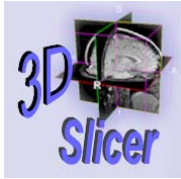


Slicer Training 10

EMAtlasBrainClassifier

Sonia Pujol, Ph.D.

Randy Gollub, M.D., Ph.D.



Acknowledgments



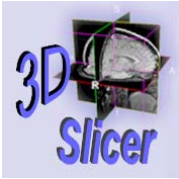
National Alliance for Medical Image Computing
NIH U54EB005149



Neuroimage Analysis Center
NIH P41RR013218

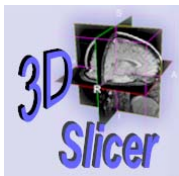


Computer Science and Artificial Intelligence Lab-MIT,
Surgical Planning Lab-Harvard Medical School
Thanks to Kilian Pohl, Sandy Wells, Martha Shenton, Sylvain Bouix,
Alex Guimond, Eric Grimson and Simon Warfield.

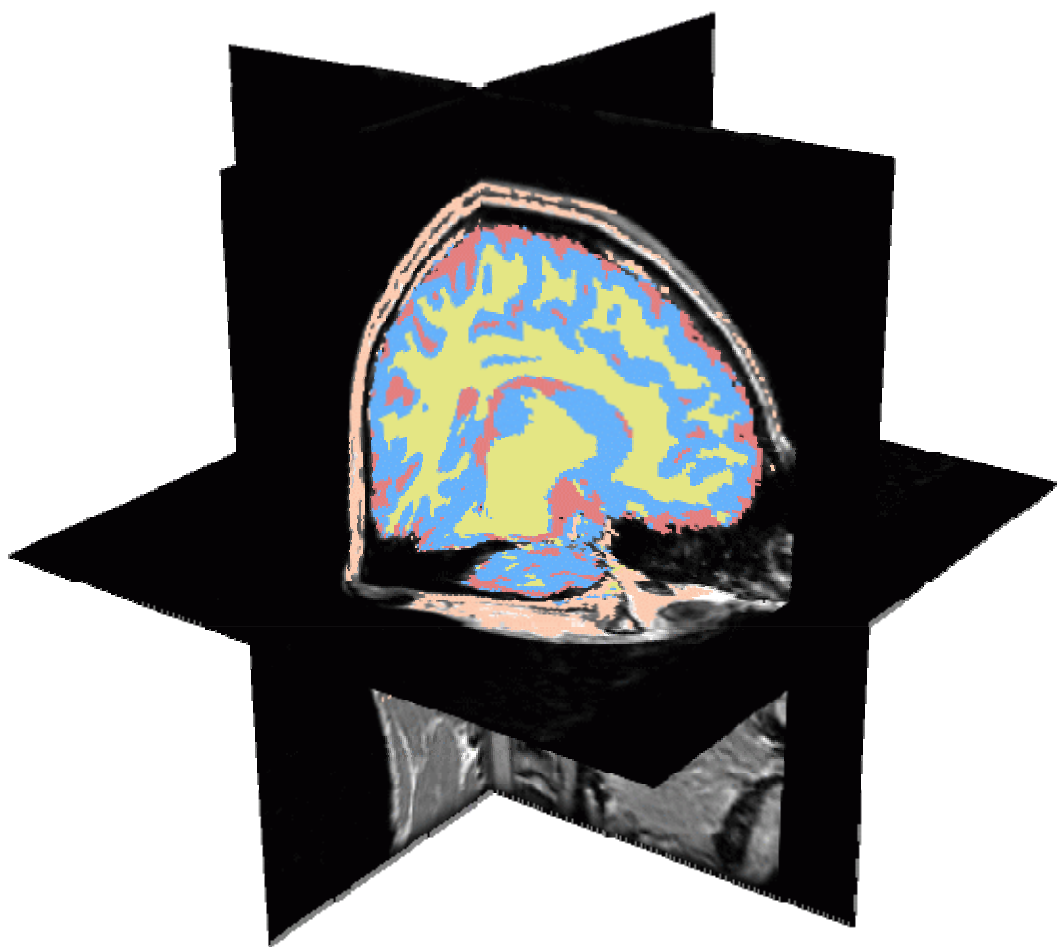


Disclaimer

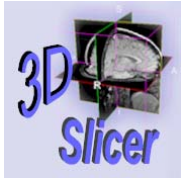
It is the responsibility of the user of 3DSlicer to comply with both the terms of the license and with the applicable laws, regulations and rules.



Goal of the tutorial



Guiding you step by step through the process of using the Expectation-Maximization algorithm to **automatically segment brain structures from MRI data** within Slicer.



Material

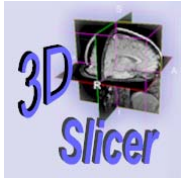
- Slicer 2.6

www.na-mic.org/Wiki/index.php/Slicer:Slicer2.6_Getting_Started

- BrainAtlasClassifierTutorial.zip

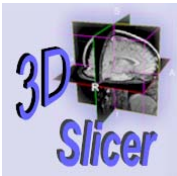
www.na-mic.org/Wiki/index.php/Slicer:Workshops:User_Training_101

- This tutorial assumes that you have already completed Slicer Basics Loading and Viewing Data (Slicer Training 1) and Saving Data (Slicer Training 7)

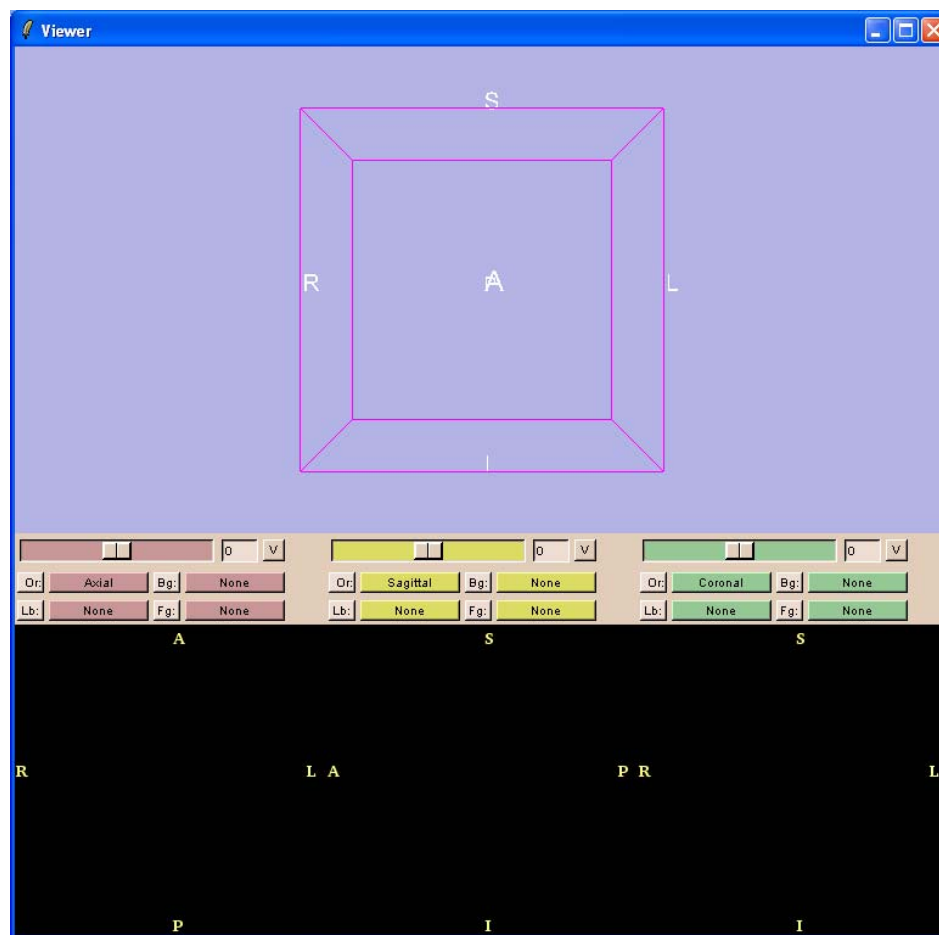
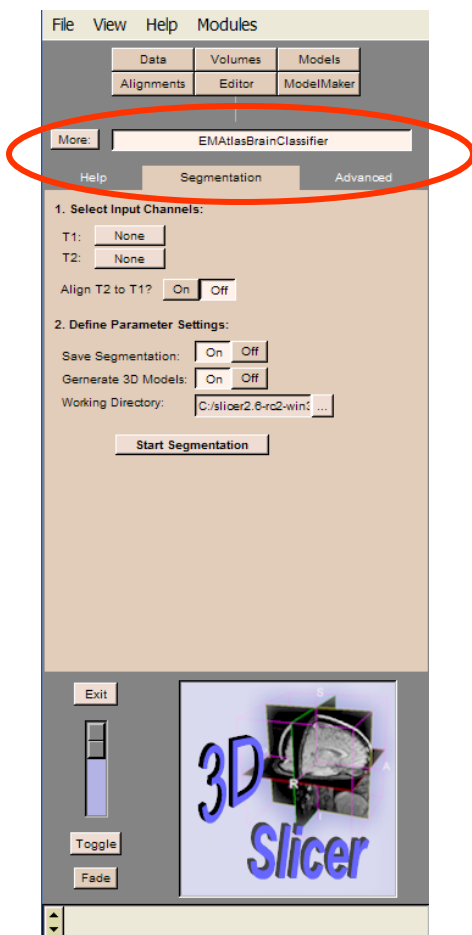


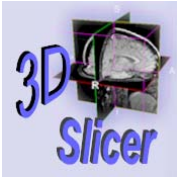
Computer Resources

- The first part of this tutorial teaches you how the module works; it uses **pre-computed** results.
- The second part guides you through processing the tutorial data yourself with the EMBrainAtlasClassifier module (Slide 40). For this part, your computer must have adequate processing speed and RAM.
- The final part shows you how to run this module on your own data (Slide 51).



EMBrainAtlasClassifier

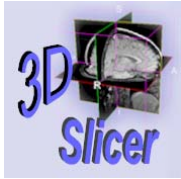




Tutorial dataset

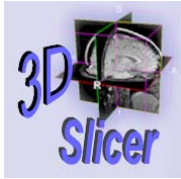
- Pre-computed Generic atlas of the brain.....
- Pre-computed T1 and T2 volumes aligned
- Pre-computed T1 and T2 volumes normalized.....
- Pre-computed Patient-specific atlas of the brain
- Pre-computed Segmentation results.....





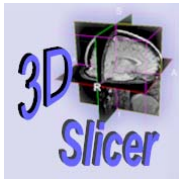
Overview

- Part 1: Generic Atlas and EM Pipeline
- Part 2: Loading tutorial data
- Part 3: Hardware requirements
- Part 4: Working with tutorial data
- Part 5: Working with your own data

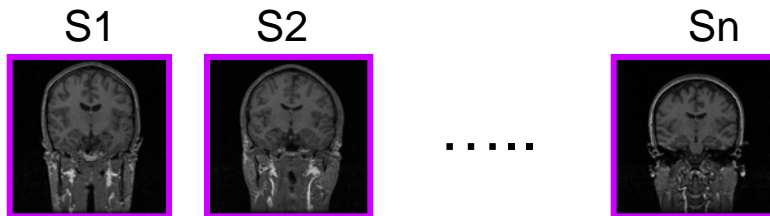


Generic Atlas and EM Pipeline

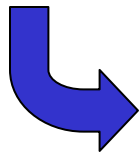
- This module relies on a previously computed generic atlas.
- Running the EM segmentation requires that you have **installed the generic atlas** and that your target datasets go through a **processing pipeline**.



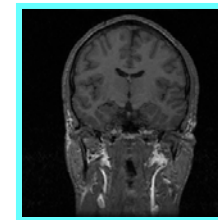
Generic Atlas Generation (Step 1)



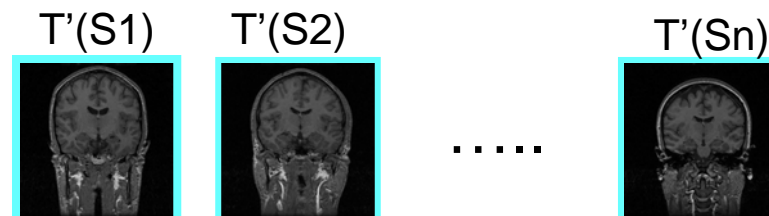
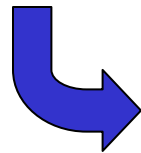
n=80 healthy subjects, ages 25-40



Register all the subjects to the training subject

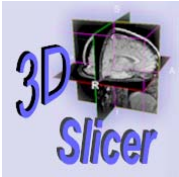


Training subject (randomly chosen)

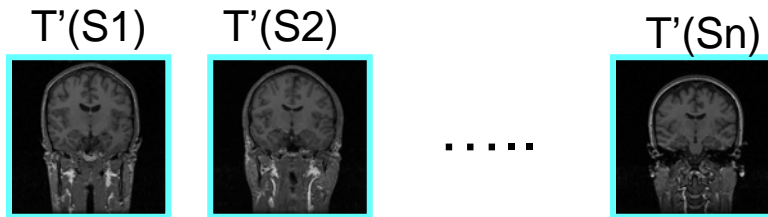


n=80 registered subjects

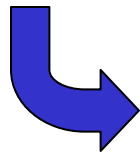
A Binary Entropy Measure to Assess Non-rigid Registration Algorithms. S. Warfield, J. Rexilius, P. Huppi, T. Inder, E. Miller, W. Wells, G. Zientara, F. Jolesz, R. Kikinis. In Proc. MICCAI 2001: Medical Image Computing and Computer-Assisted Interventions, pp 266-274.



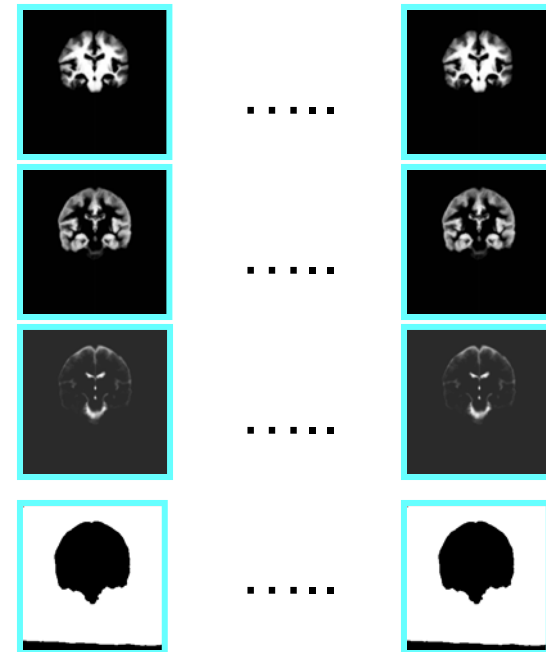
Generic Atlas Generation (Step 2)



n=80 registered subjects

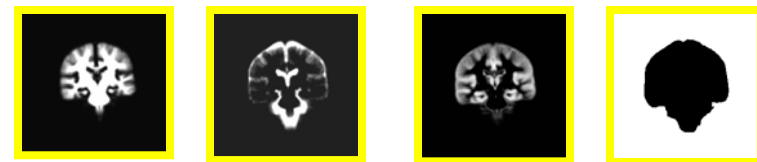
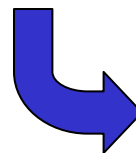


Segment all 80 images
into 4 classes



Generate the generic atlas

(voxel wise map of the number of subjects/80
possible that belong to that class)



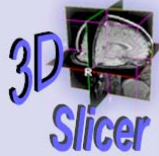
white matter

csf

grey matter

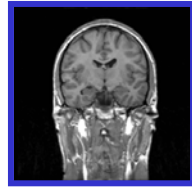
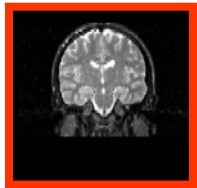
background

*Adaptive Segmentation of MRI data. Wells W.,
Grimson E., Kikinis R and Jolesz F. IEEE Transactions
on Medical Imaging, vol.15, p 429-442, 1996.*



EM Pipeline: Data Normalization

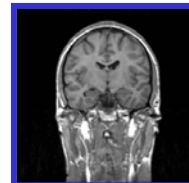
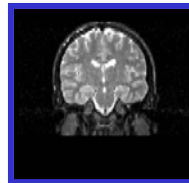
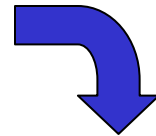
Patient data



t2

t1

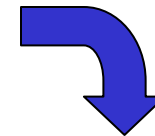
Align t2 to t1



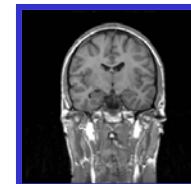
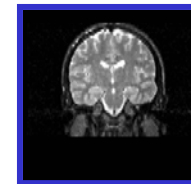
T(t2)

t1

Normalize the intensity of each image



Normalized Patient data



T(t2) normalized

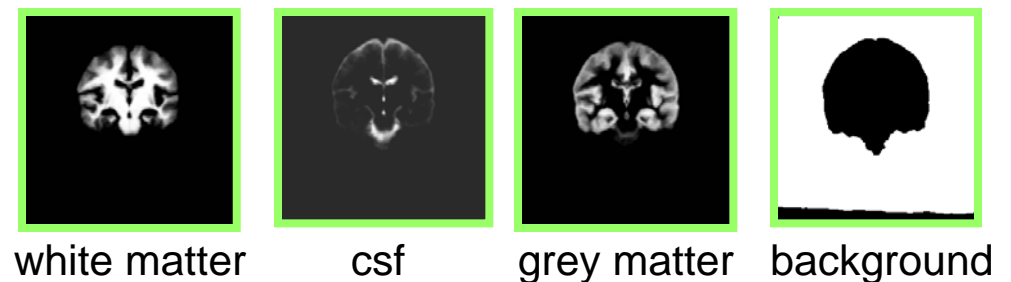
t1 normalized

EM Pipeline: Patient-Specific Atlas Generation

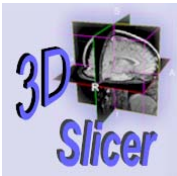


Register the generic atlas to the images to create the patient-specific atlas

Patient-specific atlas

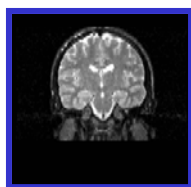


Anatomical Guided Segmentation with non-stationary tissue class distributions in an expectation maximization framework. Pohl K., Bouix S., Kikinis R. and Grimson E. In Proc.ISBIT 2004: IEEE International Symposium on Biomedical Imaging: From Nano to Macro, pp 81-84

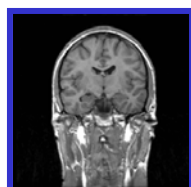


EM Pipeline: Segmentation

Normalized Patient data

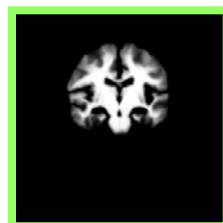


T(t2)
normalized

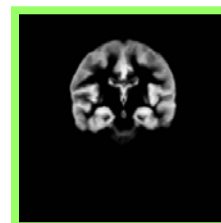


T1
normalized

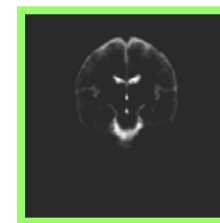
Patient-specific atlas



white matter



csf



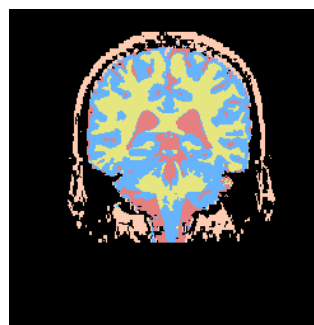
grey matter



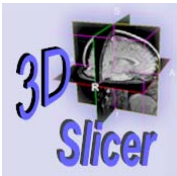
background



Anatomical Guided Segmentation with non-stationary tissue class distributions in an expectation maximization framework. Pohl K., Bouix S., Kikinis R. and Grimson E. In Proc.ISBIT 2004: IEEE International Symposium on Biomedical Imaging: From Nano to Macro, pp 81-84



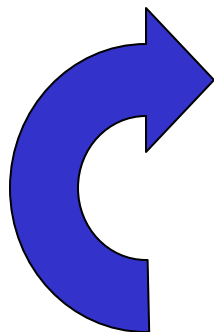
Segment using the Expectation Maximization algorithm



EP Pipeline: Algorithm

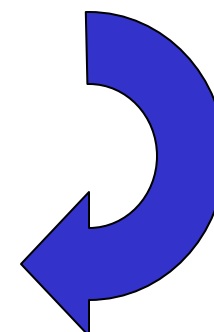
Expectation Step

classifies the MR voxels in tissue classes
Gray Matter, White Matter, CSF

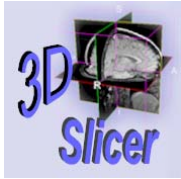


Maximization Step

applies the intensity correction as a
function of the tissue class

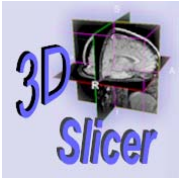


Loop iterated 4 times

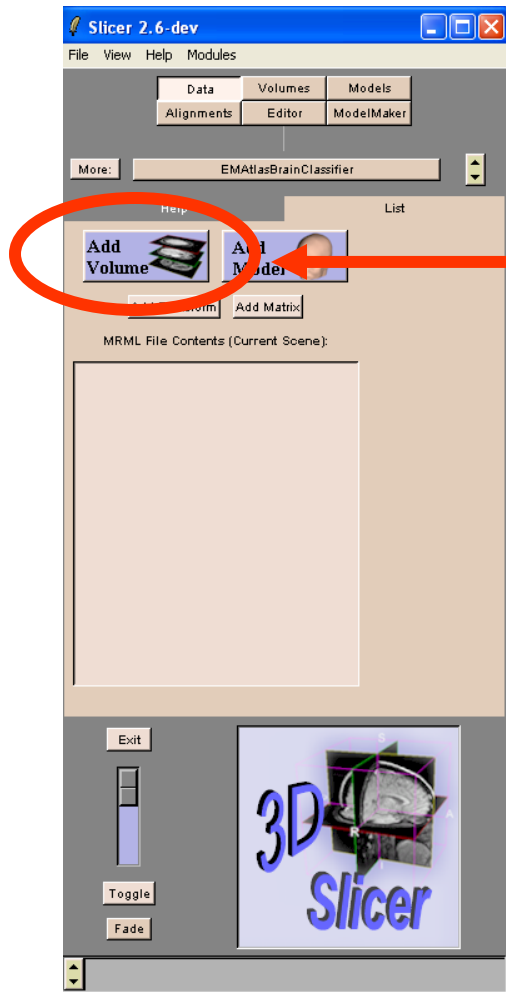


Overview

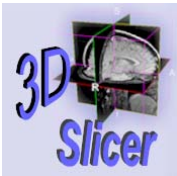
- Part 1: Generic Atlas and EM Pipeline
- **Part 2: Loading tutorial data**
- Part 3: Hardware requirements
- Part 4: Working with tutorial data
- Part 5: Working with your own data



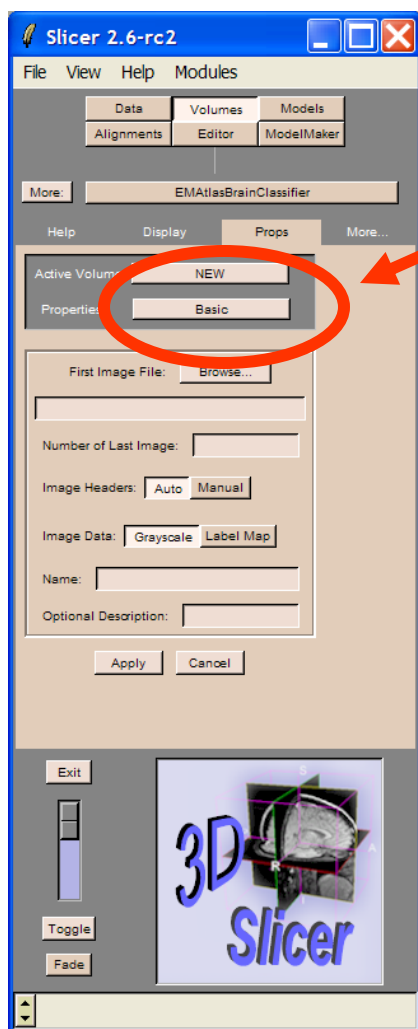
Loading T1 volume



Click Add Volume in the Panel Data



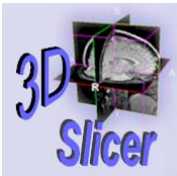
Loading T1 volume



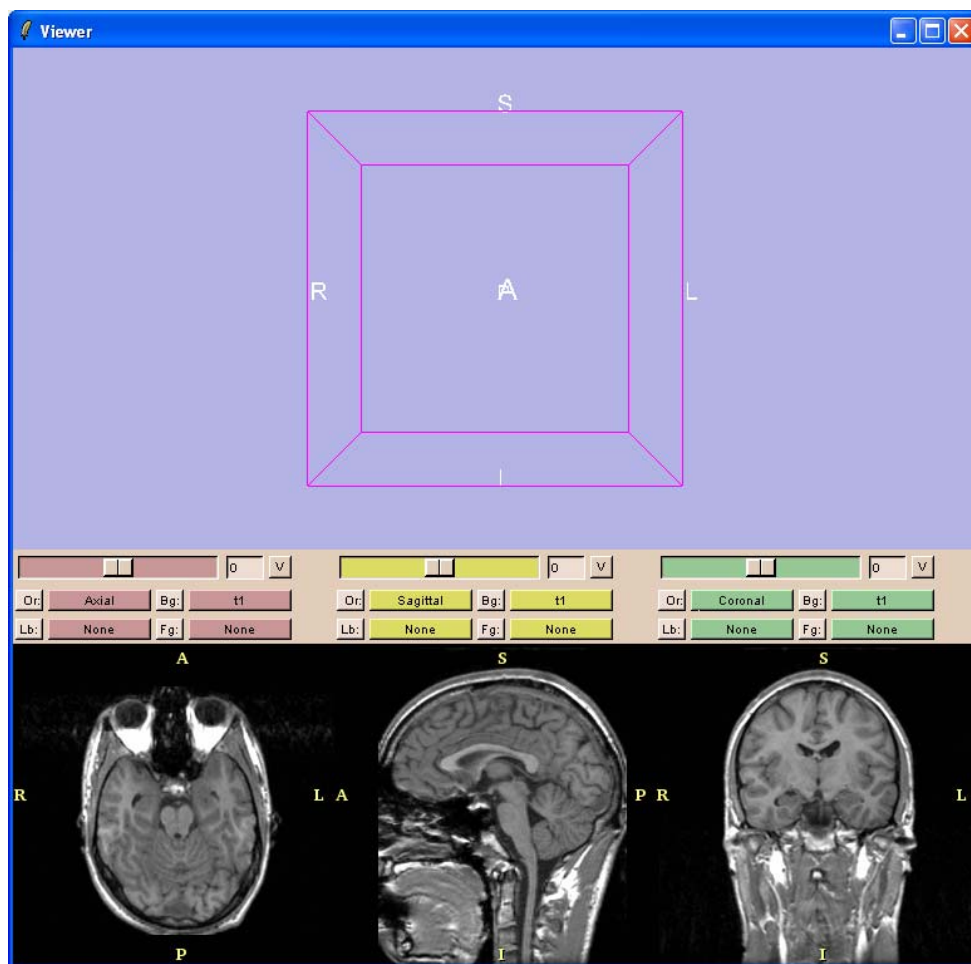
Click Add Volume and select Basic in the Panel Props of the module Volumes

Load the volume t1 from the directory named /BrainAtlasClassifier/data

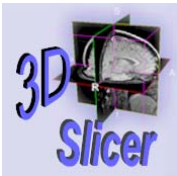
Click on Apply



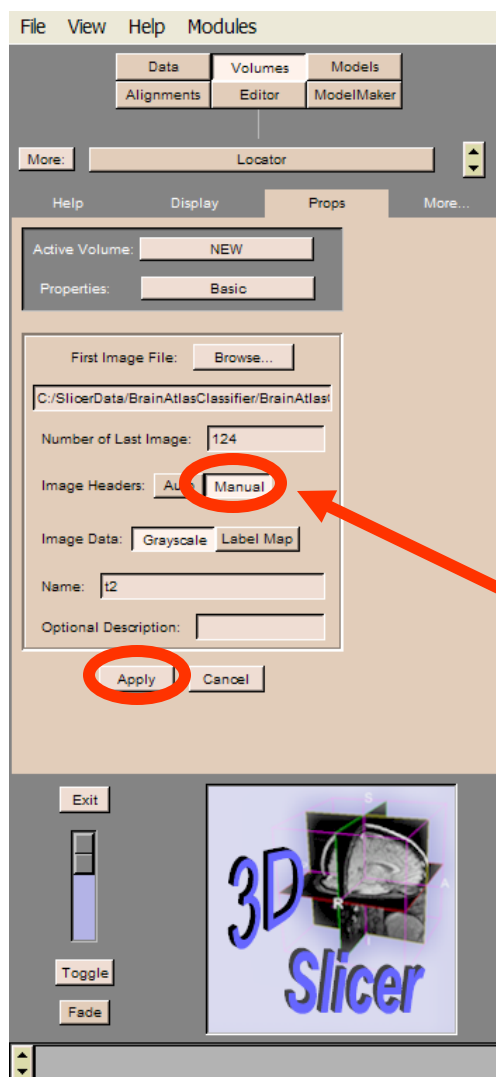
Loading T1 volume



Slicer loads the volume t1 in the viewer.



Loading T2 volume

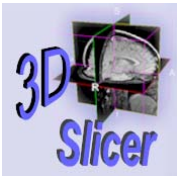


Click Add Volume and select Basic in the Panel Props of the module Volumes

Select the volume t2

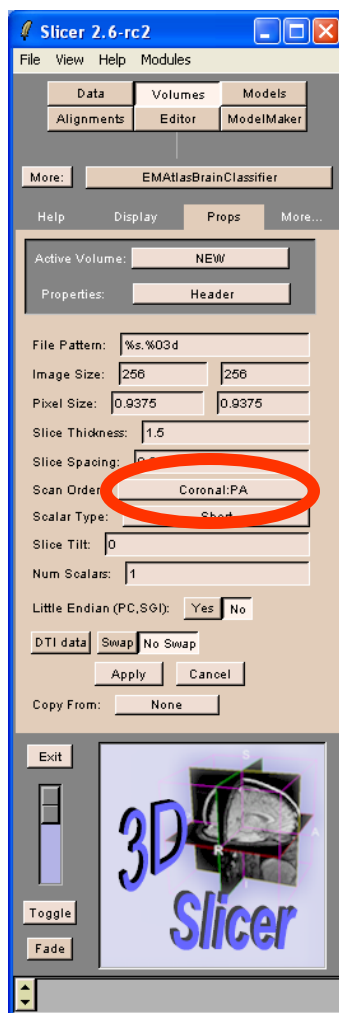
Click on Image Headers Manual

Click on Apply



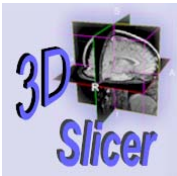
Loading T2 volume

The tutorial dataset t2 was acquired in the Coronal Posterior-Anterior orientation.

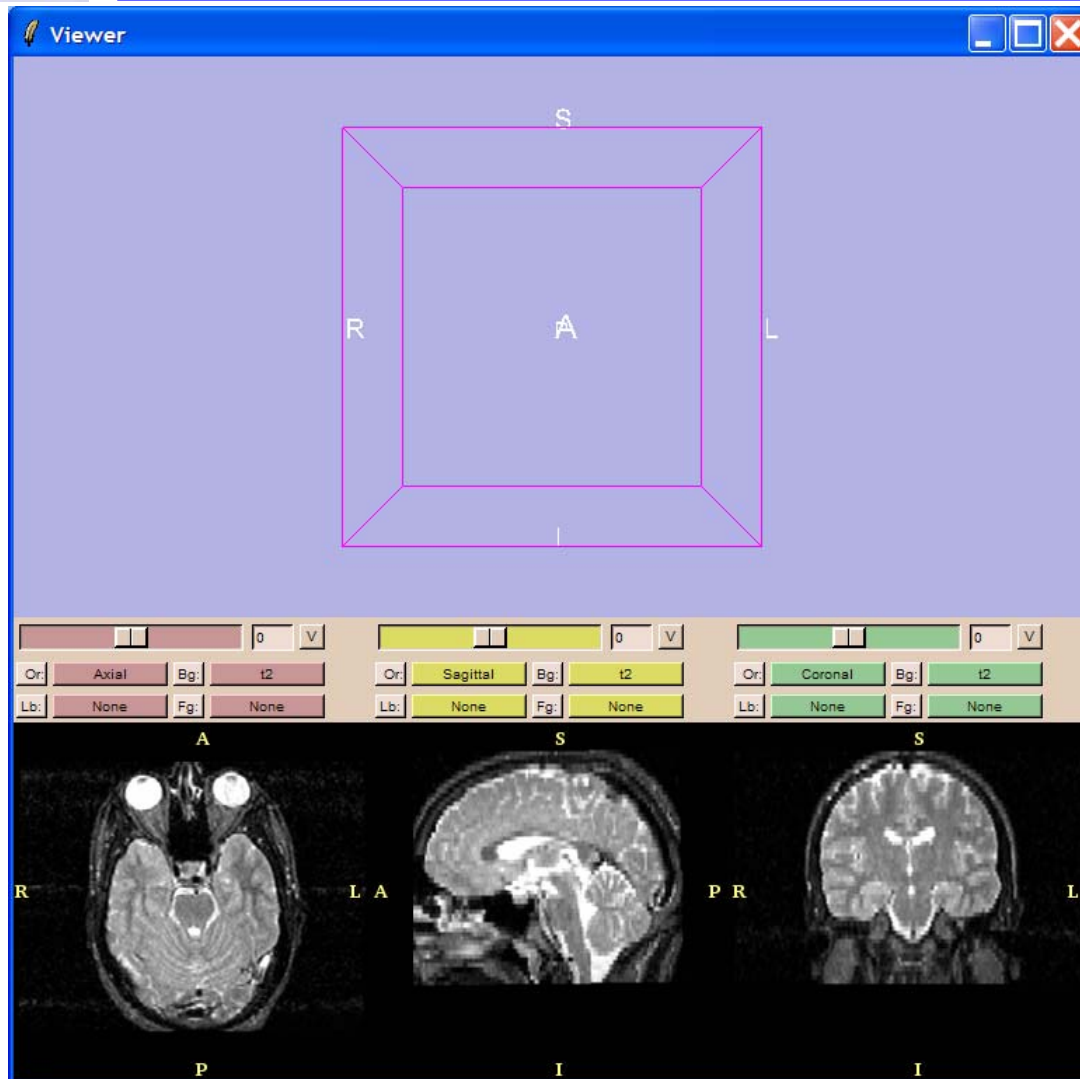


Select the Scan order Coronal:PA

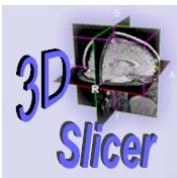
Click on Apply



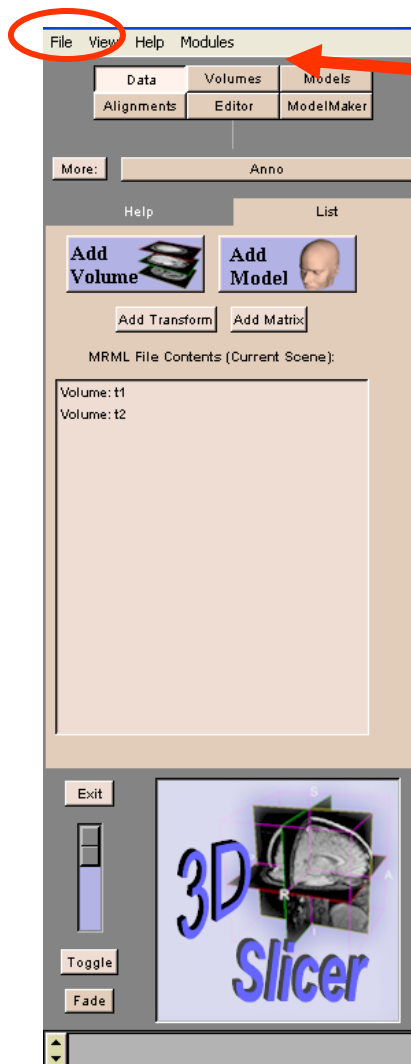
Loading T2 volume



Slicer loads the volume t2 in the viewer.

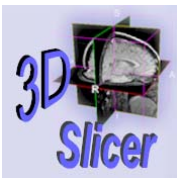


Loading the generic atlas of the brain

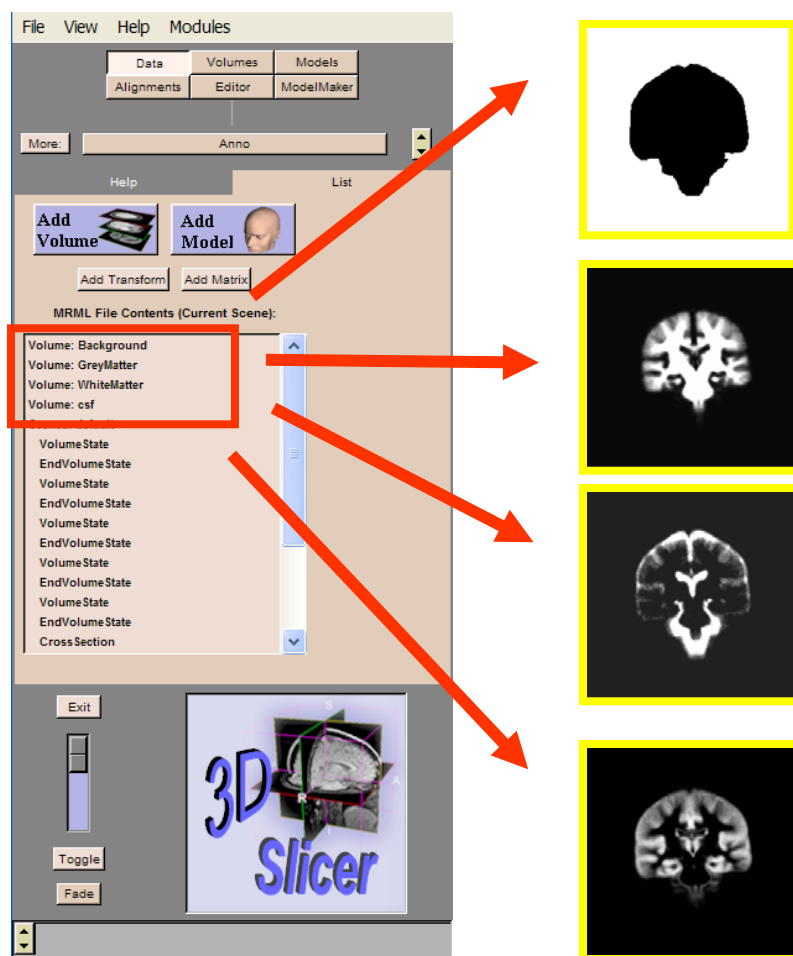


Select File → OpenScene in the Main menu.

Select the file generic_atlas.xml in the directory BrainAtlasClassifier/atlas
Click on Apply

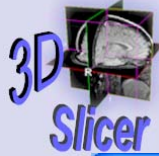


Loading the generic atlas of the brain

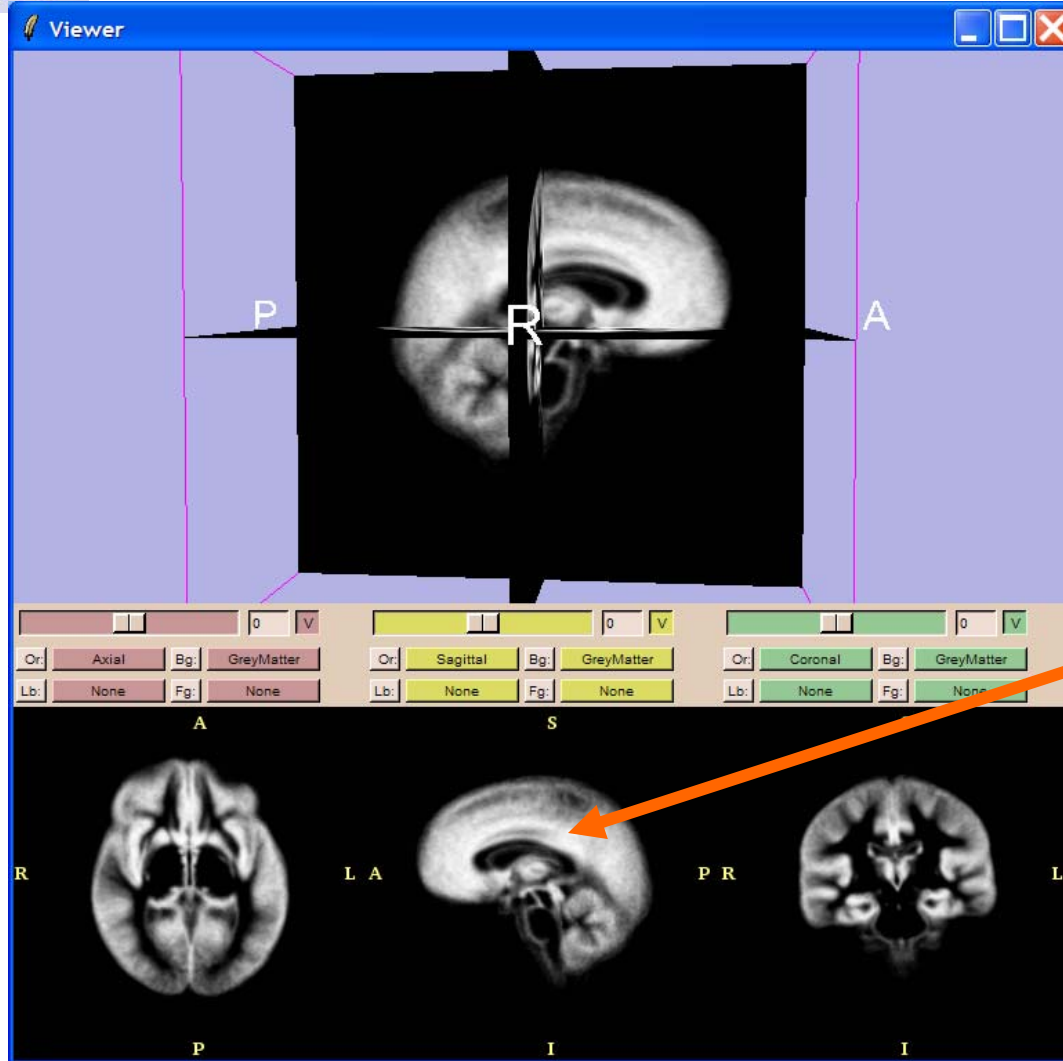


Slicer loads the generic atlas, composed of 4 volumes:

- White Matter
- Gray Matter
- CSF
- Background

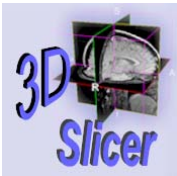


Viewing the generic atlas of the brain

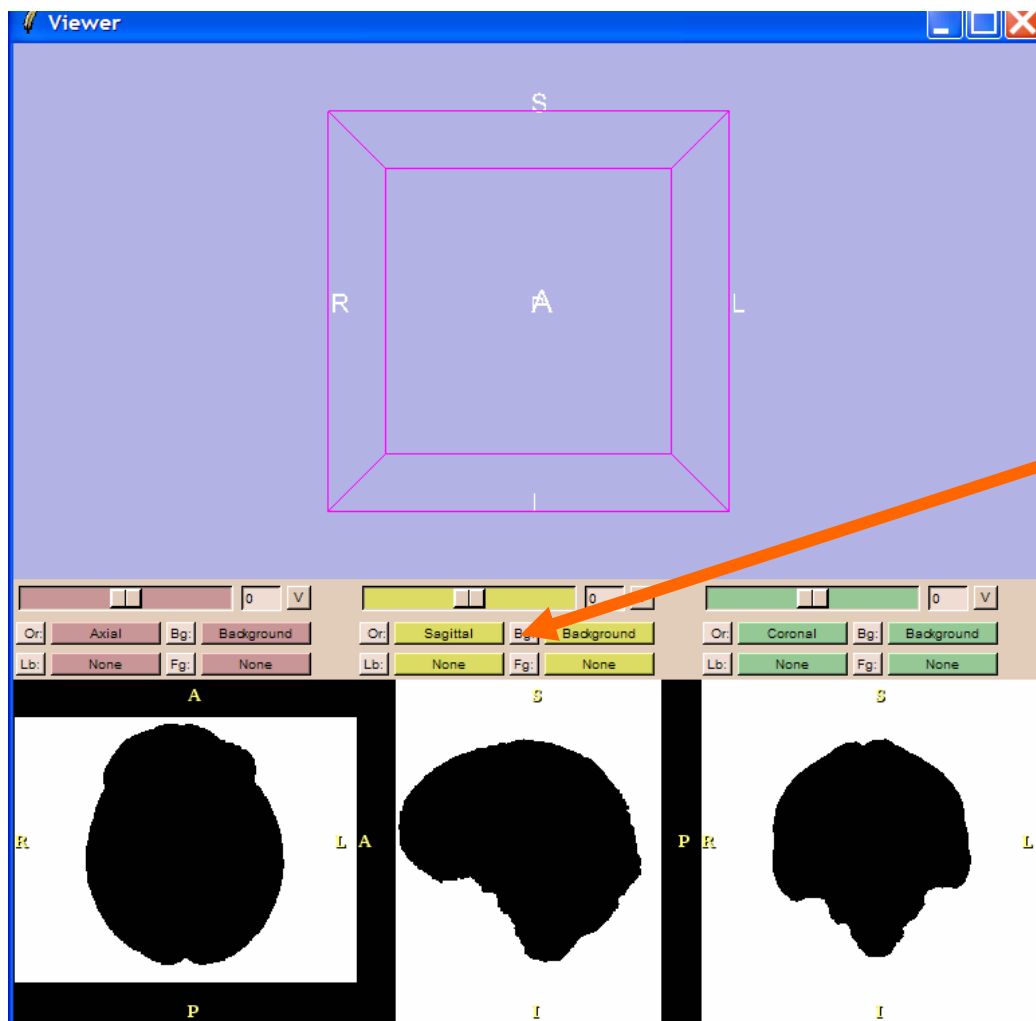


Slicer displays the generic atlas of the brain in the viewer.

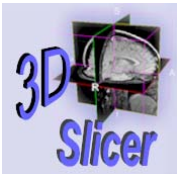
Move the mouse over the images to see atlas values (0-80) in different brain regions



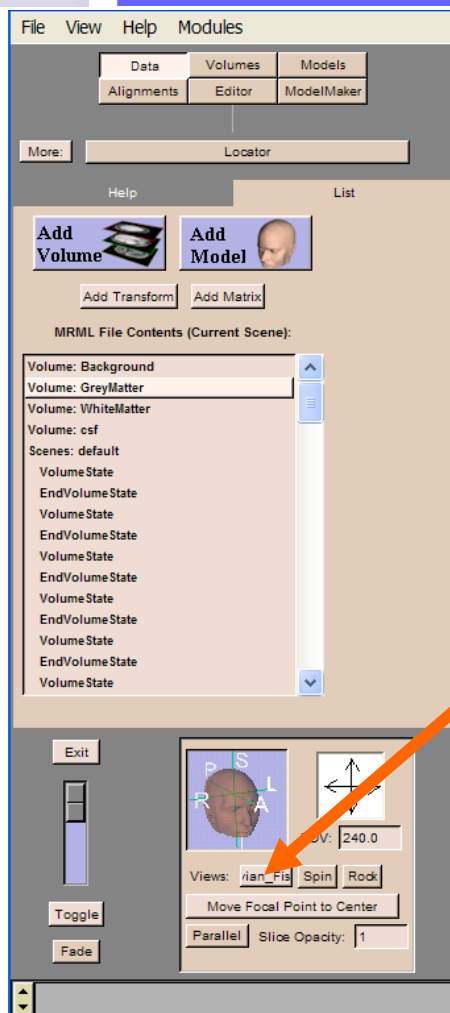
Loading the generic atlas of the brain



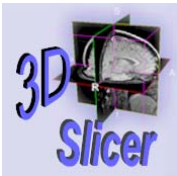
Left click on Bg to step through viewing each component.



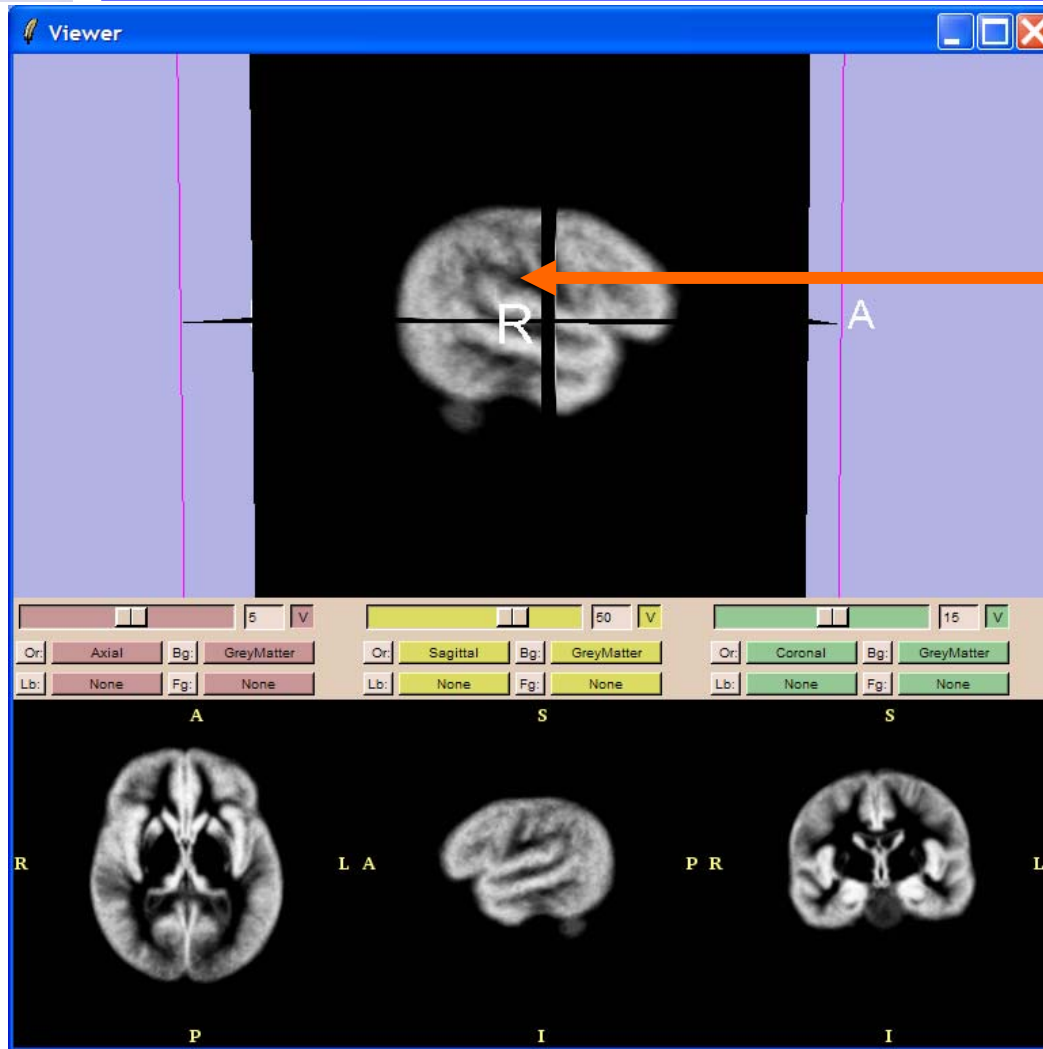
Viewing the generic atlas of the brain



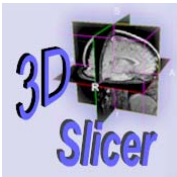
In the Control Panel left-click on Views and select the view Sylvian Fissure



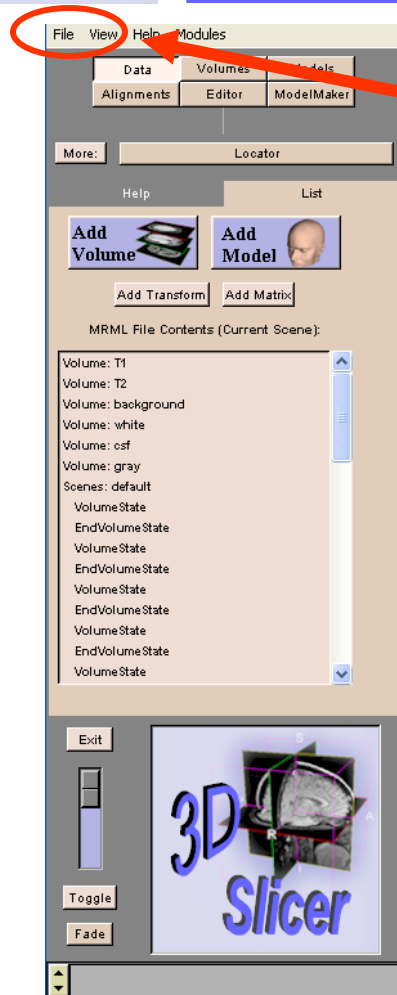
Viewing the generic atlas of the brain



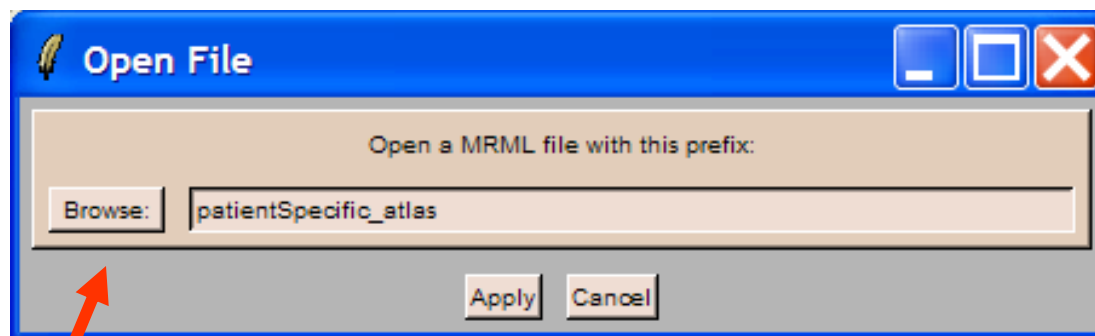
Slicer displays a coronal view of the Sylvian fissure from the Grey Matter atlas



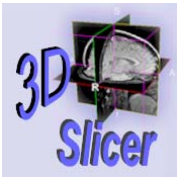
Loading the patient-specific atlas of the brain



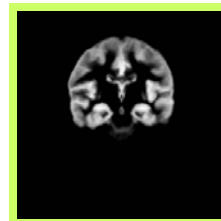
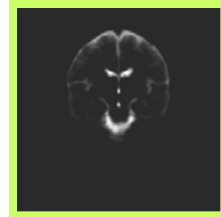
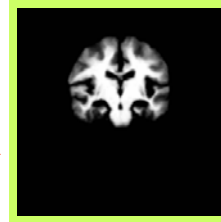
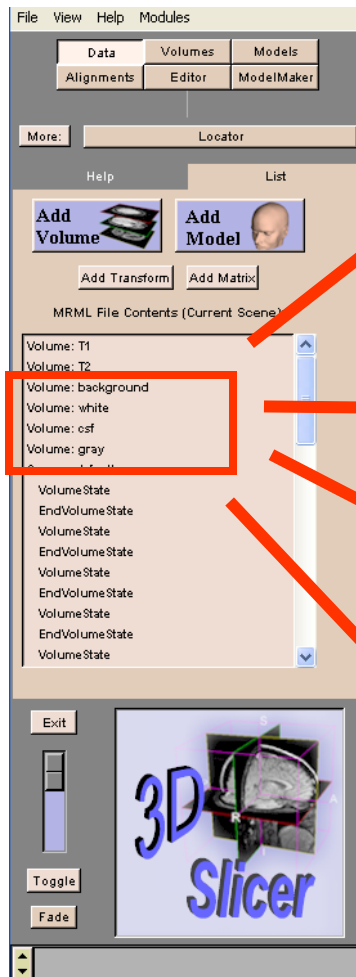
Select File → OpenScene in the Main menu



Select the file patientSpecific_atlas.xml in the directory BrainAtlasClassifier/working/atlas
Click on Apply

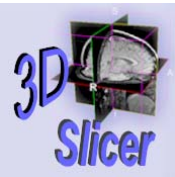


Loading the patient-specific atlas of the brain

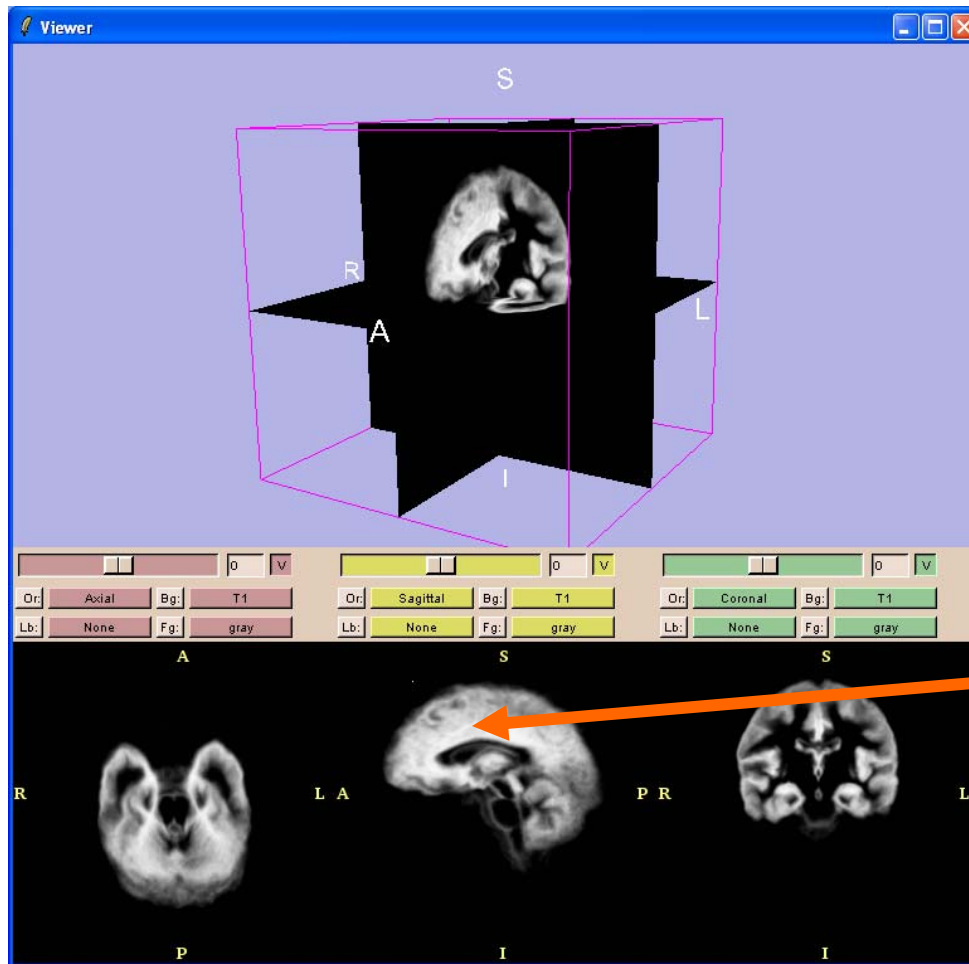


Slicer loads the patient-specific atlas, composed of 4 volumes:

- Background
- White Matter
- CSF
- Grey Matter

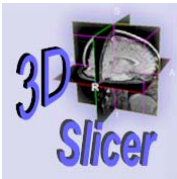


Loading the patient-specific atlas of the brain

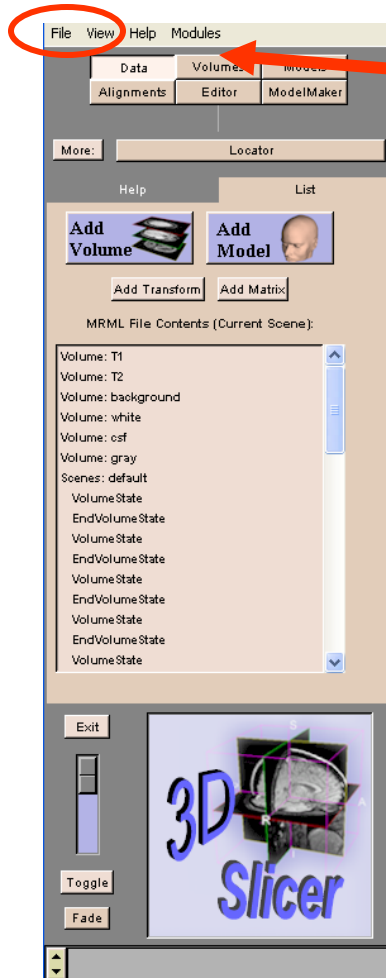


Slicer displays the Gray Matter volume of the atlas in the viewer

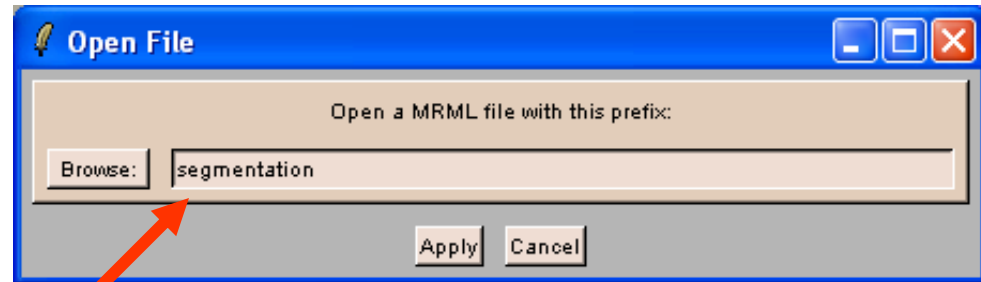
Move the mouse over the images to see atlas values (0-80) in different brain regions



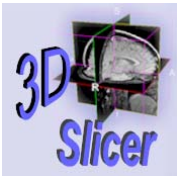
Loading the Segmentation results



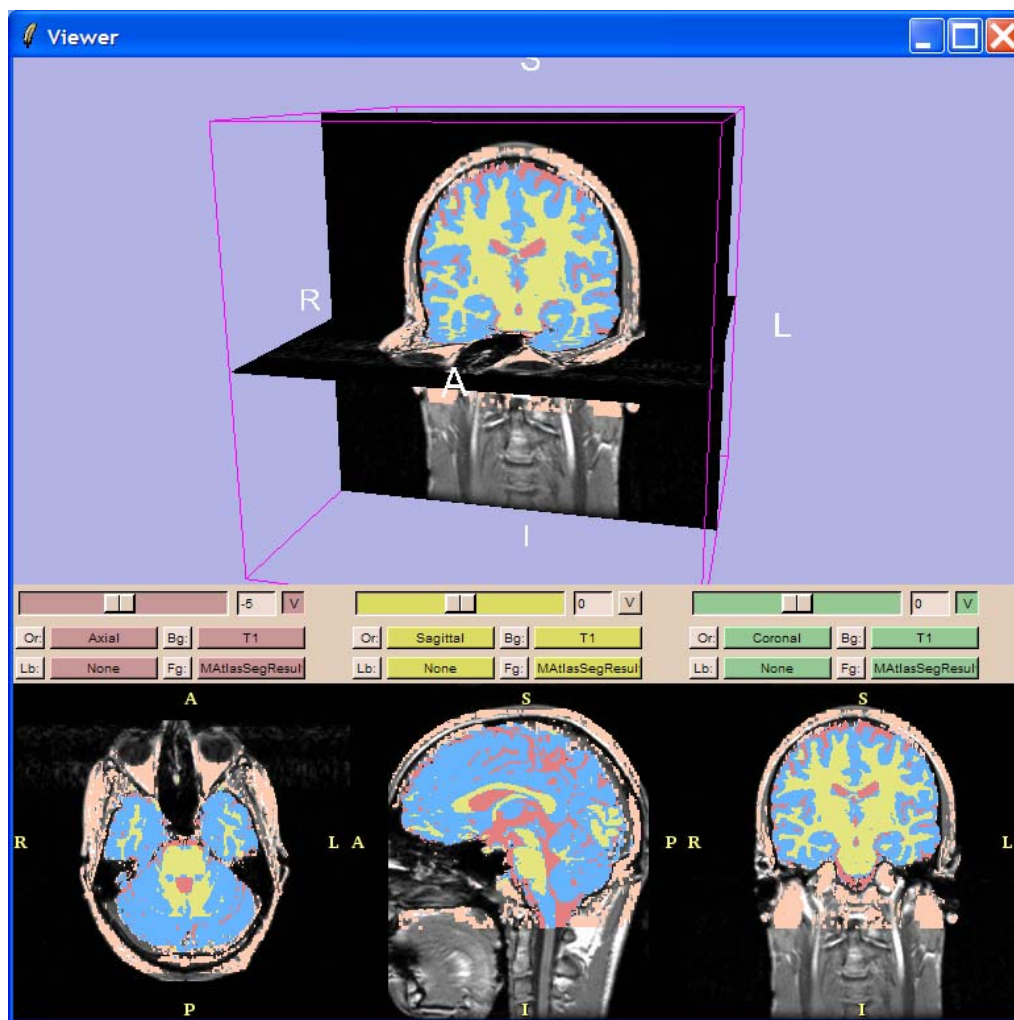
Select File → Open Scene in the Main menu.



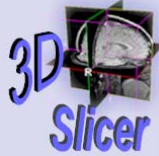
Select the file segmentation in the directory **BrainAtlasClassifier/working/EMSegmentation** and click on Apply



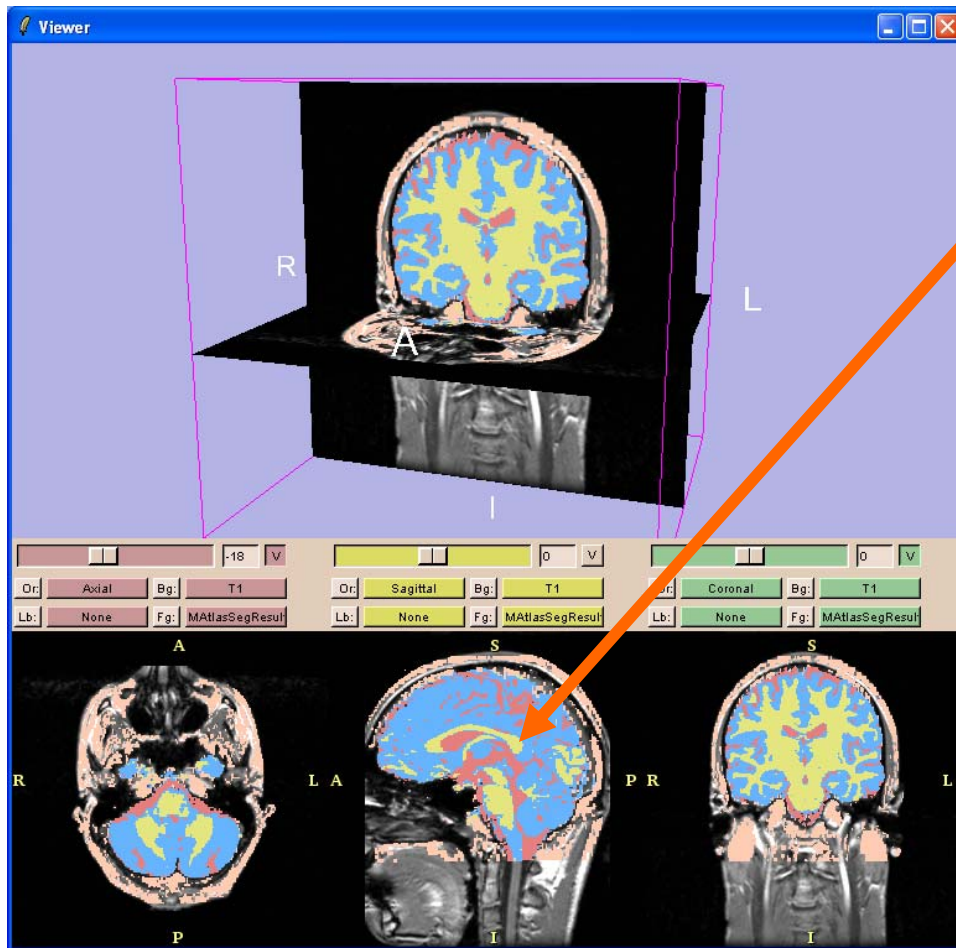
Loading the Segmentation results



Slicer superimposes the results of the segmentation on T1 images



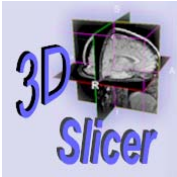
Loading the Segmentation results



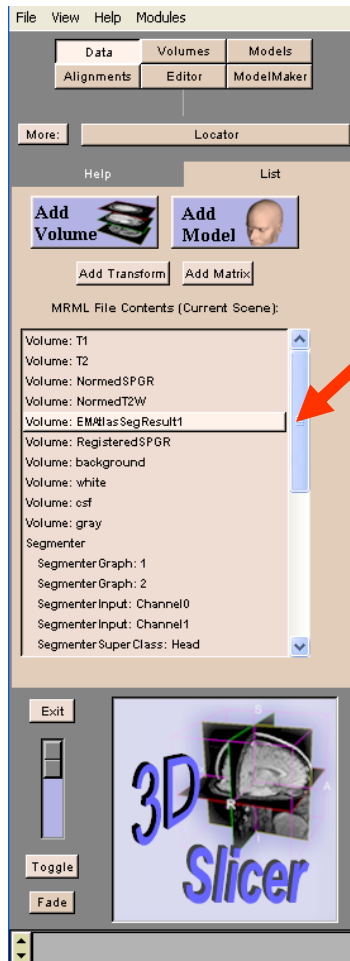
Move the mouse over the images in the 2D Viewer

Slicer displays the names of the labels corresponding to the segmented structures:

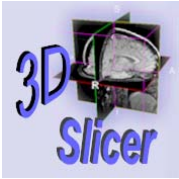
- White Matter (yellow)
- Grey Matter (blue)
- CSF (red)
- Background (pink)



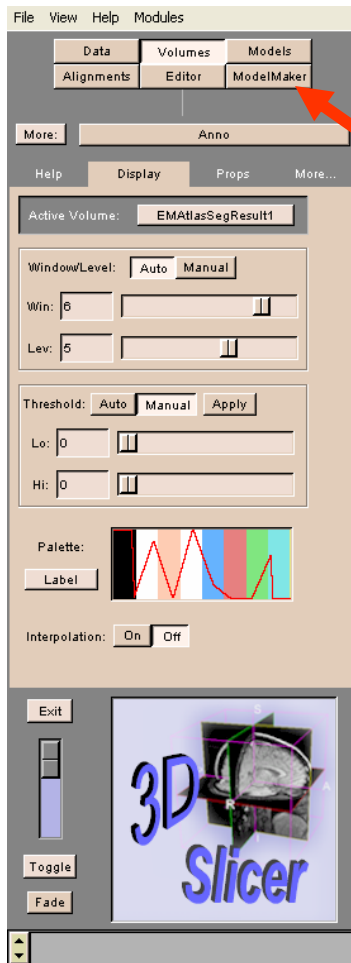
Building 3D models



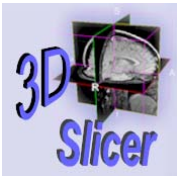
Double-click on the volume
Volume:EMBrainSegResult1



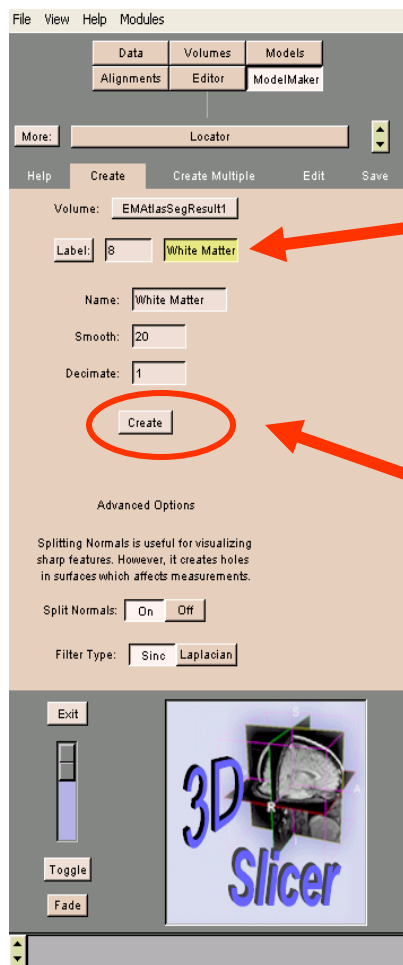
Building 3D models



Select the module ModelMaker

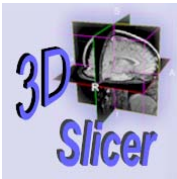


Building 3D models

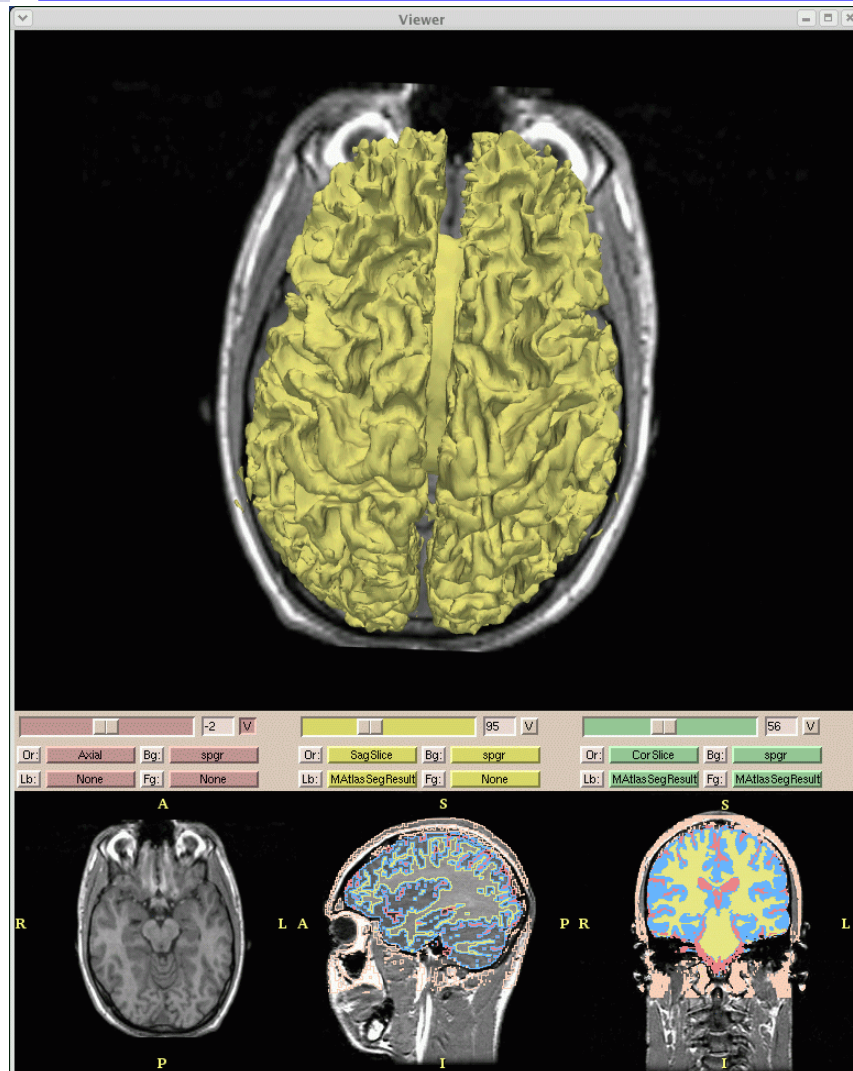


Select the label White Matter corresponding to the color label of the White Matter segmentation.

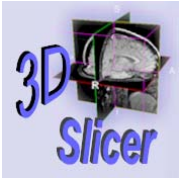
Create on Create



Building 3D models

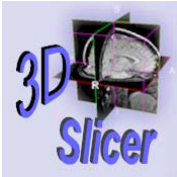


Slicer generates a 3D model of the White Matter



Overview

- Part 1: Generic Atlas and EM Pipeline
- Part 2: Loading tutorial data
- **Part 3: Hardware requirements**
- Part 4: Working with tutorial data
- Part 5: Working with your own data



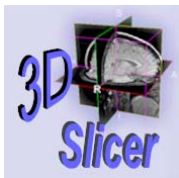
Hardware: constraints

Minimal requirements

- RAM: 1 GB
- Processor: 2 GHz



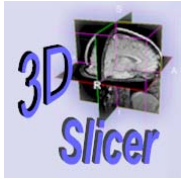
Segmentation algorithm is computationally demanding.



Module Performance

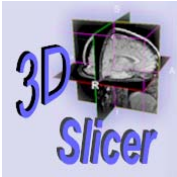
Examples of processing time for the
EMBrainAtlasClassifier

- Sun Solaris 12 UltraSparc-III
processors 10 GB RAM: **55 min**
- Debian Pentium 4-M CPU 2.4 GHz,
2 GB RAM : **45 min**
- RedHat 64 bit 4 Gig 2x 3.0 GHz
Xeon Processor: **40 min**

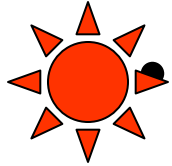


Overview

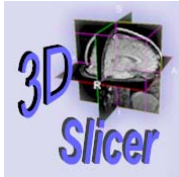
- Part 1: Generic Atlas and EM Pipeline
- Part 2: Loading tutorial data
- Part 3: Hardware requirements
- **Part 4: Working with tutorial data**
- Part 5: Working with your own data



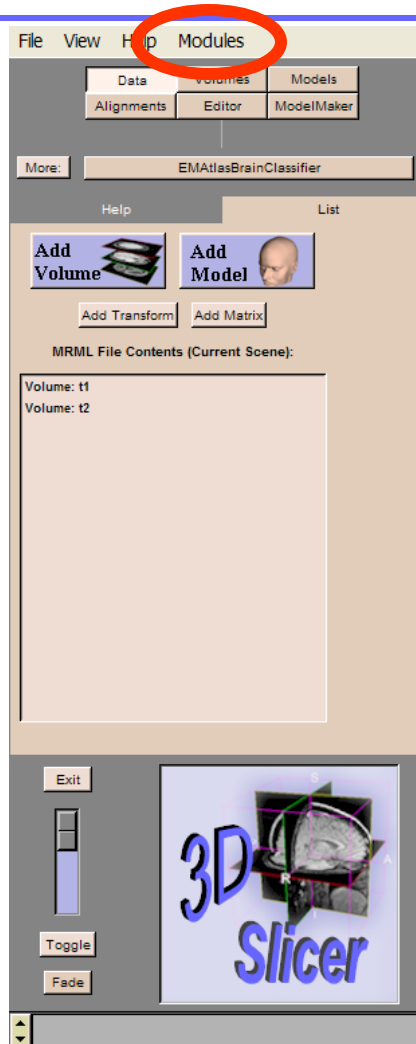
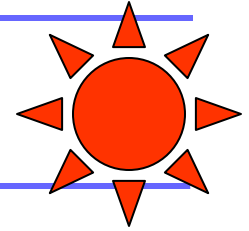
Implementing the EM algorithm



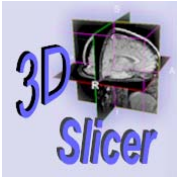
- If your **processor meets the requirements** the following steps will guide you through the process of segmenting your data using the EM algorithm
- If your processor does not, read through (slide 40) to see what you need to do when you run it on a computer with adequate processing capabilities



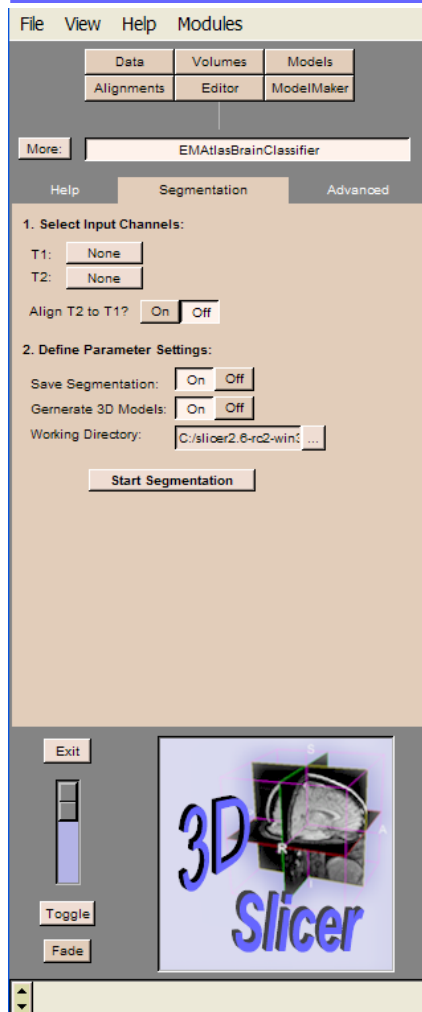
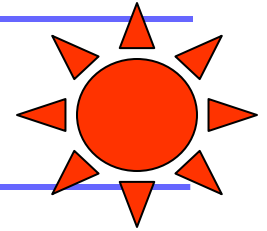
Parameter Settings



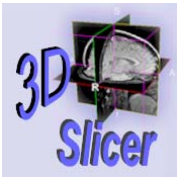
In the Main Menu select
Modules → Segmentation →
EMAtlasBrainClassifier



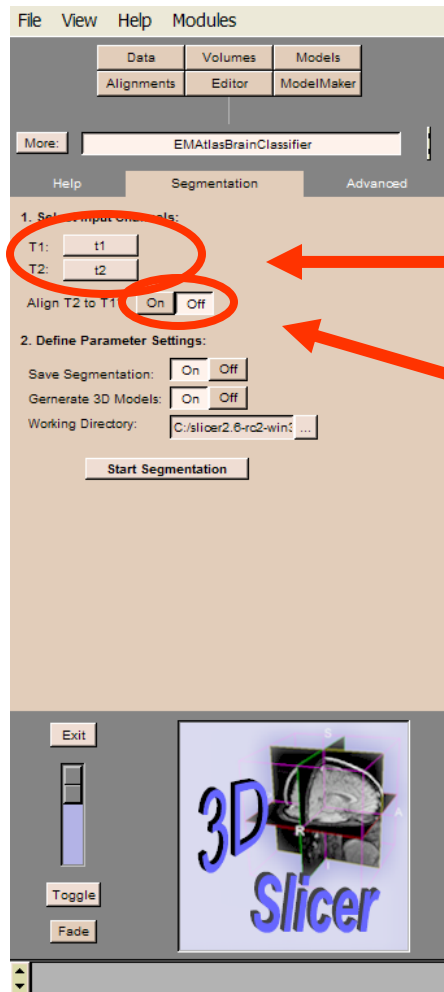
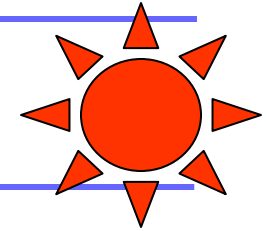
Parameter Settings



The Segmentation panel of the module EMAtlasBrainClassifier appears.

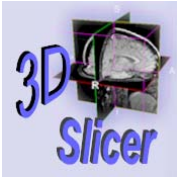


Parameter Settings

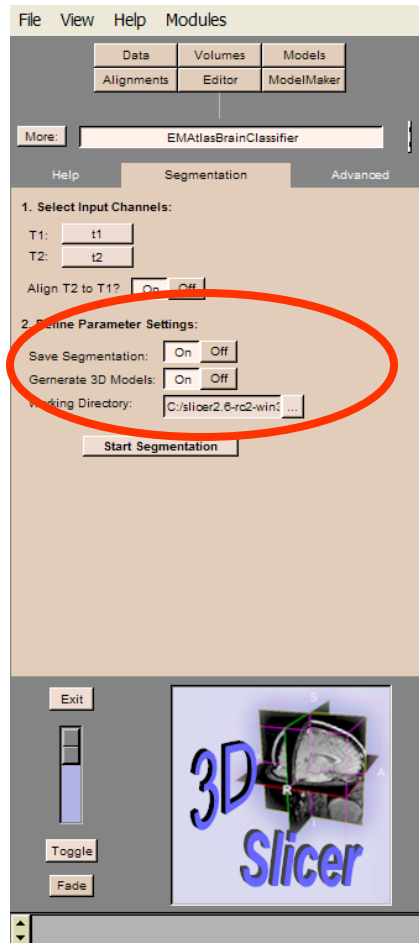
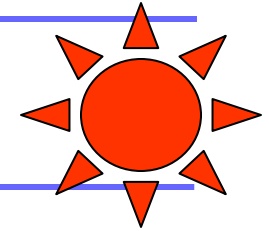


Select the panel Segmentation and select the input channels t1 and t2 that were previously loaded in the first part of the tutorial.

Set alignment to On



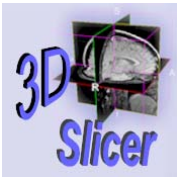
Parameter Settings



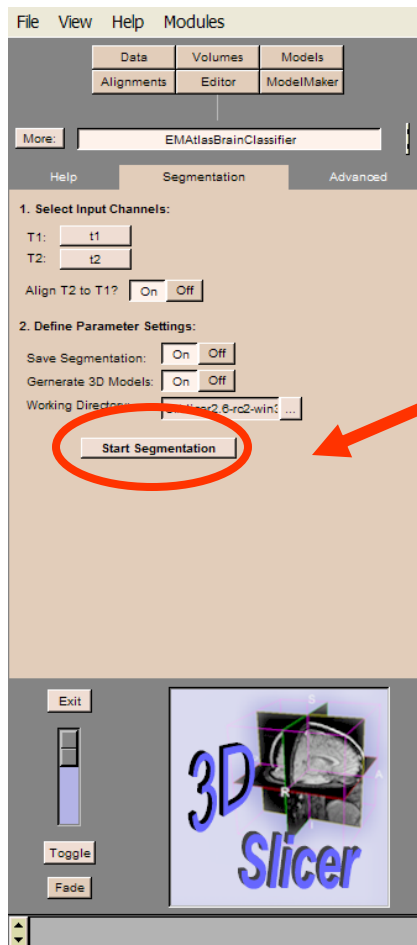
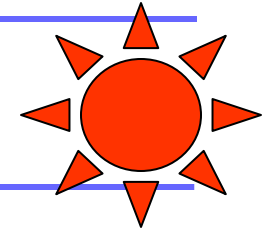
Set Save Segmentation On to save the output of the segmentation

Set Generate 3D Models On to reconstruct 3D models of the White Matter, Gray Matter and CSF.

Enter the path corresponding to the location of the directory BrainAtlasClassifier/working in the tutorial data.

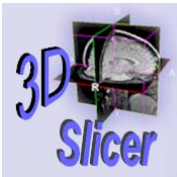


Automatic Segmentation

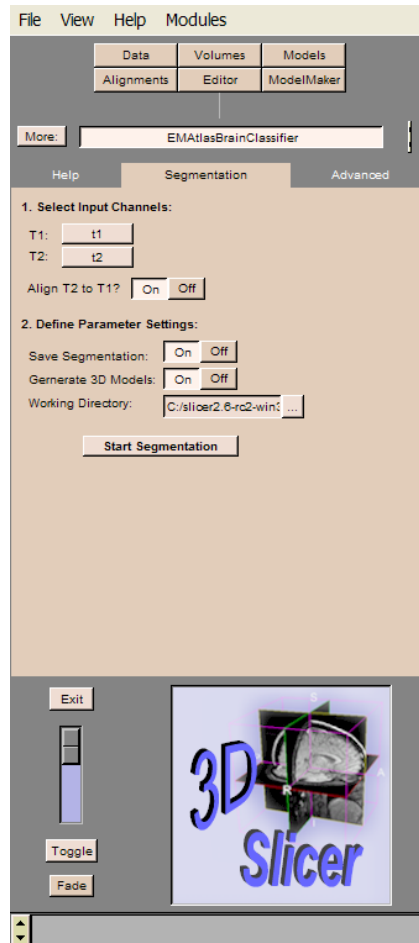


Click on Start Segmentation

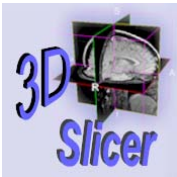
Expected mean processing time reminder : 45 min



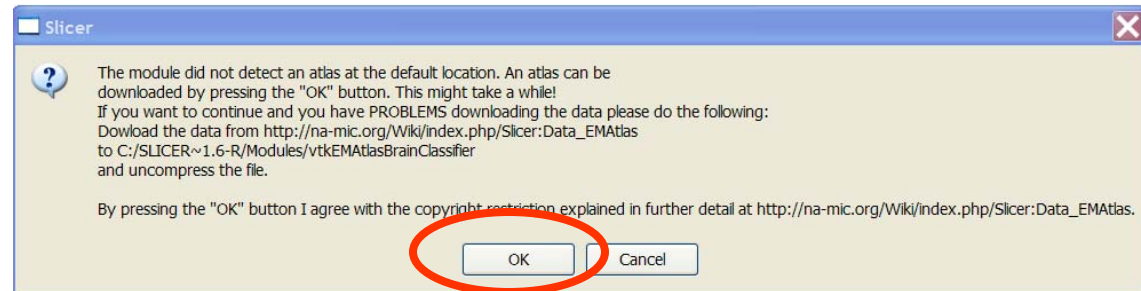
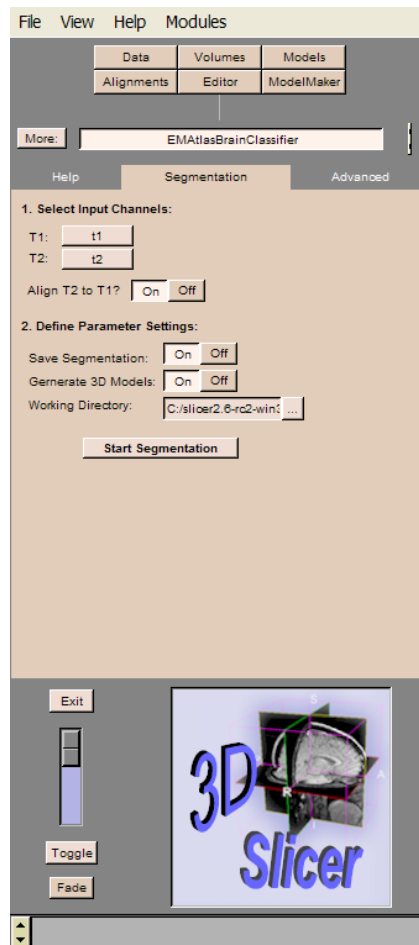
Atlas loading



The program looks for a generic atlas at the default location
Modules/vtkEMBrainAtlasClassifier

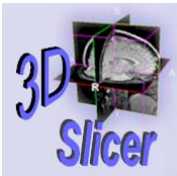


Atlas loading

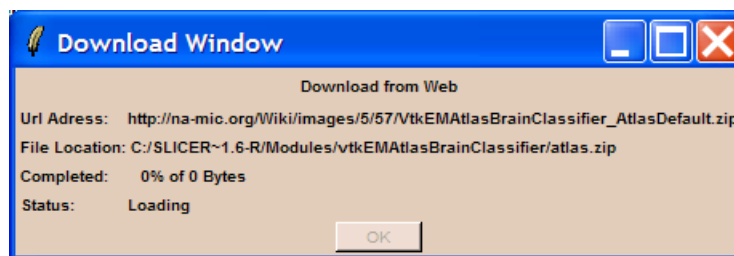
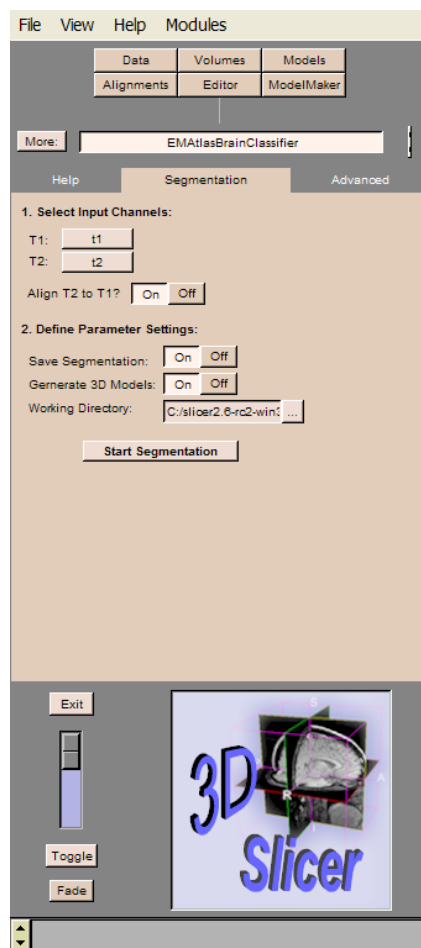


A message inviting you to download the generic atlas from the web appears. Click OK.

This message will happen only once after having installed Slicer.

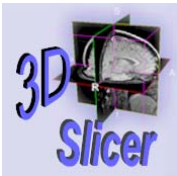


Atlas loading (automatic)



Slicer downloads the atlas from the web.

Click OK once the installation is completed.



Atlas loading (manual)

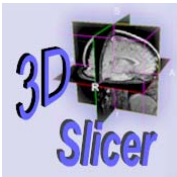
If you experience problems with the automatic atlas loading, manually download the atlas from the links stated below:

- Unix/Linux/Mac:

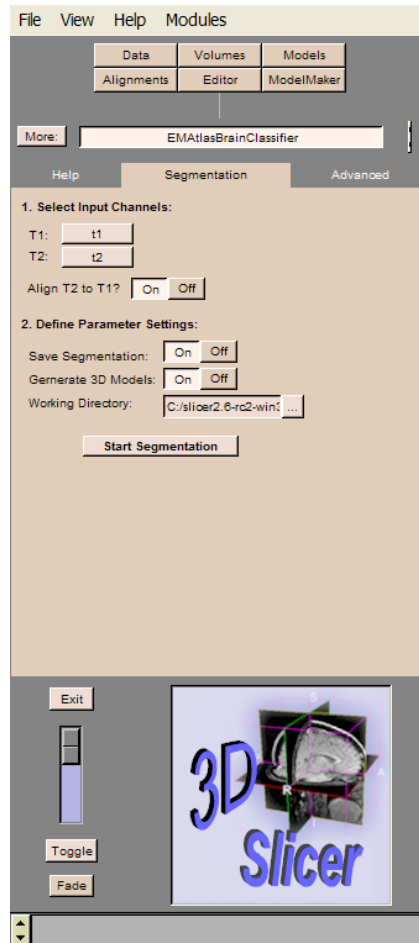
http://na-mic.org/Wiki/images/8/8d/VtkEMAtlasBrainClassifier_AtlasDefault.tar.gz

- Windows:

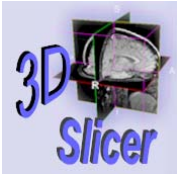
http://na-mic.org/Wiki/images/5/57/VtkEMAtlasBrainClassifier_AtlasDefault.zip



Atlas installation



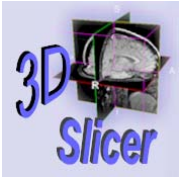
Manually unzip the archive of the atlas in the directory
Modules/vtkEMAtlasBrainClassifier/atlas



Atlas installation (Non-Windows Users)

Check that the atlas is located in the directory

Modules/vtkEMAtlasBrainClassifier/atlas



Atlas installation (additional step only required for Windows Users)

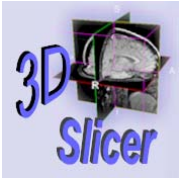
Built-in Windows unzip wizard adds an extra level of directory

Modules/vtkEMAtlasBrainClassifier/atlas/atlas

Move the atlas data one level-up to the correct directory

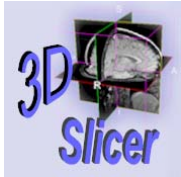
Modules/vtkEMAtlasBrainClassifier/atlas

and delete the unnecessary directory



Overview

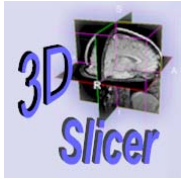
- Part 1: Generic Atlas and EM Pipeline
- Part 2: Loading tutorial data
- Part 3: Hardware requirements
- Part 4: Working with tutorial data
- Part 5: Working with your own data



Data Acquisition: Tutorial data

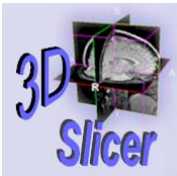
The [tutorial dataset](#) was acquired with the following parameters

- T1 volume: Coronal series of contiguous Spoiled Gradient (SPGR) images (124 slices of 1.5 mm thickness, voxel dimensions 0.9375 x 0.9375 x 1.5 mm)
- T2 volume: Axial series of contiguous double-echo images (Proton Density and T2 Weighted, 108 slices of 3 mm slice thickness, voxel dimensions 0.9375 x 0.9375 x 3 mm) isotropic t2
Dimension 0.9375mm x 0.9375mm x 3mm
- More details can be found on the NA-MIC wiki
http://www.na-mic.org/Wiki/index.php/Brockton_MRI_Scan_Parameters

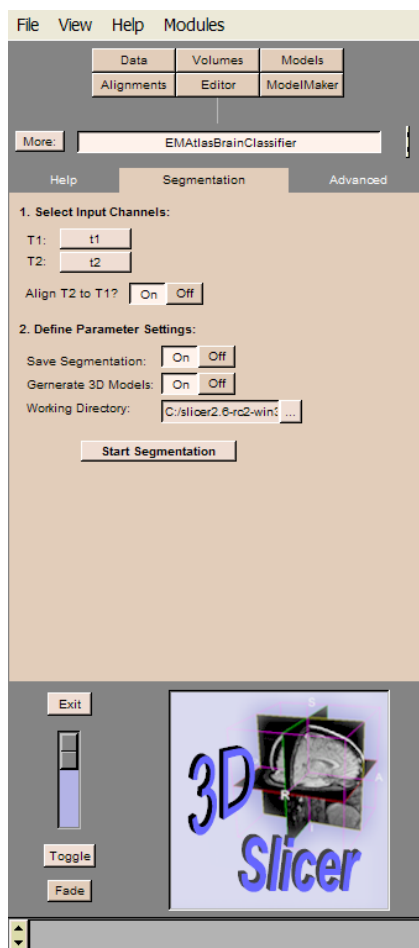


Data Acquisition: your data

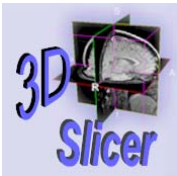
- You'll need to experiment the EMBrainAtlasClassifier module with your own data.
- We suggest **High resolution T1 and T2 weighted images.**



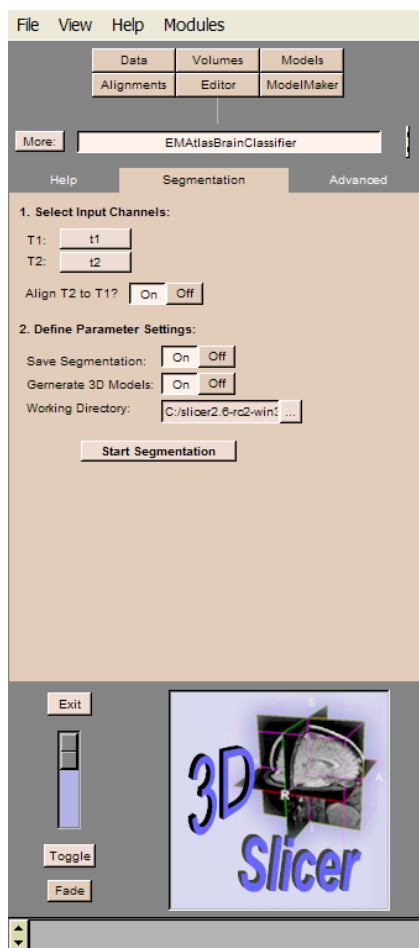
Working with your own data



Load T1 and T2 as Input Channels, and set Align T2 to T1 On to register the two volumes.



Working with your own data

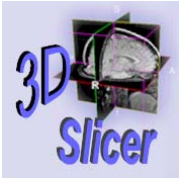


Set Save Segmentation On to save the output of the segmentation

Set Generate 3D Models On to reconstruct 3D models of the White Matter, Gray Matter and CSF.

Enter the path corresponding to the working directory for your own data

Click on Start Segmentation



Conclusion

- Automatic segmentation of MRI brain data in White Matter, Grey Matter and Cerebrospinal Fluid.
- Open-source environment