Slicer3 Training Tutorial

UNC external modules

For regional cortical thickness analysis

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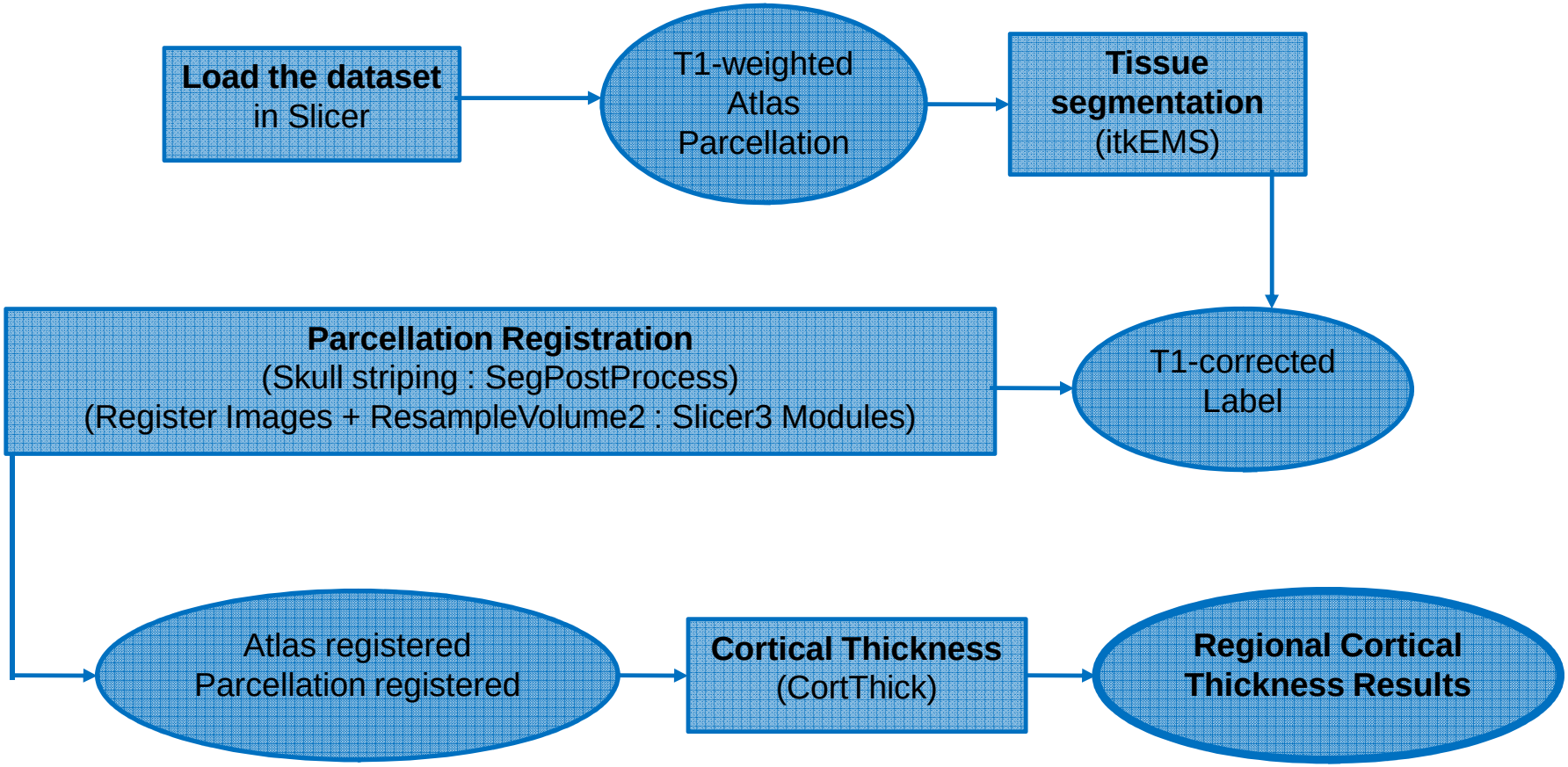
Learning Objective

Following this tutorial, you will be able to run UNC external modules, within Slicer3 or using command lines, in order to perform a regional cortical thickness analysis.

You will learn how to load input volumes, perform a **tissue segmentation** (itkEMS), **register a parcellation map** (skull-stripping -SegPostProcess-, atlas registration -Register Images-, applying the transformation to the parcellation image -ResampleVolume2-) and compute **sparse and asymmetric cortical thickness** (CortThick).

Learning Objective

How to perform a regional cortical thickness step by step?



Prerequisites

This tutorial assumes that you have already completed the tutorial **Data Loading and Visualization**. Tutorials for **Slicer3** are available at the following location:

- **Slicer3** tutorials
http://www.na-mic.org/Wiki/index.php/Slicer3.2:Training

Materials

This tutorial requires the installation of Slicer3, the tutorial dataset and the external modules. They are available at the following locations:

- Slicer3 download page (***Slicer 3.2***)

http://www.slicer.org/pages/Downloads

- Tutorial dataset download page(***ARCTIC_Tutorial_example_1.0***)
- External modules download page (***ARCTIC_Executables_1.0***)

http://www.nitrc.org/projects/arctic/

- Atlas download page(***UNC_Pediatric_Brain_Atlas***)

http://www.insight-journal.org/midas/item/view/2277

Materials: Tutorial dataset

The tutorial dataset (*ARCTIC_Tutorial_example_1.0*) is a ZIP file.

Unzip this file somewhere in your computer.

An "*ARCTIC_Tutorial_example_1.0*" folder will be created, containing:

- A pediatric case: T1-weighted and T2-weighted images.
- An "ARTIC-Results/" directory, in which results of the tutorial example will be saved.

Materials: External modules

The executables are in a ZIP file (*ARCTIC_Executables_1.0_linux32/64*) .

Unzip this file somewhere in your computer.

An "*ARCTIC_Executables_1.0_linux32/64*" folder will be created, containing executables needed to perform the cortical thickness analysis.

To add the pipeline as a Slicer3 external module :

- Open Slicer3
- Go to View → Application Settings →Module Settings
- Click on the "add a preset" button
- Select the "*ARCTIC_Executables_1.0"* folder and confirm
- Close Slicer3

Materials: Atlas

The atlas and its related files are in a ZIP file (*UNC_Pediatric_Brain_Atlas*) .

Create a “pediatric-atlas-4years-sym-T1-RAI” folder somewhere in your computer.

Unzip the ZIP file in this new folder.

The “pediatric-atlas-4years-sym-T1-RAI” folder will thus contain the atlas and its related files.

You can then unzip all the images (gunzip command).

Tutorial Overview

A-Tutorial example with dataset

1- Load the dataset in Slicer

2- Tissue segmentation : itkEMS

3- Registration : SegPostProcess, RegisterImages, ResampleVolume2

4- Cortical thickness : CortThick

B-In depth tutorial

1- Load images

2- Use itkEMS for tissue segmentation

3- Use SegPostProcess for skull stripping

4- Use CortThick for thickness assessment

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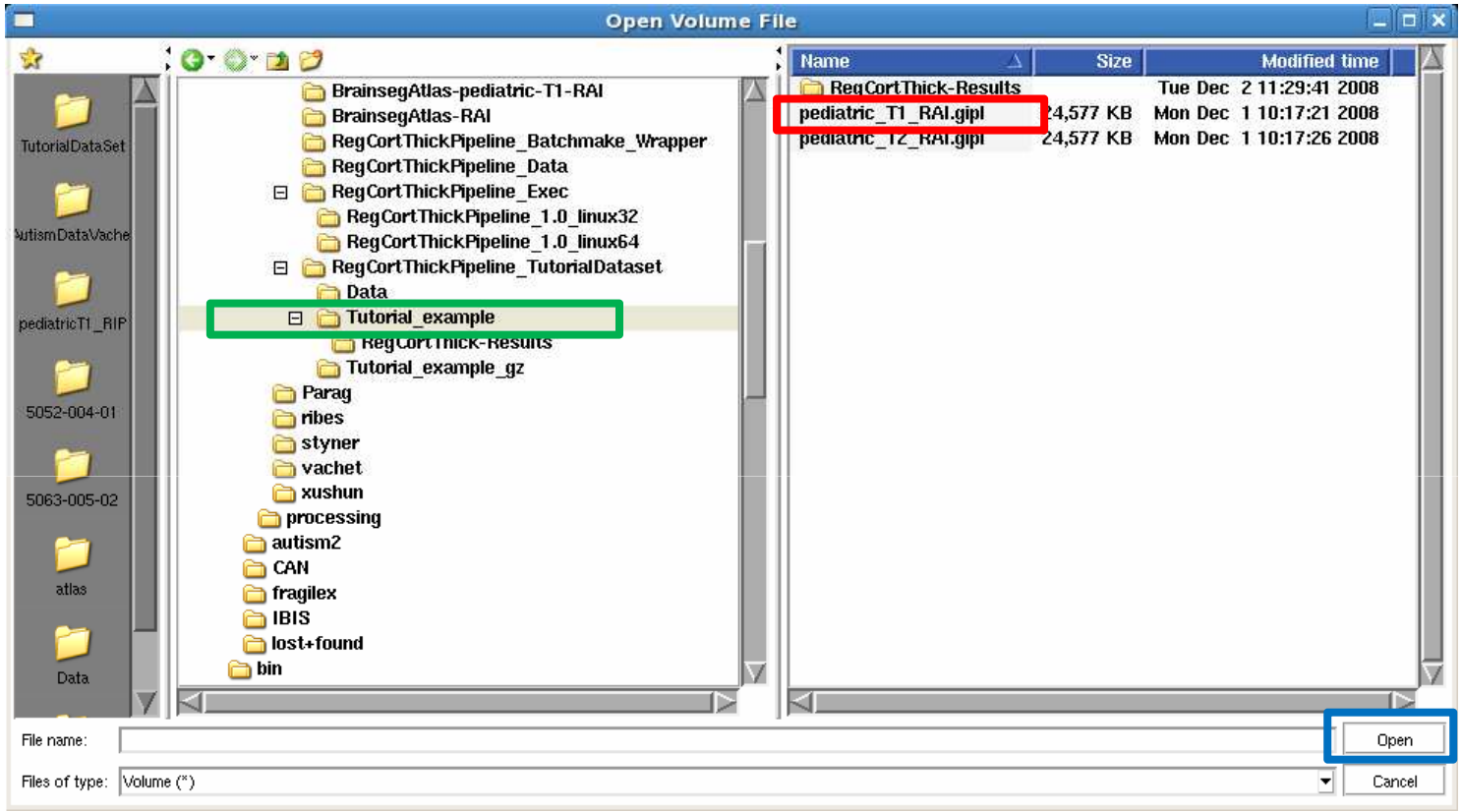
B-In depth tutorial

Load the dataset in Slicer

In Slicer, select the module « Volumes » to load the input images.

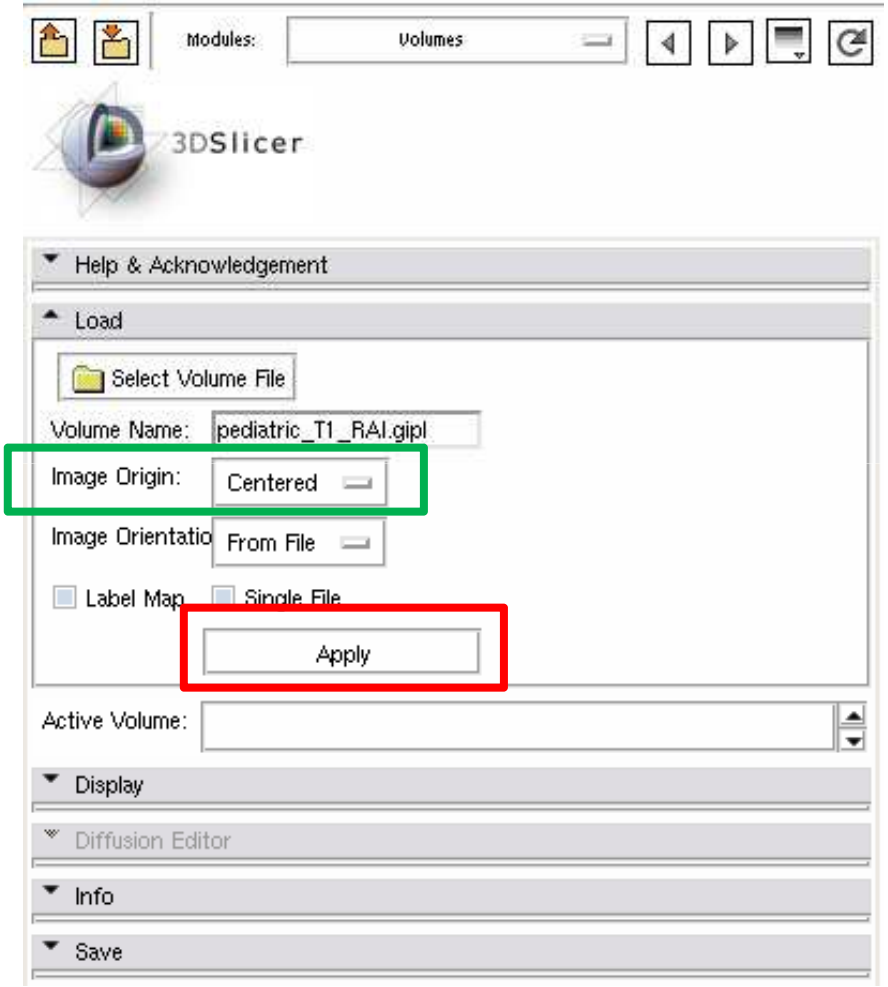
Then click on the « Select Volume File » button to load the images.

Load the dataset in Slicer



A new window ‘Open Volume File’ is now open. Select the **« Tutorial_example »** directory **.** Select the **« pediatric_T1_RAI.gipl »** file in the Data directoryand click on **« Open »**.

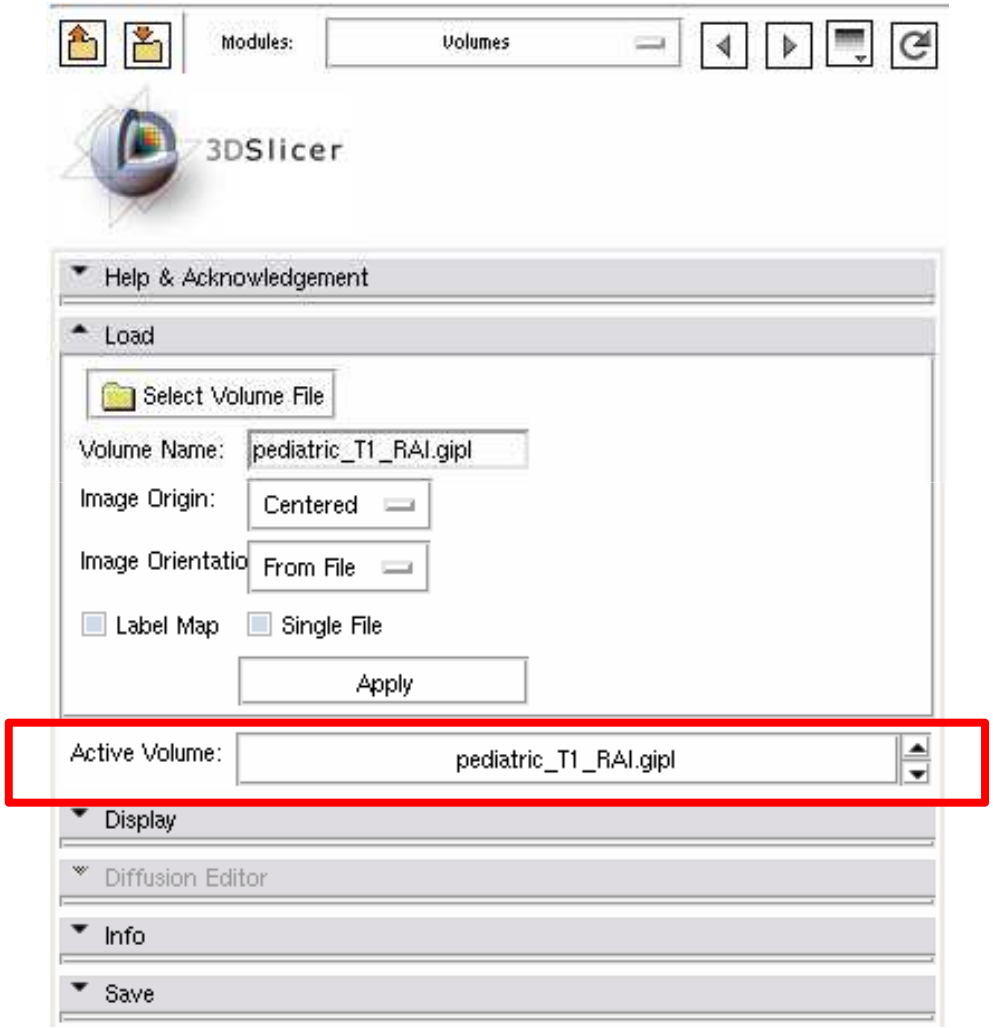
Load the dataset in Slicer



Now, select the Image Origin as **« Centered ».**

And click on **« Apply ».**

Load the dataset in Slicer



The first image is now loaded.

You can check it in the « Active Volume » widget.

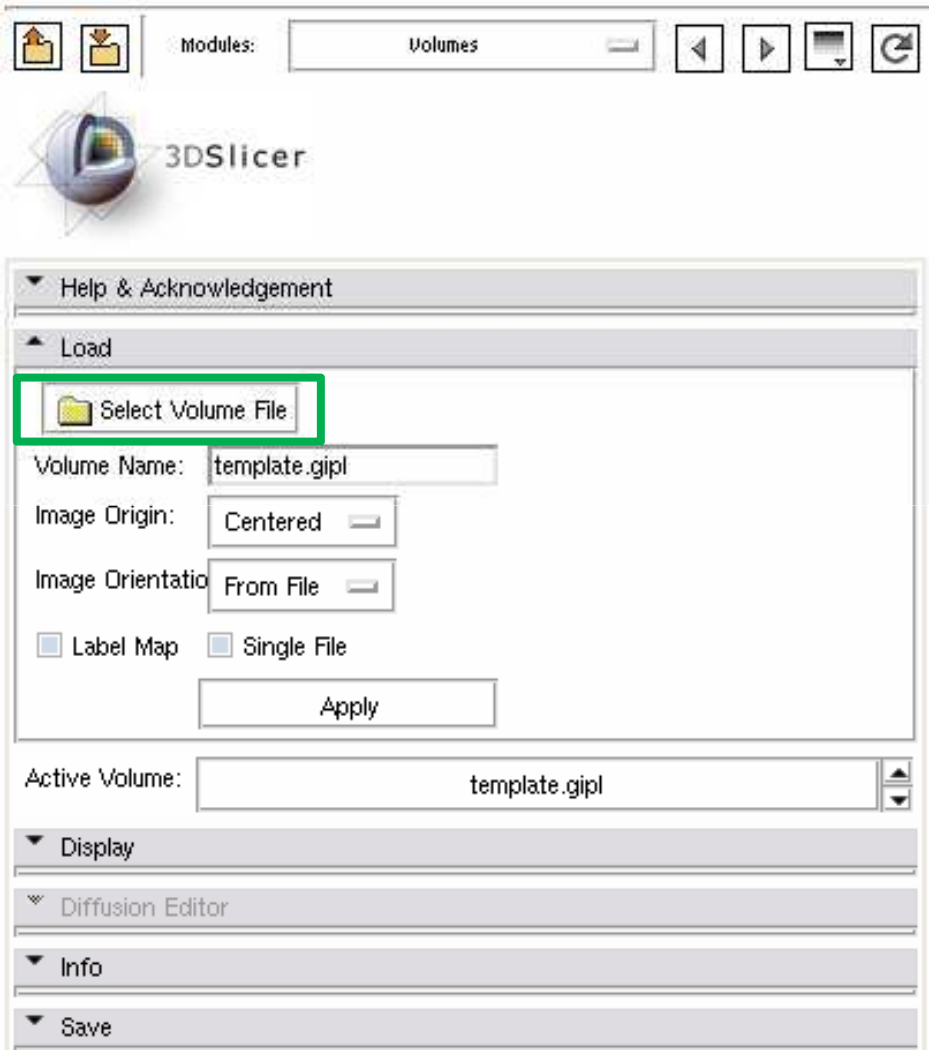
Load the dataset in Slicer

Apply the same steps to load the T2-weighted and atlas images.

One can find the T2-weighted image in the same directory than the T1-weighted.

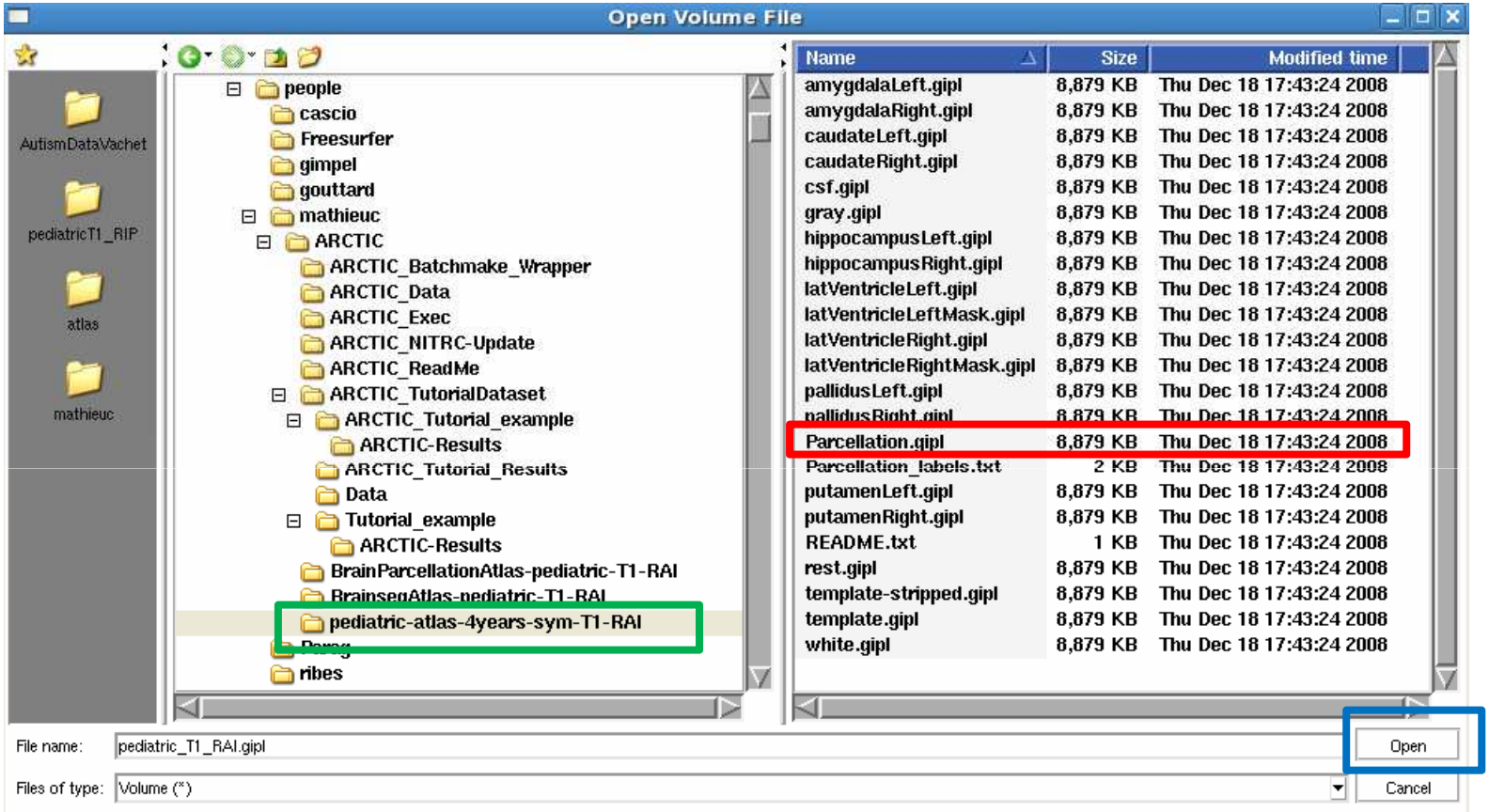
The atlas image, named « template-stripped.gipl », is in the pediatric-atlas-4years-sym-T1-RAI/ directory.

Load the dataset in Slicer



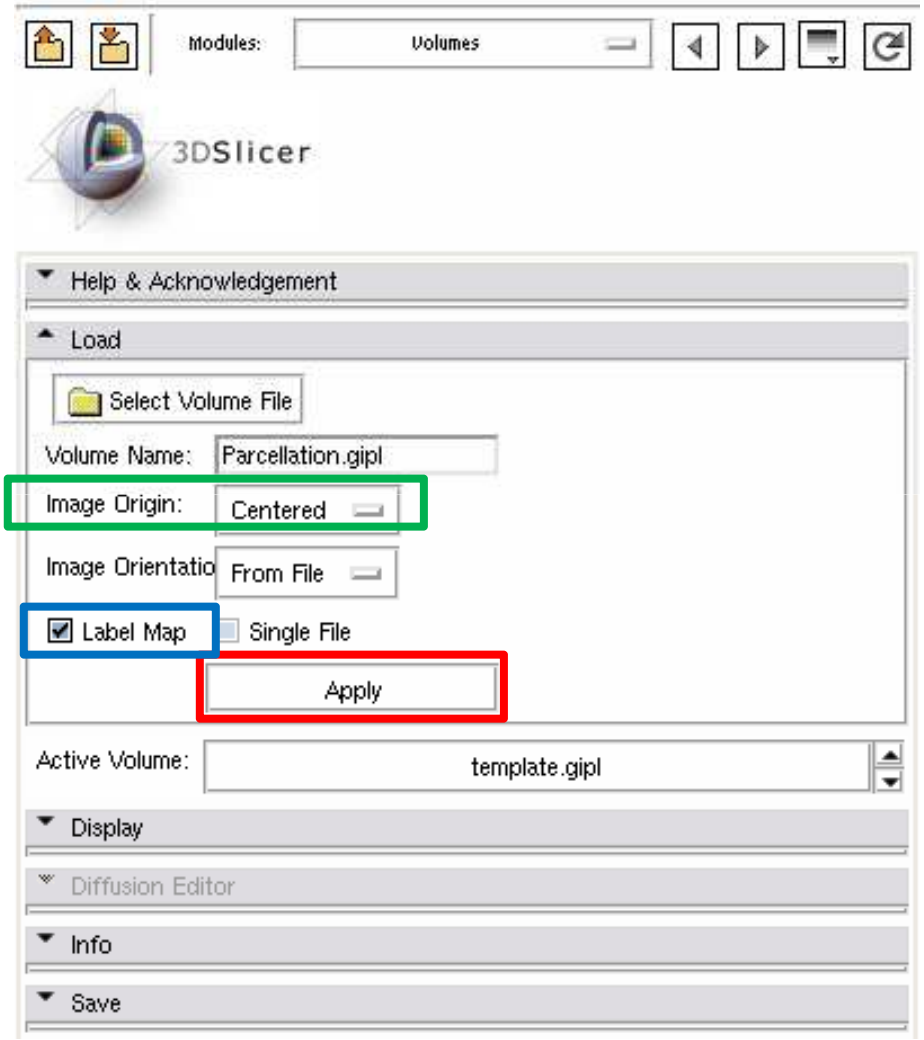
Now we will load the parcellation image.
Click on the **« Select Volume File »** button to load the parcellation.

Load the dataset in Slicer



A new window '**Open Volume File**' is now open. Select the **« BrainParcellationAtlas-pediatric-RAI»** directory . Then, select the **« Parcellation.gipl »** file and click on **« Open »** .

Load the dataset in Slicer

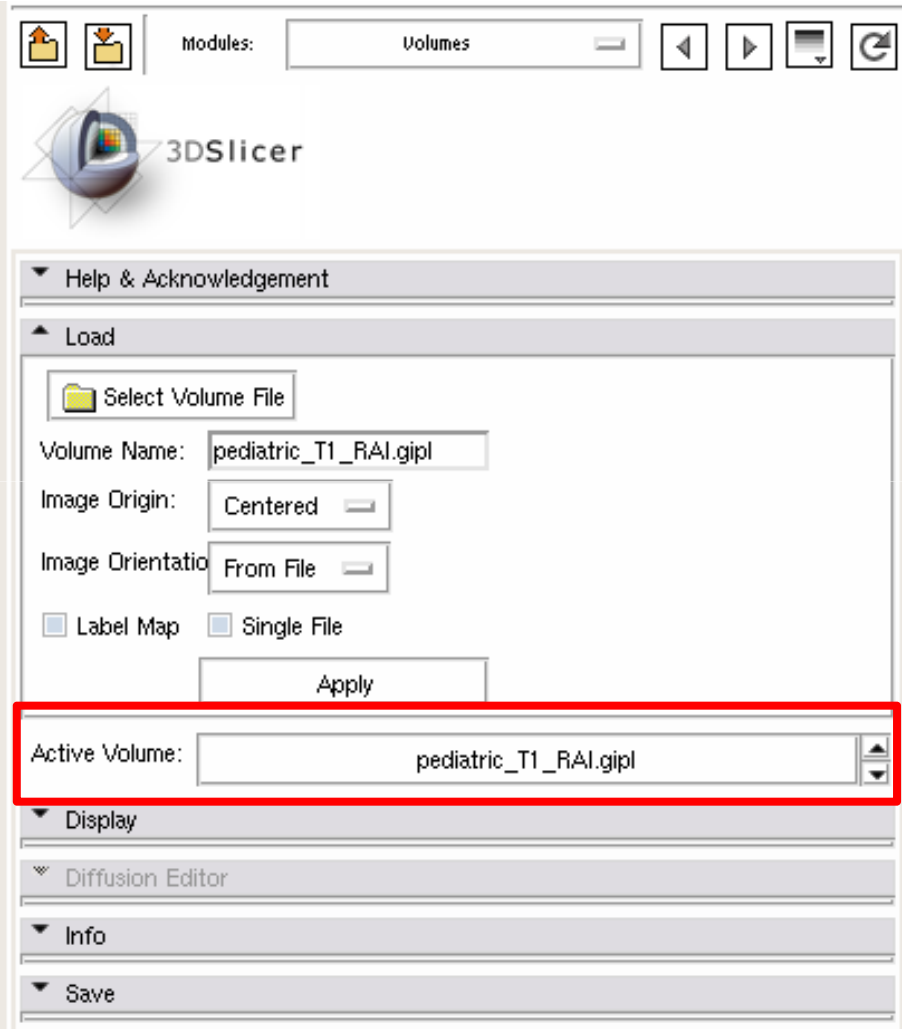


Now, select the Image Origin as **« Centered ».**

Then, check the **« Label Map »** case to load the parcellation as a label image.

And click on **« Apply »**.

Load the dataset in Slicer



The dataset is now loaded.

You can check it in the « Active Volume » widget while displaying the 4 images.

Tutorial Overview

A-Tutorial example with dataset

1- Load the dataset in Slicer

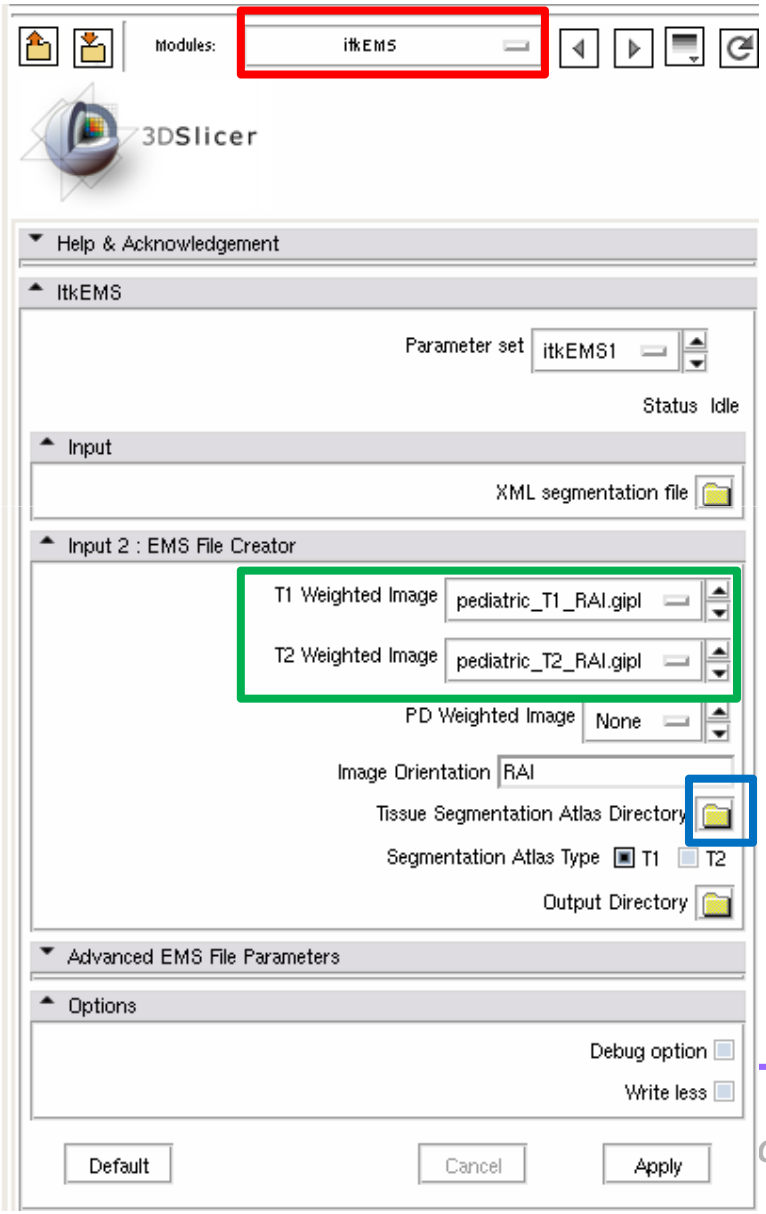
2- Tissue segmentation : itkEMS

3- Registration : SegPostProcess, RegisterImages, ResampleVolume2

4- Cortical thickness : CortThick

B-In depth tutorial

Tissue segmentation : itkEMS

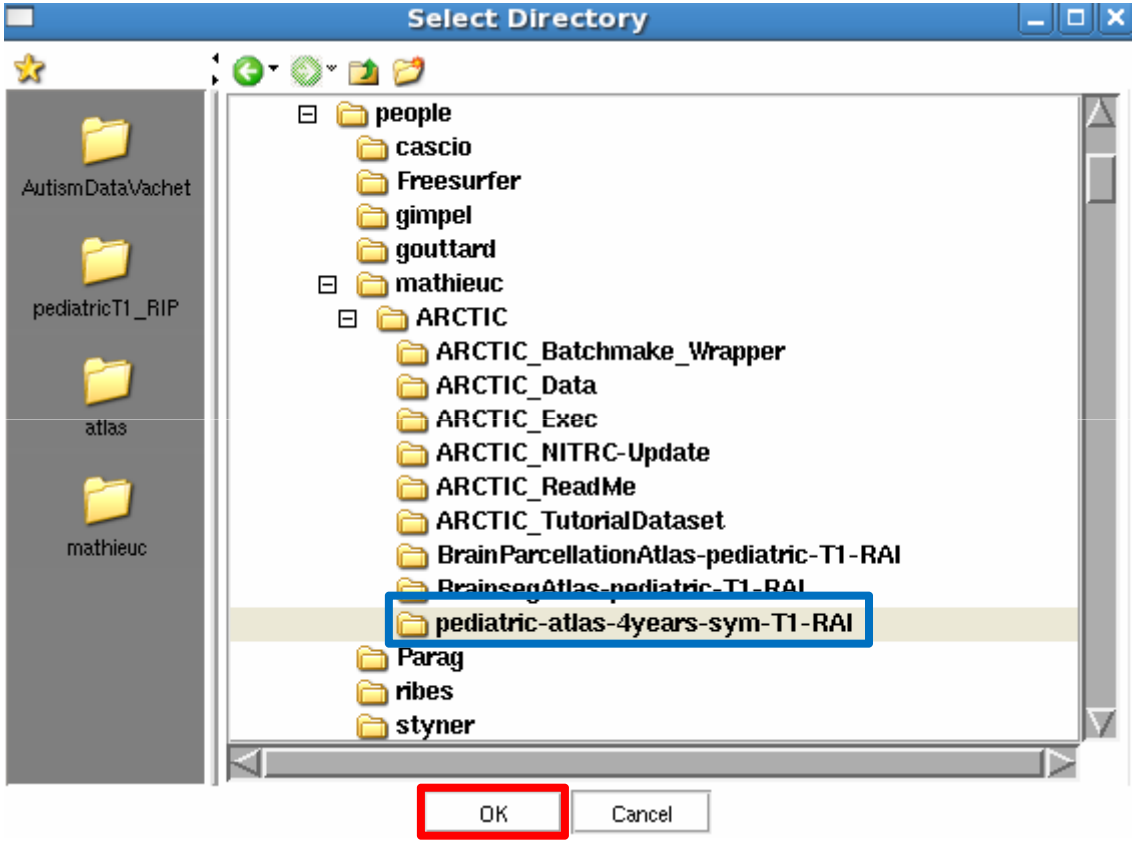


Select the **« itkEMS »** module (in All Modules).

Add the **« T1-weighted image », « T2-weighted image » and « PD-weighted image »** if available.

Click on the **« tissue segmentation atlas directory »** button.

Tissue segmentation : itkEMS

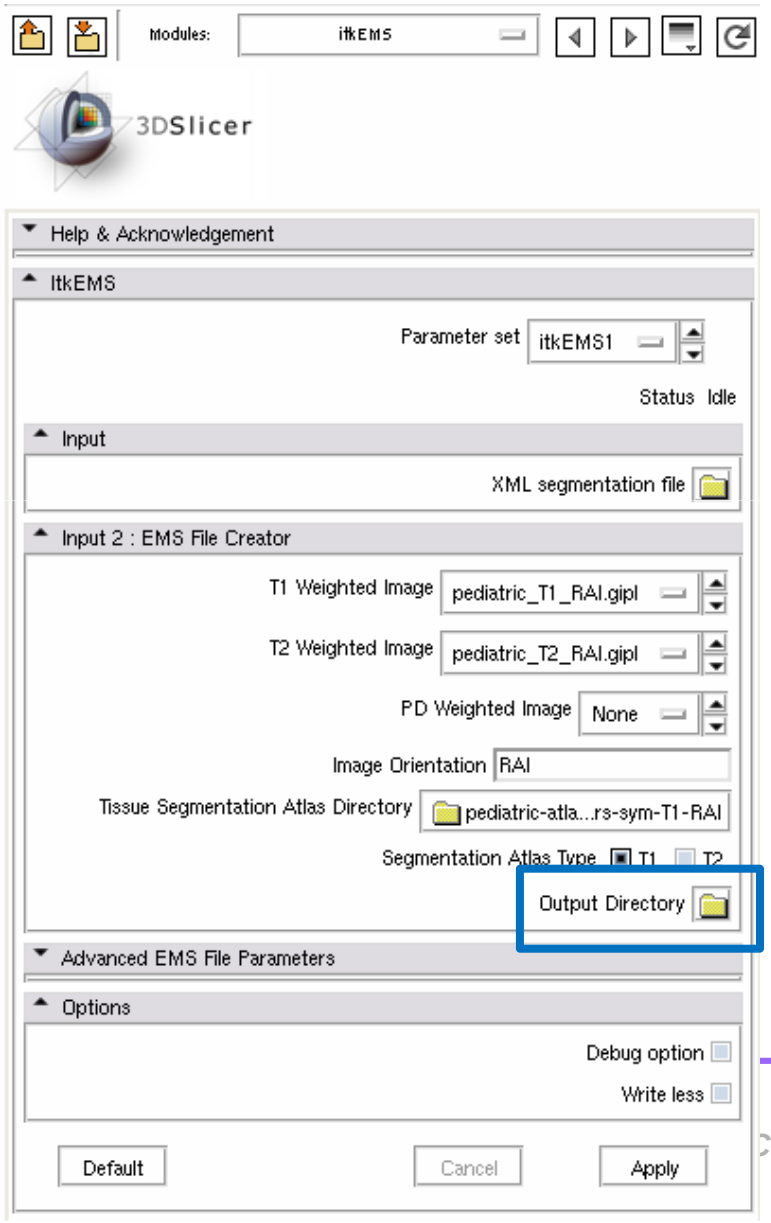


A new window is now open to select the tissue segmentation atlas.

Search and select the **« pediatric-atlas-4years-sym-T1-RAI/»** directory.

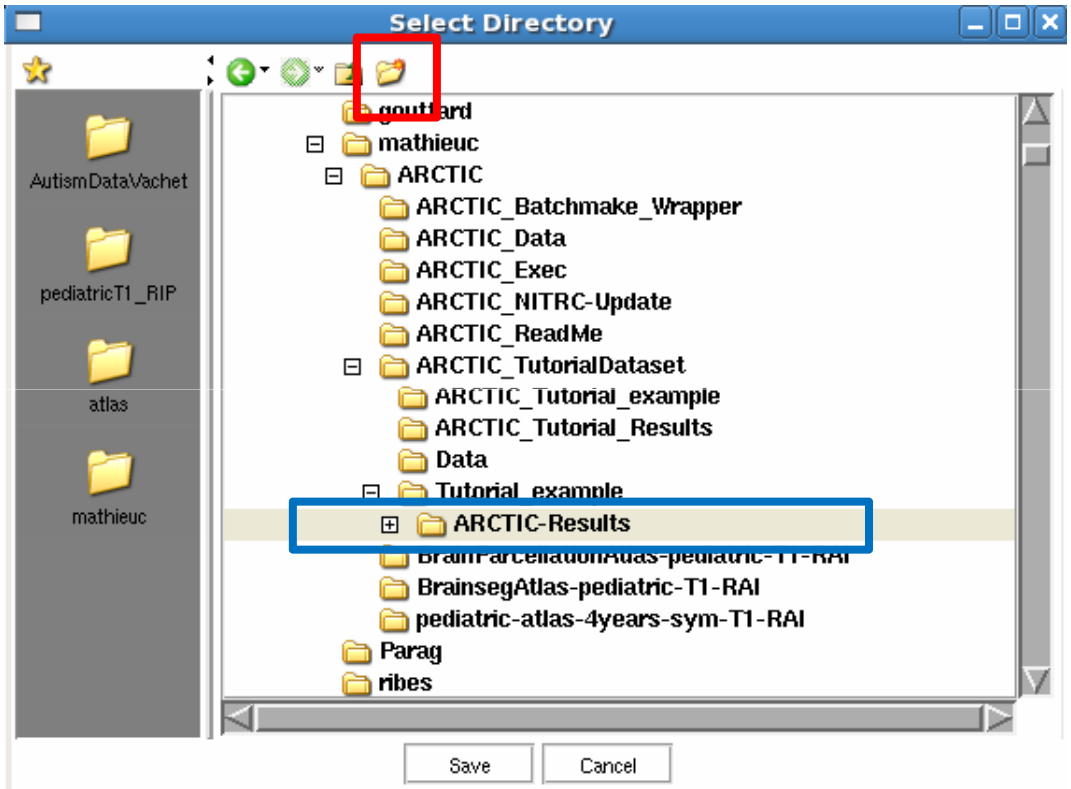
Click on the **« OK »** button to confirm.

Tissue segmentation : itkEMS



Click on the **« Output Directory »** button.

Tissue segmentation : itkEMS



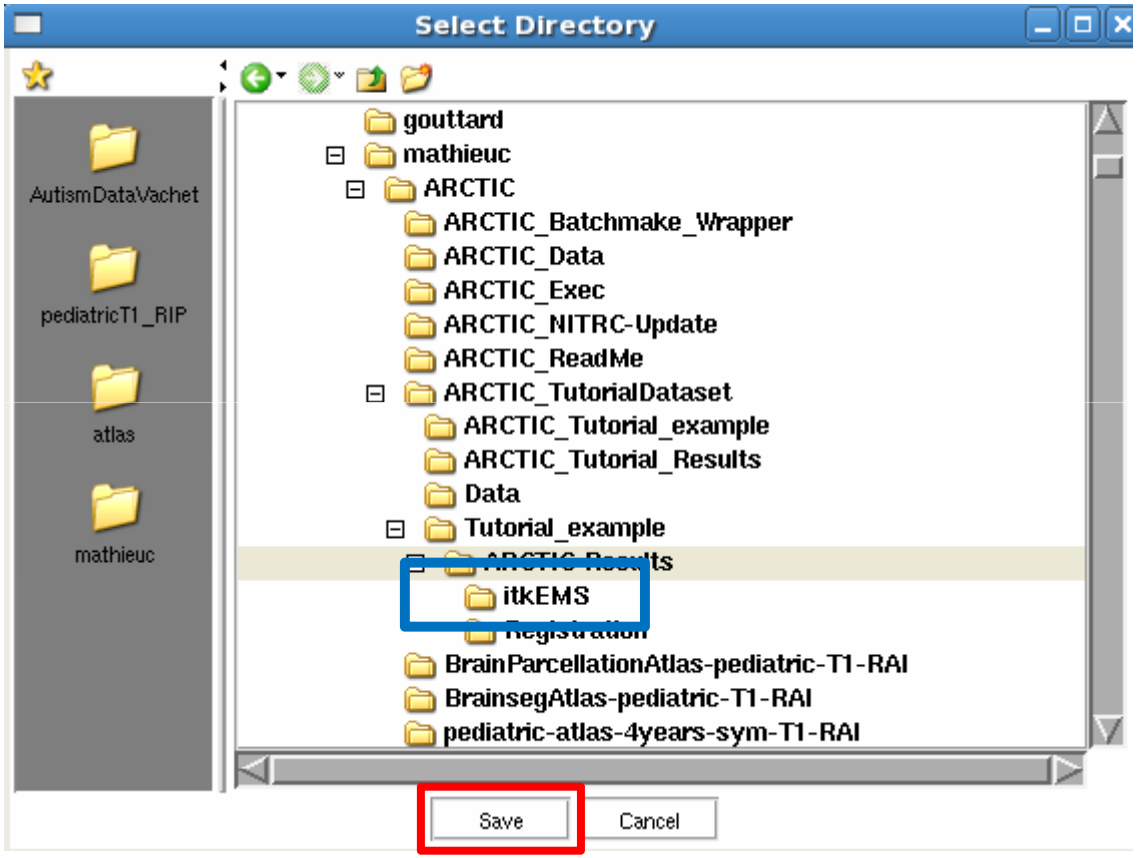
A new window is now open to select the output directory.

Select the **« ARCTIC-Results »** directory in the Tutorial example folder.

Click on the button to **« create a new directory »**. Name it « **itkEMS** ».

Tissue segmentation outputs will be saved in this new folder.

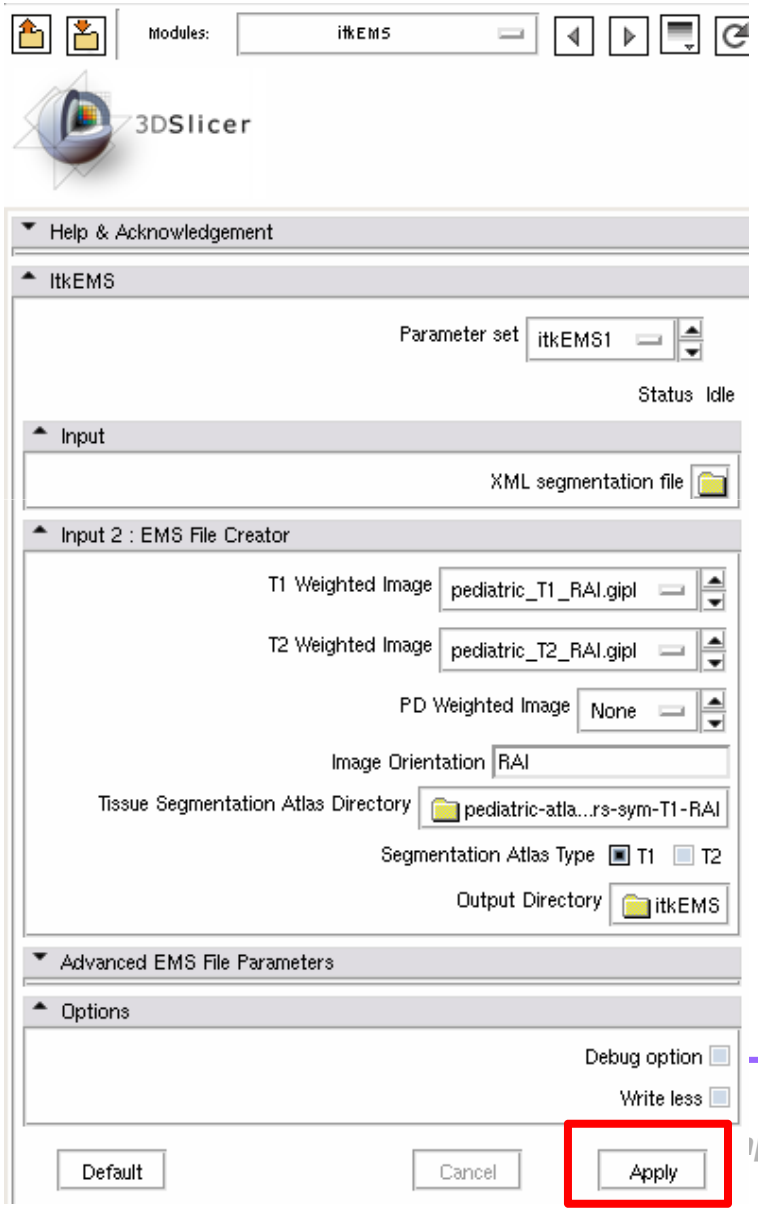
Tissue segmentation : itkEMS



Now, select **the new directory** (itkEMS).

Click on the **« Save »** button, to confirm your selection.

Tissue segmentation : itkEMS

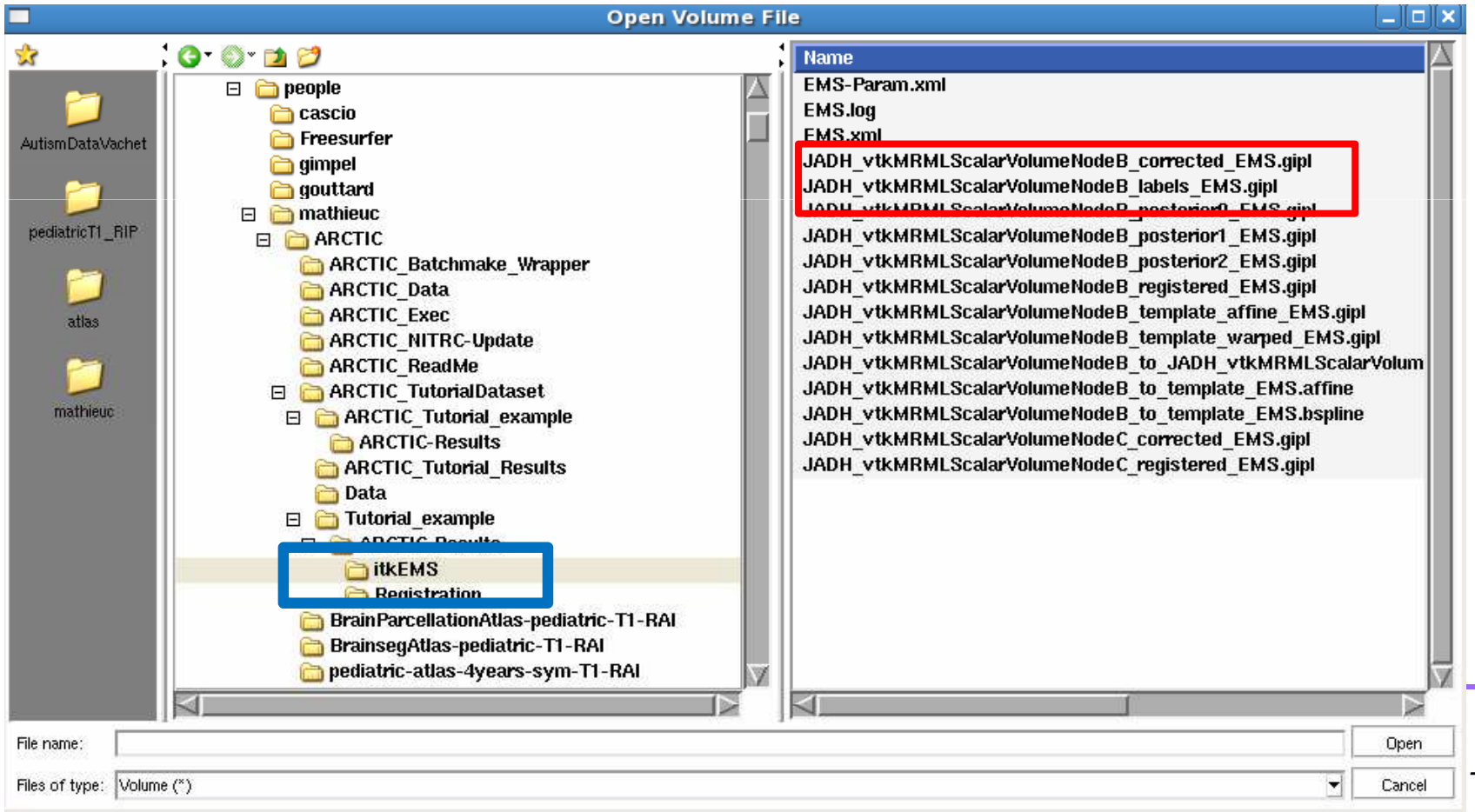


All the parameters have been set. One can use this screenshot to check if everything is set properly.

Click on the « **Apply** » button to perform a tissue segmentation.

Tissue segmentation : itkEMS

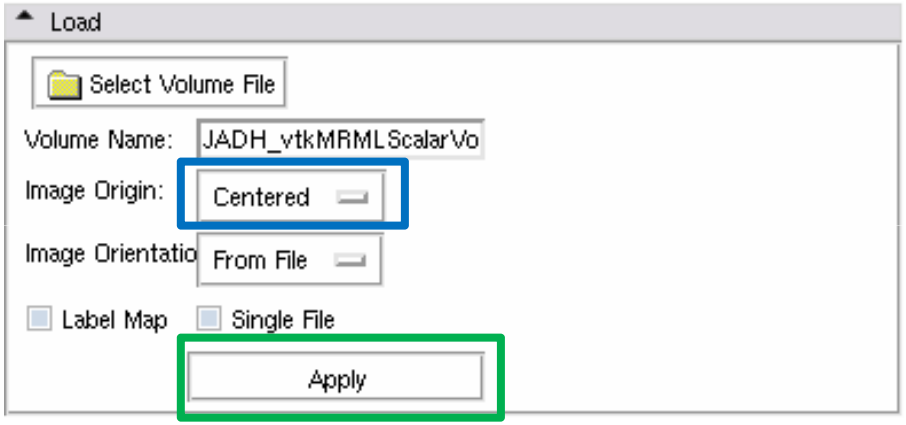
Two outputs, located in the itkEMS directory, will be used by the next step and thus need to be loaded: the tissue segmentation label image (labels_EMS) and the T1_weighted corrected image (corrected_EMS).
Load these images by selecting the **« itkEMS » directory**, and choose **the two files** one by one.



Tissue segmentation : itkEMS

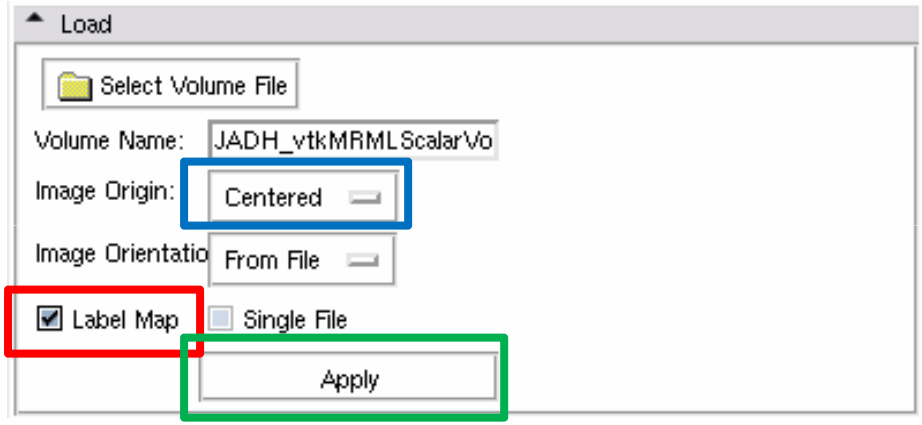
Select the following options to properly load the two files :

Corrected_EMS image



Set the image origin as **« Centered ».**
Click on the **« Apply »** button.

Labels_EMS image



Set the image origin as **« Centered ».**
Check the **« Label Map »** box.
Click on the **« Apply »** button.

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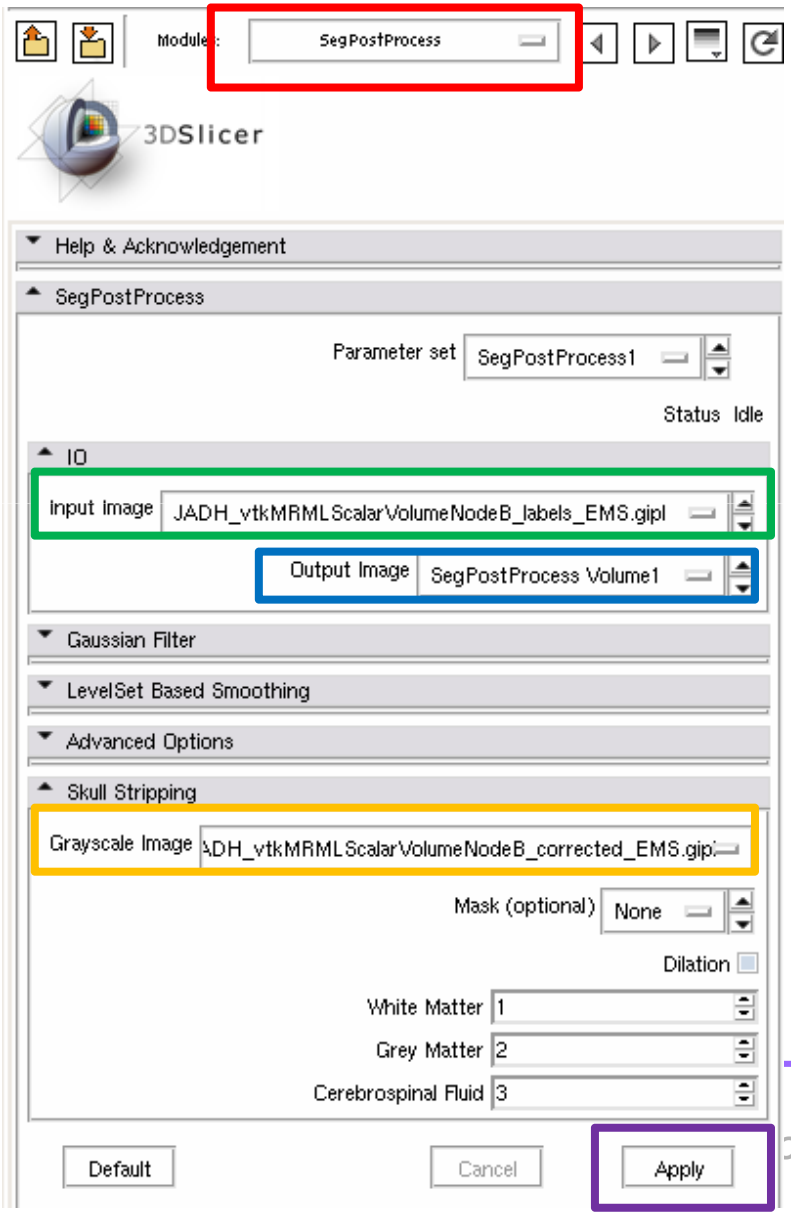
4- Cortical thickness : CortThick

B-In depth tutorial

Skull stripping : SegPostProcess



Select the « **SegPostProcess** » module (in All Modules)

Add the « **Labels_EMS** » as Input image

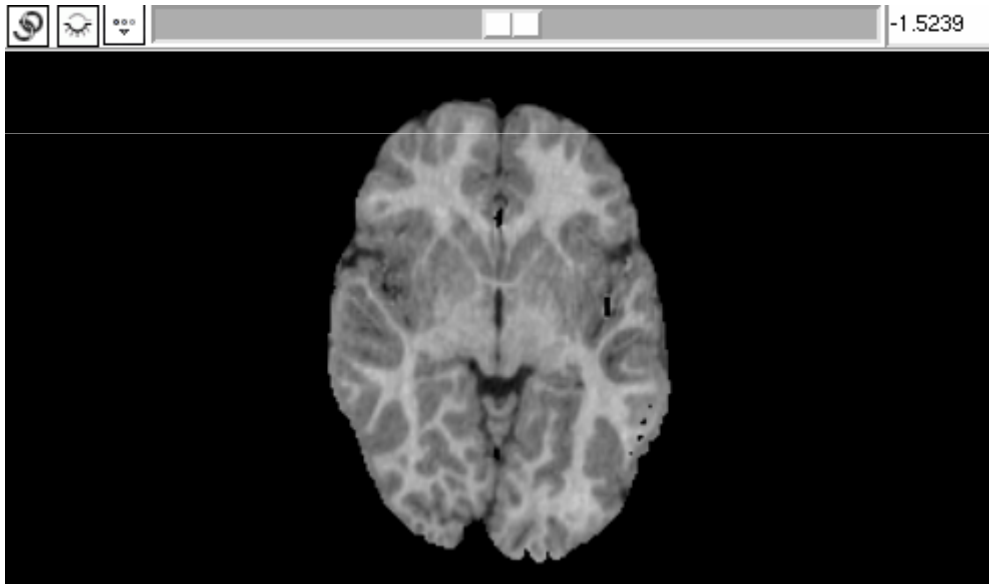
Choose « **Create a new volume** » for the output image

Add the « **Corrected_EMS** » as Greyscale image

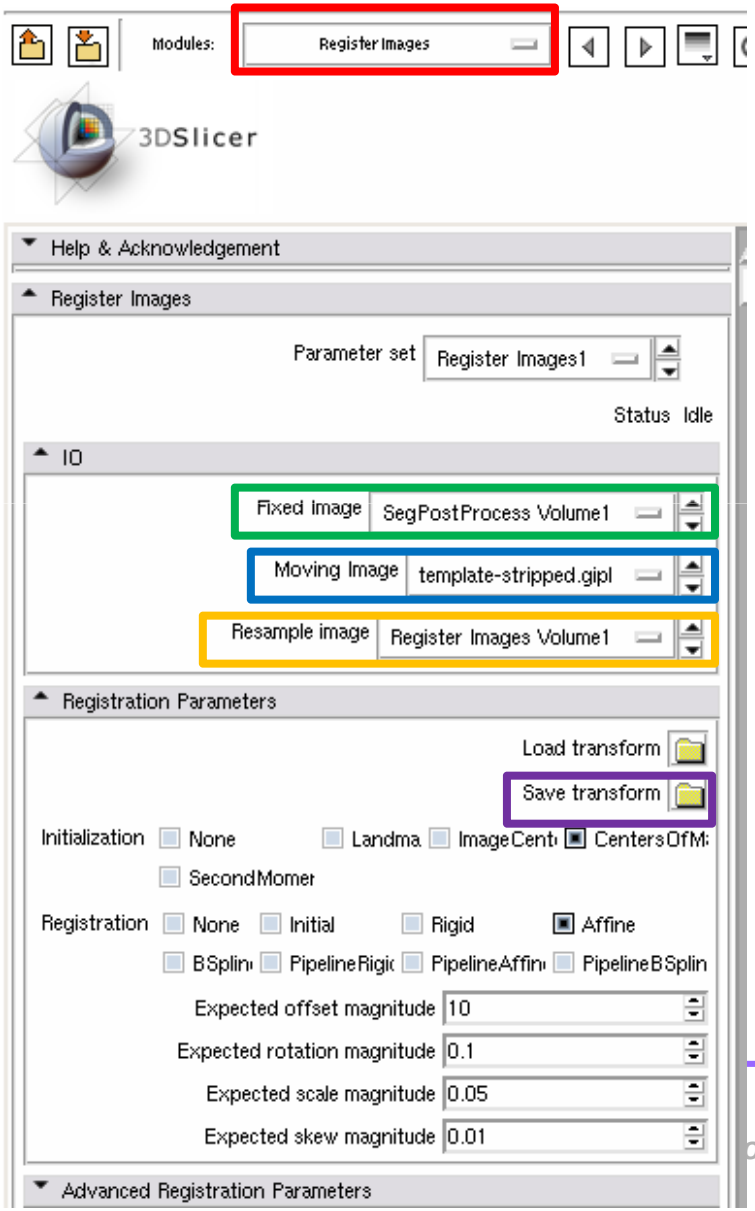
Click on the « **Apply** » button to perform a skull stripping.

Skull stripping : SegPostProcess

Now, one has the T1-weighted stripped image as an output, being named « SegPostProcess Volume 1 » in Slicer.



Registration : RegisterImages



Select the **« RegisterImages »** module (in All Modules)

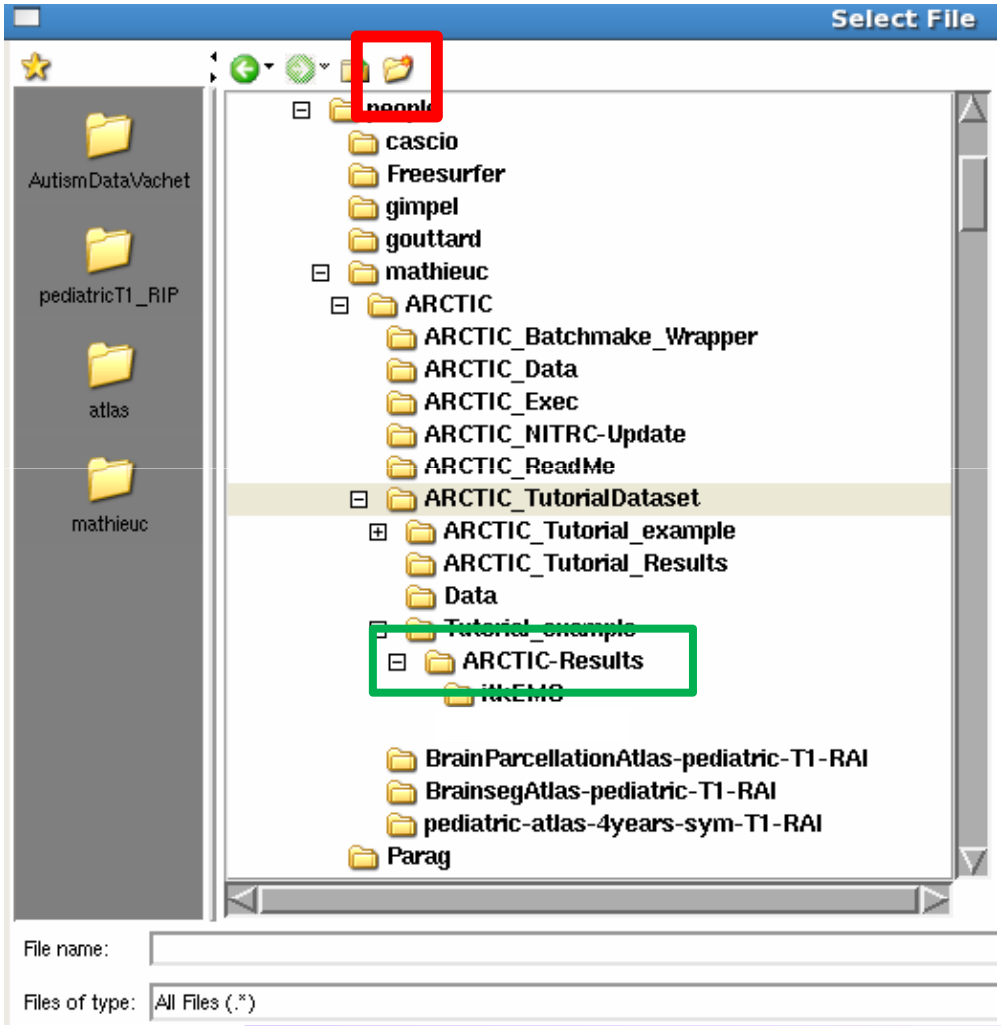
Add the **« SegPostProcess Volume 1 »** (T1-stripped image) as Fixed Image

Add the **« template-stripped.gipl »** as Moving Image

Select **« Add a new volume »** as Resample image

Click on the button **« Save Transform »**

Registration : RegisterImages

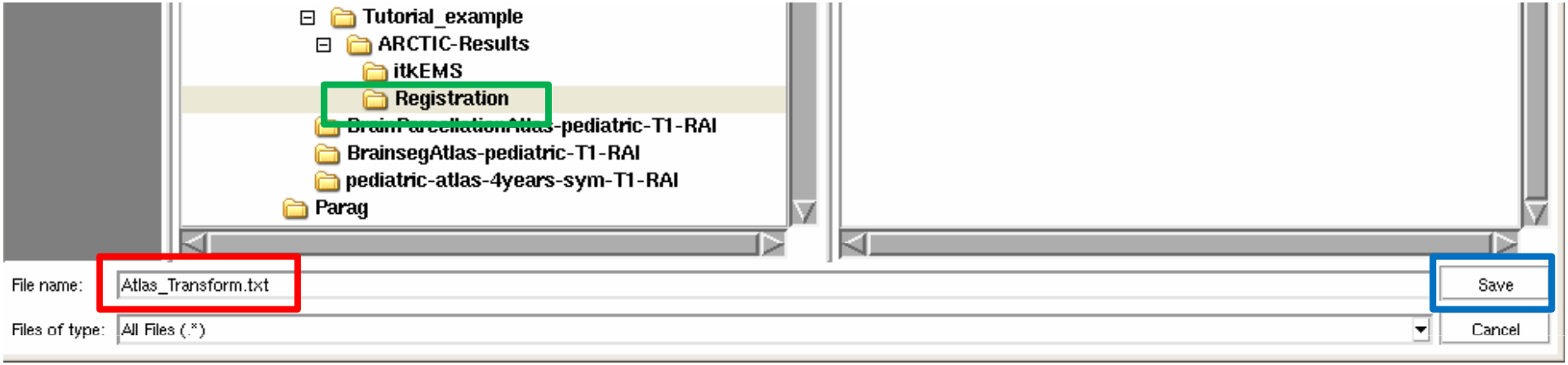


A new window is now open to save the transformation file.

Select the « **ARCTIC-Results/** » directory.

Click **here** to create a new folder and name it **« Registration ».**

Registration : RegisterImages

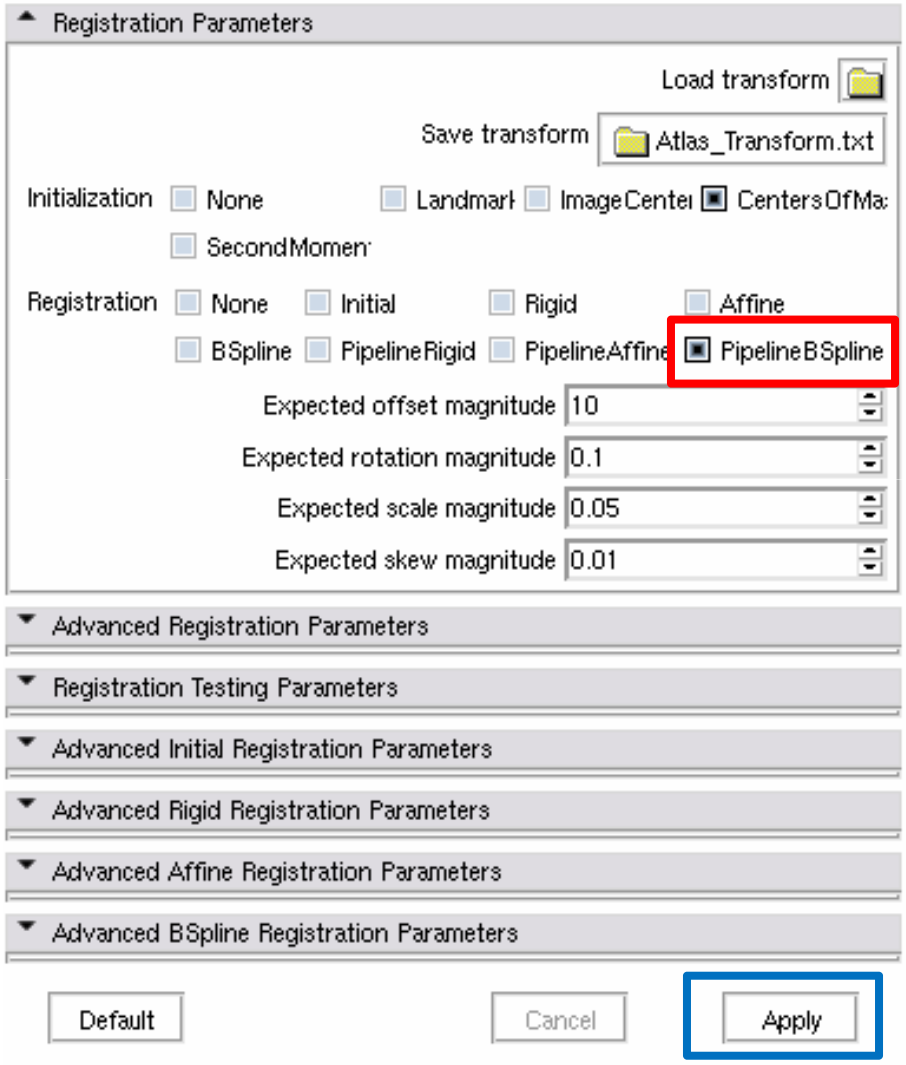


Select the **« Registration »** folder.

Call the transformation file **« Atlas_Transform.txt »**.

Click on the **« Save »** button.

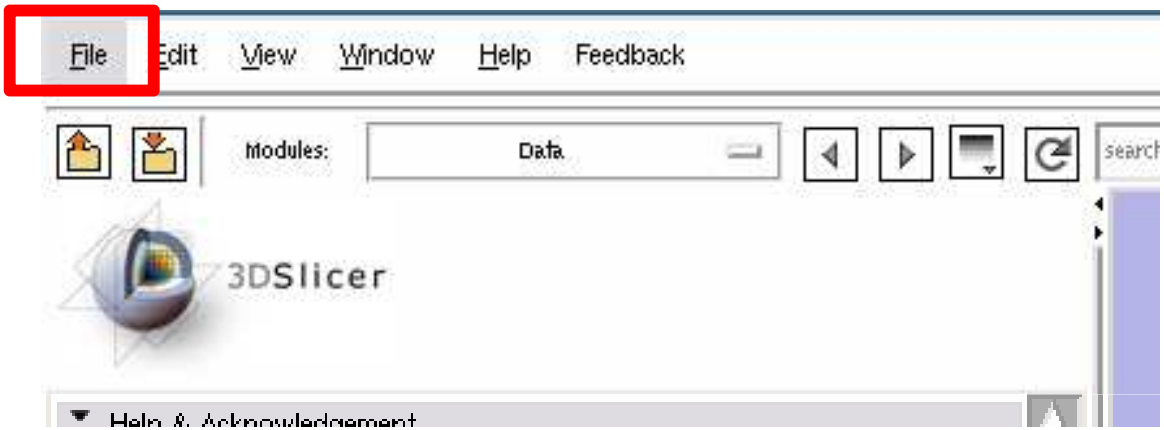
Registration : RegisterImages



In the registration parameters, check the **« PipelineBSpline »** box.

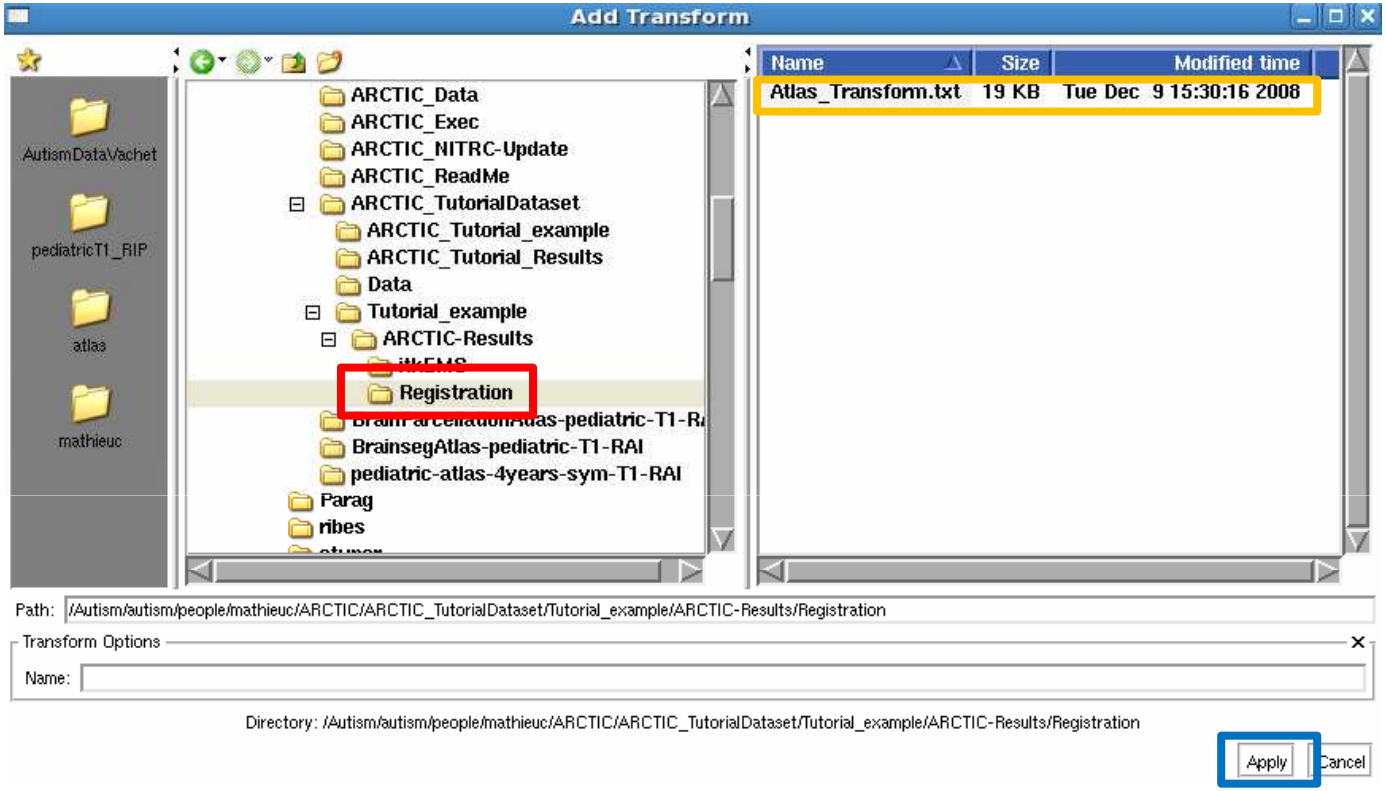
Click on the **« Apply »** button to perform the atlas to case registration.

Registration : Load the transform file



Once the registration is finished, select **« File »** and **« Add Transform… »**.

Registration : Load the transform file

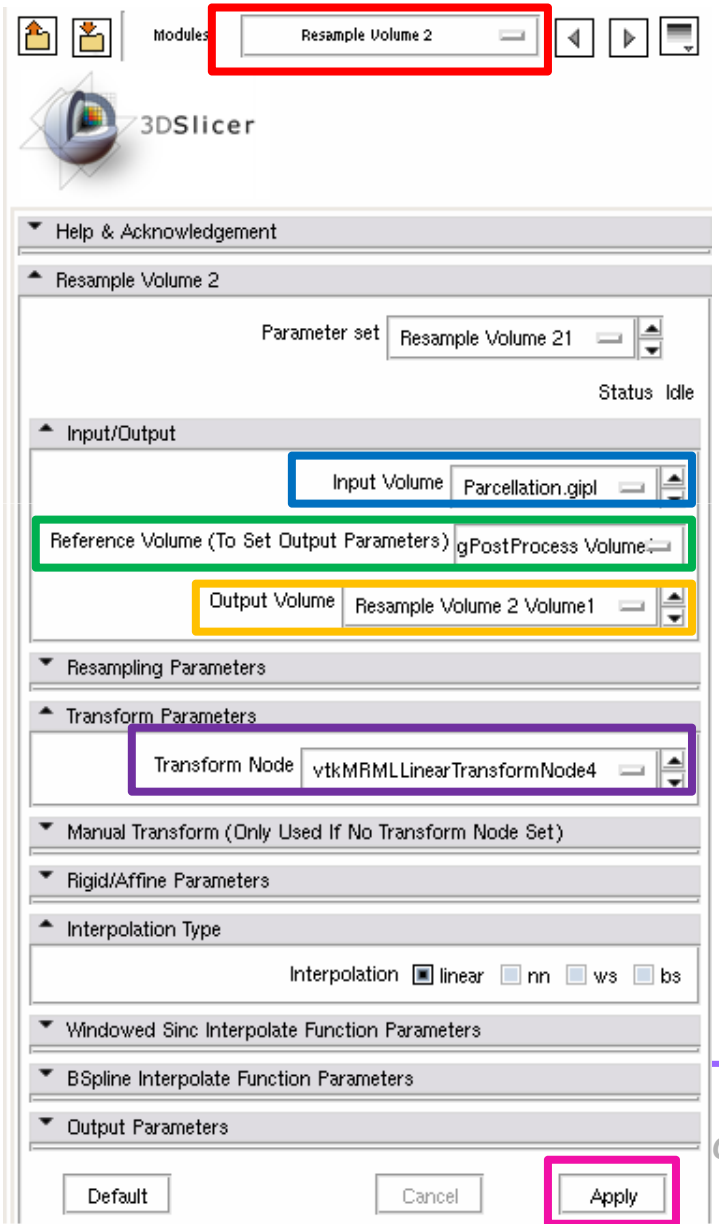


Select the **« Registration »** folder.

Select the **« Atlas_Transform »** file.

Click on the **« Apply »** button.

Registration : Resample Volume 2



Select the **« Resample Volume 2 »** module (in All Modules)

Add the **« ParcellationRAI.hdr »** as Input volume

Add the **« SegPostProcess Volume 1 »** (T1-stripped image) as Reference volume

Select **« Add a new volume »** as Resample image

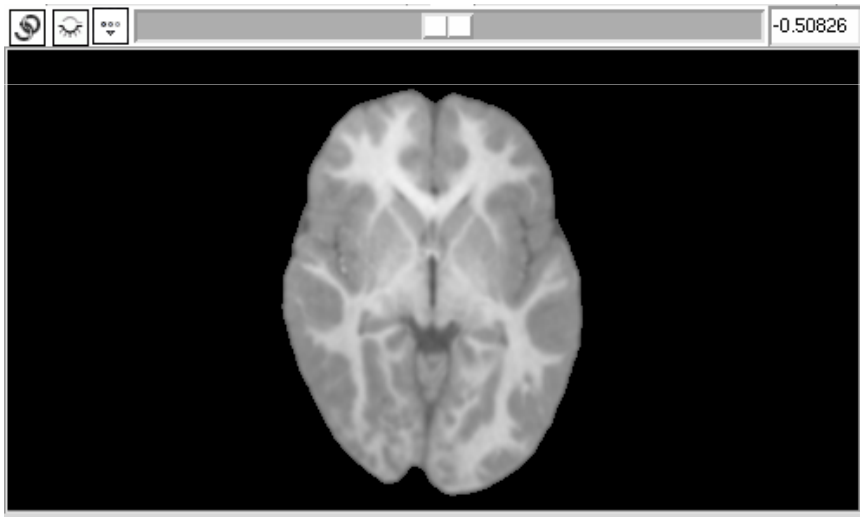
Add the transformation file **« Atlas_Transform.txt »**

Click on the **« Apply »** button to apply the transformation to the parcellation map.

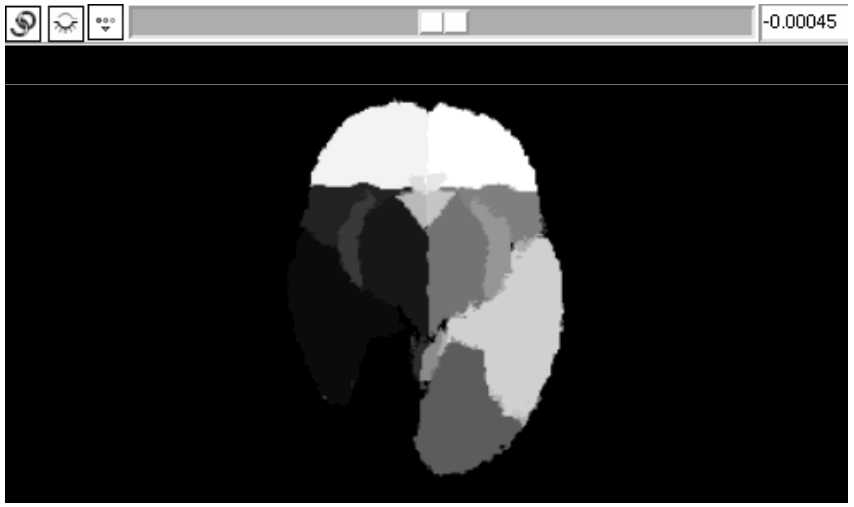
Registration

Now, one has two new images :

- the atlas that has been registered : « Register Images Volume 1 »
- the parcellation map that has been registered : « Resample Volume 2 Volume 1 »



Atlas Registered



Parcellation Registered

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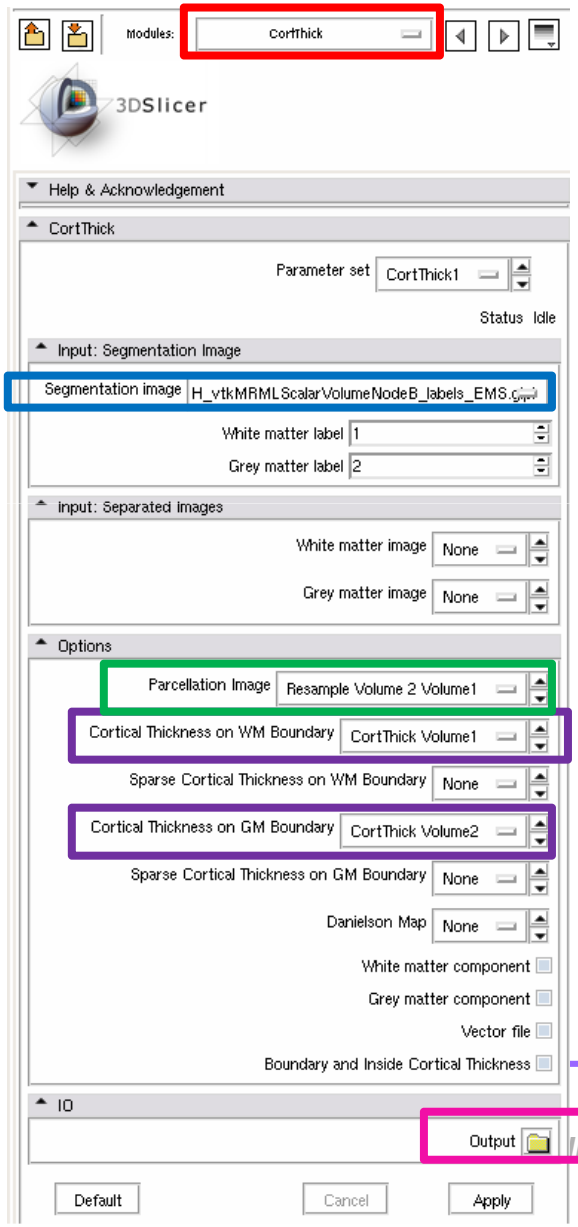
B-In depth tutorial

Cortical Thickness : CortThick



Select the « **CortThick**» module (in All Modules)

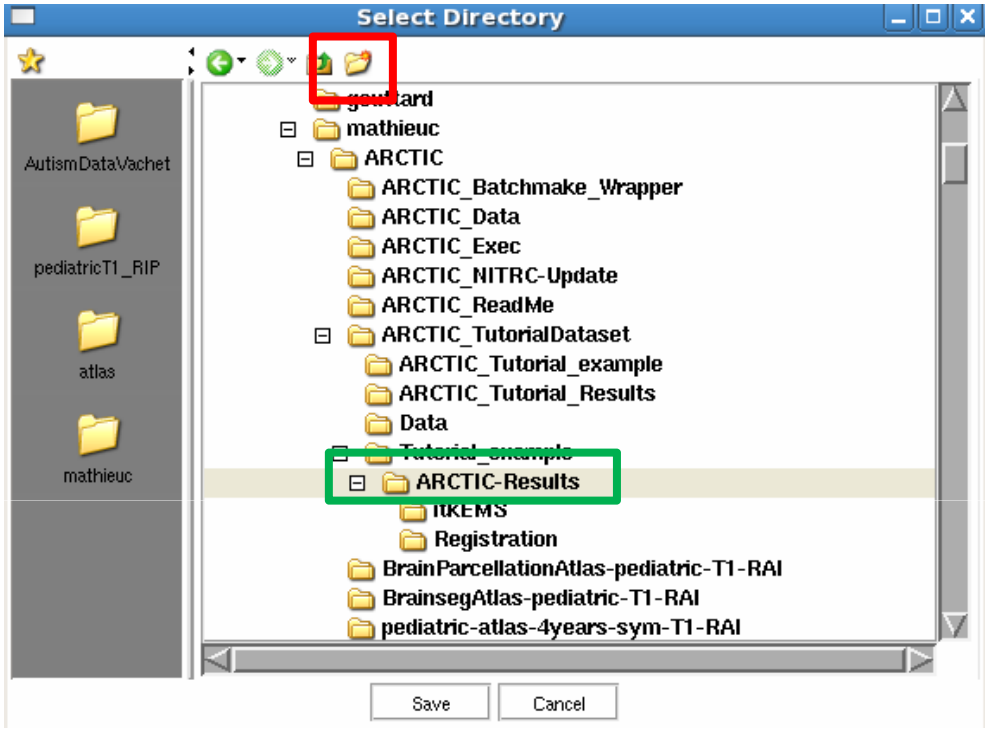
Add the « **labels_EMS.gipl** » as Segmentation image

Add the « **Resample Volume 2 Volume 1** » (T1-stripped image) as Parcellation image

Select « **Add a new volume** » to display the cortical thickness on WM and GM boundaries

Click on the « **Output** » button to select the output directory

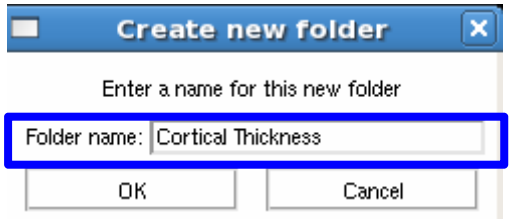
Cortical Thickness : CortThick



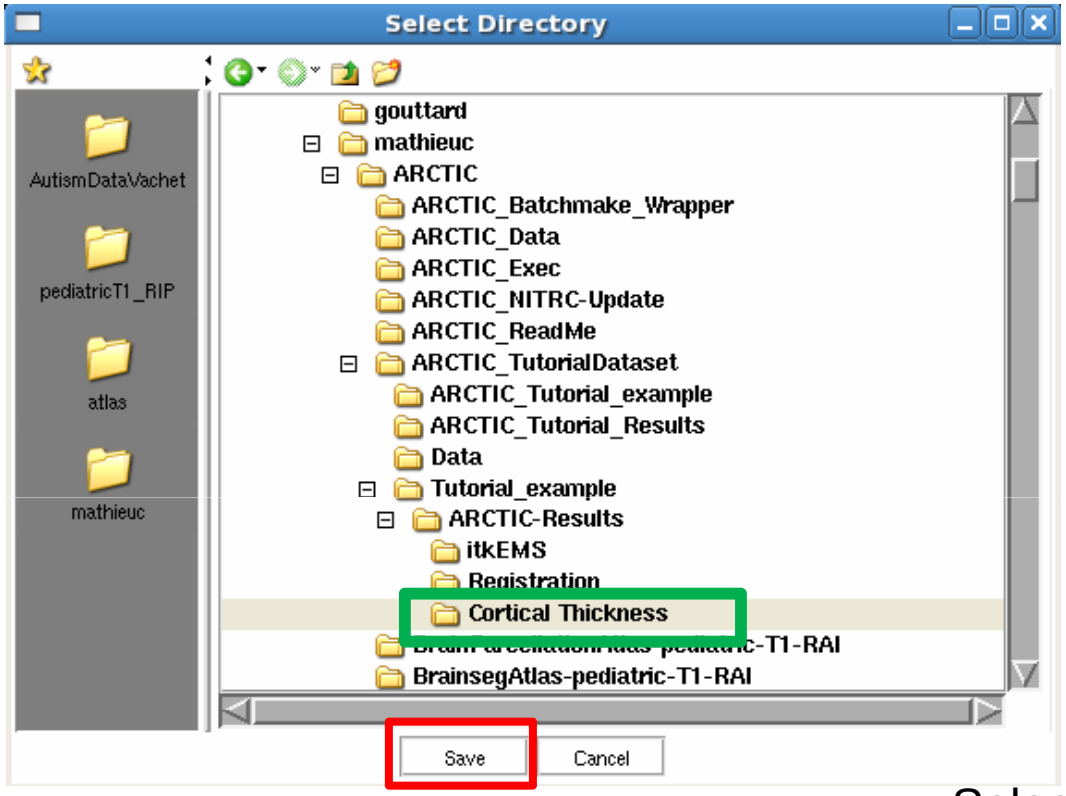
Select the « **ARCTIC-Results**» folder

Click on the « **Create a new folder** » button to create a new one

Call it « **Cortical Thickness** »



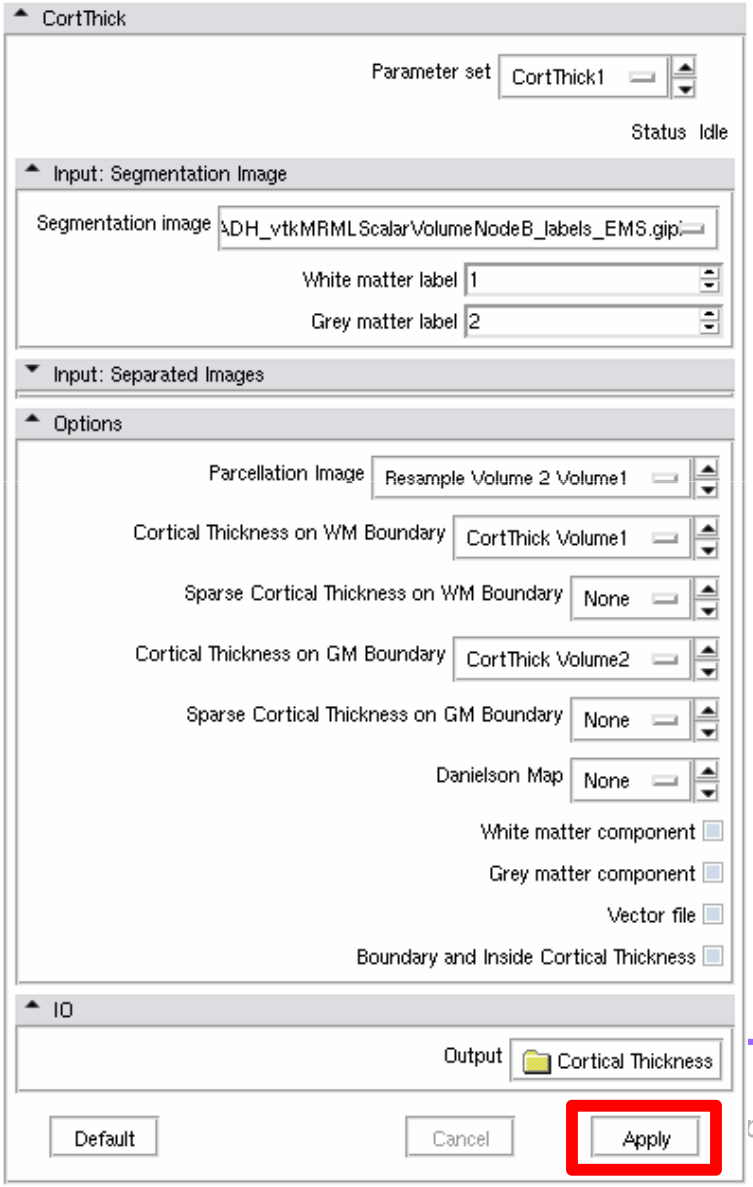
Cortical Thickness : CortThick



Select the **« Cortical Thickness»** folder

Click on the **« Save »** button to save the output directory

Cortical Thickness : CortThick



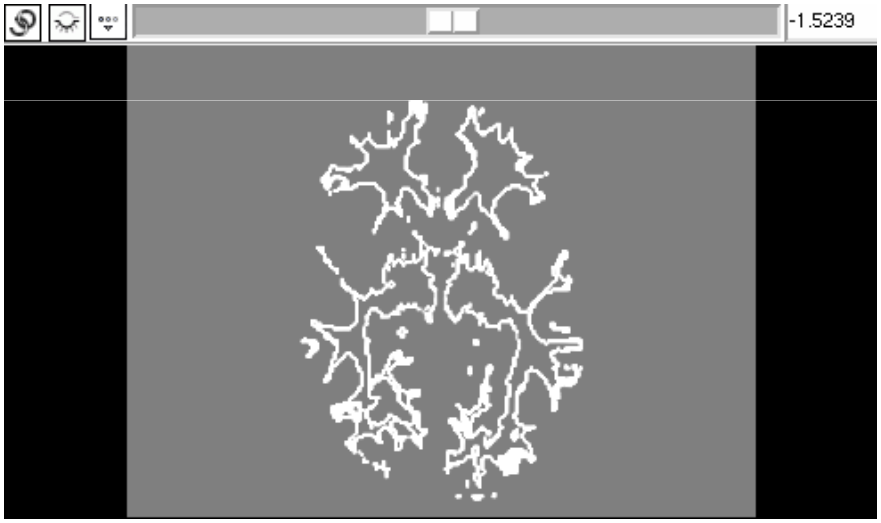
Click on the **« Apply »** button to perform a cortical thickness analysis.

Cortical thickness results will be stored in the « Cortical Thickness » directory.
Those are « .csv » files which can be opened using a spreadsheet's software.

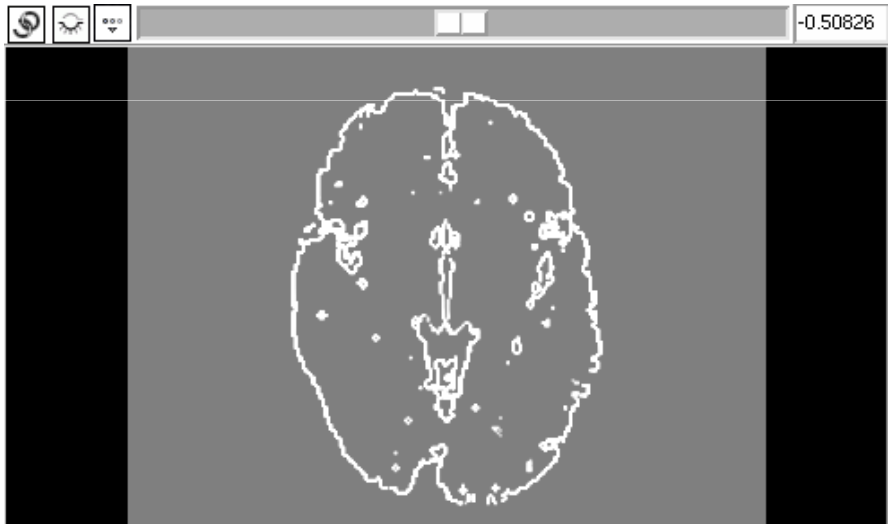
Cortical Thickness : CortThick

Now, one has two new images :

- Cortical thickness on white matter boundary: « CortThickVolume 1 »
- Cortical thickness on gray matter boundary: « CortThickVolume 2 »



Cortical thickness on WM boundary



Cortical thickness on GM boundary

Tutorial Overview

A-Tutorial example with dataset

B-In depth tutorial

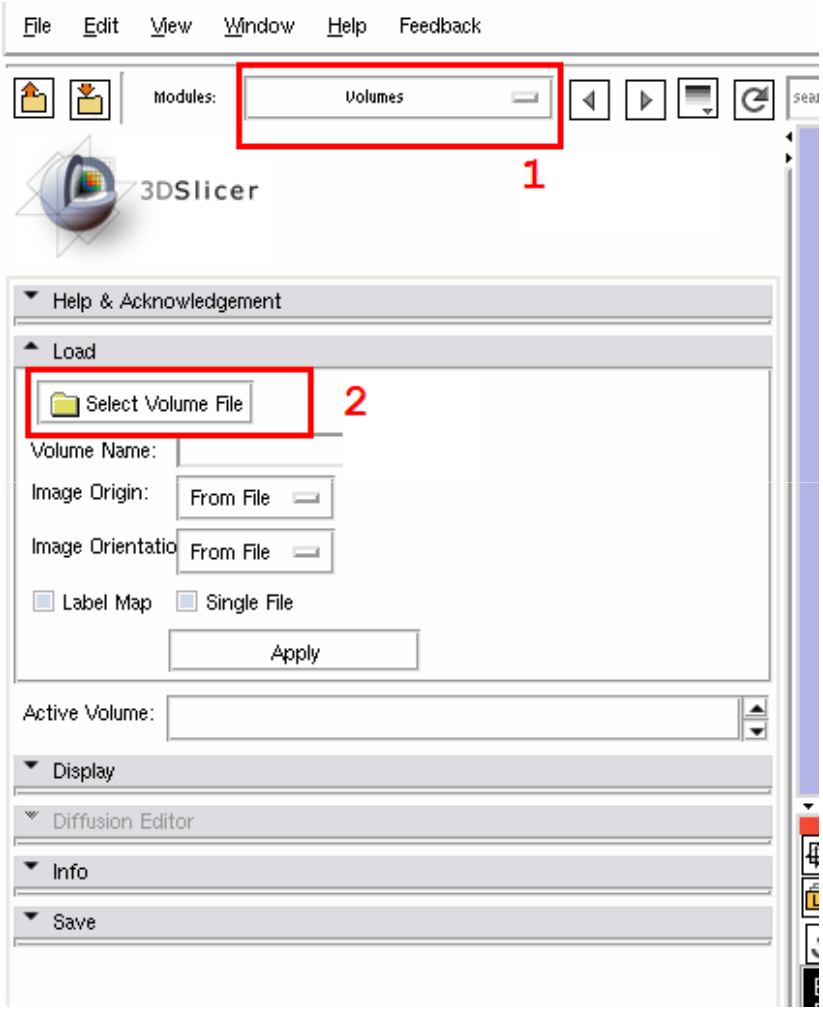
1- Load images

2- Use itkEMS for tissue segmentation

3- Use SegPostProcess for skull stripping

4- Use CortThick for thickness assessment

Load input images

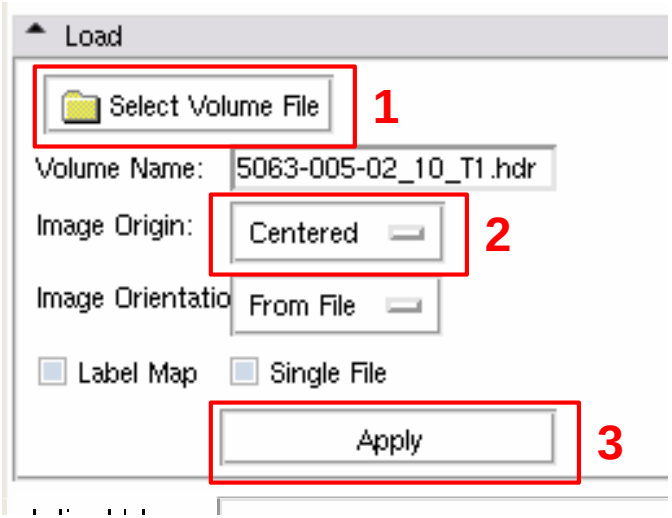


OVERVIEW

1- Select the « Volumes » module

2- Load all the files you need for the analysis (cf. Slide « Utilisation : What you need … »)

Load input images



How to load grayscale images (case and atlas)?

1- Select the image in the browser

2- Set the image origin as « centered »

3- Click on « Apply » to load

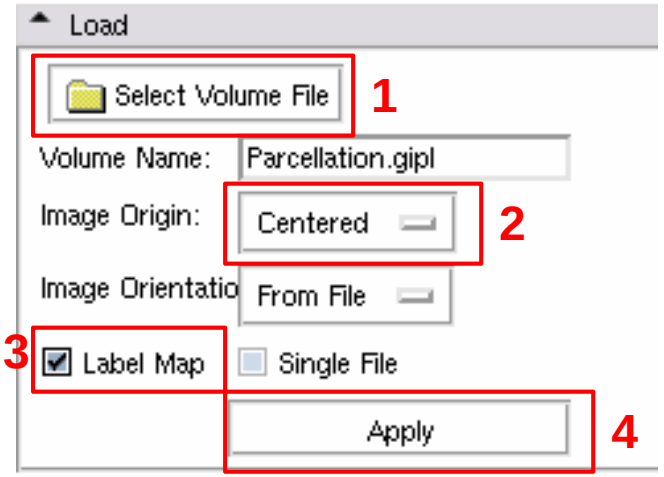
How to load parcellation and label images?

1- Select the image in the browser

2- Set the image origin as « centered »

3- Check the « label map » button

4- Click on « Apply » to load



Tutorial Overview

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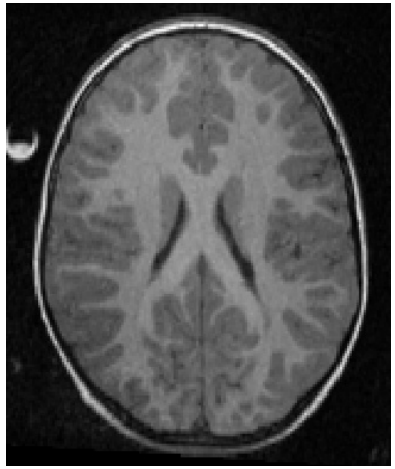
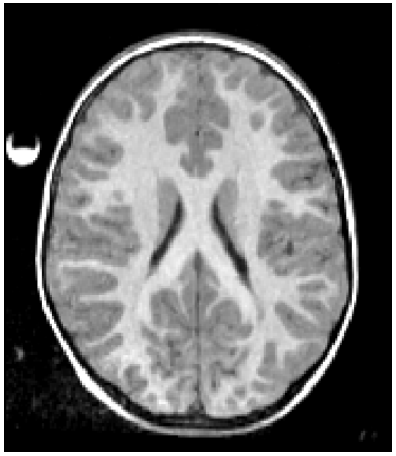
Tissue segmentation : itkEMS

Overview

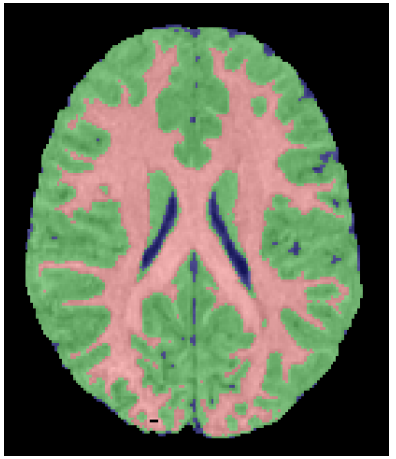
Probabilistic atlas-based automatic tissue segmentation via an Expectation-Maximization scheme. ItkEMS also performs an intensity inhomogeneity correction of the input image that removes gradual variations in the image intensities mainly due to RF coil imperfection



Input_T1-Image.gipl



Image_corrected_EMS.gipl



Image_labels_EMS.gipl

Tissue segmentation : itkEMS

itkEMS needs an XML file as an input. The Slicer3 module has been updated in order to create such a file.
One has thus 2 choices :
- Load the XML file to execute the module.
- Create the XML file within Slicer3 and execute the module.

Tissue segmentation : itkEMS

Input images

What you need…

Execute with an existing XML file

XML file

Create the XML file and execute

T1-weighted image

Tissue segmentation atlas directory

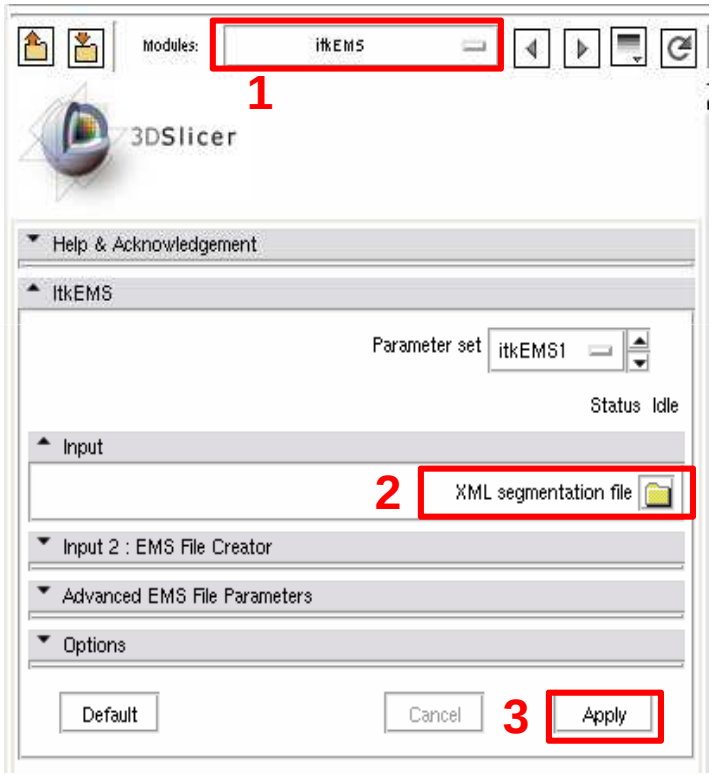
Optional

T2-weighted image

PD-weighted image

Tissue segmentation : itkEMS

Execution with an existing XML file



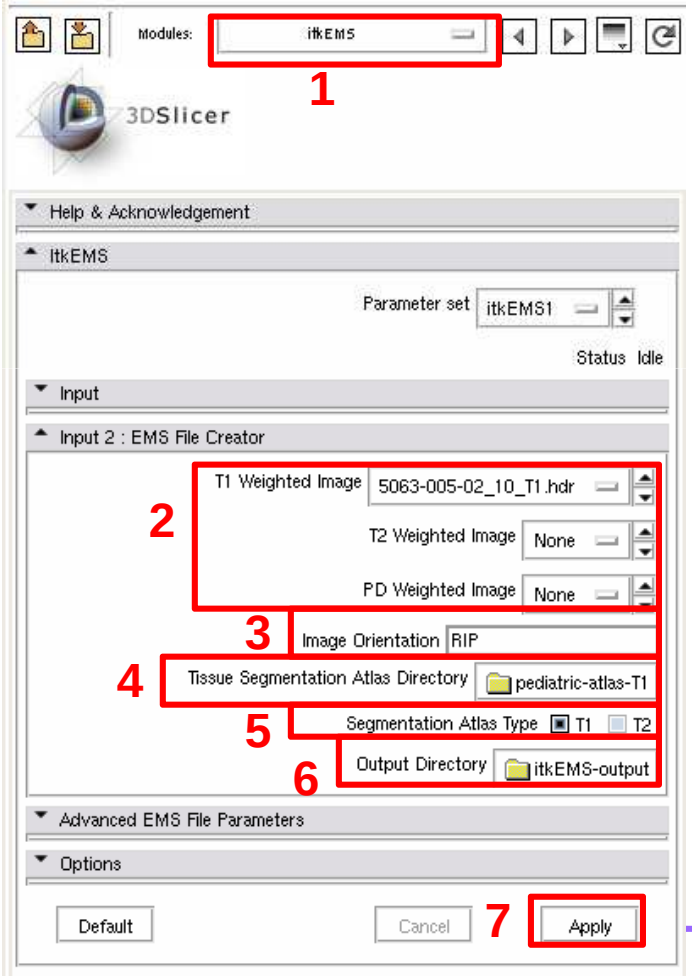
1- Select the « itkEMS » module (in All Modules)

2- Add the XML with the browser

3- Click on the « Apply » button to process the data

Tissue segmentation : itkEMS

XML file creation and execution



1- Select the « itkEMS » module (in All Modules)

2- Add the available images for the segmentation (the set of three isn't needed)

3- Check that the atlas has the same orientation than the input images

4- Set the Tissue Segmentation Atlas Directory for the tissue segmentation

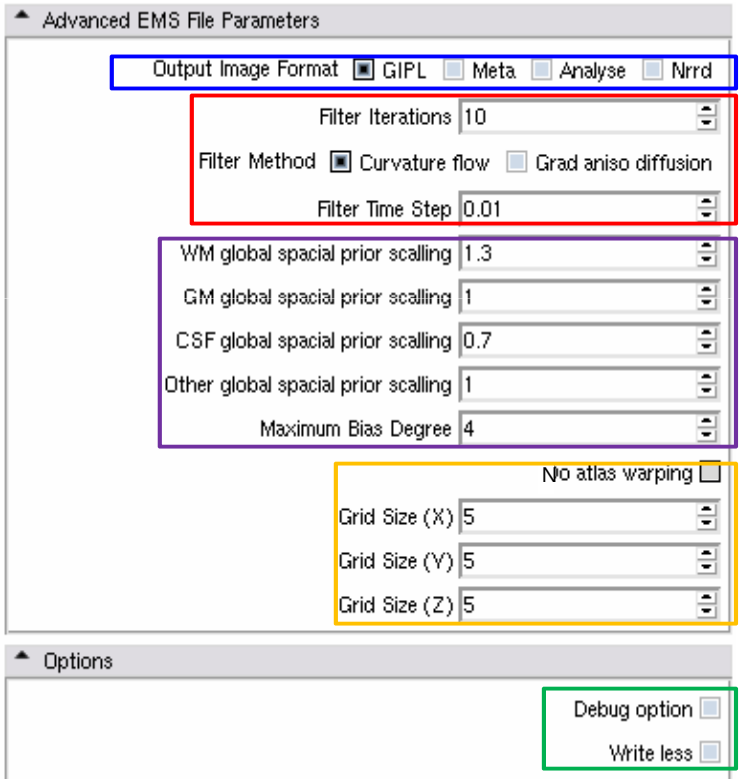
5- Check the tissue segmentation atlas type (T1-weighted or T2-weighted image)

6- Set the output directory

7- Click on the « Apply » button to process the data

Tissue segmentation : itkEMS

Advanced options (these will only need to be adjusted rarely)



Tissue segmentation parameters

-- Choose the format of the output images

-- Filter options: specifies smoothing parameters prior to segmentation

-- Priors weighting the tissue classes in the segmentation

-- Warping options for atlas: b-spline registration by default with its grid control points

-- if button checked, an affine registration is performed instead

Execution options

-- Debug option : Display debug messages during process

-- Write less : Does not write filtered and corrected images

Tissue segmentation : itkEMS

Output images

What you will find in the output directory…

Output directory/

Image_labels_EMS.gipl

if ‘write less’ option is not activated

Image_corrected_EMS.gipl
Image_posterior0_EMS.gipl
Image_posterior1_EMS.gipl
Image_posterior2_EMS.gipl

Tissue segmentation : itkEMS

Using the command line

If XML input file available :

brainsegCLP --XMLFile EMS-Param.xml

If the XML file needs to be created :

brainsegCLP --T1 T1_Image.gipl (--T2 T2_Image.gipl --pd PD_Image.gipl) --orientation ImagesAtlasOrientation --segAtlasDir TissueSegmentationAtlasDirectory/ --atlasType atlasType --outputDir outputDirectory/

with « atlasType » format : T1 or T2 (default : T1)
« orientation » format like RIP, RAI, … (default : RAI)

Tissue segmentation : itkEMS

Using the command line

Options

--help : Display help menu

Tissue segmentation parameters

--debug : To display debug messages
--writeless : To not write posteriors, filtered and bias corrected images

Execution options

--AtlasWarpingOff : To perform an atlas to subject affine registration instead of the warping
--grideSizeX (or Y,Z) <int> (default : 5) : X (Y,Z)-direction grid size for atlas warping
--maxBiasDegree <int> (default : 4): To set the maximum bias degree
--WMPrior <float> (default : 1,3) To set the white matter global spatial prior scaling
--GMPrior <float> (default : 1) To set the grey matter global spatial prior scaling
--CSFPrior <float> (default : 1,3) To set the cerebrospinal fluid global spatial prior scaling
--OtherPrior <float> (default : 1,3) To set the other matter global spatial prior scaling
--filterIteration <int> (default : 10): To set the number of filter iterations
--filterTimeStep <float> (default : 0,01): To set the filter time step
--filterMethod <Curvature flow | Grad aniso diffusion> (default : Curvature flow)

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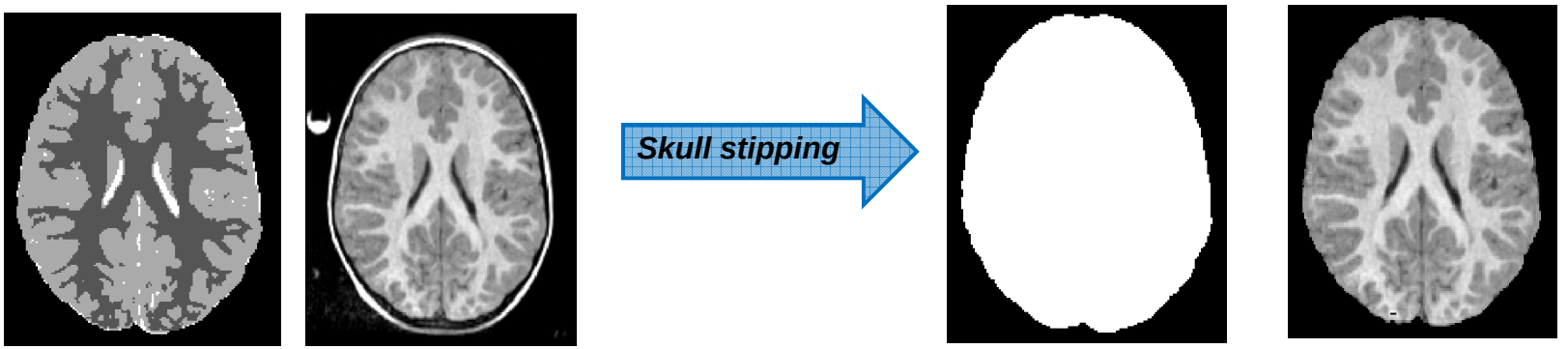
Segmentation post-processing : SegPostProcess

Overview

Using a tissue segmentation label image as an input, this module can perform a skull stripping.



Input
Label_Image.gipl

Input
Raw_Image.gipl (here T1)

Optional Output
Mask_Image.gipl

Output
T1_stripped_Image.gipl

Segmentation post-processing : SegPostProcess

Input images

What you need…

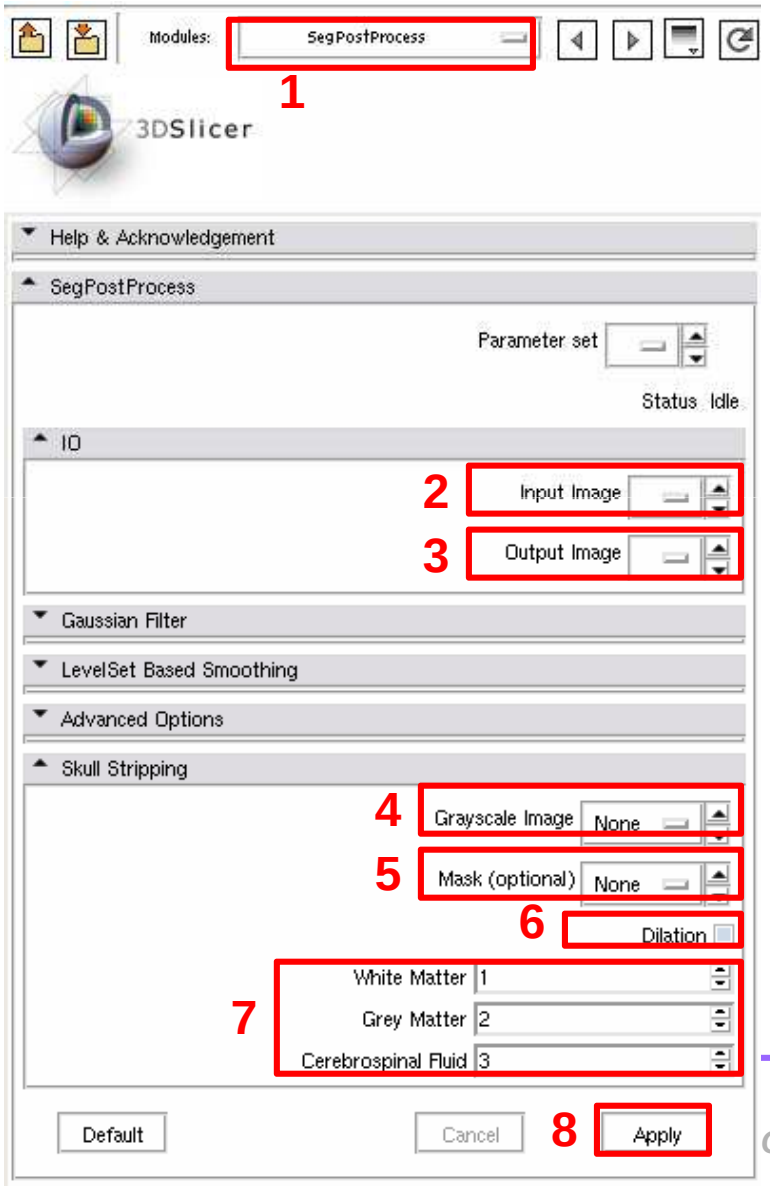
Filling

Tissue segmentation label image

Skull stripping

Tissue segmentation label image
MRI grayscale image

Segmentation post processing : SegPostProcess



Skull stripping

1- Select the « SegPostProcess » module (in All Modules)

2- Add the tissue segmentation label image

3- Set output image to be displayed in Slicer (« Create a new volume » instead of « None »)

4- Add the raw image to be stripped

5- If you want to display the mask used for the skull stripping, set « Create a new volume » instead of « None »

6- Check to apply a dilation of the mask (necessary if the tissue segmentation has a low quality)

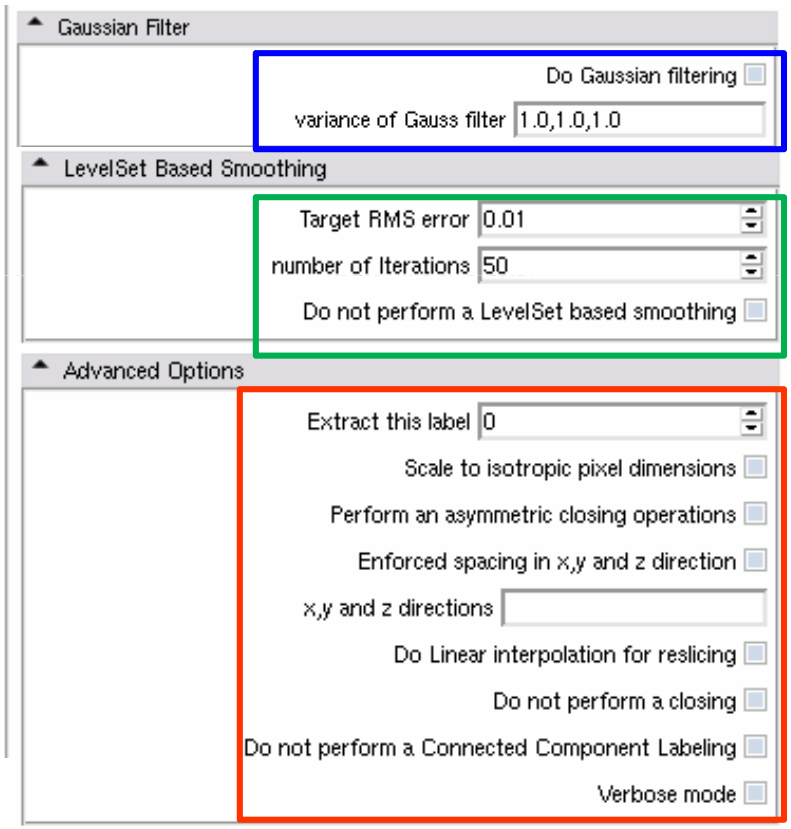
7- Set the related tissue labels

8- Click on the « Apply » button to process the data

Segmentation post processing : SegPostProcess

Advanced options

(these options should not be changed for normal processing)



Gaussian Filter

-- Check to apply a gaussian filtering

-- If checked, set the variance of the gaussian filter in all 3 dimensions, either as a single value or a set of 3 (comma separated)

LevelSet Based Smoothing

-- Uncheck not to apply a LevelSet based smoothing

-- Set the target RMS error for LevelSet smoothing

-- Set the number of iterations for the LevelSet smoothing

Advanced Options

-- Choose the label to be extracted before processing

-- Check/Uncheck buttons one wants to activate/disable

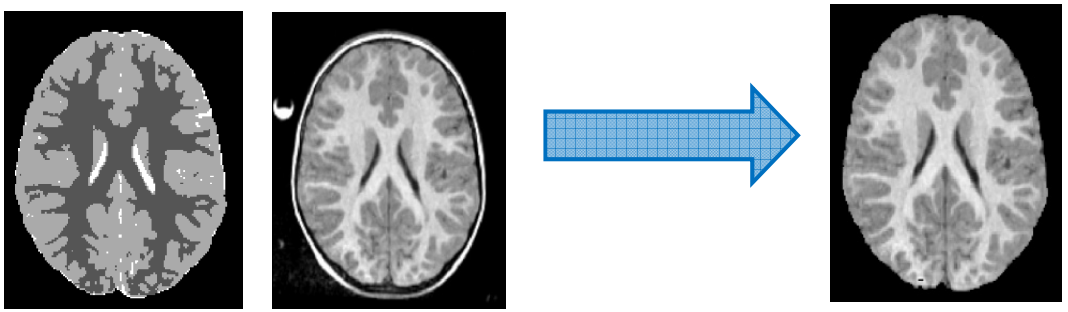
-- Set enforced spacing in x,y and z directions before any processing (comma separated values)

Segmentation post processing : SegPostProcess

Using the command line

Skull stripping:

```
SegPostProcessCLP  Label_Image.gipl  OutputImage.gipl  --skullstripping
                   Input_Image.gipl
```



Segmentation post processing : SegPostProcess

Using the command line

Skull stripping options
(if flag --skullstripping activated)

--mask Mask.gipl : To save the mask used for skull stripping

--dilate : To apply a dilation of the mask before the skull stripping necessary if the tissue segmentation has a low quality)

--WM <integer> (default : 1) : White matter intensity level

--GM <integer> (default : 2) : Gray matter intensity level

--CSF <integer> (default : 3) : Cerebrospinal fluid intensity level

Segmentation post processing : SegPostProcess

Options

Using the command line

--help : Display help menu

Gaussian filter options

--Gauss : To apply a gaussian filter
--var <x-value, y-value, z-value> (default: 1.0 , 1.0 , 1.0) : Gaussian filter variance in the 3 dimensions

LevelSet based smoothing options

--noLS : Not to perform LevelSet based smoothing
--RMS <double> (default: 0.01) : To set the target RMS error for LevelSet smoothing
--iter <integer> (default: 50): To set the number of iterations for LevelSet smoothing

Advanced options

--label <integer> : To extract a label before processing
--isotropic : To scale first to isotropic pixel dimensions
--asymClose : To perform an asymmetric closing operation
--noCCL : Not to perform a connected component labeling and threshold for the largest part
--rescale : To enforce spacing in the 3 dimensions before any processing
--space <x-direction, y-direction, z-direction> : To enforce spacing before any processing
--linear : To apply a linear interpolation for reslicing (nearest neighbor interpolation otherwise)
--verb : To activate verbose mode

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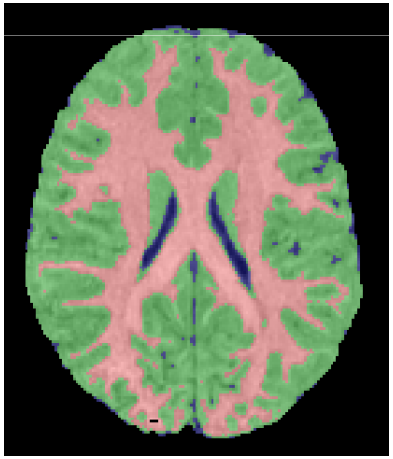
Cortical Thickness (CortThick external module)

Sparse and asymmetric local cortical thickness

Overview

This tool measures the cortical thickness of the brain, i.e. the distance between the white matter and gray matter at each point.

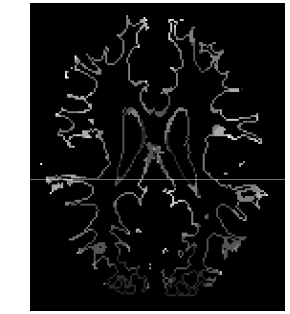


Image_labels_EMS.gipl

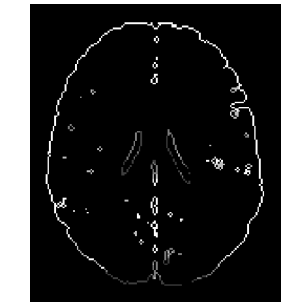
Label	Average	Std Dev	Nb Of Elem
1	2.96	1.81	1214
2	3.8	1.79	2113
3	2.93	1.89	1128
4	4.09	1.8	1796
5	3.9	2.52	897
6	4.15	1.93	9
7	4.31	1.76	90
8	3.39	1.41	2772
9	2.81	1.61	1479

Lobar cortical thickness analysis (csv file)

Optional outputs



WM_AvgBoundary.gipl



GM_AvgBoundary.gipl

Cortical Thickness (CortThick external module)

Sparse and asymmetric local cortical thickness

One can choose between two modes to compute the cortical thickness, depending on the available images:

- Use a single tissue segmentation label map as an input. This image contains white matter, gray matter and CSF labels.

- Use two different binary images: a white matter label image and a gray matter label image.

Cortical Thickness (CortThick external module)

Sparse and asymmetric local cortical thickness

Input images

What you need…

Execution with a segmentation image

Tissue segmentation label image

Optional

Parcellation image

Execution with separate WM and GM images

White matter label image
Gray matter label image

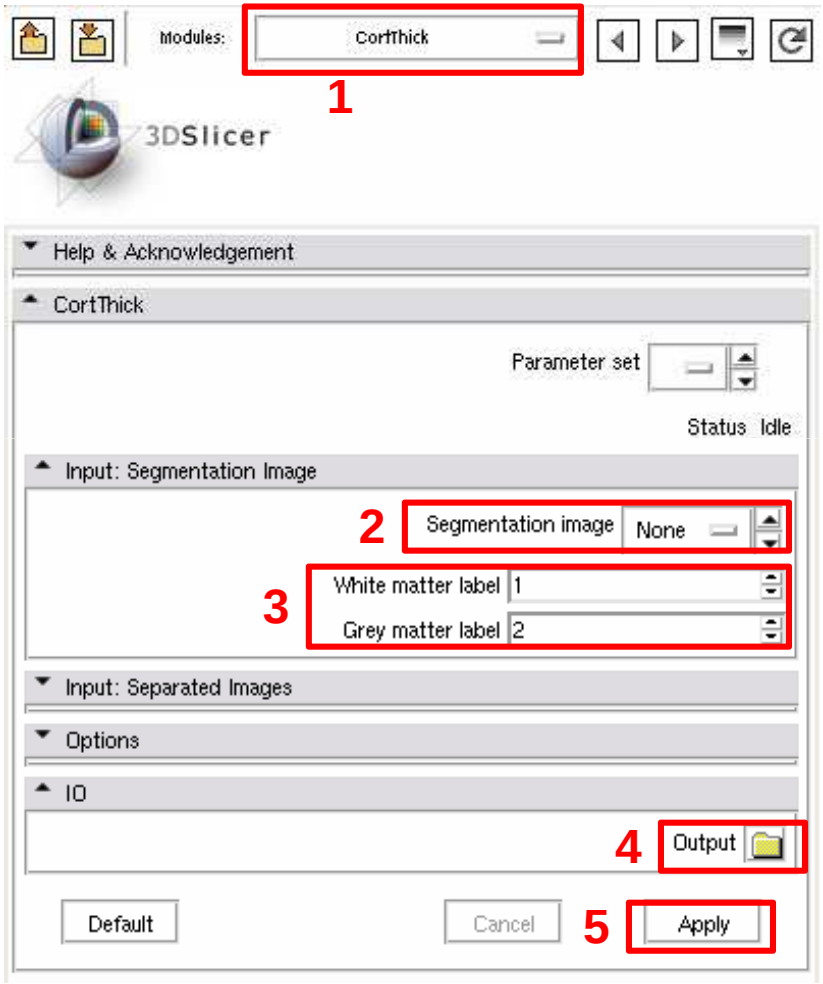
Optional

Parcellation image

Cortical Thickness (CortThick external module)

Sparse and asymmetric local cortical thickness

Segmentation image



1- Select the « SegPostProcess » module (in All Modules)

2- Add the tissue segmentation label image

3- Check if the white and gray matter label values are those of the segmentation image

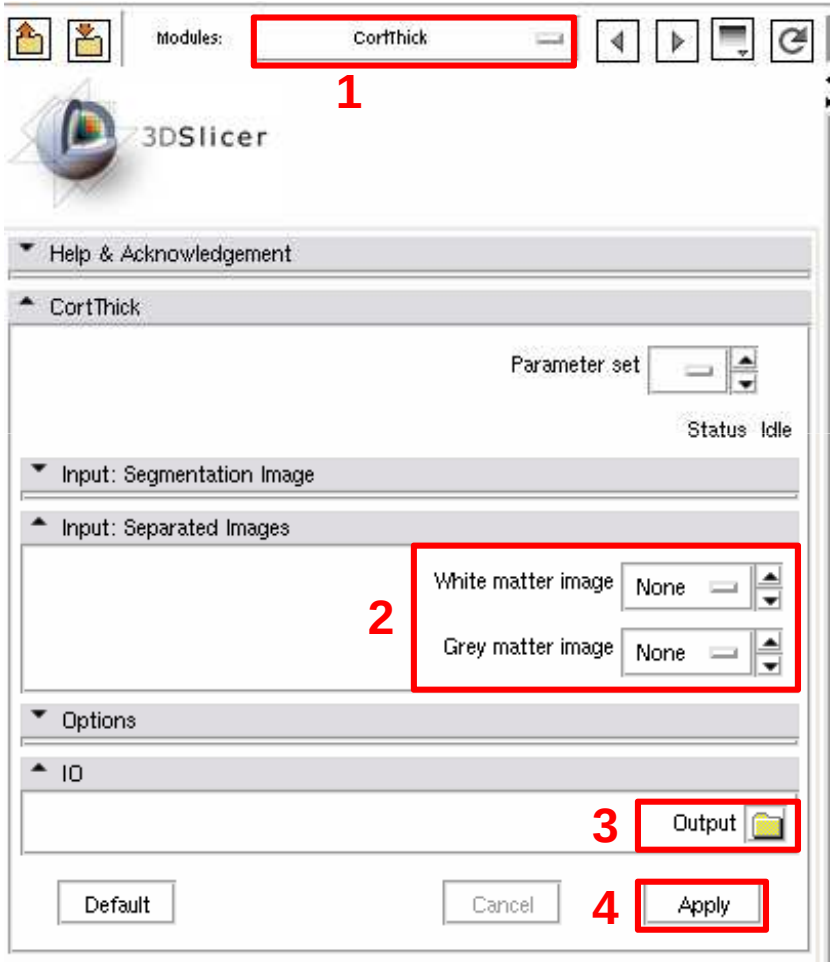
4- Select the output directory to save cortical thickness information

5- Click on the « Apply » button to process the data

Cortical Thickness (CortThick external module)

Sparse and asymmetric local cortical thickness

Separate images



1- Select the « SegPostProcess » module (in All Modules)

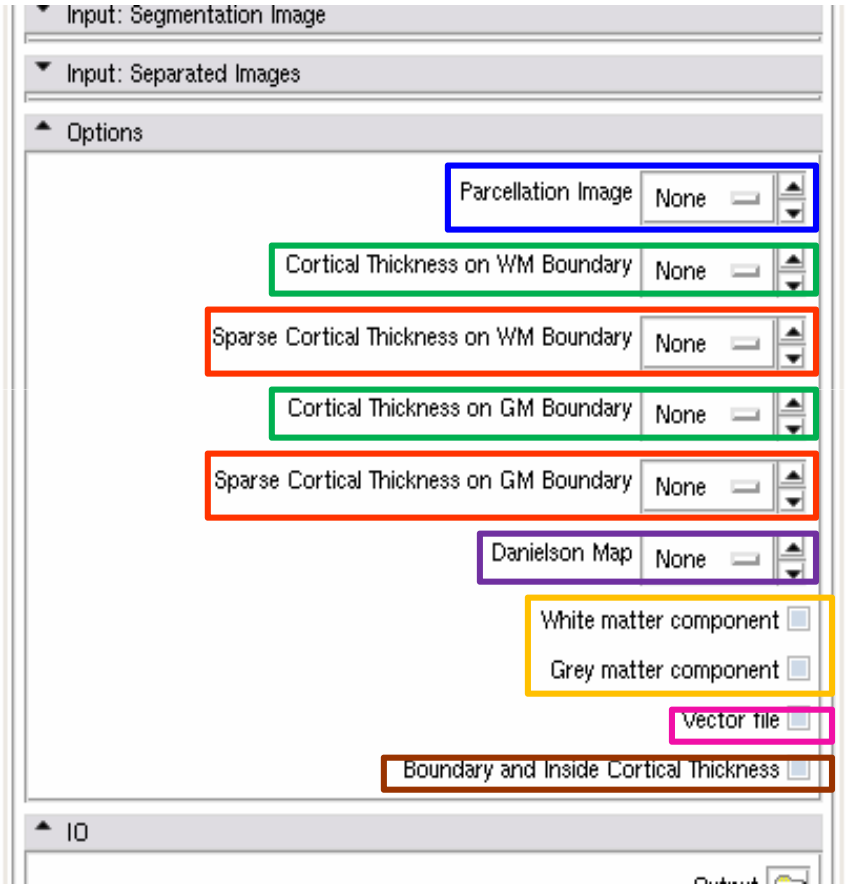
2- Add the white and gray matter label images

3- Select the output directory to save cortical thickness information

4- Click on the « Apply » button to process the data

Cortical Thickness (CortThick external module)

Sparse and asymmetric local cortical thickness



Common options

Parcellation Image

Load a parcellation image to have the results by label

Cortical Thickness on WM/GM boundary

Select « Add a new volume » to display the cortical thickness on WM/GM boundary

Rare options

Sparse cortical thickness on WM/GM boundary

Select « Add a new volume » to display the cortical thickness on WM/GM boundary

Danielsson map

Select « Add a new volume » to display the danielsson map on GM

WM/GM component

Check to apply a connected component filter

Vector file

Check to write the vector file (VtkFile)

Boundary and inside cortical thickness

Check to write two images : boundary and inside cortical thickness

Cortical Thickness (CortThick external module)

Sparse and asymmetric local cortical thickness

Using the command line

« Segmentation image » Mode

Global analysis

CortThickCLP OutputDirectory/ --inputSeg Label_Image.gipl

Lobar cortical thickness analysis
(if parcellation map is available)

CortThickCLP OutputDirectory/ --inputSeg Label_Image.gipl --par Parcellation_Image.gipl

Cortical Thickness (CortThick external module)

Sparse and asymmetric local cortical thickness

Using the command line

« Separate WM and GM images » Mode

Global analysis

CortThickCLP OutputDirectory/ --inputWM WM_Image.gipl --inputGM GM_Image.gipl

Lobar cortical thickness analysis
(if parcellation map is available)

CortThickCLP OutputDirectory/ --inputWM WM_Image.gipl --inputGM GM_Image.gipl --par Parcellation_Image.gipl

Using the command line

Options

--help : Display help menu

Segmentation image mode options

--WMLabel <integer> (default:1) : White matter label
--GMLabel <integer> (default:2) : Gray matter label

Display options

--SaveWM WM_Avg_Boundary.gipl : Save the average cortical thickness on white matter boundary
--SaveGM GM_Avg_Boundary.gipl : Save the average cortical thickness on gray matter boundary
--SaveSparseWM WM_Boundary.gipl : Save the sparse cortical thickness on white matter boundary
--SaveSparseGM GM_Boundary.gipl : Save the sparse cortical thickness on gray matter boundary
--DanGM GM_DanielssonMap.gipl : Save the Danielsson map on the gray matter boudary
--Vtk : Save the vector image
--BvsI : Save 2 images : Boundary and inside cortical thickness

Connected component options

--Wc : Apply a connected component filter on white matter
--Gc : Apply a connected component filter on gray matter

Cortical Thickness (CortThick external module)

Sparse and asymmetric local cortical thickness

Output Directory

What you will find in the output directory…

Output directory/

labels_EMS-WhiteMatDistanceMap.csv
(i.e. cortical thickness value for each voxel)

if parcellation option :

labels_EMS-WhiteMatDistanceMap_par.csv
(i.e. per lobe, cortical thickness value for each voxel)

labels_EMS-WhiteMatDistanceMap_par_array.csv
(i.e. per lobe, average cortical thickness with standard deviation and number of elements)

Conclusion

Slicer3 toolkit provides an accessible and versatile platform to conduct image processing of MRI data, in this case, regional cortical thickness analysis using individual modules.

Thanks to this tutorial you are now ready to apply the individual modules on your own dataset and perform a regional cortical thickness analysis.

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