



Slicer3 Training Compendium



Slicer3 Training Tutorial

ARCTIC (v1.2)

(Automatic Regional Cortical ThIckness)



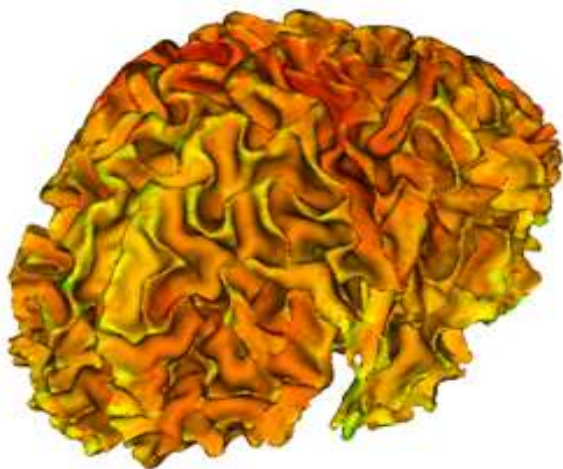
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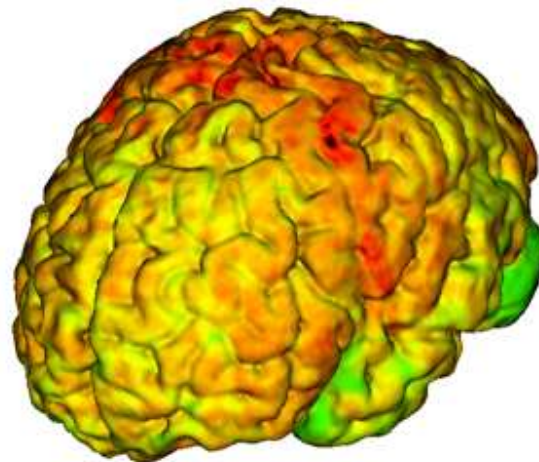
Learning Objective

Following this tutorial, you will be able to perform an individual analysis of regional cortical thickness.

You will learn how to **load input volumes**, **run the end-to-end module ARCTIC** to **generate cortical thickness information** and **display output volumes**.



Cortical thickness on WM surface



Cortical thickness on GM surface



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>



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

- Slicer3 download page (***Slicer nightly build***)
<http://www.slicer.org/pages/Downloads>
- BatchMake wrapper download page (***ARCTIC_BatchMake_Wrapper_1.2***)
- Tutorial dataset download page (***ARCTIC_Tutorial_example_1.0***)
- External modules download page (***ARCTIC_Executables_1.2***)
<http://www.nitrc.org/projects/arctic/>
- Atlas download page (***UNC_Pediatric_Brain_Atlas***)
<http://www.insight-journal.org/midas/item/view/2277>

Disclaimer: *It is the responsibility of the user of Slicer to comply with both the terms of the license and with the applicable laws, regulations, and rules.*



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_1.2_linux32/64/Mac*

Unzip this file somewhere in your computer.

An “*ARCTIC_Executables_1.2*” folder will be created, containing executables needed to perform the cortical thickness analysis.

To add the executables as Slicer3 external modules:

- Open Slicer3
- Go to View → Application Settings → Module Settings
- Click on the “add a preset” button
- Select the “*ARCTIC_Executables_1.2*” 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).



Add the executables in the PATH.

-tcsh usage : setenv PATH ARCTIC-Executables-Directory:Slicer3-Plugins-Directory:Slicer3-Bin-Directory:\${PATH}
-bash usage : export PATH=ARCTIC-Executables-Directory:Slicer3-Plugins-Directory:Slicer3-Bin-Directory:\${PATH}

Notice : To execute ARCTIC within Slicer3D, it is not necessary to add "Slicer3D-Bin-Directory" and "Slicer3-Bin-Directory" in the PATH.

Set ARCTIC environment variable

-tcsh usage : setenv BatchmakeWrapper_Dir Batchmake-Wrapper-Directory
-bash usage : export BatchmakeWrapper_Dir=Batchmake-Wrapper-Directory

WITH:

ARCTIC-Executables-Directory/ : Downloaded folder (ARTIC_Executables_1.2)

Slicer3-Plugins-Directory/ : Directory containing Slicer3 plugins

Nightly build version : "Slicer3Dir"/lib/Slicer3/Plugins

Slicer3-Bin-Directory/ : Directory containing Slicer3 binary files

Nightly build version : "Slicer3Dir"/lib/Slicer3/bin

Batchmake-Wrapper-Directory/ : Downloaded folder (ARTIC_Batchmake_Wrapper_1.2)



Set Slicer libraries variable (only for command line)

-tcsh usage : setenv SLICERLIBPATH “Slicer-nightly-build”/lib
setenv LD_LIBRARY_PATH

```
{LD_LIBRARY_PATH}:{SLICERLIBPATH}/BatchMake:{SLICERLIBPATH}/bmModuleDescriptionParser:{SLICERLIBPATH}/FreeSurfer:{SLICERLIBPATH}/GenerateCLP:{SLICERLIBPATH}/GenerateLM:{SLICERLIBPATH}/IGT:{SLICERLIBPATH}/igtl:{SLICERLIBPATH}/InsightToolkit:{SLICERLIBPATH}/ITKCommandIO:{SLICERLIBPATH}/KWWidgets:{SLICERLIBPATH}/LoadableModule:{SLICERLIBPATH}/MGHImageIO:{SLICERLIBPATH}/ModuleDescriptionParser:{SLICERLIBPATH}/MRML:{SLICERLIBPATH}/MRMLImageIO:{SLICERLIBPATH}/OpenIGTLink:{SLICERLIBPATH}/Python/lib:{SLICERLIBPATH}/Qdec:{SLICERLIBPATH}/RemoteIO:{SLICERLIBPATH}/Slicer3:{SLICERLIBPATH}/SlicerIO:{SLICERLIBPATH}/tclap:{SLICERLIBPATH}/TclTk/lib:{SLICERLIBPATH}/Teem-1.10.0:{SLICERLIBPATH}/vtk-5.2:{SLICERLIBPATH}/vtkITK:{SLICERLIBPATH}/vtkTeem
```

-bash usage : export SLICERLIBPATH=“Slicer-nightly-build”/lib
export

```
LD_LIBRARY_PATH={LD_LIBRARY_PATH}:{SLICERLIBPATH}/BatchMake:{SLICERLIBPATH}/bmModuleDescriptionParser:{SLICERLIBPATH}/FreeSurfer:{SLICERLIBPATH}/GenerateCLP:{SLICERLIBPATH}/GenerateLM:{SLICERLIBPATH}/IGT:{SLICERLIBPATH}/igtl:{SLICERLIBPATH}/InsightToolkit:{SLICERLIBPATH}/ITKCommandIO:{SLICERLIBPATH}/KWWidgets:{SLICERLIBPATH}/LoadableModule:{SLICERLIBPATH}/MGHImageIO:{SLICERLIBPATH}/ModuleDescriptionParser:{SLICERLIBPATH}/MRML:{SLICERLIBPATH}/MRMLImageIO:{SLICERLIBPATH}/OpenIGTLink:{SLICERLIBPATH}/Python/lib:{SLICERLIBPATH}/Qdec:{SLICERLIBPATH}/RemoteIO:{SLICERLIBPATH}/Slicer3:{SLICERLIBPATH}/SlicerIO:{SLICERLIBPATH}/tclap:{SLICERLIBPATH}/TclTk/lib:{SLICERLIBPATH}/Teem-1.10.0:{SLICERLIBPATH}/vtk-5.2:{SLICERLIBPATH}/vtkITK:{SLICERLIBPATH}/vtkTee
```

WITH:

“Slicer-nightly-build” : path of Slicer nightly build in your computer

- 1- Pipeline overview
- 2- Input images
- 3- Pipeline description
- 4- Output images and organisation
- 5- Execution within Slicer
- 6- Example with tutorial dataset
- 7- Command line execution

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Pipeline Overview

All the tools used in the current pipeline are Slicer3 modules, some of them being UNC external modules. The user can thus perform a regional cortical thickness analysis on an individual subject within Slicer3.

Two different modes can be used, depending on the input images:

- Raw images (T1-weighted, T2-weighted, PD)
- Tissue segmentation label image

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- 2- **Input images**
- 3- Pipeline description
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What you need...

Raw images

T1-weighted image
Tissue segmentation atlas directory

Optional

T2-weighted image
PD-weighted image
Atlas raw image + its parcellation
Case parcellation image

Segmented image

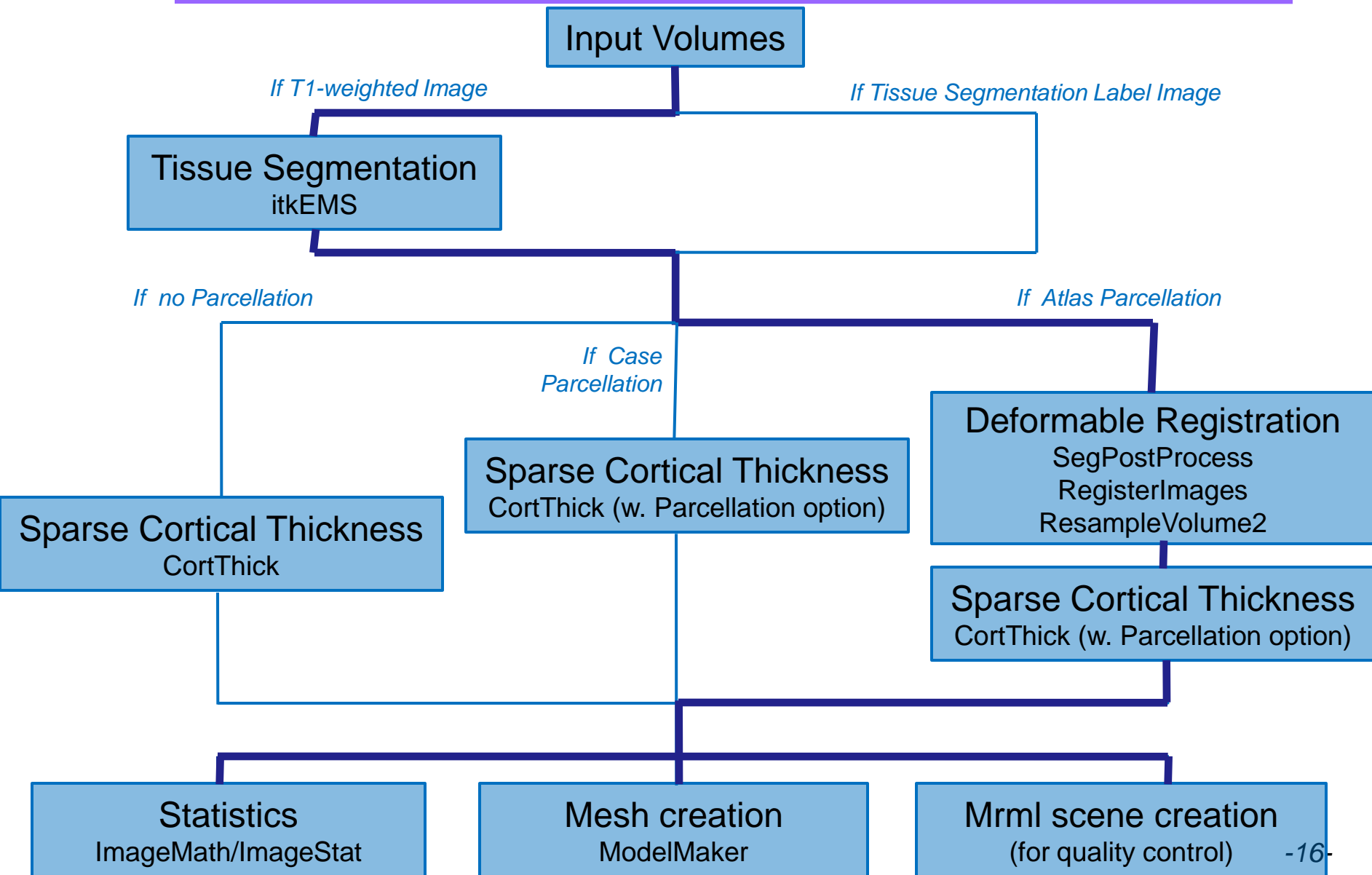
Raw image
Tissue segmentation label image

Optional

Atlas raw image + its parcellation
Case parcellation image

- 1- Pipeline overview
- 2- Input images
- 3- **Pipeline description**
- 4- Output images and organisation
- 5- Execution within Slicer
- 6- Example with tutorial dataset
- 7- Command line execution

Pipeline Description





Pipeline Description

1. Tissue segmentation

Module : itkEMS (UNC Slicer3 external module)

2. Regional atlas deformable registration

3.1. Skull stripping

Module : SegPostProcess (UNC Slicer3 external module)

3.2. Deformable registration of T1-weighted atlas

Module : RegisterImages (Slicer3 module)

3.3. Applying transformation to its parcellation map

Module : ResampleVolume2 (Slicer3 module)

3. Sparse and asymmetric Cortical Thickness

Module : CortThick (UNC Slicer3 module)

4. Statistics

Modules : ImageMath, ImageStat (UNC Slicer3 external modules)

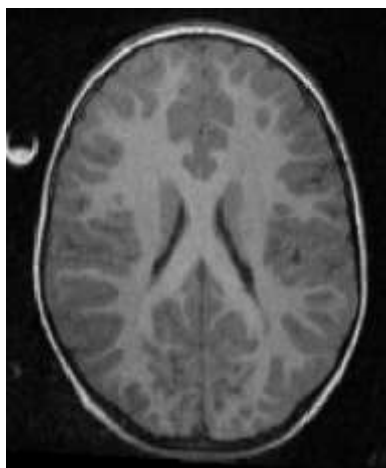
5. Mesh Creation

Module : ModelMaker (Slicer3 module)

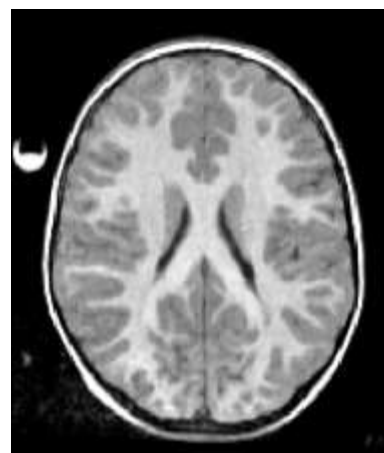
6. Mxml scene Creation

Tissue segmentation (itkEMS external module)

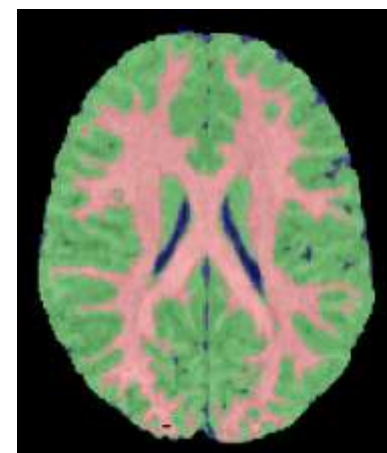
Probabilistic atlas-based automatic tissue segmentation via an Expectation-Maximization scheme. ItkEMS also performs an intensity inhomogeneity correction of the input image that removes gradual variations in the image intensities mainly due to RF coil imperfection



Input_T1-Image.nrrd



Image_corrected_EMS.nrrd

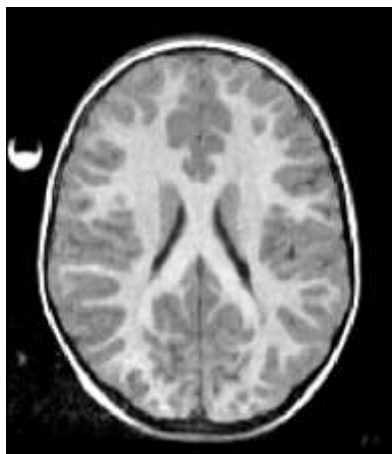


Image_labels_EMS.nrrd

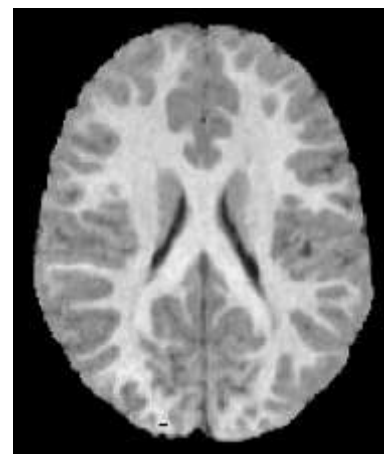
Pipeline Description

Skull Stripping (SegPostProcess external module)

This step is performed using the previously computed tissue segmentation label image.



Image_corrected_EMS.nrrd



Image_corrected_EMS_stripped.nrrd

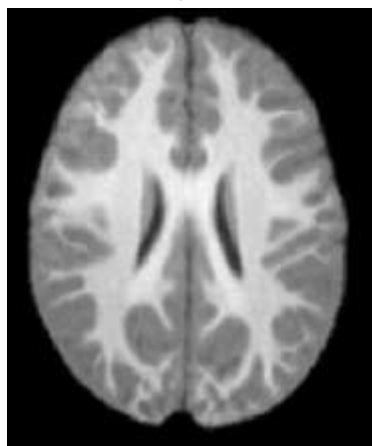
Deformable registration of T1-weighted atlas (RegisterImages module)

B-spline pipeline registration.

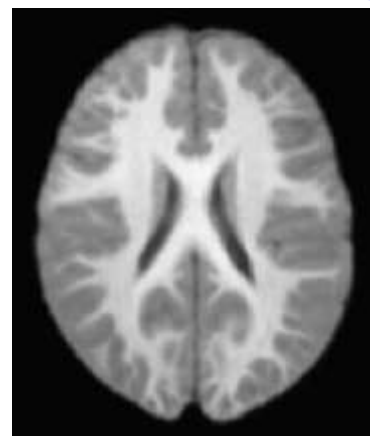
A transformation file is created and will be used by the next step.

Module link

http://www.na-mic.org/Wiki/index.php/ITK_Registration_Optimization#Pipeline_Registration



Atlas.nrrd



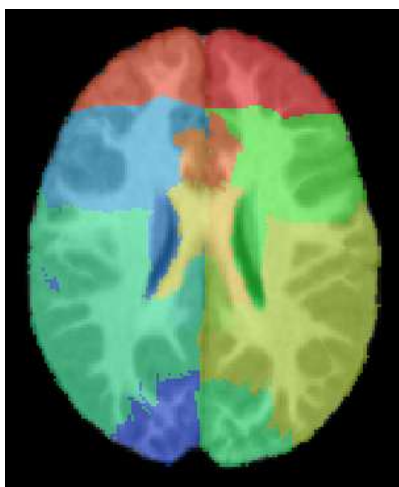
AtlasRegistered_Image_corrected_EMS_stripped.nrrd

Pipeline Description

Applying transformation to the atlas' parcellation map (ResampleVolume2 module)

Module link :

<http://slicer.spl.harvard.edu/slicerWiki/index.php/Modules:ResampleVolume2-Documentation>



Parcellation.nrrd

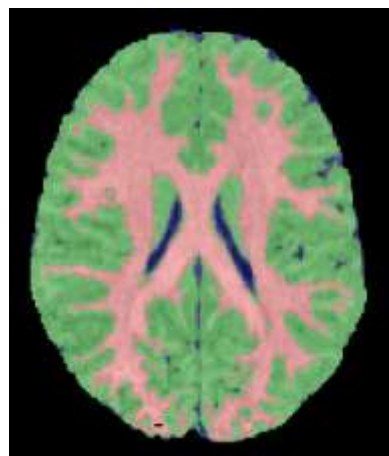


ParcellationRegistered_Image_corrected_EMS_stripped.nrrd

Pipeline Description

Cortical Thickness (CortThick external module)

Sparse and asymmetric local cortical thickness



Image_labels_EMS.nrrd



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

Regional Cortical Thickness information

Optional Outputs



WM_AvgBoundary.nrrd



GM_AvgBoundary.nrrd



Pipeline Description

Statistics (ImageStat and ImageMath modules)

Both modules are used to generate volume information in the following files :

- TissueSegmentationVolumes.csv
White matter, gray matter and CSF volumes.
- ParcellationMapVolumes.csv (if the parcellation image is provided)
White matter, gray matter and CSF volumes per lobe.

Notice : values are in mm



Pipeline Description

Mesh creation (ModelMaker module)

Module link :

<http://www.slicer.org/slicerWiki/index.php/Modules:Modelmaker-Documentation-3.2>

Two meshes are created :

- WM_Surface.vtk
White matter mesh.
- GM_Surface.vtk
Gray matter mesh.



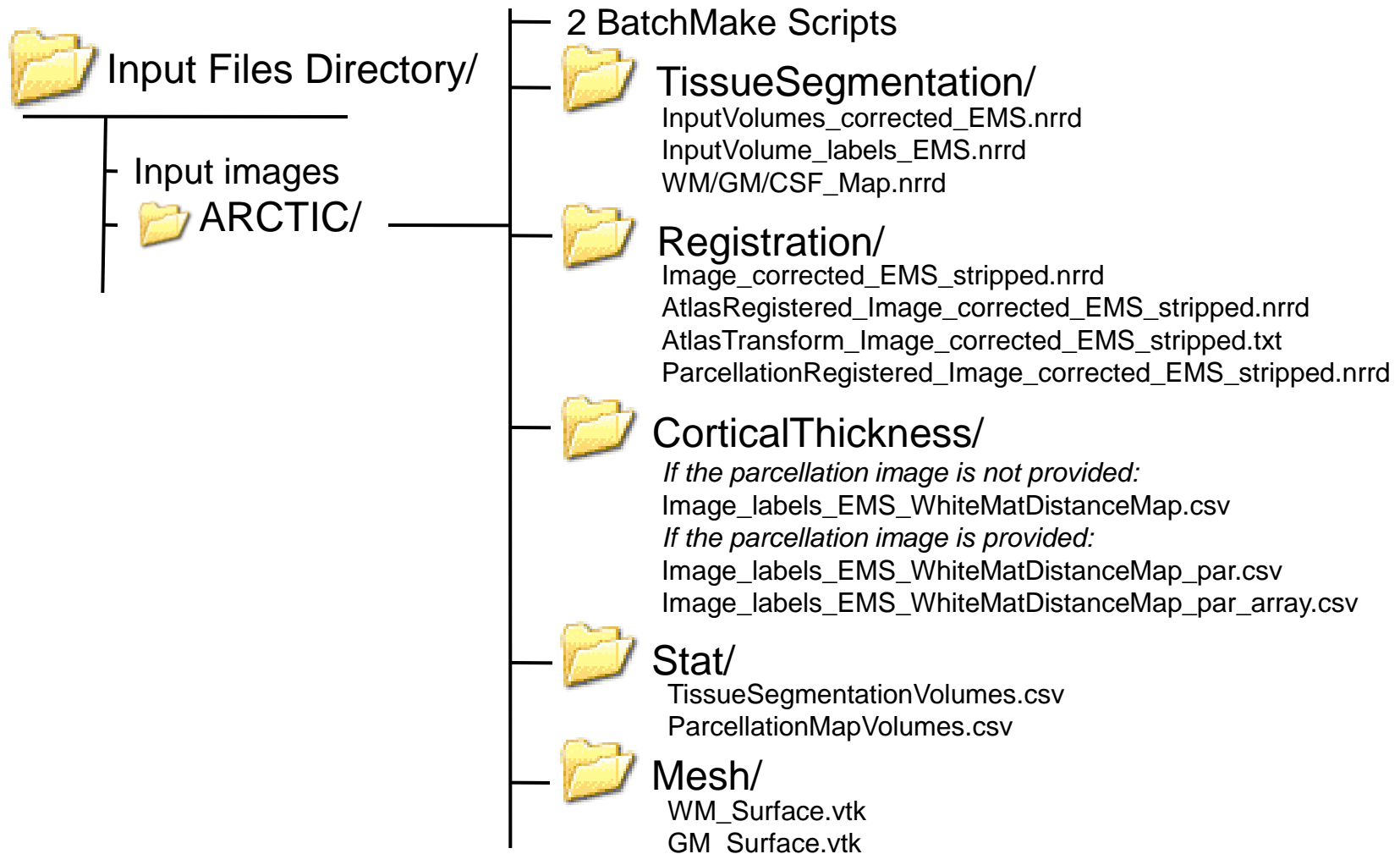
Pipeline Description

Mrml scene creation

A Mrml scene is created to display all the steps of the pipeline.
There is one snapshot per step.
This Mrml scene is created to make a quality control.

- 1- Pipeline overview
- 2- Input images
- 3- Pipeline description
- 4- **Output images and organization**
- 5- Execution within Slicer
- 6- Example with tutorial dataset
- 7- Command line execution

Output and Organisation



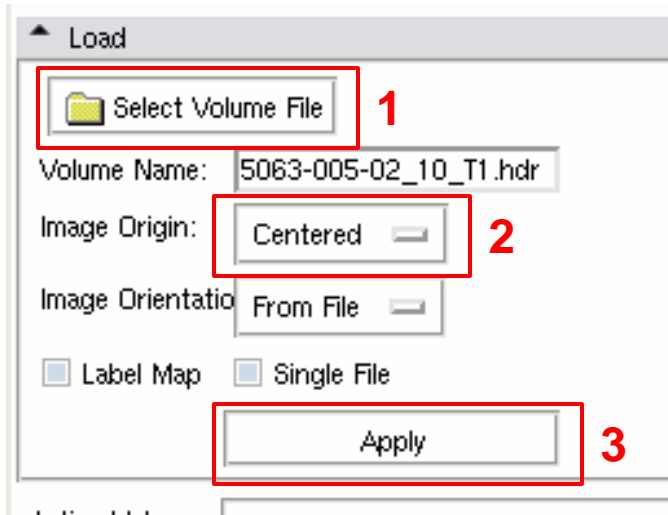
- 1- Pipeline overview
- 2- Input images
- 3- Pipeline description
- 4- Output images and organisation
- 5- **Execution within Slicer**
- 6- Example with tutorial dataset
- 7- Command line execution



Execution within Slicer

- **Load input images**
- Demonstration with « Raw Images »
- Demonstration with « Segmented Image »

Demonstration : Load the input images

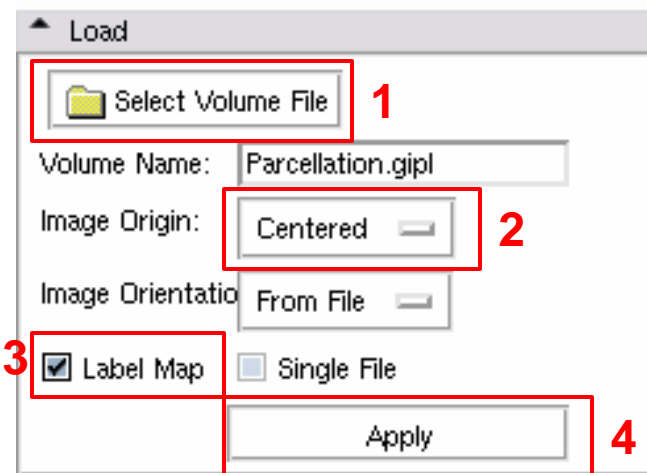


How to load raw images (case and atlas)?

- 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



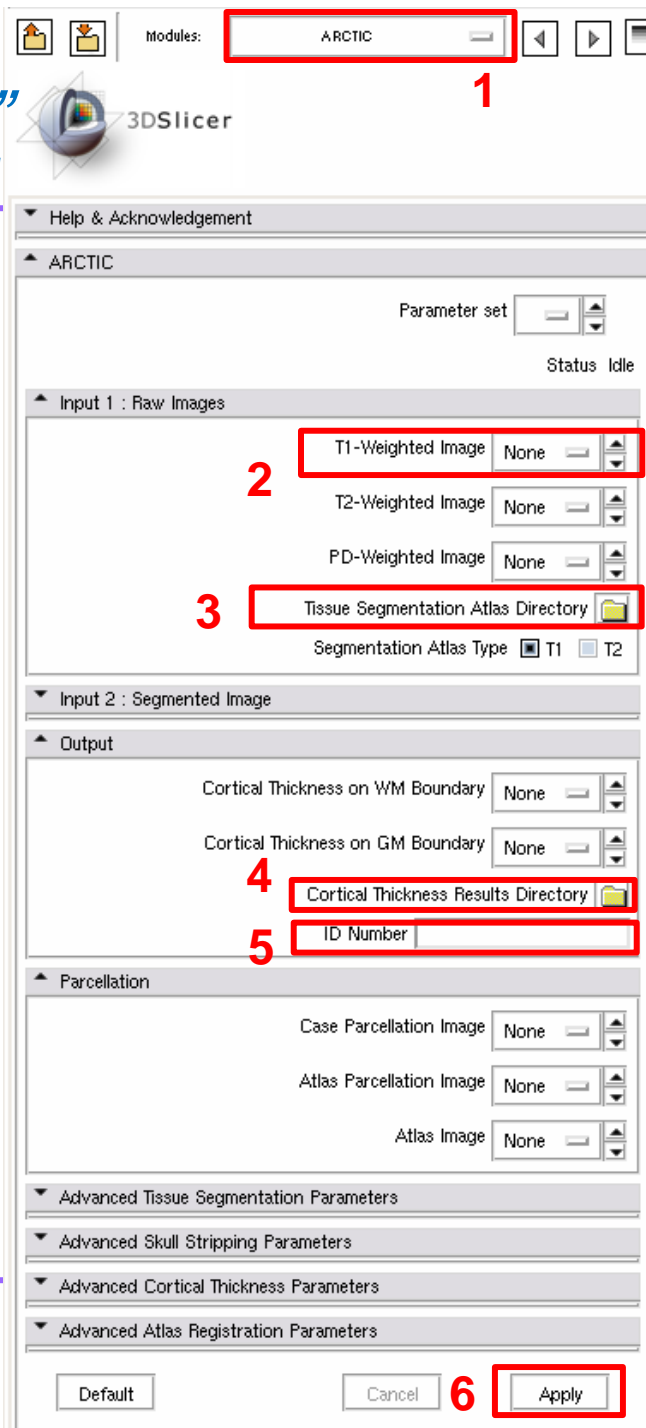


Demonstration in Slicer

- Load input images
- **Demonstration with « Raw Images »**
- Demonstration with « Segmented Image »
- Parcellation option
- Advanced parameters



Demonstration : "Raw Images" Input 1



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

2- Add the T1-weighted image

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

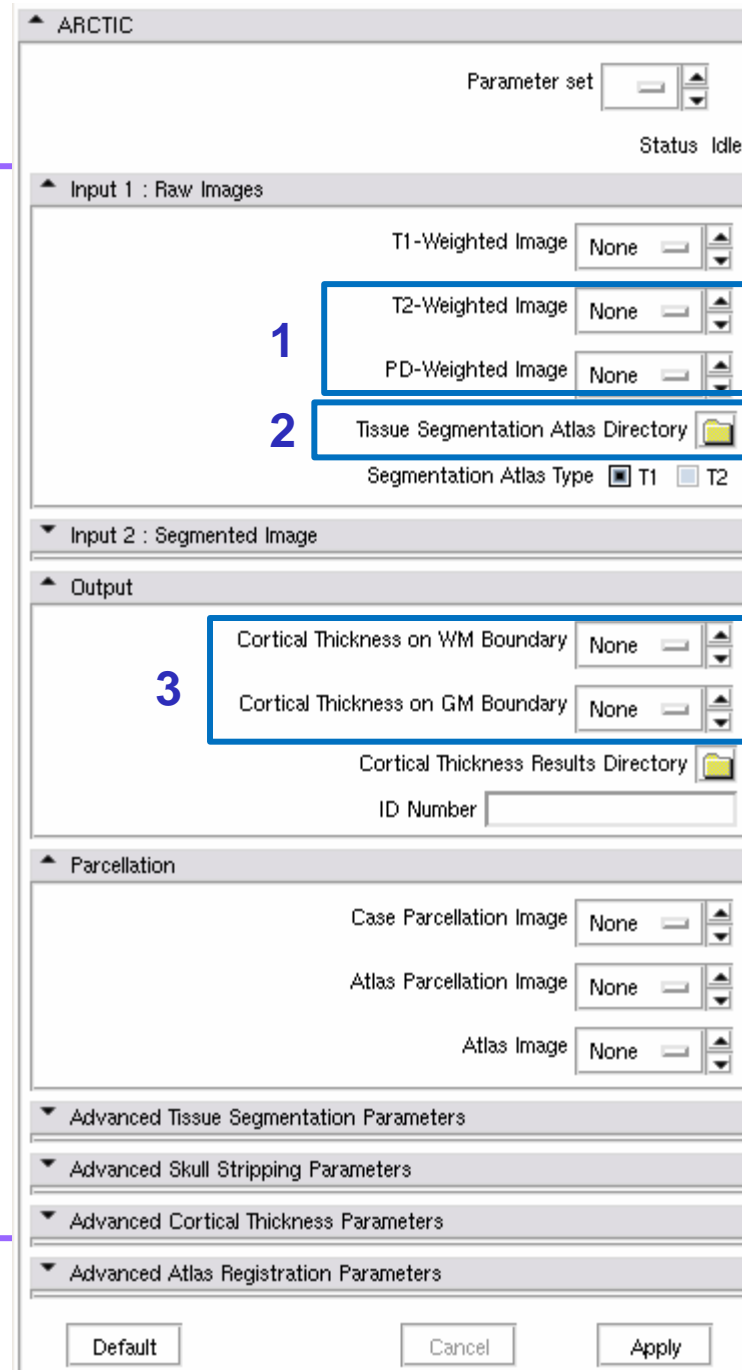
4- Set the output directory

5- Set a prefix which will be added to all the outputs

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

Verifications / Options

- 1- If available, set the T2 and/or PD-weighted images to improve the tissue segmentation
- 2- Check the tissue segmentation atlas type (T1-weighted or T2-weighted image)
- 3- Set the output images to be displayed in Slicer (« Create a new volume » instead of « None »)





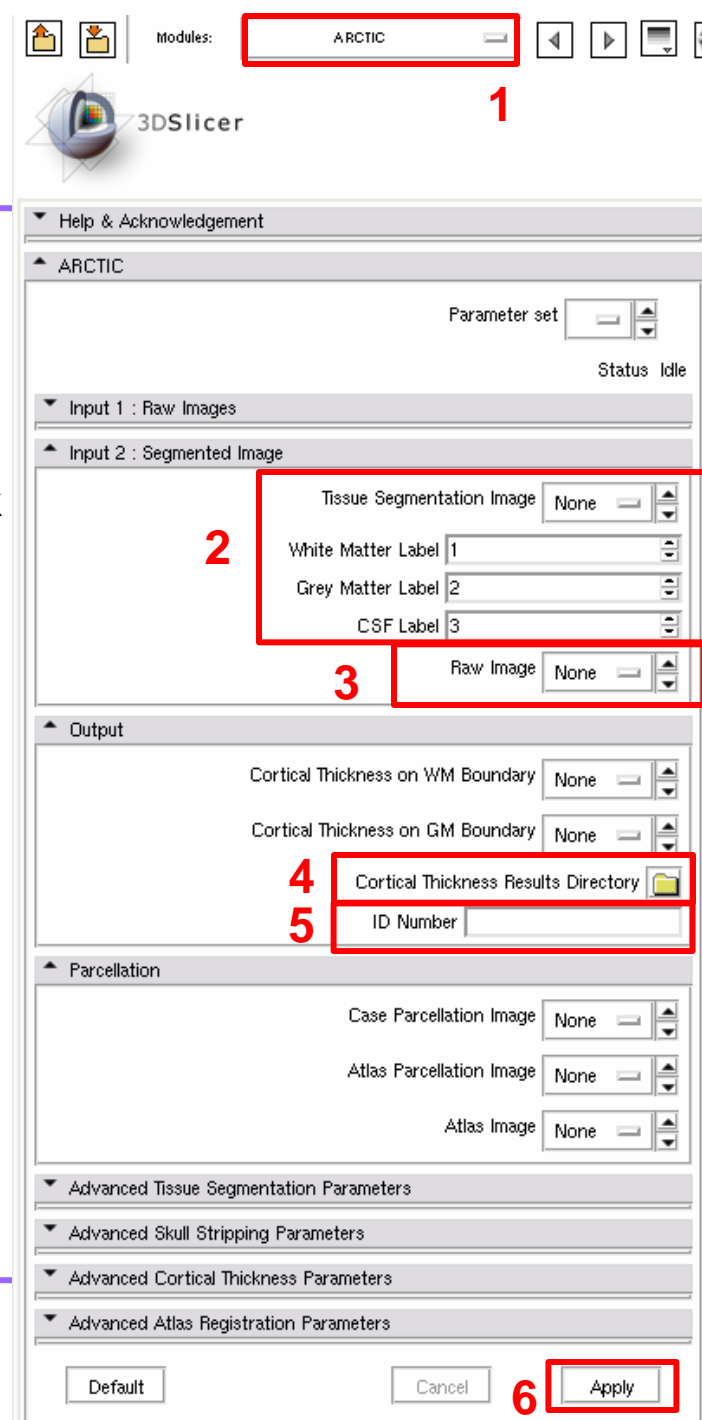
Demonstration in Slicer

- Load input images
- Demonstration with « Raw Images »
- **Demonstration with « Segmented Image »**
- Parcellation option
- Advanced parameters



Demonstration : “Segmented Image” Input 2

- 1- Select the « ARCTIC » module (in All Modules)
- 2- Set the tissue segmentation label image and check the related tissue labels
- 3- Set its raw image (T1-weighted, T2-weighted, PD-weighted) and change the orientation if necessary
- 4- Set the output directory
- 5- Set a prefix which will be added to all the outputs
- 6- Click on the « Apply » button to process the data



Options

- 1- Set the output images to be displayed in Slicer (« Create a new volume » instead of « None »)



Cortical Thickness on WM Boundary



Cortical Thickness on GM Boundary

ARCTIC

Parameter set: ARCTIC

Status: Idle

Input 1 : Raw Images

Input 2 : Segmented Image

Tissue Segmentation Image: None

White Matter Label: 1

Grey Matter Label: 2

CSF Label: 3

Raw Image: None

Orientation: RAI

Output

1 Cortical Thickness on WM Boundary: None

Cortical Thickness on GM Boundary: None

Cortical Thickness Results Directory: [Folder Icon]

ID Number: [Text Field]

Parcellation

Case Parcellation Image: None

Atlas Parcellation Image: None

Atlas Image: None

Atlas/Parcellation Orientation: RAI

Advanced Tissue Segmentation Parameters

Advanced Skull Stripping Parameters

Advanced Atlas Registration Parameters

Default Cancel Apply



Demonstration in Slicer

- Load input images
- Demonstration with « Raw Images »
- Demonstration with « Segmented Image »
- **Parcellation option**
- Advanced parameters

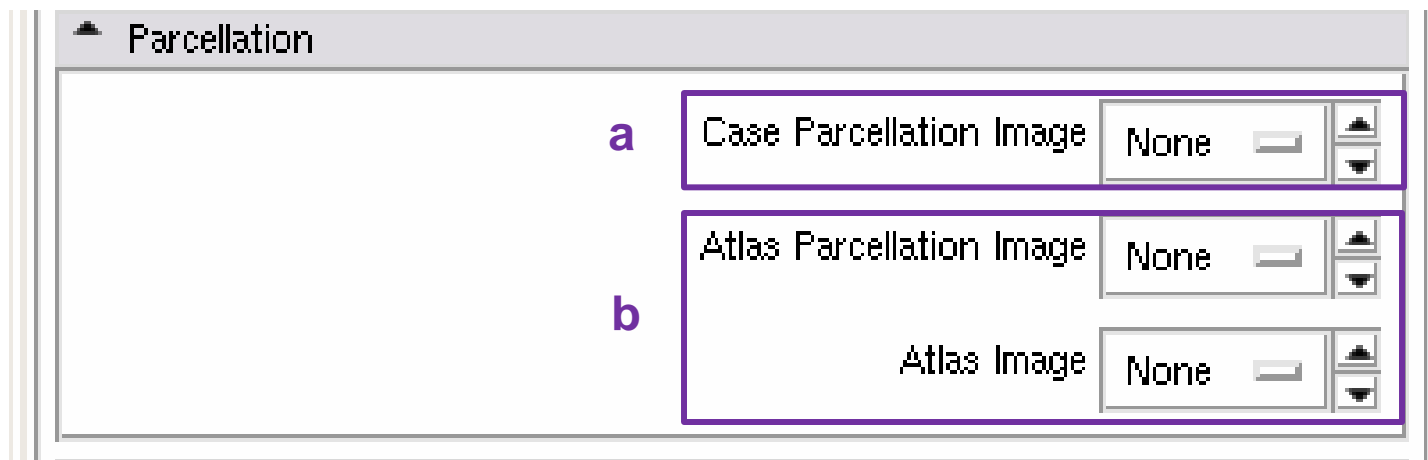
Parcellation options

Parcellation options

If you want to perform a lobar cortical thickness analysis, choose between the two possibilities

a- Add a parcellation image which is defined in the input coordinate space (« Case Parcellation Image »)

b- Add the atlas raw image **and** its parcellation, defined in the atlas coordinate space (« Atlas Parcellation Image »)





Demonstration in Slicer

- Load input images
- Demonstration with « Raw Images »
- Demonstration with « Segmented Image »
- Parcellation option
- **Advanced parameters**



Advanced parameters

Tissue segmentation parameters

- a-** Filter options: specifies smoothing parameters prior to the segmentation
- b-** Priors weighting the tissue classes for the segmentation
- c-** Atlas warping options:
 - No atlas warping:
 - Unchecked by default: atlas to subject B-Spline registration is performed
 - Checked: atlas to subject affine registration is performed instead of the warping
 - Grid size X,Y,Z: grid controls points for atlas warping

Skull stripping parameters

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

Cortical Thickness parameters

- a-** To remove the interpolation of the cortical thickness or set the threshold used to match the cortical thickness map with the parcellation

Atlas registration parameters

- a-** Different initialization methods

The screenshot shows the 'Advanced Parameters' dialog box in 3DSlicer, divided into several sections. Annotations 'a', 'b', and 'c' are placed next to specific parameter groups.

- Advanced Tissue Segmentation Parameters:**
 - a:** Filter Iterations (10), Filter Time Step (0.01), Filter Method (Curvature flow checked, Grad aniso diffusion unchecked).
 - b:** WM global spacial prior scaling (1.2), GM global spacial prior scaling (1), CSF global spacial prior scaling (0.7), Other global spacial prior scaling (1), Maximum Bias Degree (4).
 - c:** No tissue segmentation masking (unchecked), No atlas warping (unchecked), Grid Size (X) (5), Grid Size (Y) (5), Grid Size (Z) (5).
- Advanced Skull Stripping Parameters:**
 - a:** Mask Dilation (unchecked).
- Advanced Cortical Thickness Parameters:**
 - a:** InterpOff (unchecked), Threshold (1.8).
- Advanced Atlas Registration Parameters:**
 - a:** Initialization (None, Landma, ImageCent, CentersOfM: checked, SecondMomer).

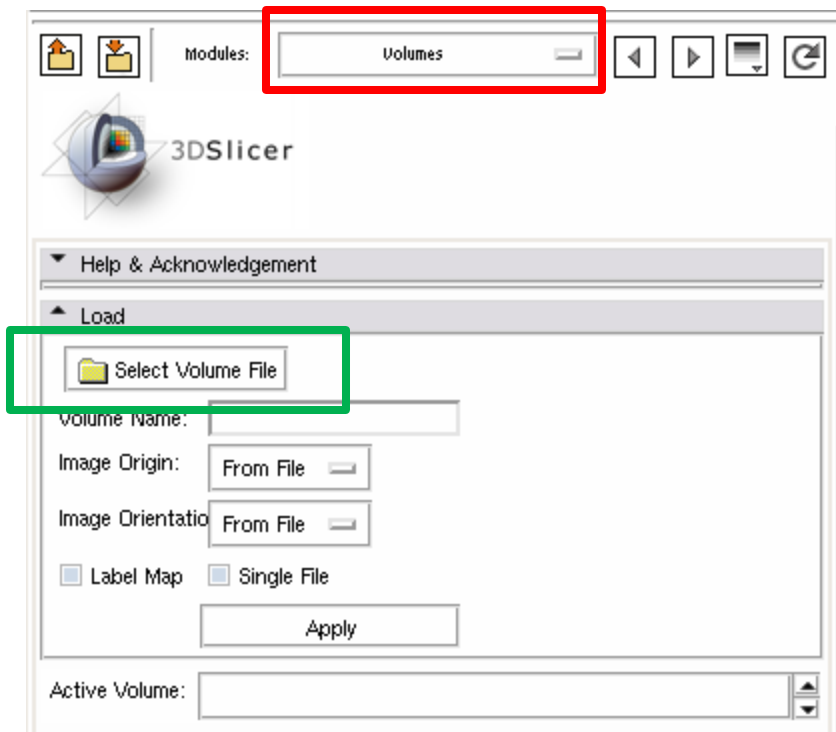
- 1- Pipeline overview
- 2- Input images
- 3- Pipeline description
- 4- Output images and organisation
- 5- Execution within Slicer
- 6- **Example with tutorial dataset**
- 7- Command line execution



Example with tutorial dataset

- Load input images
- Run ARCTIC

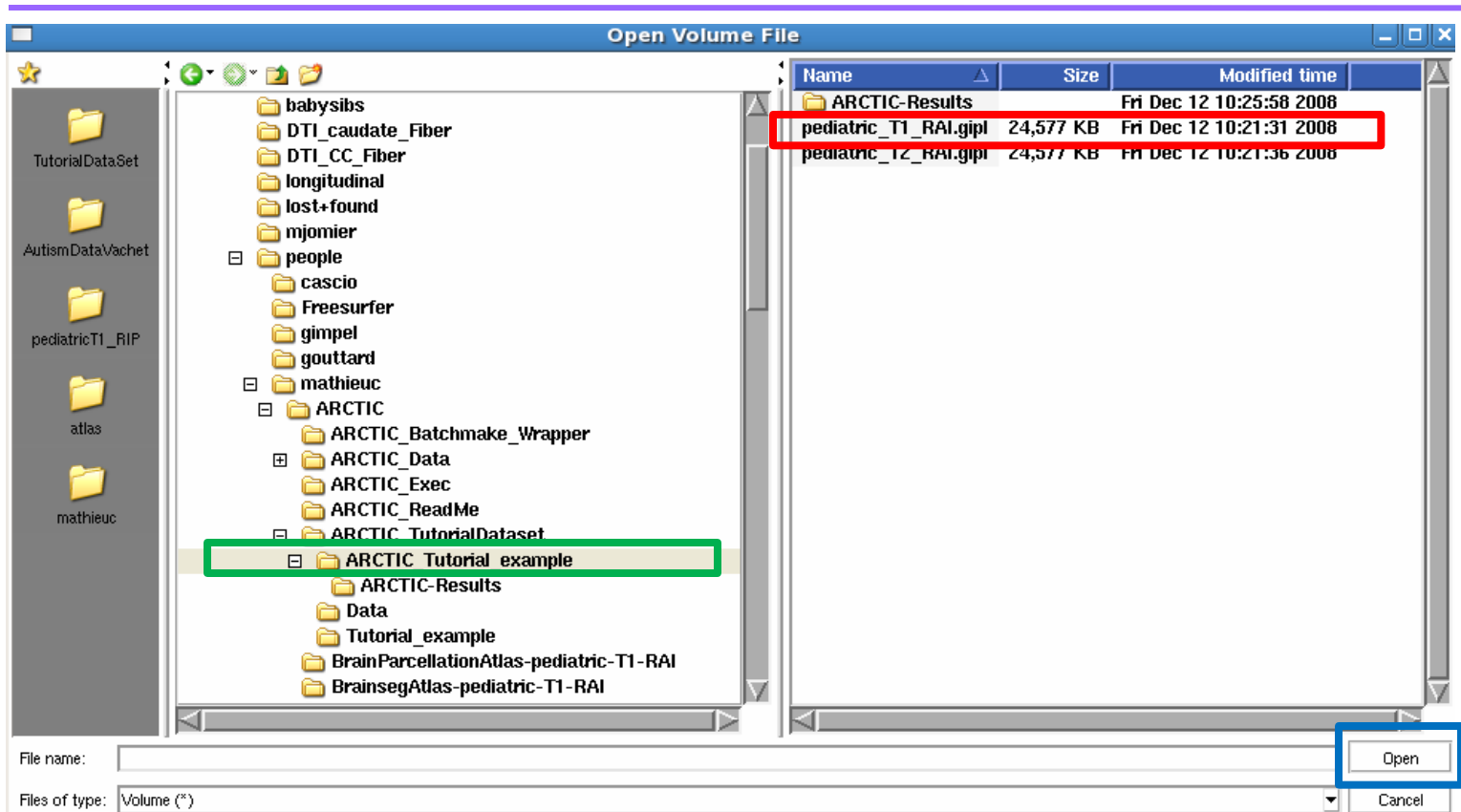
Load input images



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

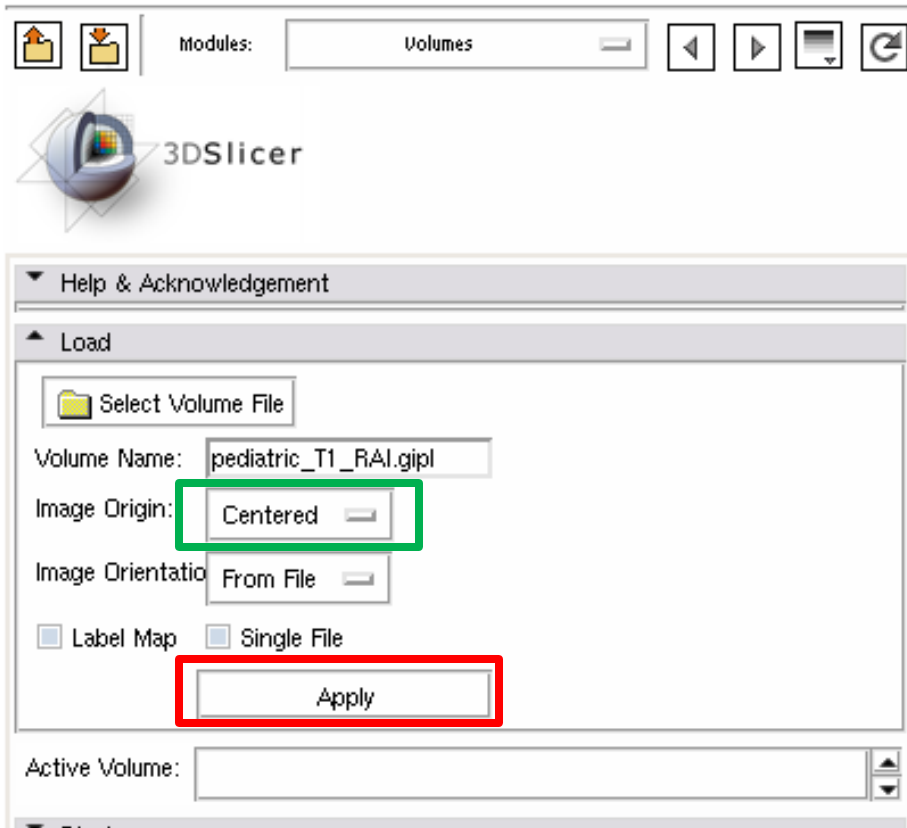
Then click on the « **Select Volume File** » button to load the images.

Load input images



A new window 'Open Volume File' is now open. Select the « **ARCTIC_Tutorial_example** » directory. Select the « **pediatric_T1_RAI.nrrd** » file in the Data directory and click on « **Open** ».

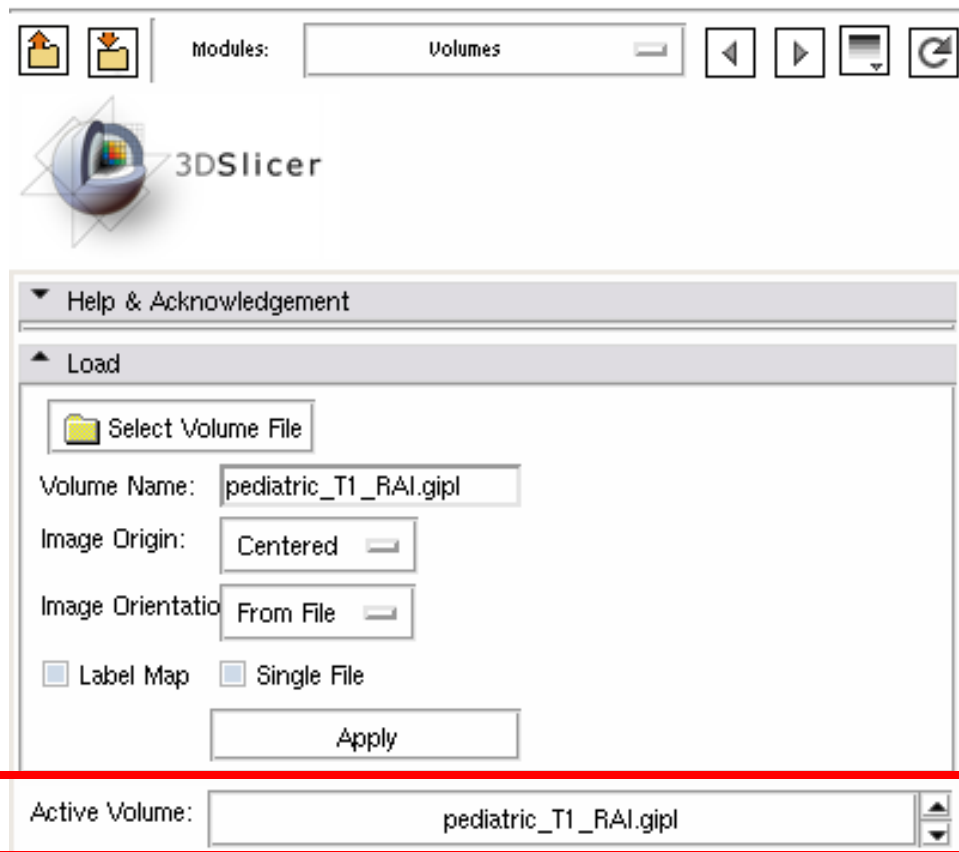
Load input images



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

And click on « **Apply** ».

Load input images



The first image is now loaded.

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



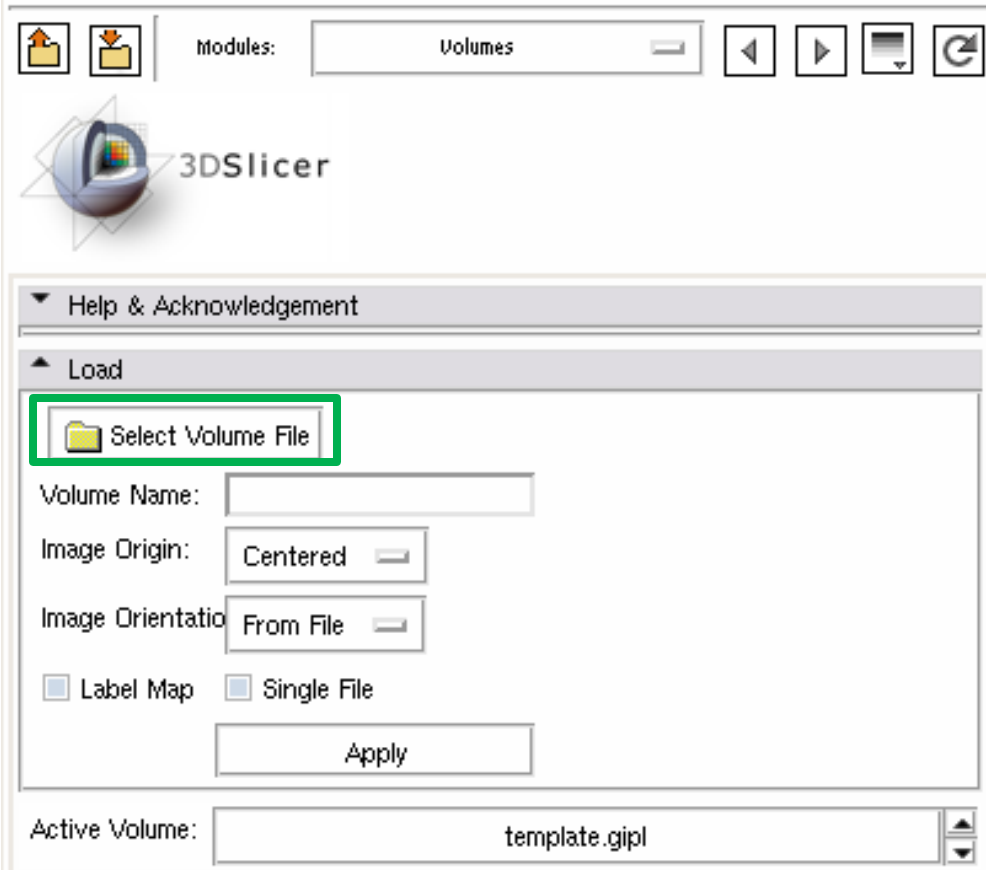
Load input images

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 one.

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

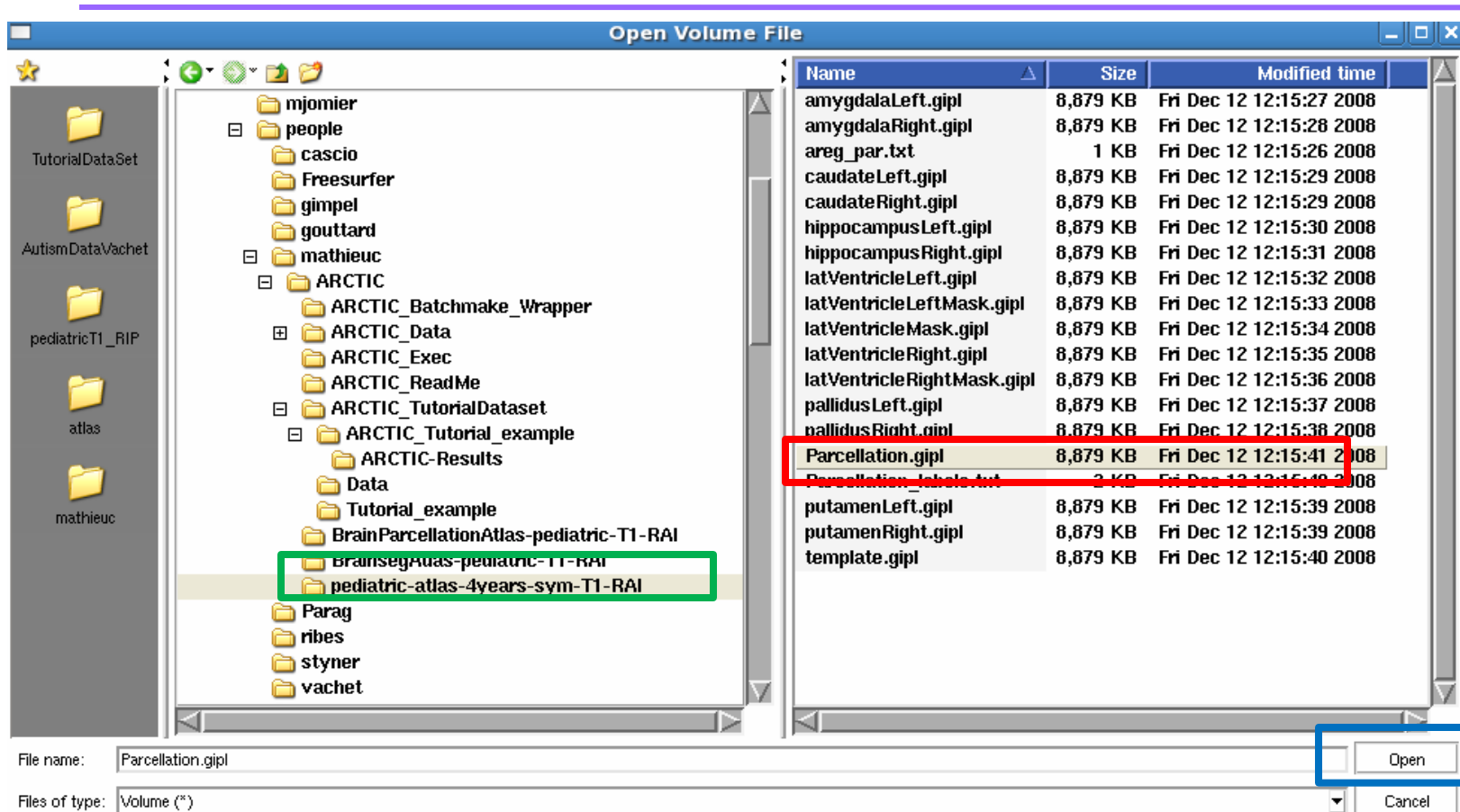
Load input images



Now we will load the parcellation image.

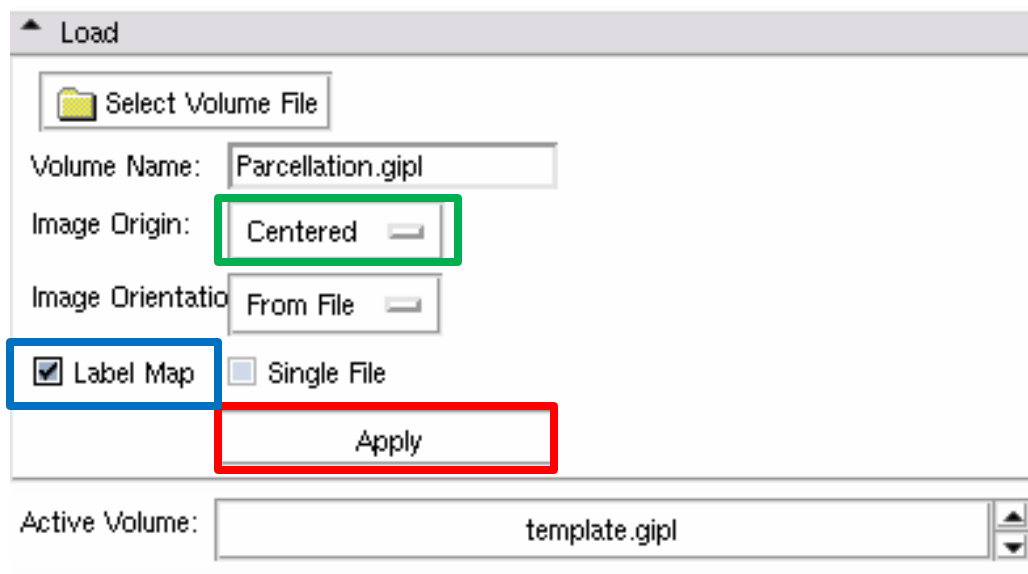
Click on the « **Select Volume File** » button to load the parcellation.

Load input images



A new window 'Open Volume File' is now open. Select the « **pediatric-atlas-4years-sym-T1-RAI** » directory . Select the « **Parcellation.nrrd** » file and click on « **Open** » .

Load input images

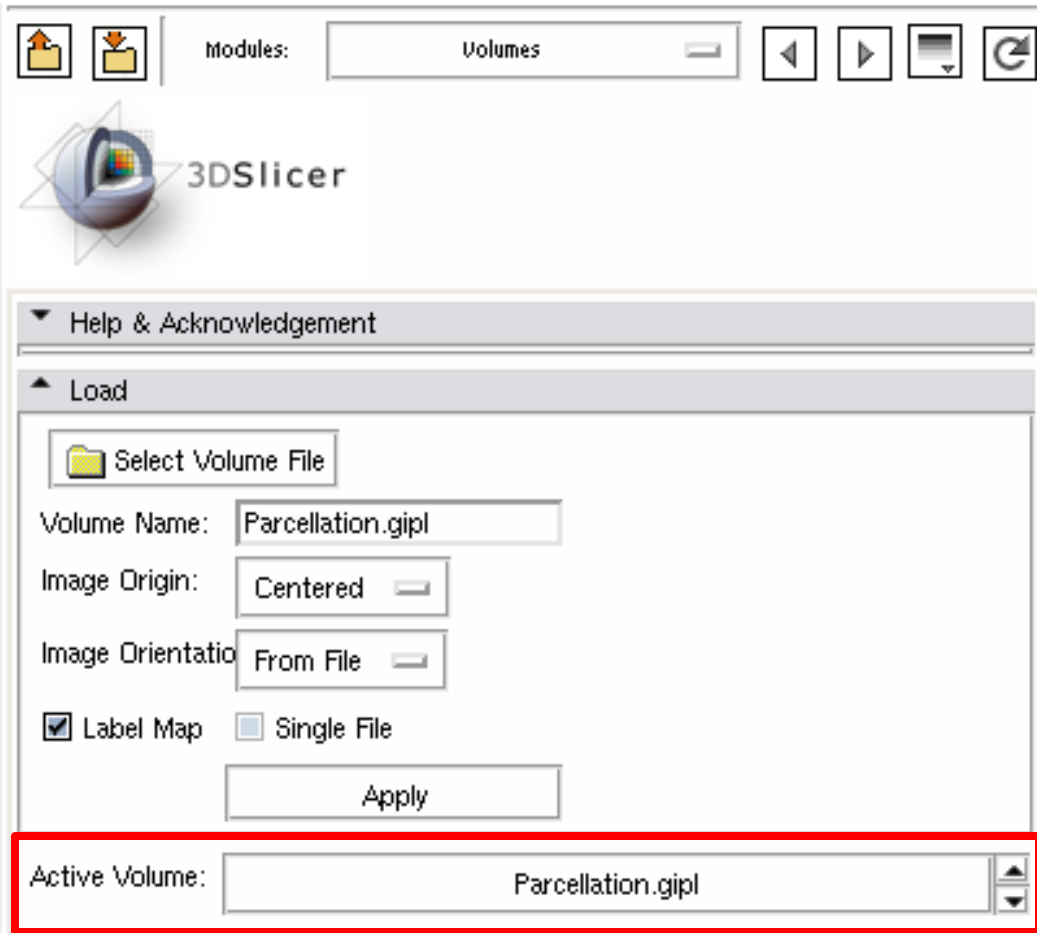


Now, select the Image Origin as « **Centered** ».

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

And click on « **Apply** ».

Load input images



The dataset is now loaded.

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



Example with tutorial dataset

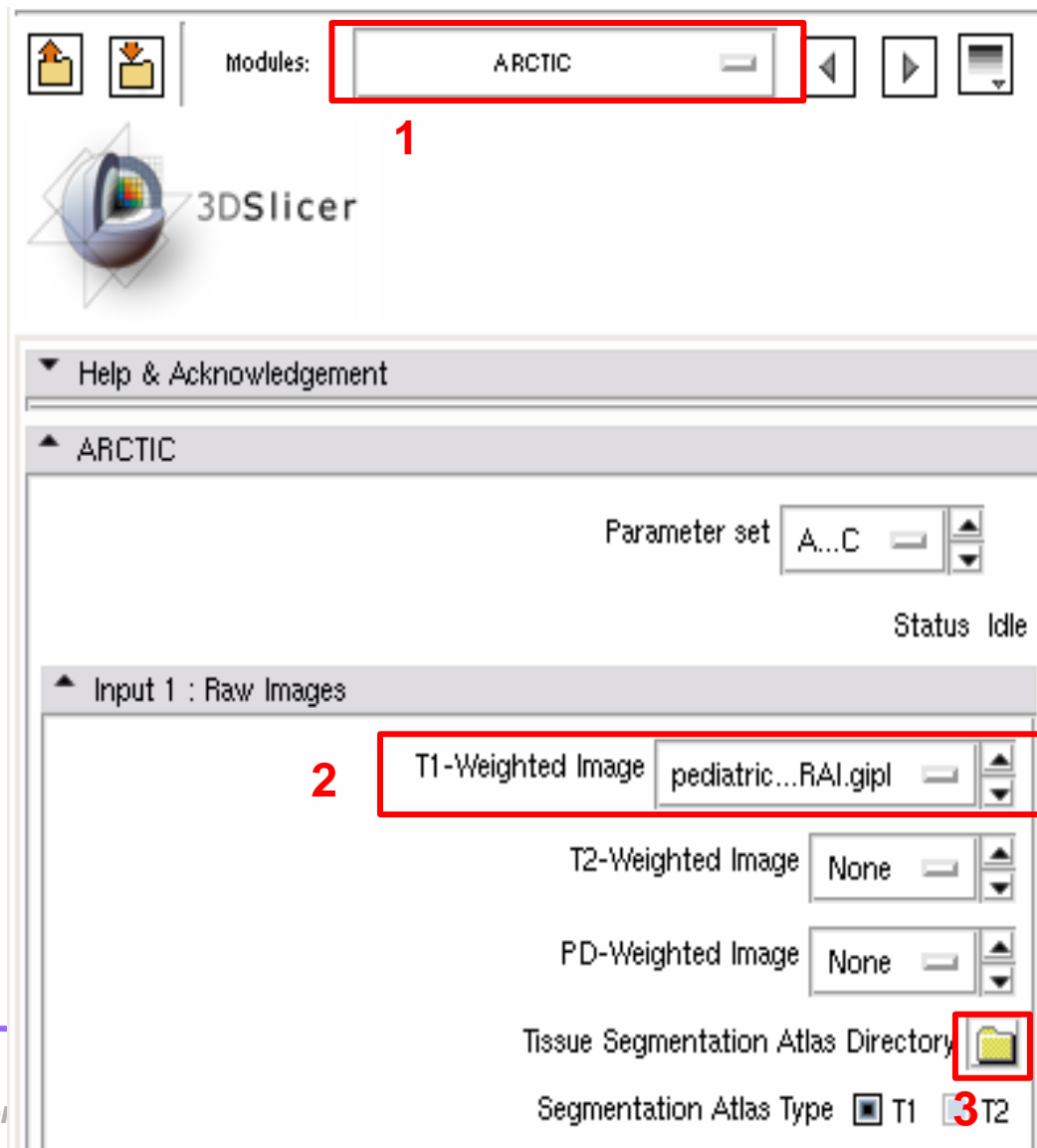
- Input images loading
- ARCTIC execution

Module execution

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

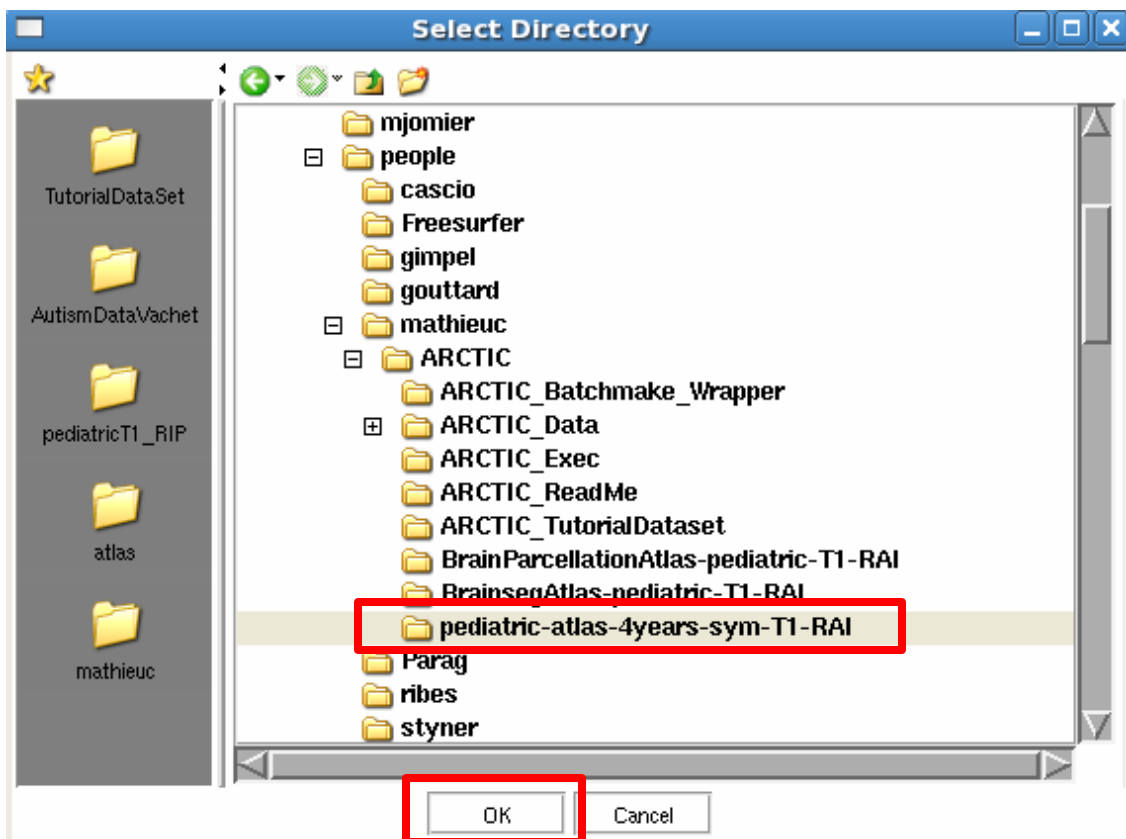
2- Set the T1-weighted images (**pediatric_T1_RAI.gipl**)

3- Click on the « **Tissue Segmentation Atlas Directory** » button



The screenshot shows the 3DSlicer interface with the ARCTIC module selected. The 'Modules' dropdown menu is set to 'ARCTIC', highlighted with a red box and a red '1'. Below it, the 'Parameter set' is 'A...C'. The 'Input 1 : Raw Images' section is expanded, showing 'T1-Weighted Image' set to 'pediatric...RAI.gipl', highlighted with a red box and a red '2'. The 'T2-Weighted Image' and 'PD-Weighted Image' are both set to 'None'. The 'Tissue Segmentation Atlas Directory' button is highlighted with a red box and a red '3'. The 'Segmentation Atlas Type' is set to 'T1' (checked) and 'T2' (unchecked).

Module execution



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

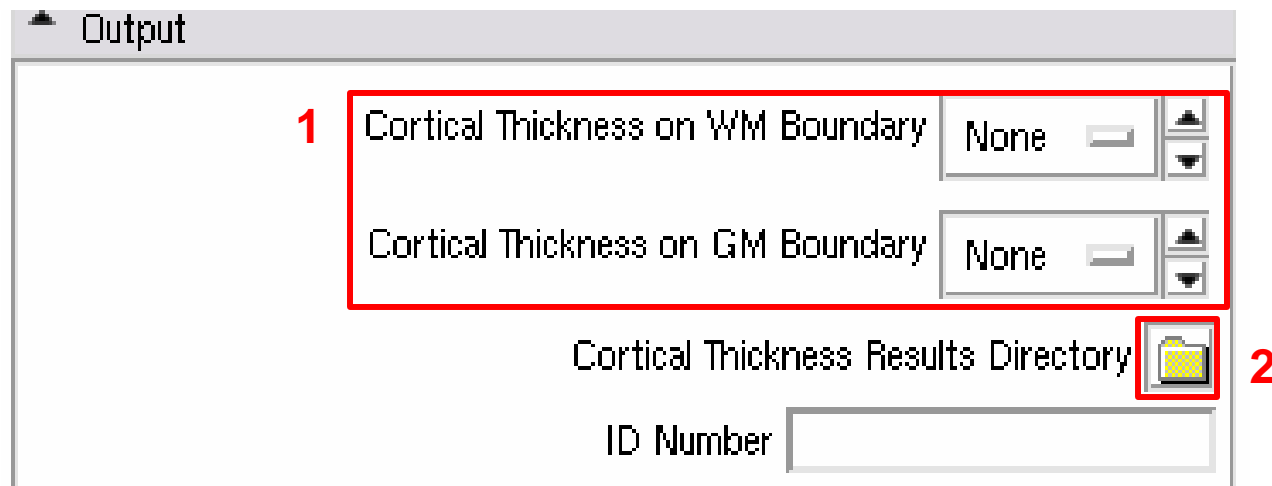
Search and select the « **pediatric-atlas-4years-sym-T1-RAI/** » folder.

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

Module execution

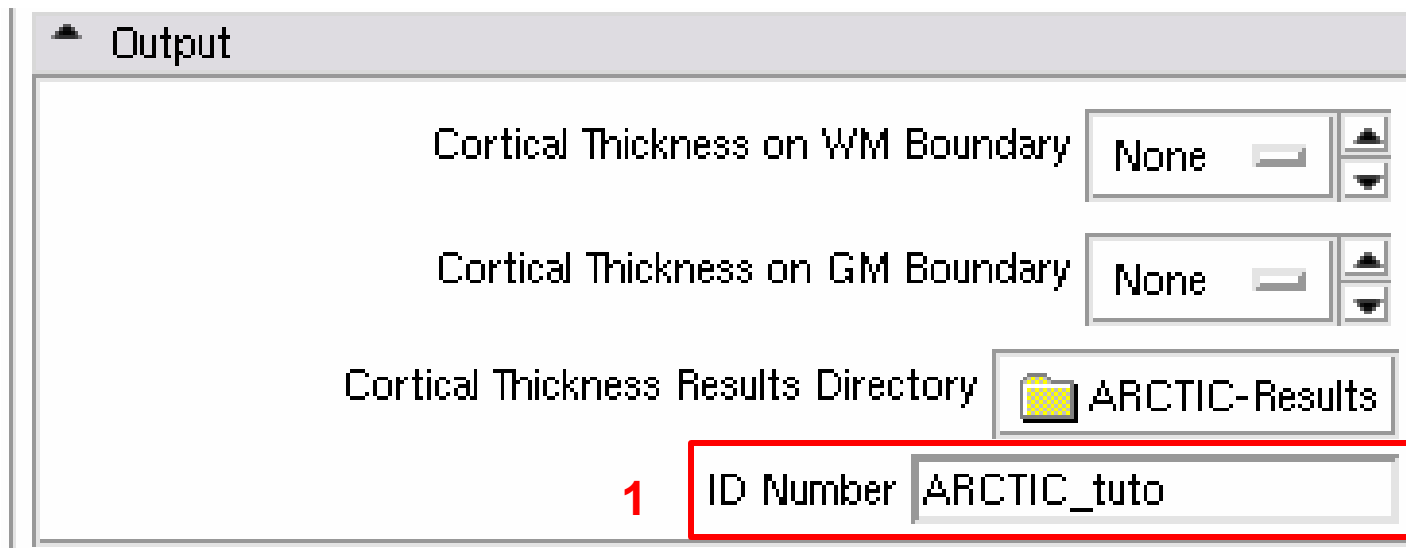
1- Select « **Create a new volume** » to display output images

2- Click on the « **Cortical Thickness Results Directory** » button

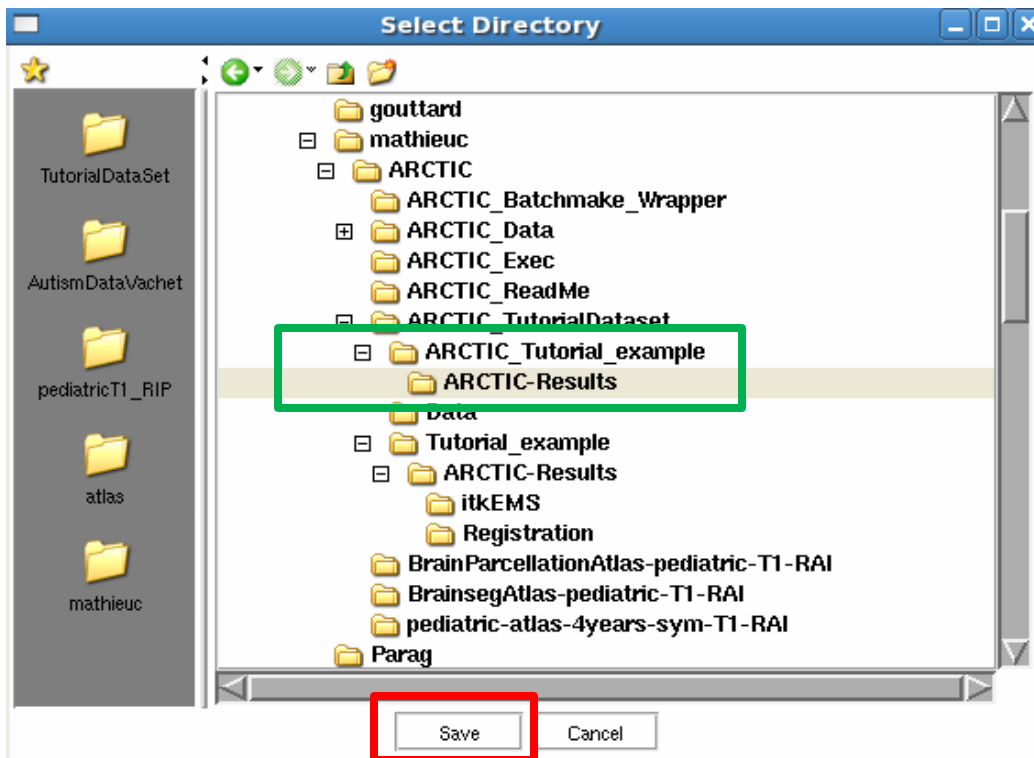


Module execution

- 1- Set the prefix for the outputs.



Module execution



Select the « **ARCTIC-Results** » folder in the ARCTIC_Tutorial_Example directory

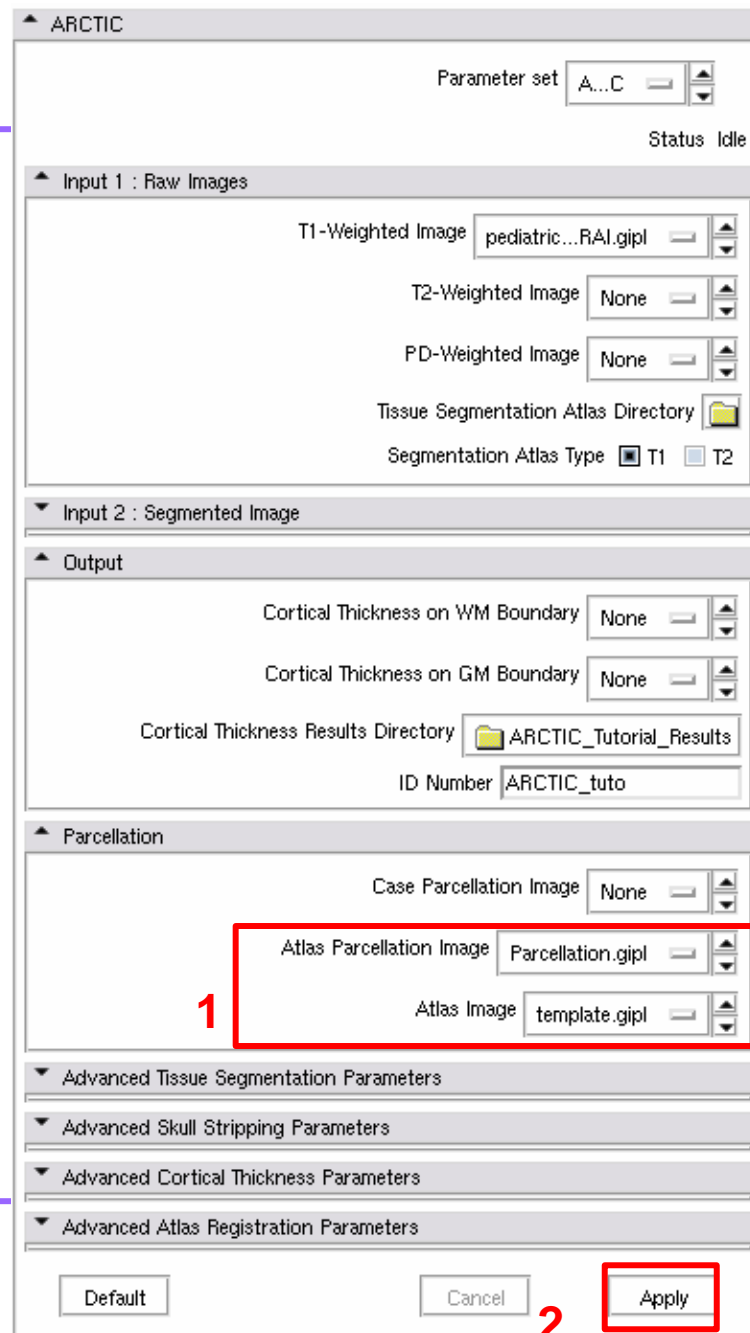
Click on the « **Save** » button to confirm your choice.



Module execution

1- Add the « **Parcellation.gipl** » as Atlas Parcellation Image, and the « **template-stripped.gipl** » as Atlas Image

2- Click on the « **Apply** » button to start the process.



Module execution

Once the execution is finished, several images are displayed within Slicer. You can compare your images with the following ones to perform a quick quality control.



Cortical Thickness on WM Boundary



Cortical Thickness on GM Boundary

- 1- Pipeline overview
- 2- Input images
- 3- Pipeline description
- 4- Output images and organisation
- 5- Execution within Slicer
- 6- Example with tutorial dataset
- 7- **Command line execution**



Use the command line

« Raw Images » Mode

Global analysis

```
ARCTIC --T1 Image_T1.nrrd --segAtlasDir TissueSegmentationAtlasDirectory/
```

Lobar cortical thickness analysis

If the atlas raw image and its parcellation are provided:

```
ARCTIC --T1 Image_T1.nrrd --segAtlasDir TissueSegmentationAtlasDirectory/  
--atlas Atlas.nrrd --atlasParcellation Parcellation.nrrd
```

If the case parcellation image is provided:

```
ARCTIC --T1 Image_T1.nrrd --segAtlasDir TissueSegmentationAtlasDirectory/  
--caseParcellation CaseRegisteredParcellation.nrrd
```



Use the command line

« Raw Images » Mode

Complementary flags

--T2 *Image_T2.gipl* / **--pd** *Image_PD.gipl* : T2 and/or Pd-weighted image(s) can be added to improve tissue segmentation

--atlasOrientation *RAI* : if the orientation of your atlas/parcellation is different than the default value (RAI), add this flag to set the right orientation

--atlasType *T1* : if the type of your tissue segmentation atlas is different than T1 (default value)

--outputDir *output_directory/* : if you want to select the output directory, add this flag and indicate the path an existing folder

--IDNumber *prefix* : if you want to add a prefix before all the outputs generated by the pipeline

--SaveWM *WMCorticalThicknessMap.gipl* / **--SaveGM** *GMCorticalThicknessMap.gipl* : those flags are used to save a volume with information of the average cortical thickness on WM/GM boundary(ies), the fileName needed is a path with the name of the output volume



Use the command line

« Segmented Image » Mode

Global analysis

```
ARCTIC --label TissueSegmentationImage.nrrd --rawImage Image_T1.nrrd
```

Lobar cortical thickness analysis

If the atlas raw image and its parcellation are provided:

```
ARCTIC --label TissueSegmentationImage.nrrd --rawImage Image_T1.nrrd  
--atlas Atlas.nrrd --atlasParcellation Parcellation.nrrd
```

If the case parcellation image is provided:

```
ARCTIC --label TissueSegmentationImage.nrrd --rawImage Image_T1.nrrd  
--caseParcellation CaseRegisteredParcellation.nrrd
```



Use the command line

« Segmented Image » Mode

Complementary flags

--WMLabel *1* / **--GMLabel** *2* / **--CSFLabel** *3* : if your label are different than the default value

--outputDir *output_directory/* : if you want to select the output directory, add this flag and indicate the path an existing folder

--IDNumber *prefix* : if you want to add a prefix before all the outputs generated by the pipeline

--SaveWM *WMCorticalThicknessMap.gipl* / **--SaveGM** *GMCorticalThicknessMap.gipl* : those flags are used to save a volume with information of the average cortical thickness on WM/GM boundary(ies), the fileName needed is a path with the name of the output volum



Conclusion

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

Thanks to this tutorial you are now ready to perform a regional cortical thickness analysis on your own dataset.



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