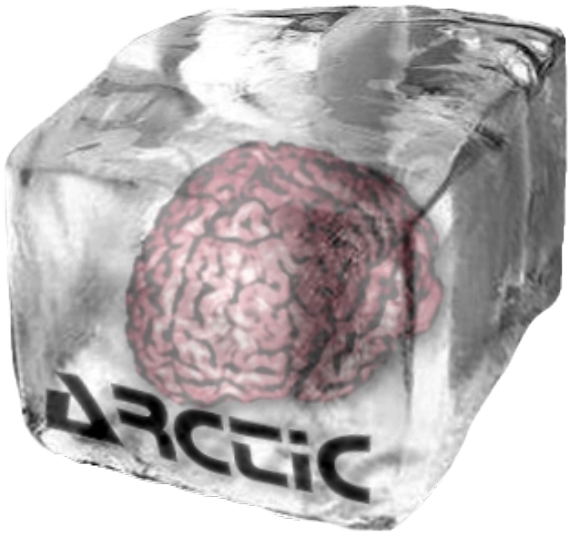
# Slicer3 Training Tutorial

# ARCTIC (v1.2)

## (Automatic Regional Cortical ThICkness)

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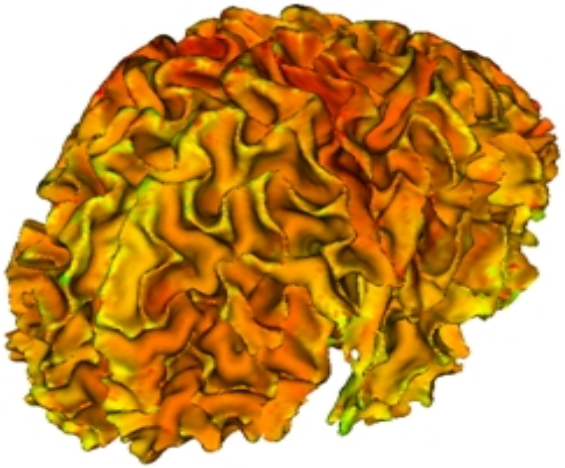
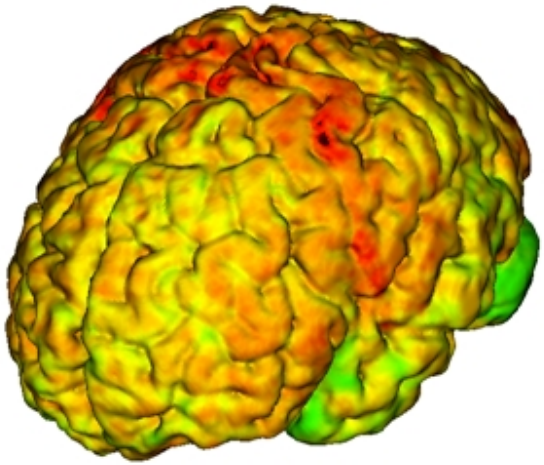
# Learning Objective

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

# Materials

**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

# 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).

# Prerequisites

## 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)

# Prerequisites

## 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}/MRMLIDImageIO:${SLICERLIBPATH}/OpenIGTLink:${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}/MRMLIDImageIO:${SLICERLIBPATH}/OpenIGTLink:${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

# Overview

1- Pipeline overview
2- Input images
3- Pipeline description
4- Ouput 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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# Input images

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

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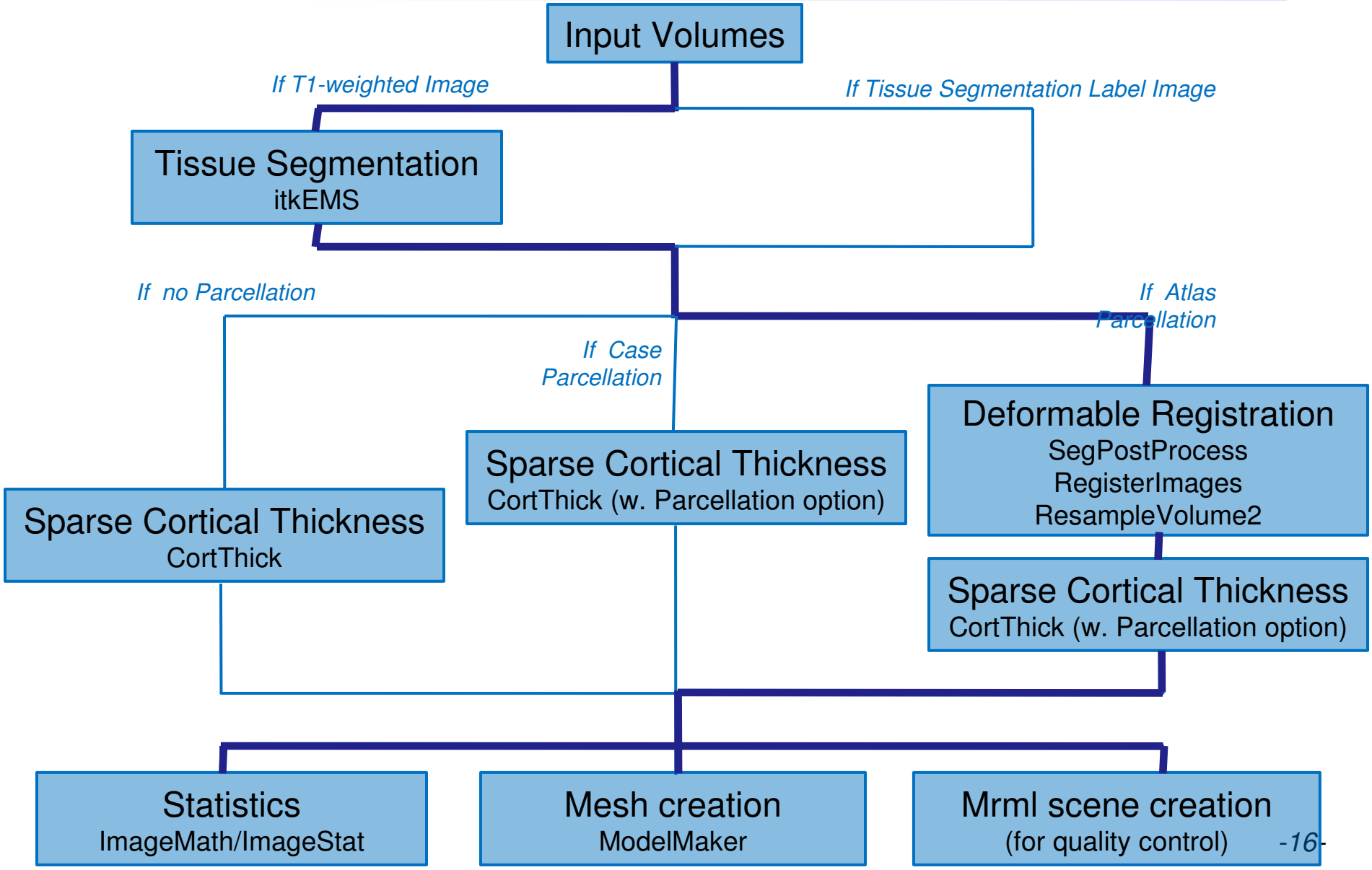
# Pipeline Description



# 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

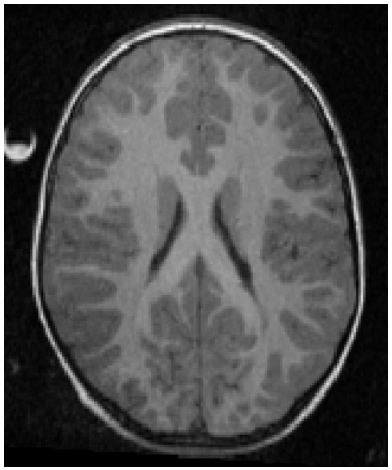
Module : ModelMaker (Slicer3 module)

## 6. Mrml scene Creation

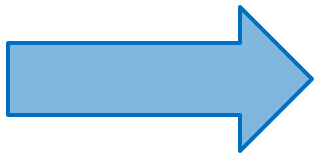
# Pipeline Description

## 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*

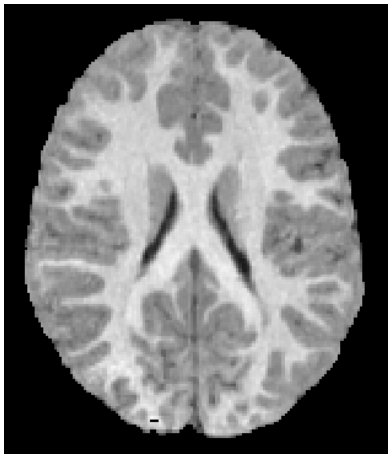
*Image_labels_EMS.nrrd*

# Pipeline Description

## Skull Stripping (SegPostProcess external module)

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

*Image_corrected_EMS.nrrd*



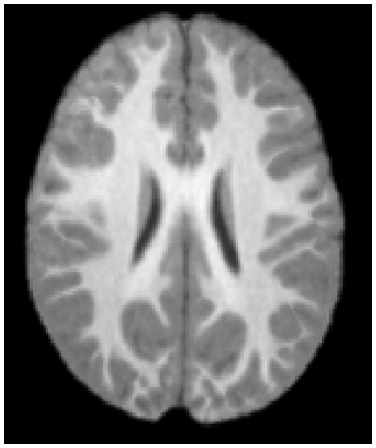
*Image_corrected_EMS_stripped.nrrd*

# Pipeline Description

## Deformable registration of T1-weighted atlas (RegisterImages module)

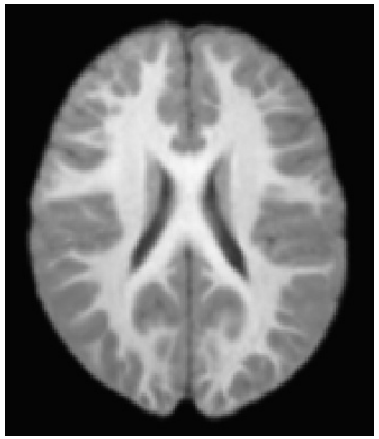
B-spline pipeline registration.
A transformation file is created and will be used by the next step.

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



*Atlas.nrrd*

*TransformFile.txt*



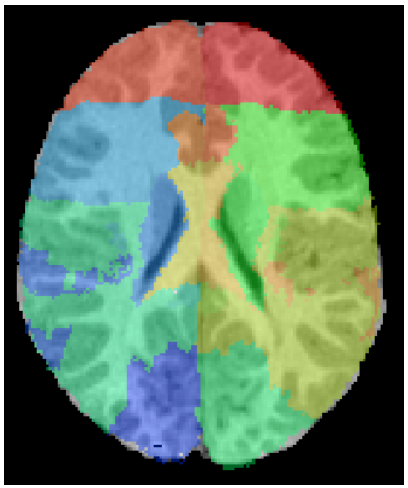
*AtlasRegistered_Image_corrected_EMS_stripped.nrrd*

# 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 cubic 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

In order to perform a quality control, a Mrml scene is created to display all the steps of the pipeline.
There is one snapshot per step.

# Overview

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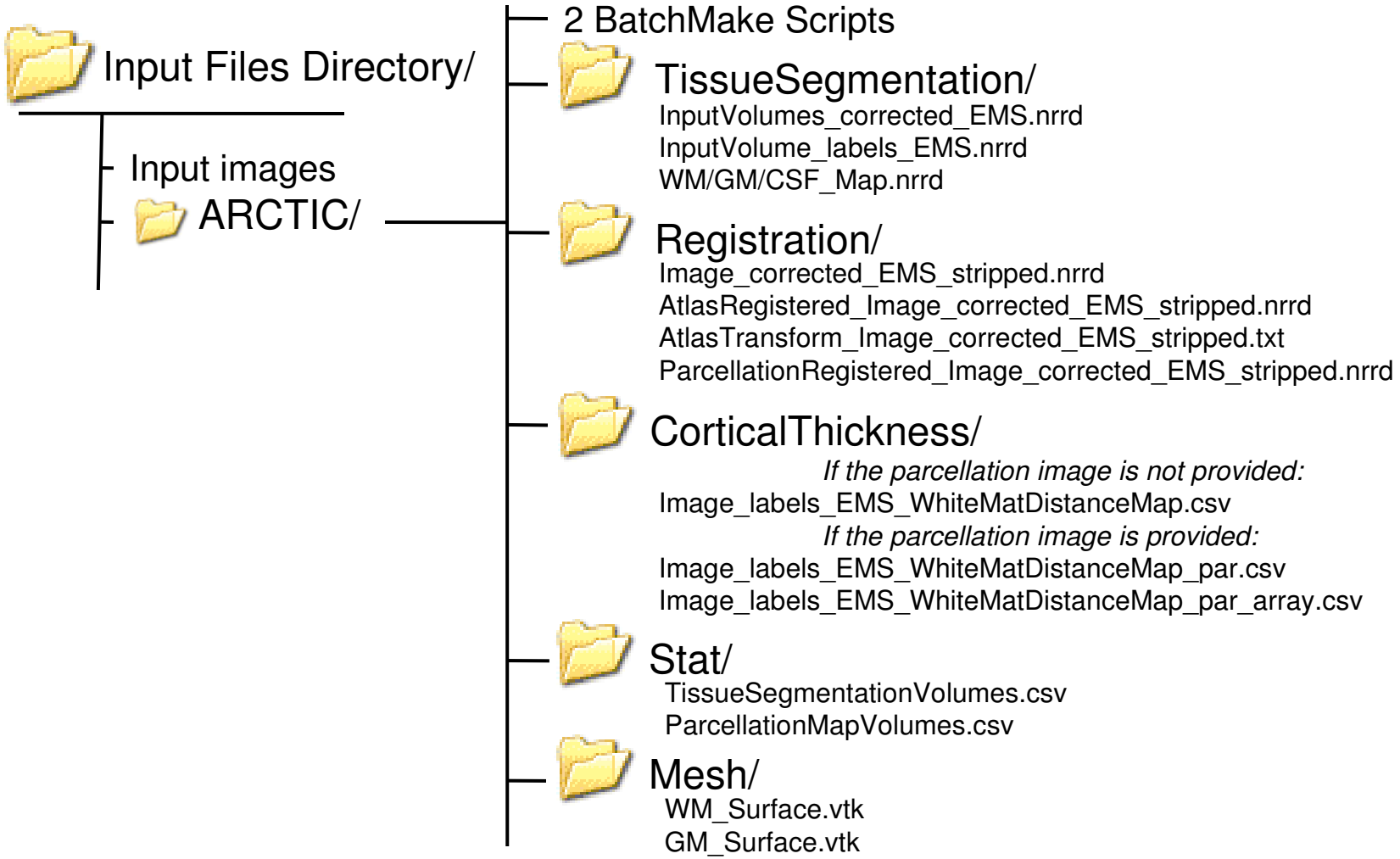
# Output and Organisation



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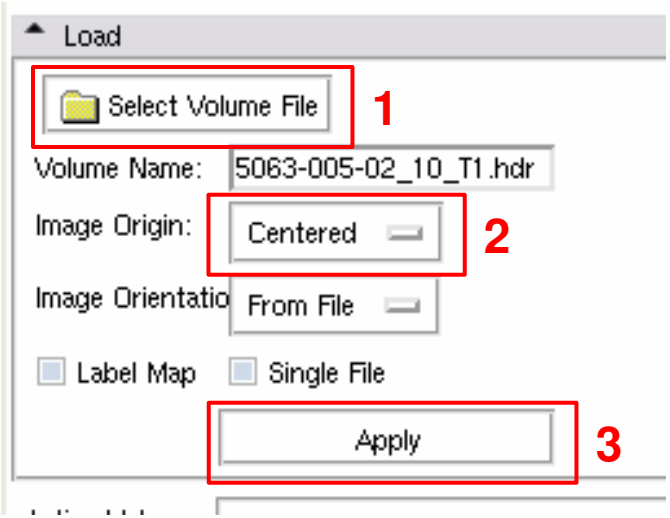
# Execution within Slicer

- **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

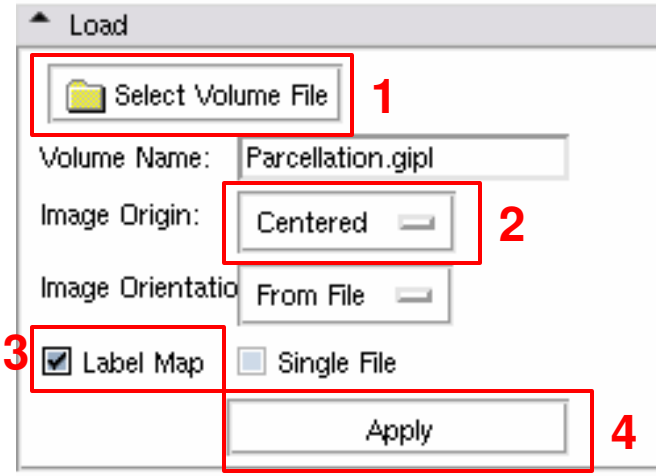
## How to load parcellation and label images?

**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)

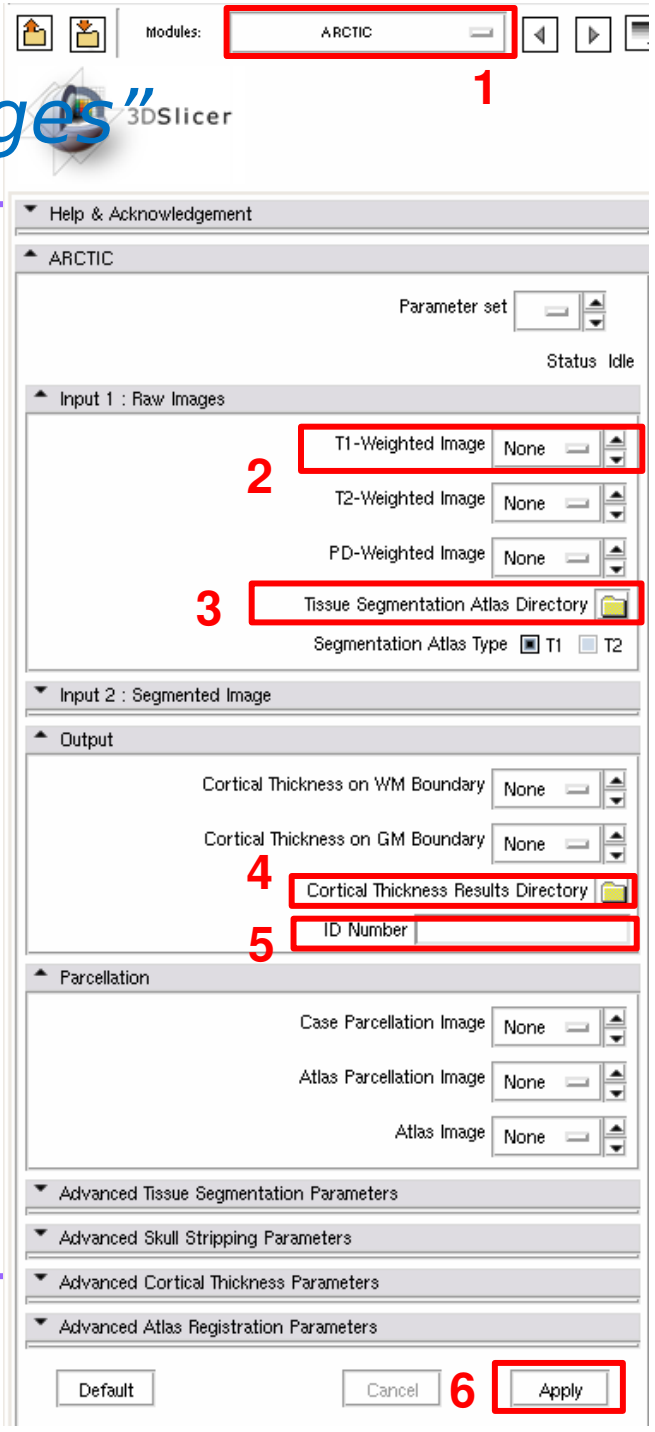
**2-** Add the T1-weighted image

**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



# Demonstration : “Raw Images”

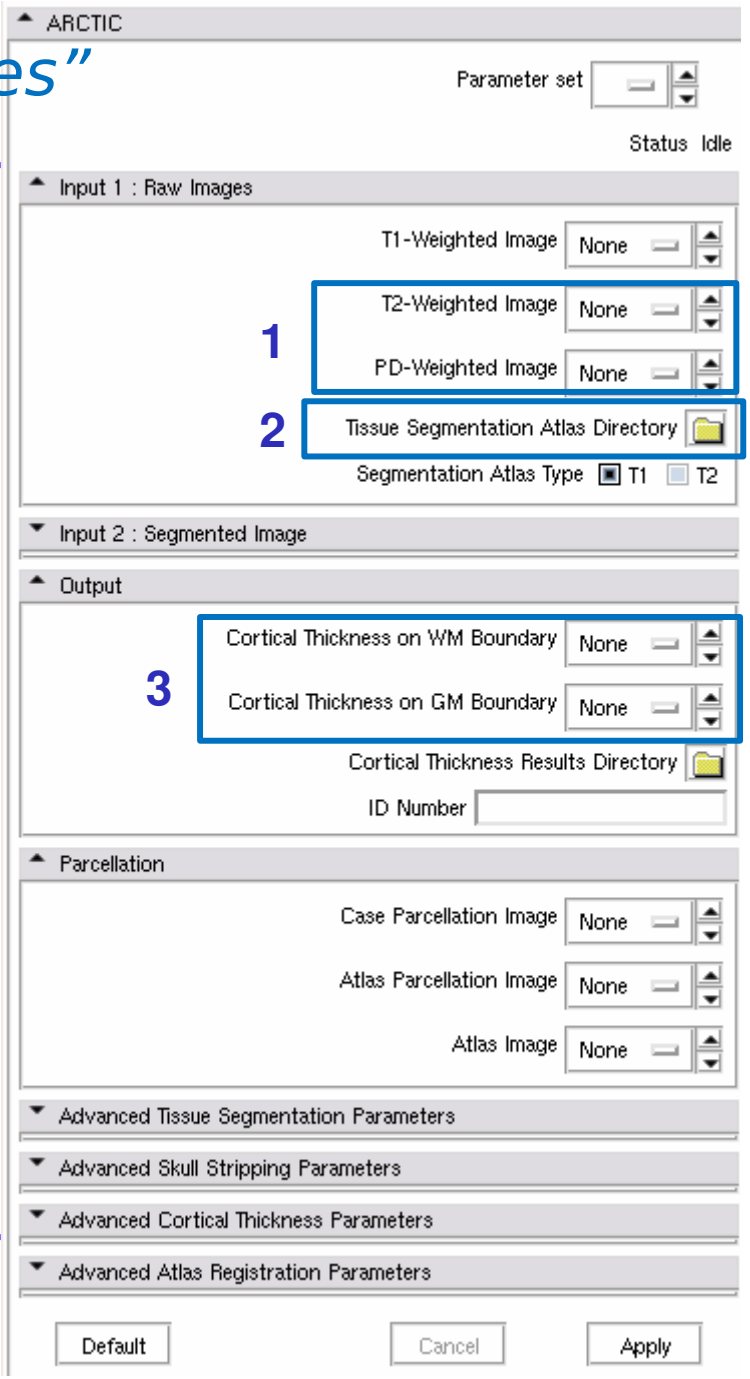
## Input 1

## 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)

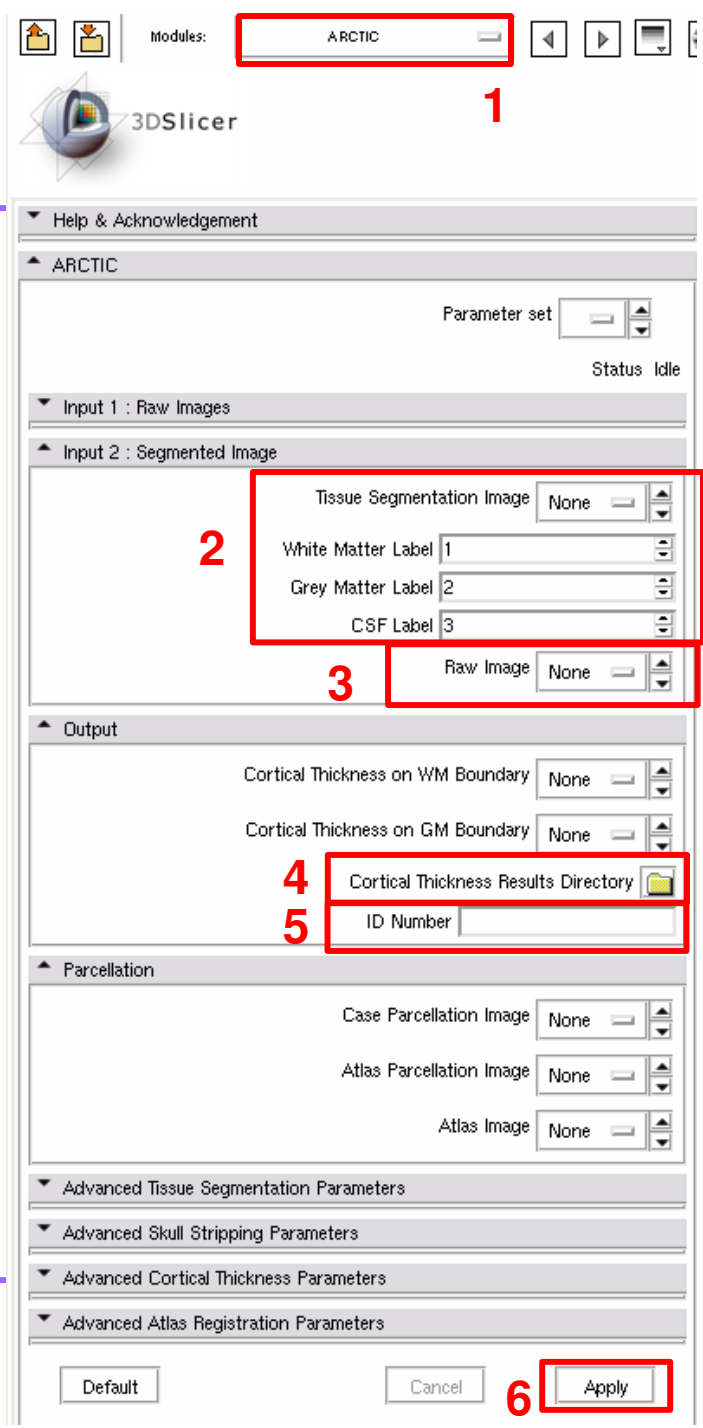
**2-** Set the tissue segmentation label image and check the related tissue labels

**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



# Demonstration : “Segmented Image”

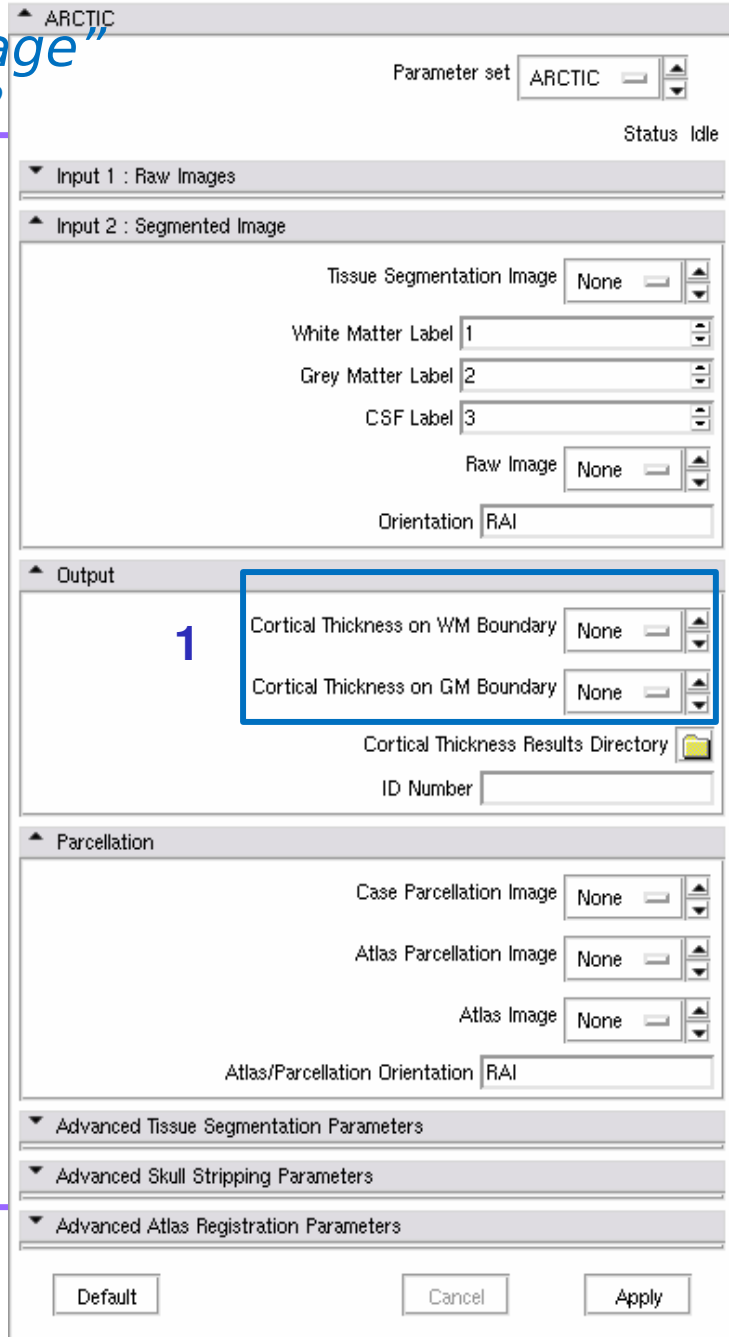
## *Input 2*

## 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*



# Demonstration in Slicer

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

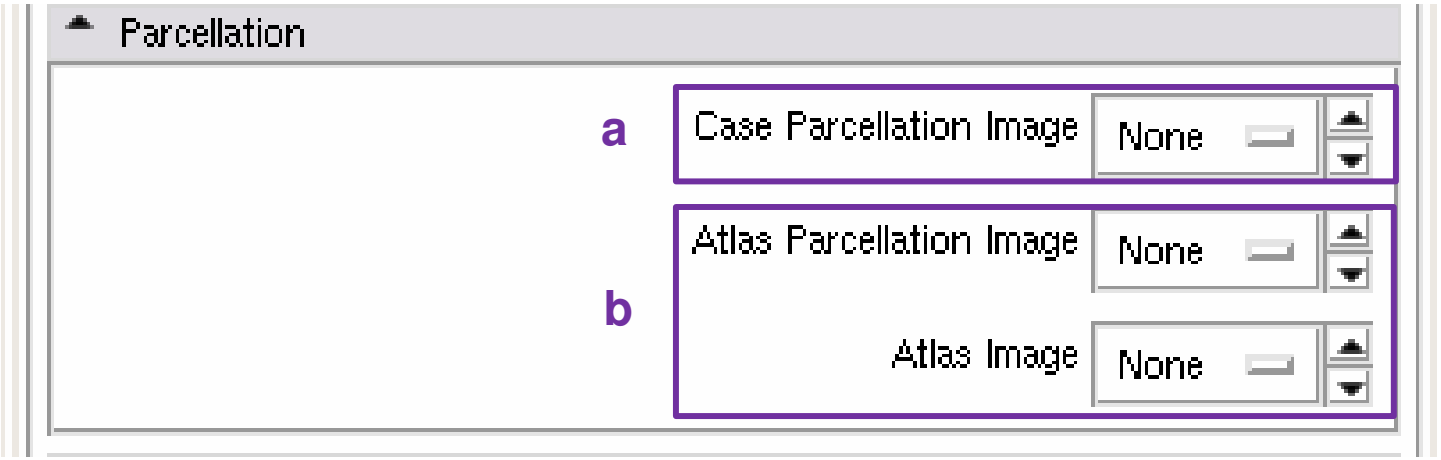
# Parcellation options

## 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

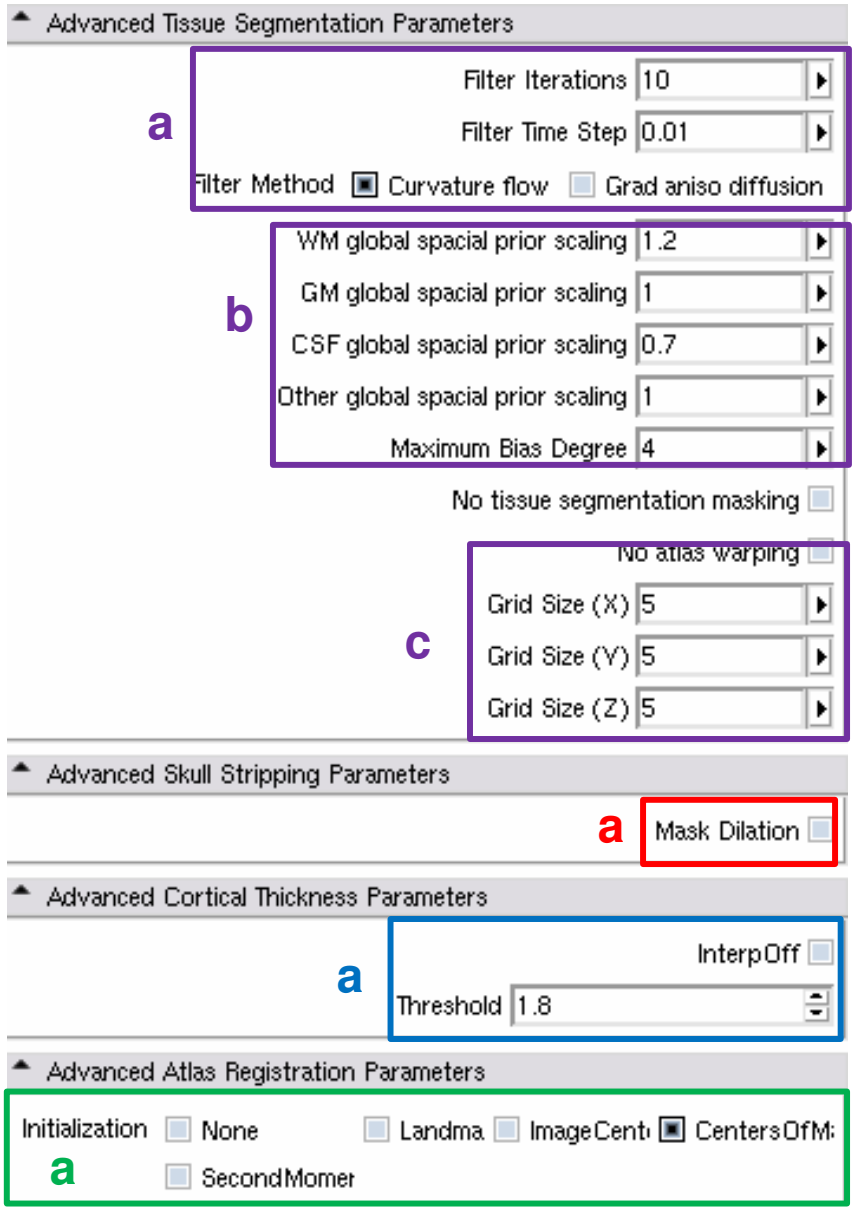
**a-** Check to apply a dilation of the mask (necessary if the tissue segmentation has a low quality)

## 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



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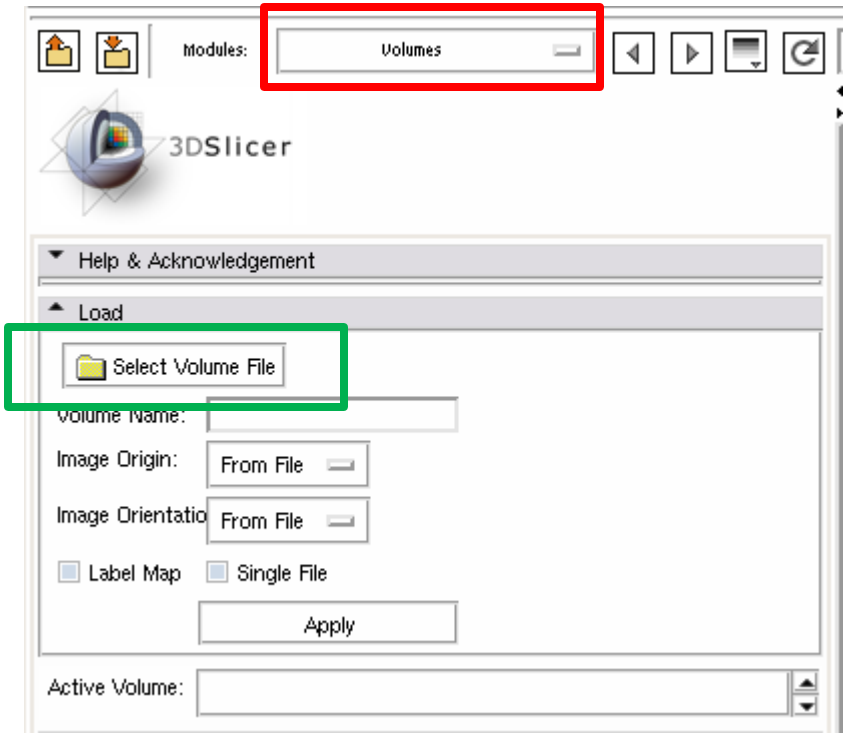
# Example with tutorial dataset

- Load input images
- Run ARCTIC

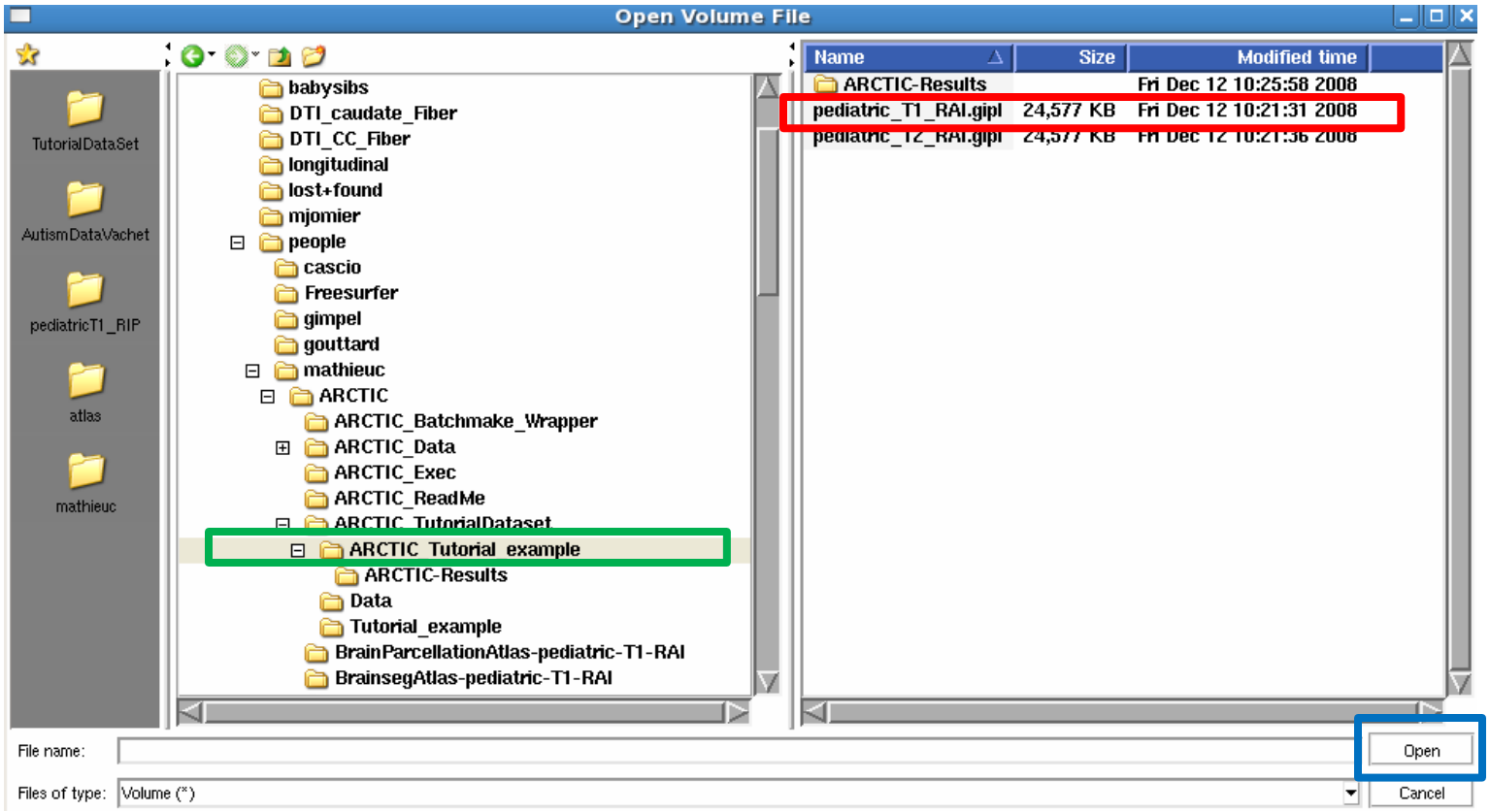
# Load input images




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

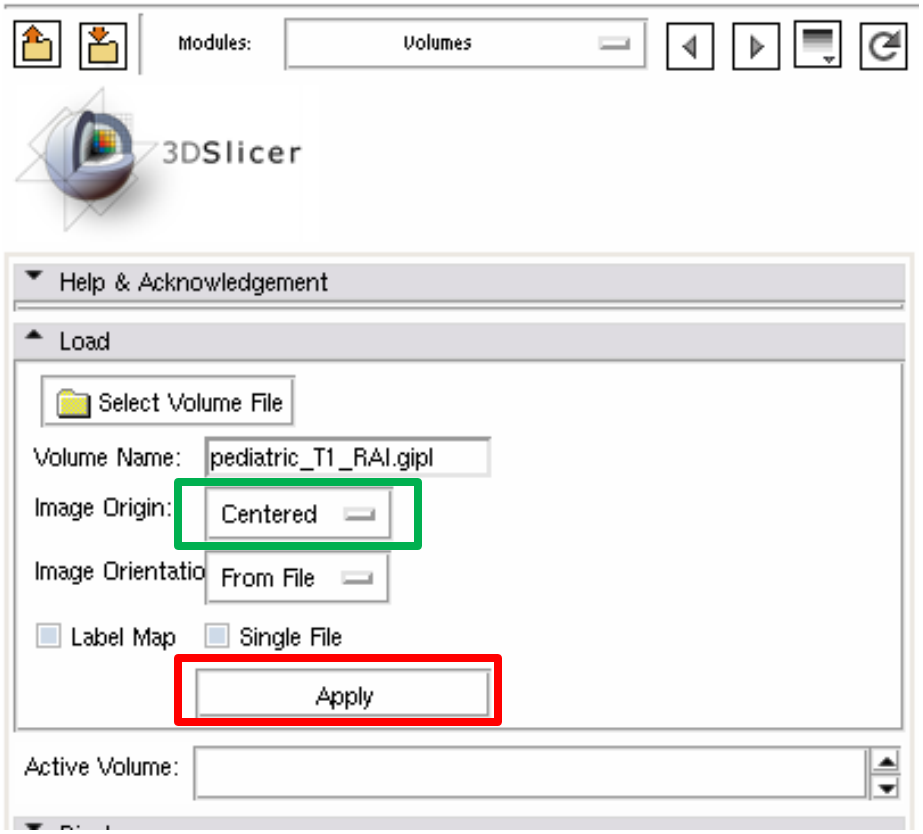
Then click on the « Select Volume File » button to load the images.

# 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 »**.

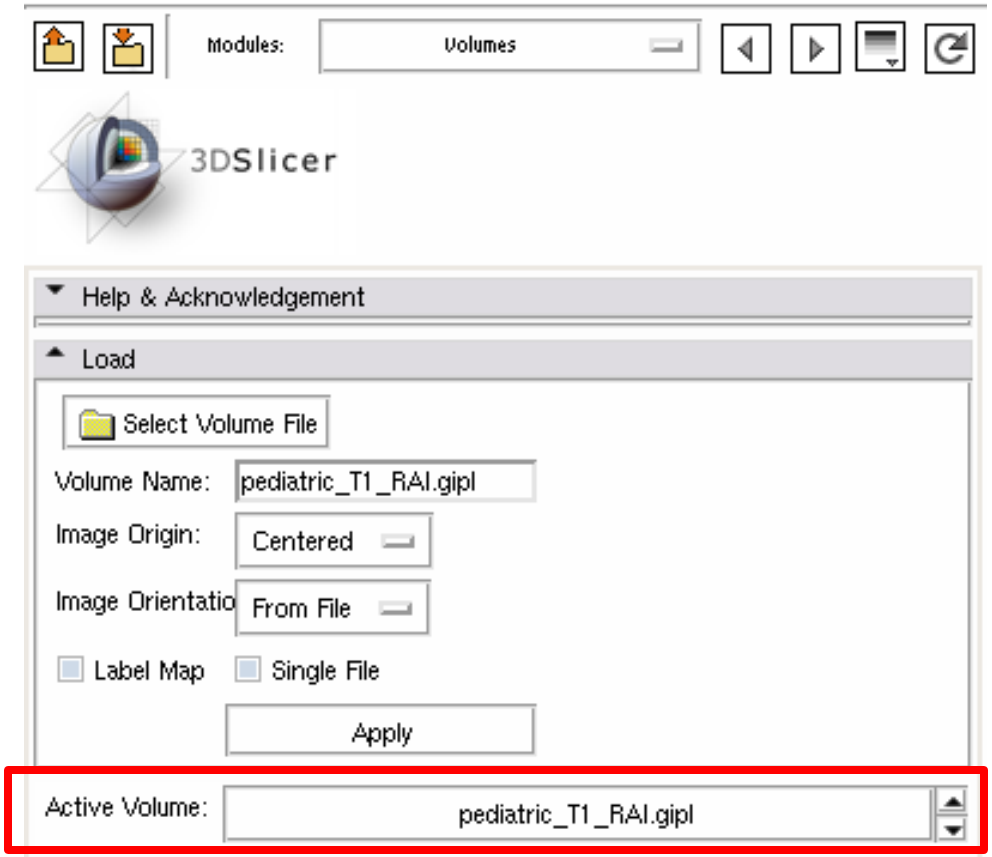
# Load input images




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.

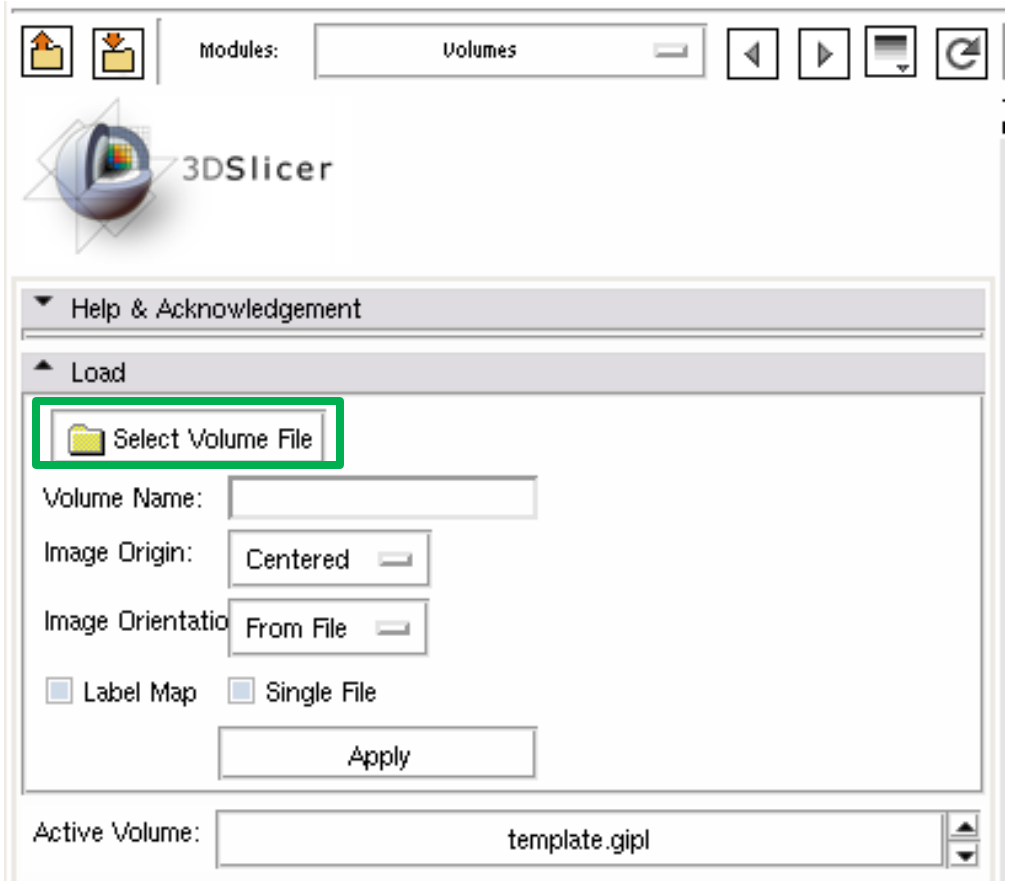
# Load input images

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.

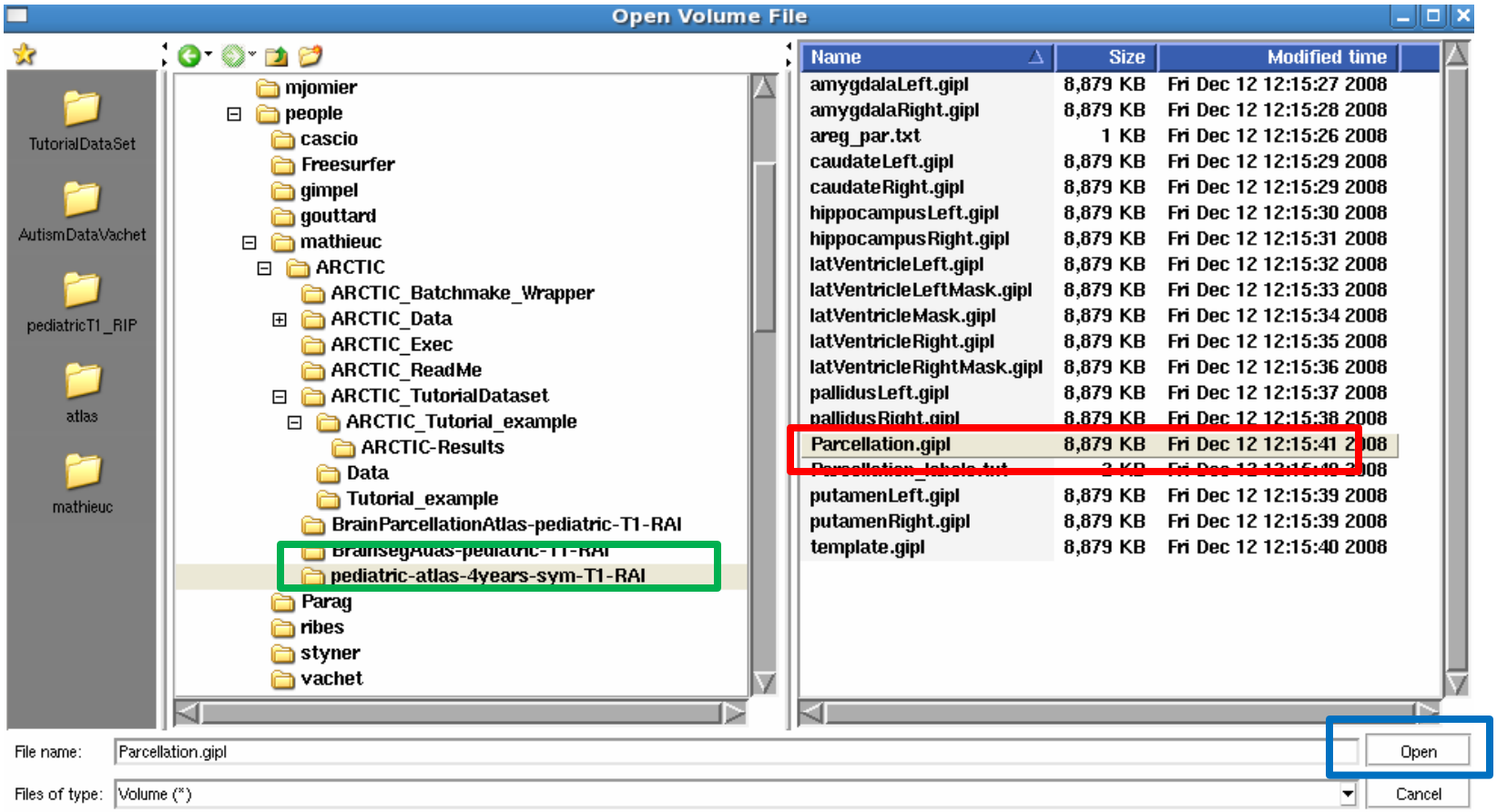
The atlas image, named « template-stripped.nrrd » is in the « pediatric-atlas-4years-sym-T1-RAI » directory.

# Load input images



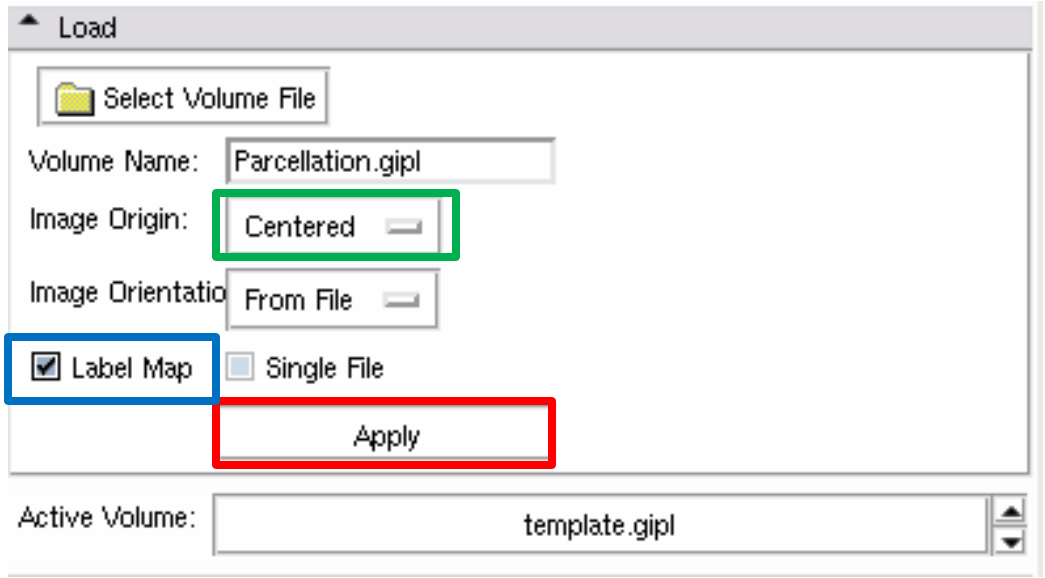

Now we will load the parcellation image.
Click on the « Select Volume File » button to load the parcellation.

# 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

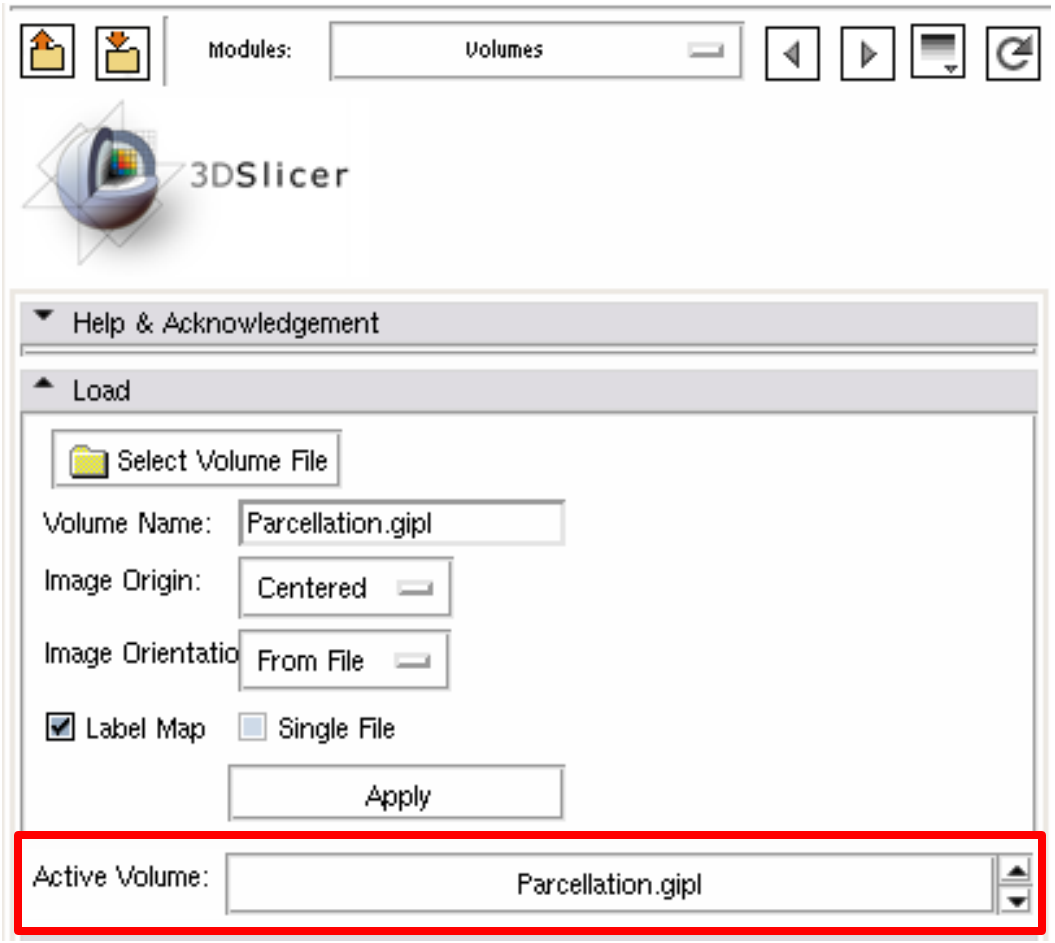



Now, select the Image Origin as « **Centered** ».

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

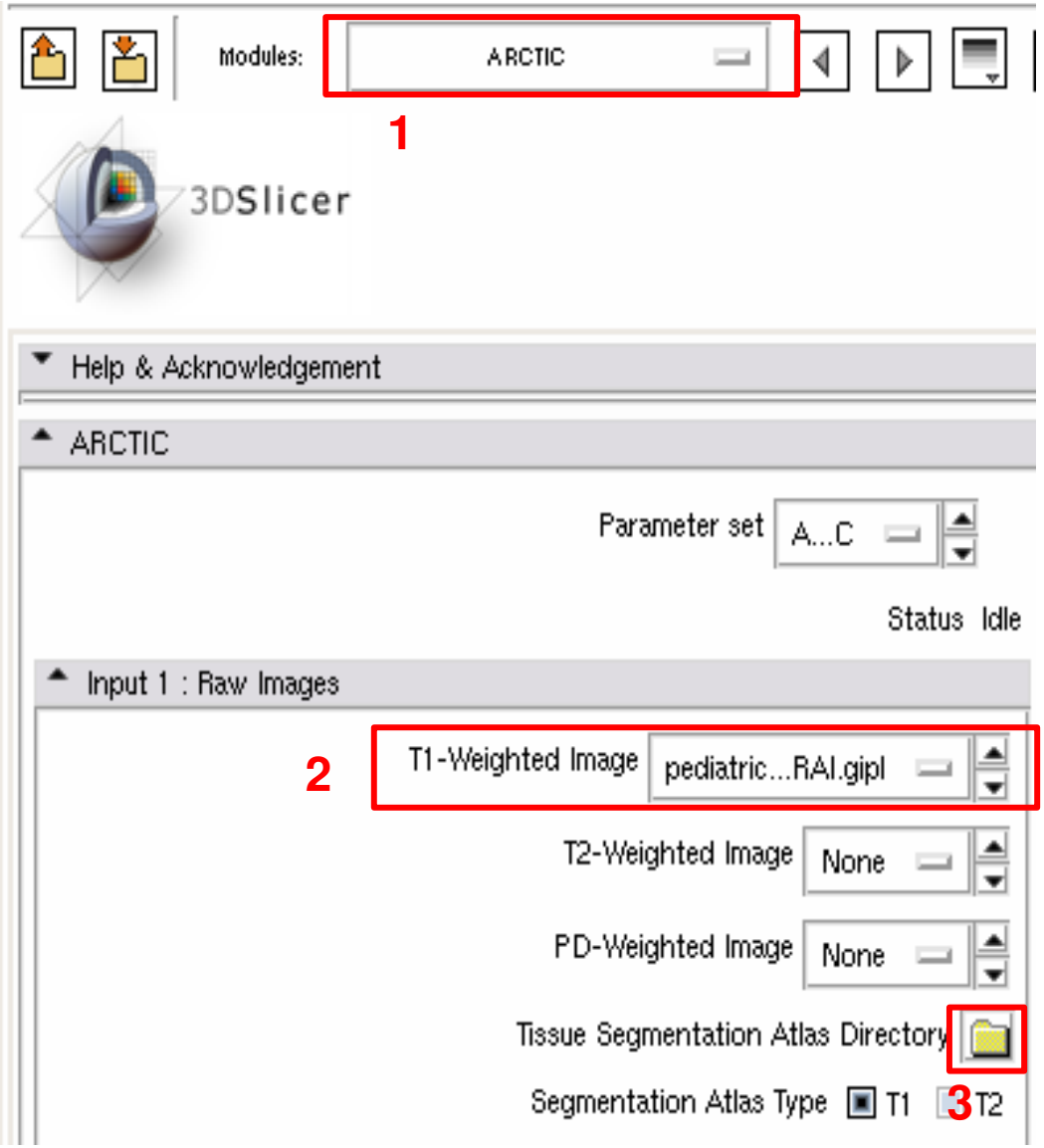
- Input images loading
- ARCTIC execution

# Module execution

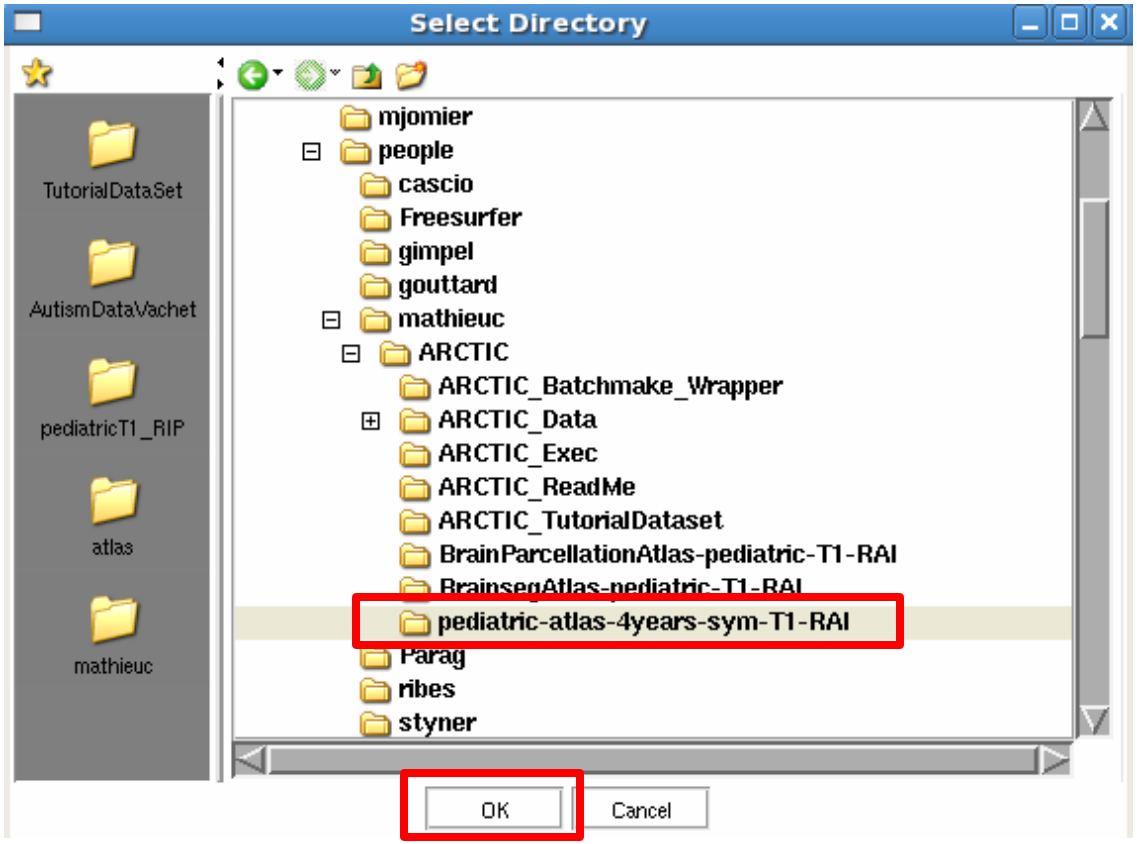
**1-** Select the « **ARCTIC** » module (in All Modules)

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

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



# Module execution




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

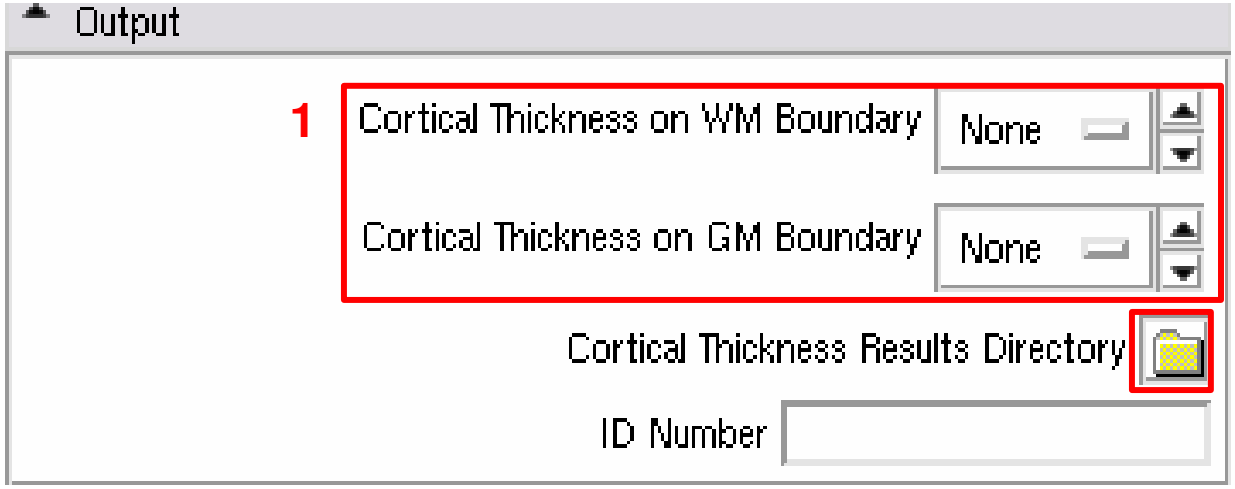
Search and select the « **pediatric-atlas-4years-sym-T1-RAI/**» folder.

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

# Module execution

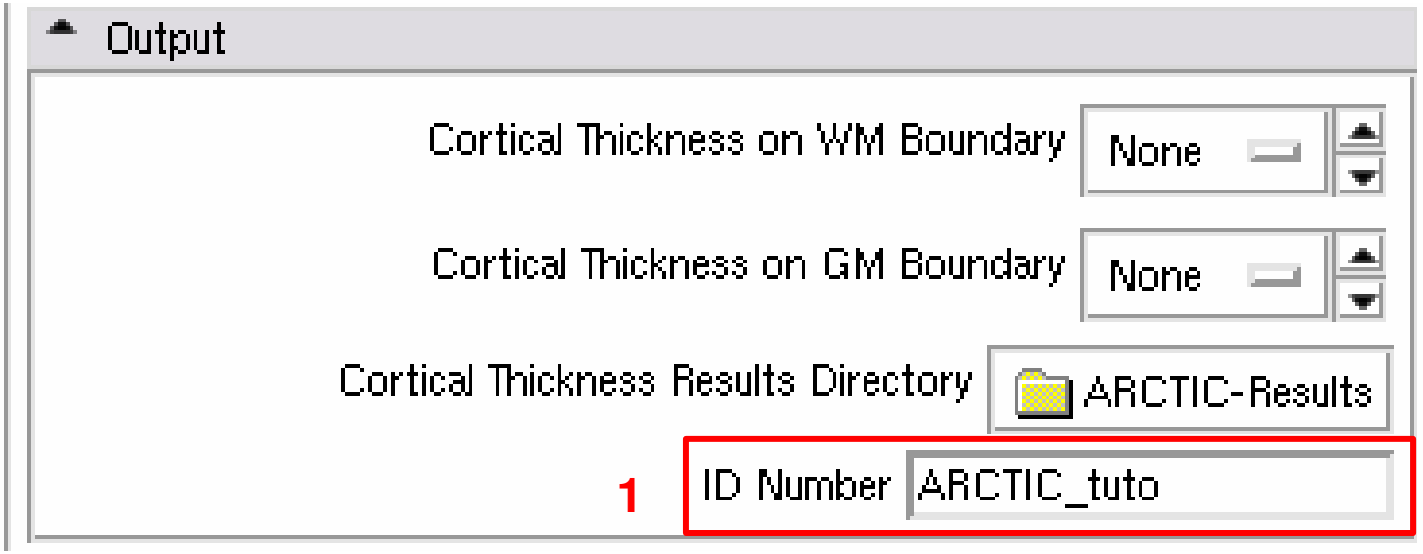
**1-** Select « **Create a new volume** » to display output images

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

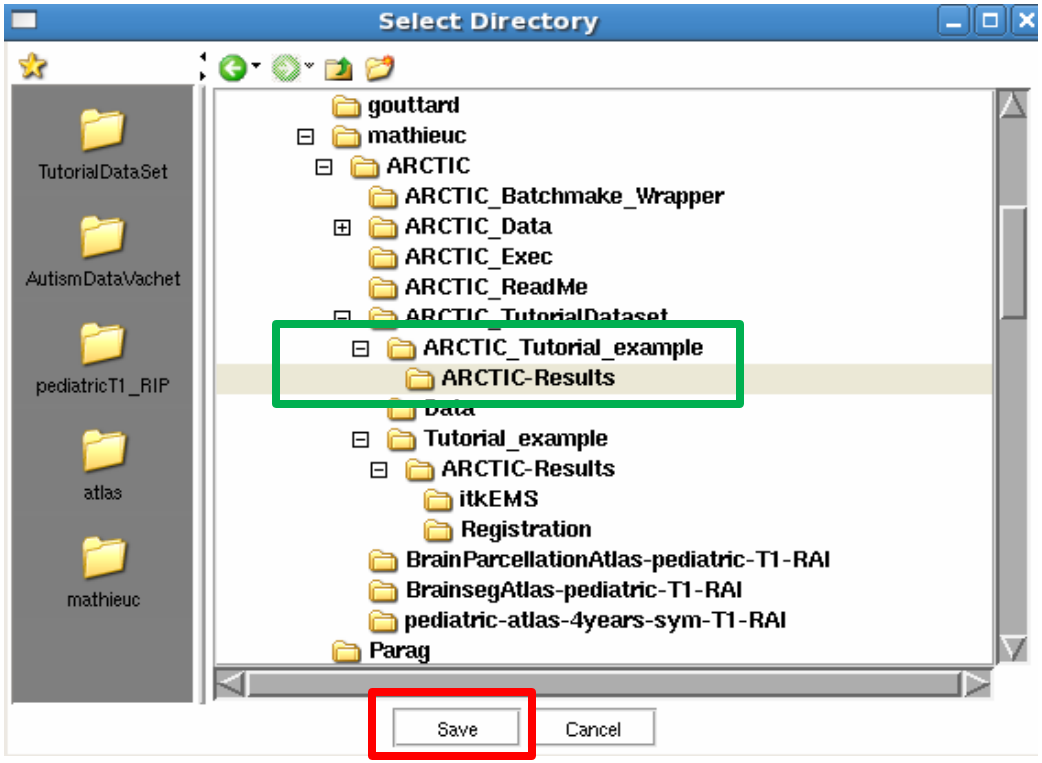


# Module execution

**1-** Set the prefix for the outputs.



# Module execution



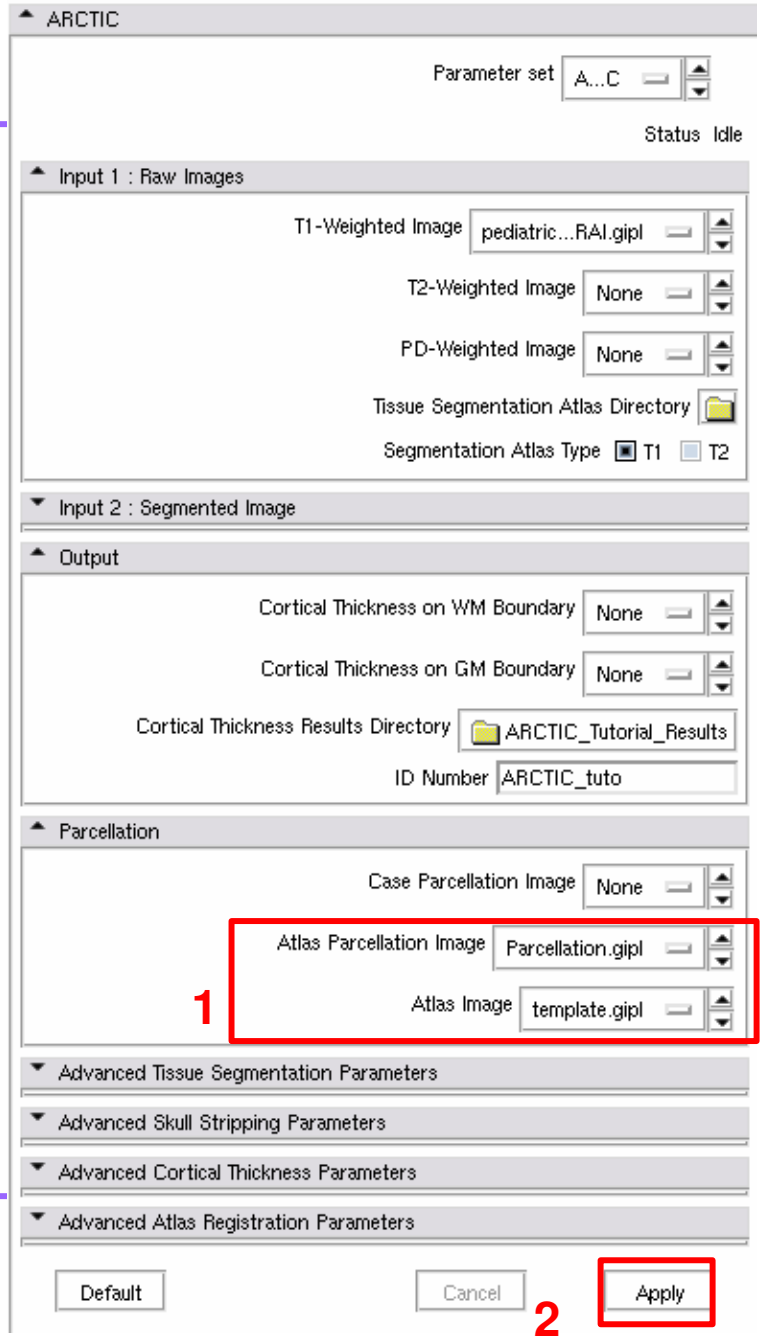

Select the « **ARCTIC-Results** » folder in the ARCTIC_Tutorial_Example directory

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*

# Overview

1- Pipeline overview
2- Input images
3- Pipeline description
4- Ouput 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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