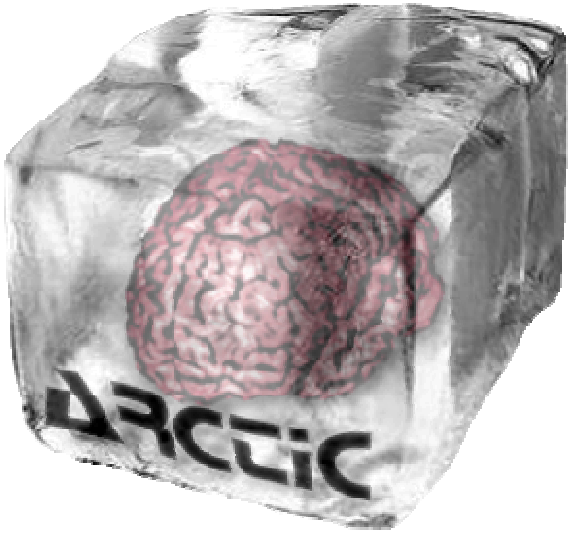
Slicer3 Training Tutorial

ARCTIC

(Automatic Regional Cortical ThICkness)



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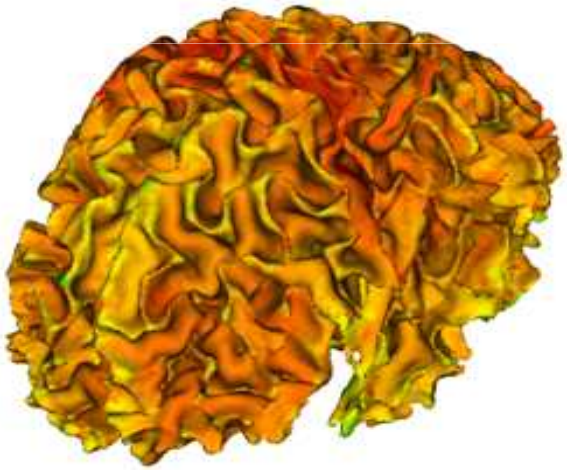
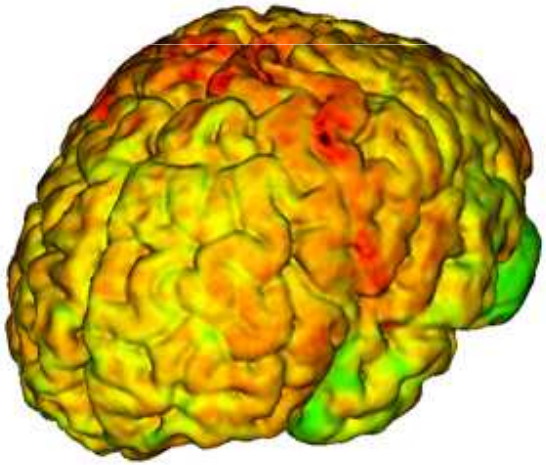
Learning Objective

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, BatchMake wrappers, 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

- BatchMake download page (***BatchMake 1.0.6***)

http://www.batchmake.org/batchmake/resources/software.html

- BatchMake wrapper download page (***ARCTIC_BatchMake_Wrapper_1.0***)
- 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 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_1.0"* 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).

Prerequisites

Add the executables in the PATH.

-**tcsh usage :** setenv PATH ARCTIC-Executables-Directory/:Slicer3D-Plugins-Directory/:Batchmake-Directory/:${PATH}
-**bash usage** : export PATH=ARCTIC-Executables-Directory/:Slicer3D-Plugins-Directory/:Batchmake-Directory/:${PATH}

Notice : To execute ARCTIC within Slicer3, it is not necessary to add "Slicer3D-Plugins-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_1.0)
Slicer3D-Plugins-Directory/ : Directory containing Slicer3 plugins
- Release: “Slicer3Dir”/lib/Slicer3/Plugins
- Compiled Version: “Slicer3Dir”/Slicer3-build/lib/Slicer3/Plugins

Batchmake-Directory/ : Directory containing BatchMake application
Batchmake-Wrapper-Directory/ : Downloaded folder (ARTIC_Batchmake_Wrapper_1.0)

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

Overview

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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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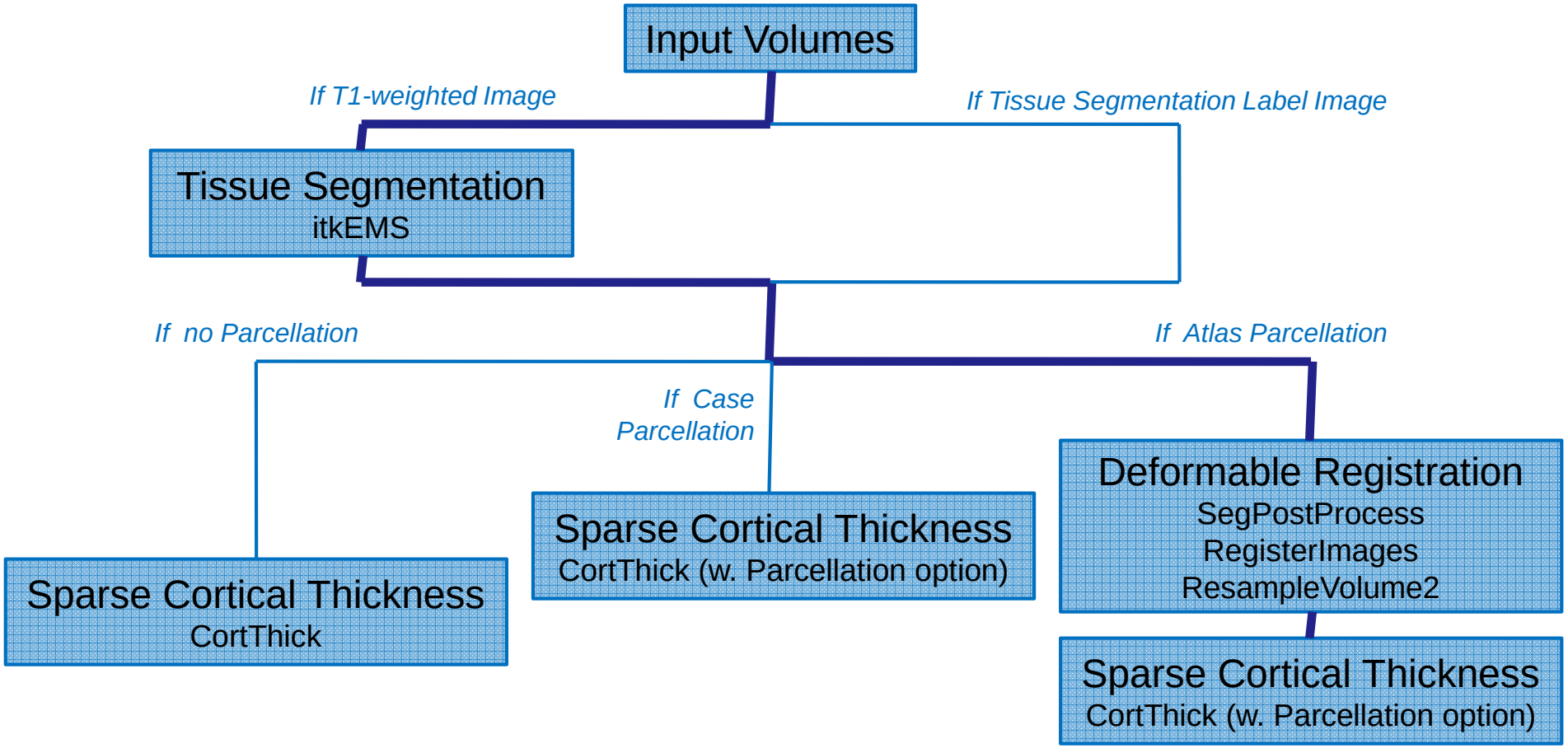
Pipeline Description



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)

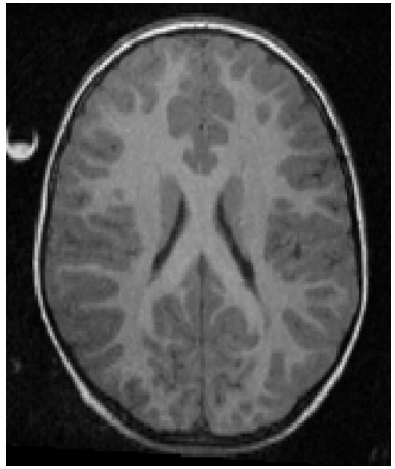
3. Sparse and asymmetric Cortical Thickness

Module : CortThick (UNC Slicer3 module)

Pipeline Description

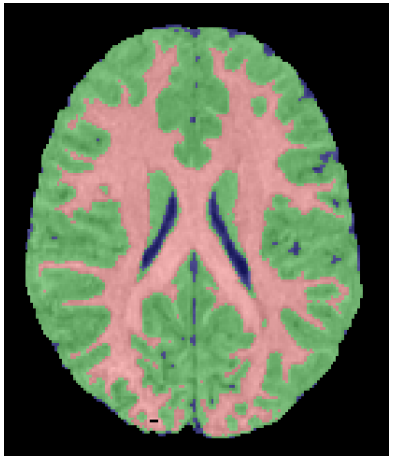
Tissue segmentation (itkEMS external module)

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.gipl

Image_corrected_EMS.gipl

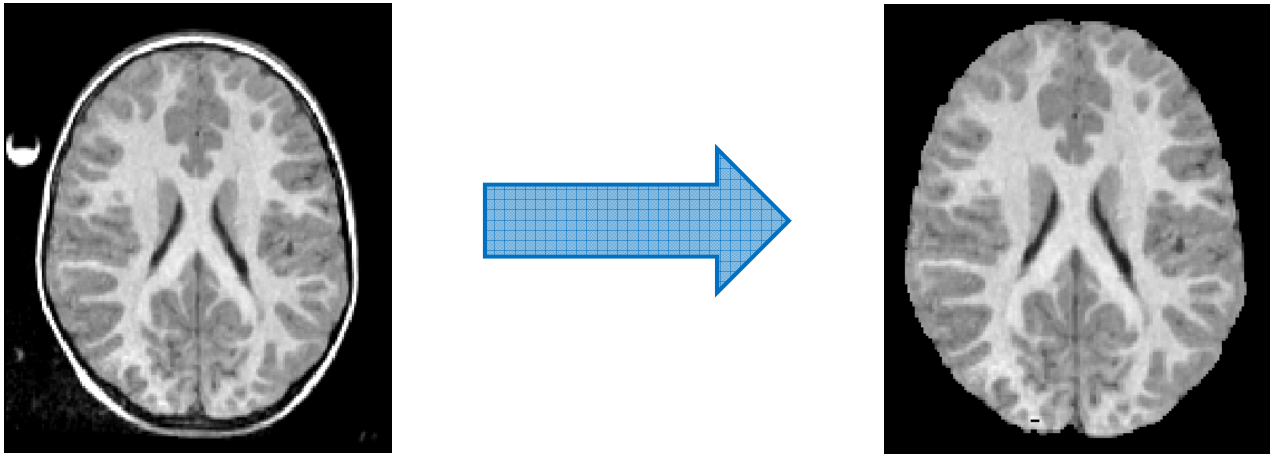


Image_labels_EMS.gipl

Pipeline Description

Skull Stripping (SegPostProcess external module)

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



Image_corrected_EMS.gipl

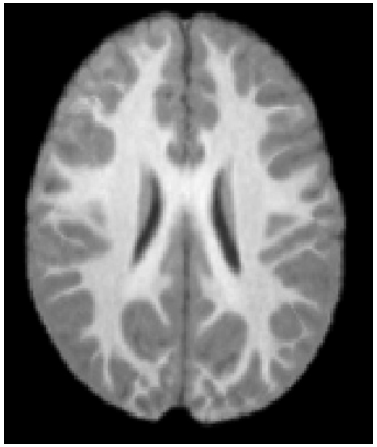
Image_corrected_EMS_stripped.gipl

Pipeline Description

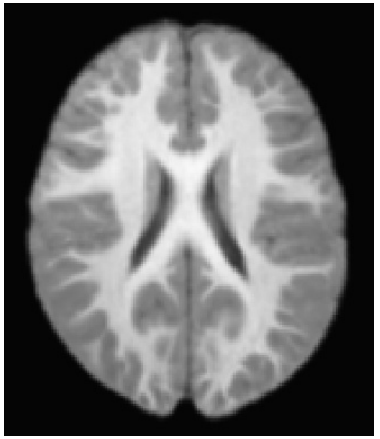
Deformable registration of T1-weighted atlas (RegisterImages module)

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.gipl

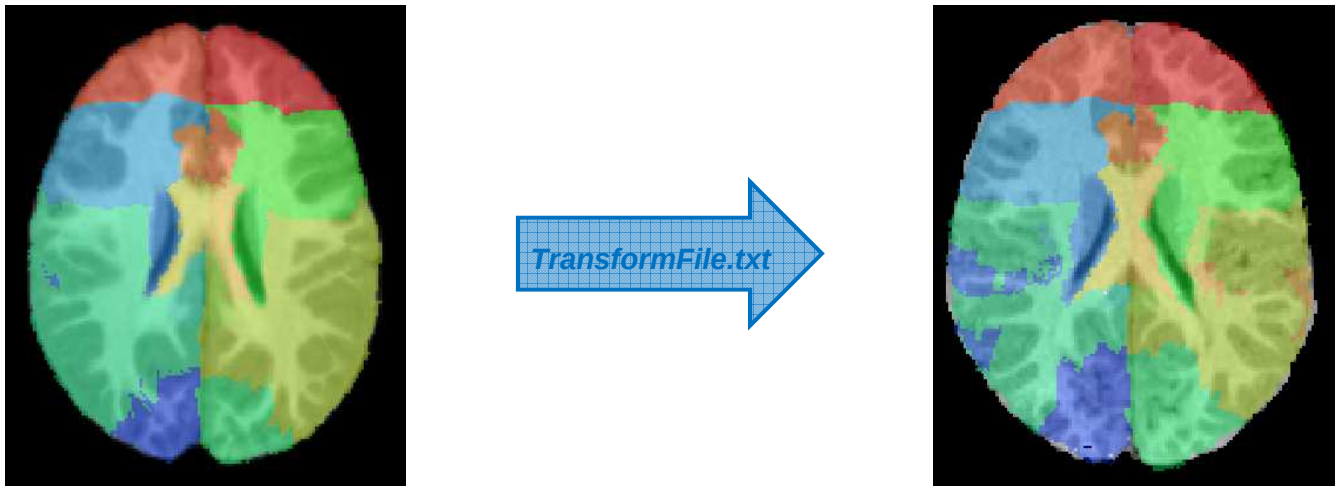


AtlasRegistered_Image_corrected_EMS_stripped.gipl

Pipeline Description

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

Module link :
http://slicer.spl.harvard.edu/slicerWiki/index.php/Modules:ResampleVolume2-Documentation



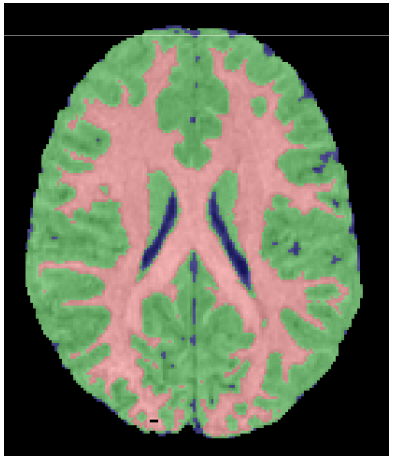
Parcellation.gipl

ParcellationRegistered_Image_corrected_EMS_stripped.gipl

Pipeline Description

Cortical Thickness (CortThick external module)

Sparse and asymmetric local cortical thickness

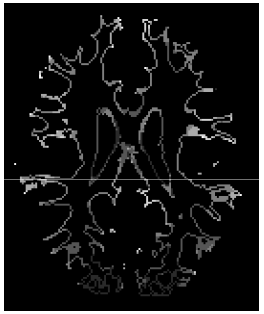


Image_labels_EMS.gipl

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

Regional Cortical Thickness information

Optional Outputs



WM_AvgBoundary.gipl

GM_AvgBoundary.gipl

Pipeline Description

Volume information (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.

Overview

1- Pipeline overview

2- Input images

3- Pipeline description

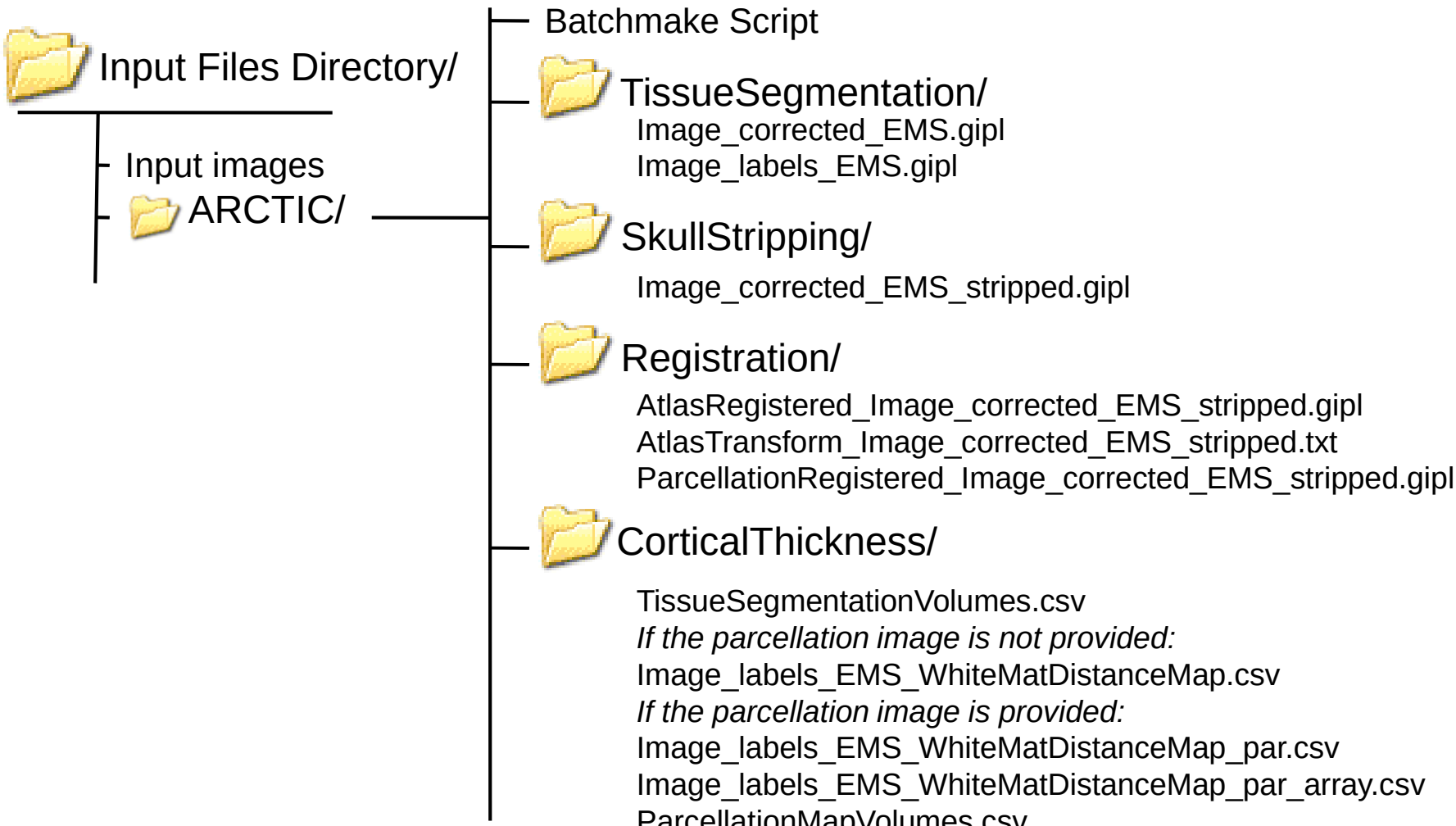
4- **Output images and organization**

5- Execution within Slicer

6- Example with tutorial dataset

7- Command line execution

Output and Organisation



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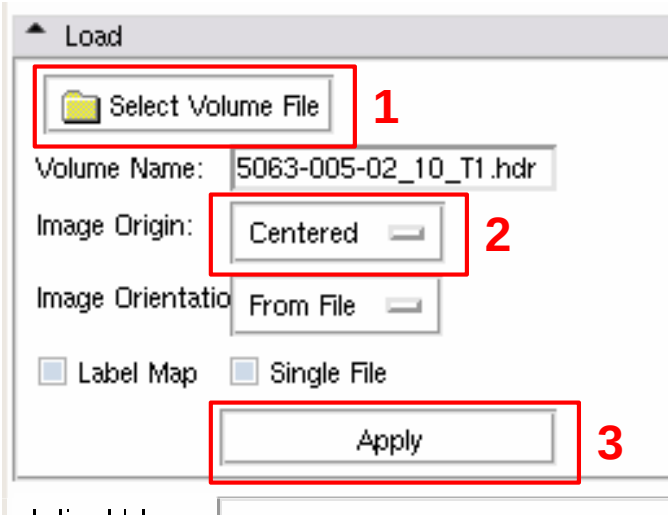
Execution within Slicer

- **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

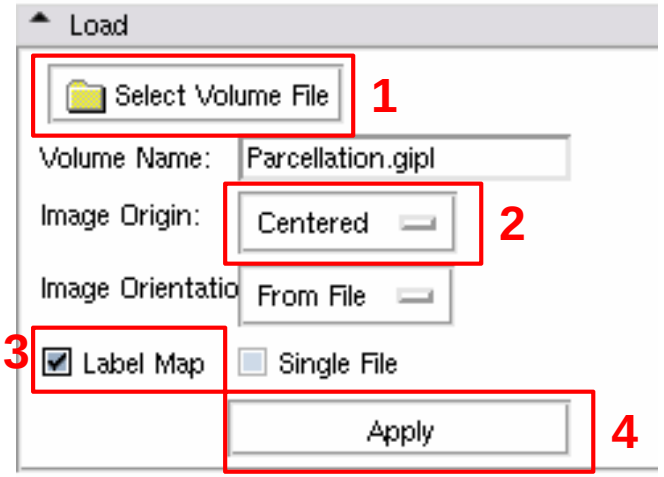
How to load parcellation and label images?

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

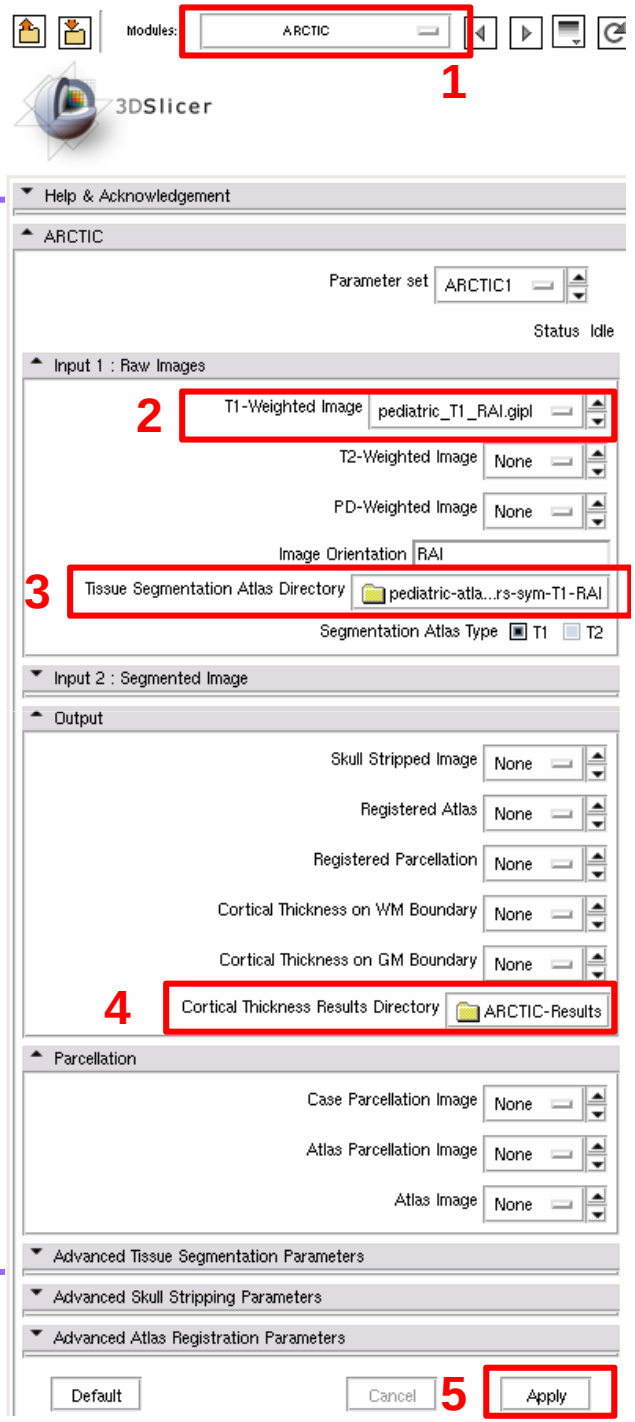
1- Select the « ARCTIC » module (in All Modules)

2- Add the T1-weighted image

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

4- Set the output directory

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



Demonstration : "Raw Images"

Input 1

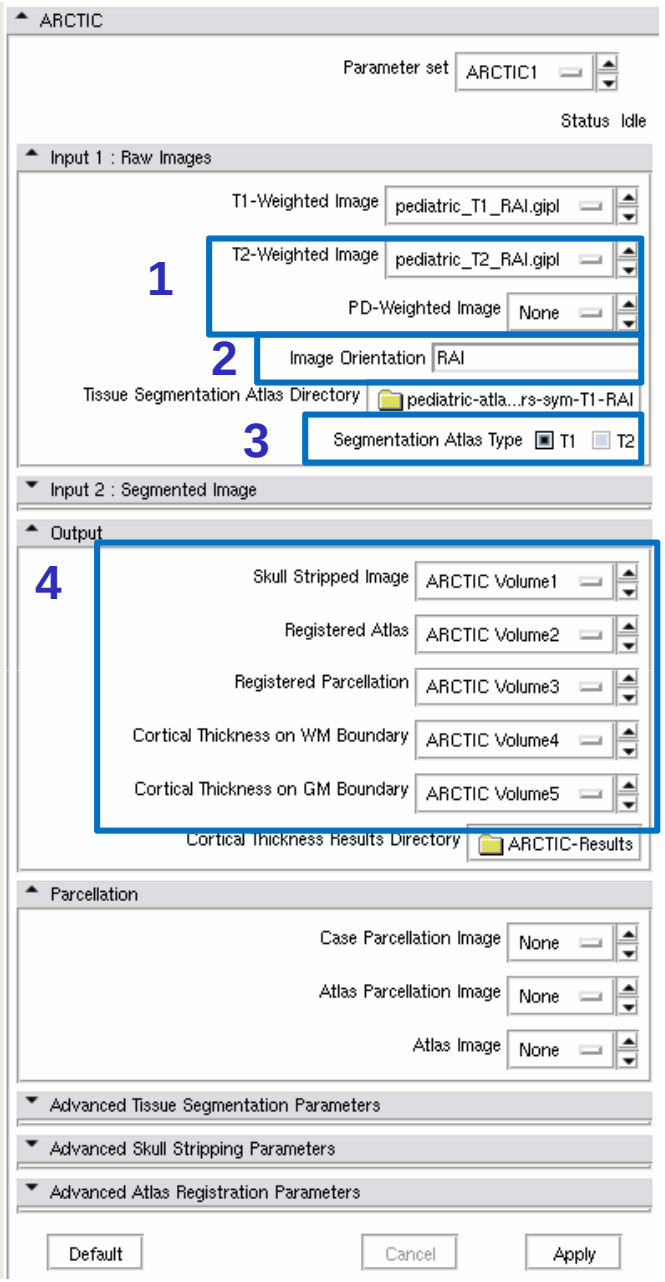
Verifications / Options

1- If available, set the T2 and/or PD-weighted images to improve the tissue segmentation

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

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

4- 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

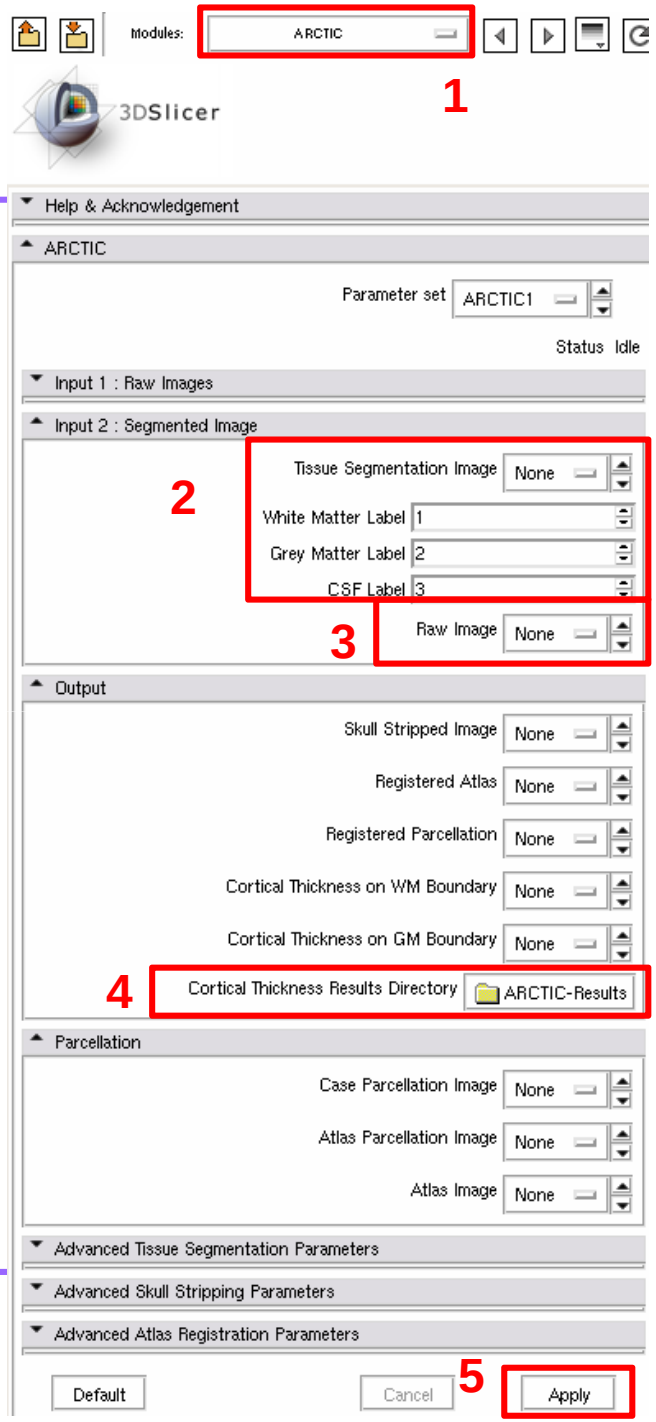
1- Select the « ARCTIC » module (in All Modules)

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

3- Set its raw image (T1-weighted, T2-weighted, PD-weighted)

4- Set the output directory

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



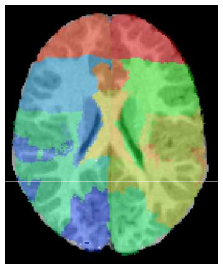
Demonstration : "Segmented Image"
Input 2

Options

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

Skull Stripped Image

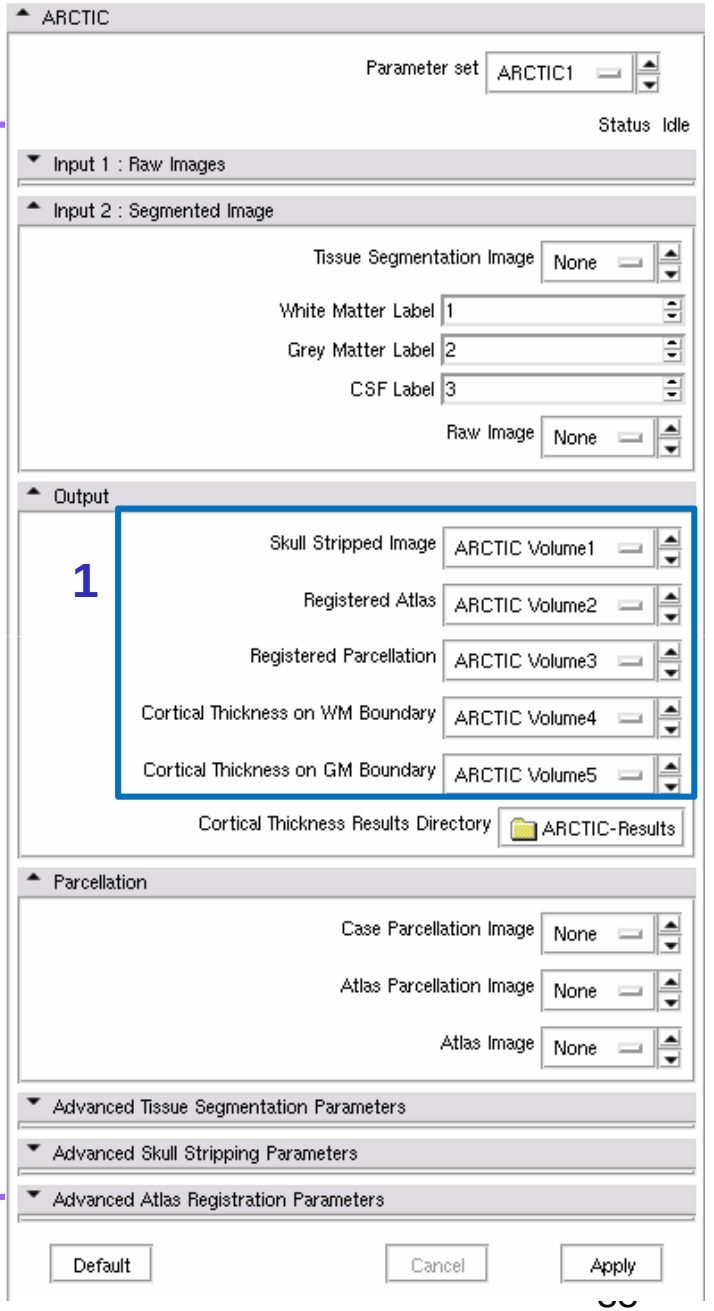
Registered Atlas



Registered Parcellation

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

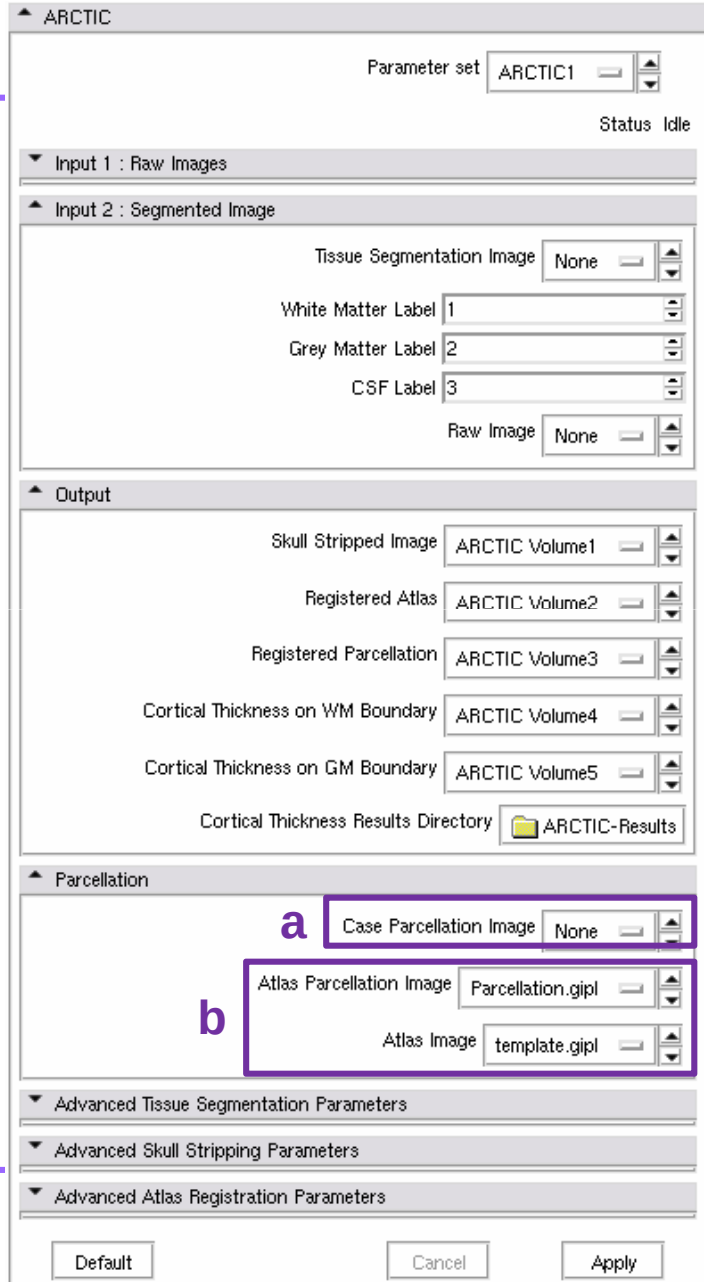
Parcellation options

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

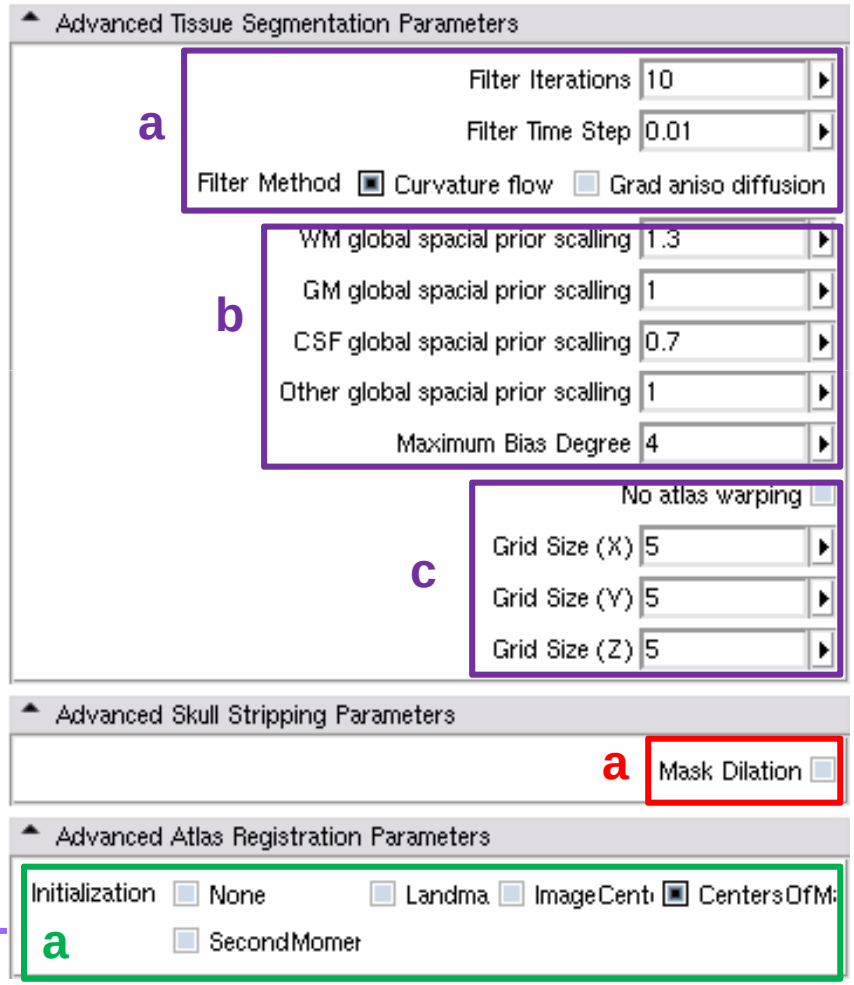
- Grid size X,Y,Z: grid controls points for atlas warping

Skull stripping parameters

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

Atlas registration parameters

a- Different initialization methods



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Example with tutorial dataset

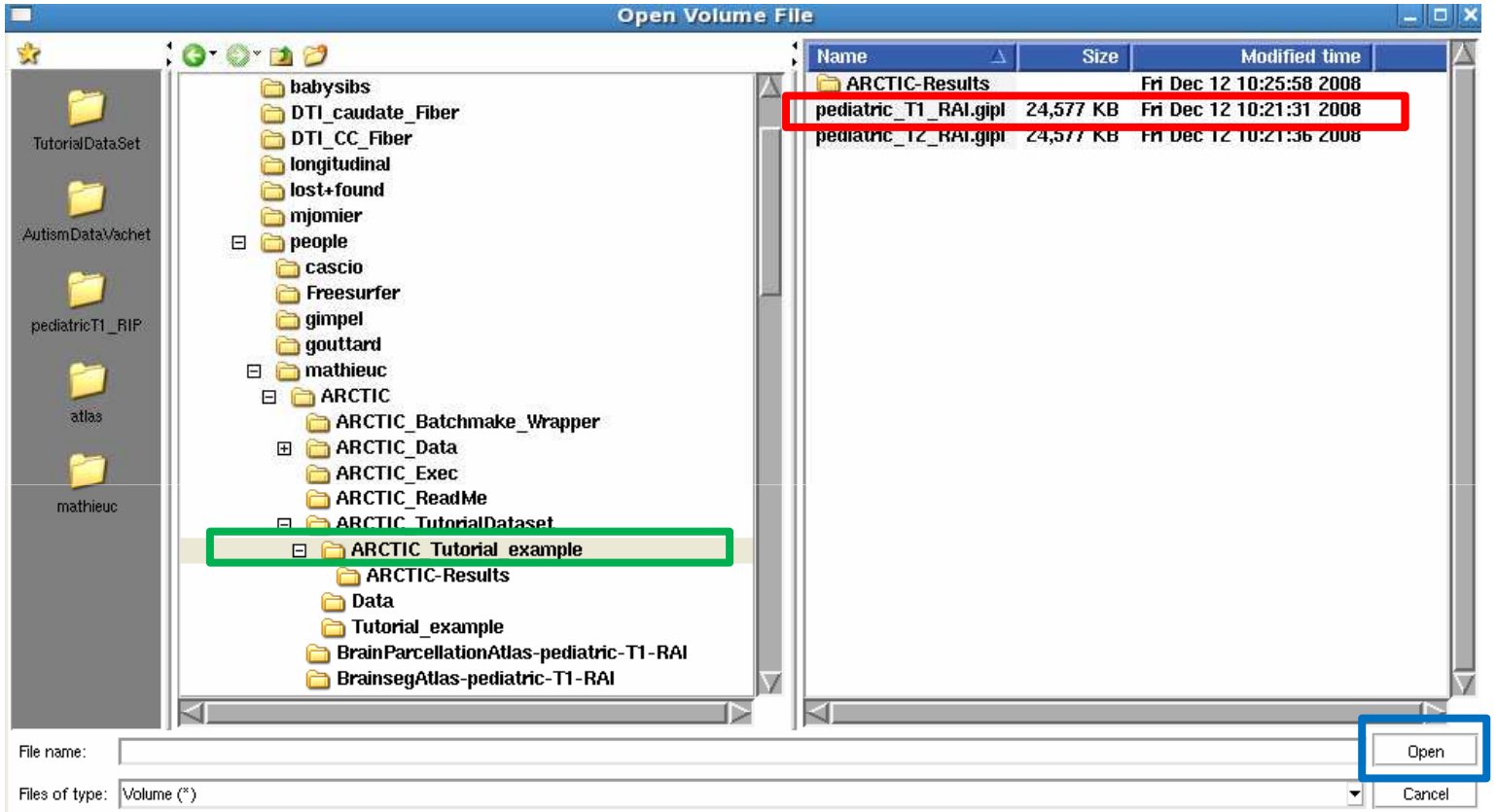
- Load input images
- Run ARCTIC

Load input images

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

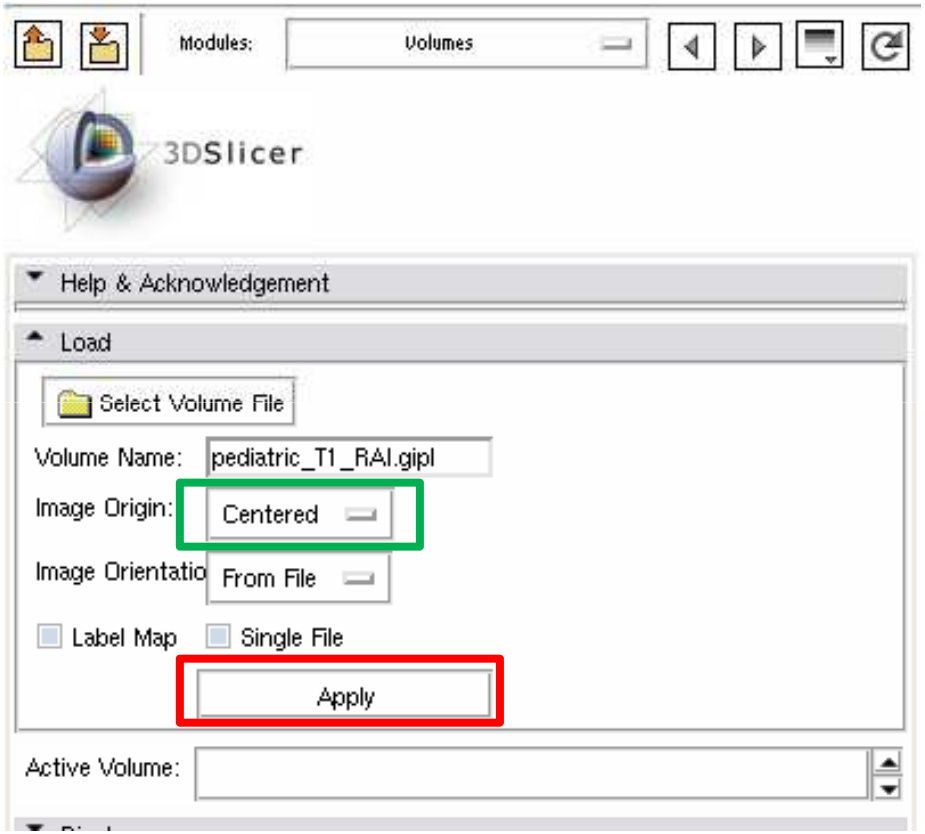
Then click on the « Select Volume File » button to load the images.

Load input images



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

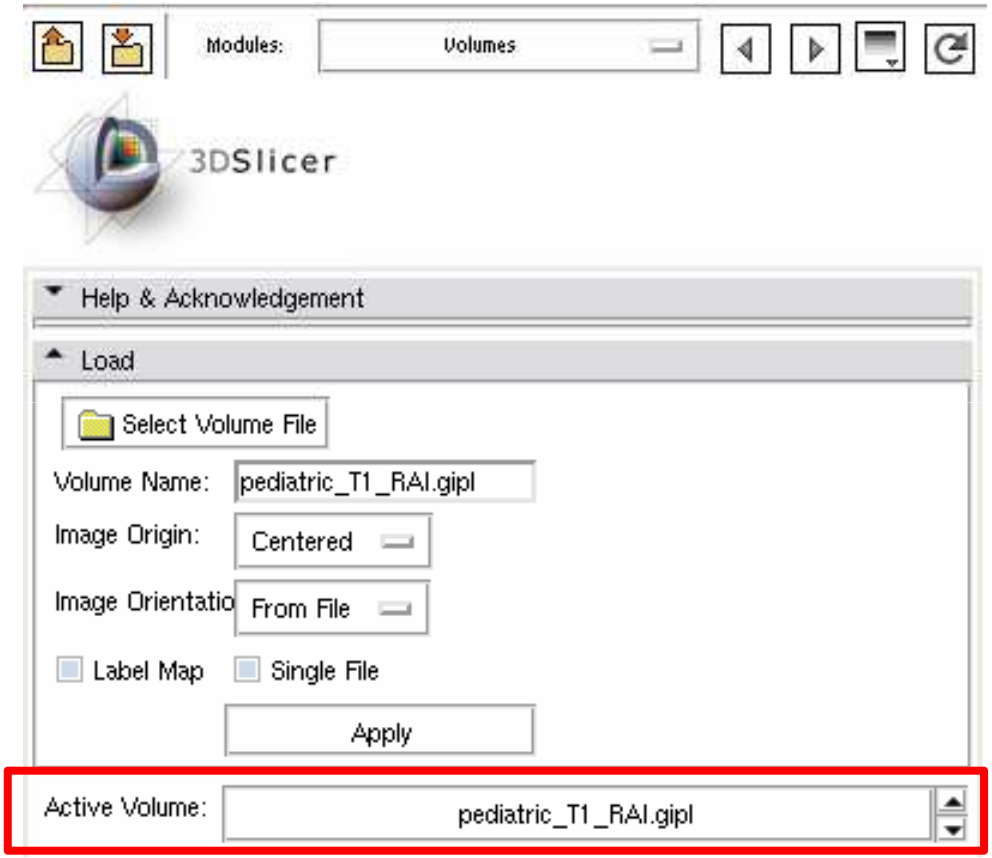
Load input images



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.

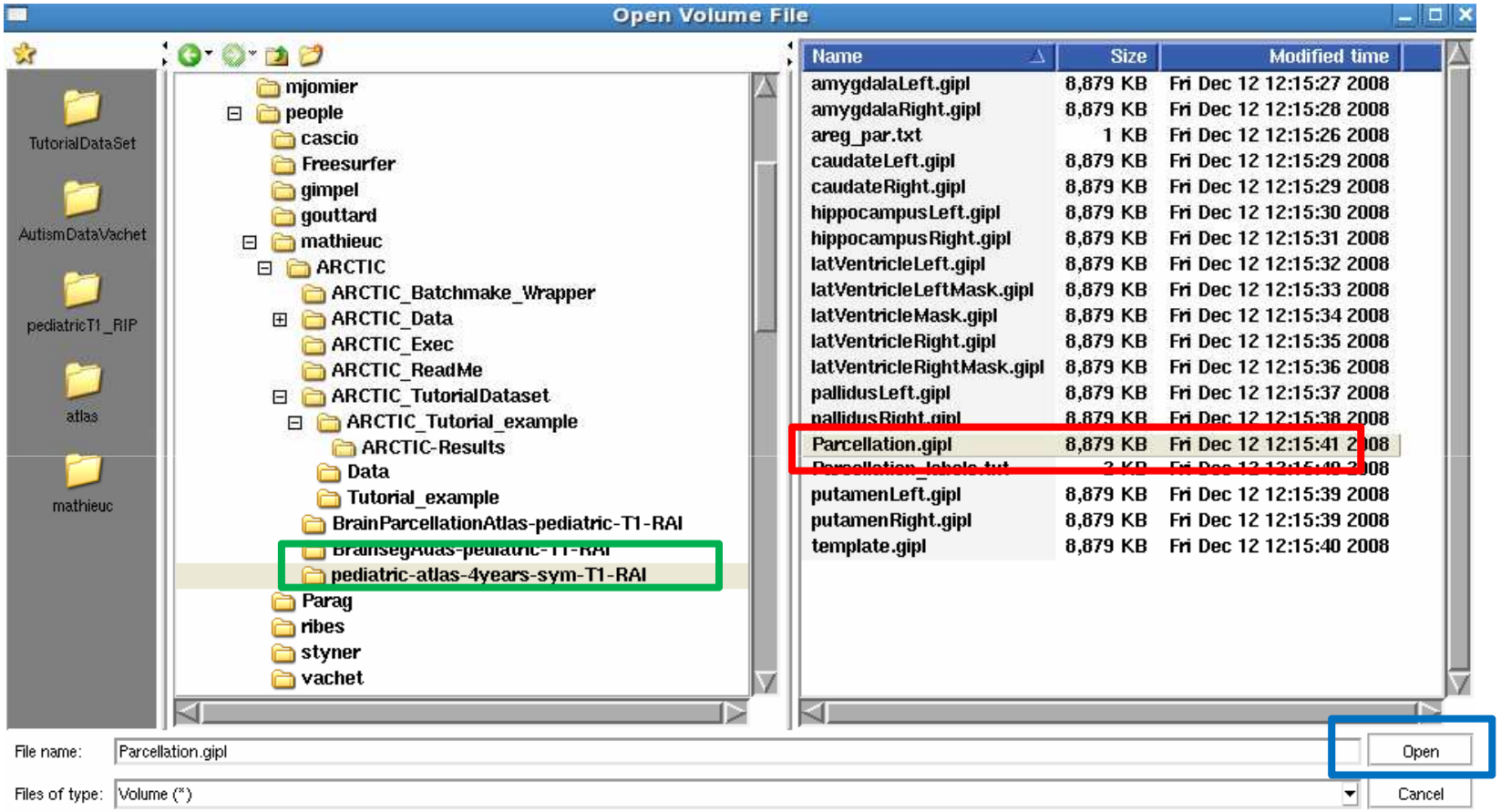
One can find the T2-weighted image in the same directory than the T1-weighted one.

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

Load input images

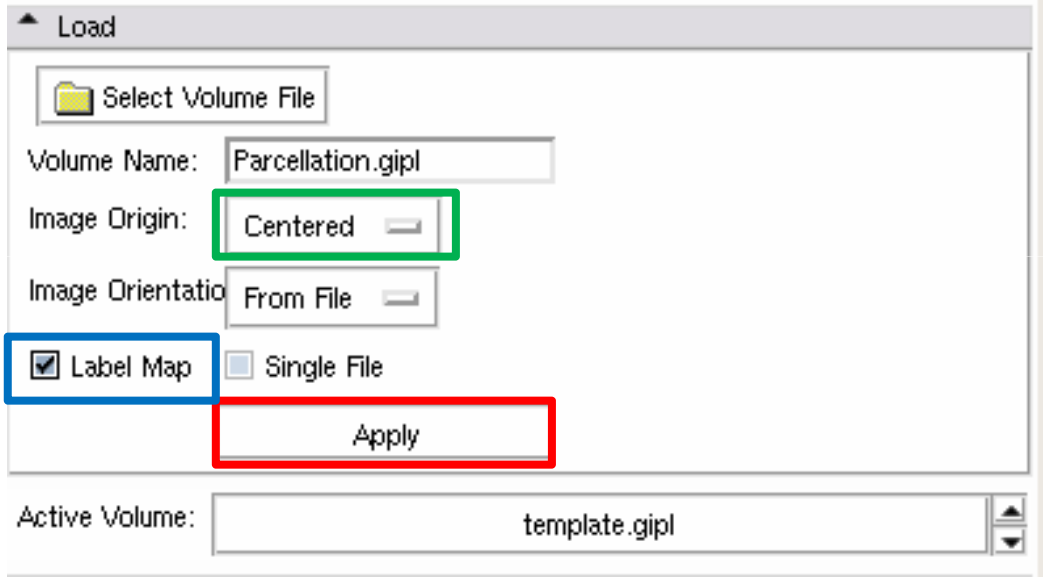
Now we will load the parcellation image.
Click on the « Select Volume File » button to load the parcellation.

Load input images



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

Load input images

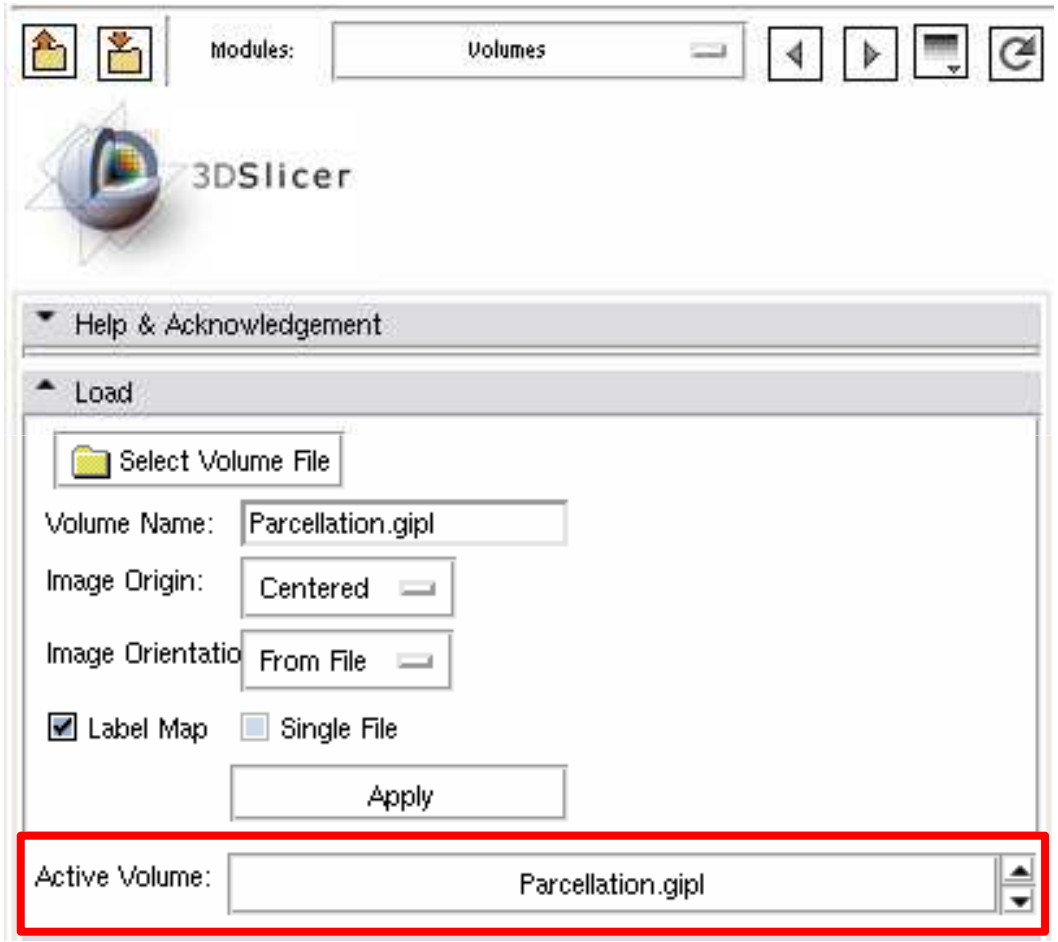


Now, select the Image Origin as **« Centered ».**

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

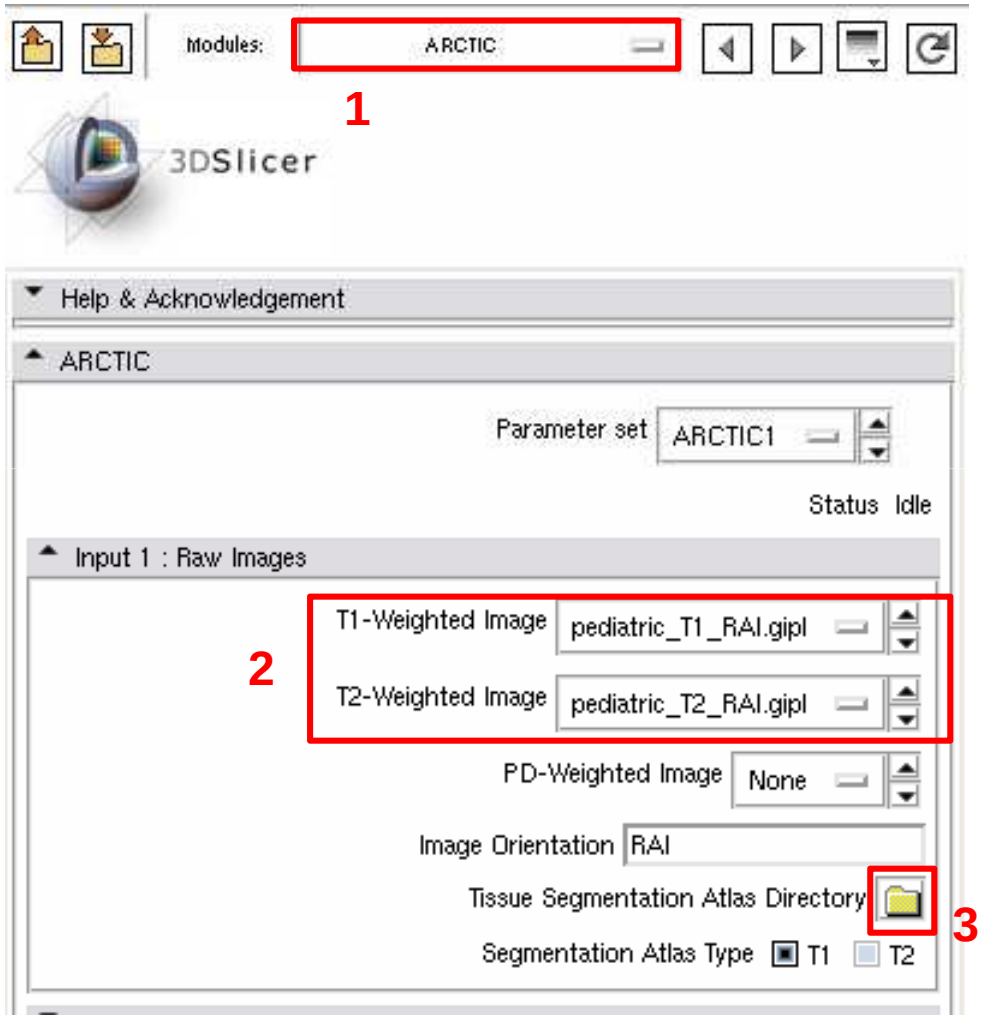
- Input images loading
- ARCTIC execution

Module execution

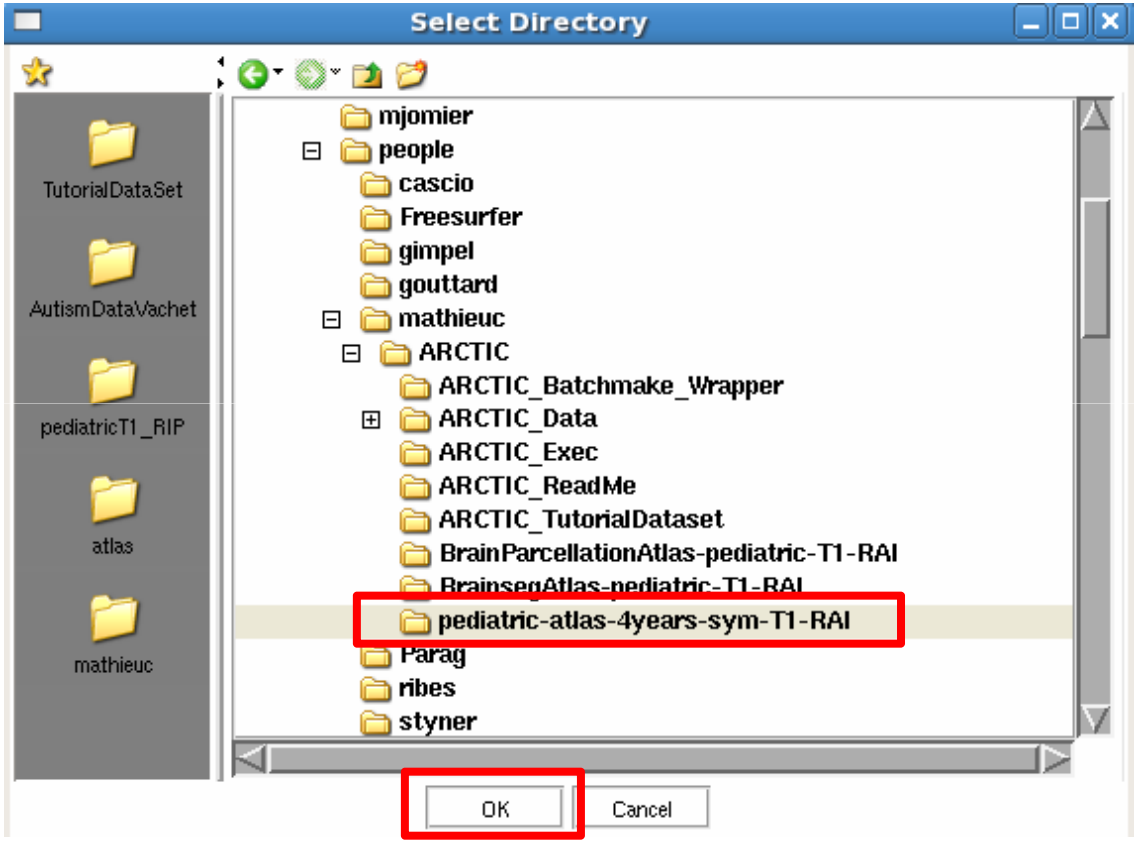
1- Select the « **ARCTIC** » module (in All Modules)

2- Set the T1 and T2-weighted images (**pediatric_T1/T2_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.

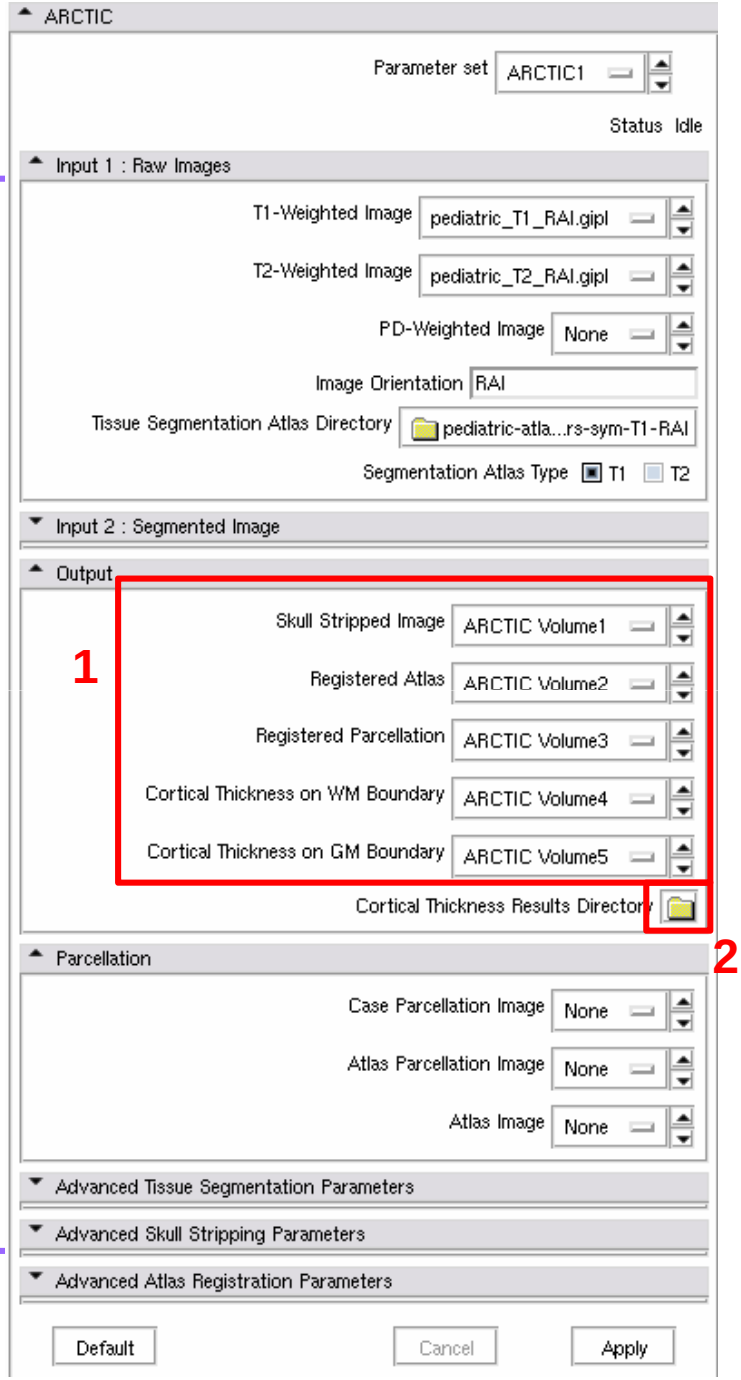
Search and select the « **pediatric-atlas-4years-sym-T1-RAI/**» folder.

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

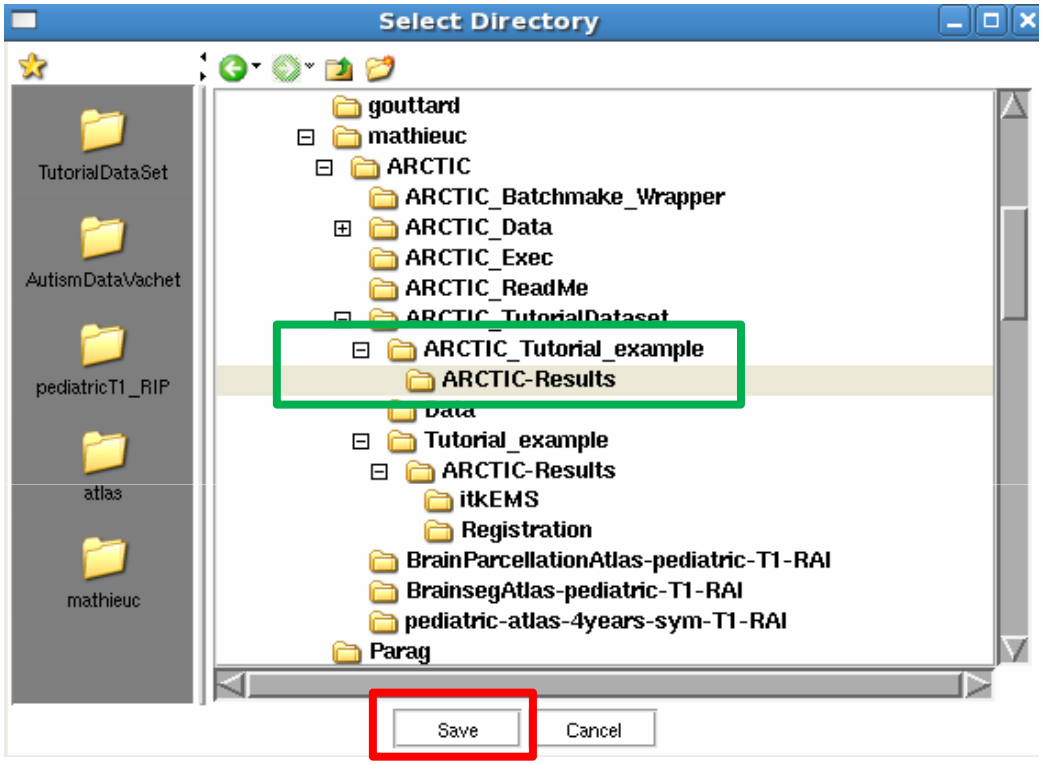
Module execution

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

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



Module execution



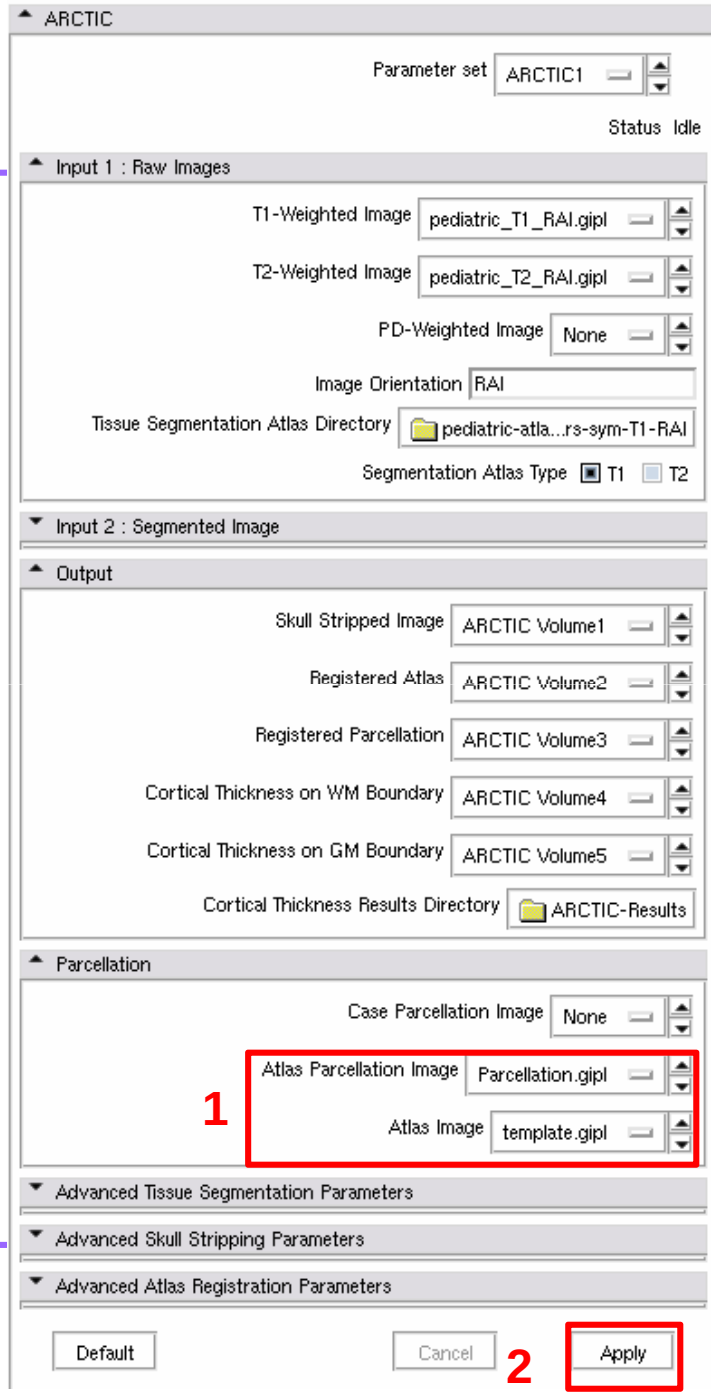
Select the « **ARCTIC-Results** » folder in the ARCTIC_Tutorial_Example directory

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.

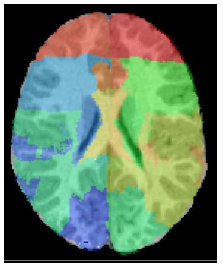


Module execution

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.

Skull Stripped Image
ARCTIC Volume1

Registered Atlas
ARCTIC Volume2



Registered Parcellation
ARCTIC Volume3

Cortical Thickness on WM Boundary
ARCTIC Volume4

Cortical Thickness on GM Boundary
ARCTIC Volume5

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.gipl --segAtlasDir TissueSegmentationAtlasDirectory/

Lobar cortical thickness analysis

If the atlas raw image and its parcellation are provided:

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

If the case parcellation image is provided:

ARCTIC --T1 Image_T1.gipl --segAtlasDir TissueSegmentationAtlasDirectory/
--caseParcellation CaseRegisteredParcellation.gipl

Use the command line

« Segmented Image » Mode :

Global analysis

ARCTIC --label TissueSegmentationImage.gipl --rawImage Image_T1.gipl

Lobar cortical thickness analysis

If the atlas raw image and its parcellation are provided:

ARCTIC --label TissueSegmentationImage.gipl --rawImage Image_T1.gipl
--atlas Atlas.gipl --atlasParcellation Parcellation.gipl

If the case parcellation image is provided:

ARCTIC --label TissueSegmentationImage.gipl --rawImage Image_T1.gipl
--caseParcellation CaseRegisteredParcellation.gipl

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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