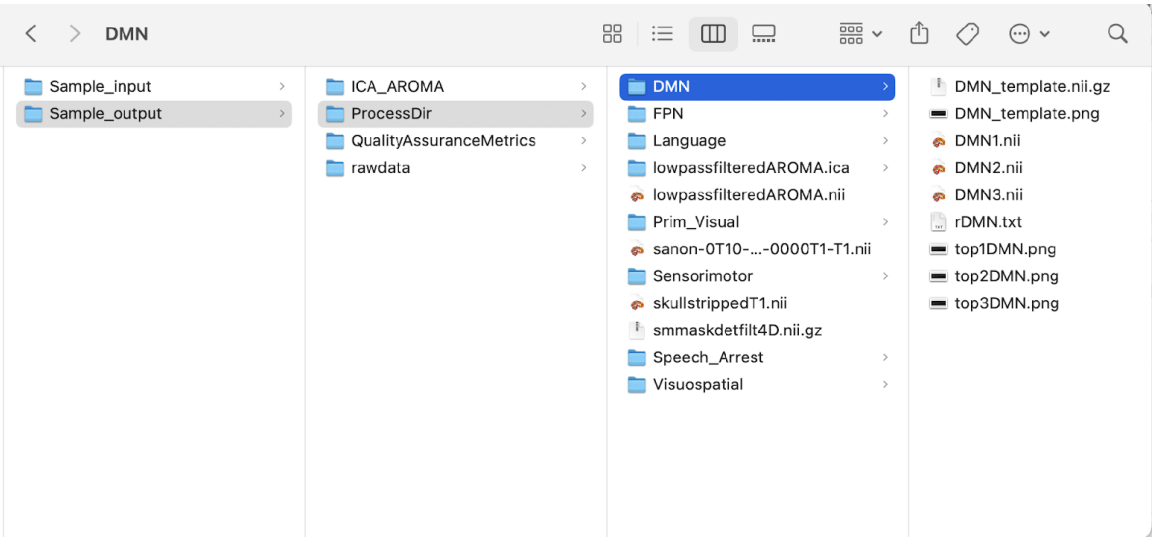

Figure 7 : Structure of the ProcessDir folder.

For each of the seven resting state networks (DMN, FPN, Language, Prim_Visual, Sensorimotor, Speech_Arrest, Visuospatial), three images (top1*.png, top2*.png, top3*.png) showing the spatial maps of the Independent Components selected by ReStNeuMap will be created (fig. 8, fig. 9, fig. 10).

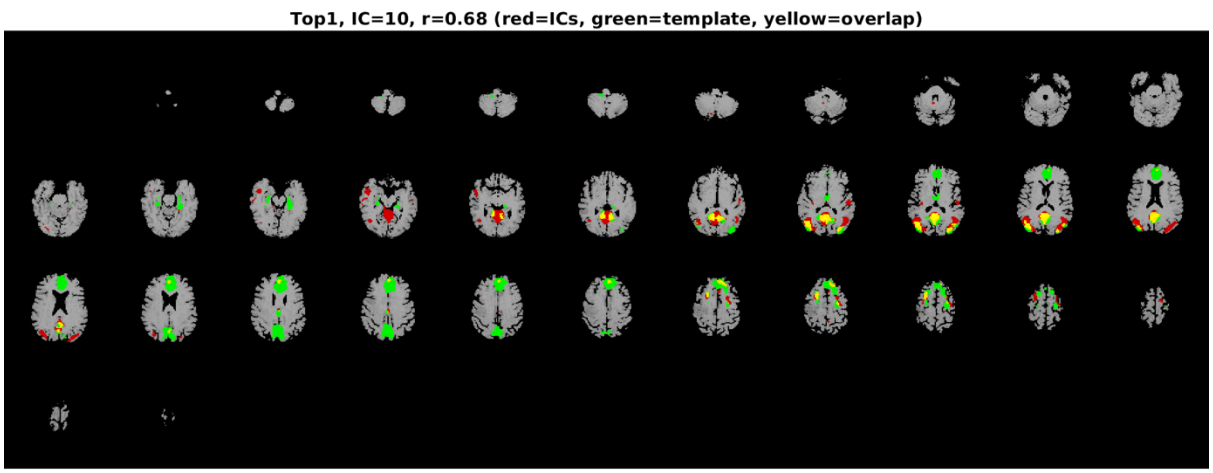

Figure 8 : top1DMN.png file showing the top1 IC extracted by ReStNeuMap (red), matching the Default Mode Network template (green), overlaid on patient's T1 image. The title reports the cross-correlation value (r=0.68).

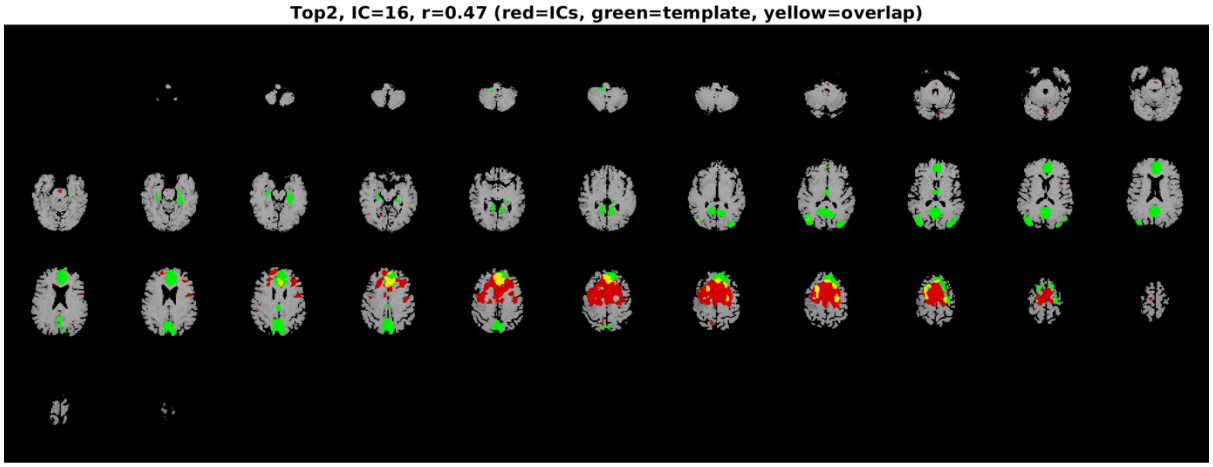

Figure 9 : top2DMN.png file showing the top2 IC extracted by ReStNeuMap (red), matching the Default Mode Network template (green), overlaid on patient's T1 image. The title reports the cross-correlation value (r=0.47).

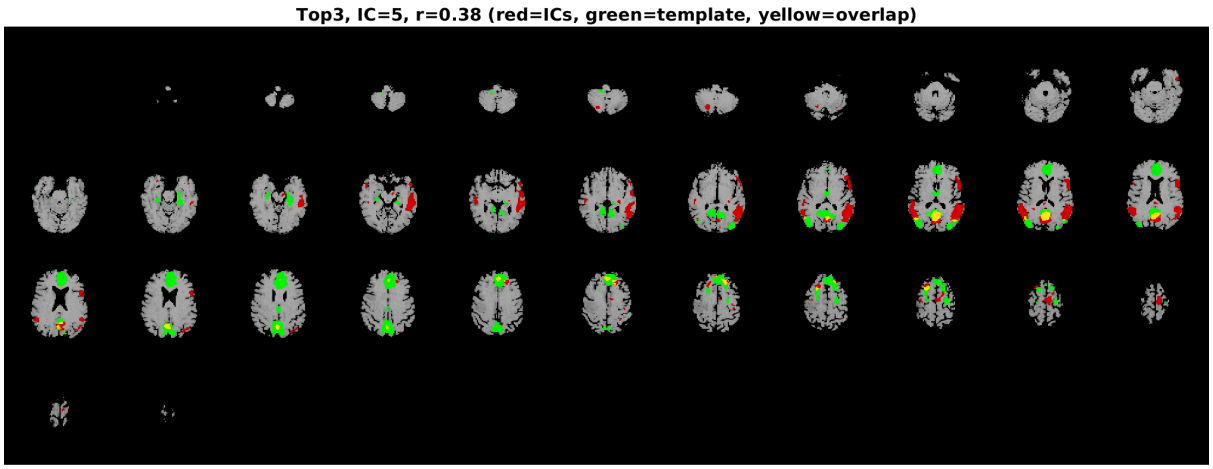

Figure 10 : top3DMN.png file showing the top3 IC extracted by ReStNeuMap (red), matching the Default Mode Network template (green), overlaid on patient's T1 image. The title reports the cross-correlation value (r=0.38).

Each of the seven resting state networks folders (NETWORK = DMN, FPN, Language, Prim_Visual, Sensorimotor, Speech_Arrest, Visuospatial) contains the following files:

File name	Description
NETWORK_template.nii.gz	Nifti file containing the network's template overlayed onto the T1w image.
NETWORK_template.png	Figure displaying the network's template (green) overlayed onto the T1w image.
NETWORK1.nii	Nifti file containing the top1 selected IC aligned to the T1w image.
NETWORK2.nii	Nifti file containing the top2 selected IC aligned to the T1w image.
NETWORK3.nii	Nifti file containing the top3 selected IC aligned to the T1w image.
rNETWORK.txt	txt file reporting the cross-correlation values between ICs and the network's template
top1NETWORK.png	Figure displaying the top1 selected IC (red), the network's template (green) and their intersection (yellow) overlayed onto the T1w image.
top2NETWORK.png	Figure displaying the top2 selected IC (red), the network's template (green) and their intersection (yellow) overlayed onto the T1w image.
top3NETWORK.png	Figure displaying the top3 selected IC (red), the network's template (green) and their intersection (yellow) overlayed onto the T1w image.

The ProcessDir folder contains also:

- lowpassfilteredAROMA.ica folder, with fsl's melodic outputs
- lowpassfilteredAROMA.nii : final preprocessed rs-fMRI nifti file (after ICA-AROMA)
- sanon-0T10-000T1-0000T1-T1.nii : T1w nifti file
- skullstrippedT1.nii : skull-stripped T1w nifti file
- smmaskdetfilt4D.nii.gz : smoothed rs-fMRI nifti file (before ICA-AROMA)

2.1.4 QualityAssuranceMetrics folder

The following files will be created within the QualityAssuranceMetrics folder (fig. 11):

File name	Description
checkreg_output.png	Figure displaying the registration between the T1w image and the rs-fMRI data.
NETWORK_2_T1.nii	Nifti file containing the network's template aligned with the T1w image.
rNETWORK.nii	Nifti file containing the network's template aligned with the rs-fMRI data.
top1NETWORK.nii	Nifti file containing the top1 selected IC, the network's template, and their intersection, overlayed onto the T1w image.
top2NETWORK.nii	Nifti file containing the top2 selected IC, the network's template, and their intersection, overlayed onto the T1w image.
top3NETWORK.nii	Nifti file containing the top3 selected IC, the network's template, and their intersection, overlayed onto the T1w image.

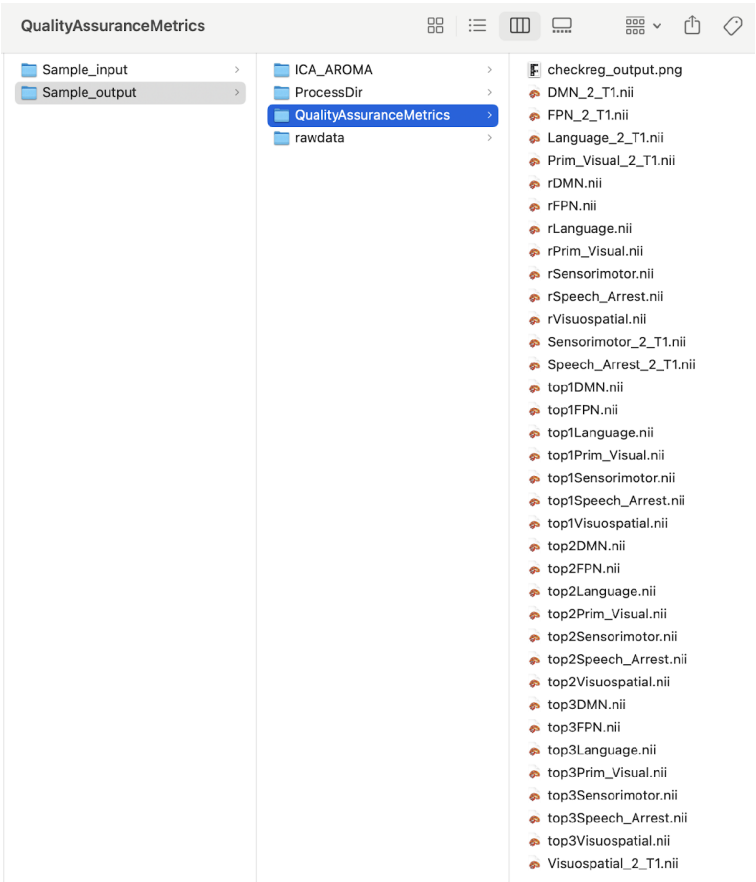

Figure 11 : Structure of the QualityAssuranceMetrics folder.

3. Credits

This software was initially written by Domenico Zacà, Lisa Novello, and Jorge Jovicich, and then updated by Manuela Moretto and Beatrice Federica Luciani 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 these works:

- Moretto M., Luciani B.F., Zigiotto L., Saviola F., Tambalo S., Cabalo D.G., Annicchiarico L., Venturini M., Jovicich J., and Sarubbo S. *Resting state functional networks in gliomas: validation with Direct Electric Stimulation of a new tool for planning brain resections.* Neurosurgery (2024)
- 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.

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 accompanying publication, and no formal support or maintenance is provided or implied.

We would like to acknowledge Lisa Novello and Domenico Zacà for help in developing, documenting and testing this software.
This work was supported by the Autonomous Province of Trento, Italy (Project: “NeuSurPlan and integrated approach to neurosurgery planning based on multimodal data"), the Fondazione Paolina Lucarelli Irion, Rovereto (Trento), Italy, and the Ministry of Education and Research (Department of Excellence Project, 2018-2022).