Local EACSF Tutorial

About LocalEACSF tool

➡ LocalEACSF is a tool that locally quantifies the extra-axial cerebrospinal fluid (EA-CSF).

➡ LocalEACSF use a pipeline that combines probabilistic brain tissue segmentation, cortical surface reconstruction and streamline-based local EA-CSF quantification.

➡ This tutorial is focused in how the LocalEACSF tool works. But if you are interested to more understand the pipeline behind it (recommended), here are two paper that explain it clearly:

- [A Novel Method for High-Dimensional Anatomical Mapping of Extra-Axial Cerebrospinal Fluid: Application to the Infant Brain](#)

- [Local Extraction of Extra-Axial CSF from structural MRI](#)

Installing LocalEACSF tool

➡ For NIRAL users LocalEACSF is already installed locally and in Longleaf (please make sure to use the latest version of the tool):

- Locally : /work/tools/Local_EACSF

- Longleaf : /proj/NIRAL/tools/Local_EACSF

➡ For other users you can :

- Clone the LocalEACSF github repository , then build it by following the readme . For that you will need a python with a version higher than 3.7, Qt5 and Qt4.

- Clone the LocalEACSF github repository, then by using the DockerFile build an image of the tool and run it in a docker container.

   ❖ In the directory containing DockerFile build the image by running this command :

      docker build -t localeacsf .

   ❖ Then run this image in a container.

   ❖ Be sure that your workstation is configured with X so it can display the GUI.

Necessary data for LocalEACSF

Before running the tool make sure you have the following data :

- A tissue segmentation of gray matter, white matter and CSF (3 labels) in nrrd format.

- A probability map of CSF (nrrd format).

- The left and right middle (MID) surfaces. The MID surface is the average between the gray matter and white matter surfaces and should be given in vtk format. (For NIRAL users you can find those surfaces in CIVET)
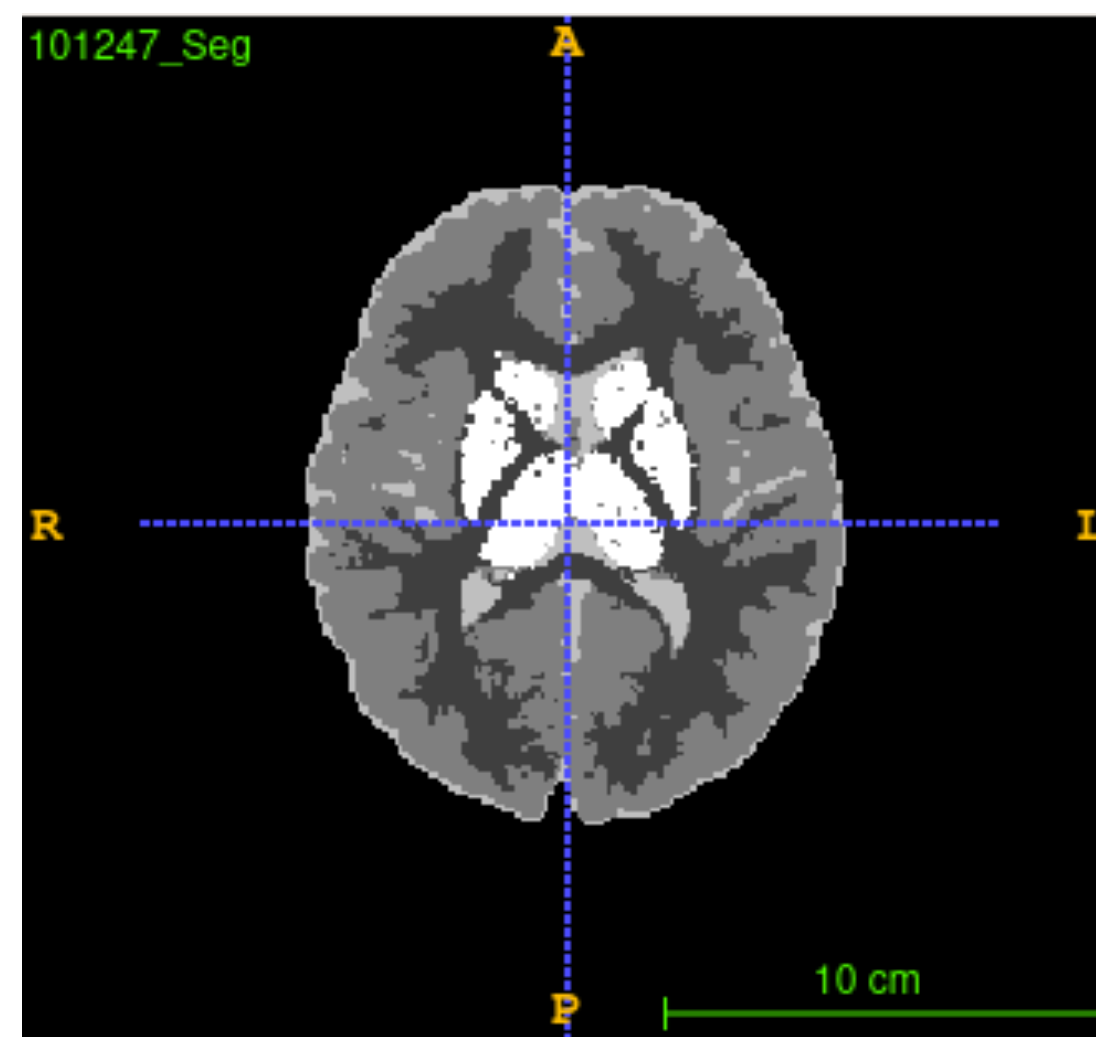
Tissue Segmentation
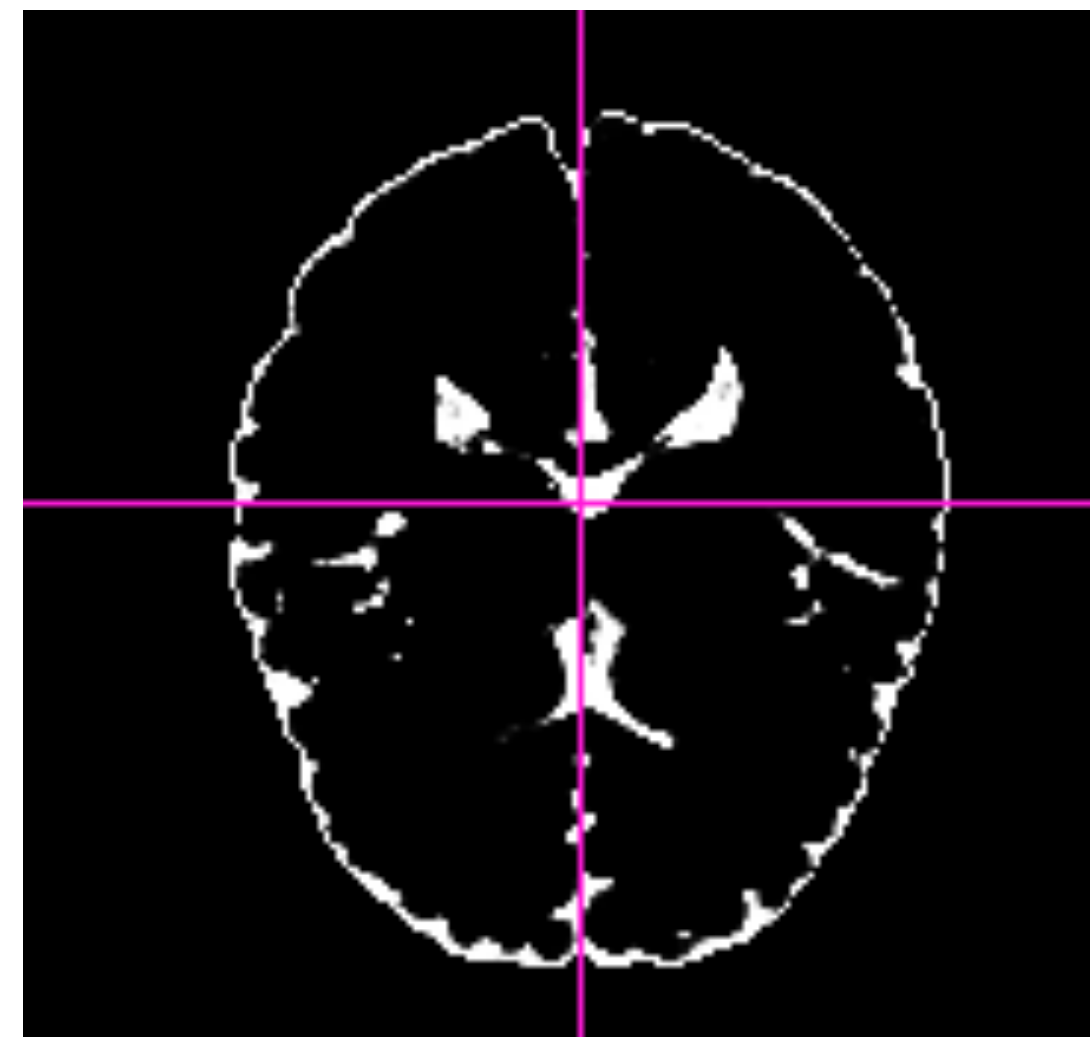
CSF Probability Map
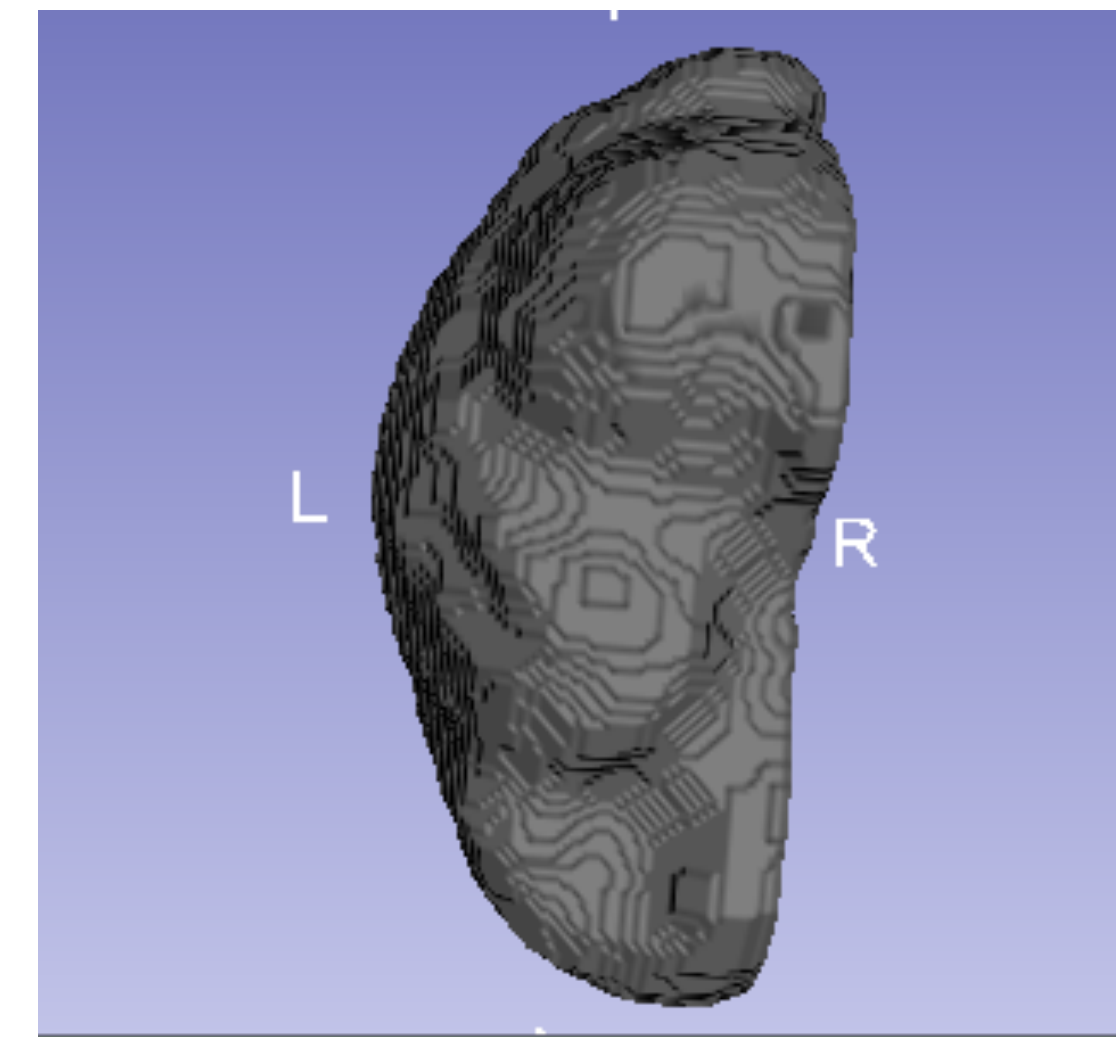
RH MID Surface

Running LocalEACSF tool

➡ Run LocalEACSF with GUI :

- without specifying a Json file : ./Local_EACSF

- with Json file: ./Local_EACSF —param <path to the Json file>

➡ Run LocalEACSF without GUI :

- One case : ./Local_EACSF —param <path to the Json file> —noGUI

- Many cases ./Local_EACS —param <path to the Json file —csv <path to the csv file> —noGUI —BatchProcessing

- For more details type : ./Local_EACSF —help

NB: Be sure to run the tool on a machine with many CPUs.

LocalEACSF inputs

Mandatory :

- Tissue segmentation of the gray, white matter and CSF (nrrd format).

- CSF probability Map (nnrd format).

- The left and right MID surfaces (vtk format).

- Path to the output directory where you want to have the LocalEACSF outputs.

- Label : it could be the case's ID it should be different to each subject.

Optional :

If you want to use 75P Surface (3/4) instead of the MID surface you should provide the gray matter surfaces (vtk) beside the MID surfaces.

If you want to compute regional sum and mean of EACSF you should provide left and right surfaces labeling (txt files).

If you want to put the EACSF scalars on an inflated surfaces for better visualization (quality control) please provide those inflated surfaces (vtk format).

LocalEACSF executables
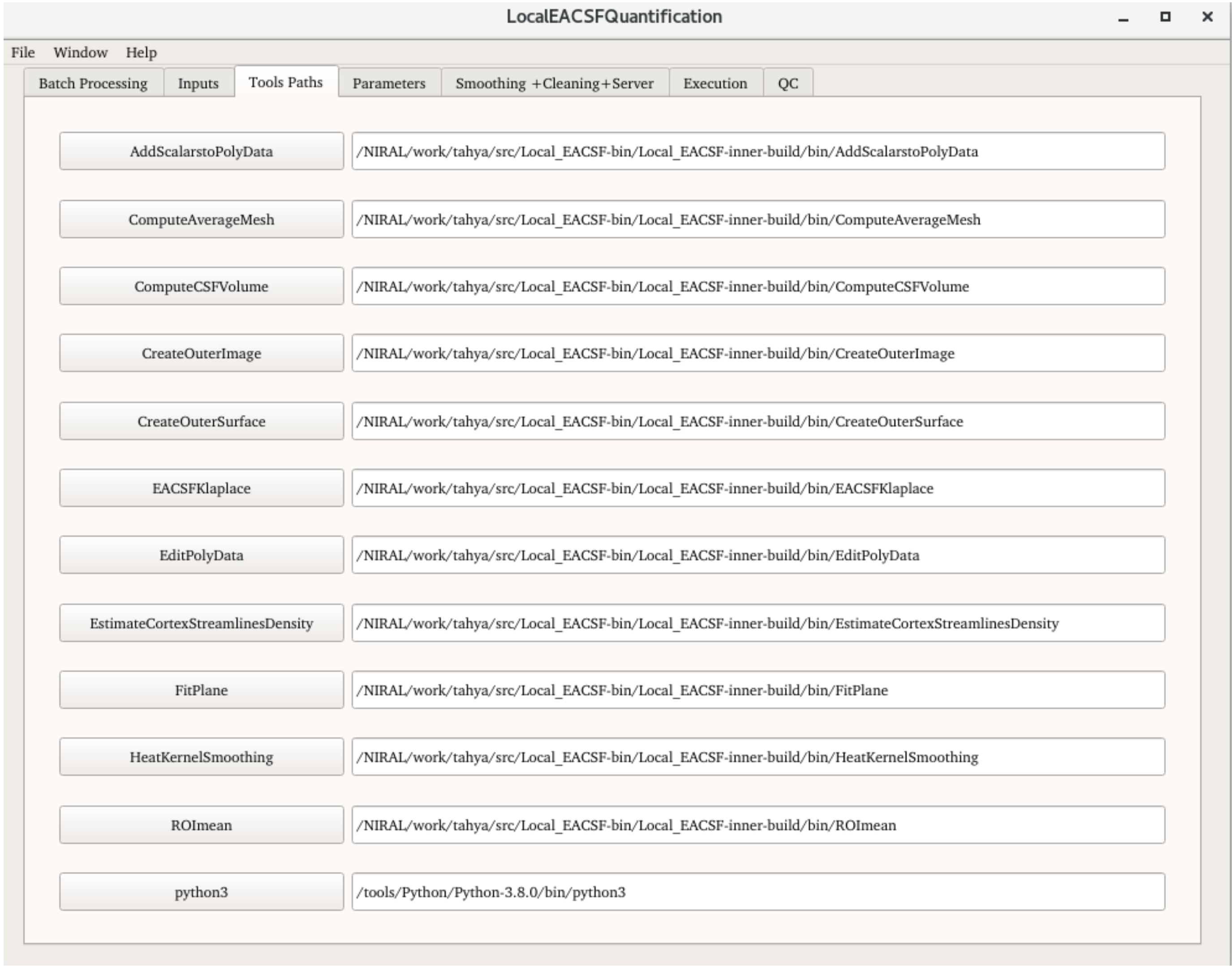
➡ Those are the paths to all executables used by the tool.

➡ All executables are build with the tool and their paths are set by default.

➡ The paths are editable in case you want to use others executables.

➡ To know more about each executable type :

./<path to the executable> —help

➡ For python you will need a version 3.7 or higher.

LocalEACSF parameters

➡ For the creation of CSF outer surface you   will need:

  • Closing radius (voxel).

  • Dilation radius (voxel).

  • Smoothing number of iterations.

➡ For the generation of streamlines the surfaces are divided to many images so you will need :

  The image size (voxel) which is the size of each image (by default 300).

    • Use 'always use CSF density at image size' to compute the EACSF only at image size.

    • Use 'Use optimal CSF density' to optimize the EACSF computation by computing it at 3 values of image size (here for example 20, 19 and 21) then doing a linear interpolation.

Smoothing, Cleaning, Server

➡ Smoothing:

  For the heat kernel smoothing you should provide:

    • Number of iterations. Generally a value of 5 to 10 work well. But if your surface still not smoothed feel free to increase the number of iterations.

    • Kernel band with (mm).

➡ Cleaning:

  This option remove the intermediate outputs generated while the creation of streamlines and while the linear interpolation. Those intermediate outputs take a lot of memory and are not important to keep.

➡ Server:

  You can run the tool :

    • Locally

    • On Slurm in this case you should provide the Slurm parameters(number of nodes, number of cores, time and memory).

Json file

➡ All the previous parameters and data can be provide as a Json file, for that click on 'File' in the menubar and then on 'Load Config File' then choose your Json file.

➡ You can also save your configuration as a Json file by clicking on 'File' and then 'Save Config File'

➡ You have here an example of the Json file: Json File

LocalEACSF tool execution
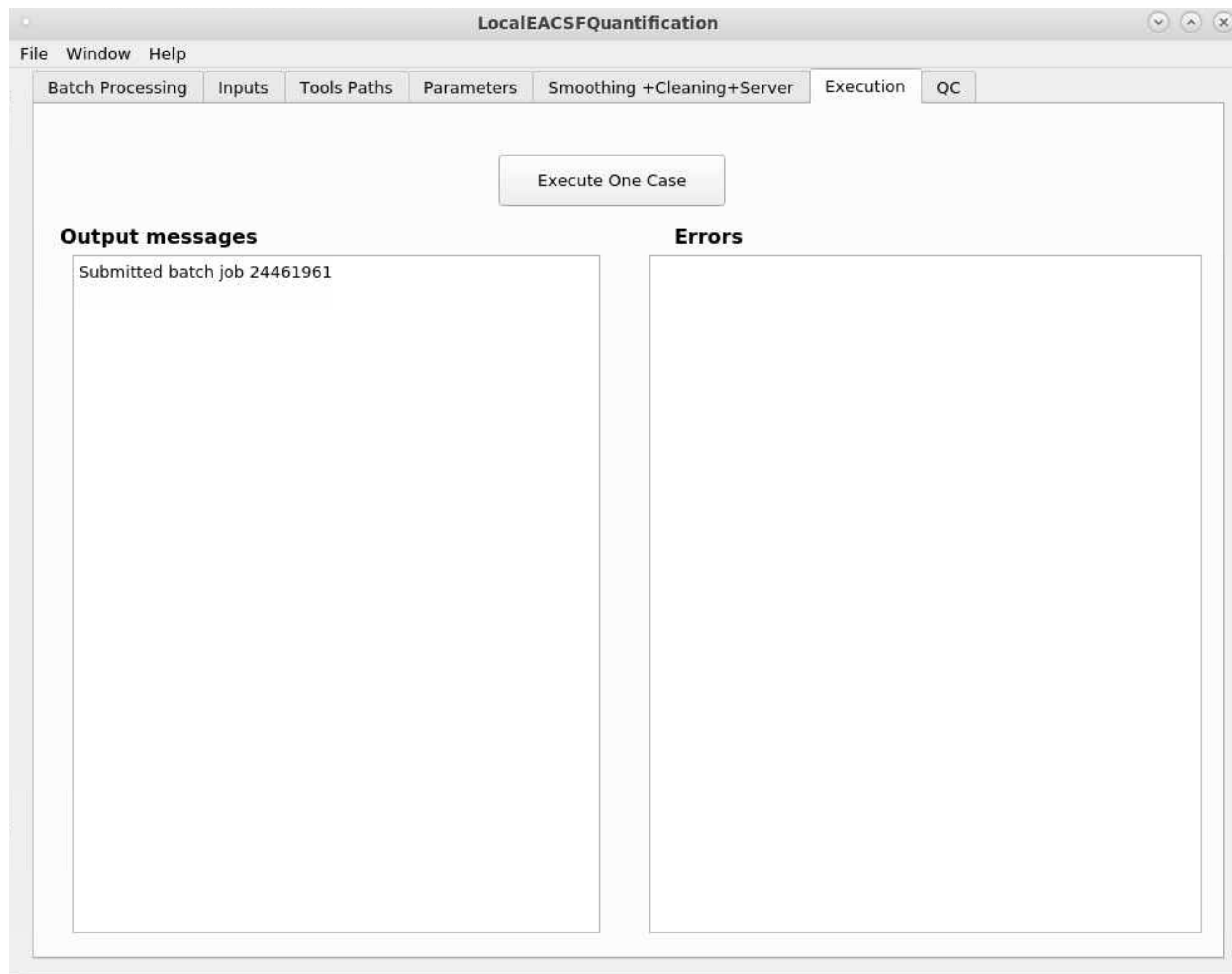
By clicking on "Execute One Case" the tool will launch the LocalEACSF script in the background and show you a message that the batch job was submitted if slurm or your job was started if local.

You can watch the output messages and the errors in real time in the error and output files localized in the output directory .

LocalEACSF tool outputs

➡ At the end of the LocalEACSF processing the output directory will contain a LocalEACSF directory.

➡ LocalEACSF directory contains two directories one for the left and another for the right hemisphere, A text file with the EA-CSF volume and the sum of densities, an error and output text files and a Json file with all all the parameters used to run the tool.

➡ Each side directory (LH and RH directories) will contains the following files:

‣ The CSF probability map given as an input.

‣ GM Dilated which is a binary image created from the tissue segmentation and will be used to create the CSF outer surface.

‣ MID surface given as an input.

‣ CSF outer surface.

‣ CSF density (vtk).

‣ CSF density final, final smoothed, interpolated and original text files.

‣ Inflated surface in case you gave it as in input.

‣ Outer streamelines: a vtk file containing all the streamlines.

‣ Visitation a binary file indicating all the voxels visited during the EA-CSF computation.

‣ Visitation length a nrrd file that associate to each voxel the total length of streamlines passing through it.

‣ Tissue segmentation given as an input.

‣ Regional mean and sum txt files.

‣ 75P and gray matter surfaces if you use the 75P instead of MID surface.

‣ New GM Dilated which is the GM Dilated after fitting a mid-sagittal plan to elimina

Quality Control

After finishing the execution of LocalEACSF you can visualize and check your output by using the quality control tab (QC).

One Case:

➡ The 'Output Directory' is the output directory given as in input it should contain a LocalEACSF directory with all the necessary data.

➡ You can visualize the EACSF for both left and right hemispheres:

EACSF for the left and right hemispheres

About ShapePopulationViewer
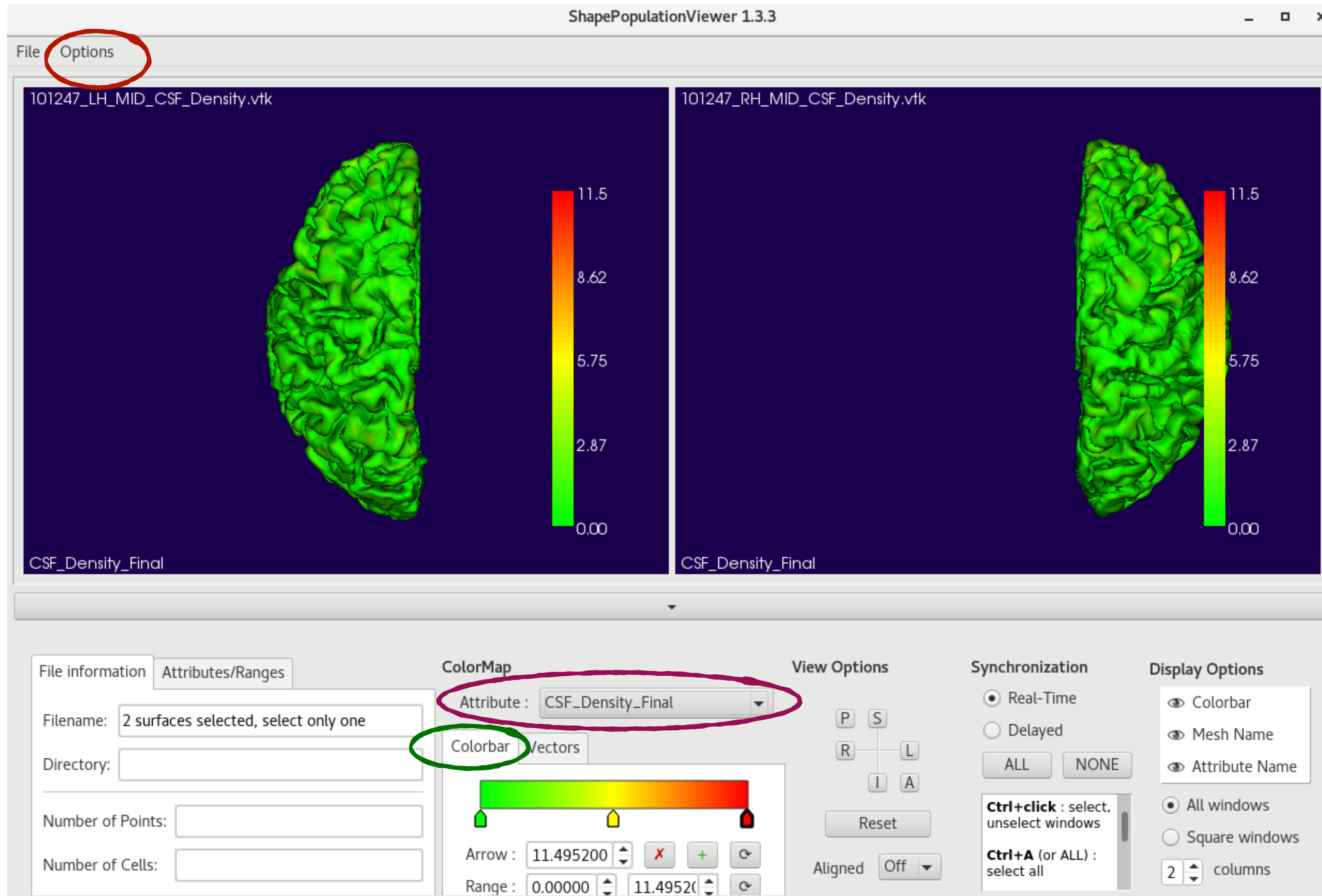
➡ You can choose the scalars that you want to visualise in 'Attribute'. For example : CSF_Desnity_Final, CSF_Desnity_Final_Smoothed …

➡ Adjust the Colorbar (max, min ..).

➡ Using 'Option' you can save your Colorbar.

Quality Control

Quality Control

One Case:

➡Compare the value of volume and the sum of density of EACSF and compute the asymmetries between the left and the right for both :

$$X_{Asymmetry} = 2 * \frac{(X_{left} - X_{right})}{X_{left} + X_{right}} * 100$$

Batch Processing

➡The tool provide a batch processing to proceed many data. For that you should provide the 'Data Directory' where you have all your subjects data and then click 'Find'.

➡For more information about the Data Directory click on Help.

➡You can also give to the tool a CSV file instead of the Data directory 'Load a CSV file' (the header of the CSV file is given in Help)

➡You can save all the data informations as a CSV file using 'Export To a CSV file'

➡Choose local or Slurm to run batch processing.

➡Before running the batch processing be sure to set all the other parameters (Inputs, Tools Paths, Parameters, Smoothing …)

➡All the cases in batch will be proceed with the same parameters , the same surfaces labeling for regional computation and the same inflated surfaces.

➡You can run the Batch process by clicking on 'Run Batch process'

Batch Processing

Warning :

If you start Batch Processing please keep the GUI open, otherwise the tool will crash

Batch Processing/QC

Many Cases:

➡️To visualize many cases in the same time for group analysis you should provide a CSV file to the tool. This CSV file is created while batch processing. See Help for more details.

➡️After providing the CSV file you can choose to visualize the CSF density for all cases in this CSV file in ShapePopulationViewer, or to visualize all the visitations map for the left or for the right hemisphere

Left EACSF for 3 cases

If you have any question about the tutorial or the tool feel free to mention it in the GitHub repository by using 'Issues'.