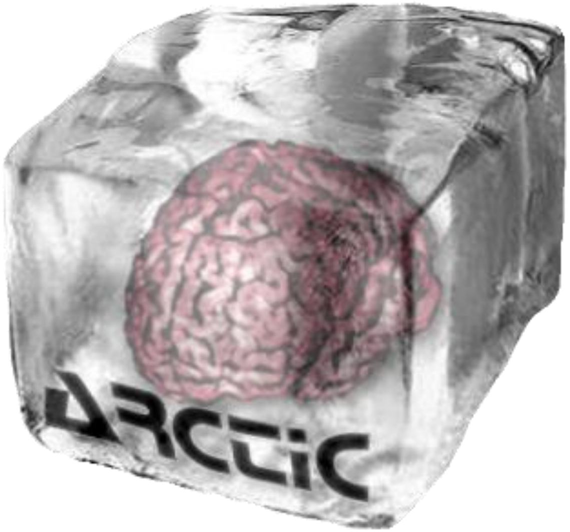
Slicer3 Training Tutorial
ARCTIC (v1.1)
(Automatic Regional Cortical ThICkness)



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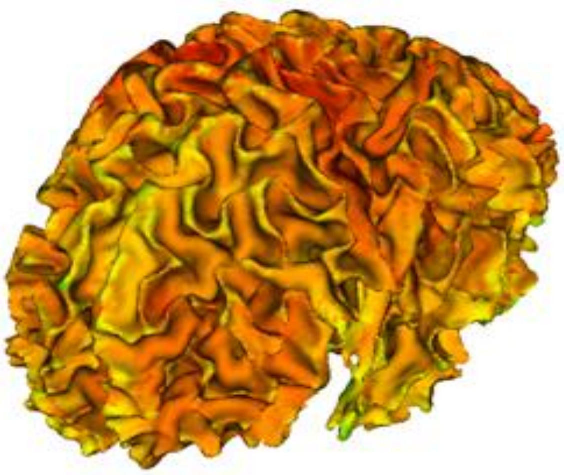
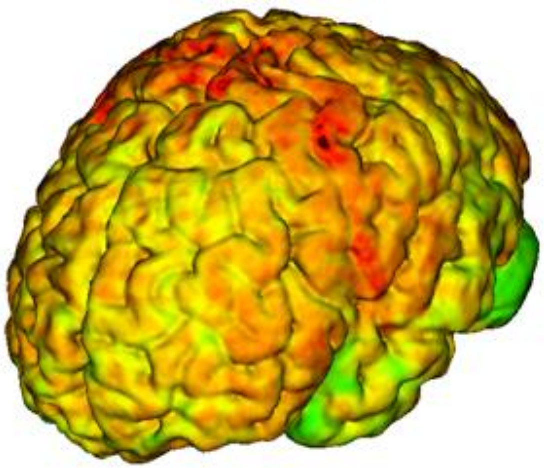
Learning Objective

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_1.1***)
- Tutorial dataset download page(***ARCTIC_Tutorial_example_1.0***)
- External modules download page (***ARCTIC_Executables_1.1***)

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_1.1*) is a ZIP file.

Unzip this file somewhere in your computer.

An “*ARCTIC_Tutorial_example_1.1*” 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_1.1*” 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_1.1”* 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}`

<u>Notice</u> : 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_1.1)
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_1.1)

Prerequisites

Set Slicer libraries variable

-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

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

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

3DSlicer

Overview

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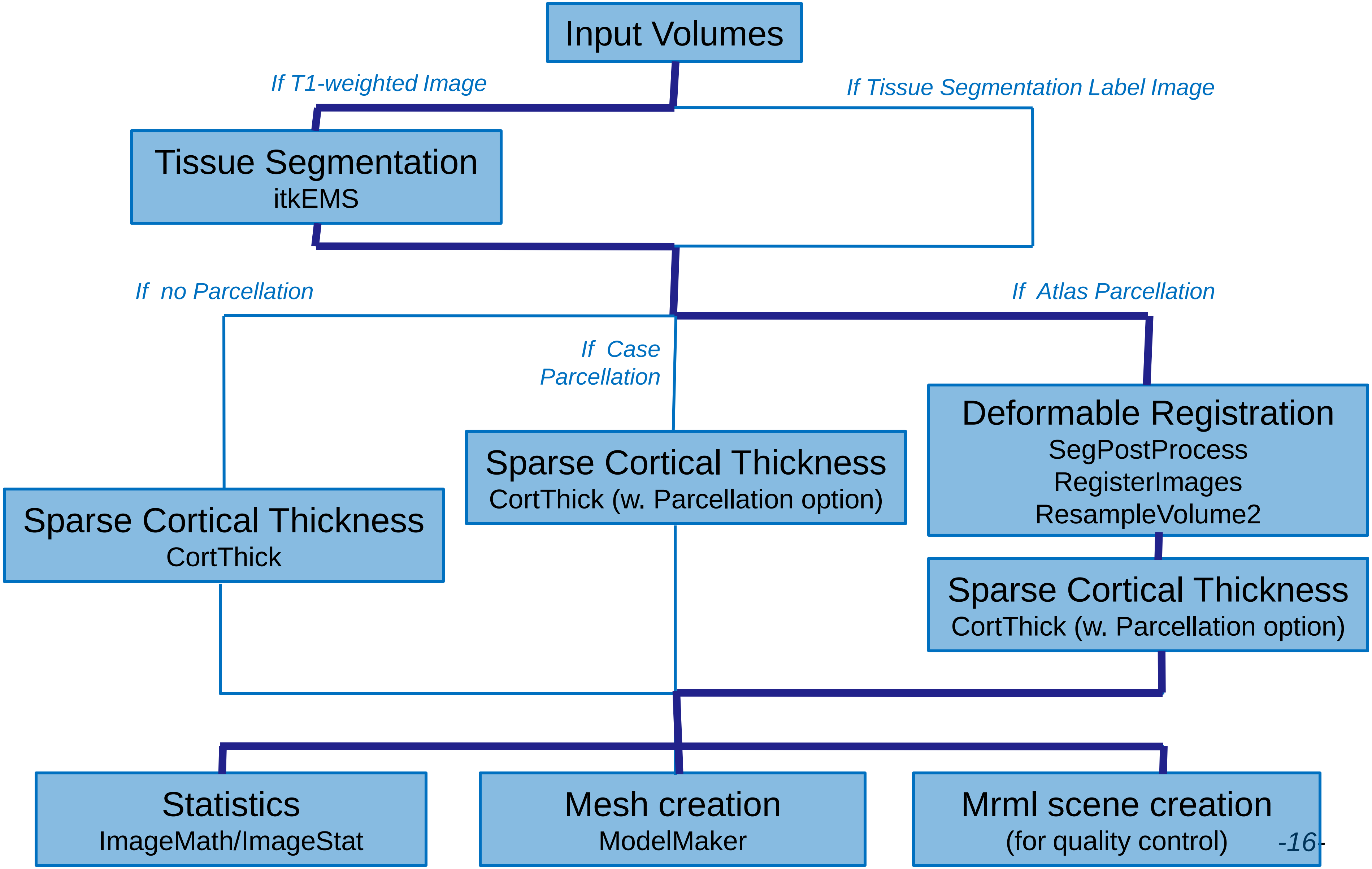
Pipeline Description



Input Volumes

If T1-weighted Image

If Tissue Segmentation Label Image

Tissue Segmentation
itkEMS

If no Parcellation

If Atlas Parcellation

If Case Parcellation

Deformable Registration
SegPostProcess
RegisterImages
ResampleVolume2

Sparse Cortical Thickness
CortThick (w. Parcellation option)

Sparse Cortical Thickness
CortThick

Sparse Cortical Thickness
CortThick (w. Parcellation option)

Statistics
ImageMath/ImageStat

Mesh creation
ModelMaker

Mrml scene creation
(for quality control)

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

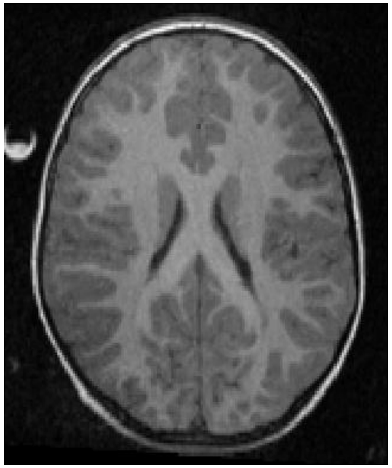
Module : ModelMaker (Slicer3 module)

6. Mrml scene Creation

Pipeline Description

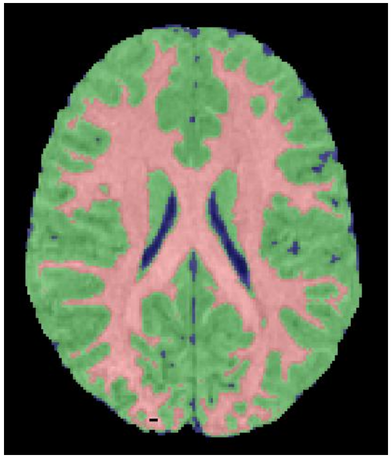
Tissue segmentation (itkEMS external module)

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

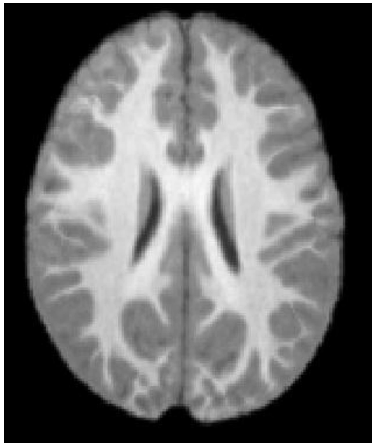
Image_corrected_EMS_stripped.nrrd

Pipeline Description

Deformable registration of T1-weighted atlas (RegisterImages module)

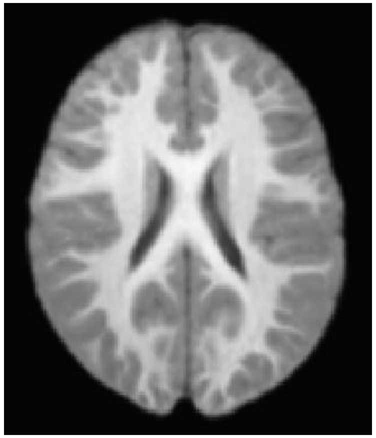
B-spline pipeline registration.
A transformation file is created and will be used by the next step.

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



Atlas.nrrd

TransformFile.txt



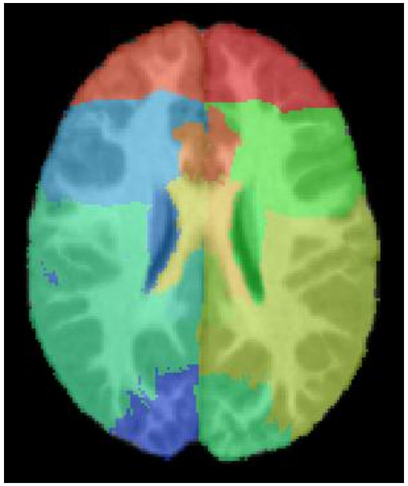
AtlasRegistered_Image_corrected_EMS_stripped.nrrd

Pipeline Description

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

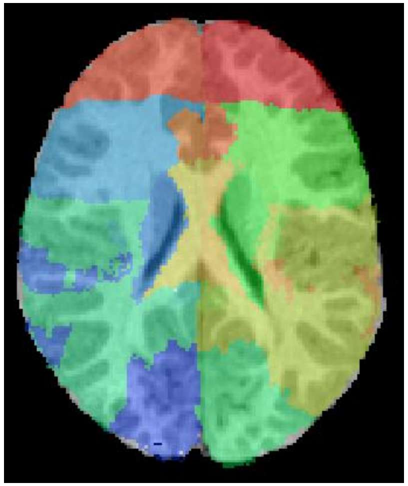
Module link :

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



Parcellation.nrrd

TransformFile.txt



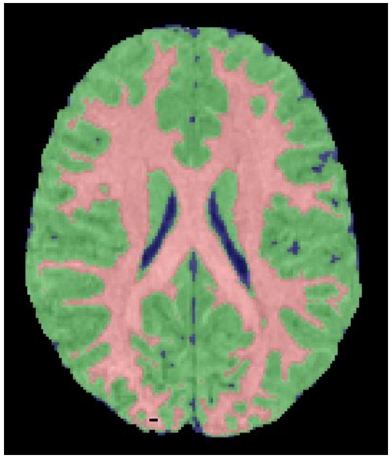
ParcellationRegistered_Image_corrected_EMS_stripped.nrrd

Pipeline Description

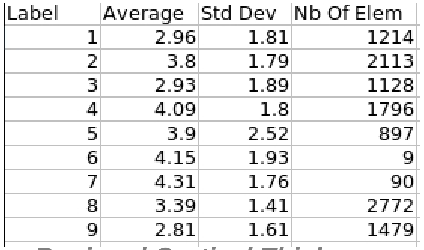
Cortical Thickness (CortThick external module)

Sparse and asymmetric local cortical thickness

Optional Outputs

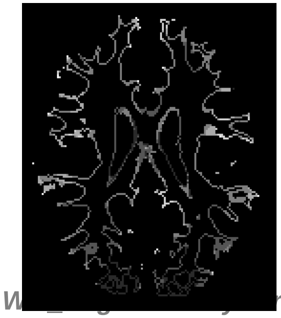


Image_labels_EMS.nrrd



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



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.

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

- Input Files Directory/
  - Input images
  - ARCTIC/
    - 2 BatchMake Scripts
    - TissueSegmentation/
      - InputVolumes_corrected_EMS.nrrd
      - InputVolume_labels_EMS.nrrd
      - WM/GM/CSF_Map.nrrd
    - Registration/
      - Image_corrected_EMS_stripped.nrrd
      - AtlasRegistered_Image_corrected_EMS_stripped.nrrd
      - AtlasTransform_Image_corrected_EMS_stripped.txt
      - ParcellationRegistered_Image_corrected_EMS_stripped.nrrd
    - CorticalThickness/
      - *If the parcellation image is not provided:*
      - Image_labels_EMS_WhiteMatDistanceMap.csv
      - *If the parcellation image is provided:*
      - Image_labels_EMS_WhiteMatDistanceMap_par.csv
      - Image_labels_EMS_WhiteMatDistanceMap_par_array.csv
    - Stat/
      - TissueSegmentationVolumes.csv
      - ParcellationMapVolumes.csv
    - Mesh/
      - WM_Surface.vtk
      - GM_Surface.vtk

Overview

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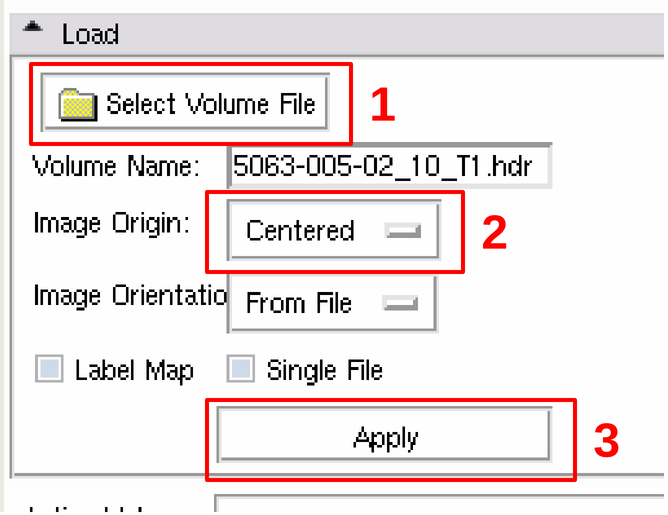
Execution within Slicer

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

Demonstration : Load the input images



Volume Name: 5063-005-02_10_T1.hdr

Image Origin: Centered

Image Orientatio From File

☐ Label Map ☐ Single File

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

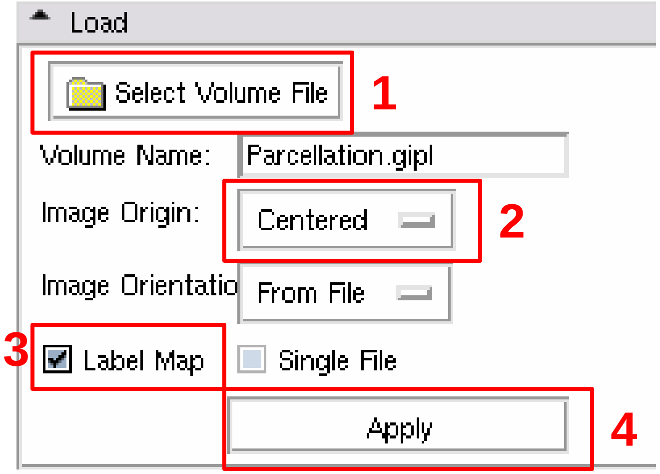
How to load parcellation and label images?

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



Volume Name: Parcellation.gipl

Image Origin: Centered

Image Orientatio From File

☑ Label Map ☐ Single File

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)

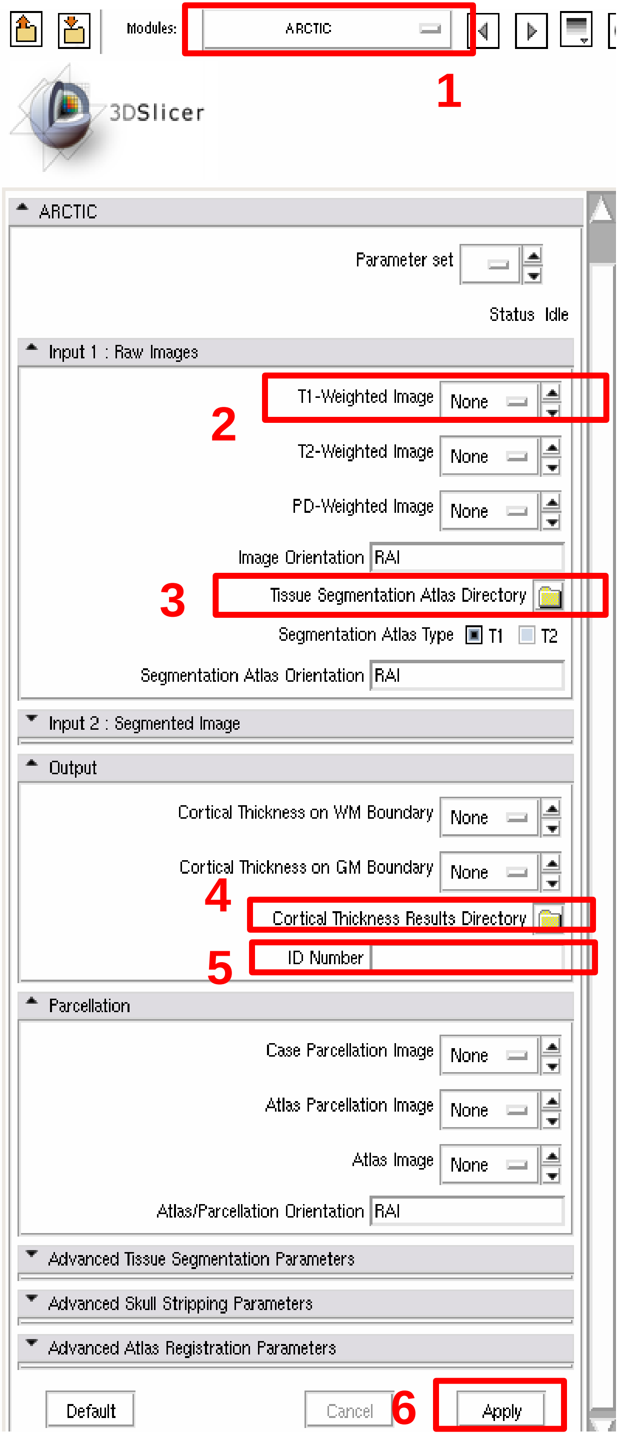
2- Add the T1-weighted image

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



Modules: ARCTIC

ARCTIC

Parameter set

Status Idle

Input 1 : Raw Images

T1-Weighted Image None

T2-Weighted Image None

PD-Weighted Image None

Image Orientation RAI

Tissue Segmentation Atlas Directory

Segmentation Atlas Type ▣ T1 ☐ T2

Segmentation Atlas Orientation RAI

Input 2 : Segmented Image

Output

Cortical Thickness on WM Boundary None

Cortical Thickness on GM Boundary None

Cortical Thickness Results Directory

ID Number

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

Demonstration : “Raw Images”

Input 1

Verifications / Options

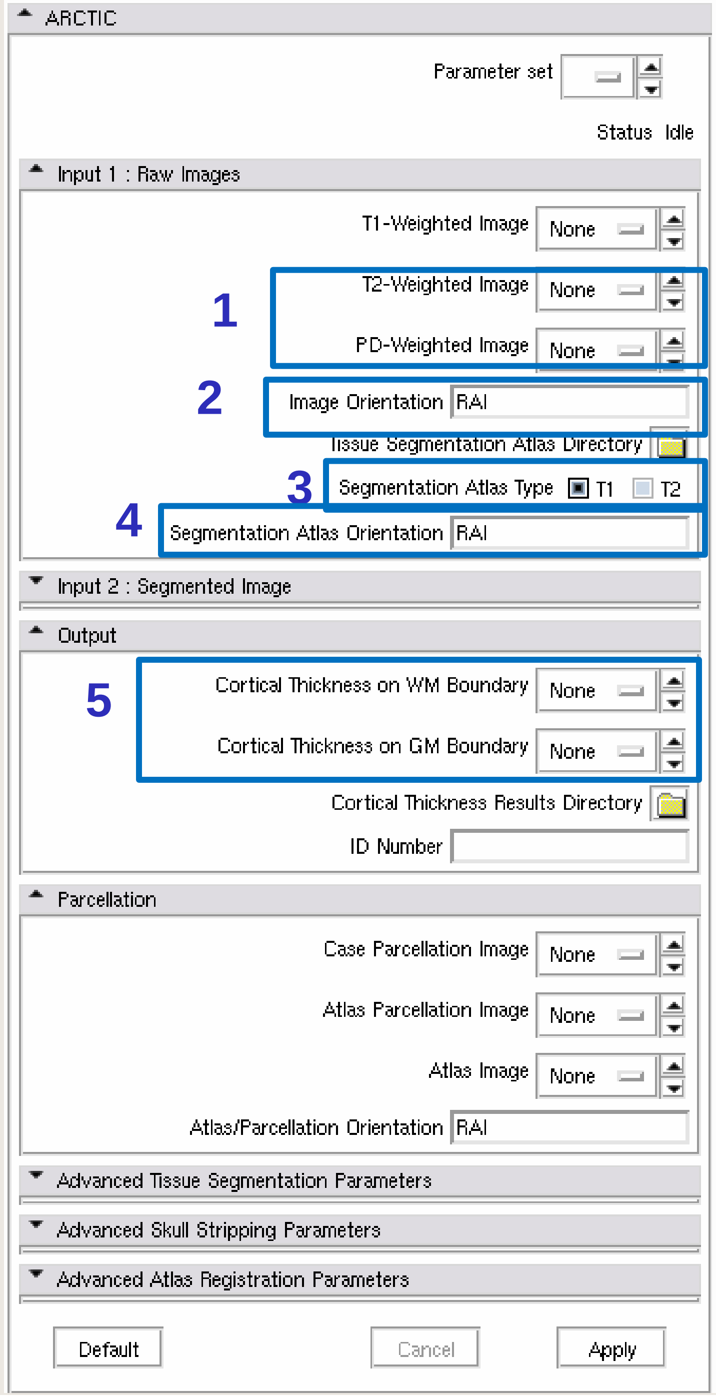
1- If available, set the T2 and/or PD-weighted images to improve the tissue segmentation

2- Set the images’ orientation if it is different than the default value

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

4- Set the images’ orientation if it is different than the default value

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



ARCTIC

Parameter set

Status Idle

Input 1 : Raw Images

T1-Weighted Image None

T2-Weighted Image None

PD-Weighted Image None

Image Orientation RAI

Tissue Segmentation Atlas Directory

Segmentation Atlas Type ▣ T1 ☐ T2

Segmentation Atlas Orientation RAI

Input 2 : Segmented Image

Output

Cortical Thickness on WM Boundary None

Cortical Thickness on GM Boundary None

Cortical Thickness Results Directory

ID Number

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

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)

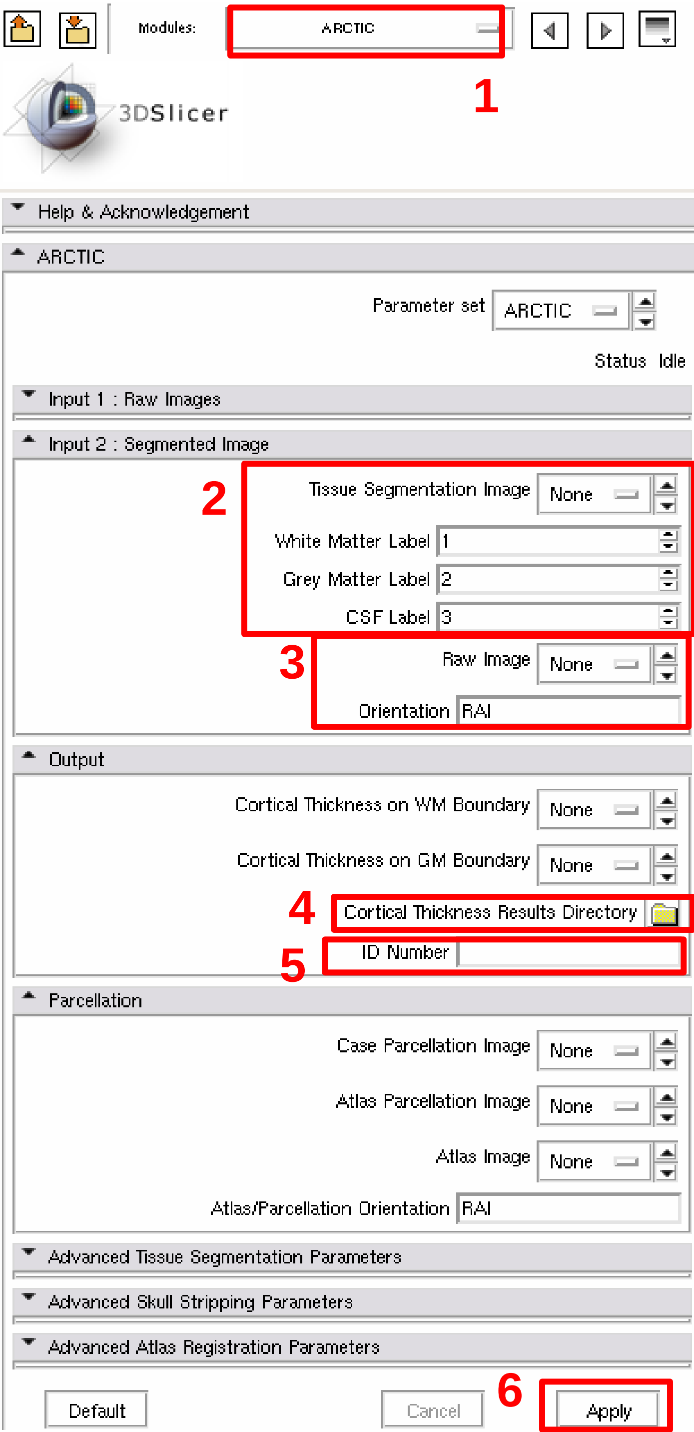
2- Set the tissue segmentation label image and check the related tissue labels

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



Modules: ARCTIC

Parameter set ARCTIC

Status Idle

Tissue Segmentation Image None

White Matter Label 1

Grey Matter Label 2

CSF Label 3

Raw Image None

Orientation RAI

Cortical Thickness on WM Boundary None

Cortical Thickness on GM Boundary None

Cortical Thickness Results Directory

ID Number

Case Parcellation Image None

Atlas Parcellation Image None

Atlas Image None

Atlas/Parcellation Orientation RAI

Demonstration : “Segmented Image”

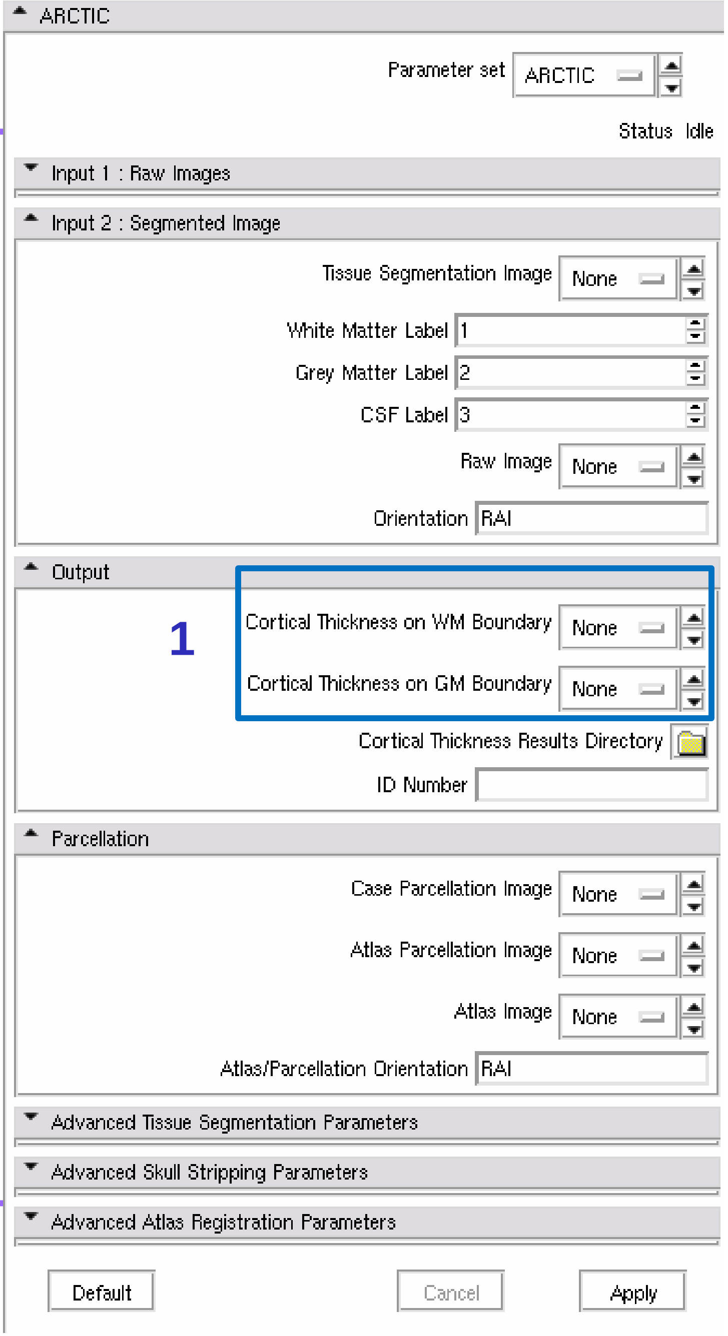
Input 2

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



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

ID Number

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

Demonstration in Slicer

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

Parcellation options

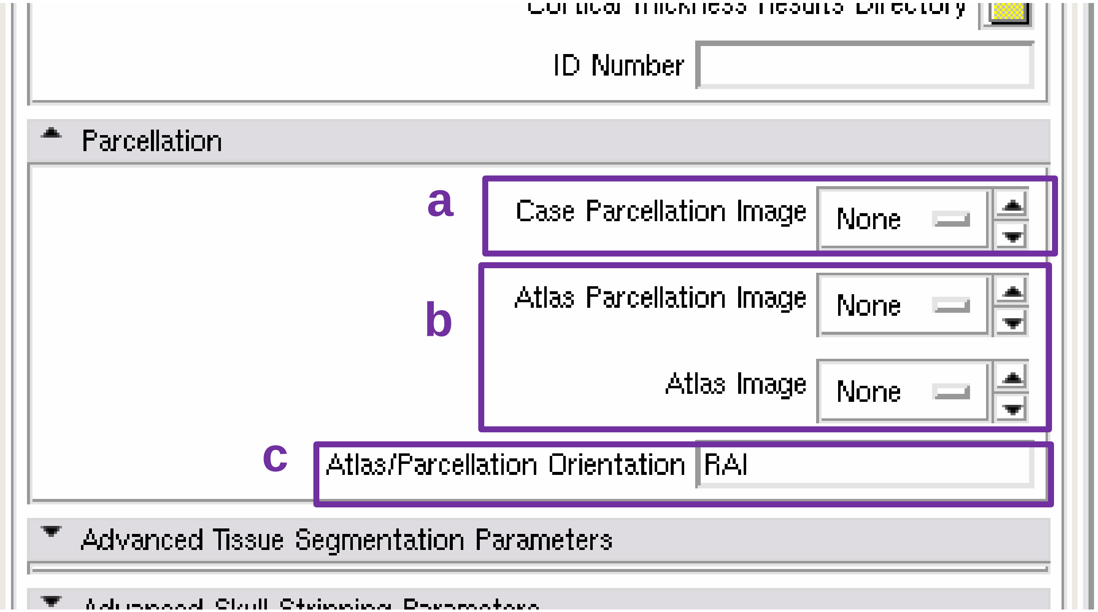
Parcellation options

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 »)

c- Change the orientation if yours is different than the default value.



ID Number

Case Parcellation Image: None

Atlas Parcellation Image: None

Atlas Image: None

Atlas/Parcellation Orientation: RAI

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:

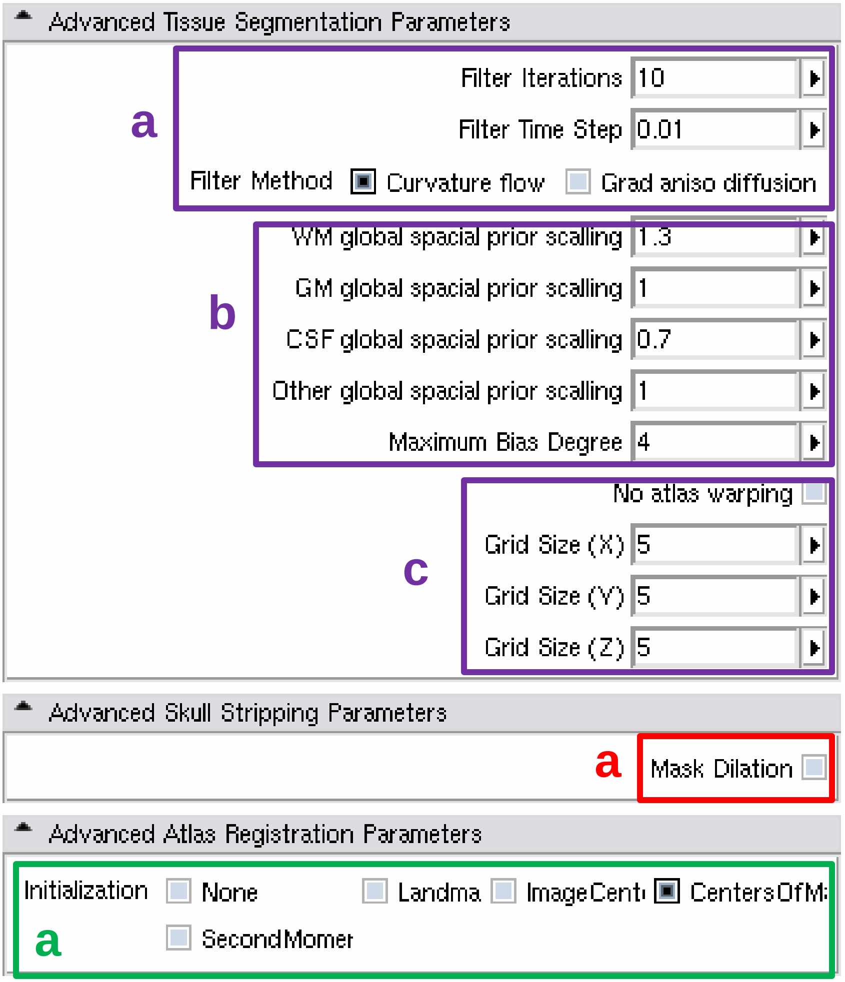
- No atlas warping:
  - Unchecked by default: atlas to subject B-Spline registration is performed
  - Checked: atlas to subject affine registration is performed instead of the warping
- Grid size X,Y,Z: grid controls points for atlas warping

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



Advanced Tissue Segmentation Parameters

Filter Iterations: 10
Filter Time Step: 0.01
Filter Method: ☒ Curvature flow ☐ Grad aniso diffusion

WM global spacial prior scalling: 1.3
GM global spacial prior scalling: 1
CSF global spacial prior scalling: 0.7
Other global spacial prior scalling: 1
Maximum Bias Degree: 4

No atlas warping ☐
Grid Size (X): 5
Grid Size (Y): 5
Grid Size (Z): 5

Advanced Skull Stripping Parameters

Mask Dilation ☐

Advanced Atlas Registration Parameters

Initialization: ☐ None ☐ Landma ☐ ImageCent ☒ CentersOfM ☐ SecondMomer

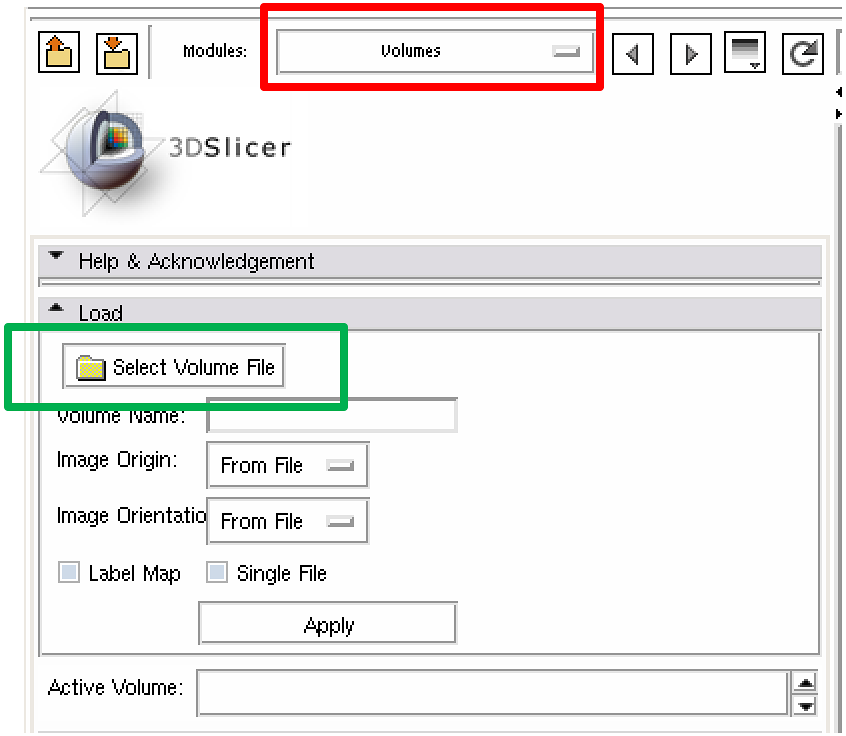
Overview

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

Example with tutorial dataset

- Load input images
- Run ARCTIC

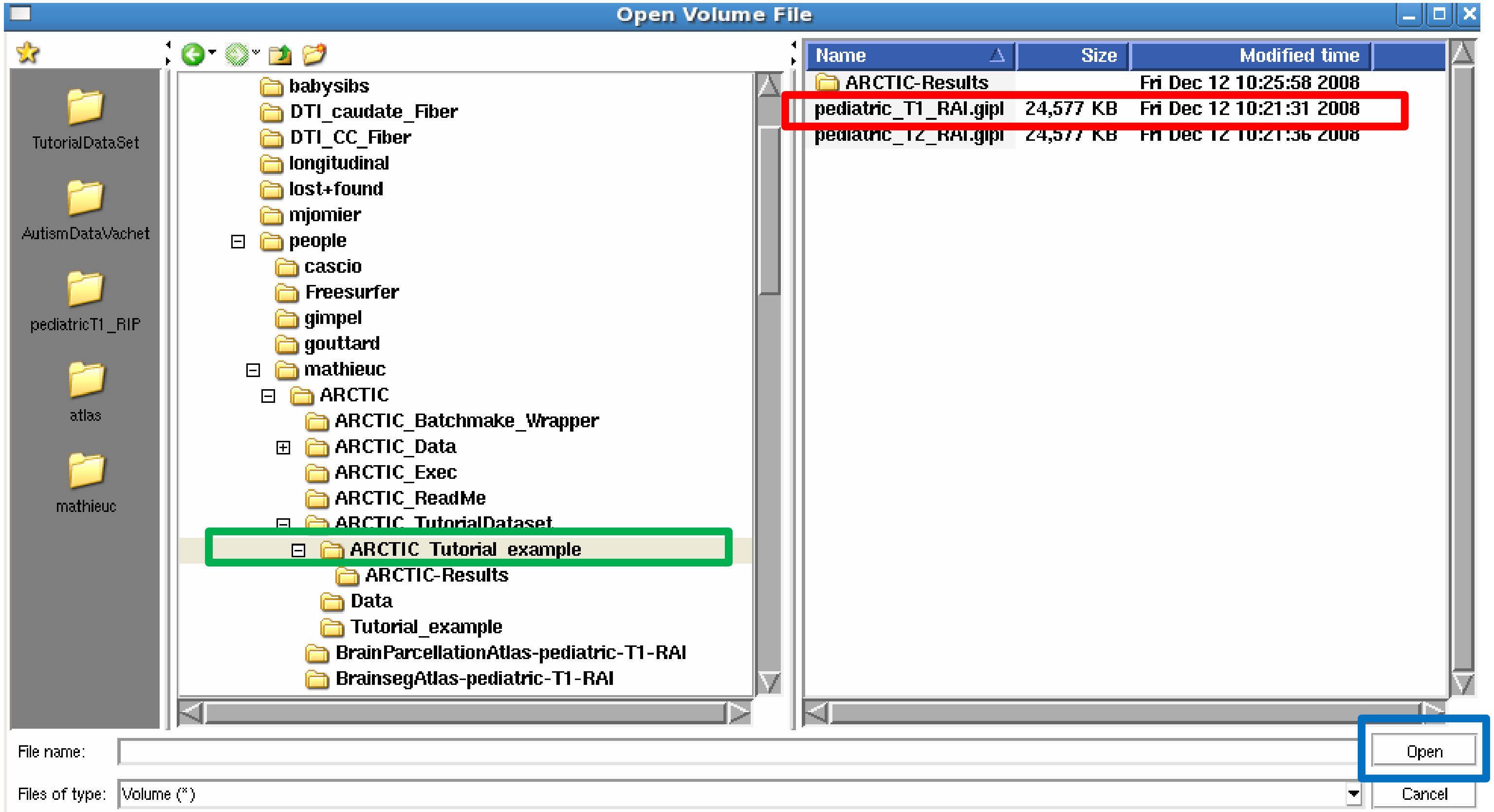
Load input images



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



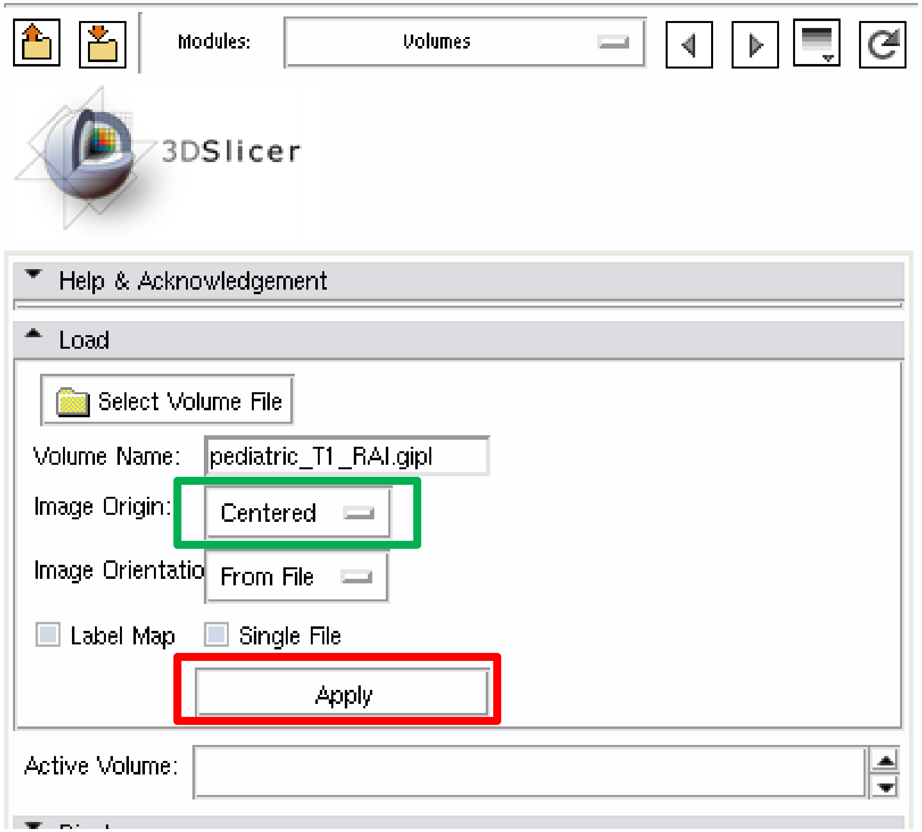
Name	Size	Modified time
ARCTIC-Results		Fri Dec 12 10:25:58 2008
pediatric_T1_RAI.gipl	24,577 KB	Fri Dec 12 10:21:31 2008
pediatric_T2_RAI.gipl	24,577 KB	Fri Dec 12 10:21:36 2008

File name:

Files of type: Volume (*)

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



Volume Name: pediatric_T1_RAI.gipl

Image Origin: Centered

Image Orientation: From File

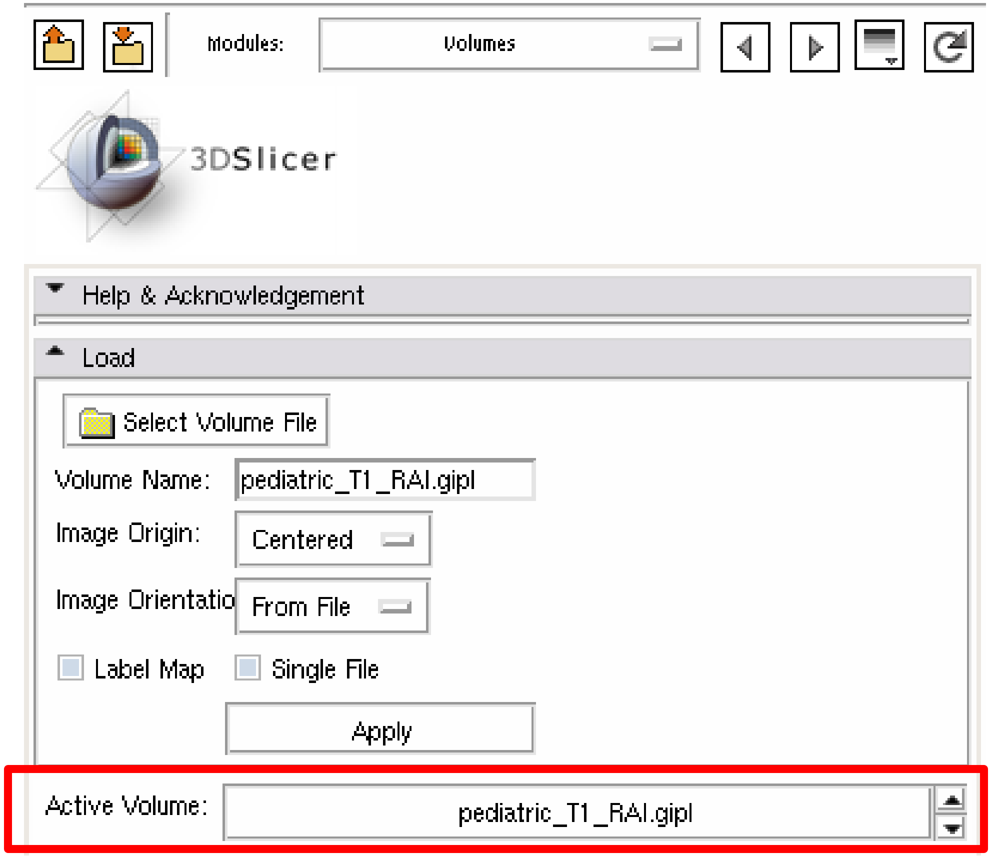
☐ Label Map ☐ Single File

Active Volume:

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

And click on **« Apply ».**

Load input images



Modules: Volumes

Volume Name: pediatric_T1_RAI.gipl

Image Origin: Centered

Image Orientatio From File

☐ Label Map ☐ Single File

Active Volume: pediatric_T1_RAI.gipl

The first image is now loaded.

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

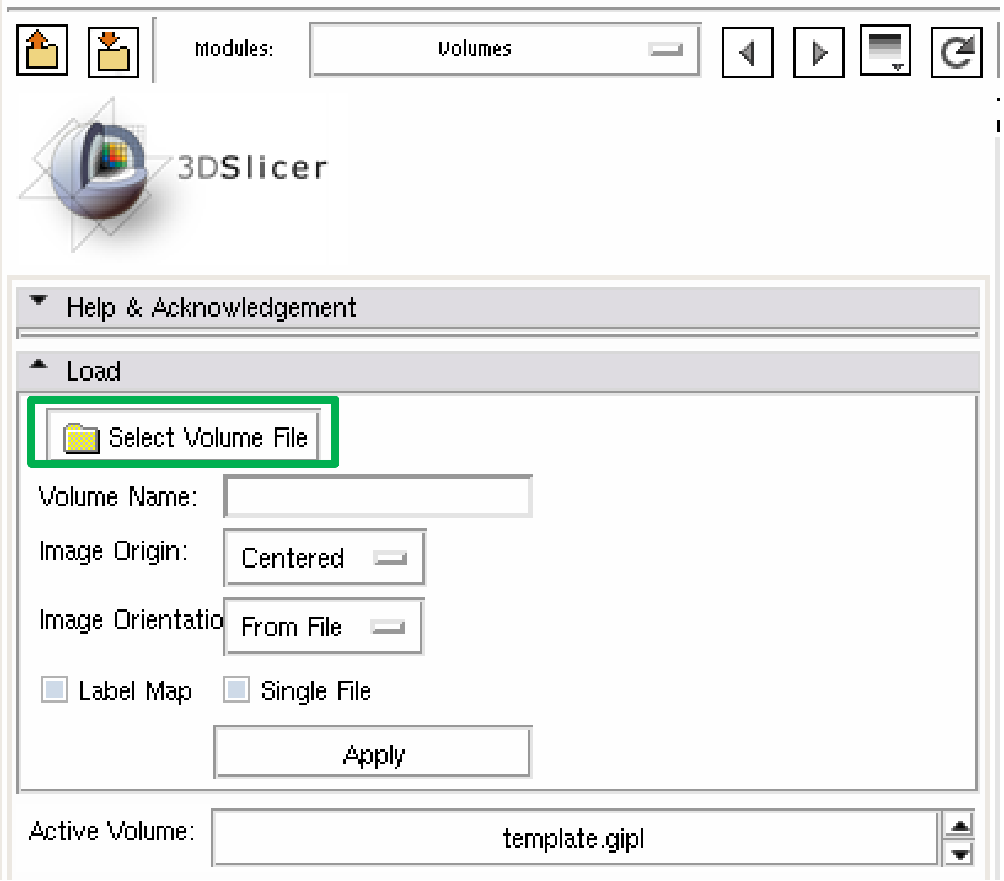
Load input images

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



Volume Name:

Image Origin: Centered

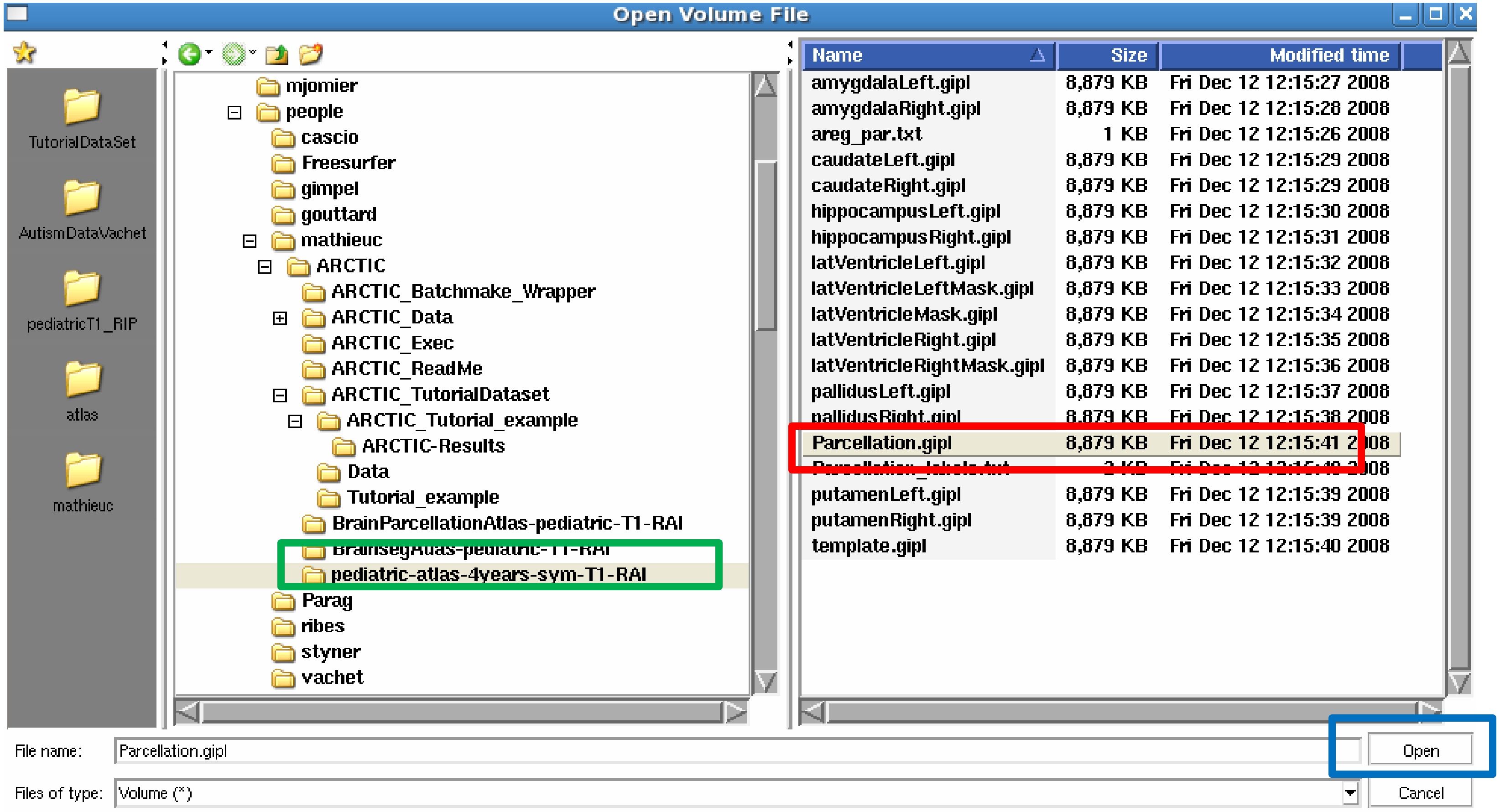
Image Orientatio From File

☐ Label Map ☐ Single File

Active Volume: template.gipl

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

Load input images



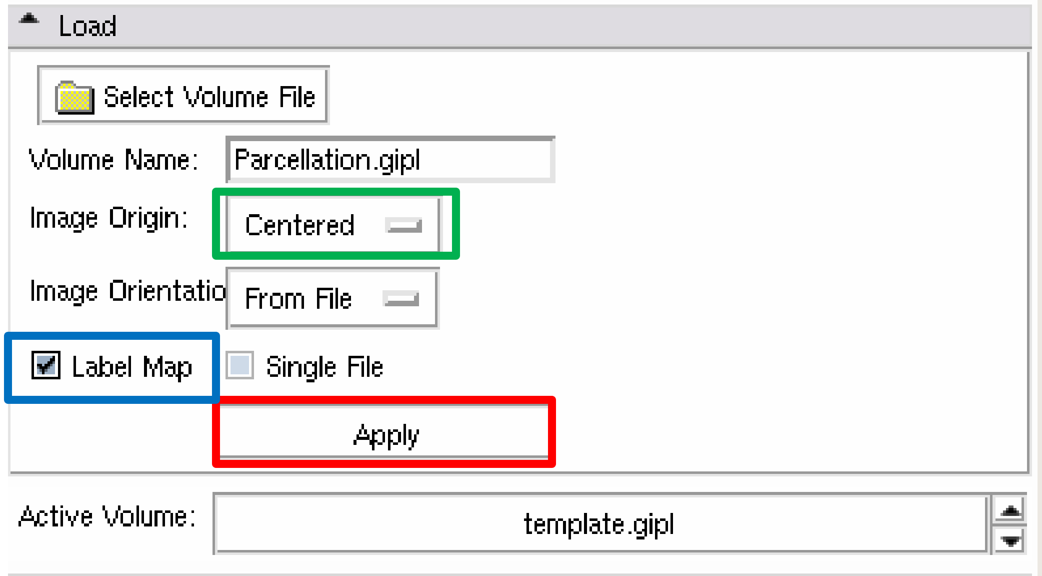
Name	Size	Modified time
amygdalaLeft.gipl	8,879 KB	Fri Dec 12 12:15:27 2008
amygdalaRight.gipl	8,879 KB	Fri Dec 12 12:15:28 2008
areg_par.txt	1 KB	Fri Dec 12 12:15:26 2008
caudateLeft.gipl	8,879 KB	Fri Dec 12 12:15:29 2008
caudateRight.gipl	8,879 KB	Fri Dec 12 12:15:29 2008
hippocampusLeft.gipl	8,879 KB	Fri Dec 12 12:15:30 2008
hippocampusRight.gipl	8,879 KB	Fri Dec 12 12:15:31 2008
latVentricleLeft.gipl	8,879 KB	Fri Dec 12 12:15:32 2008
latVentricleLeftMask.gipl	8,879 KB	Fri Dec 12 12:15:33 2008
latVentricleMask.gipl	8,879 KB	Fri Dec 12 12:15:34 2008
latVentricleRight.gipl	8,879 KB	Fri Dec 12 12:15:35 2008
latVentricleRightMask.gipl	8,879 KB	Fri Dec 12 12:15:36 2008
pallidusLeft.gipl	8,879 KB	Fri Dec 12 12:15:37 2008
pallidusRight.gipl	8,879 KB	Fri Dec 12 12:15:38 2008
Parcellation.gipl	8,879 KB	Fri Dec 12 12:15:41 2008
Parcellation_labels.txt	2 KB	Fri Dec 12 12:15:40 2008
putamenLeft.gipl	8,879 KB	Fri Dec 12 12:15:39 2008
putamenRight.gipl	8,879 KB	Fri Dec 12 12:15:39 2008
template.gipl	8,879 KB	Fri Dec 12 12:15:40 2008

File name: Parcellation.gipl

Files of type: Volume (*)

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



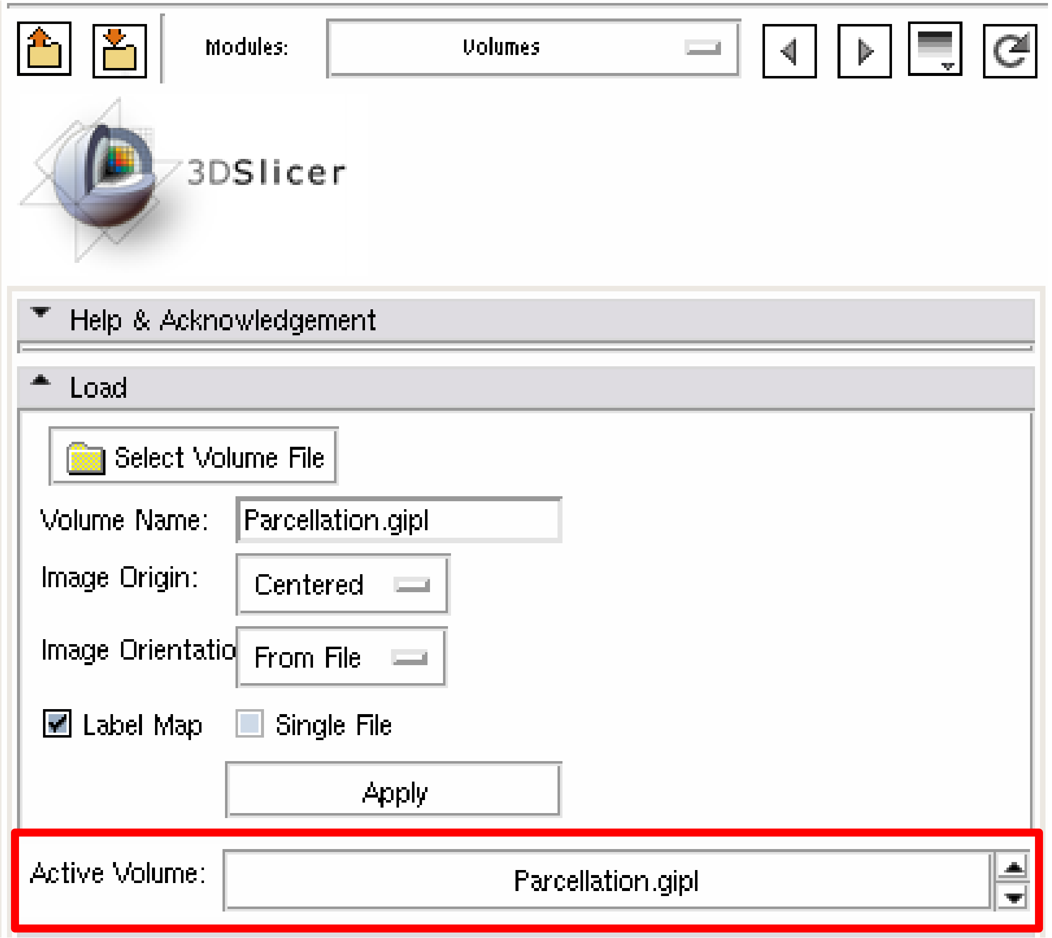
Volume Name: Parcellation.gipl
Image Origin: Centered
Image Orientatio From File
☑ Label Map ☐ Single File
Active Volume: template.gipl

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



Volume Name: Parcellation.gipl

Image Origin: Centered

Image Orientatio: From File

☑ Label Map ☐ Single File

Active Volume: Parcellation.gipl

The dataset is now loaded.

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

Example with tutorial dataset

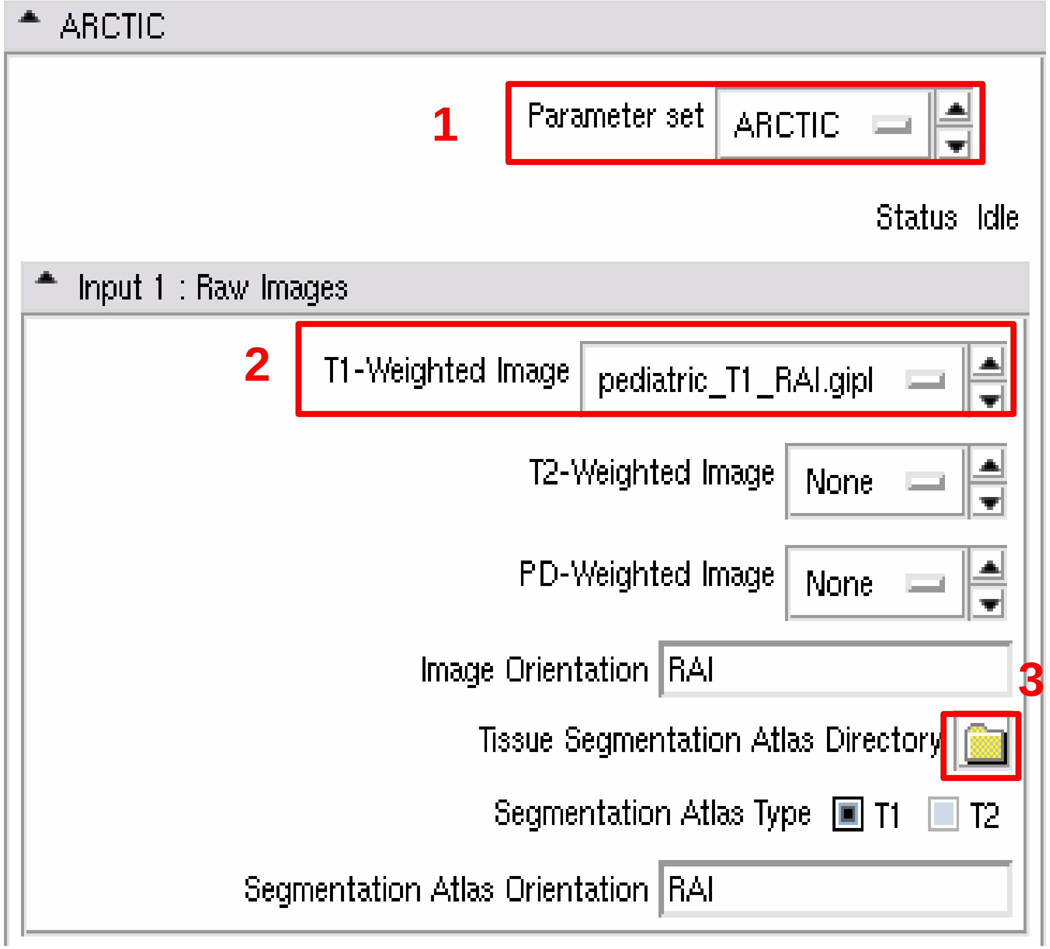
- Input images loading
- ARCTIC execution

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



Parameter set: ARCTIC

Status: Idle

T1-Weighted Image: pediatric_T1_RAI.gipl

T2-Weighted Image: None

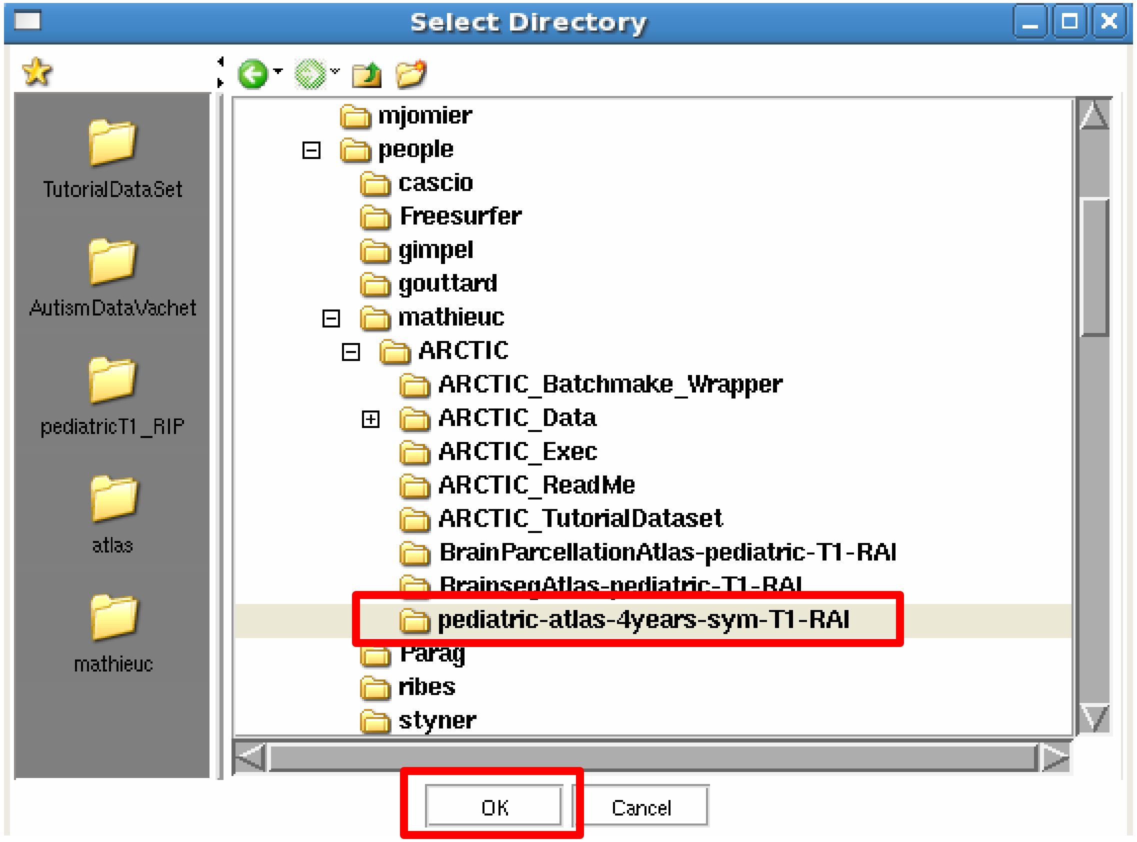
PD-Weighted Image: None

Image Orientation: RAI

Segmentation Atlas Type: ▣ T1 ☐ T2

Segmentation Atlas Orientation: RAI

Module execution



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

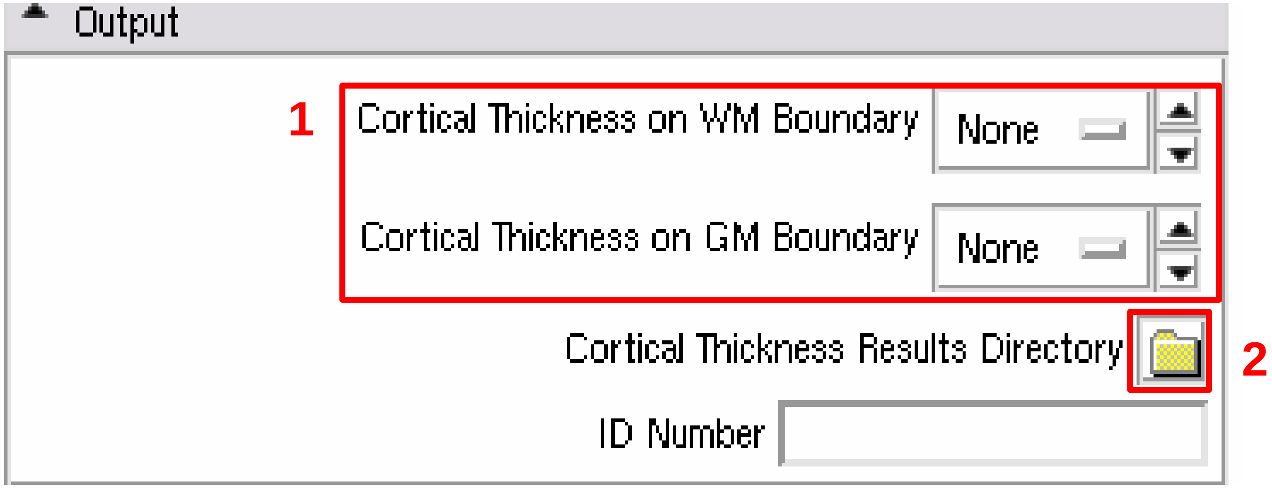
Search and select the **« pediatric-atlas-4years-sym-T1-RAI/»** folder.

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

Module execution

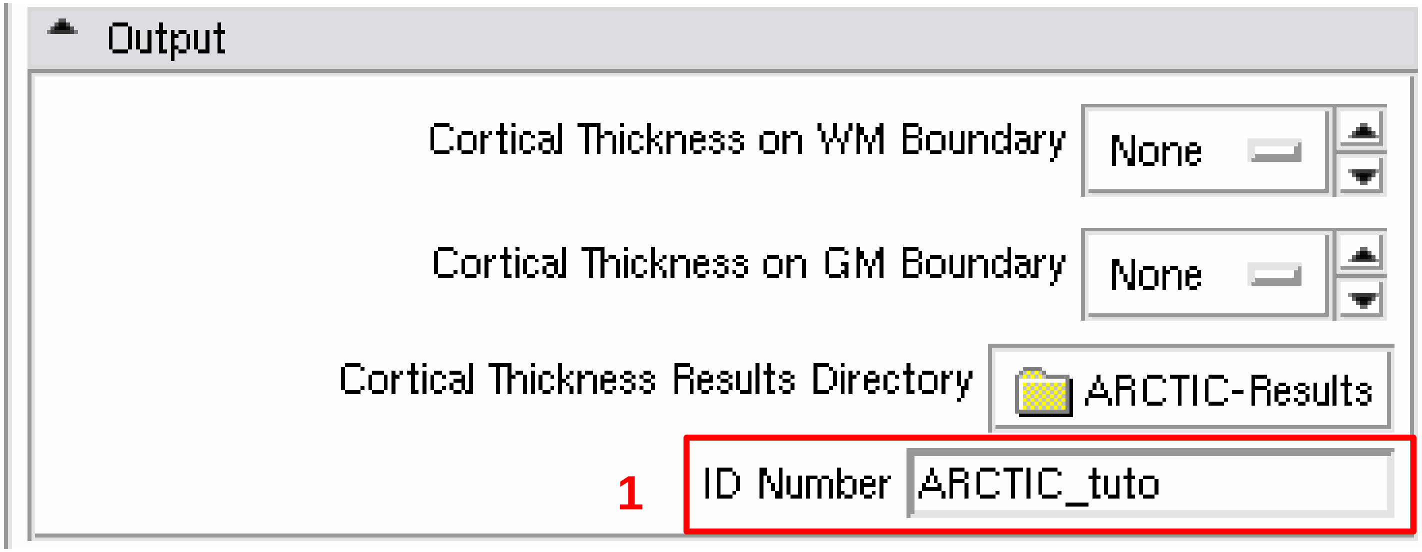
1- Select « **Create a new volume** » to display output images

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



Module execution

1- Set the prefix for the outputs.



Output

Cortical Thickness on WM Boundary: None

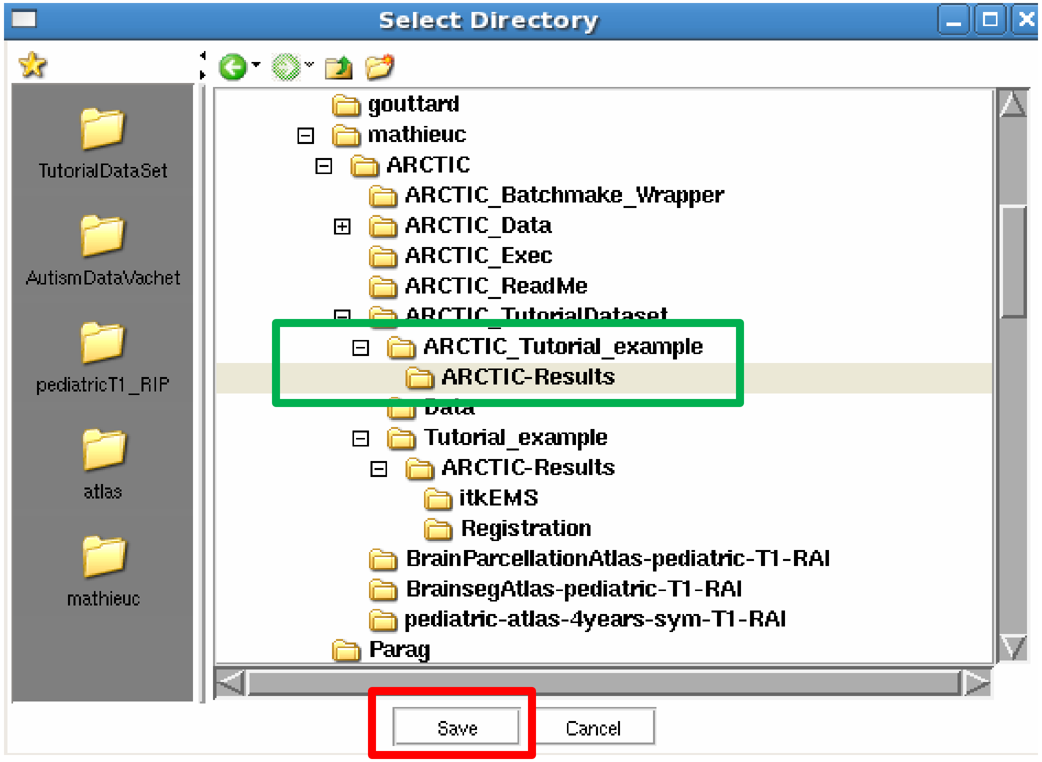
Cortical Thickness on GM Boundary: None

Cortical Thickness Results Directory: ARCTIC-Results

1

ID Number: ARCTIC_tuto

Module execution



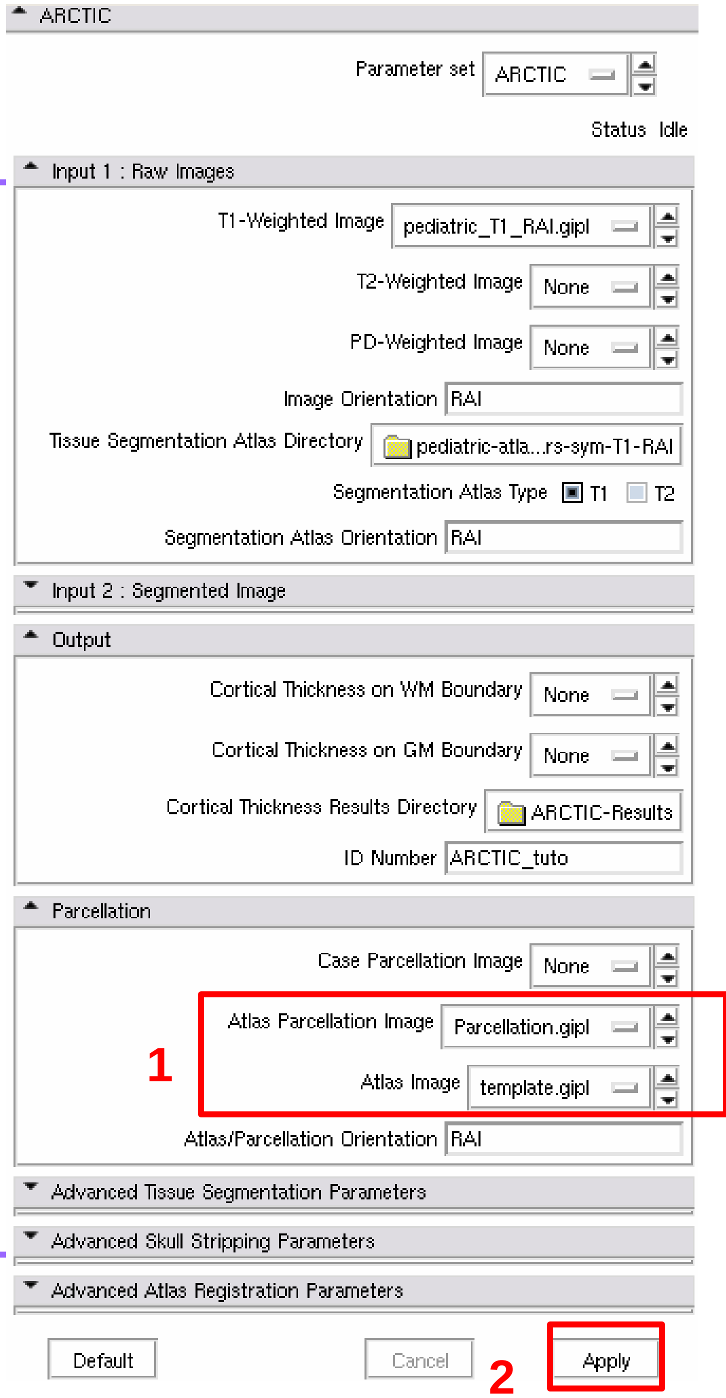
Select the « **ARCTIC-Results** » folder in the ARCTIC_Tutorial_Example directory

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.



ARCTIC

Parameter set: ARCTIC

Status: Idle

Input 1 : Raw Images

T1-Weighted Image: pediatric_T1_RAI.gipl

T2-Weighted Image: None

PD-Weighted Image: None

Image Orientation: RAI

Tissue Segmentation Atlas Directory: pediatric-atla...rs-sym-T1-RAI

Segmentation Atlas Type: ▣ T1 ☐ T2

Segmentation Atlas Orientation: RAI

Input 2 : Segmented Image

Output

Cortical Thickness on WM Boundary: None

Cortical Thickness on GM Boundary: None

Cortical Thickness Results Directory: ARCTIC-Results

ID Number: ARCTIC_tuto

Parcellation

Case Parcellation Image: None

Atlas Parcellation Image: Parcellation.gipl

Atlas Image: template.gipl

Atlas/Parcellation Orientation: RAI

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

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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

--orientation *RAI* : if the orientation of your file(s) is different than the default value (RAI), add this flag to set the right orientation

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

--segAtlasOrientation *RAI* : if the orientation of your tissue segmentation atlas 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

--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

--rawImageOrientation *RAI* : if the orientation of your files is different than the default value (RAI), add this flag to set the right orientation

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

--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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