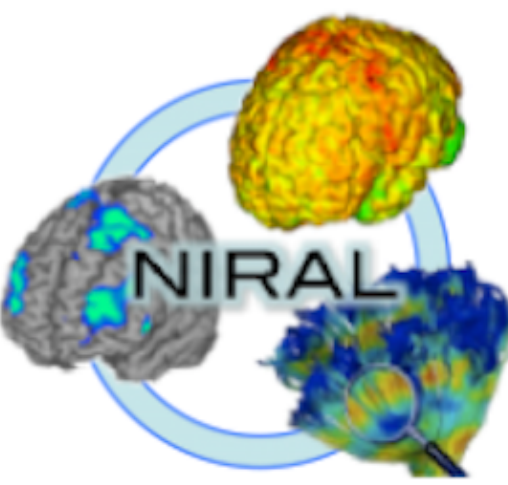




THE UNIVERSITY
of NORTH CAROLINA
at CHAPEL HILL



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](#)

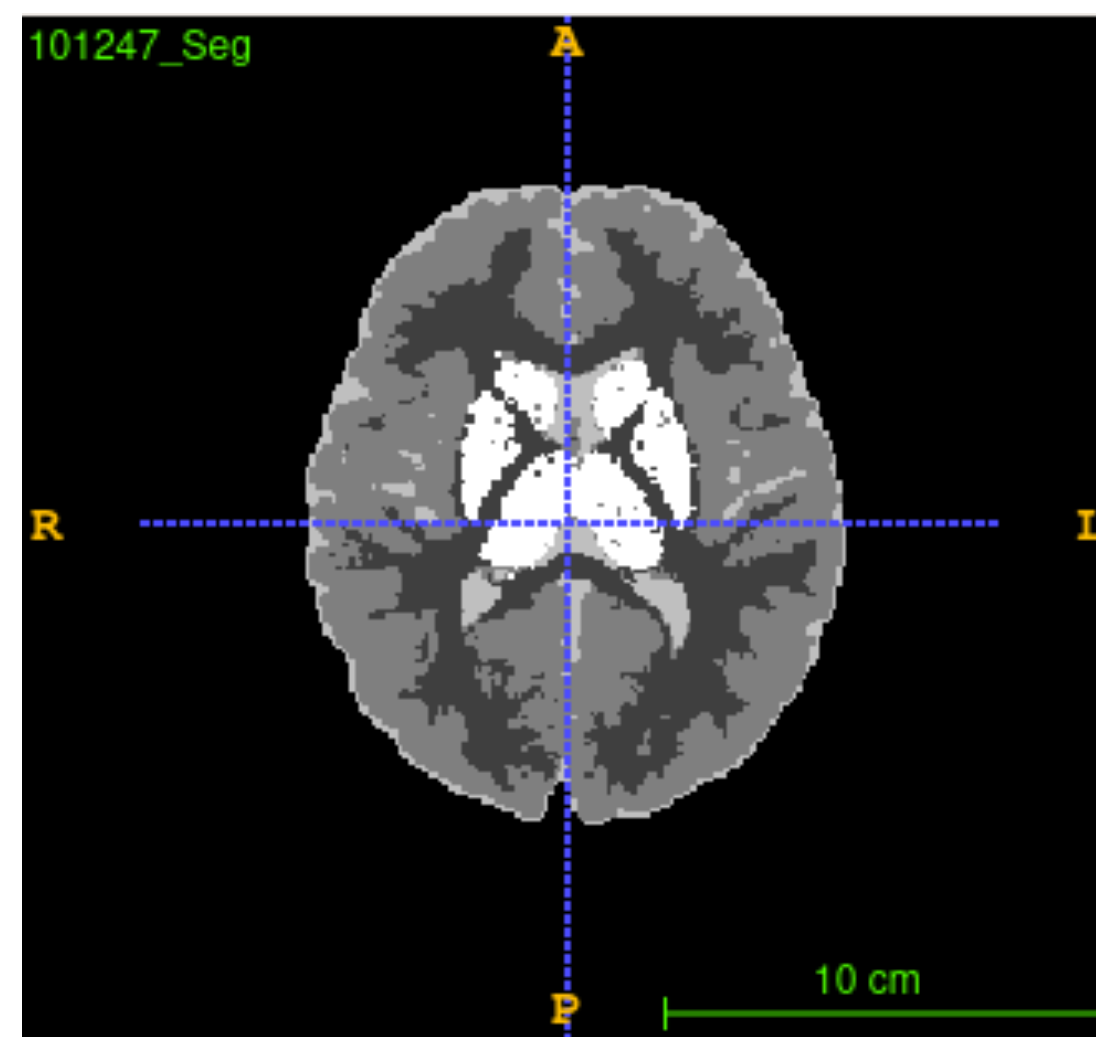
installing LocalEACSF tool

- ➔ 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.

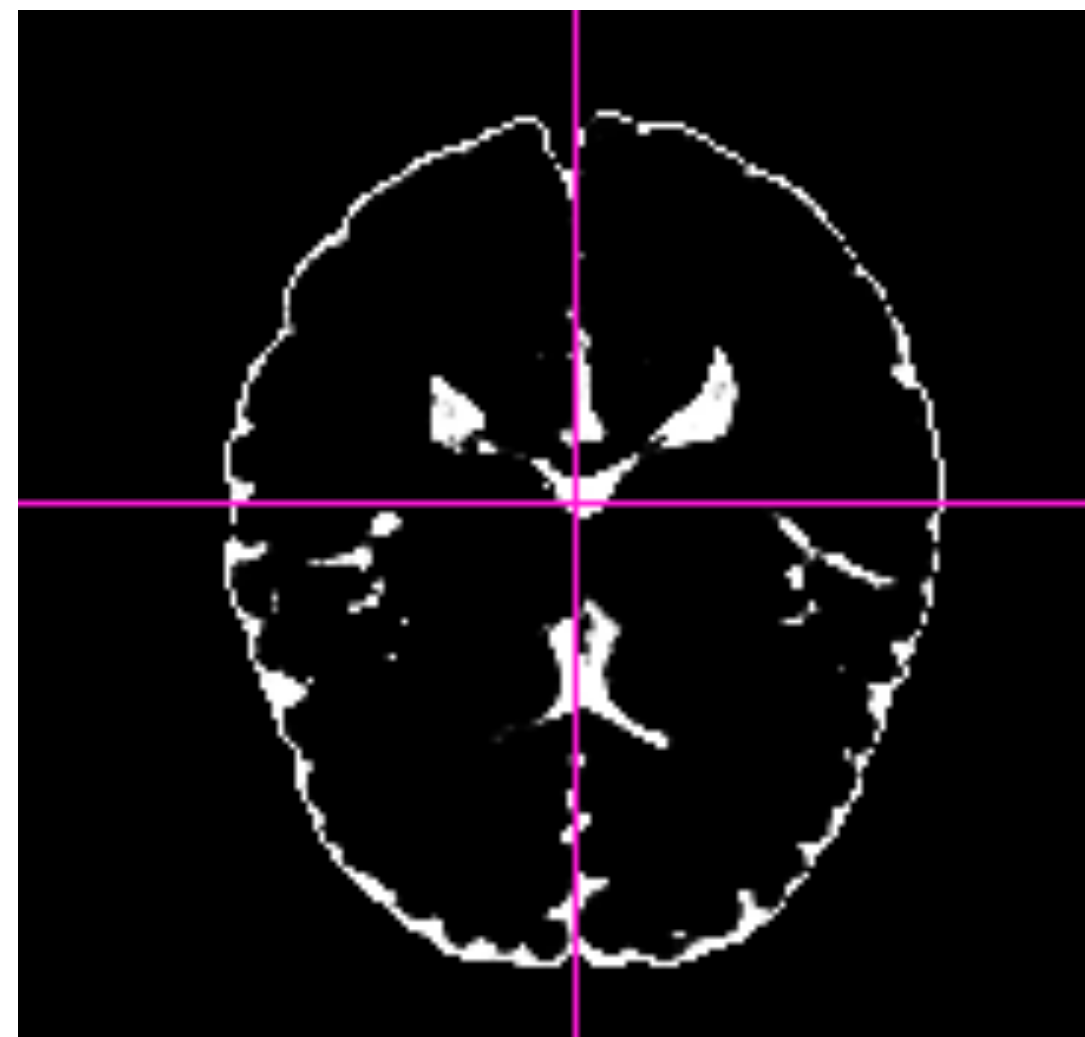
Necessary data for LocalEACSF

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

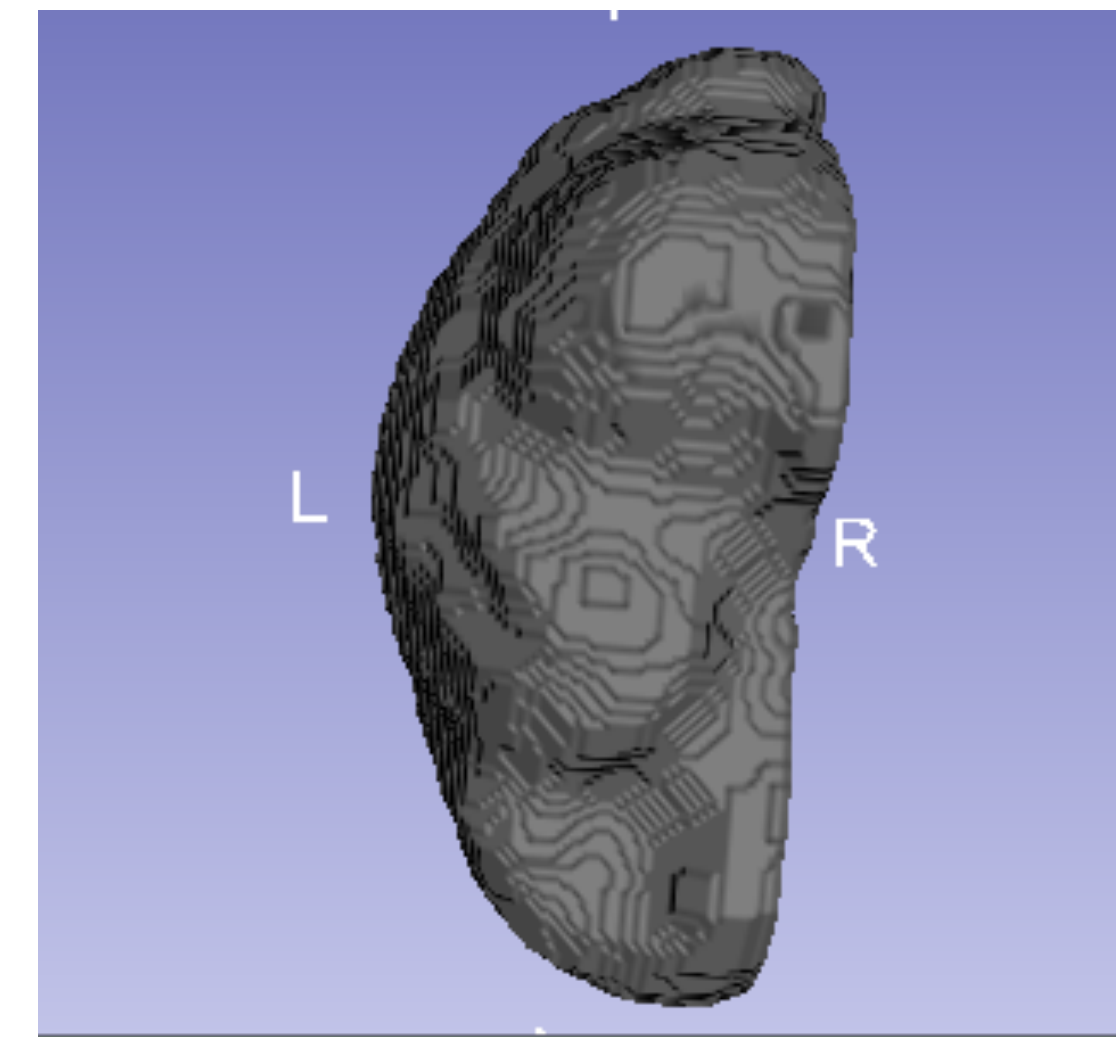
- A tissue segmentation of gray matter, white matter and CSF (3 labels) in nrrd format.
- A probability map of CSF (nrrd format).
- The left and right middle (MID) surfaces. The MID surface is the average between the gray matter and white matter surfaces and should be given in vtk format. (For NIRAL 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 case `./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 tool inputs

The screenshot shows the 'LocalEACSFQuantification' application window. It has a menu bar (File, Window, Help) and a tabbed interface with tabs for Batch Processing, Inputs, Tools Paths, Parameters, Smoothing +Cleaning+Server, Execution, and QC. The 'Inputs' tab is active, displaying several input sections:

- Input Images:** Tissue Segmentation (path: /NIRAL/work/tahya/Data/local_EACSF_Extraction/Ben_Test/101247/101247_Seg.nrrd) and CSF Probability Map (path: /NIRAL/work/tahya/Data/local_EACSF_Extraction/Ben_Test/101247/101247_CSF_Prop.nrrd).
- MID Surfaces:** LH MID Surface (path: /NIRAL/work/tahya/Data/local_EACSF_Extraction/Ben_Test/101247/101247_LH_MID.vtk) and RH MID Surface (path: /NIRAL/work/tahya/Data/local_EACSF_Extraction/Ben_Test/101247/101247_RH_MID.vtk).
- Gray Matter Surfaces:** LH GM Surface and RH GM Surface (both empty).
- Regional CSF Density:** A checked checkbox 'Compute regional CSF density (at the case of batch processing the same atlas is used for all cases)' is followed by 'Left Atlas Surface Labeling' (path: /NIRAL/tools/atlas/Surface/CIVET_160K/icbm_surface/Destrieux/Atlas_Left_Destrieux.txt) and 'Right Atlas Surface Labeling' (path: /NIRAL/tools/atlas/Surface/CIVET_160K/icbm_surface/Destrieux/Atlas_Right_Destrieux.txt).
- Inflated Surfaces:** A note '(at the case of batch processing the same template is used for all cases)' is above 'LH Inflated Template (Optional)' (path: /NIRAL/tools/atlas/Surface/CIVET_160K/icbm_surface/icbm_avg_mid_sym_mc_left_hires.vtk) and 'RH Inflated Template (Optional)' (path: /NIRAL/tools/atlas/Surface/CIVET_160K/icbm_surface/icbm_avg_mid_sym_mc_right_hires.vtk).
- Output Directory:** Output Directory (path: /NIRAL/work/tahya/final_test/test_atlas).
- Label:** Label (The cases's ID for example) with the value 101247.

Four colored dashed boxes highlight specific areas: a red box around the Gray Matter Surfaces section, a green box around the Regional CSF Density section, an orange box around the Inflated Surfaces section, and a blue box around the Output Directory and Label fields. Arrows point from these boxes to the explanatory text on the right.

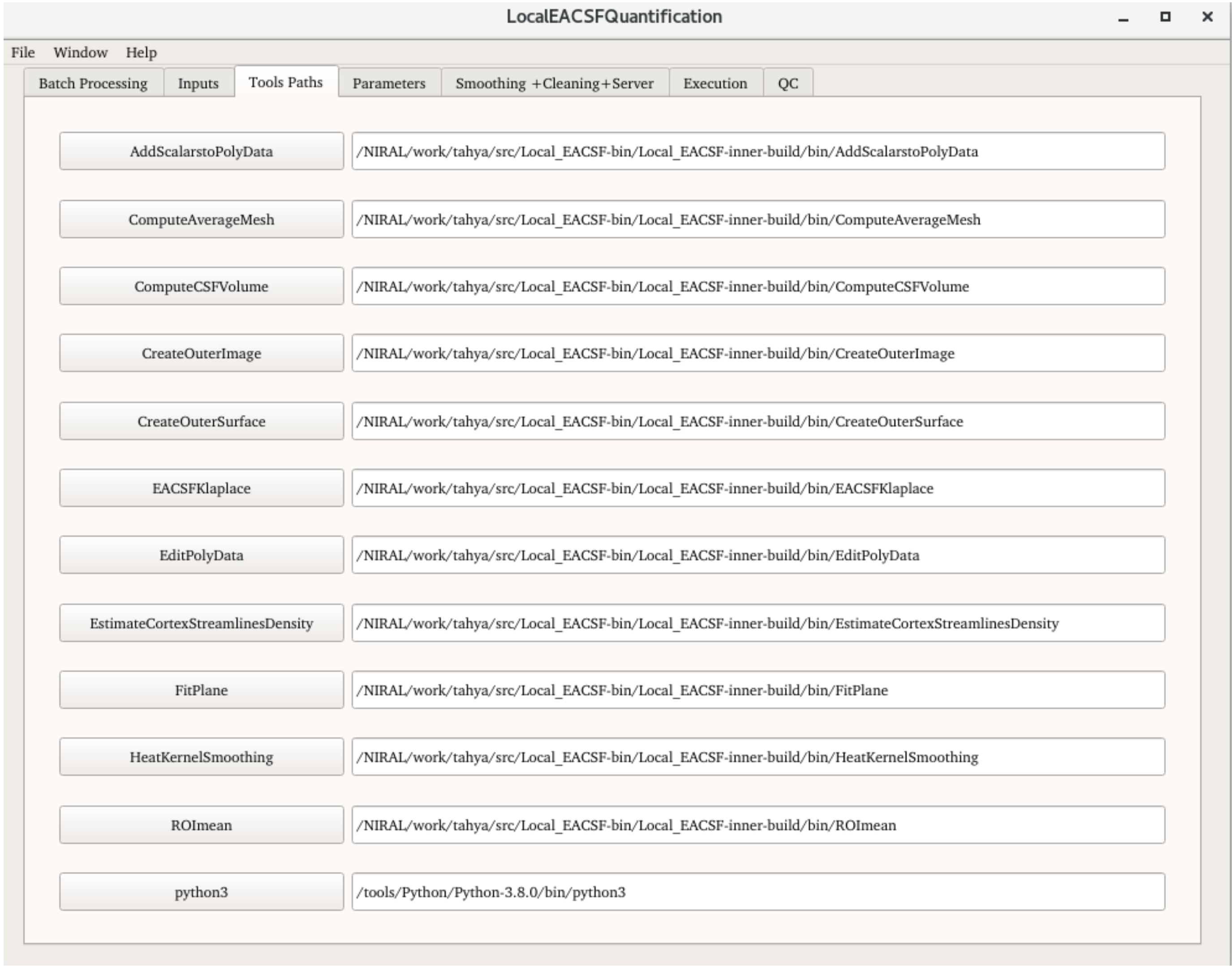
➡ Mandatory :

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

LocalEACSFQuantification

FileWindowHelp

Batch ProcessingInputsTools PathsParametersSmoothing +Cleaning+ServerExecutionQC

Please don't change the following parameters if you don't konw what you are doing

Outer Surface Creation Parameters

Closing Radius

structuring element radius for closing the tissu segmentation image

15

Dilation Radius

structuring element radius for dilating the tissu segmentation image

2

Smoothing Number of Iterartions

the number of iterations for smoothing the Outer CSF Hull

1

Surfaces Correspondance Parameters

Image Size

the size of the images used to establish the correspondence of surfaces

A higher value will give more precise results with a cost in time and memory

20

(+/-)

1

☐ Use optimal CSF density (image size +/- margin value)

☒ always use CSF density at image size

➡ 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.

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Smoothing, Cleaning, Server

LocalEACSFQuantification

File Window Help

Batch Processing Inputs Tools Paths Parameters Smoothing + Cleaning + Server Execution QC

1.Smooth the CSF density:

☒ Smooth the CSF density with heat kernel smoothing

Smoothing Parameters

Smoothing number of iterations

Smoothing kernel bandwidth

2.Clean the output directory of intermediate outputs:

☒ Clean up

3.Run this program in:

☐ Option1 : Local

☒ Option2 : SLURM/Longleaf

Slurm Parameters :

-Nodes number (-N)

-Cores number (-n)

-Time (-t) [days-hh:mm:ss]

-Memory (-mem)

➡ 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:

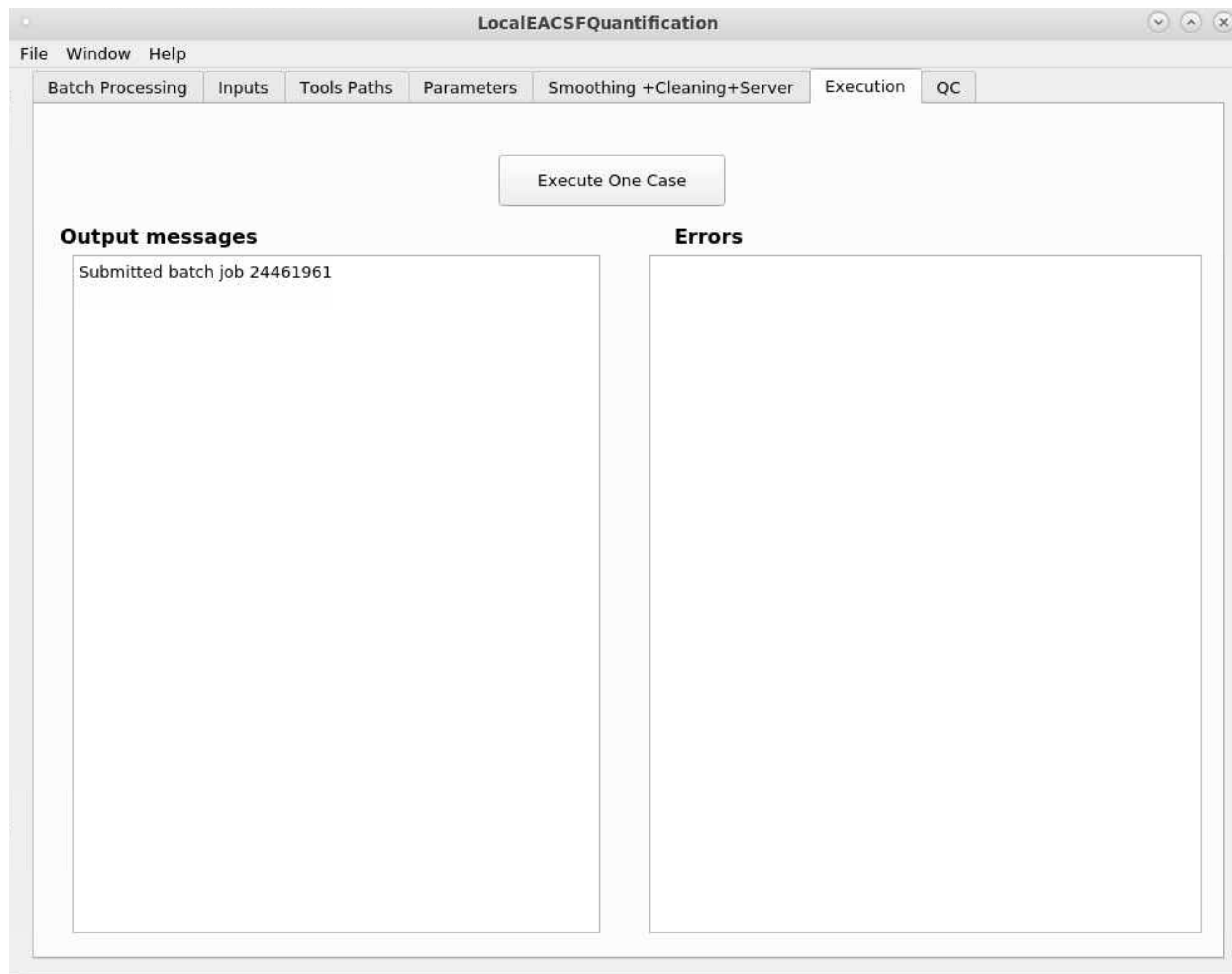
You can run the tool :

- 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 the 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 .

Quality Control

LocalEACSFQuantification

FileWindowHelp

Batch ProcessingInputsTools PathsParametersSmoothing +Cleaning+ServerExecutionQC

One Case:

Output Directory Path

Output Directory

/NIRAL/work/tahya/final_test/original

☐ Visualize the CSF density for both hemispheres in ShapePopulationViewer

☐ Visualize the CSF density for both hemispheres in ShapePopulationViewer (Inflated Surfaces)

☐ Visualize the visitation map and the CSF probability for left side in MriWatcher

☐ Visualize the visitation map and the CSF probability for right side in MriWatcher

Compare the EACSF Density sum with the EACSF Volume :

Compare

	Left	Right	Asymmetry(%)
Volume	113046	84809	28.54
Density Sum	166368	149419	10.73

Many Cases:

CSV File

Help

☐ Visualize the CSF density in ShapePopulationViewer

☐ Visualize all visitation maps for the left hemisphere

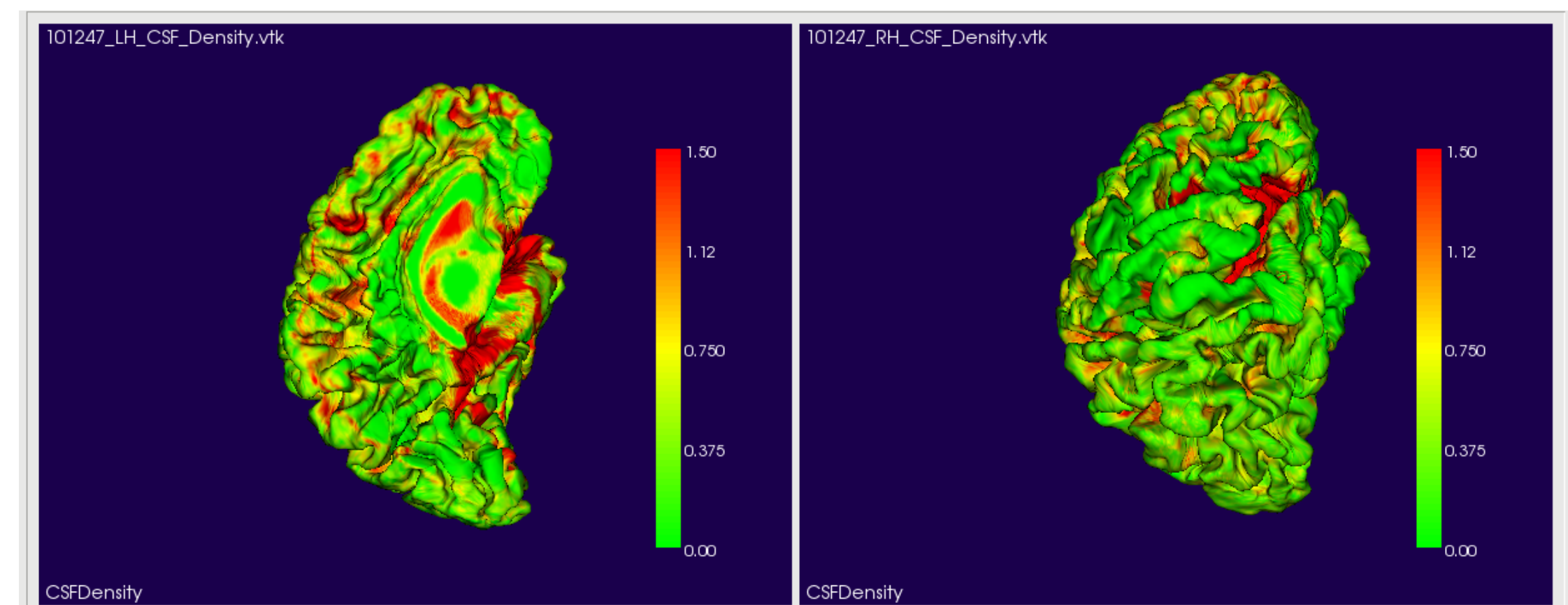
☐ Visualize all visitation maps for the right hemisphere

Visualize

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

Quality Control

LocalEACSFQuantification

File

Window

Help

Batch Processing

Inputs

Tools Paths

Parameters

Smoothing +Cleaning+Server

Execution

QC

One Case:

Output Directory Path

Output Directory

/NIRAL/work/tahya/final_test/original

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☐ Visualize the CSF density for both hemispheres in ShapePopulationViewer (Inflated Surfaces)

☒ Visualize the visitation map and the CSF probability for left side in MriWatcher

☐ Visualize the visitation map and the CSF probability for right side in MriWatcher

Visualize

Compare the EACSF Density sum with the EACSF Volume :

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Many Cases:

CSV File

Help

☐ Visualize the CSF density in ShapePopulationViewer

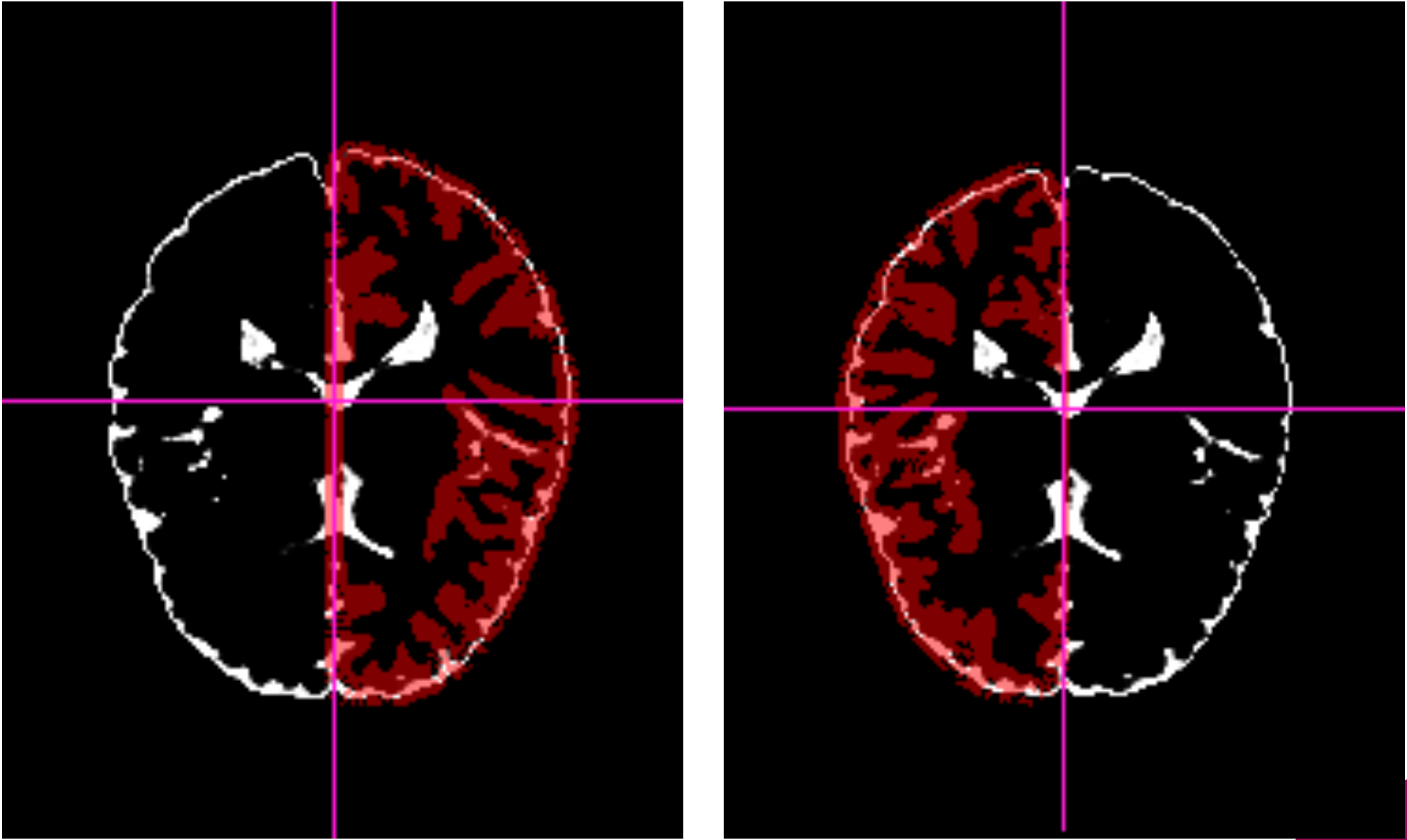
☐ Visualize all visitation maps for the left hemisphere

☐ Visualize all visitation maps for the right hemisphere

Visualize

One Case:

- ➡ You can visualize the visitation map and the CSF Probability Map for the left and for the right in MriWatcher.



Quality Control

LocalEACSFQuantification

File

Window

Help

Batch Processing

Inputs

Tools Paths

Parameters

Smoothing +Cleaning+Server

Execution

QC

One Case:

Output Directory Path

Output Directory

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☐ Visualize the visitation map and the CSF probability for left side in MriWatcher

☐ Visualize the visitation map and the CSF probability for right side in MriWatcher

Visualize

Compare the EACSF Density sum with the EACSF Volume :

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	Left	Right	Asymmetry(%)
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Density Sum	166368	149419	10.73

Many Cases:

CSV File

Help

☐ Visualize the CSF density in ShapePopulationViewer

☐ Visualize all visitation maps for the left hemisphere

☐ Visualize all visitation maps for the right hemisphere

Visualize

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

LocalEACSFQuantification

File Window Help

Batch Processing Inputs Tools Paths Parameters Smoothing +Cleaning+ Server Execution QC

Data Directory: /NIRAL/work/tahya/Test/tahya/Similarity

Seg filter: Seg.*\.(nrrd) LH MID filter: LH.*MID\.vtk LH GM filter: LH.*GM\.vtk

CSF Prob filter: CSF_Pro.*\.(nrrd) RH MID filter: RH.*MID\.vtk

☐ Use 75P Surface

Find Help

	CSF Probability Map	LH MID Surface	Label	Output Directory	RH MID Surface	Tissu Segmentation
0	...a/Similarity/103430/CSF_Pro.nrrd	...0/LH_MID.vtk	103430	...ularity/103430	...0/RH_MID.vtk	...Similarity/103430/Seg.nrrd
1	...a/Similarity/103831/CSF_Pro.nrrd	...1/LH_MID.vtk	103831	...ularity/103831	...1/RH_MID.vtk	...Similarity/103831/Seg.nrrd
2	...a/Similarity/107524/CSF_Pro.nrrd	...4/LH_MID.vtk	107524	...ularity/107524	...4/RH_MID.vtk	...Similarity/107524/Seg.nrrd
3	...a/Similarity/110940/CSF_Pro.nrrd	...0/LH_MID.vtk	110940	...ularity/110940	...0/RH_MID.vtk	...Similarity/110940/Seg.nrrd
4	...a/Similarity/119906/CSF_Pro.nrrd	...6/LH_MID.vtk	119906	...ularity/119906	...6/RH_MID.vtk	...Similarity/119906/Seg.nrrd
5	...a/Similarity/121007/CSF_Pro.nrrd	...7/LH_MID.vtk	121007	...ularity/121007	...7/RH_MID.vtk	...Similarity/121007/Seg.nrrd
6	...a/Similarity/123794/CSF_Pro.nrrd	...4/LH_MID.vtk	123794	...ularity/123794	...4/RH_MID.vtk	...Similarity/123794/Seg.nrrd
7	...a/Similarity/136345/CSF_Pro.nrrd	...5/LH_MID.vtk	136345	...ularity/136345	...5/RH_MID.vtk	...Similarity/136345/Seg.nrrd
8	...a/Similarity/136846/CSF_Pro.nrrd	...6/LH_MID.vtk	136846	...ularity/136846	...6/RH_MID.vtk	...Similarity/136846/Seg.nrrd
9	...a/Similarity/138494/CSF_Pro.nrrd	...4/LH_MID.vtk	138494	...ularity/138494	...4/RH_MID.vtk	...Similarity/138494/Seg.nrrd
10	...a/Similarity/141335/CSF_Pro.nrrd	...5/LH_MID.vtk	141335	...ularity/141335	...5/RH_MID.vtk	...Similarity/141335/Seg.nrrd
11	...a/Similarity/145656/CSF_Pro.nrrd	...6/LH_MID.vtk	145656	...ularity/145656	...6/RH_MID.vtk	...Similarity/145656/Seg.nrrd

Add Remove Selected rows Clear Export To a CSV file Load a CSV file

☐ Local: Serial Batch Processing ☐ Slurm: Parallel Batch Processing

Run Batch process

➡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/QC

LocalEACSFQuantification

FileWindowHelp

Batch ProcessingInputsTools PathsParametersSmoothing +Cleaning+ServerExecutionQC

One Case:

Output Directory Path

Output Directory

/NIRAL/work/tahya/final_test/original

☐ Visualize the CSF density for both hemispheres in ShapePopulationViewer

☐ Visualize the CSF density for both hemispheres in ShapePopulationViewer (Inflated Surfaces)

☐ Visualize the visitation map and the CSF probability for left side in MriWatcher

☐ Visualize the visitation map and the CSF probability for right side in MriWatcher

Visualize

Compare the EACSF Density sum with the EACSF Volume :

Compare

	Left	Right	Asymmetry(%)
Volume	113046	84809	28.54
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Many Cases:

CSV File

Help

☐ Visualize the CSF density in ShapePopulationViewer

☐ Visualize all visitation maps for the left hemisphere

☐ Visualize all visitation maps for the right hemisphere

Visualize

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

The figure displays three side-by-side brain surface maps, each representing the left hemisphere (LH) CSF density for a different case. The cases are labeled as 103430_LH_CSF_Density.vtk, 101247_LH_CSF_Density.vtk, and 240946_LH_CSF_Density.vtk. Each map shows a lateral view of the brain with a color scale ranging from 0.00 (green) to 2.00 (red). The maps are labeled 'CSFDensity' at the bottom.

Left EACSF for 3 cases

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If you have any question about the tutorial or the tool feel free to contact:
tahya.deddah@cpe.fr