



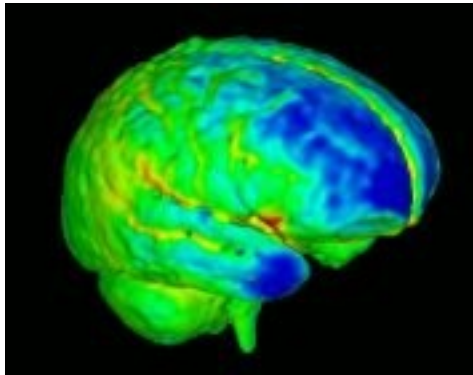
NA-MIC

National Alliance for Medical Image Computing

<http://na-mic.org>

GAMBIT: Group-wise Automatic Mesh-Based analysis of cortical Thickness

Clement Vachet, Heather Cody Hazlett, Martin Styner



University of North Carolina, Chapel Hill:
Neuro Image Research and Analysis Lab
Neurodevelopmental Disorders Research Center

Contact: cvachet@email.unc.edu

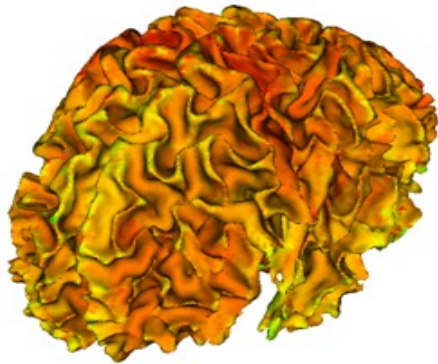
NA-MIC Tutorial Contest: Summer 2010



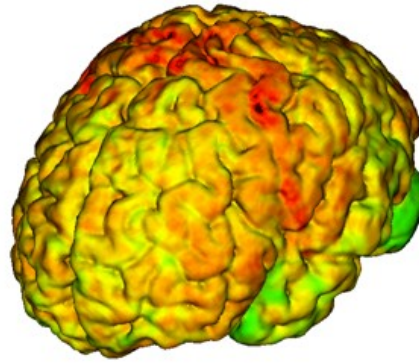
Learning Objective

Following this tutorial, you will be able to perform group-wise automatic mesh-based analysis of cortical thickness.

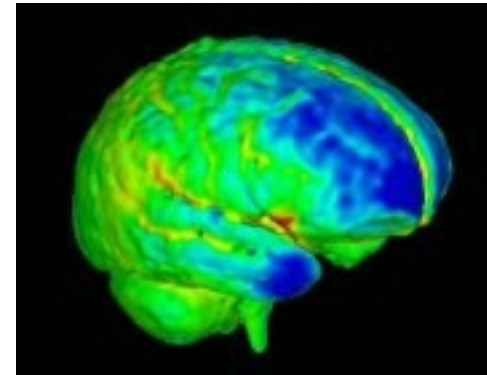
You will learn how to **create a CSV file to set the input dataset**, **run the end-to-end module GAMBIT** to **generate cortical thickness measurements** and **display MRML scenes for quality control**.



Cortical thickness on
WM surface



Cortical thickness on
GM surface



Brain development



Platform

- GAMBIT has been developed and tested on linux.
- GAMBIT will be cross-platform soon and directly available as a 3D Slicer extension.



Pre-requisite

This tutorial assumes that you have already completed tutorials for first-time and beginning users.

Tutorials are available at the following location:

http://www.slicer.org/slicerWiki/index.php/Slicer_3.6:Training

Tutorials:

- Slicer3 Minute tutorial (Author: Sonia Pujol, Ph.D.)
- Slicer3 Visualization tutorial (Author: Sonia Pujol, Ph.D.)



Material

This tutorial requires the installation of 3D Slicer, external modules, tutorial dataset and related atlas. They are available at the following locations:

- 3D Slicer download page (***Slicer 3.6 release***)
<http://www.slicer.org/pages/Special:SlicerDownloads>
- ABC (Atlas Based Classification) available as a 3D Slicer extension
- External modules and tutorial dataset download page
(***GAMBIT_Tutorial_Example_1.0 and GAMBIT_Executables_1.0***)
<http://www.nitrc.org/projects/gambit/>
- ShapeWorks download page (***ShapeWorks-0.3.0***)
<https://gforge.sci.utah.edu/gf/project/shapeworks/frs/>
- Atlas download page (***UNC_Pediatric_Brain_Atlas***)
<http://hdl.handle.net/1926/1508>

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.*



Material: Tutorial dataset

- Download and unzip “*GAMBIT_Tutorial_example_1.0.zip*” from the following download page:

http://www.nitrc.org/frs/?group_id=384

- A “*GAMBIT_Tutorial_example_1.0*” folder will be created, containing:
 - 5 pediatric cases: T1-weighted images.
 - A “*GAMBIT-Results/*” directory, in which results of the tutorial example will be saved.



Material: External modules

- ABC is a 3D Slicer external module available directly as an extension
 - Open 3D Slicer
 - Go to View → Extension Manager
 - Click next on the new window to search for available extensions
 - Select ABC and Click “Download and Install”
 - Click “Next”
 - Choose to “Restart 3D Slicer now”
- ABC will then appear as a 3D Slicer module



Material: External modules

- Download and unzip “*GAMBIT_Executables_1.0_linux64.zip*” from the following download page:

http://www.nitrc.org/frs/?group_id=384

- A “*GAMBIT_Executables_1.0*” folder will be created, containing executables needed to perform cortical thickness analysis.

- Download and unzip “*ShapeWorks-0.3.0.zip*” from the following page:

<https://gforge.sci.utah.edu/gf/project/shapeworks/frs/>

- ShapeWorks needs to be compiled locally
- Several executables will be created
- The executable “ShapeWorksRun” needs to be copied to the “*GAMBIT_Executables_1.0*” folder

Note: ShapeWorks will be soon directly available as an executable on several platforms as well as a 3D Slicer extension



Material: Add External modules

- To add the executables as 3D Slicer external modules:
 - Open 3D Slicer
 - Go to View → Application Settings → Module Settings
 - Click on the “add a preset” button
 - Select the “*GAMBIT_Executables_1.0*” folder and confirm
 - Close and restart 3D Slicer
- Several modules should appear within 3D Slicer



Material: Atlas

- Create a “pediatric-atlas-4years-sym-T1-RAI” folder somewhere in your system.
- Download the “*UNC_Pediatric_Brain_Atlas*” from the following page:
<http://hdl.handle.net/1926/1508>
 - Download everything:
 - Horizontal menu: item -> Download item (.zip)
 - Unzip the ZIP file in this new folder.
 - OR Download only needed files in this new folder:
1.mha, 2.mha, 3.mha, 4.mha, AbsoluteWMMaskImage.nrrd, latVentricleMask.nrrd, Parcellation_98Lobes.nrrd, Parcellation.nrrd, RemoveGMMaskImage.nrrd, template.mha, template-stripped.nrrd,

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



Pre-requisites

- Add the executables in the PATH:

-tcsh usage : setenv PATH GAMBIT-Executables-Directory:Slicer3-Plugins-Directory:Slicer3-Bin-Directory:\${PATH}

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

Notice : To execute GAMBIT within 3D Slicer, it is not necessary to add "Slicer3-Plugins-Directory" and "Slicer3-Bin-Directory" in the PATH.

- Set GAMBIT environment variable

-tcsh usage : setenv BatchmakeWrapper_Dir GAMBIT-Executables-Directory

-bash usage : export BatchmakeWrapper_Dir=GAMBIT-Executables-Directory

WITH:

- GAMBIT-Executables-Directory/ : Downloaded folder (GAMBIT_Executables_1.2)
- Slicer3-Plugins-Directory/ : Directory containing Slicer3 plugins
Slicer 3.6 release : "Slicer3Dir"/lib/Slicer3/Plugins
- Slicer3-Bin-Directory/ : Directory containing Slicer3 binary files
Slicer 3.6 release : "Slicer3Dir"/lib/Slicer3/bin



Pre-requisites

Set Slicer libraries variable (ONLY FOR COMMAND LINE)

-tcsh usage : setenv SLICERLIBPATH "Slicer3Dir"/lib

```
setenv LD_LIBRARY_PATH ${LD_LIBRARY_PATH}:${SLICERLIBPATH}/BatchMake:$
${SLICERLIBPATH}/bmModuleDescriptionParser:${SLICERLIBPATH}/FreeSurfer:${SLICERLIBPATH}/GenerateCLP:$
${SLICERLIBPATH}/GenerateLM:${SLICERLIBPATH}/IGT:${SLICERLIBPATH}/InsightToolkit:$
${SLICERLIBPATH}/ITKCommandIO:${SLICERLIBPATH}/KWWidgets:${SLICERLIBPATH}/LoadableModule:$
${SLICERLIBPATH}/MGHImageIO:${SLICERLIBPATH}/ModuleDescriptionParser:${SLICERLIBPATH}/MRML:$
${SLICERLIBPATH}/MRMLCLI:${SLICERLIBPATH}/MRMLIDImageIO:${SLICERLIBPATH}/OpenIGTLink:$
${SLICERLIBPATH}/Python/lib:${SLICERLIBPATH}/RemoteIO:${SLICERLIBPATH}/Slicer3:$
${SLICERLIBPATH}/SlicerIO:${SLICERLIBPATH}/tclap:${SLICERLIBPATH}/TcITk/lib:${SLICERLIBPATH}/Teem-
1.11.0:${SLICERLIBPATH}/vtk-5.6:${SLICERLIBPATH}/vtkITK:${SLICERLIBPATH}/vtkTeem
```

-bash usage : export SLICERLIBPATH="Slicer3Dir"/lib

```
export LD_LIBRARY_PATH=${LD_LIBRARY_PATH}:${SLICERLIBPATH}/BatchMake:$
${SLICERLIBPATH}/bmModuleDescriptionParser:${SLICERLIBPATH}/FreeSurfer:${SLICERLIBPATH}/GenerateCLP:$
${SLICERLIBPATH}/GenerateLM:${SLICERLIBPATH}/IGT:${SLICERLIBPATH}/InsightToolkit:$
${SLICERLIBPATH}/ITKCommandIO:${SLICERLIBPATH}/KWWidgets:${SLICERLIBPATH}/LoadableModule:$
${SLICERLIBPATH}/MGHImageIO:${SLICERLIBPATH}/ModuleDescriptionParser:${SLICERLIBPATH}/MRML:$
${SLICERLIBPATH}/MRMLCLI:${SLICERLIBPATH}/MRMLIDImageIO:${SLICERLIBPATH}/OpenIGTLink:$
${SLICERLIBPATH}/Python/lib:${SLICERLIBPATH}/RemoteIO:${SLICERLIBPATH}/Slicer3:$
${SLICERLIBPATH}/SlicerIO:${SLICERLIBPATH}/tclap:${SLICERLIBPATH}/TcITk/lib:${SLICERLIBPATH}/Teem-
1.11.0:${SLICERLIBPATH}/vtk-5.6:${SLICERLIBPATH}/vtkITK:${SLICERLIBPATH}/vtkTeem
```

WITH: "Slicer3Dir" : path of Slicer 3.6 release in your computer



Overview

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



Overview

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



Input dataset CSV file

- As GAMBIT performs group analysis, an input dataset needs to be set. Instead of loading input images one by one, the current solution include the use of a CSV file (file with comma separated values), created prior to the use of the software.
- Example of such input CSV file:

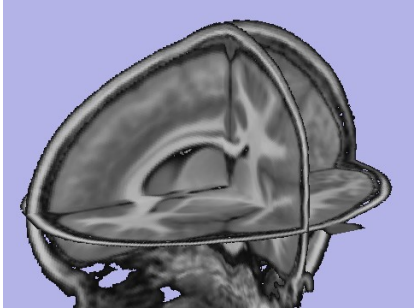
```
Caseld,Age,InputImage1,InputImage2, ...  
Subject1,2,Subject1_T1.nrrd, Subject1_T2.nrrd, ...  
Subject2,4,Subject2_T1.nrrd, Subject2_T2.nrrd, ...  
Subject3,2,Subject3_T1.nrrd, Subject3_T2.nrrd, ...  
...
```

- Note: In the future, the use of such CSV files will be replaced by the use of a 3D Slicer widget, allowing data selection, either locally or via XNAT (images with meta data used for statistical analysis)



Input segmentation atlas

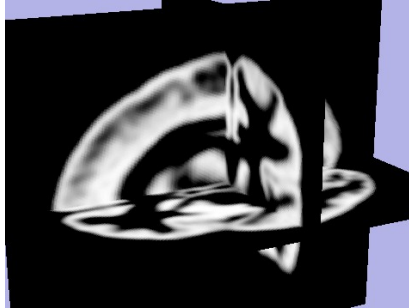
- Atlas used for tissue segmentation:
 - T1-weighted atlas image
 - Atlas class priors: white matter, grey matter, CSF, rest probability maps



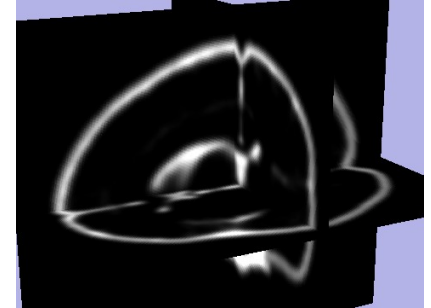
T1w atlas



White matter
probability map



Grey matter
probability map



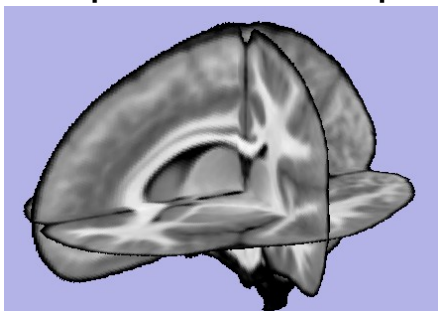
CSF
probability map



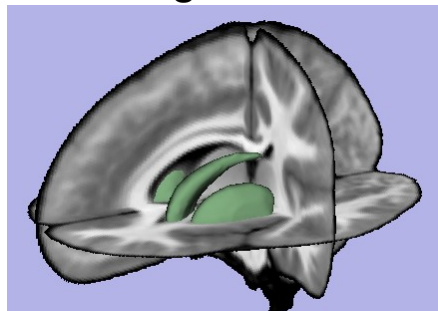
Input ROI atlas

T1w skull-stripped ROI atlas with its label images used to create white matter map:

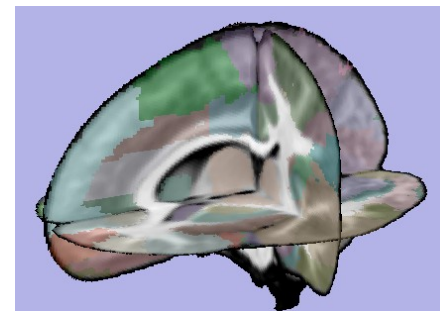
- Absolute white matter mask image: binary mask considered as absolute white matter (default: caudate, pallidus, putamen)
- CSF to white matter mask image: large binary mask which will be combined with CSF tissue map to segment lateral ventricles
- Remove GM mask image: binary mask which will be removed from white matter map (default: amygdala, hippocampus, brainstem, cerebellum)
- Label image for particle initialization: label map image used to initialize particle for correspondence step. One particle will be created per label
- Optional: lobar parcellation image



T1w ROI atlas



Absolute WM mask



Particle initialization label map

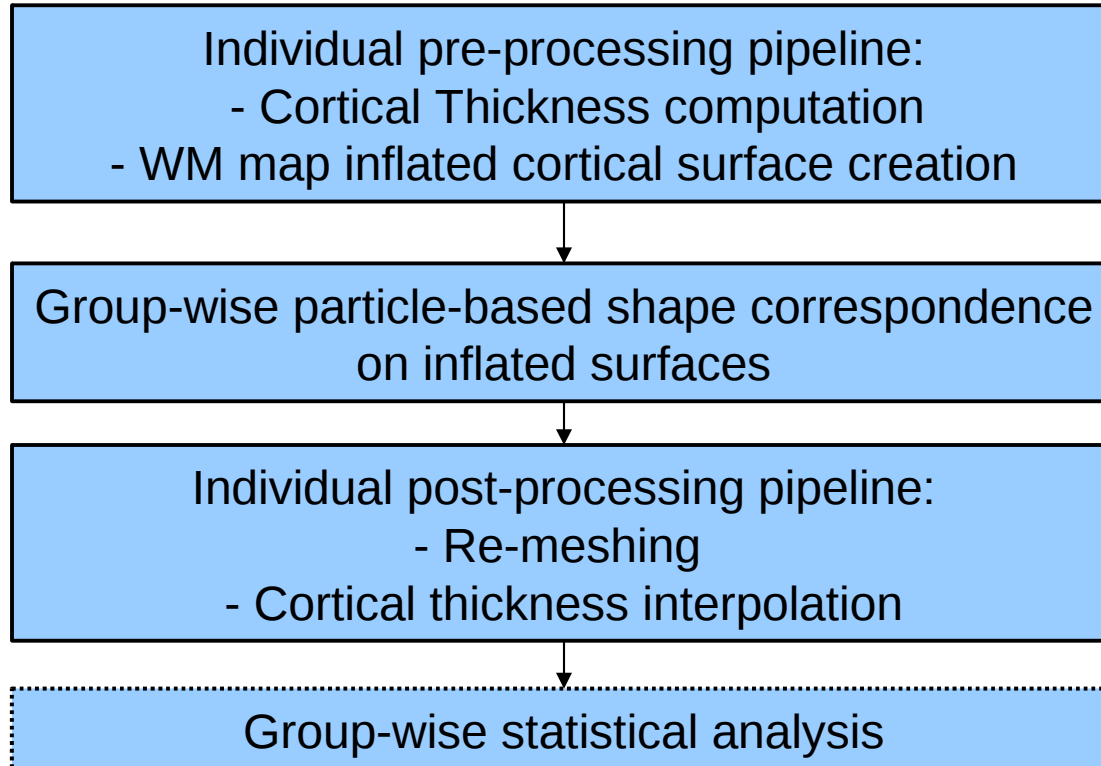


Overview

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



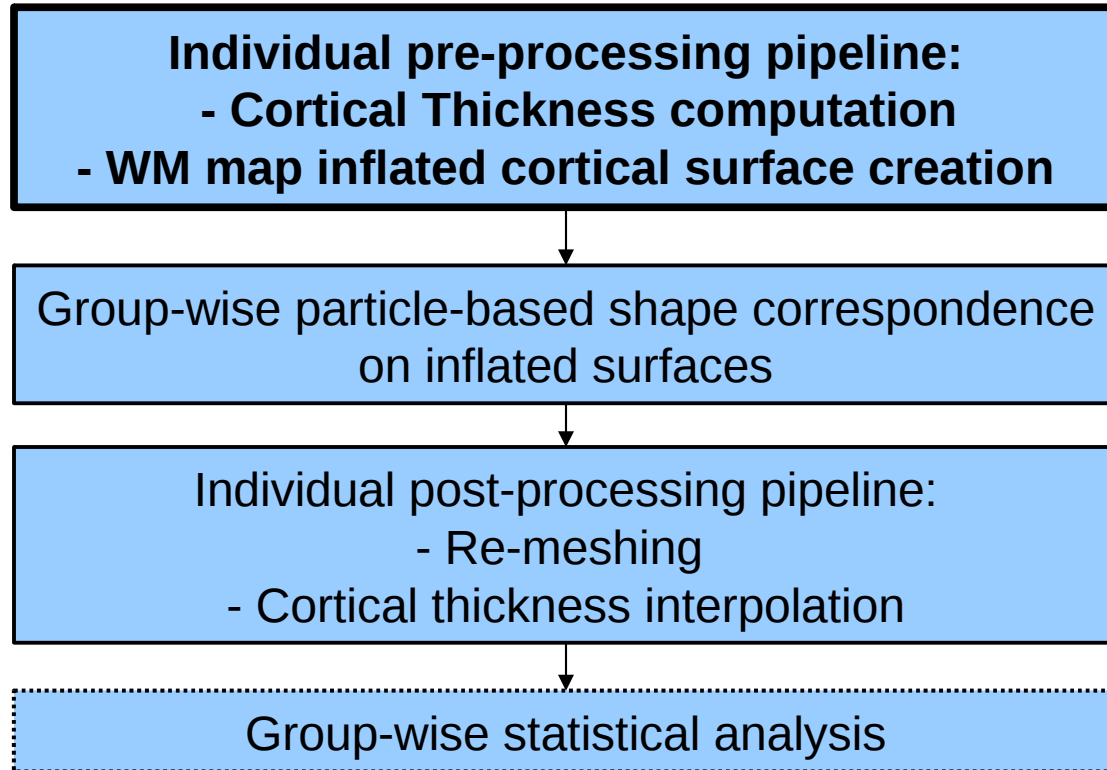
Pipeline description



Note: Statistical analysis is not performed by GAMBIT. Several 3D Slicer modules can be used in that regard, e.g shapeAnalysisMancova (UNC 3D Slicer external module)



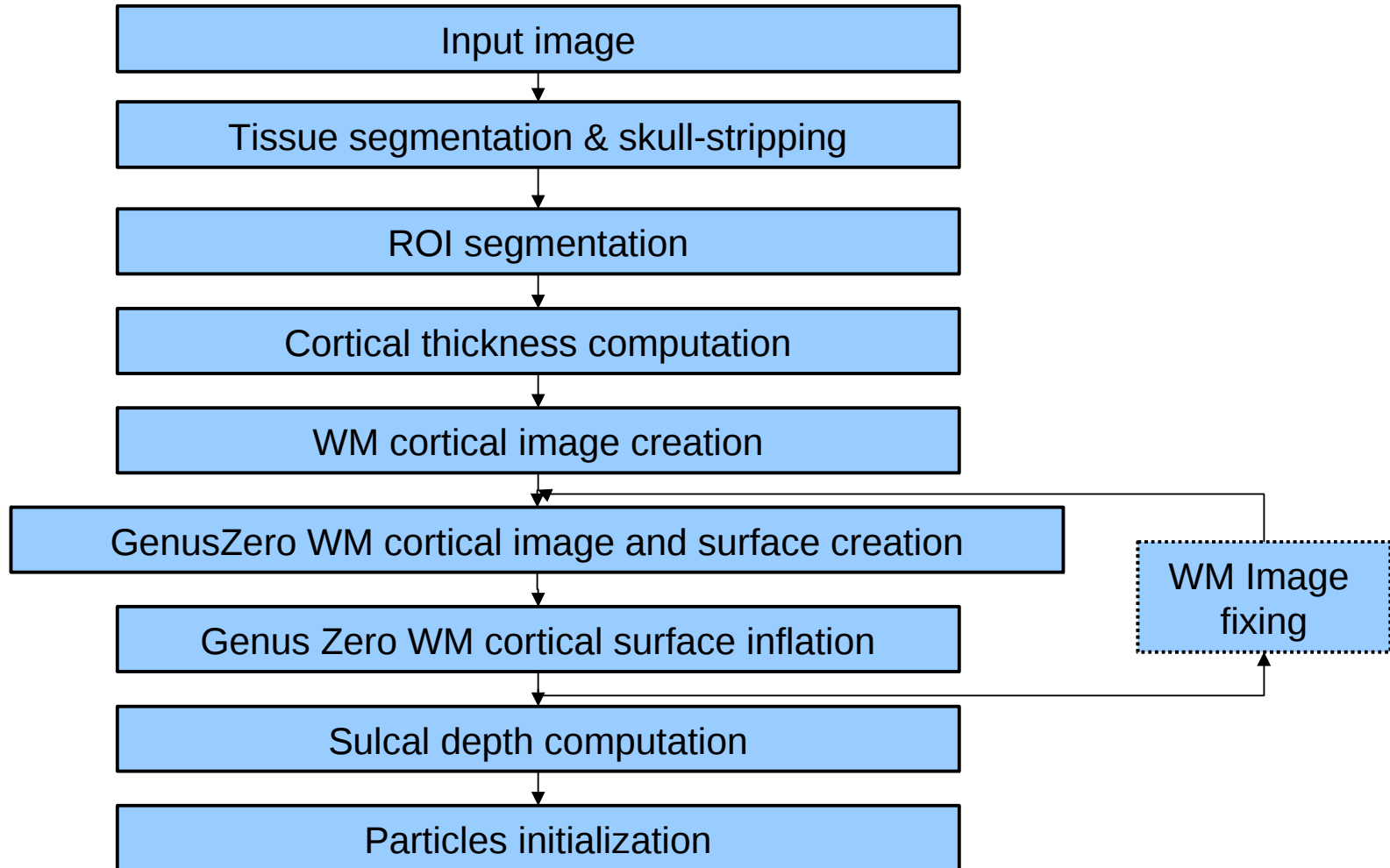
Pipeline description



Note: Statistical analysis is not performed by GAMBIT. Several 3D Slicer modules can be used in that regard, e.g shapeAnalysisMancova (UNC 3D Slicer external module)



Individual pipeline description

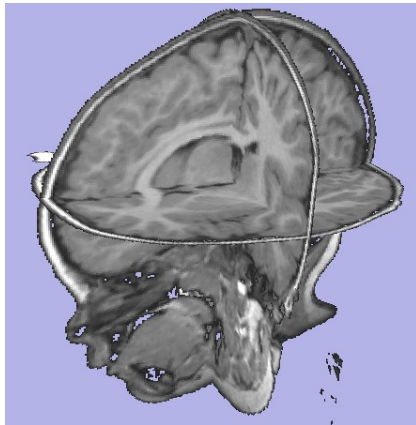




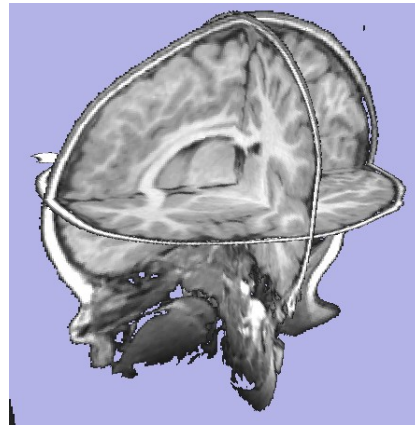
Individual pipeline

Tissue segmentation (ABC, 3D Slicer module)

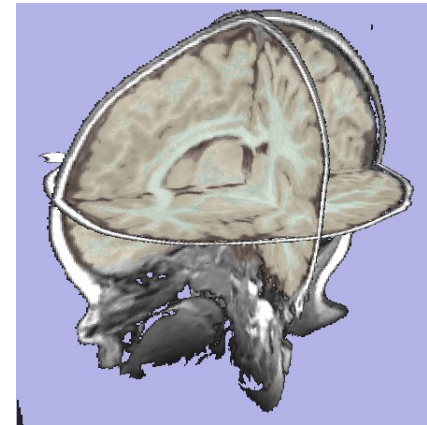
Probabilistic atlas-based automatic tissue segmentation via an Expectation-Maximization scheme. ABC also performs an intensity inhomogeneity correction of the input image that removes gradual variations in the image intensities mainly due to RF coil imperfection



T1w image



Corrected image



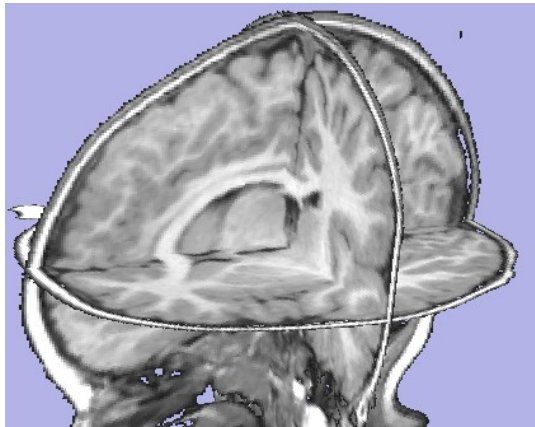
Label image



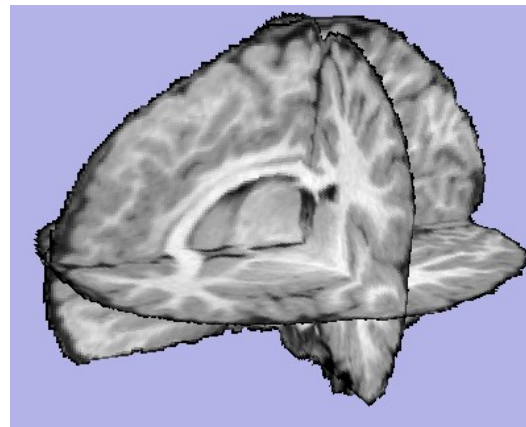
Individual pipeline

Skull-stripping (ImageMath, UNC 3D Slicer external module)

Skull-stripping is performed using the previously computed tissue segmentation label map.



Corrected image



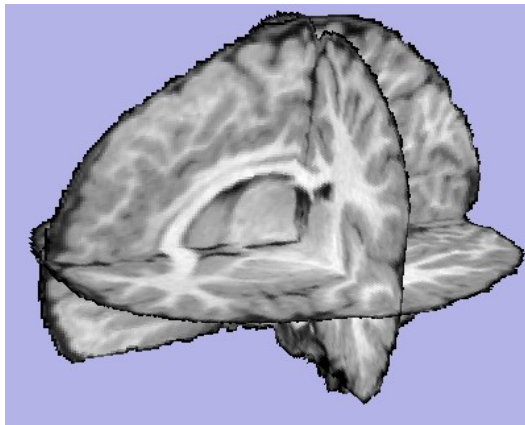
Stripped image



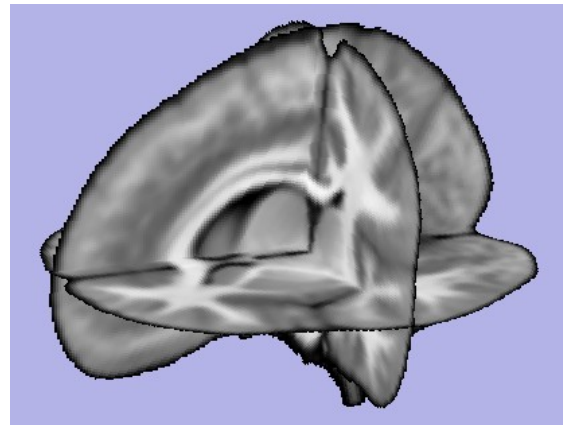
Individual pipeline

Deformable registration of T1-weighted atlas (RegisterImages, 3D Slicer module)

B-Spline based registration from atlas to skull-stripped T1-weighted image, whose ITK transformation is used in the following step to apply transformation to related images



Stripped image



T1w atlas

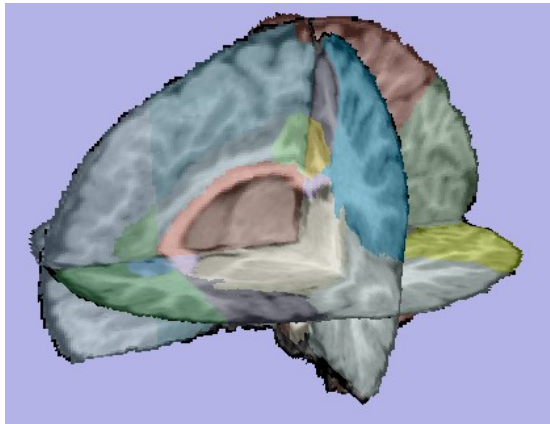


Individual pipeline

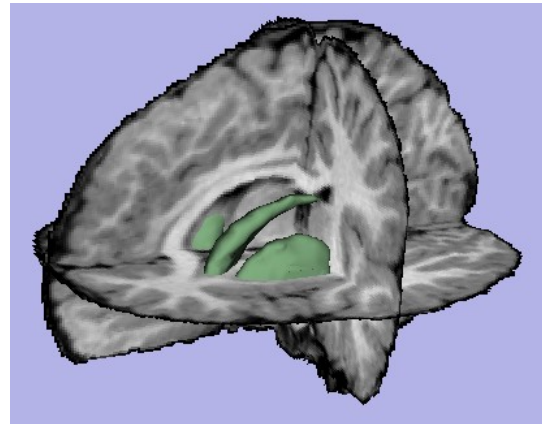
Applying deformation to the atlas label images (ResampleScalar/Vector/DWI, 3D Slicer module)

Previously computed atlas-to-subject transformation are applied to:

- Absolute white matter mask image
- Remove grey matter mask image
- Lobar parcellation image
- CSF to white matter mask image
- Particle initialization label image



Parcellation image

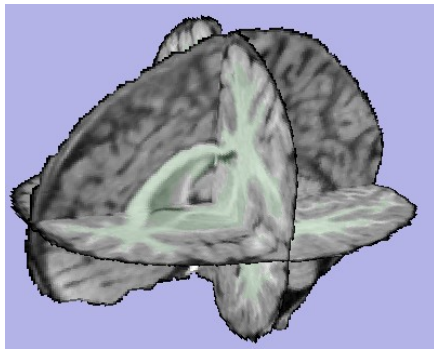


Absolute WM mask image

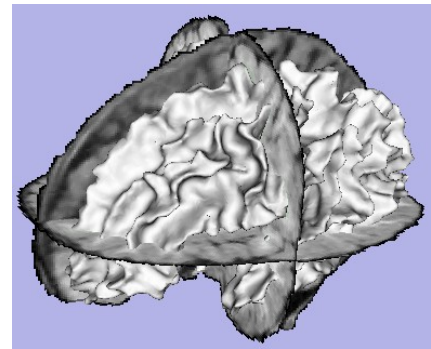


Individual pipeline

- **White matter map image creation** (ImageMath, UNC external module)
WM from tissue segmentation is combined with:
 - Absolute WM mask image (caudate, pallidus, putamen)
 - Lateral ventricles segmentation (obtained from CSF tissue segmentation combined with 'CSF to white matter mask image')
 - GM mask image is then subtracted to the resulted WM map image
- **White matter map image post-processing**
(WMSegPostProcess, UNC 3D Slicer external module)
Filling, connectivity enforcement, smoothing...



WM map image

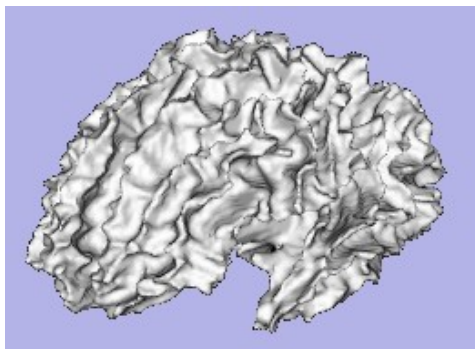


WM map surface

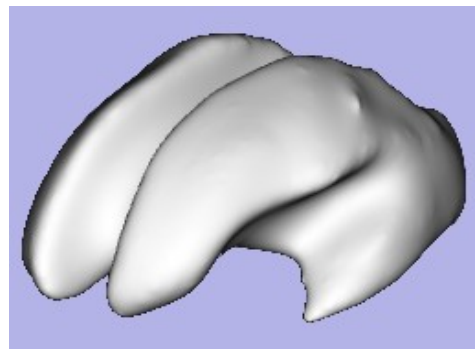


Individual pipeline

- **Genus-zero WM map image and surface creation** (GenusZeroImageFilter, UNC external module)
- **WM map surface inflation** (MeshInflation, UNC external module)
Iterative smoothing using relaxation operator (considering average vertex) and L2 norm of the mean curvature as a stopping criterion
- **WM map image fixing if necessary** (Fix Image, UNC external module)
White matter map correction with connectivity enforcement for bad vertices (really high curvature, due to tissue segmentation)
- **Back to genus-zero surface creation step if necessary**



GenusZero surface

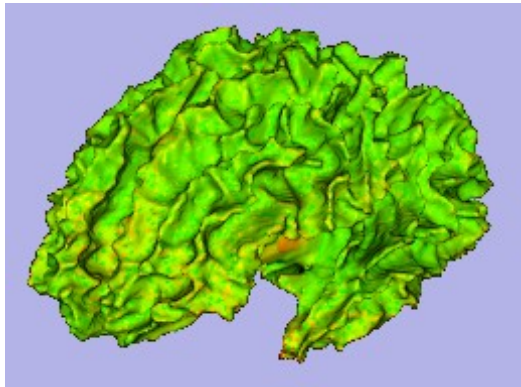


Inflated surface

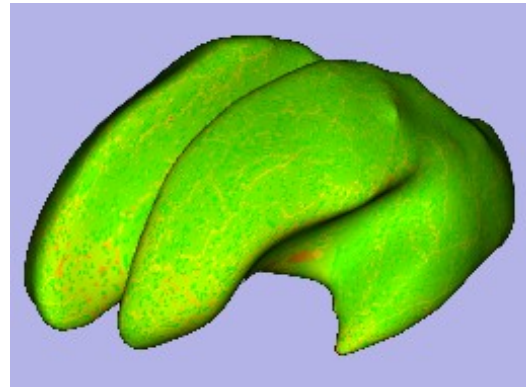


Individual pipeline

- **Cortical thickness computation** (CortThick, UNC external module)
Voxel-based cortical thickness computation using tissue segmentation label map
- **Optional:** cortical thickness interpolation on genus-zero white matter map surface



Cortical thickness on
genus-zero surface



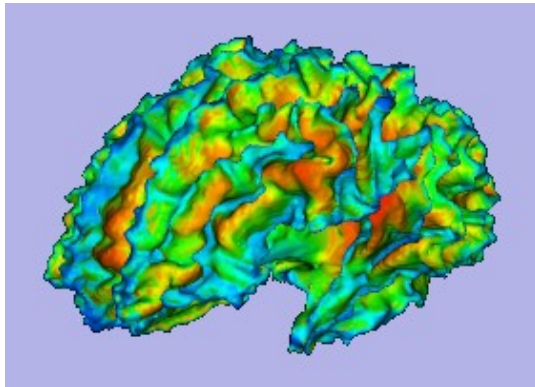
Cortical thickness on
inflated genus-zero
surface



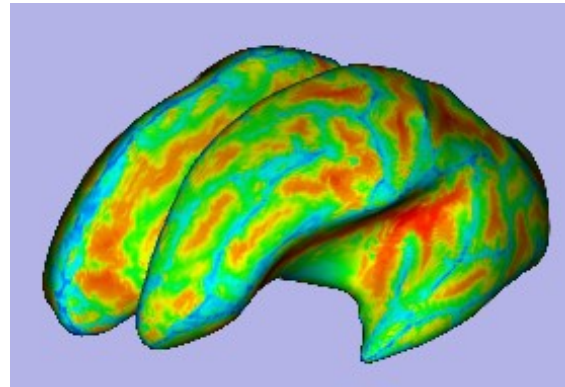
Individual pipeline

Sulcal depth computation (MeshMath, 3D Slicer external module)

Sulcal depth computation considering genus-zero white matter map surface and inflated surface



Sulcal depth on genus-zero surface



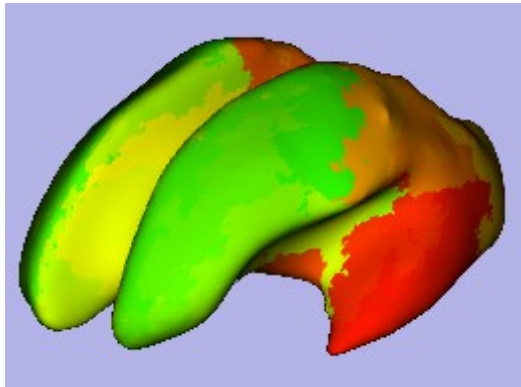
Sulcal depth on inflated genus-zero surface



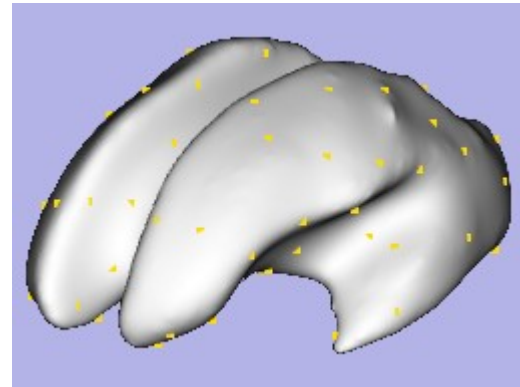
Individual pipeline

Particle initialization (ParticleInitializer, MeshMath, external modules)

Initialization of particles on inflated white matter map surface, by interpolating label map for particle initialization. One centered particle is created per lobe.



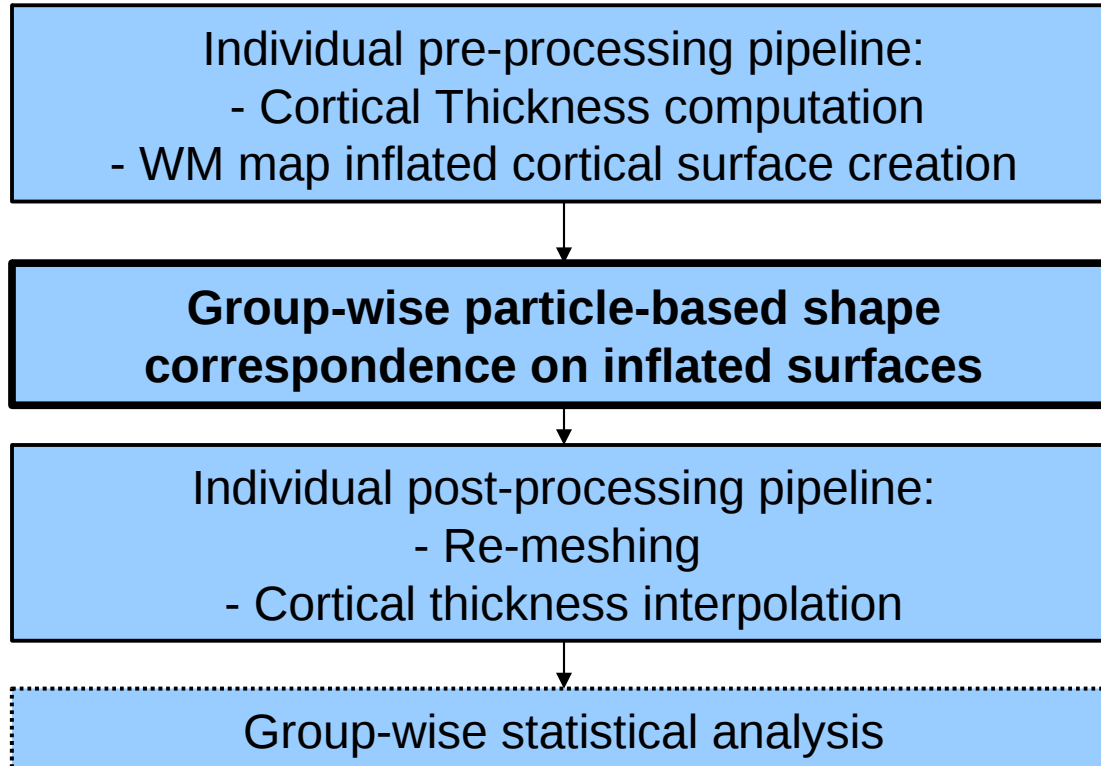
Particle initialization map
on inflated surface



Initialization particles
on inflated surface



Pipeline description



Note: Statistical analysis is not performed by GAMBIT. Several 3D Slicer modules can be used in that regard, e.g shapeAnalysisMancova (UNC 3D Slicer external module)



Pipeline: Group-wise correspondence

- **Particle correspondence pre-processing**

(ParticleCorrespondencePreprocessing, UNC 3D Slicer external module)

Smoothed white matter map distance maps (volumes) creation used as input for shape correspondence

- **Group-wise particle-based shape correspondence**

(ShapeWorks, Utah 3D Slicer external module)

Correspondence on inflated surfaces using dynamic particle system

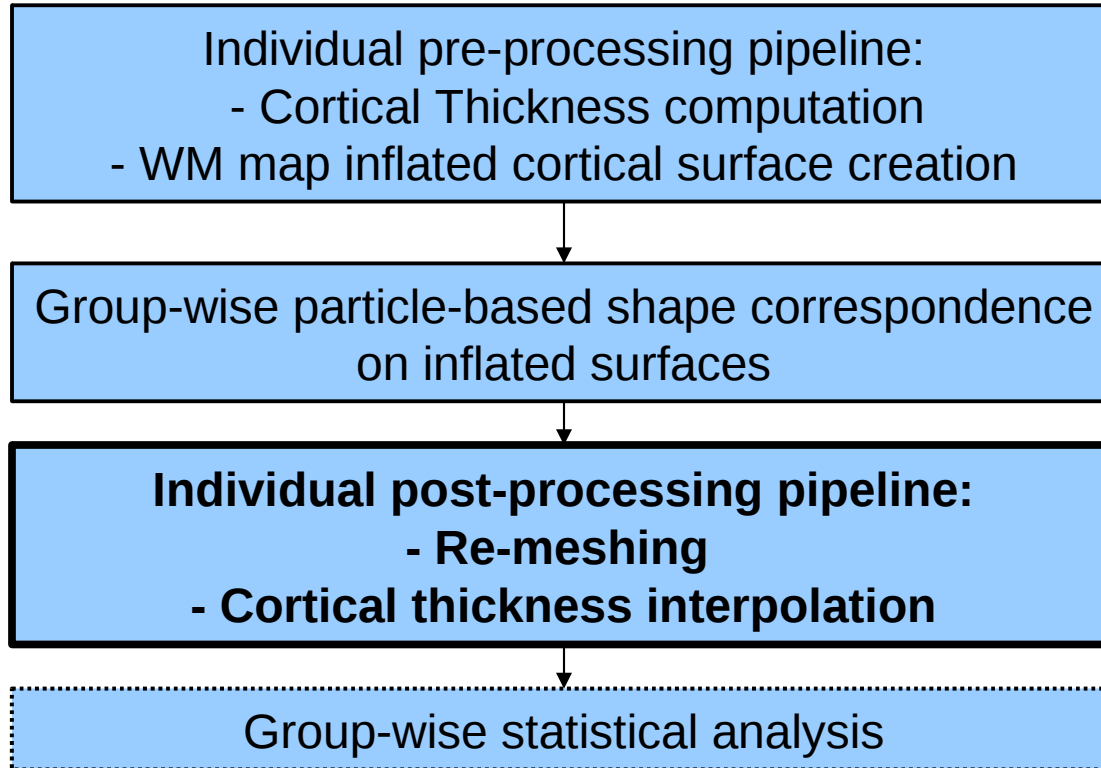
Energy minimization by gradient descent of function balancing negative entropy of the distribution of particles on each cortical surface with positive entropy of the distribution of the shape samples shape space

Documentation available online (ShapeWorksManual.pdf)

<https://gforge.sci.utah.edu/gf/project/shapeworks/frs/>



Pipeline description



Note: Statistical analysis is not performed by GAMBIT. Several 3D Slicer modules can be used in that regard, e.g shapeAnalysisMancova (UNC 3D Slicer external module)



Pipeline: post-processing

- **Particle correspondence post-processing**

(ParticleCorrespondencePostprocessing, UNC 3D Slicer external module)

White matter inflated surfaces re-meshing using template mesh

Interpolation by Thin Plate Spline using corresponding particles as control-points. Interpolated surfaces are projected to original surfaces

- **Surface measurements interpolation**

(MeshMath, UNC 3D Slicer external module)

Surface measurements (cortical thickness, sulcal depth) are interpolated on final white matter cortical surfaces

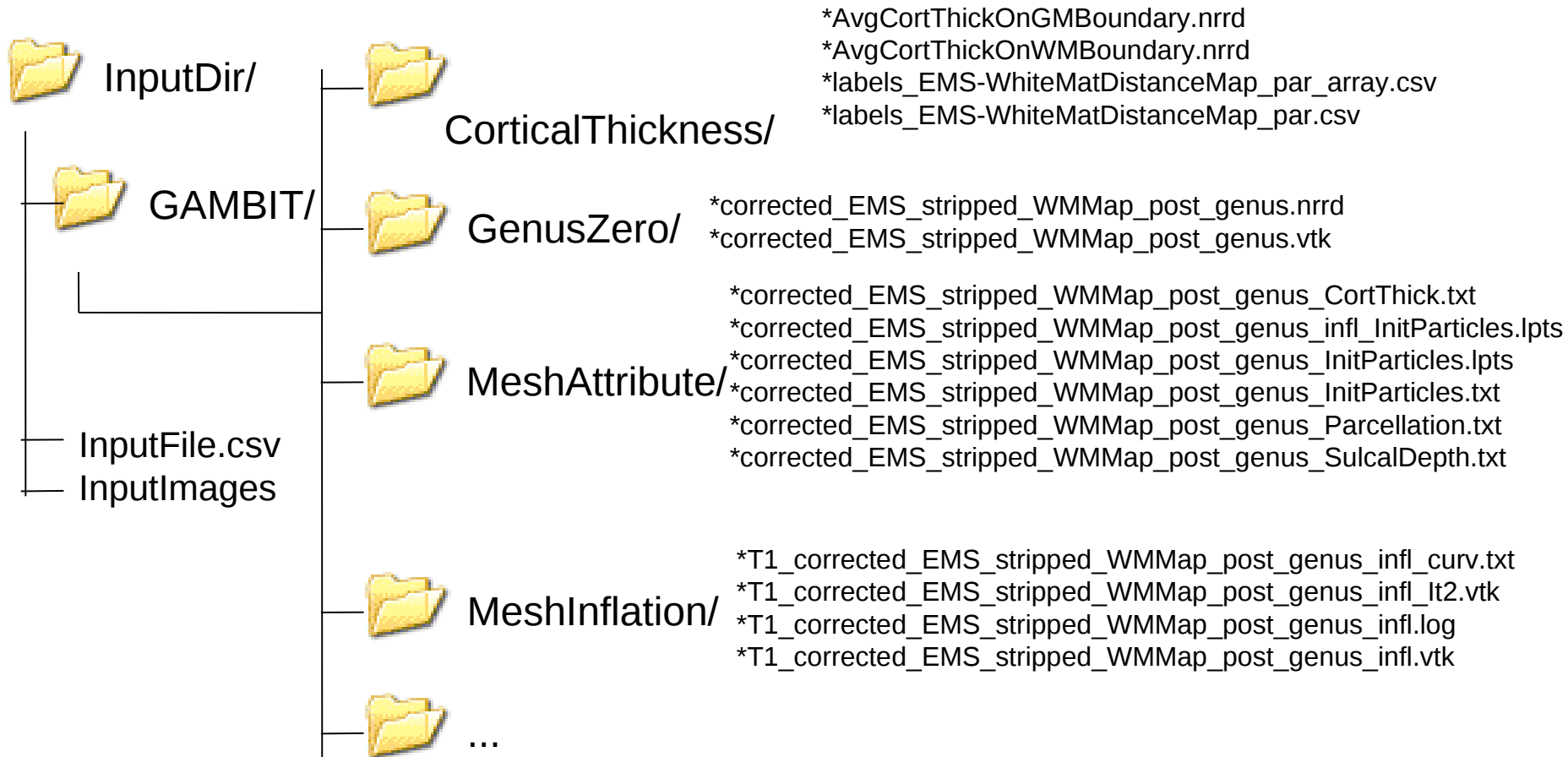


Overview

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

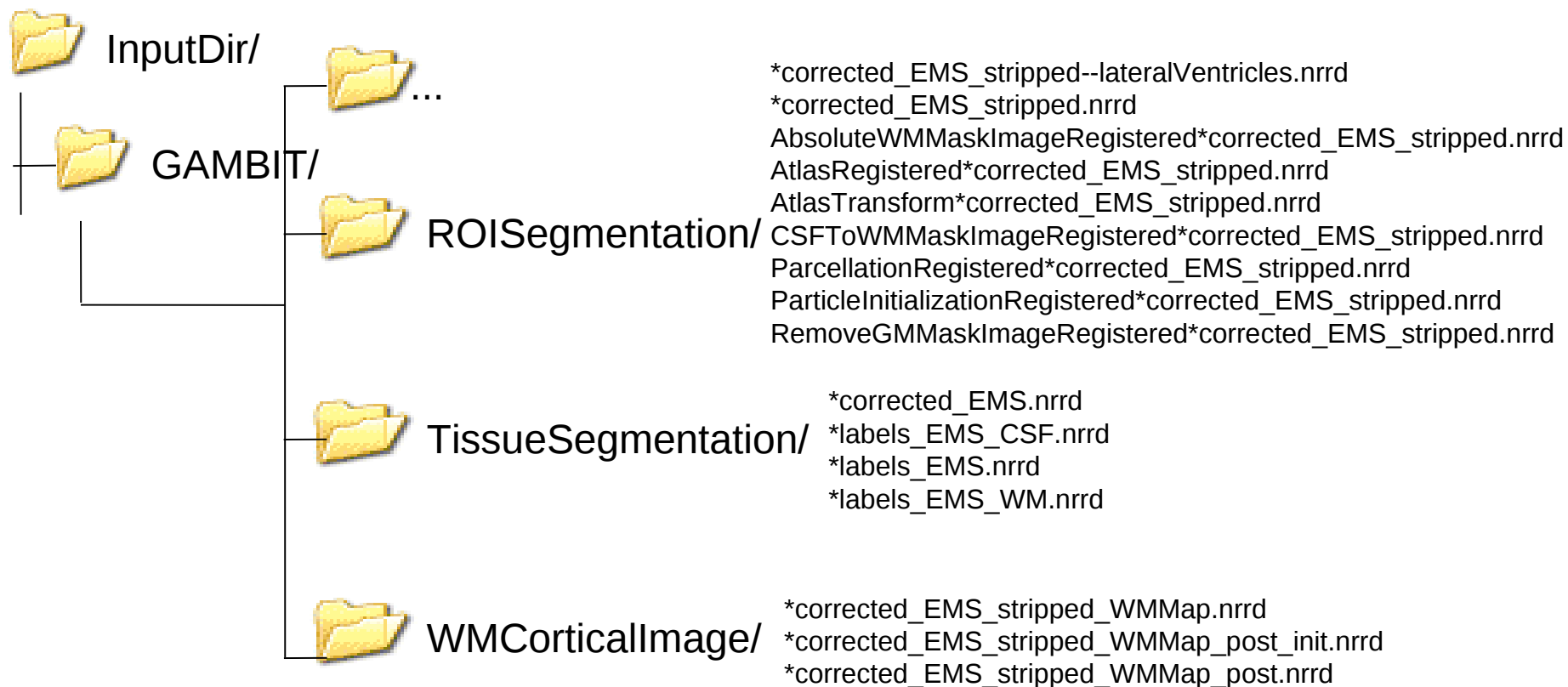


Output organization



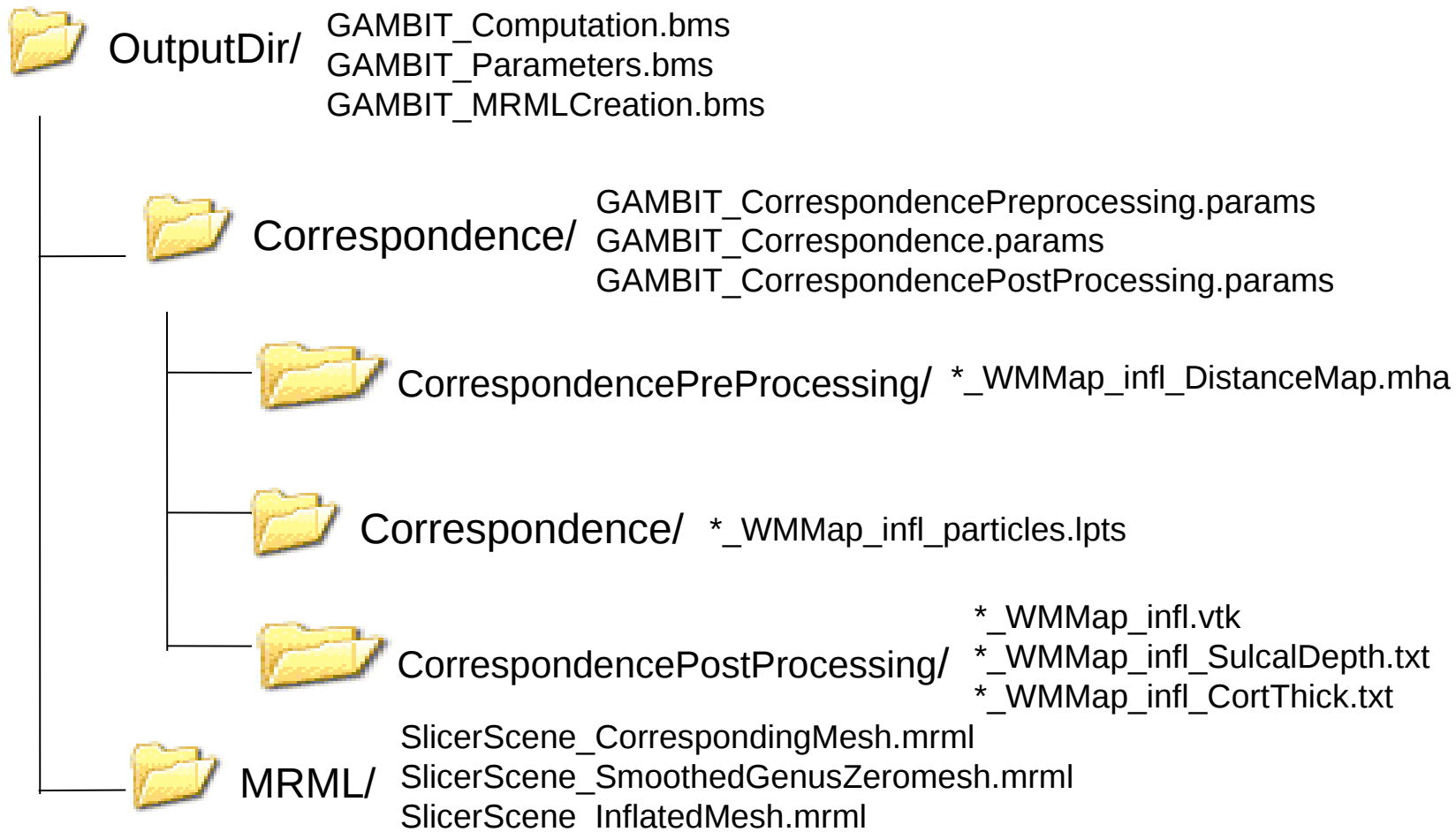


Output organization





Output organization





Overview

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



Execution within Slicer

4.1- Default execution

4.2- Advanced parameters



Default execution

1. Select “GAMBIT” module (in All modules)
2. Set new parameter set
3. Set dataset input CSV file
4. Set output directory
5. Set tissue segmentation atlas directory and atlas type
6. Set ROI atlas image and its label images
7. Click on the “Apply” button to process the dataset

1 module: GAMBIT

3DSlicer

Help & Acknowledgement

GAMBIT

2 Parameter set

Status Idle

3 Input group file: None

4 Output directory: None

Tissue Segmentation:

5 Segmentation atlas directory:

Segmentation atlas type: T1 T2

Atlas Registration:

6 T1 w ROI atlas image: N.e

Atlas absolute white matter mask image: N.e

Atlas CSF to white matter mask image: N.e

Atlas remove grey matter mask image: N.e

Atlas label image for particle initialization: N.e

Atlas parcellation image: N.e

Advanced Input File Parameters:

Advanced Tissue Segmentation Parameters:

Advanced Skull Stripping Parameters:

Advanced Atlas Registration Parameters:

Advanced Surface Inflation Parameters:

Advanced Correspondence Parameters:

Default Cancel 7 Apply



Execution within Slicer

4.1- Default execution

4.2- **Advanced parameters**



Advanced input file parameters

1. Manual input column selection: check if dataset should be found manually using **parameter 2**
2. Set column number of T1w input image for manual selection (**parameter 1** must be set)
3. Check to include T2w images (useful for tissue segmentation) in the dataset
4. Set column number of T2w input images for manual selection (**parameter 3** must be set)
5. Check to include PDw images (useful for tissue segmentation) in the dataset
6. Set column number of PDw input images for manual selection (**parameter 3** must be set)

Advanced Input File Parameters:

- 1 Manual Input column selection:
- 2 Column number of T1w input image: 0
- 3 Input T2 image:
- 4 Column number of T2w input image: 0
- 5 Input PD image:
- 6 Column number of PDw input image: 0



Advanced tissue segmentation parameters

1. Set maximum bias degree parameter
2. Set atlas class prior weights (for WM,GM,CSF,rest)
3. Set number of iterations for atlas-to case warping (fluid deformation)
4. Set type of linear mapping (prior to warping)
5. If several input images, set linear mapping type (second image registered to first one)

Advanced Tissue Segmentation Parameters:

Maximum bias degree: 4 **1**

Class prior weights: 1.2,1,0.7,1 **2**

Atlas warp fluid iterations: 10 **3**

Atlas linear map type: affine rigid identity **4**

Image linear map type: rigid identity affine **5**



Advanced skull-stripping and atlas registration parameters

1. Check/uncheck to dilate tissue segmentation label map used for skull-stripping, useful is the segmentation is not perfect.
2. Set initialization for atlas to subject B-Spline pipeline-based registration (default: center of mass)

The image shows a screenshot of a software interface with two parameter panels. The top panel, titled 'Advanced Skull Stripping Parameters', contains a checkbox for 'Mask dilation'. The bottom panel, titled 'Advanced Atlas Registration Parameters', contains an 'Initialization' section with five radio button options: 'None', 'Landma', 'ImageCent', 'CentersOfM', and 'SecondMomei'. The 'CentersOfM' option is selected. A red box highlights both panels, with a red '1' next to the top panel and a red '2' next to the bottom panel.



Advanced inflation parameters

1. Set number of iterations until inflation is stopped, if necessary, to fix the cortical surface
2. Set maximum curvature to save only vertices whose curvature is higher than max curvature once inflation is stopped after **parameter 1**
3. Set maximum number of iterations during inflation
4. Set minimum mean surface curvature used as a stopping criterion to stop inflation. Curvature keeps decreasing until minimum mean curvature is reached.
5. Set surface inflation relaxation operator (0=no smoothing, 1=full smoothing)

Parameter	Value	Label
Max iterations before fixing	50	1
Maximum curvature	2	2
Maximum number of iterations	2000	3
Mean curvature	3.5	4
Smoothing weight	0.8	5



Advanced correspondence parameters

1. Set gaussian smoothing for preprocessing
2. Set number of particles to sample surfaces
3. Set number of iterations to run between successive particle splits during an initialization phase until number of particles (**param 2**) is reached
4. The starting regularization (added to the covariance matrix of the correspondences) decays to the ending regularization over the specified number of optimization iterations
5. Set number of iterations between successive save of the optimized correspondence positions
6. Weighting factor balancing a tradeoff between compactness and accurate shape representation
7. Set procrustes registration performed based on the current correspondence positions at each specified interval, with scaling is analysis is done independently of shape
8. Set weighted projection of the interpolated surface to the original surface during correspondence post-processing (re-meshing)

Advanced Correspondence Parameters:

1	Preprocessing gaussian smoothing size:	1
2	Number of Particles:	3136
3	Iterations per split:	200
4	Starting regularization:	2000
	Ending regularization:	0.1
	Optimization iterations:	400
5	Checkpointing intervals:	50
6	Relative weighting factor:	30.1
	Procrustes off:	<input type="checkbox"/>
7	Procrustes interval:	50
	Procrustes Scaling Off:	<input type="checkbox"/>
8	Postprocessing projection to surface Off:	<input type="checkbox"/>
	Postprocessing projection factor:	0.9



Overview

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



Example with tutorial dataset

5.1- Create input CSV file

5.2- Load input atlas images

5.3- Run GAMBIT



Create input CSV file

- In the “*GAMBIT_Tutorial_example_1.0*” folder create a CSV file “*GAMBIT_InputFile.csv*” containing input images separated by commas:

Caseld,Age,InputFile1

Subject1,2,“InputDir”/Subject1_T1.nrrd

Subject2,2,“InputDir”/Subject2_T1.nrrd

Subject3,2,“InputDir”/Subject3_T1.nrrd

Subject4,2,“InputDir”/Subject4_T1.nrrd

Subject5,2,“InputDir”/Subject5_T1.nrrd

With “InputDir”: full path on your system of the “*GAMBIT_Tutorial_example_1.0*” directory



Example with tutorial dataset

5.1- Create input CSV file

5.2- Load input atlas images

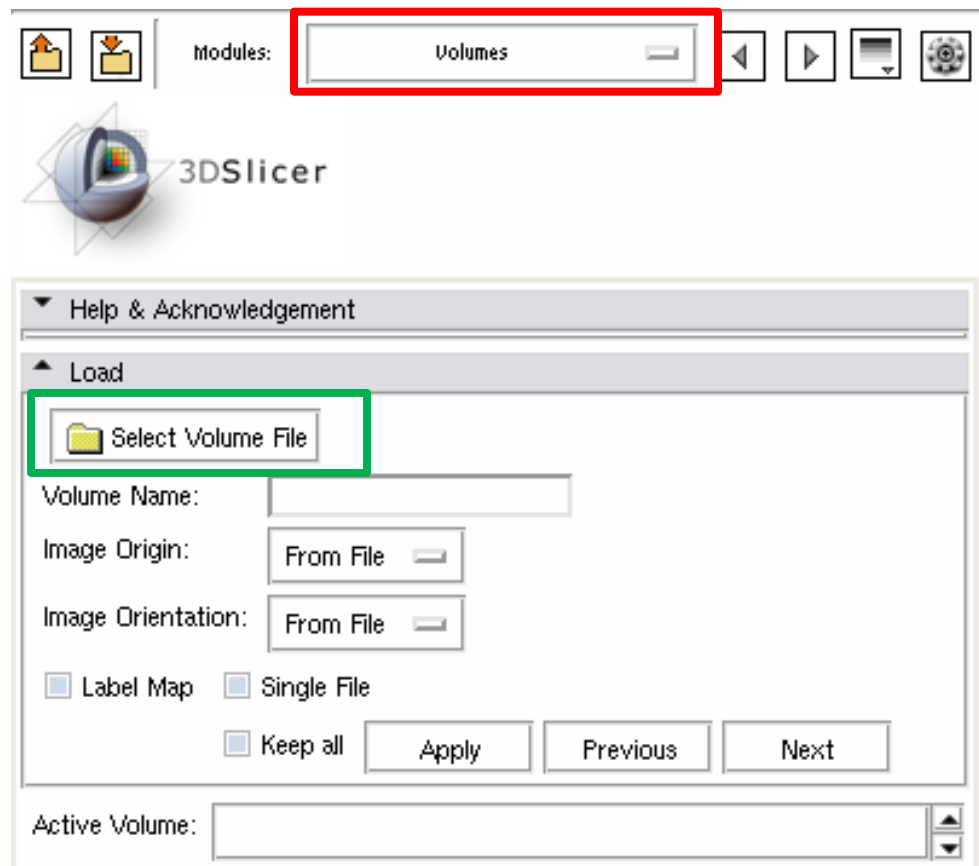
5.3- Run GAMBIT



Load input atlas images

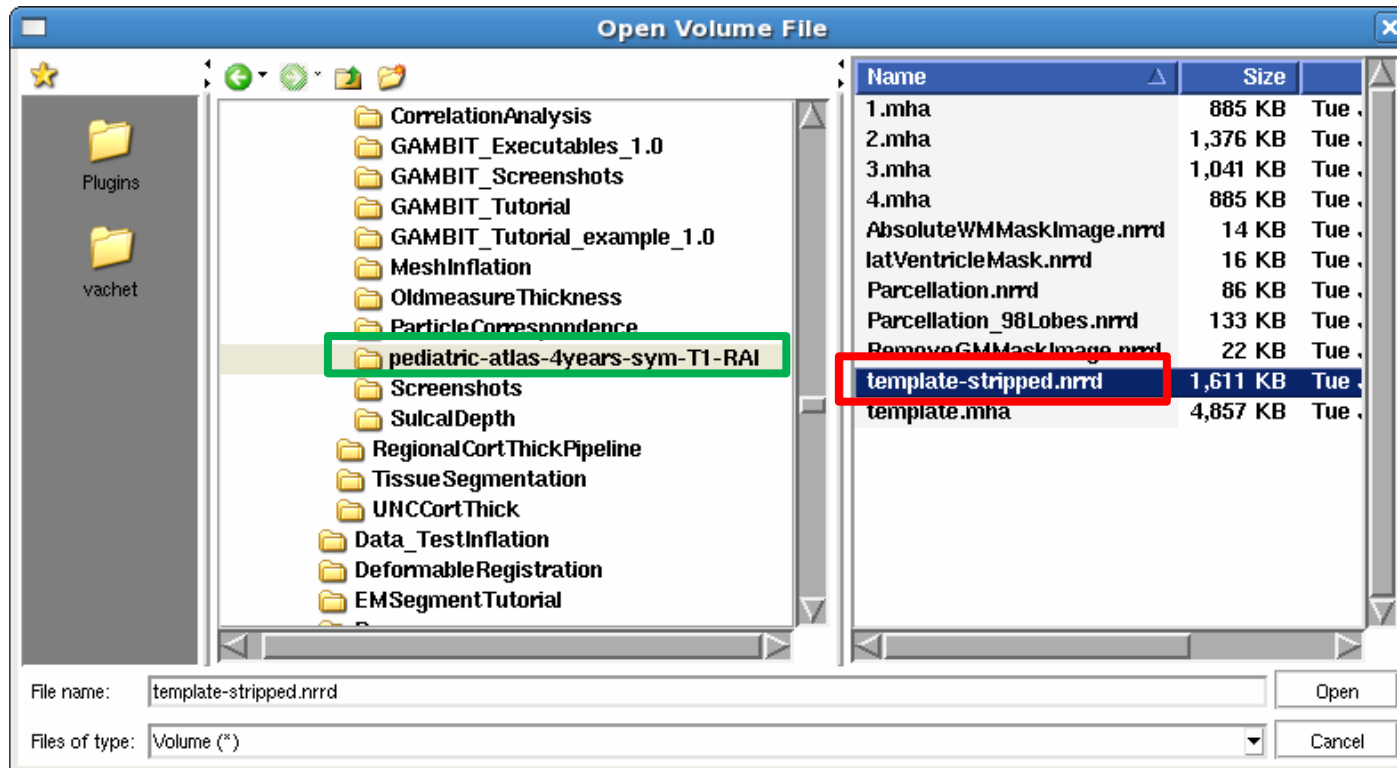
In 3d Slicer, select the module « **Volumes** » to load the input atlas images.

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





Load input atlas images



A window 'Open Volume File' pops up. Select the **«pediatric-atlas-4year-sym-T1-RAI»** directory, then select the **« template-stripped.nrrd »** file and click **« Open »**.

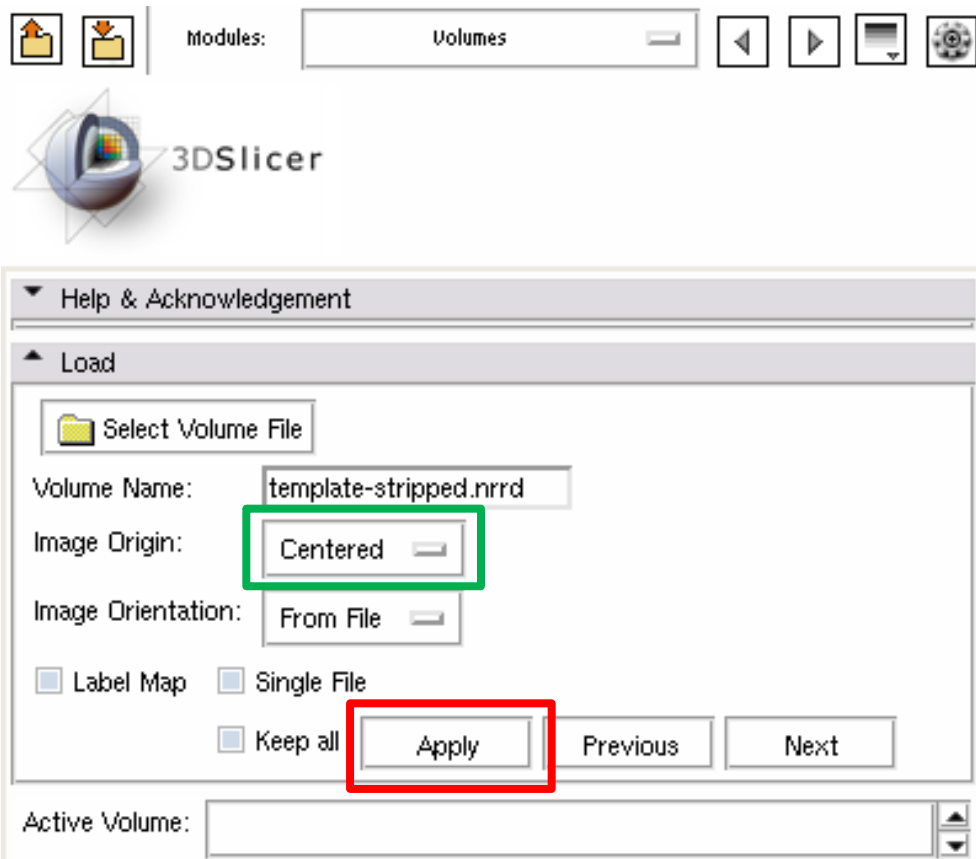


Load input atlas images

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

And click on « **Apply** ».

The atlas is now loaded.



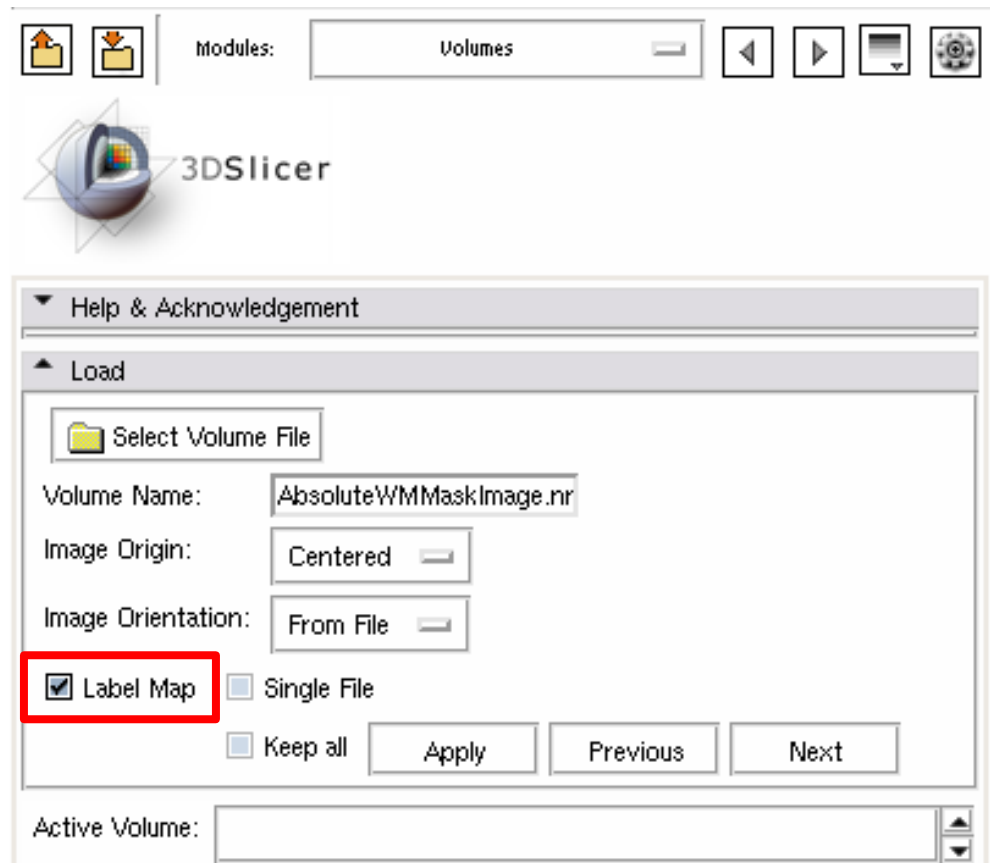


Load input atlas images

Repeat the same process to load the atlas label images:

- AbsoluteWMMaskImage.nrrd
- latVentricleMask.nrrd
- Parcellation_98Lobes.nrrd
- Parcellation.nrrd
- RemoveGMMaskImage.nrrd

However you need to check the « **Label map** » button to display them properly.





Example with tutorial dataset

5.1- Create input CSV file

5.2- Load input atlas images

5.3- Run GAMBIT



Module execution

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

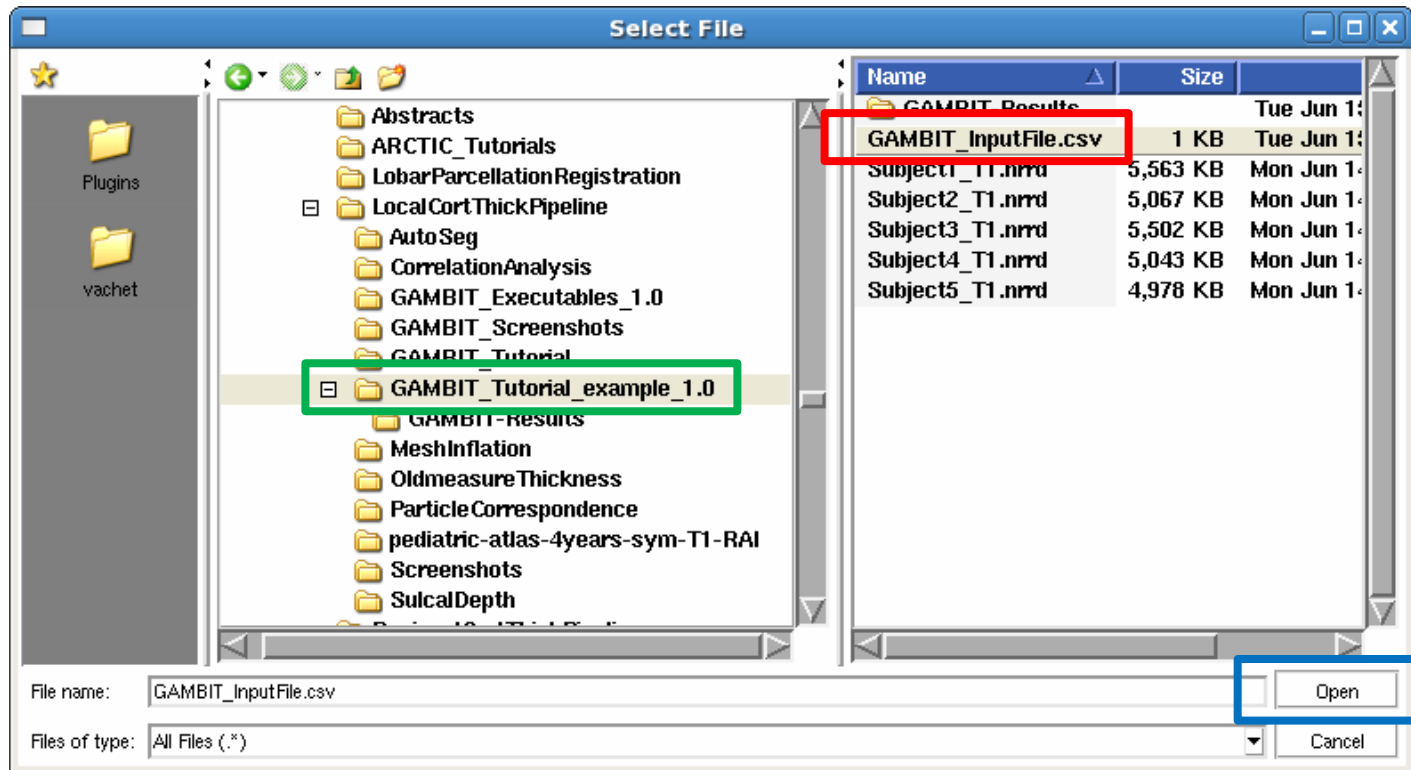
2- Set a new **parameter set**

3- Click on the « **input group file** » button. A new window will pop up.

The screenshot shows the 3DSlicer interface. At the top, the 'Modules' dropdown menu is set to 'GAMBIT', highlighted with a red box and the number 1. Below this, the 'GAMBIT' module configuration panel is visible. The 'Parameter set' dropdown is set to 'G...T', highlighted with a red box and the number 2. The 'Input group file' dropdown is set to 'None', highlighted with a red box and the number 3. The 'Output directory' dropdown is also set to 'None'. The status is 'Idle'.



Module execution

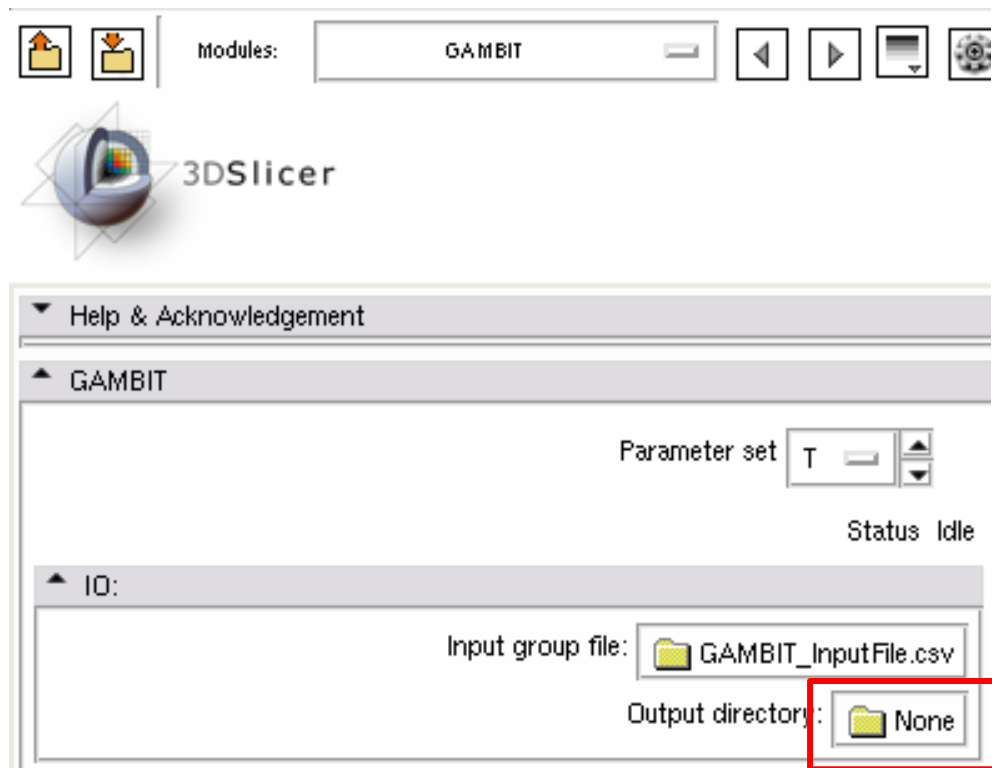


A new window 'Select File' pops up. Select the «**GAMBIT_Tutorial_example_1.0**» directory, then select the «**GAMBIT_InputFile.csv**» file and click «**Open**».



Module execution

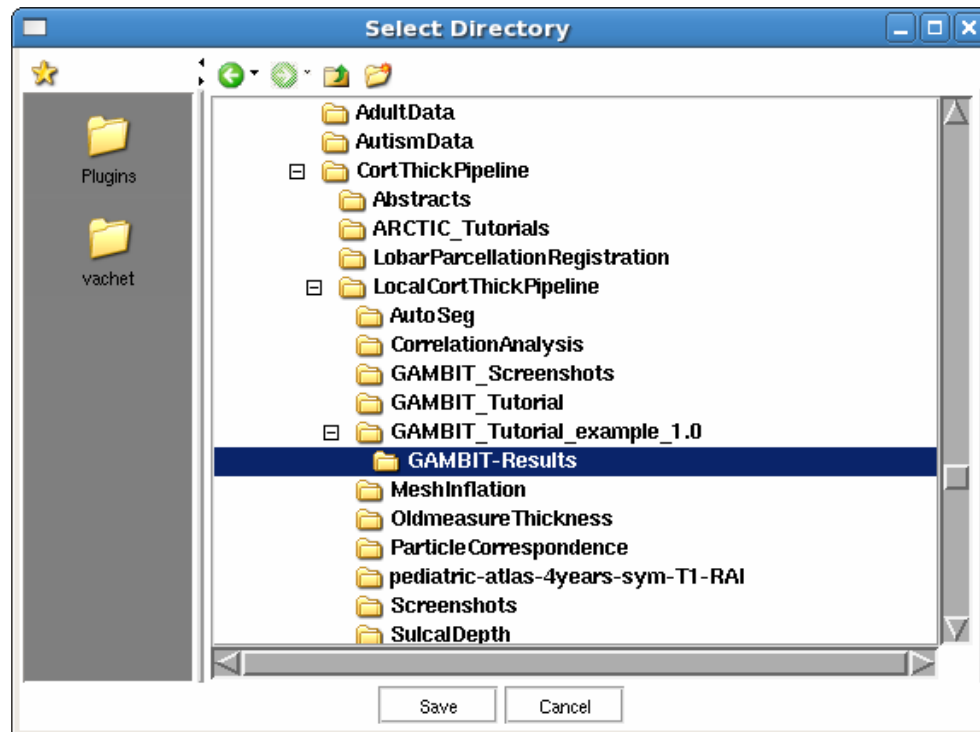
Click on the « **output directory** » button. A new window will pop up.





Module execution

Select the « **GAMBIT-Results** » directory, located in the “GAMBIT_Tutorial_example_1.0” directory





Module execution

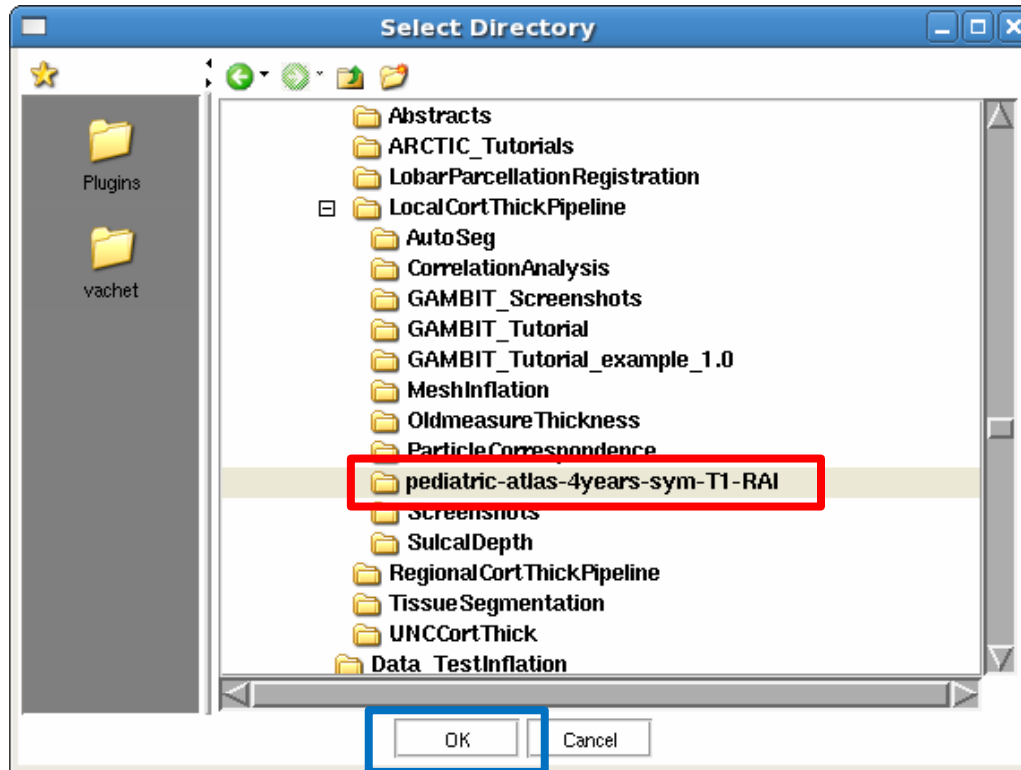
Click on the « **segmentation atlas directory** » button. A new window will pop up.

The screenshot shows the 3DSlicer software interface. At the top, there is a toolbar with icons for file operations and a 'Modules:' dropdown menu set to 'GAMBIT'. Below the toolbar is the 3DSlicer logo. The main interface is divided into several sections:

- Help & Acknowledgement**: A collapsed section at the top.
- GAMBIT**: The active module section, containing:
 - Parameter set**: A dropdown menu set to 'T'.
 - Status**: Displayed as 'Idle'.
 - ID:** A section containing:
 - Input group file:** A text field with a folder icon and the text 'GAMBIT_InputFile.csv'.
 - Output directory:** A text field with a folder icon and the text 'GAMBIT-Results'.
 - Tissue Segmentation:** A section containing:
 - Segmentation atlas directory:** A text field with a folder icon, which is highlighted with a red box.
 - Segmentation atlas type:** Radio buttons for 'T1' (selected) and 'T2'.



Module execution



A new window 'Select Directory' pops up. Select the « **pediatric-atlas-sym-T1-RAI** » directory and click « **Ok** ».



Module execution

1- Set the « **input atlas images** ».

T1w ROI atlas image

-> template-stripped.nrrd

Atlas absolute WM mask image

-> AbsoluteWMMaskImage.nrrd

Atlas CSF to WM mask image

-> latVentricleMask.nrrd

Atlas remove GM mask image

-> RemoveGMMaskImage.nrrd

Atlas label image for particle initialization

-> Parcellation_98Lobes.nrrd

Atlas parcellation image

-> Parcellation.nrrd

2- Click « **Apply** » to process the dataset.

Atlas Registration:

1

T1w ROI atlas image: t.d

Atlas absolute white matter mask image: Ad

Atlas CSF to white matter mask image: l..d

Atlas remove grey matter mask image: Rd

Atlas label image for particle initialization: Pd

Atlas parcellation image: Pd

Advanced Input File Parameters:

Advanced Tissue Segmentation Parameters:

Advanced Skull Stripping Parameters:

Advanced Atlas Registration Parameters:

Advanced Surface Inflation Parameters:

Advanced Correspondence Parameters:

Default Cancel 2 Apply



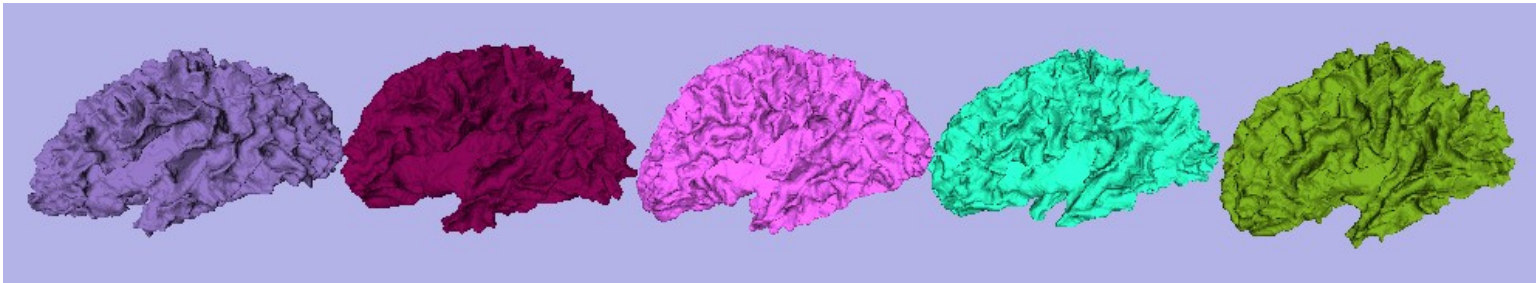
Module execution: QC

- It may take up to one day to process the tutorial dataset.
- 3D Slicer MRML scenes are created at the end of the pipeline:
 - SlicerScene_SmoothedGenusZeroMesh.mrml
 - SlicerScene_InflatedMesh.mrml
 - SlicerScene_CorrespondingMesh.mrml
- Once the dataset has been processed, one can load these scenes one by one for an efficient quality control:
 - File -> Load Scene
 - Select “GAMBIT_Tutorial_example_1.0/GAMBIT-Results/MRML” directory
 - Click “Open”

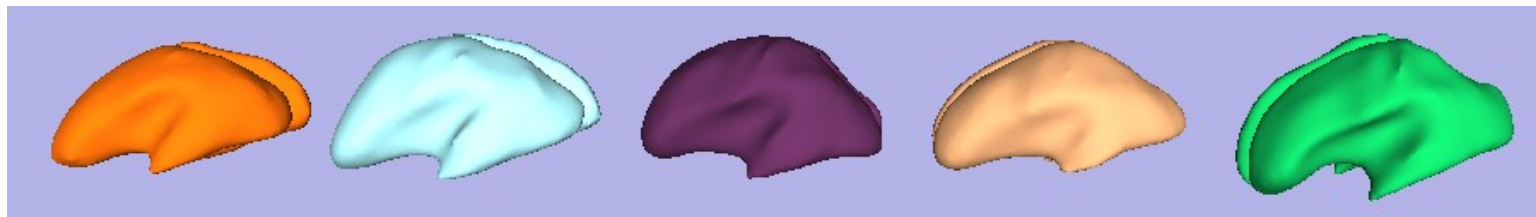


Module execution: QC

Example: SlicerScene_SmoothedGenusZeroMesh.mrml



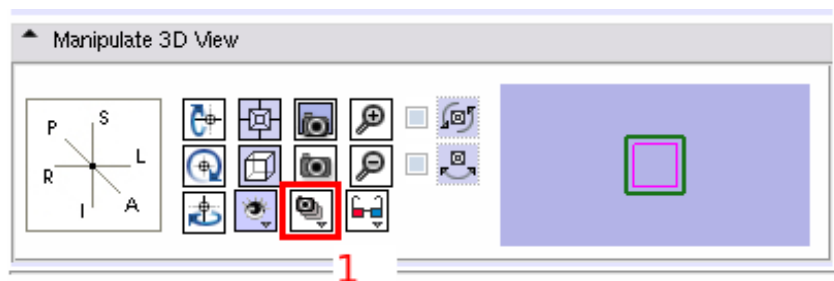
Example: SlicerScene_CorrespondingMesh.mrml





Module execution: QC

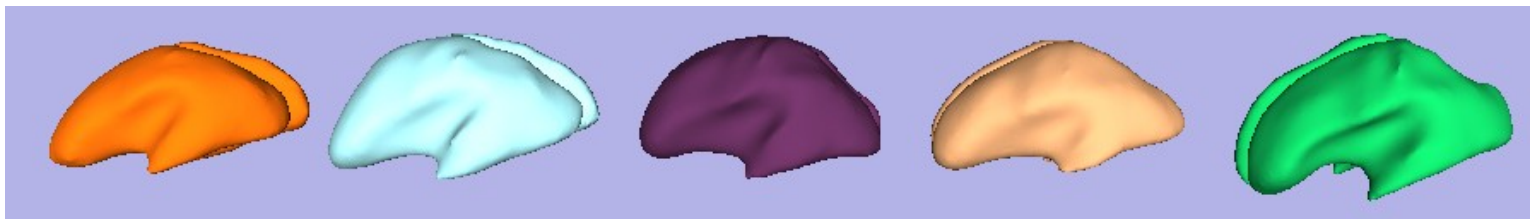
- Each MRML scene contains 3 snapshots allowing color map display
- To display the color maps:
 1. Click on the "Snapshots" button.
 2. Select 'SulcalDepth' or 'CorticalThickness'.
 3. Click on 'Restore'.



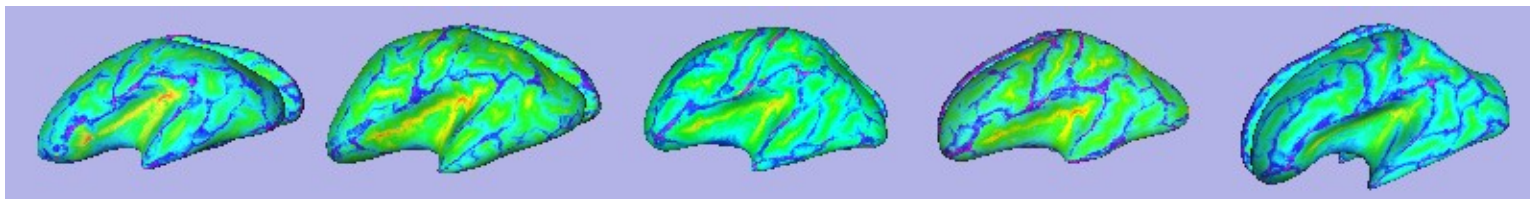


Module execution: QC

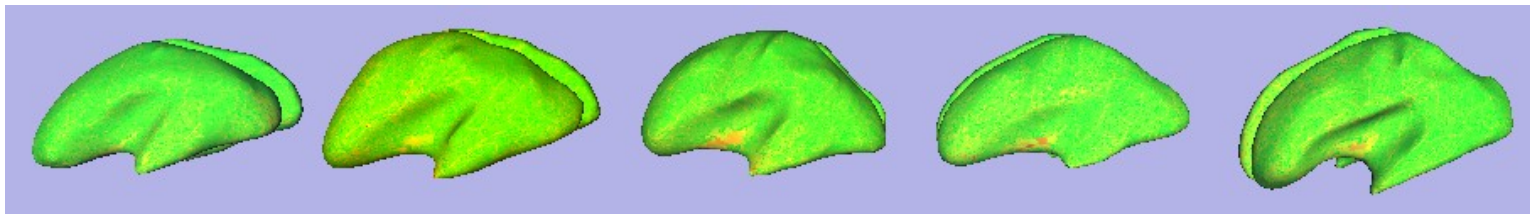
Example: SlicerScene_CorrespondingMesh.mrml



Snapshot 1: Inflated white matter cortical surfaces



Snapshot 2: Sulcal depth overlayed on inflated cortical surfaces



Snapshot 3: Cortical thickness overlayed on inflated cortical surfaces



Overview

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



Command line execution

Default analysis:

```
GAMBIT GAMBIT_InputFile.csv TestGAMBIT
--segAtlasDir segAtlas
--ROIAtlas ROIAtlas/template-stripped.nrrd
--atlasParcellationImage ROIAtlas/Parcellation.nrrd
--atlasParticleInitializationImage ROIAtlas/Parcellation_98Lobes.nrrd
--atlasAbsoluteWMMaskImage ROIAtlas/AbsoluteWMMaskImage.nrrd
--atlasCSFToWMMaskImage ROIAtlas/latVentricleMask.nrrd
--atlasRemoveGMMaskImage ROIAtlas/RemoveGMMaskImage.nrrd
```



Command line execution

Complementary flags:

- Input selection parameters:

- inputColumnSelection : set manual input column selection
- inputColumnNumberT1 T1ColumnNumber : set T1 column number
- inputT2Image : Enable/disable use of T2-weighted images
- inputColumnNumberT2 T2ColumnNumber : Set T2 column number
- inputPDImage : Enable/disable use of PD-weighted images
- inputColumnNumberPD PDColumnNumber : Set PD column number



Command line execution

Complementary flags:

- Tissue segmentation parameters:
 - ABCMaxBiasDegree MaxBiasDegree : set maximum bias degree
 - ABCPriors WMPrior,GMPrior,CSFPrior,RestPrior : set atlas class priors
 - ABCAtlasWarplIterations WarplIterations : set number of fluid iterations
 - ABCAtlasLinearMapType AtlasMapType : set atlas linear mapping type
 - ABCImageLinearMapType ImageMapType : set image linear mapping type
- Skull-stripping parameters:
 - maskDilation : tissue segmentation label map dilation
- Registration parameters:
 - registrationInit Init : Atlas registration initialization method



Command line execution

Complementary flags:

- Inflation parameters:

- inflationMaxIterationsBeforeFixing `MaxFixingIterations` : set maximum number of iterations until cortical surface is fixed if necessary

- inflationMaxCurvature `MaxCurvature` : set maximum curvature to save only vertices whose curvature is higher than max curvature once inflation is stopped

- inflationMaxIteration `MaxIteration` : set maximum number of iterations

- inflationMeanCurvature `MeanCurvature` : set minimum mean surface curvature used as a stopping criterion to stop inflation. Curvature keeps decreasing until this minimum mean curvature is reached.

- inflationSmoothing `InflationSmoothing` : set relaxation operator (0=no smoothing, 1=full smoothing)

- Skull-stripping parameters:

- maskDilation : tissue segmentation label map dilation

- Registration parameters:

- registrationInit `Init` : Atlas registration initialization method



Command line execution

Complementary flags:

- Correspondence parameters:

- correspondencePreprocessingSmoothing Smoothing : set gaussian smoothing element size

- correspondenceNbParticles Nbparticles : set number of particles to sample shape

- correspondenceIterationsPerSplit SplitIterations : set number of iterations to run between successive particle splits during an initialization phase

- correspondenceStartingRegularization StartRegularization --correspondenceEndingRegularization EndRegularization --correspondenceOptimizationIterations OptimizationIt : The starting regularization (added to the covariance matrix of the correspondences) decays to the ending regularization over the specified number of iterations

- correspondenceCheckPointingIntervals Interval : set number of iterations between successive saves of the optimized correspondence positions

- correspondenceRelativeWeightin Alpha : set weighting factor balancing a tradeoff between model compactness and accurate shape representation

- correspondenceProcrustesOff : enable/disable Procrustes registration

- correspondenceProcrustesInterval EndRegularization : procrustes registration is performed based on the current correspondence positions at each specified interval



Command line execution

Complementary flags:

- Correspondence post-processing parameters:

`--correspondencePostProcessingProjectToSurfaceOff` : enable/disable projection of the interpolated surface to the original surface

`--correspondencePostProcessingProjectionFactor Factor` : Projection factor (0=no projection, 1=full projection with possibly collapsed triangles)



Future improvement

The development of the presented software is an ongoing process, further improvements including:

- Quality control improvement with new MRML scenes and snapshots
- Use of 3D Slicer widget to set input dataset
- Consider sulcal depth as attribute to improve correspondence
- Use of average inflated white matter map cortical surface as an unbiased template for shape-based correspondence
- Allow correspondence on new dataset by fixing particles on already existing sample dataset
- New options/methods thanks to user feedback...



Conclusion

3D Slicer, is a free, open source software package for visualization and image analysis, in this case, Group-wise mesh-based analysis of cortical thickness using GAMBIT.

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



Acknowledgments



National Alliance for Medical Image Computing
NIH U54EB005149



UNC Chapel Hill
Neurodevelopmental Disorders Research Center
Neuro Image Research Analysis Laboratories



University of Utah
Scientific Computing and Imaging Institute



Acknowledgments

- **Marcel Prastawa**, Scientific Computing and Imaging Institute, Utah (ABC)
- **Steven Aylward**, Kitware Inc. (RegisterImages)
- **François Budin**, NIRAL, UNC Chapel Hill (Resample Scalar/Vector/DWI Volume)
- **Steve Haker and Marc Niethammer**, UNC Chapel Hill (GenusZeroImageFilter)
- **Delphine Ribes, Sylvain Gouttard, Cassian Marc**, NIRAL, UNC (CortThick)
- **Joshua Cates, Manasi Data, Thomas Fletcher, Ross Whitaker**, Scientific Computing and Imaging Institute, Utah (ShapeWorks)
- **Ipek Oguz**, NIRAL, UNC Chapel Hill (ParticleCorrespondencePreProcessing and ParticleCorrespondencePostProcessing)
- **Beatriz Paniagua**, NIRAL, UNC Chapel Hill (Slicer visualization)
- **Corentin Hamel**, NIRAL, UNC Chapel Hill (Quality Control)
- **Julien Jomier**, Kitware Inc. (BatchMake)
- **Steve Pieper**, Isomics Inc.
- **Joseph Piven**, Neurodevelopmental Disorders Research Center, UNC Chapel Hill