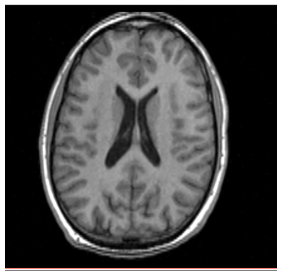
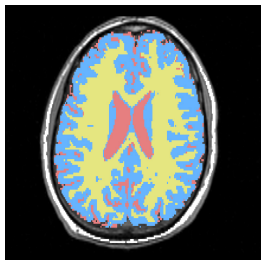
Automatic Segmentation of Brain Structures



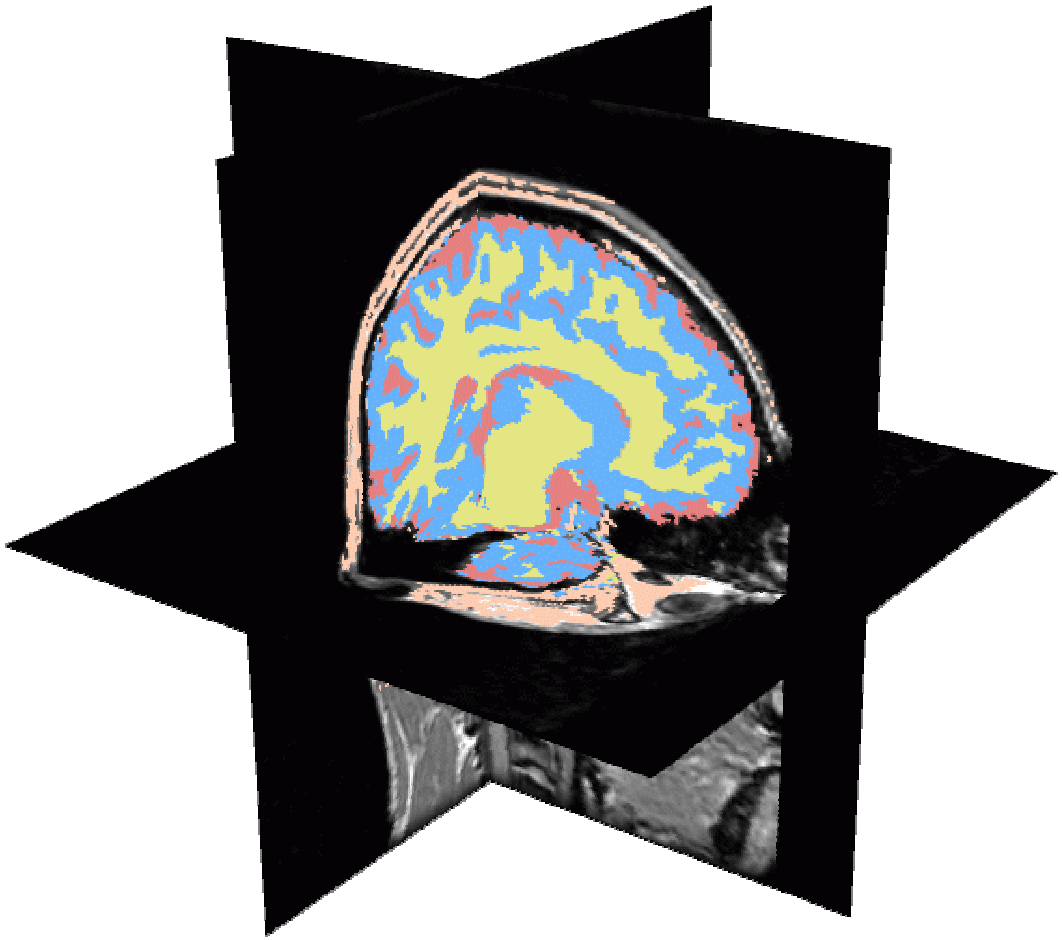
Sonia Pujol, Ph.D.

Surgical Planning Laboratory

Harvard Medical School



Goal of the course



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

Algorithm History

12-year of algorithm development

- 1996: Williams Wells et al.

EM framework for simultaneous estimation of bias field a label map. IEEE Transactions on Medical Imaging.

- 1999: Kapur et al.

Model noise via Markov Random Field . MIT PhD Thesis

- 2002: Van Leemput et al.

Non-spatial tissue priors. IEEE Transactions on Medical Imaging

- Since 2002: Pohl et al.

Deformable registration to align atlas (MICCAI)
Hierarchical framework to model anatomical dependencies (ISBI)

- 2007: Brad Davis et al.: EMSegmenter in Slicer3

Material

- **Slicer 3.4 Software**

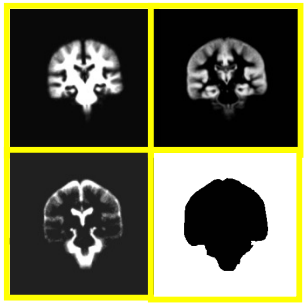
./Slicer.exe (Windows) or ./Slicer (Linux/Mac)

- **AutomaticSegmentation.zip** dataset

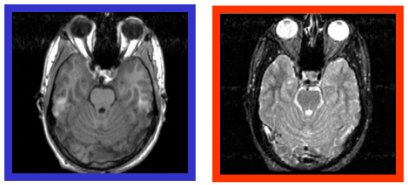
Disclaimer: It is the responsibility of the user of 3DSlicer to comply with both the terms of the license and with the applicable laws, regulations and rules.

Tutorial dataset

- Pre-computed generic atlas of the brain……



- T1 and T2 volumes ……..



Anatomical Tree

- The **anatomical tree** defines the hierarchy of structures that will be segmented.

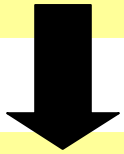
- In this course, we focus on the following hierarchy

  - Intracranial Cavity
    - White Matter (WM)
    - Grey Matter (GM)
    - Cerebrospinal Fluid (CSF)

  - Background
    - Air
    - Skull

EM Pipeline

Step 1: Pre-processing

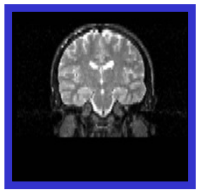


Step 2: Patient-specific atlas generation

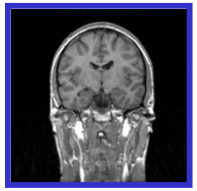
Step 3: Automatic segmentation

EM Pipeline: Preprocessing

Patient data

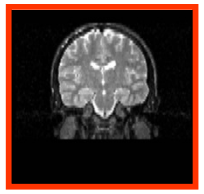


t2

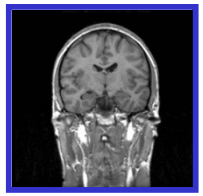


t1

Intensity Normalization
Normalize the intensity of t1 and t2

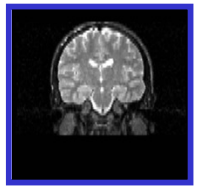


t2 normalized

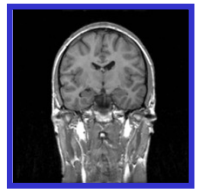


t1 normalized

Target to Target Registration
Align t2 to t1



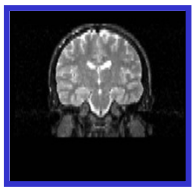
T(t2n)



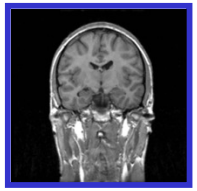
t1n

EM Pipeline: Patient-Specific Atlas Generation

Registered Normalized Patient data

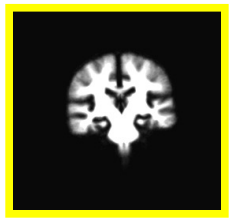


T(t2n)

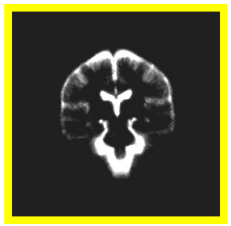


t1n

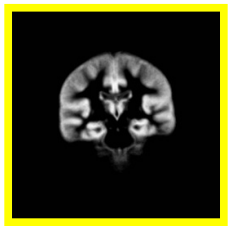
Generic atlas



white matter



csf

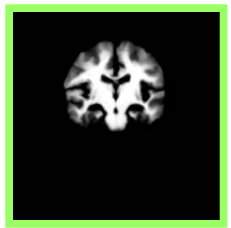


grey matter

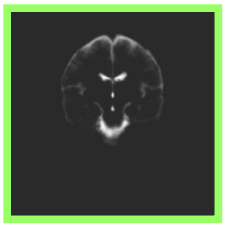
background

Atlas to target registration
Register the generic atlas to the images to create the patient-specific atlas

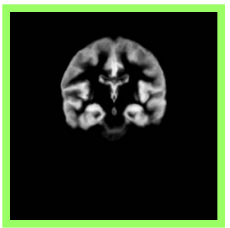
Patient-specific atlas



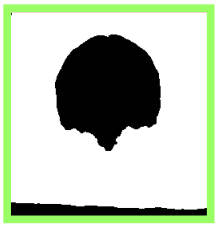
white matter



csf



grey matter

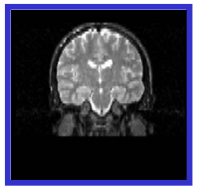


background

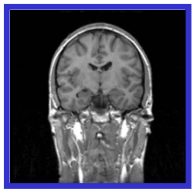
Anatomical Guided Segmentation with non-stationary tissue class distributions in an expectation maximization framework. Pohl K., Bouix S., Kikinis R. and Grimson E. In Proc.ISBIT 2004: IEEE International Symposium on Biomedical Imaging:From Nano to Macro, pp 81-84

EM Pipeline: Segmentation

Normalized Patient data

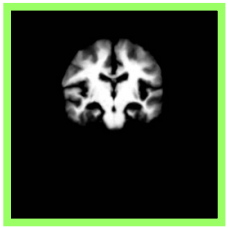


T(t2) normalized

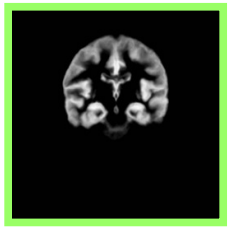


T1 normalized

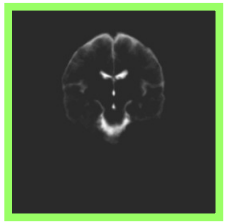
Patient-specific atlas



white matter

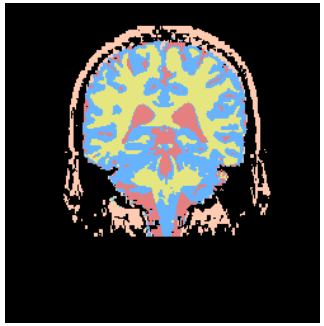


csf



grey matter

background



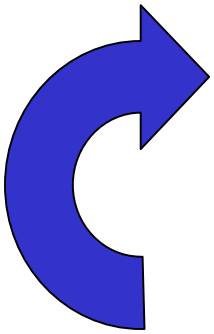
Segment using the Expectation Maximization algorithm

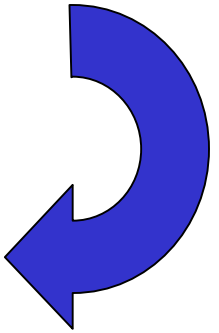
Anatomical Guided Segmentation with non-stationary tissue class distributions in an expectation maximization framework. Pohl K., Bouix S., Kikinis R. and Grimson E. In Proc.ISBIT 2004: IEEE International Symposium on Biomedical Imaging:From Nano to Macro, pp 81-84

EP Pipeline: Segmentation 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

Running Slicer3

Mac/Linux

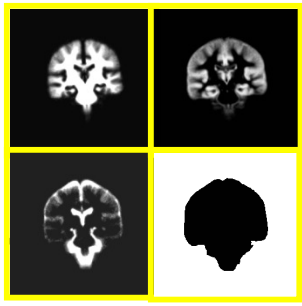
Run **./Slicer3** in Slicer3-build/

Windows

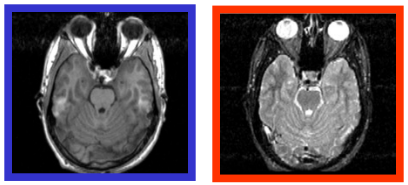
Run **./Slicer3.exe** in Slicer3-build/

Tutorial dataset

- Pre-computed generic atlas of the brain……

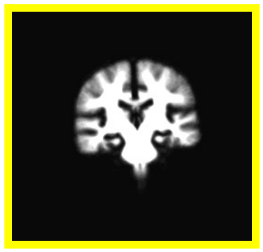
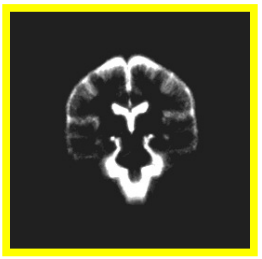
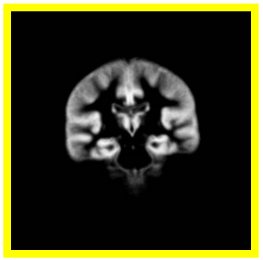


- T1 and T2 volumes ……..

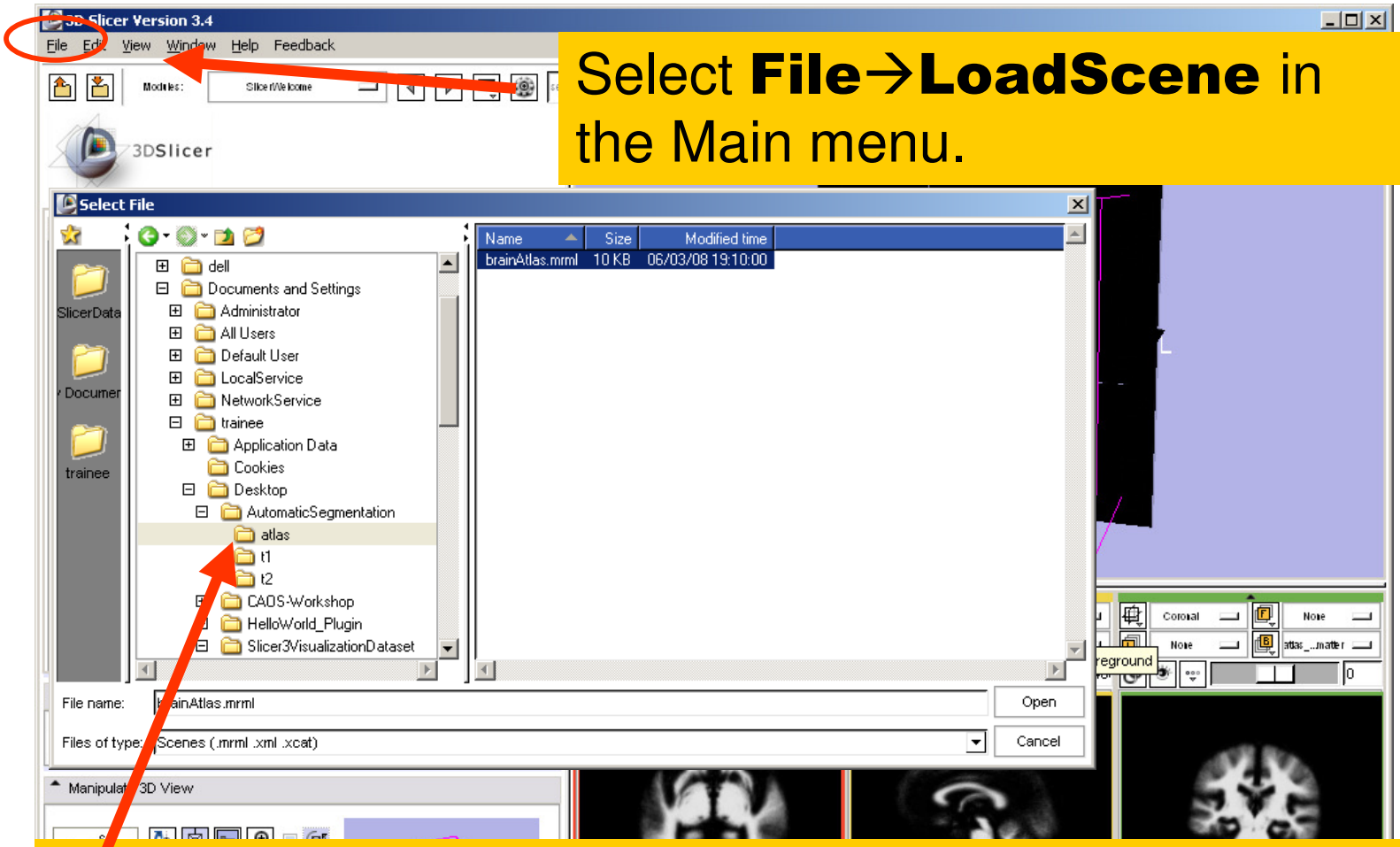


Generic Brain Atlas

The Generic Brain Atlas is composed of four grey-levels volumes which correspond to the structures that will be automatically segmented in the MRI example datasets.

White Matter (WM)	Cerebrospinal Fluid (CSF)	Grey Matter (WM)	Background (Bg)
			

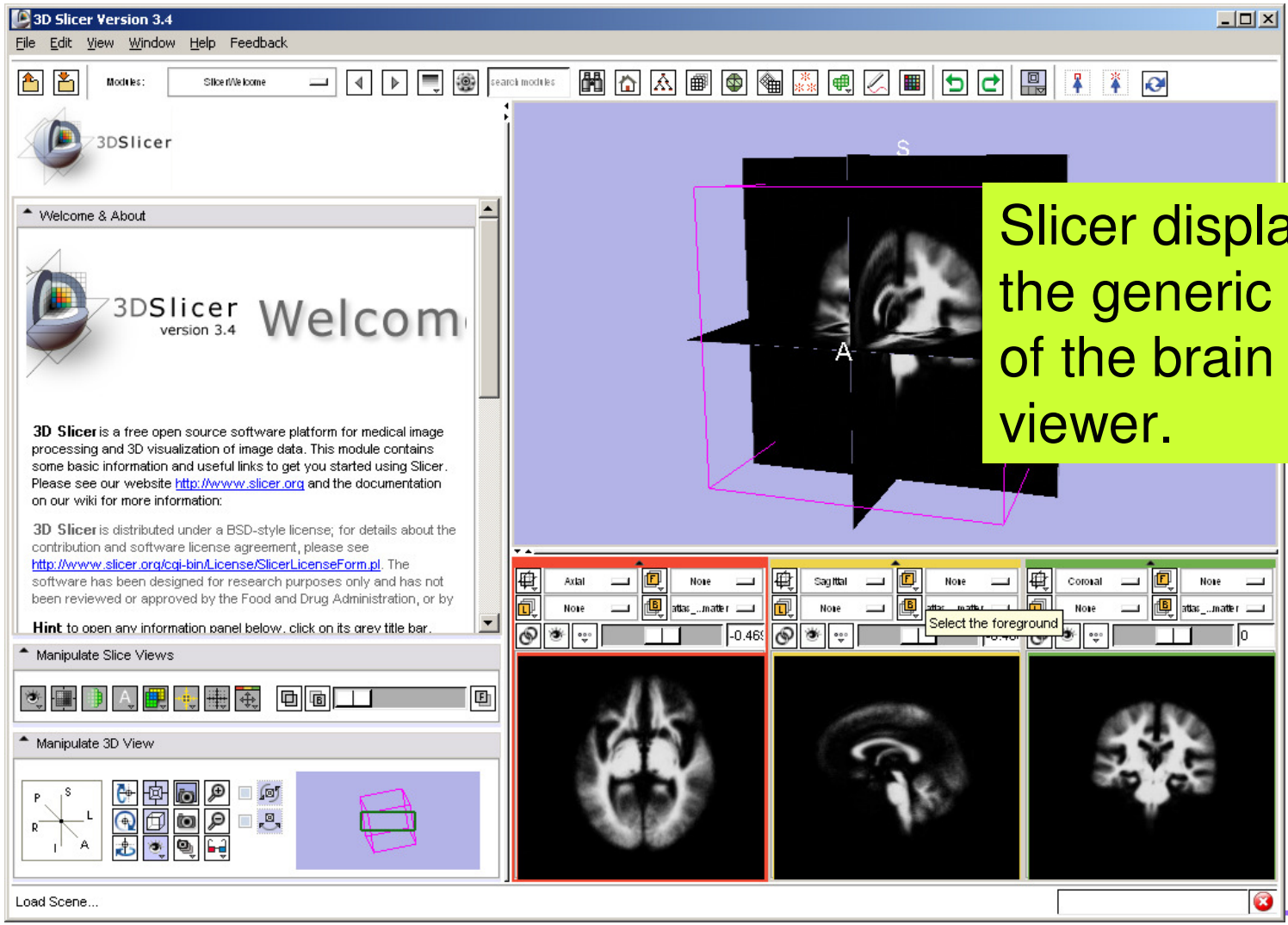
Loading the generic atlas of the brain



Select **File→LoadScene** in the Main menu.

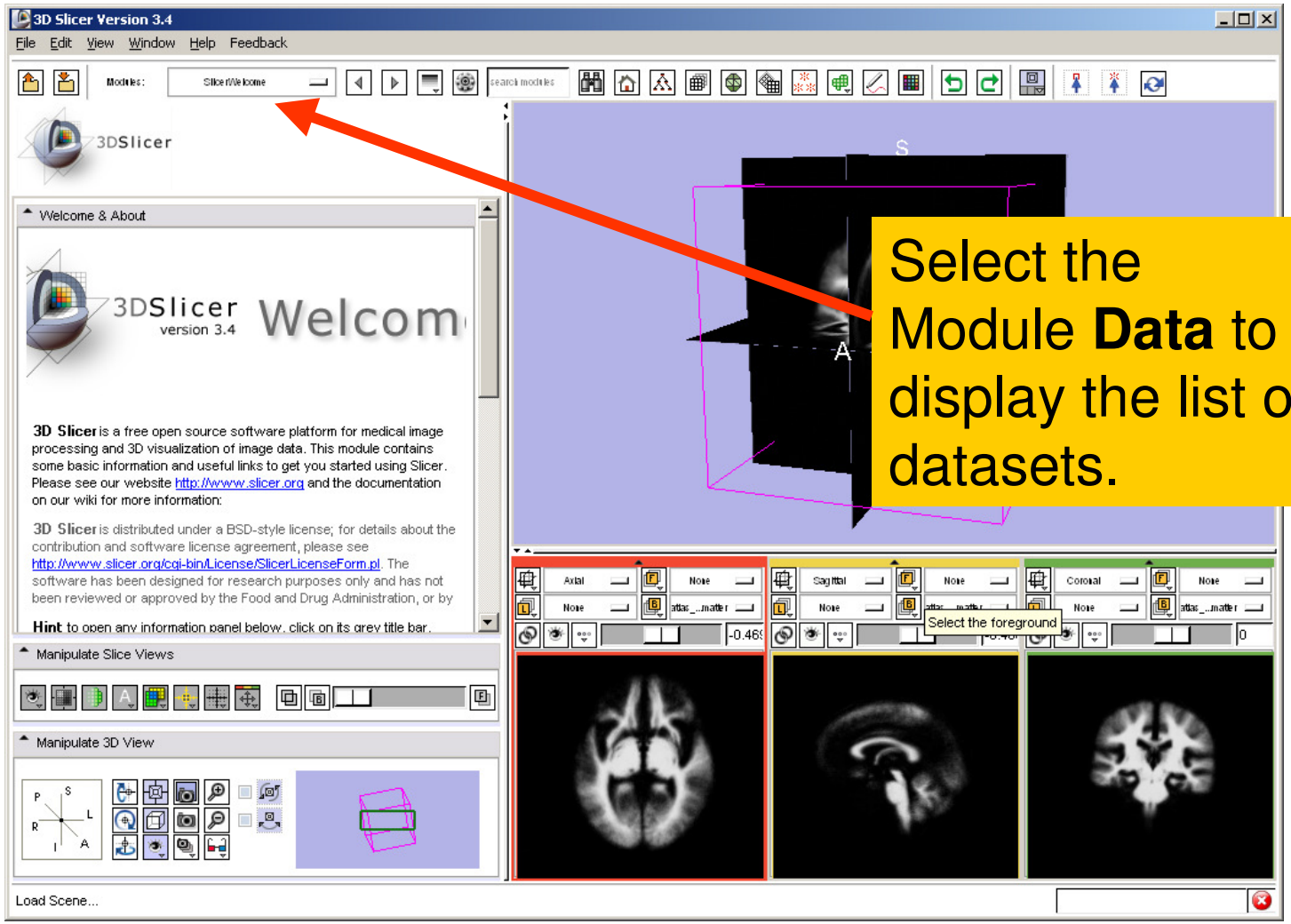
Select the file **brainAtlas.mrml** in the directory **AutomaticSegmentation/atlas** and click on **Open**

Viewing the generic atlas of the brain

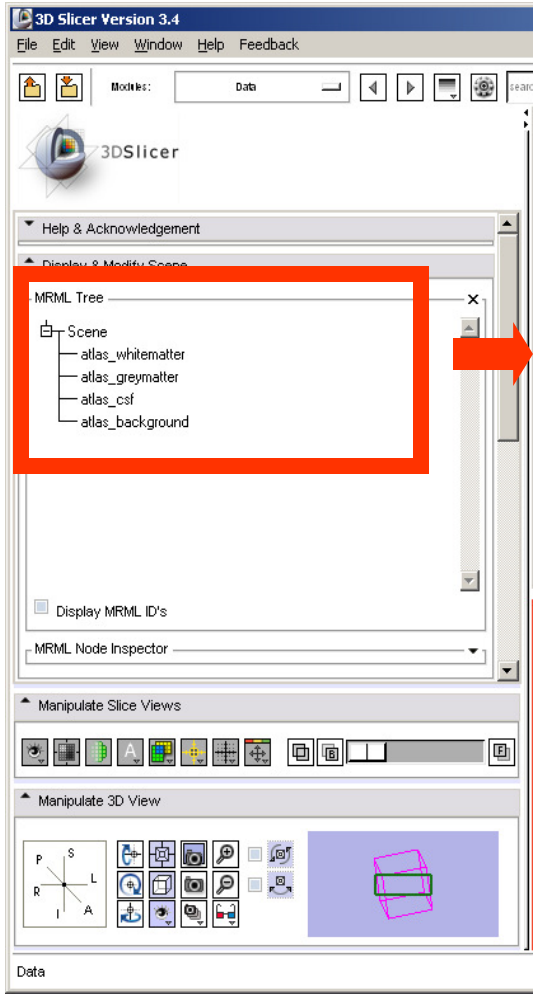


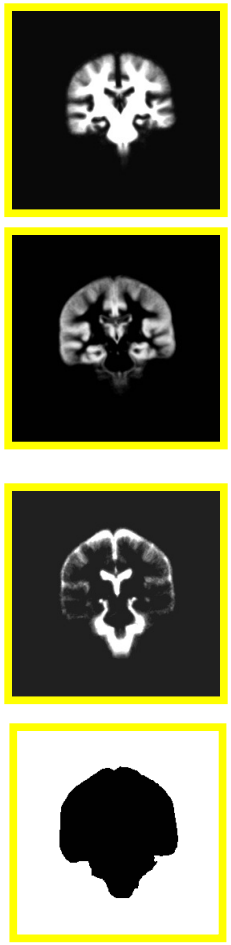
Slicer displays the generic atlas of the brain in the viewer.

Viewing the generic atlas of the brain



Viewing the generic atlas of the brain





The generic atlas is composed of 4 volumes:

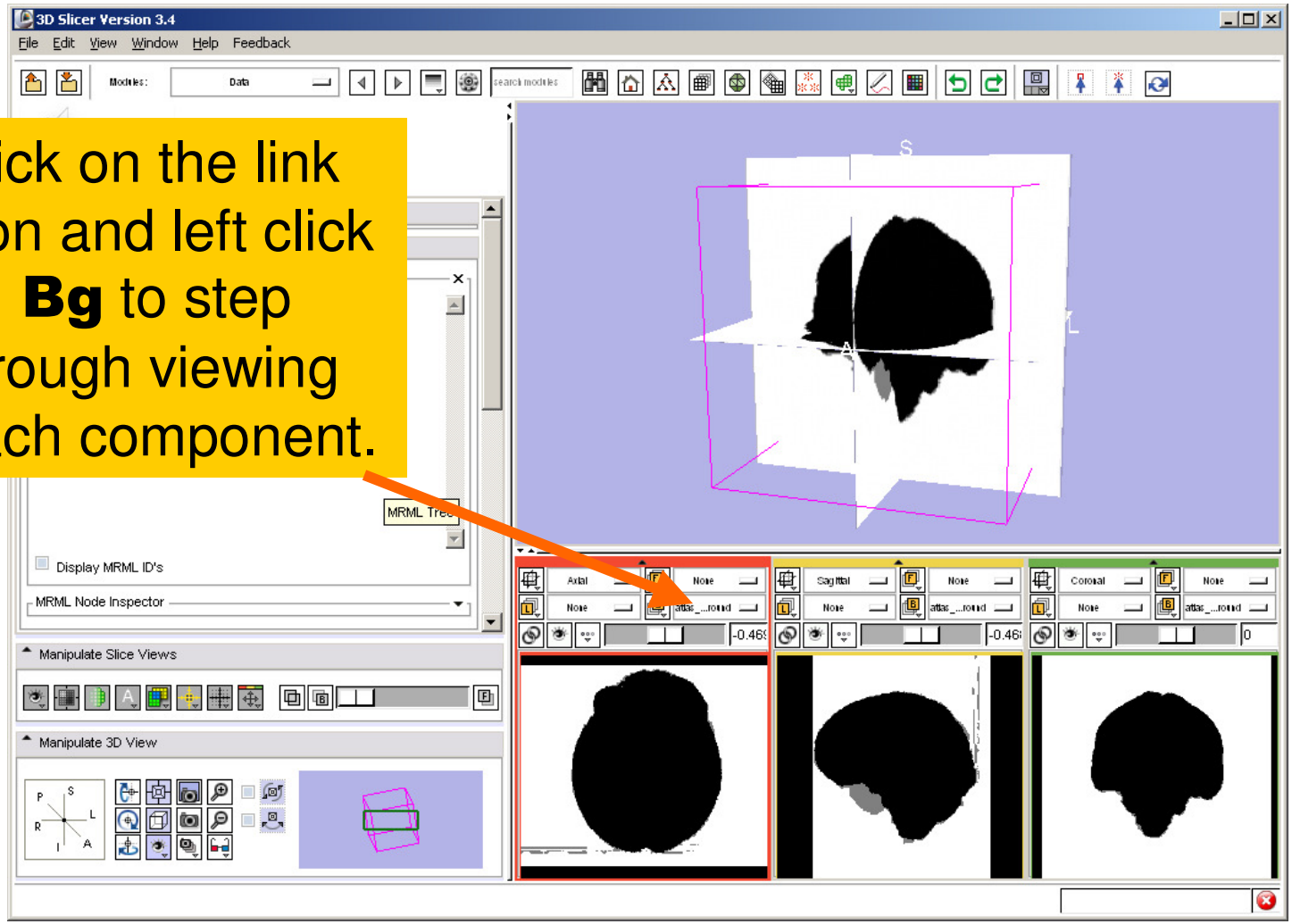
-White Matter

-Grey Matter

-CSF

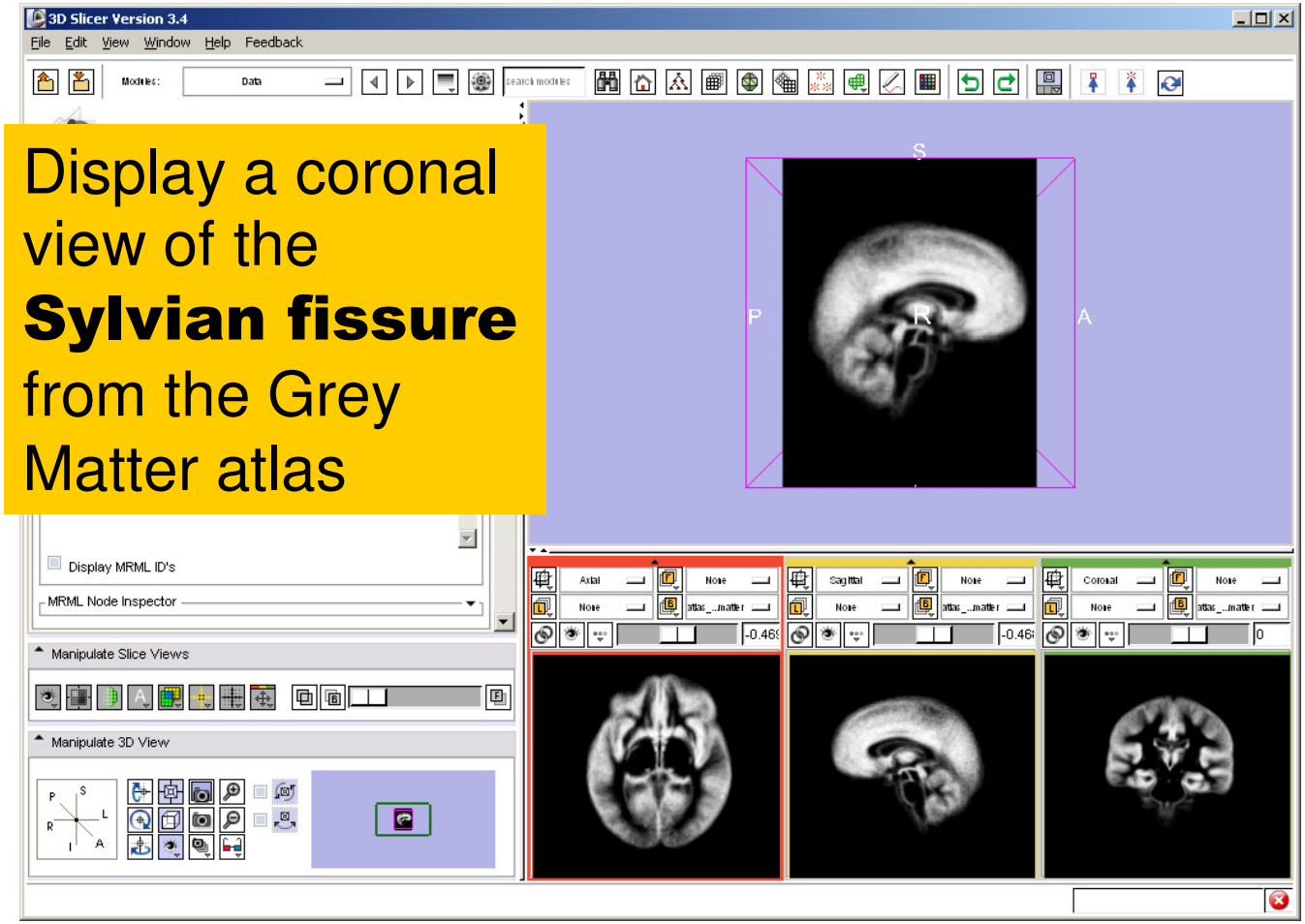
-Background

Loading the generic atlas of the brain



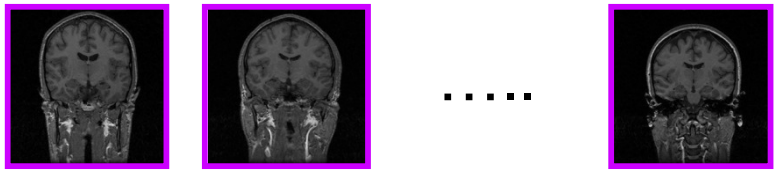
Click on the link icon and left click on **Bg** to step through viewing each component.

Viewing the generic atlas of the brain



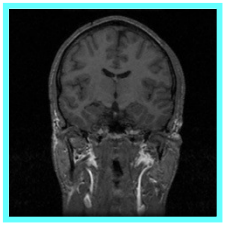
Display a coronal view of the **Sylvian fissure** from the Grey Matter atlas

Generic Atlas Generation (Step 1)

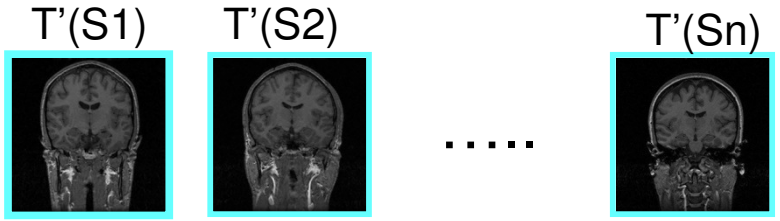


n=82 healthy subjects, ages 25-40

Register all the subjects to the training subject



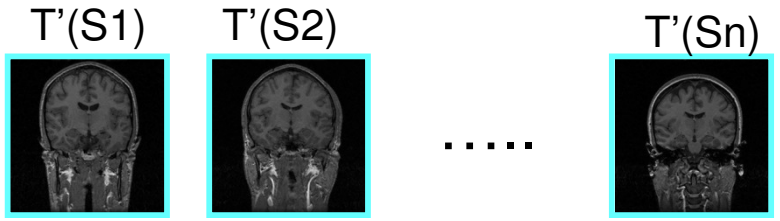
Training subject (randomly chosen)



n=82 registered subjects

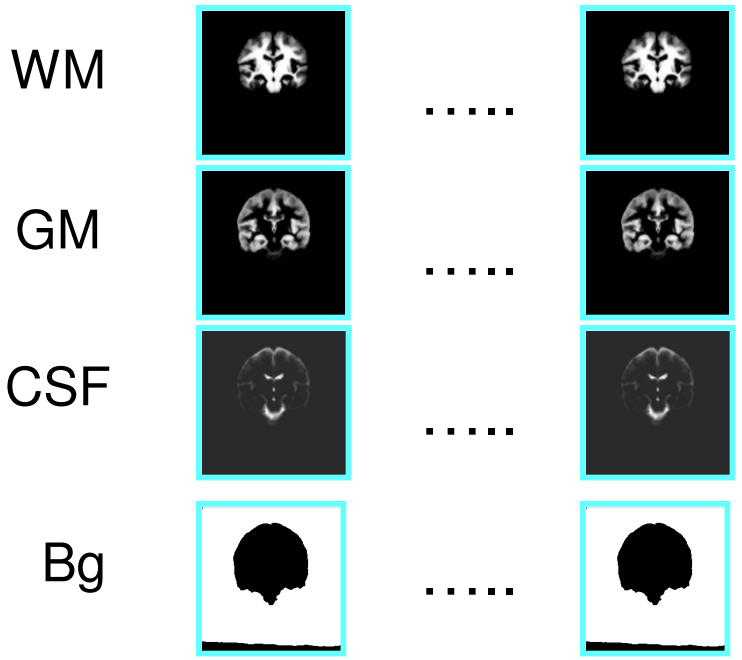
A Binary Entropy Measure to Assess Non-rigid Registration Algorithms. S.Warfield, J. Rexilius, P. Huppi, T.Inder, E. Miller, W.Wells, G. Zientara, F. Jolesz, R. Kikinis. In Proc. MICCAI 2001: Medical Image Computing and Computer-Assisted Interventions, pp 266-274.

Generic Atlas Generation (Step 2)

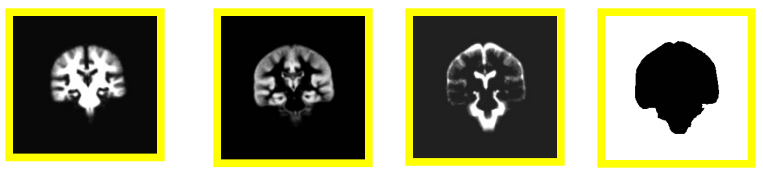


n=82 registered subjects

Segment all n images into 4 classes



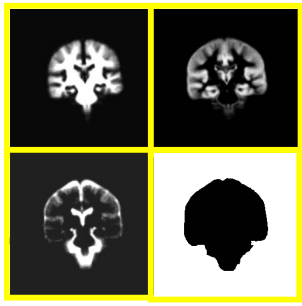
Generate the generic atlas



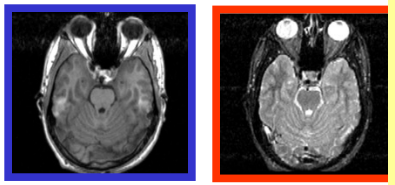
Adaptative Segmentation of MRI data. Wells W., Grimson E., Kikinis R and Jolesz F. IEEE Transactions on Medical Imaging, vol.15, p 429-442, 1996.

Tutorial dataset

- Pre-computed generic atlas of the brain……

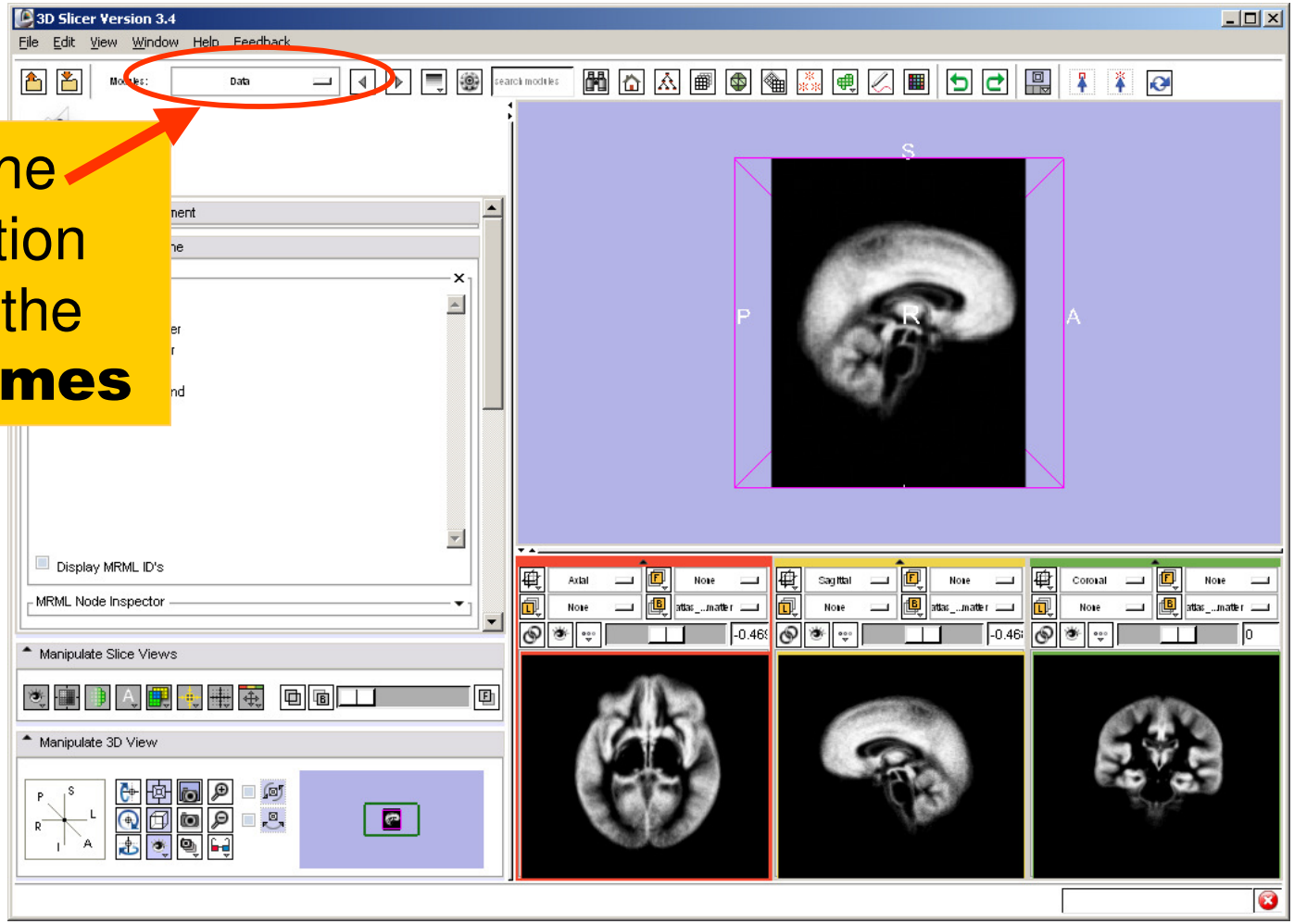


- T1 and T2 volumes ……..



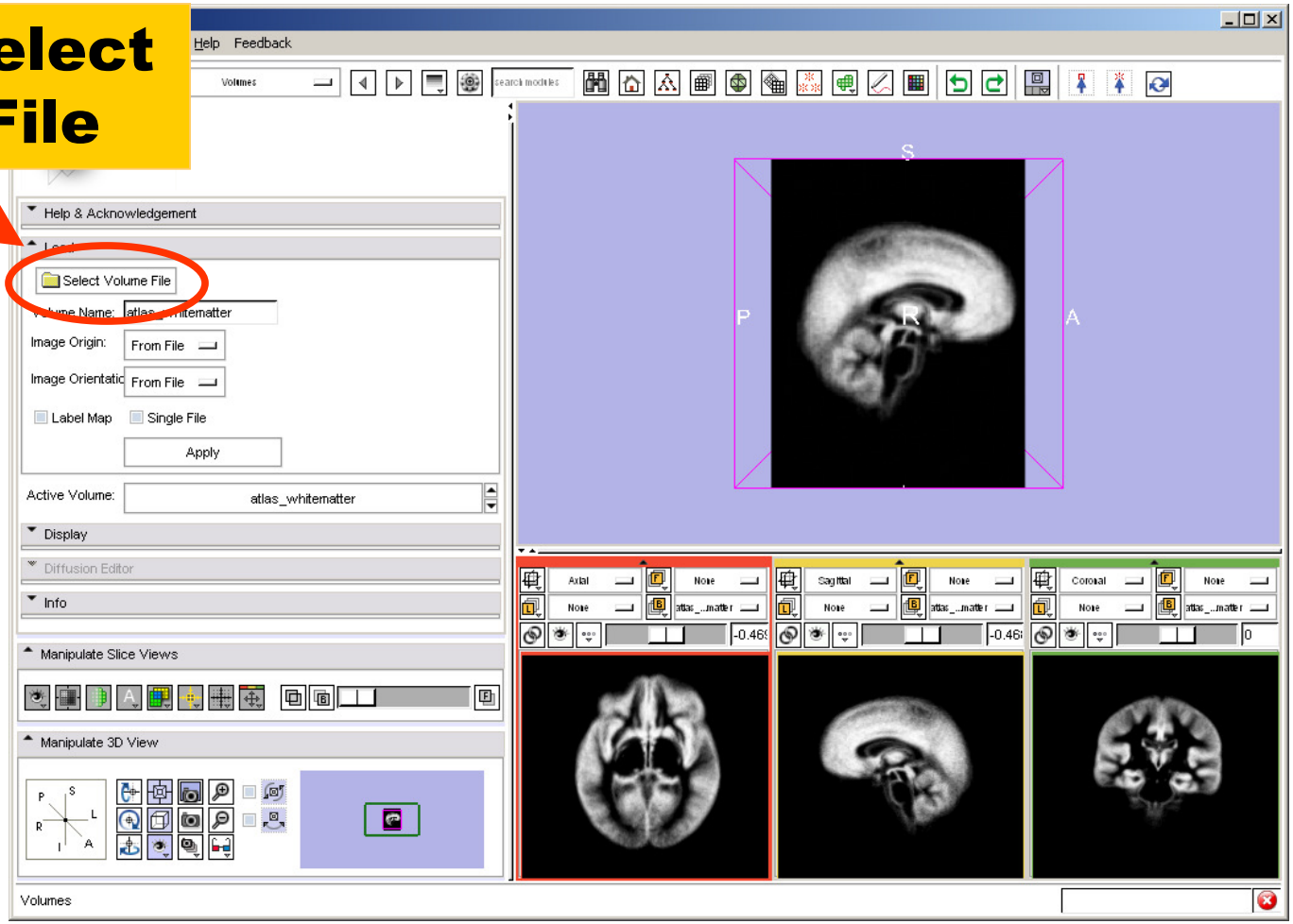
Loading T1 Volume

Left-click on the module selection menu to load the module **Volumes**

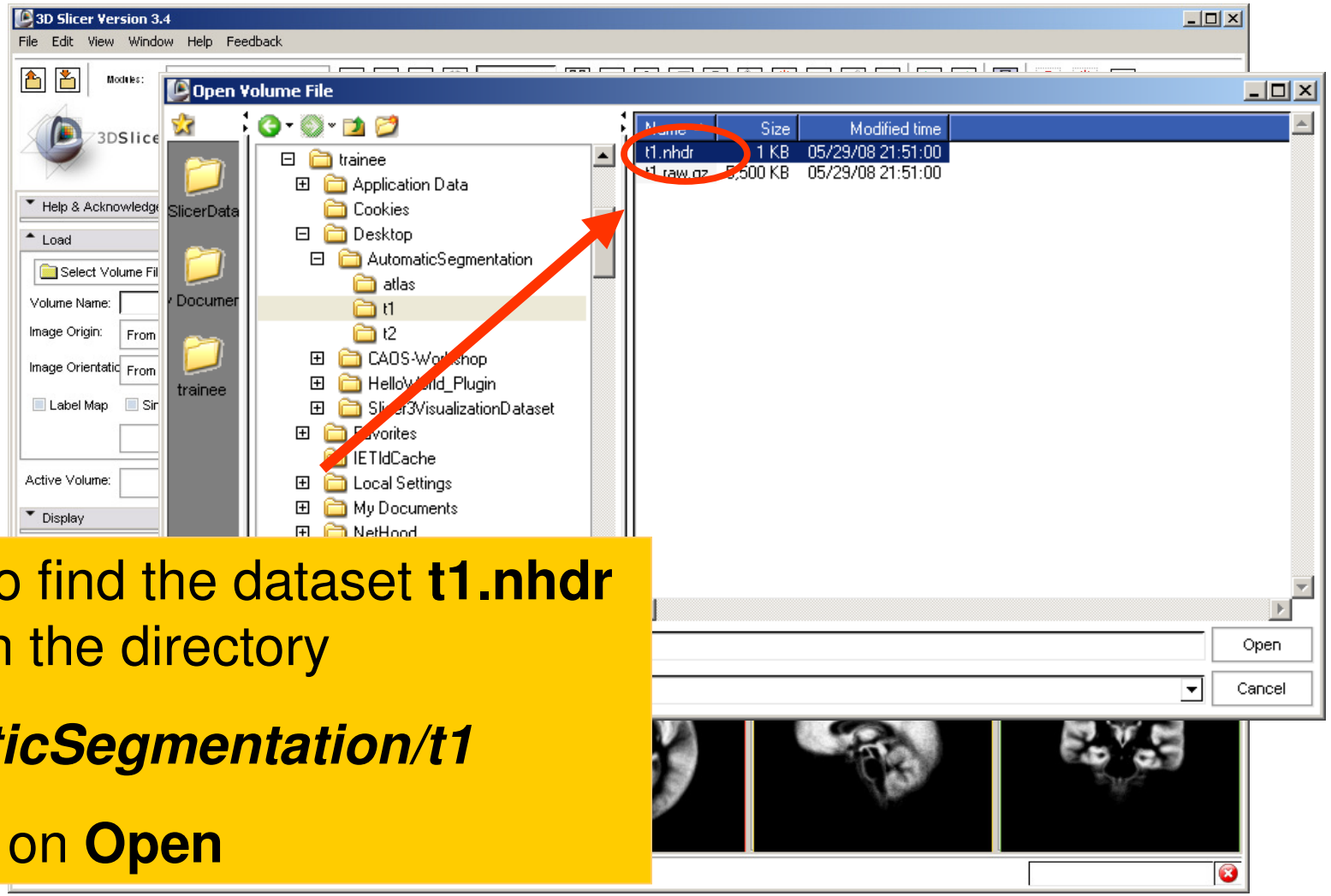


Loading T1 Volume

Click on **Select Volume File**



Loading T1 Volume

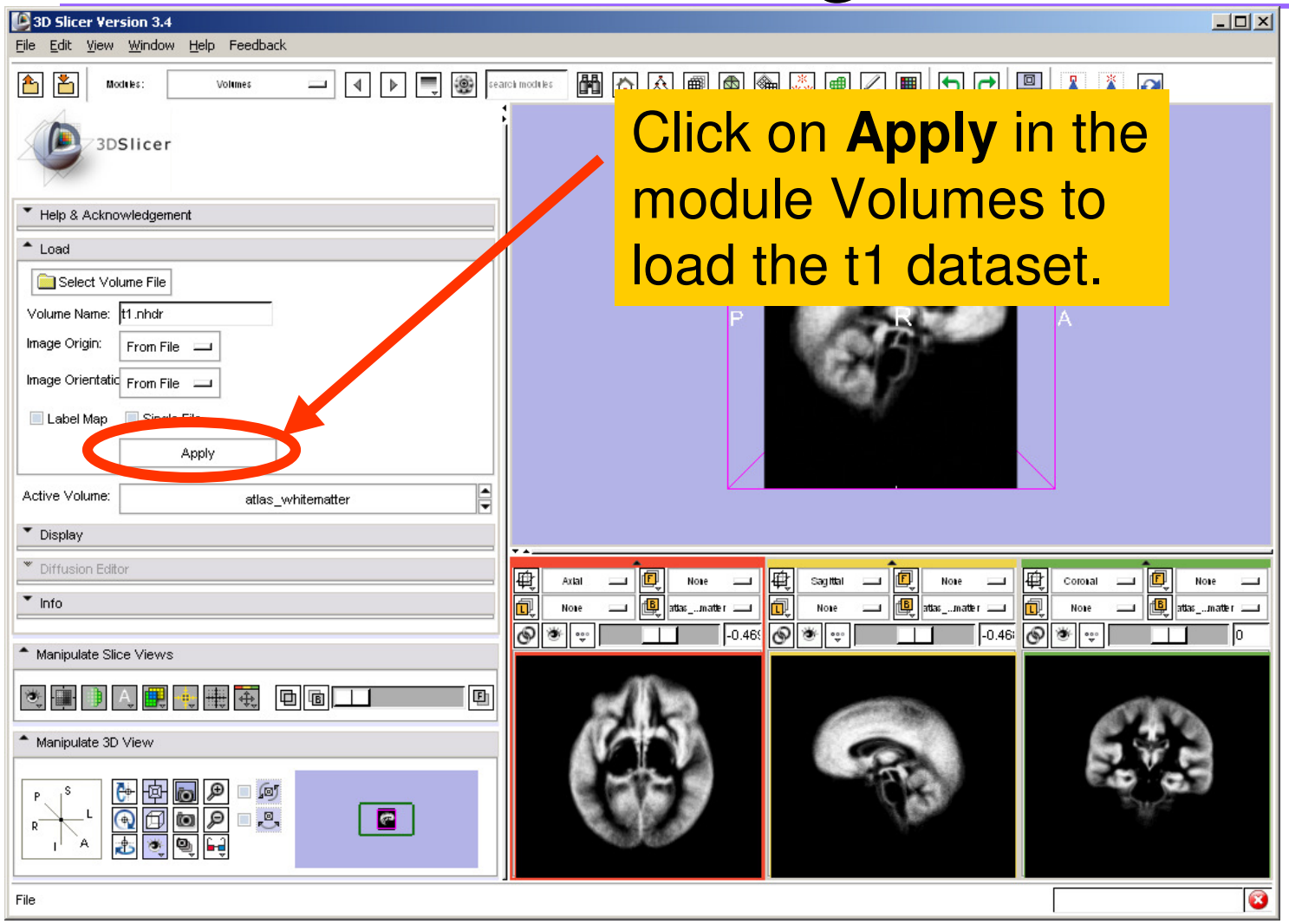


Browse to find the dataset **t1.nhdr** located in the directory

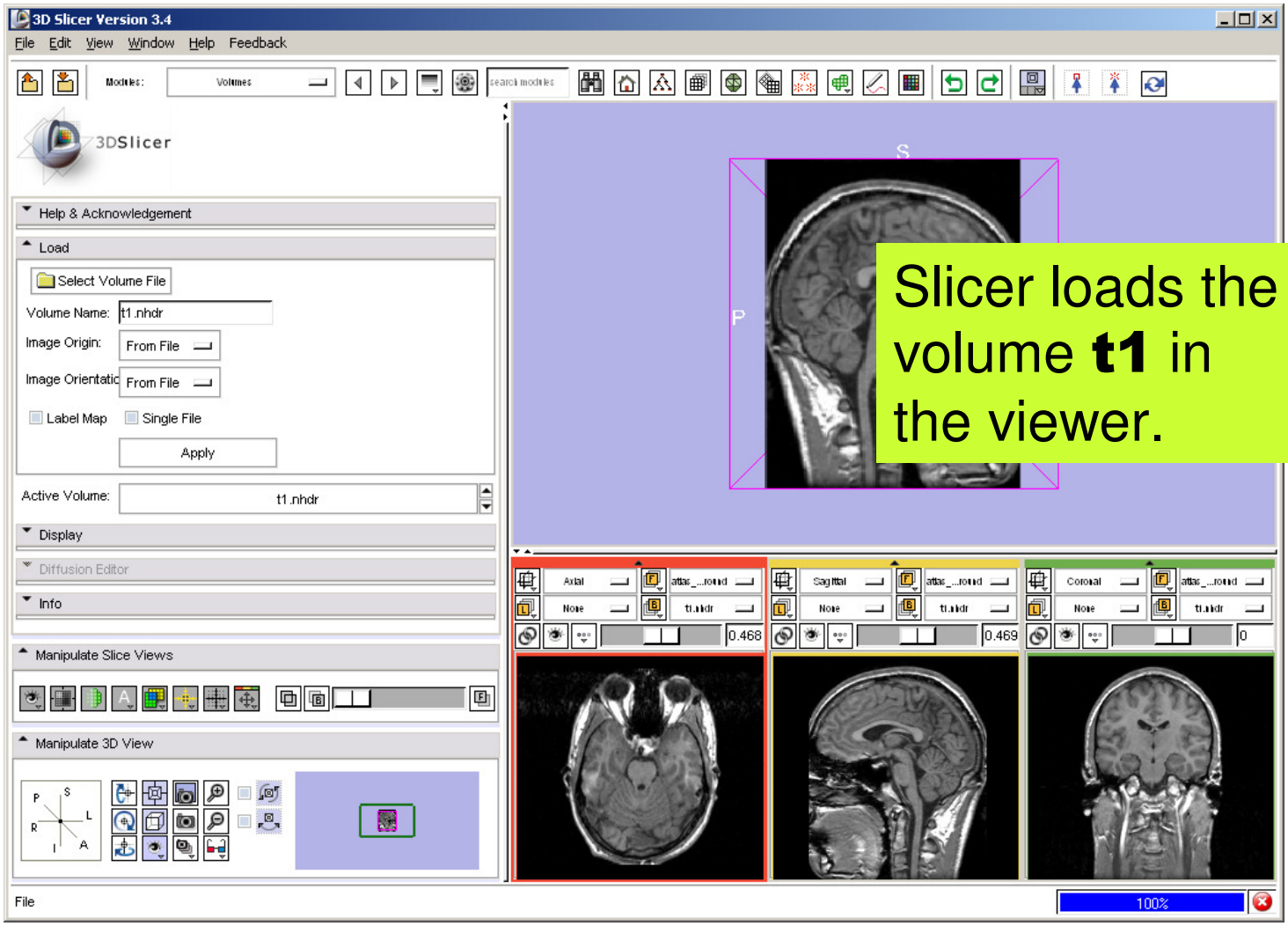
AutomaticSegmentation/t1

and click on **Open**

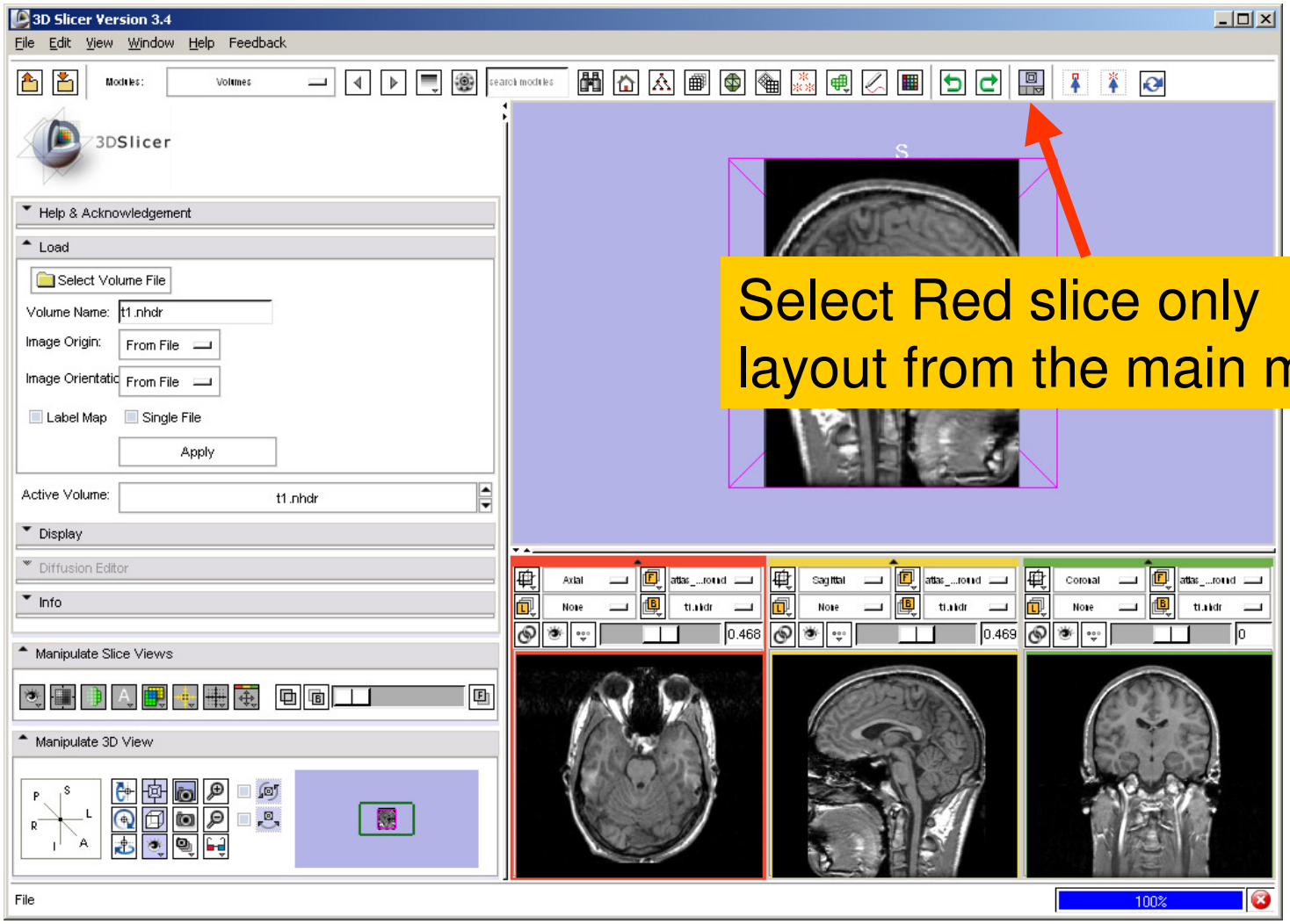
Loading T1 volume



Loading T1 volume

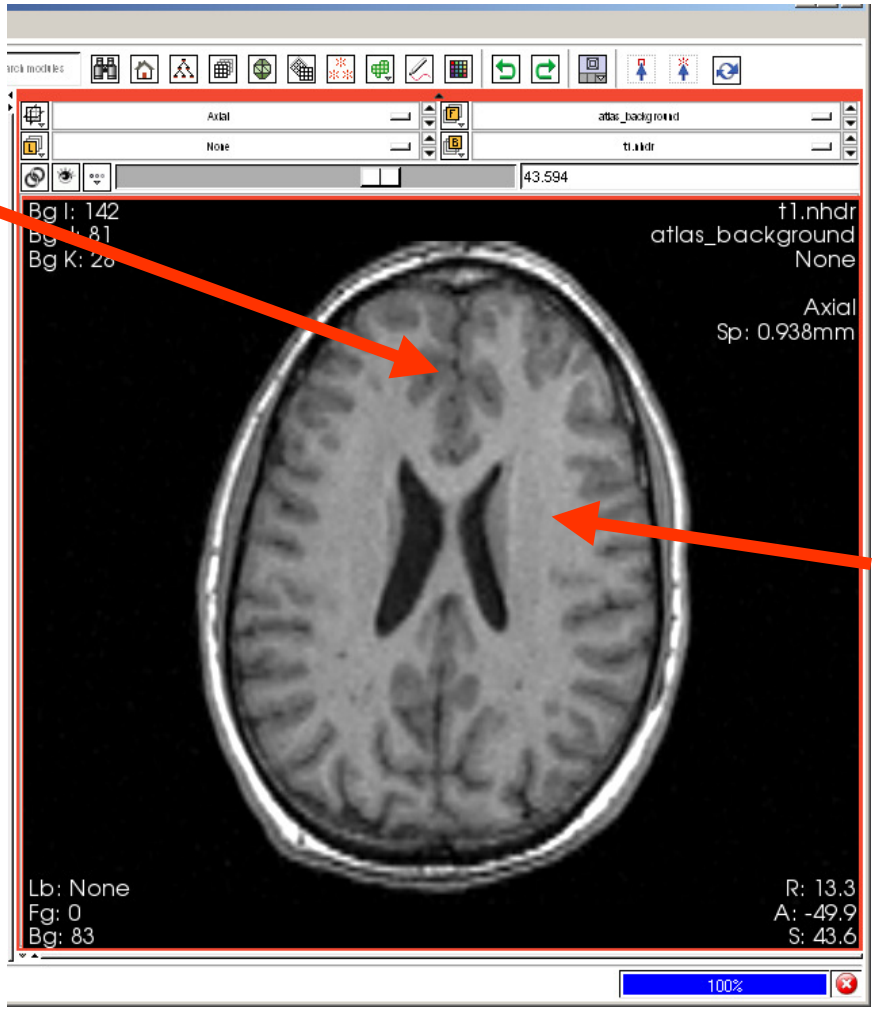


Loading T1 volume



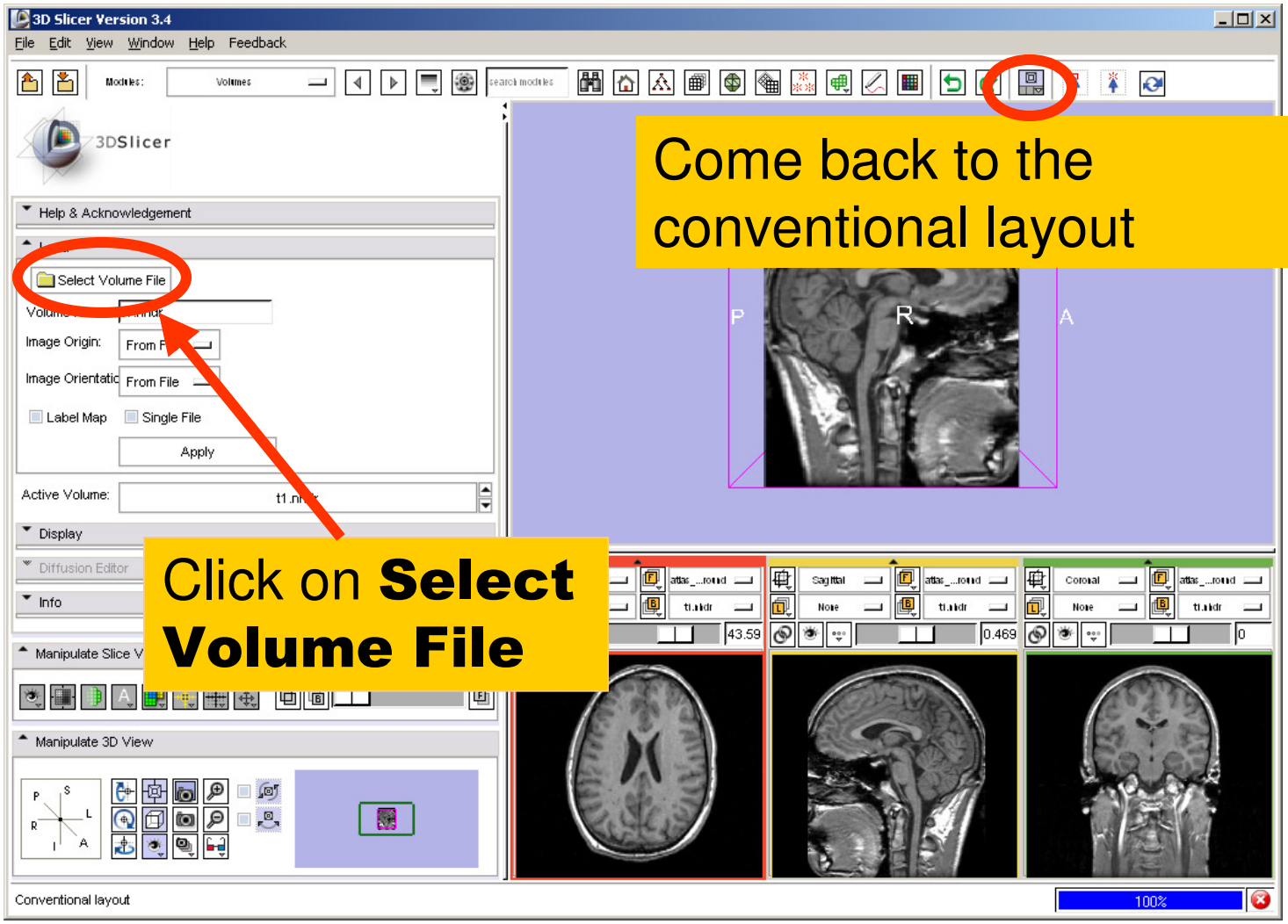
T1 contrast

Grey Matter

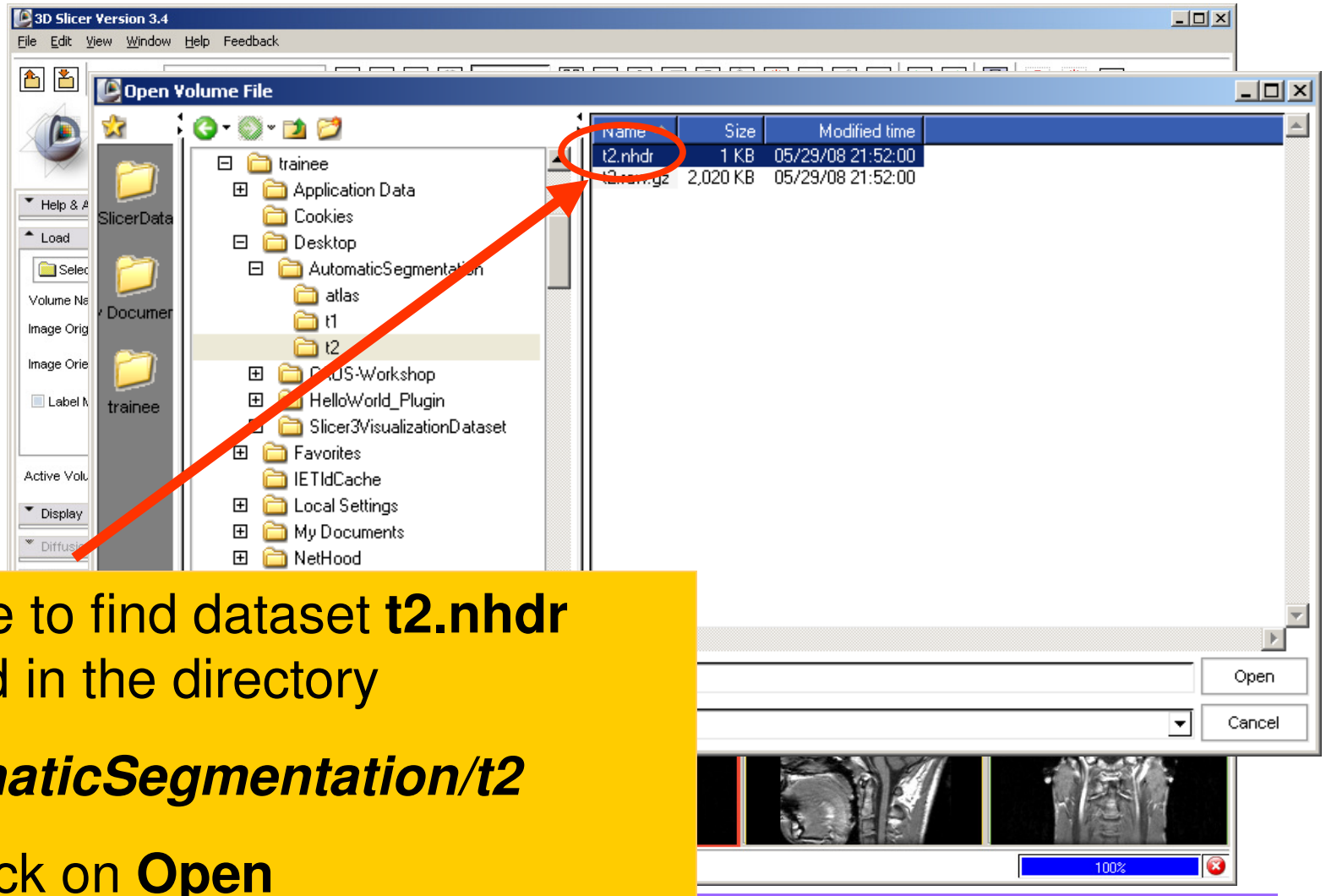


White Matter

Loading T2 volume



Loading T2 volume

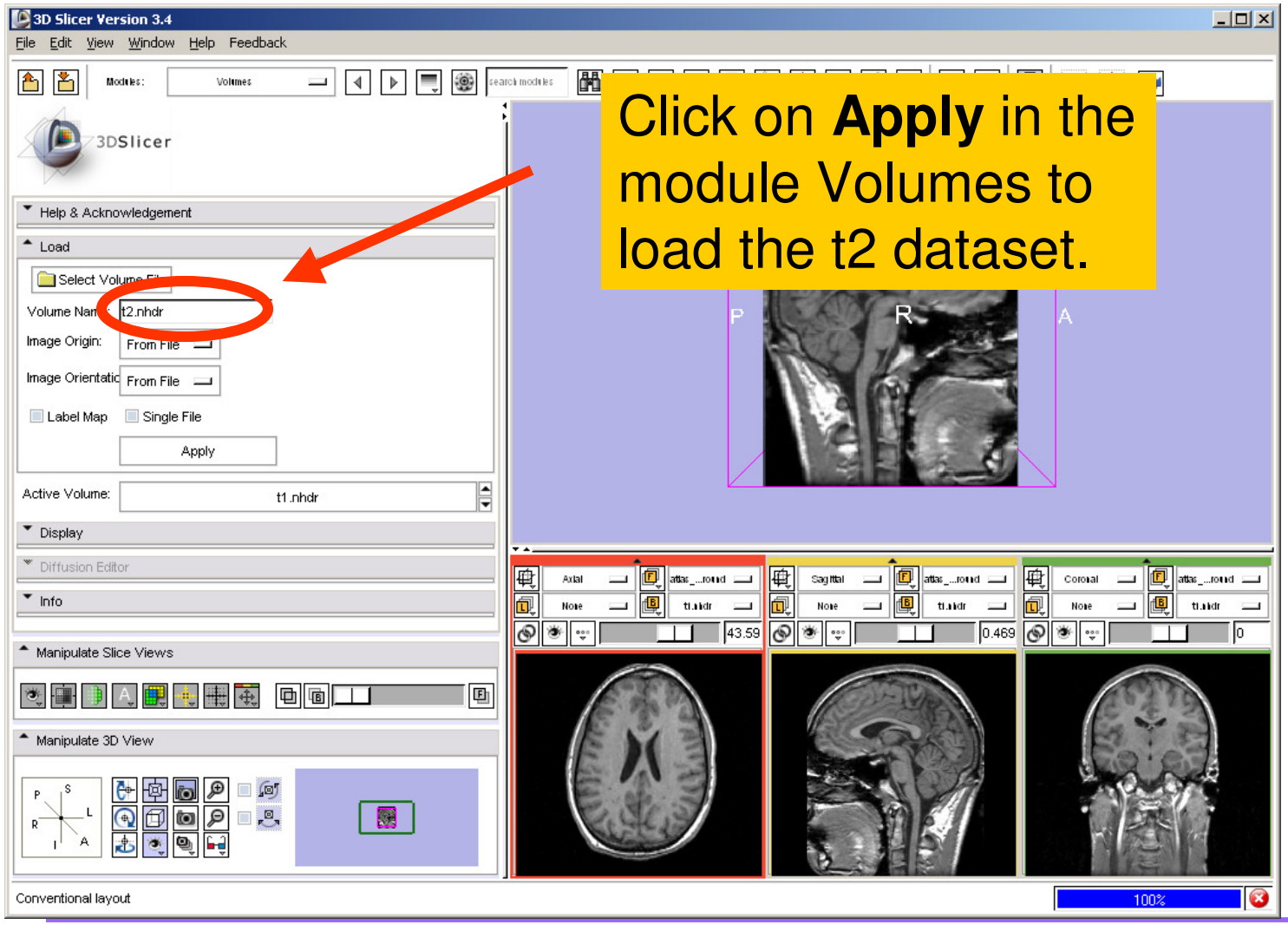


Browse to find dataset **t2.nhdr** located in the directory

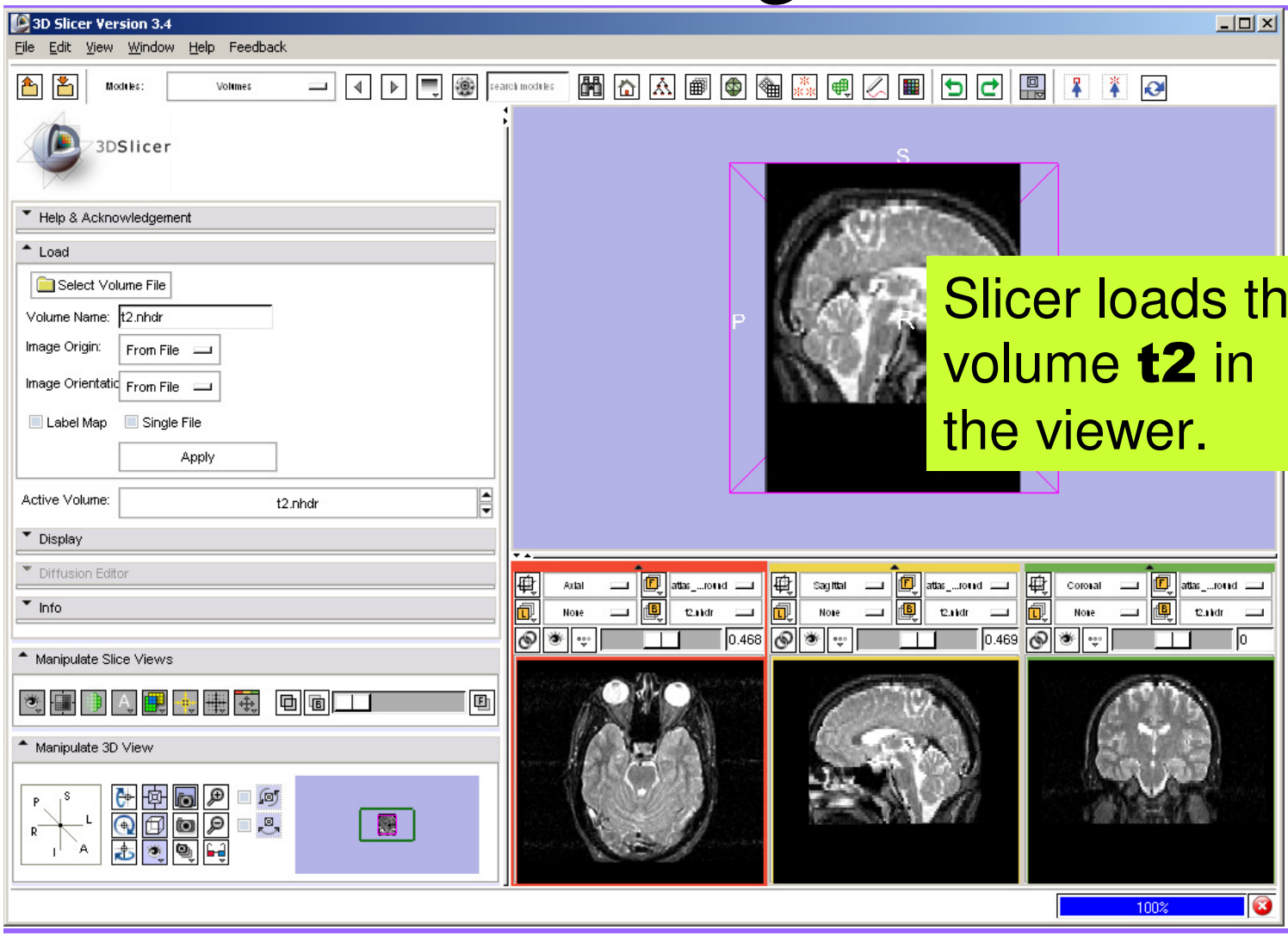
AutomaticSegmentation/t2

and click on **Open**

Loading T2 volume

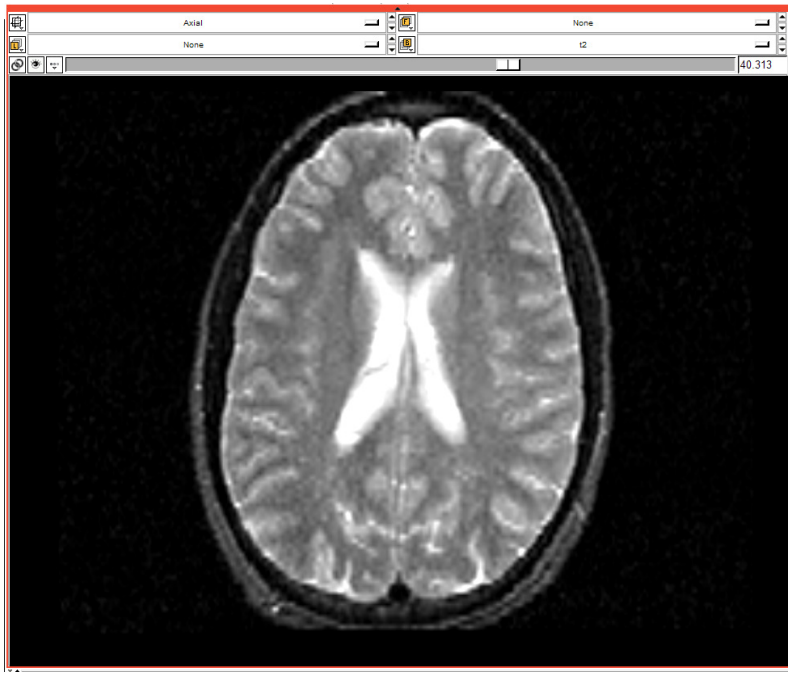


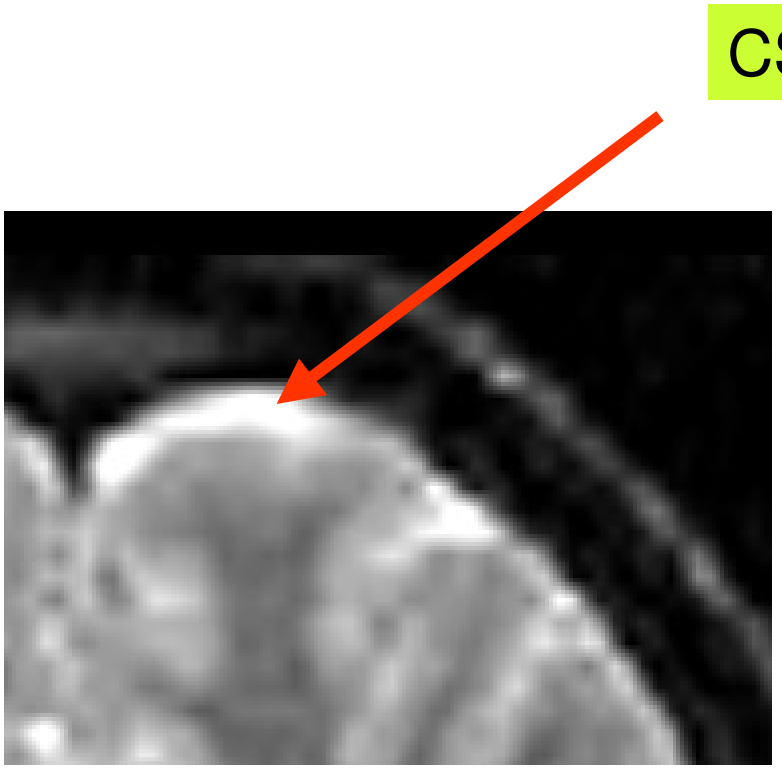
Loading T2 volume



Slicer loads the volume **t2** in the viewer.

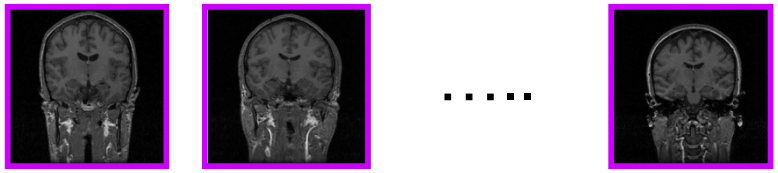
T2 contrast



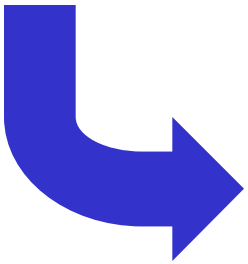


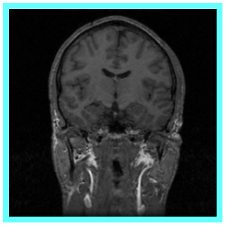
Generic Atlas

S1 S2 ..... Sn

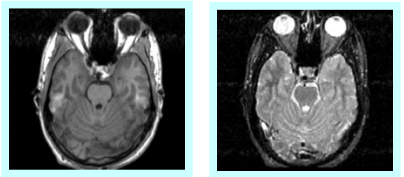


n=82 healthy subjects, ages 25-40



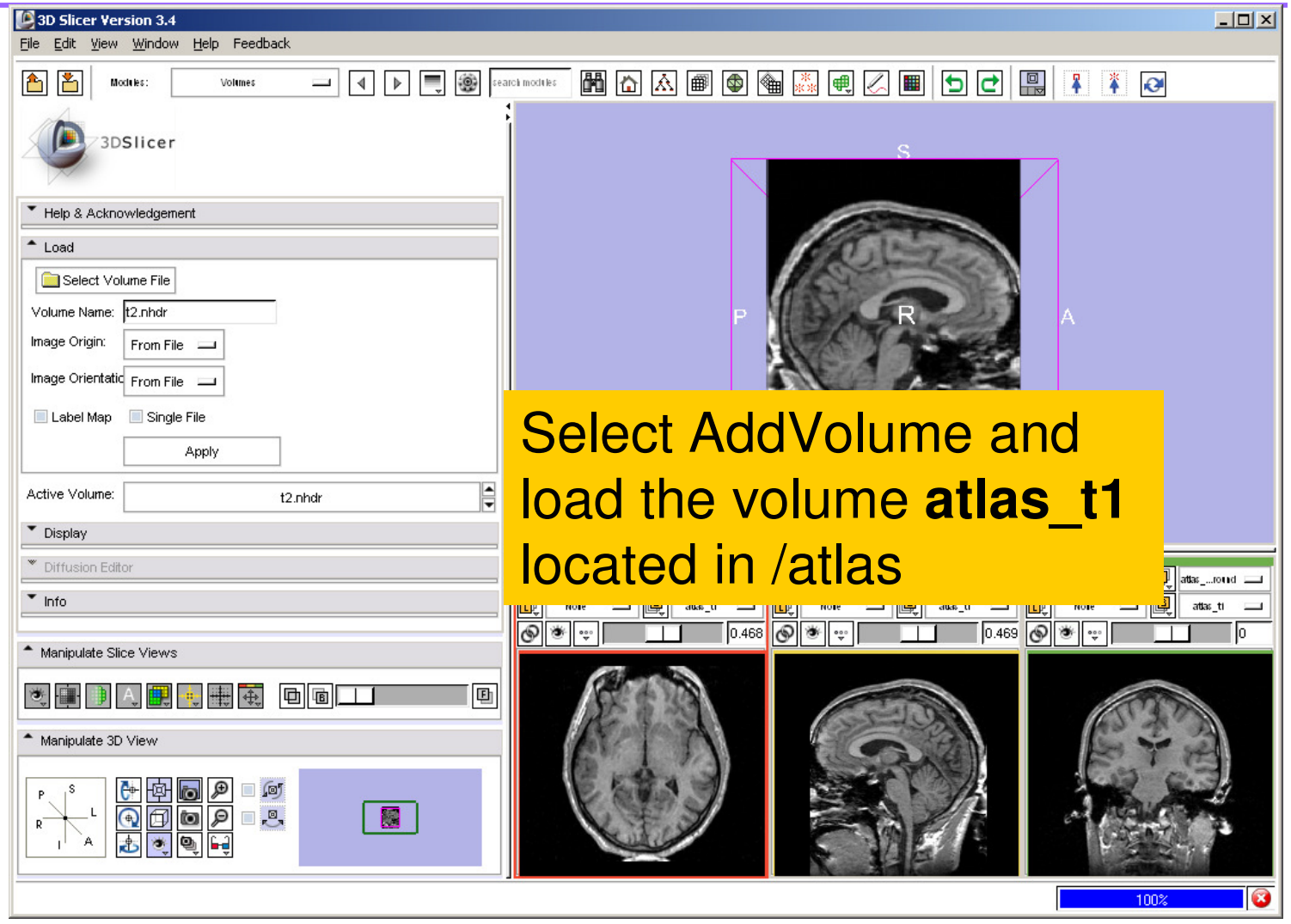


Training subject (randomly chosen)

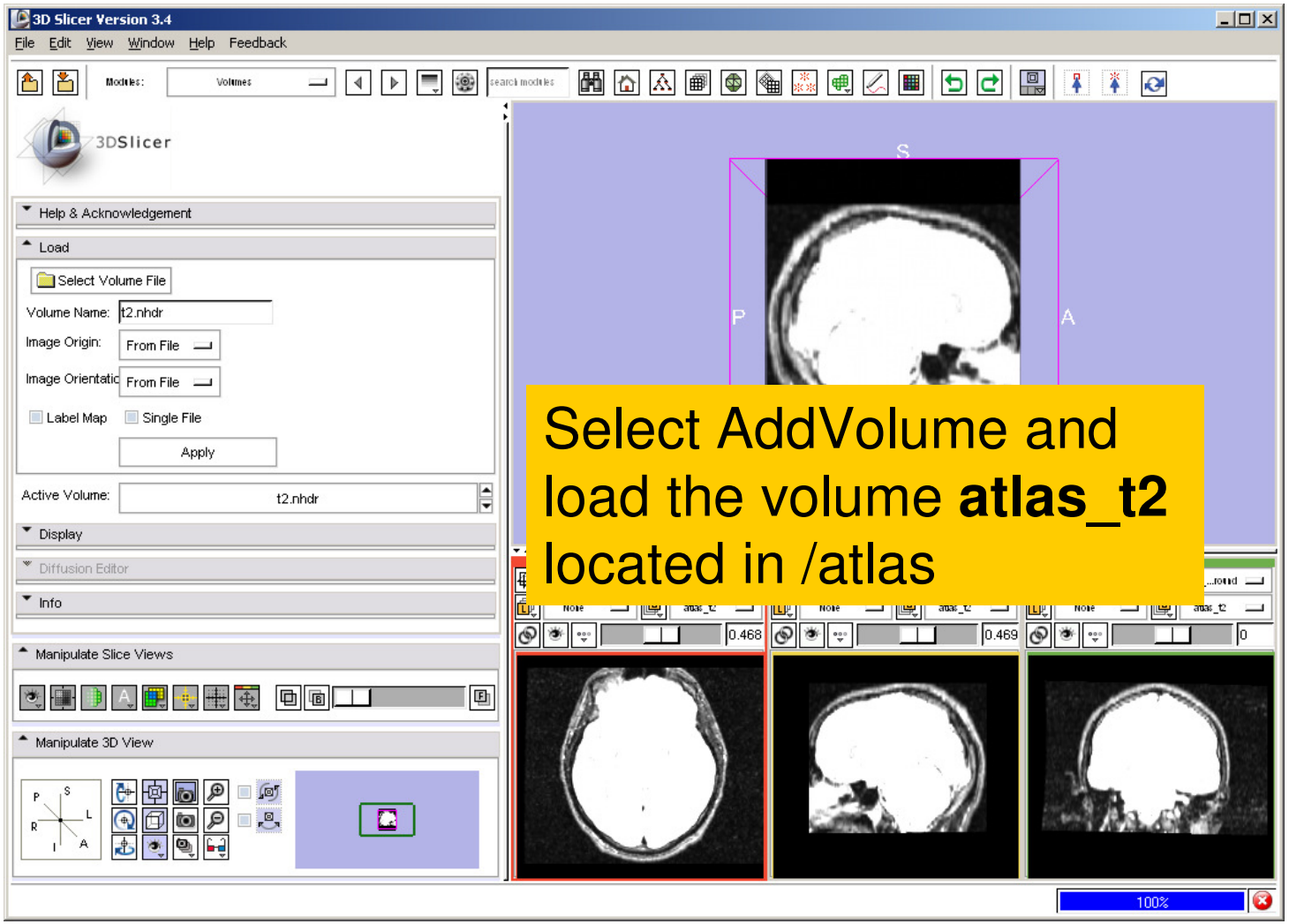


t1 and t2 of the training subject

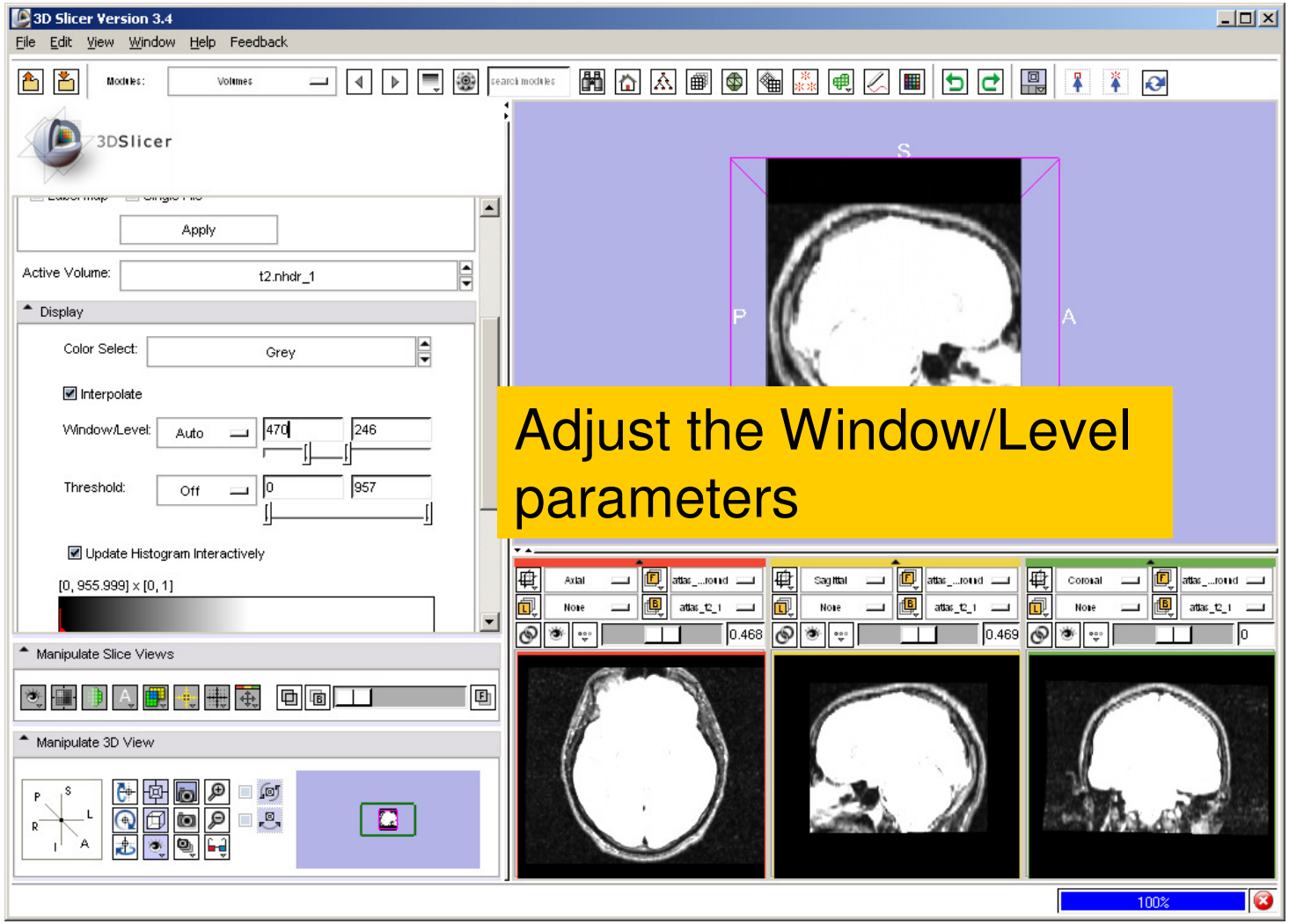
Atlas T1


3D Slicer Version 3.4
File Edit View Window Help Feedback
Modules:
Volumes
3DSlicer
Help & Acknowledgement
Load
Select Volume File
Volume Name:
t2.nhdr
Image Origin:
From File
Image Orientatic
From File
Label Map
Single File
Apply
Active Volume:
t2.nhdr
Display
Diffusion Editor
Info
Manipulate Slice Views
Manipulate 3D View
S
P
R
A
0.468
0.469
100%
Select AddVolume and load the volume **atlas_t1** located in /atlas

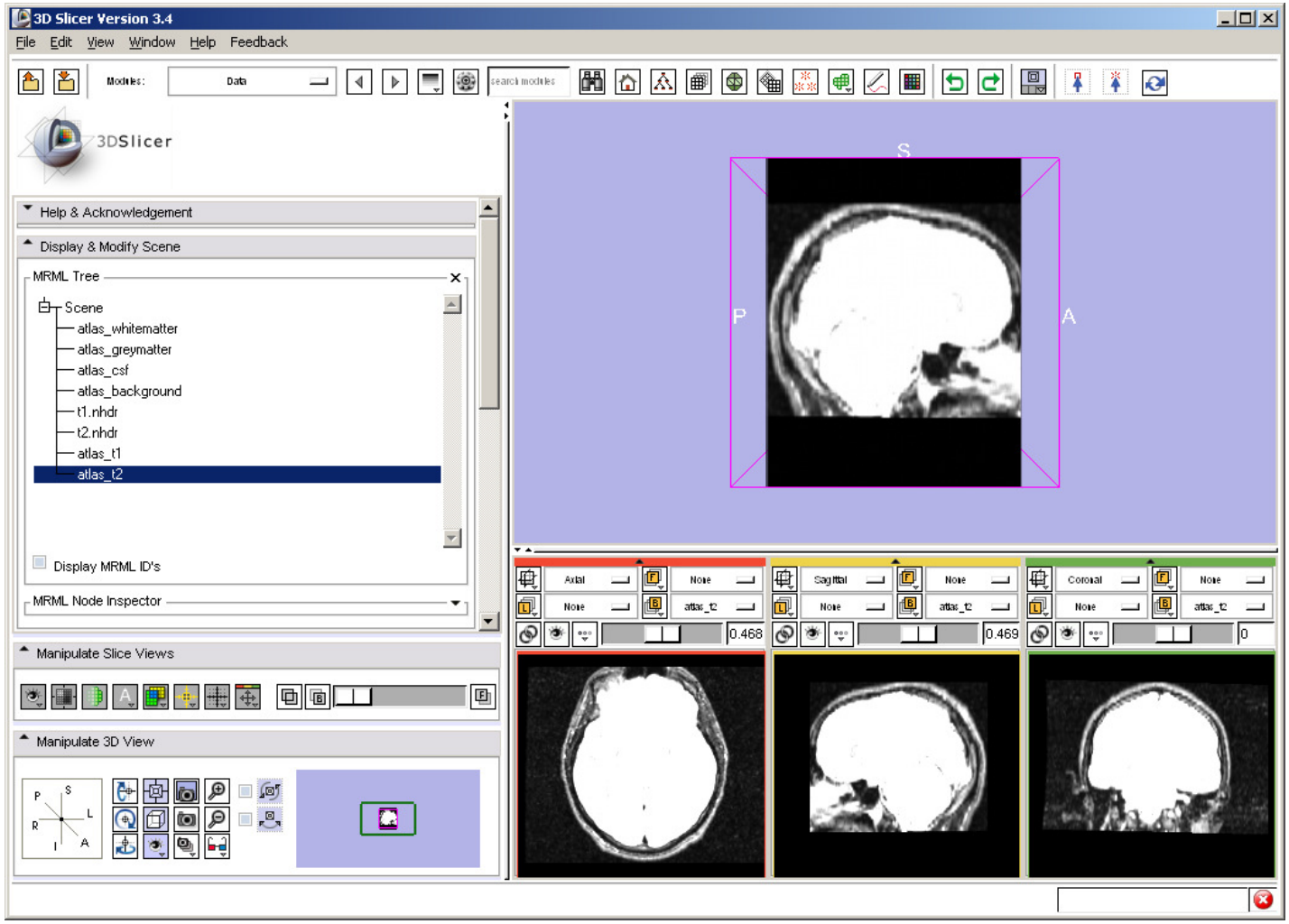
Atlas T2


3D Slicer Version 3.4
File Edit View Window Help Feedback
Modules:
Volumes
3DSlicer
Help & Acknowledgement
Load
Select Volume File
Volume Name: t2.nhdr
Image Origin: From File
Image Orientatic From File
Label Map
Single File
Apply
Active Volume: t2.nhdr
Display
Diffusion Editor
Info
Manipulate Slice Views
Manipulate 3D View
S
P
A
Select AddVolume and load the volume **atlas_t2** located in /atlas
0.468
0.469
100%

Atlas T2

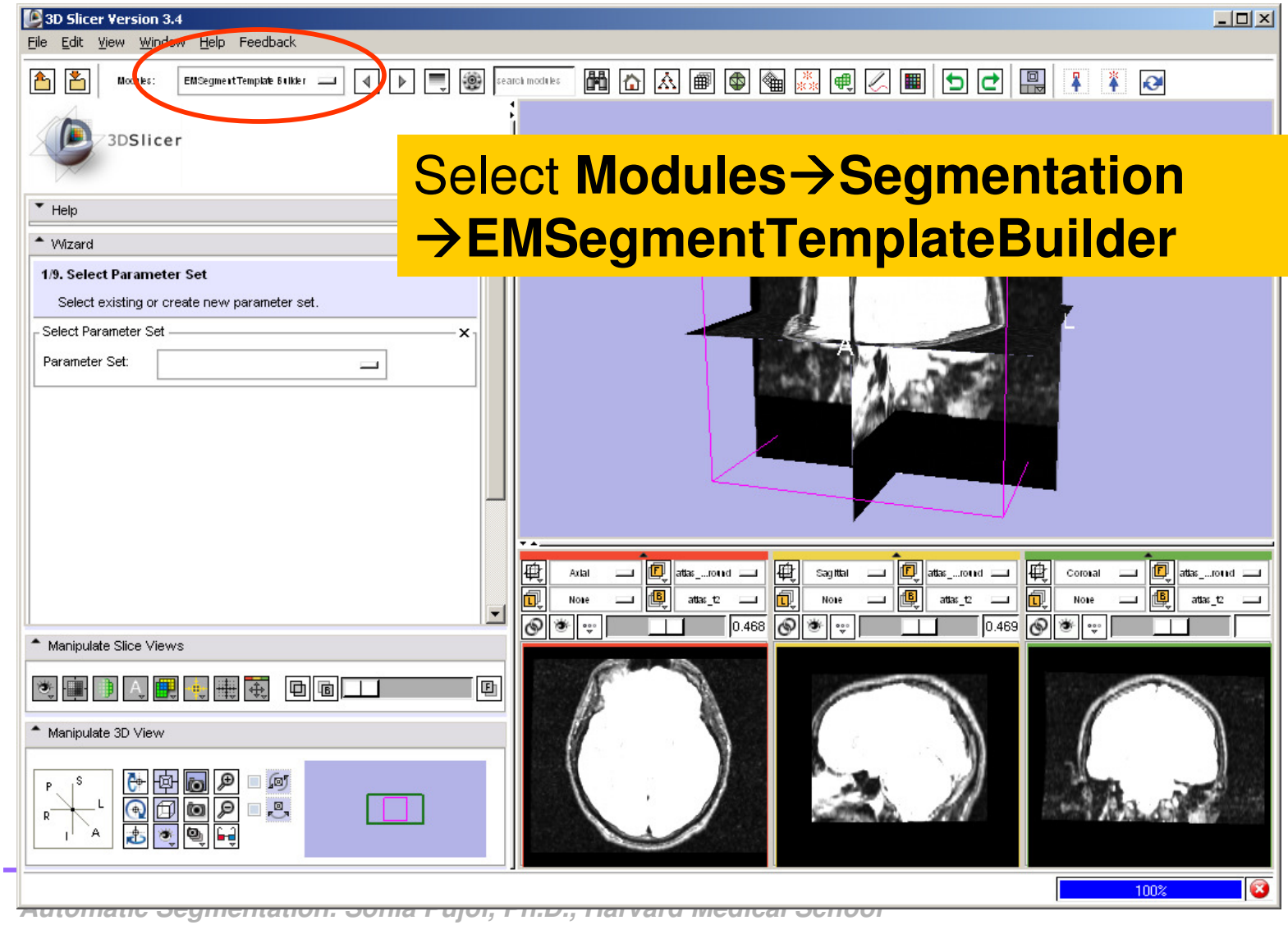

3D Slicer Version 3.4
File Edit View Window Help Feedback
Modules:
Volumes
3DSlicer
Apply
Active Volume:
t2.nhdr_1
Display
Color Select:
Grey
Interpolate
Window/Level:
Auto
470
246
Threshold:
Off
0
957
Update Histogram Interactively
[0, 955.999] x [0, 1]
Manipulate Slice Views
Manipulate 3D View
S
P
A
Adjust the Window/Level parameters
Axial
Sagittal
Coronal
None
0.468
0.469
100%

Training Datasets



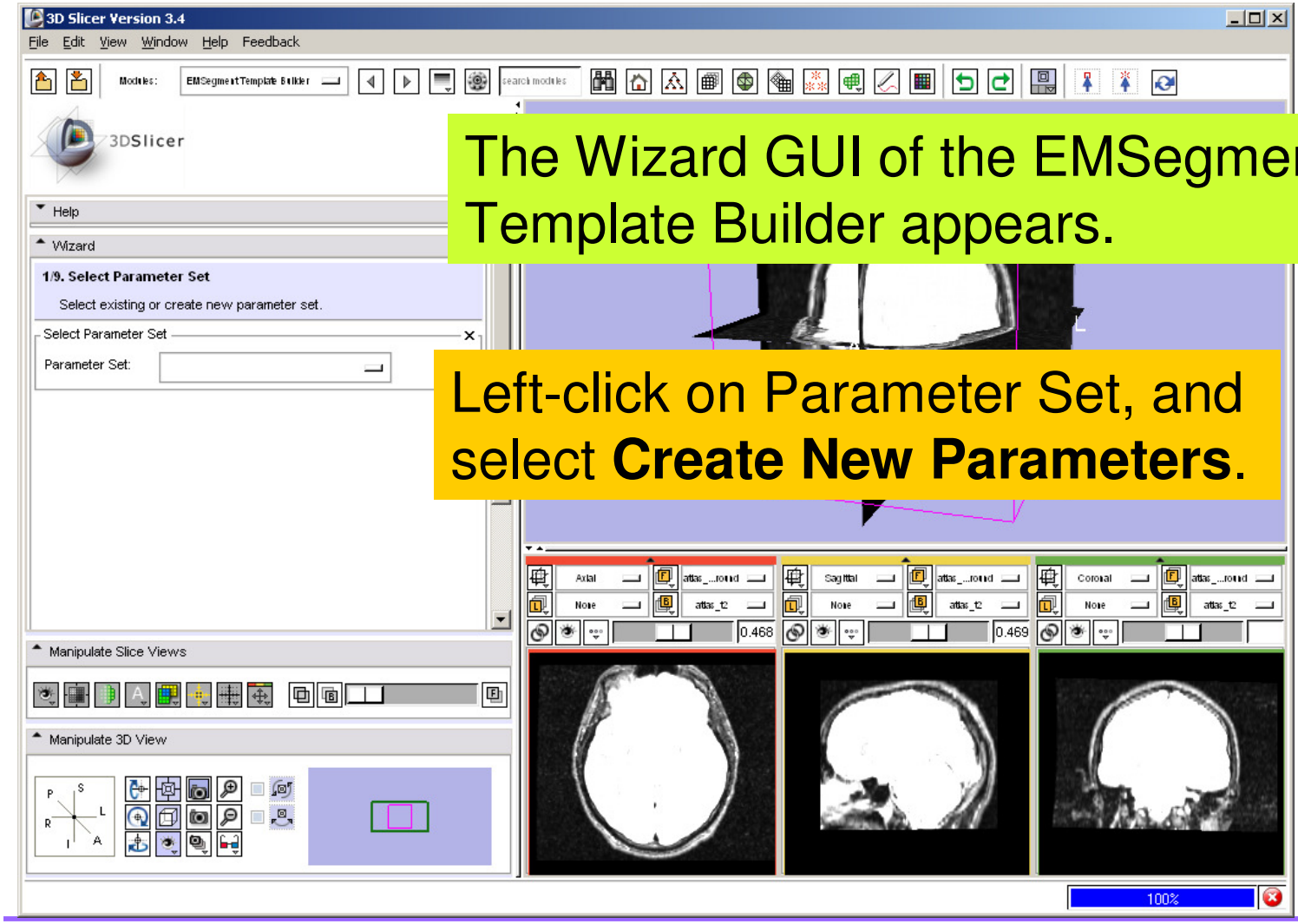
Template Builder: Parameters Settings

Template Builder



Select **Modules→Segmentation →EMSegmentTemplateBuilder**

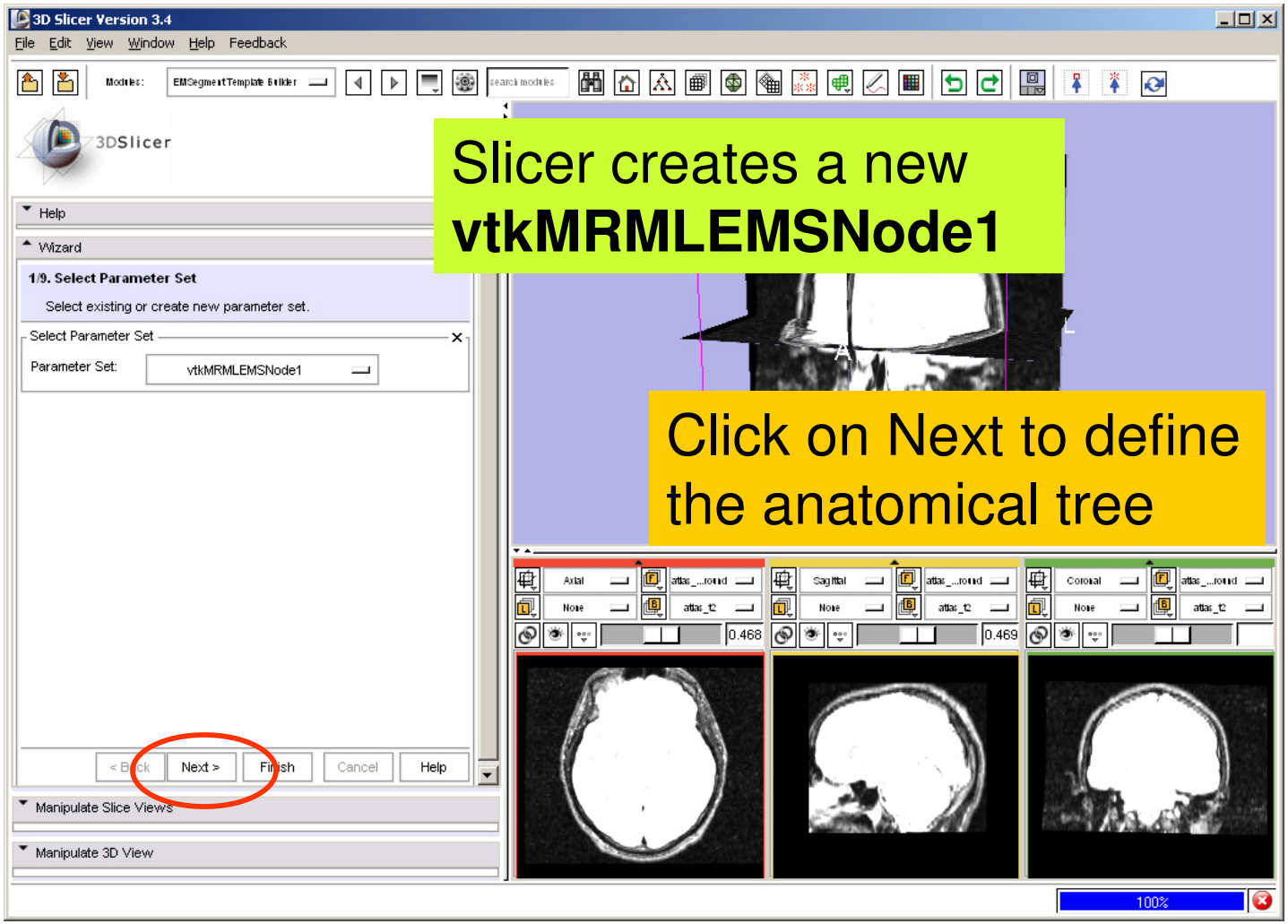
Template Builder



The Wizard GUI of the EMSegment Template Builder appears.

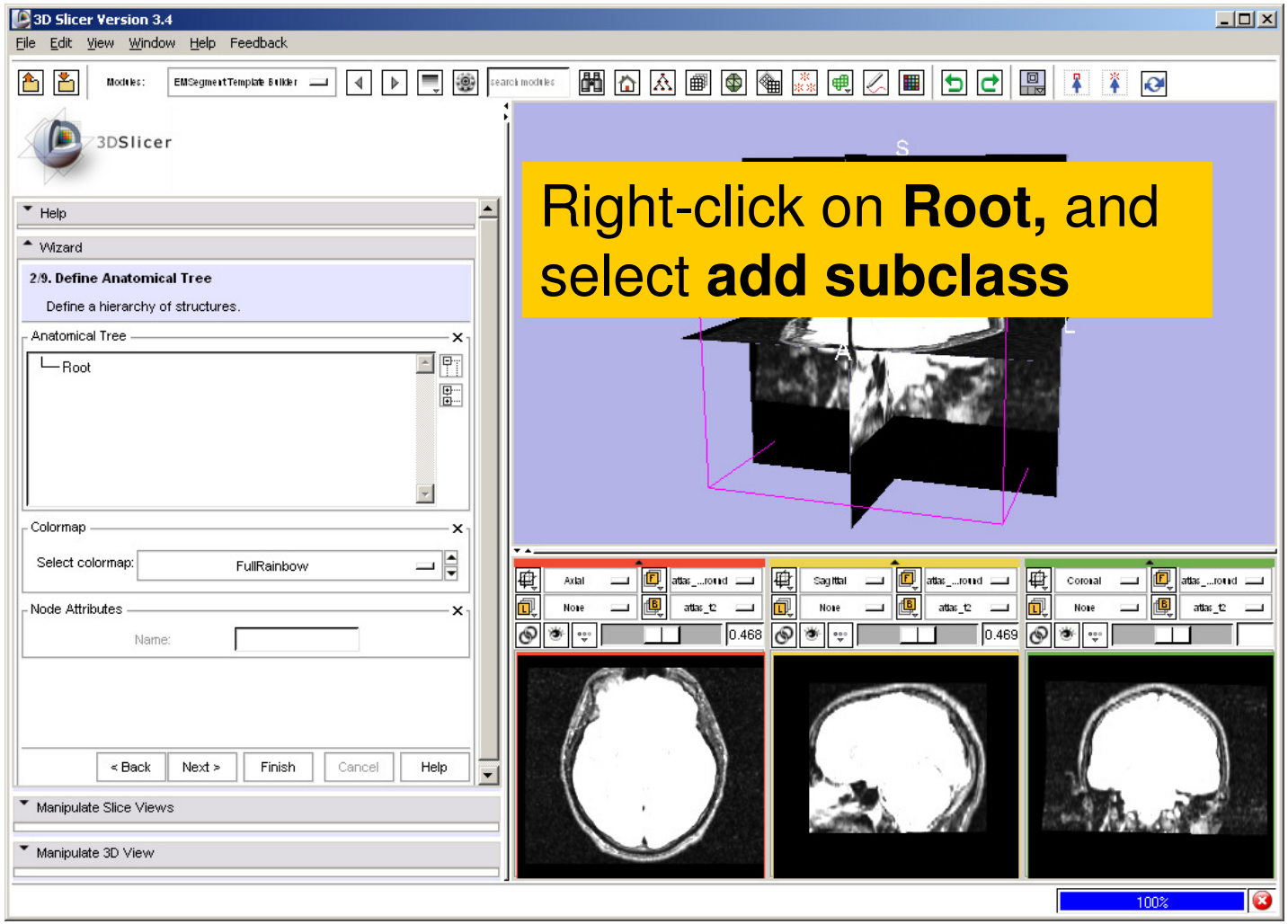
Left-click on Parameter Set, and select **Create New Parameters**.

Template Builder

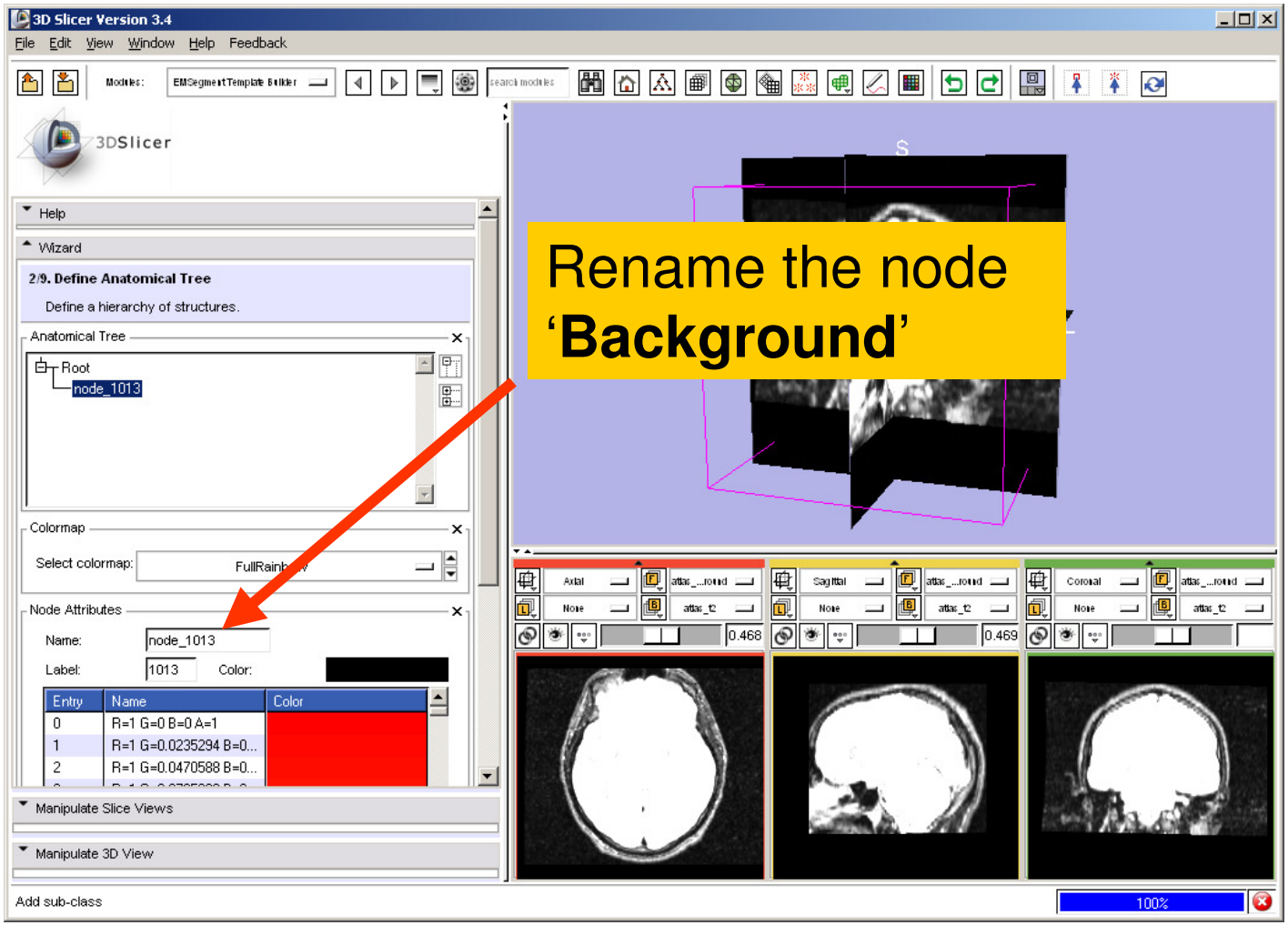


Anatomical Tree

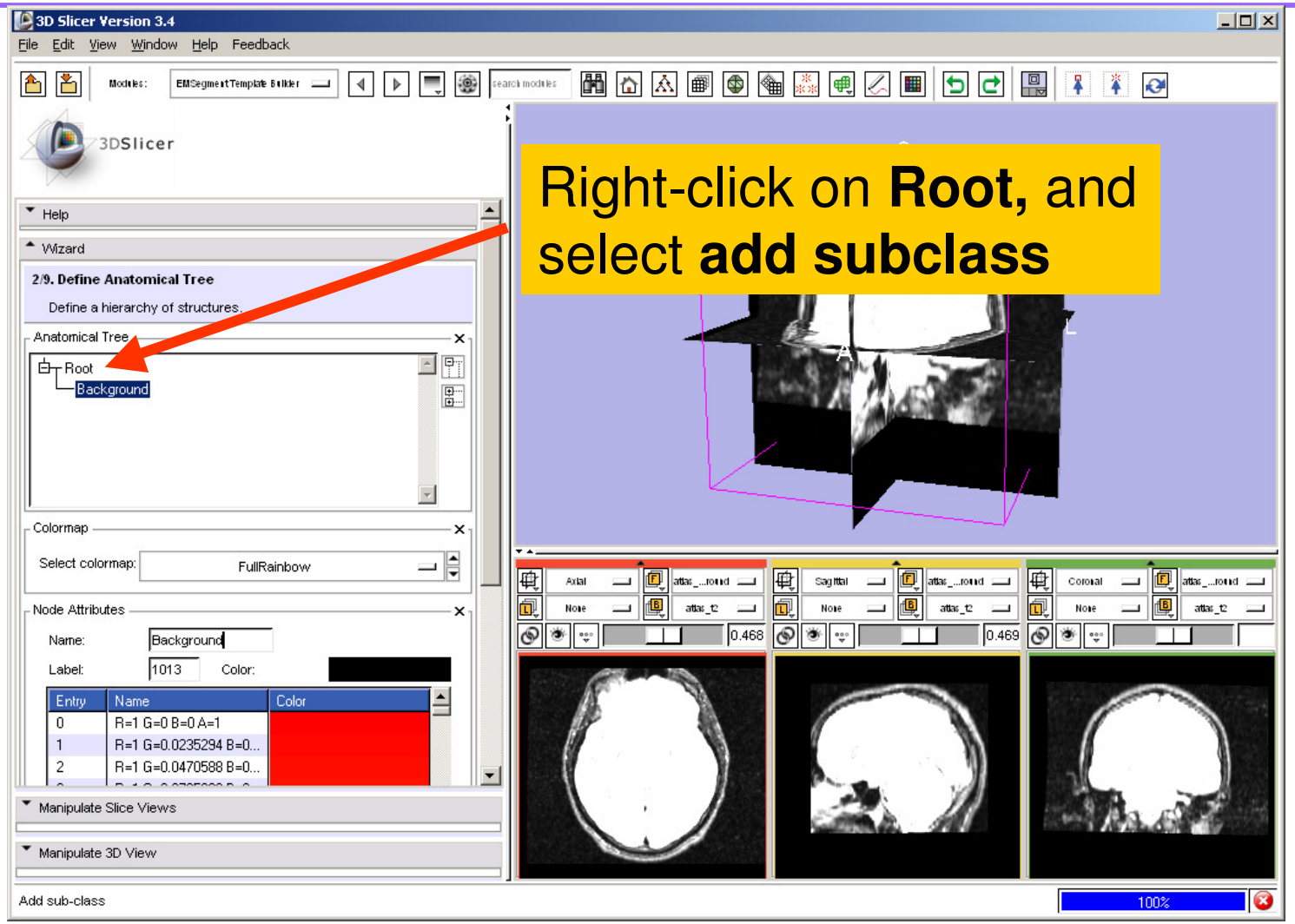
Anatomical Tree



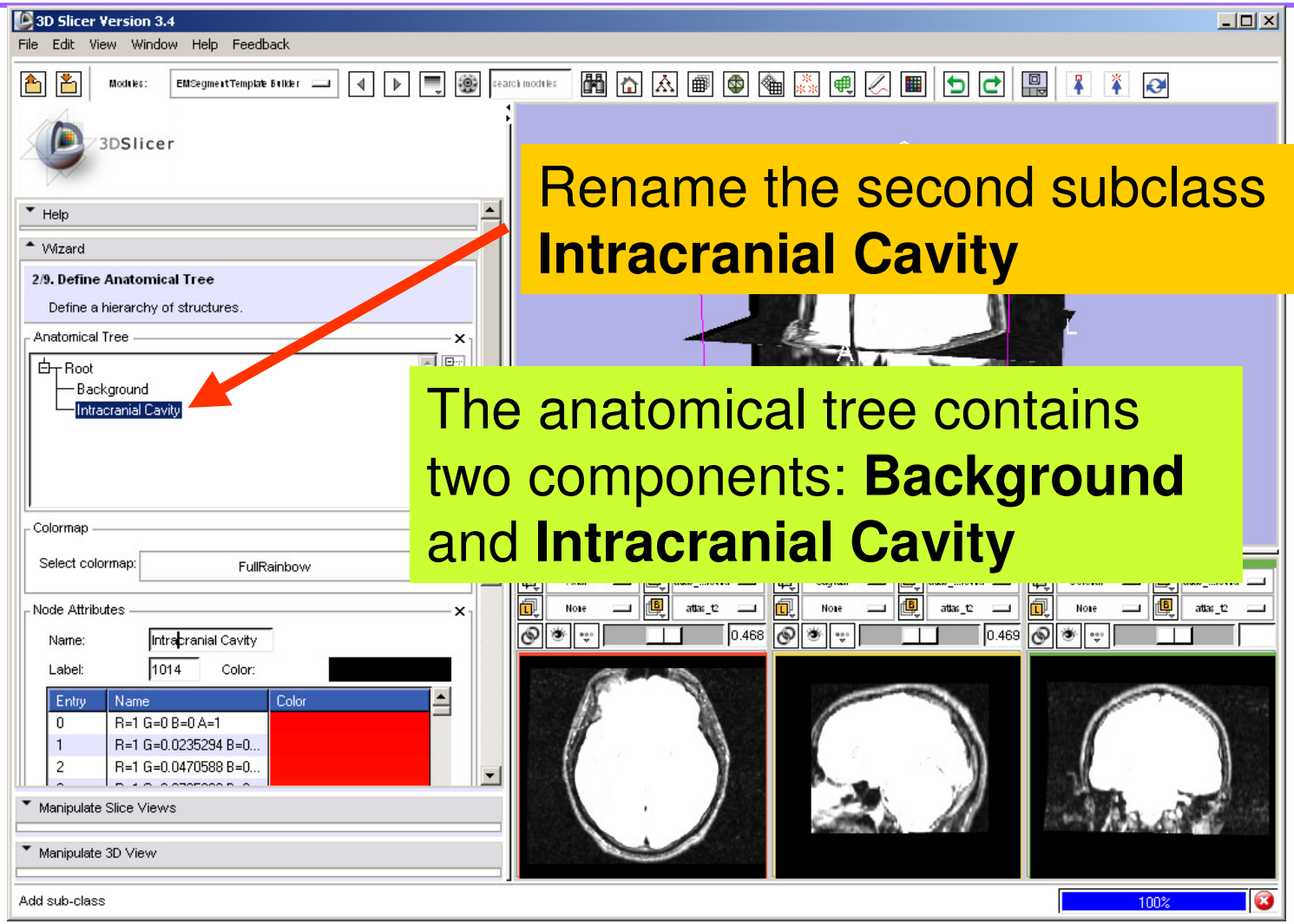
Anatomical Tree



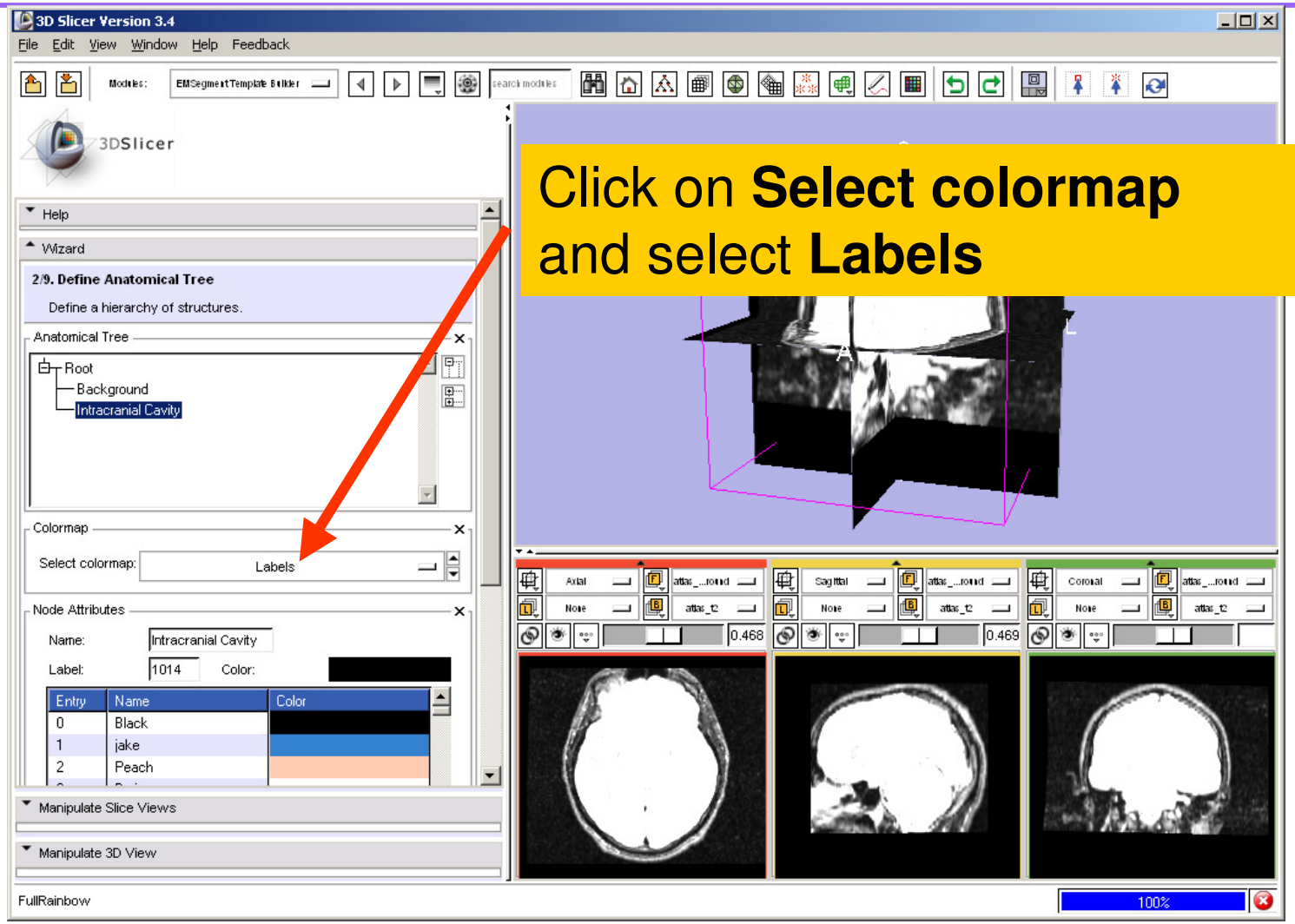
Anatomical Tree



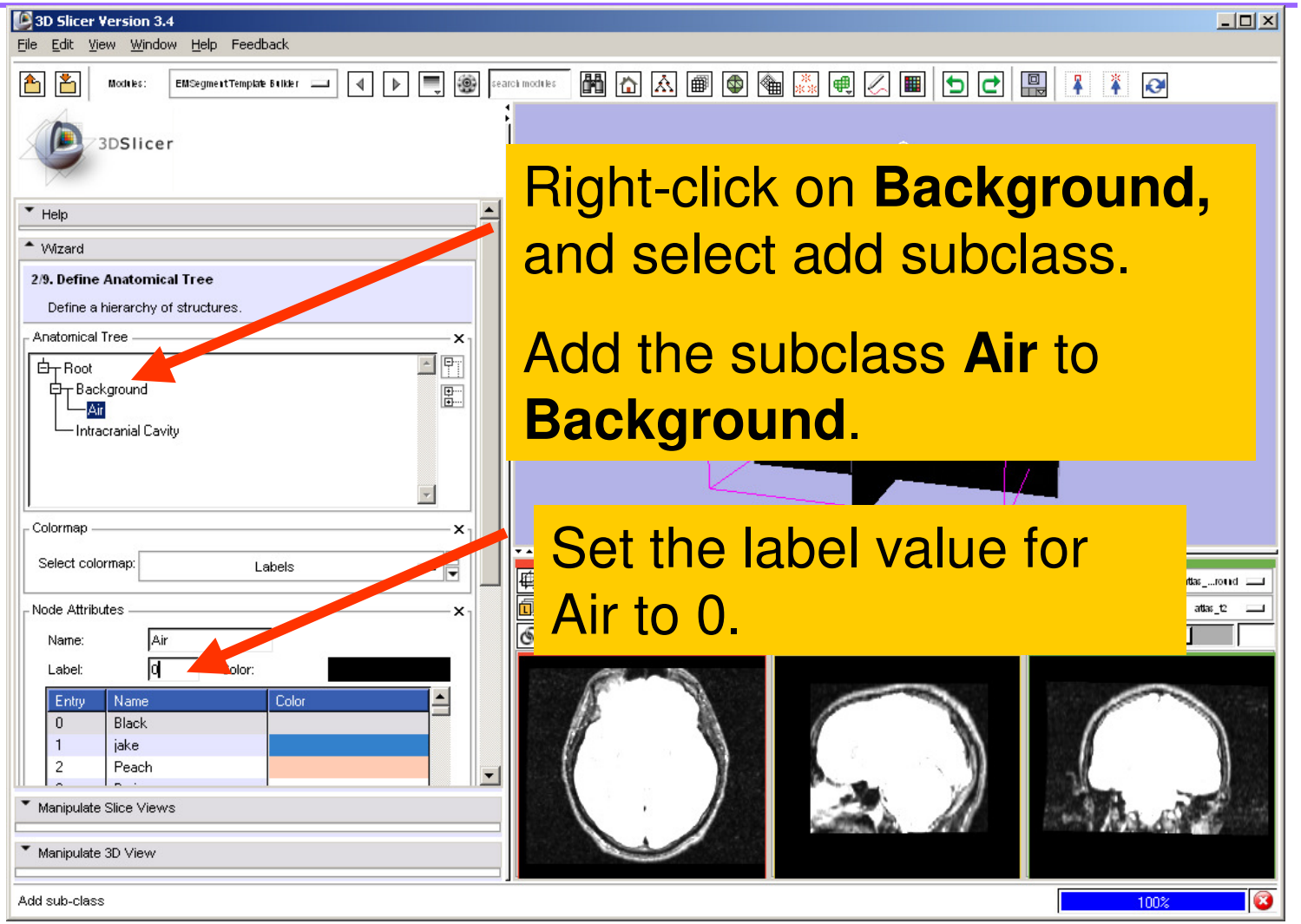
Anatomical Tree



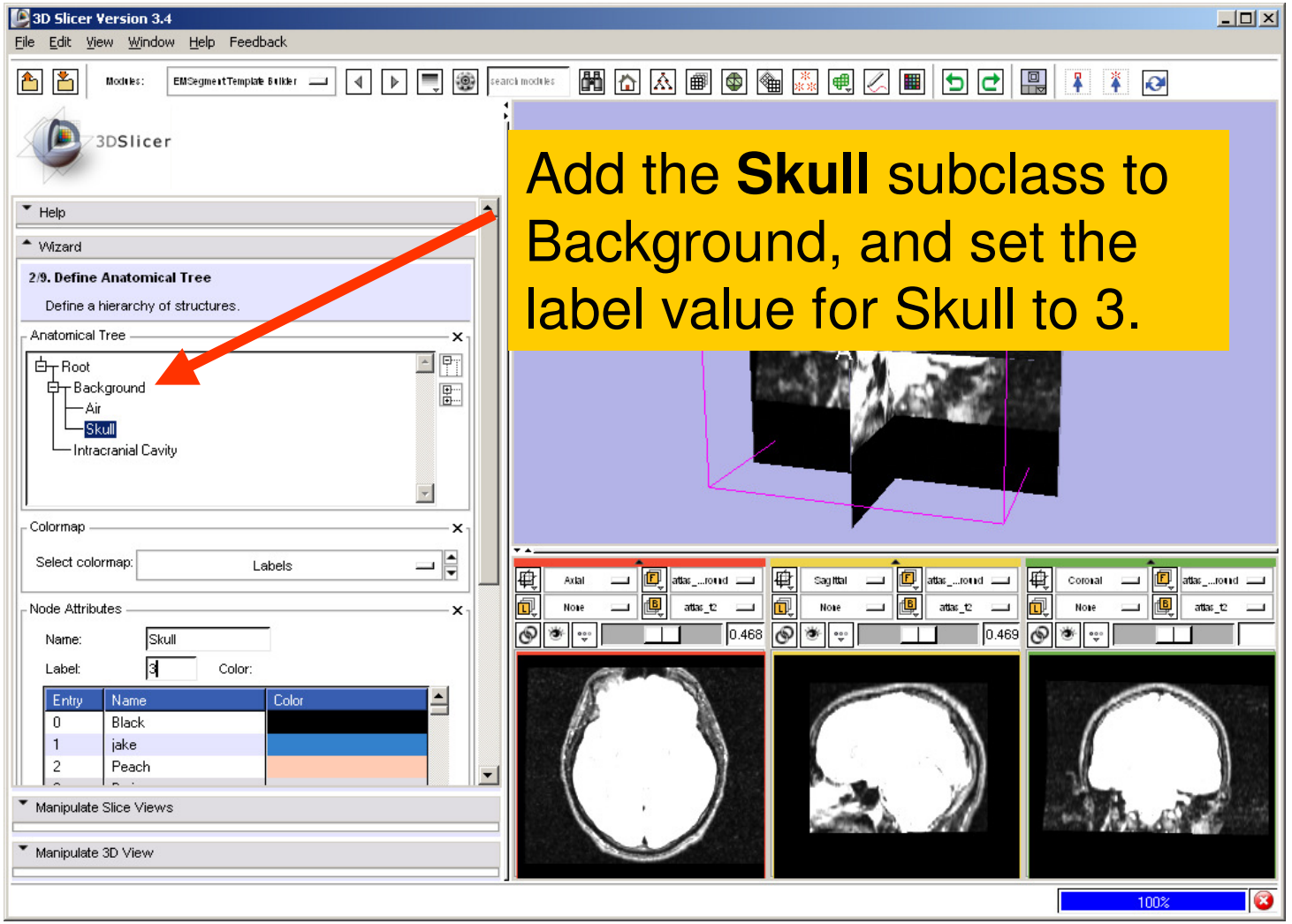
Anatomical Tree



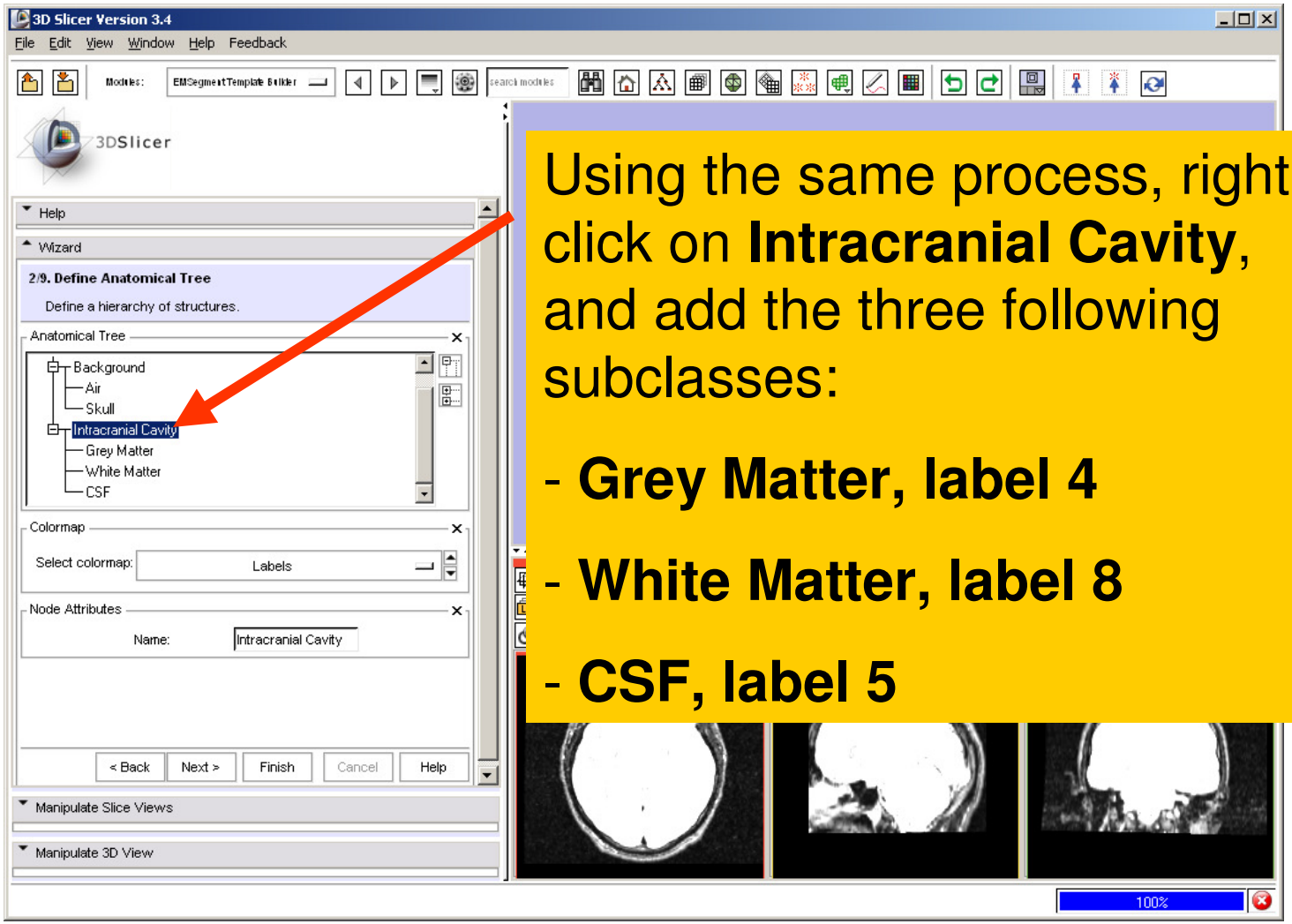
Anatomical Tree



Anatomical Tree



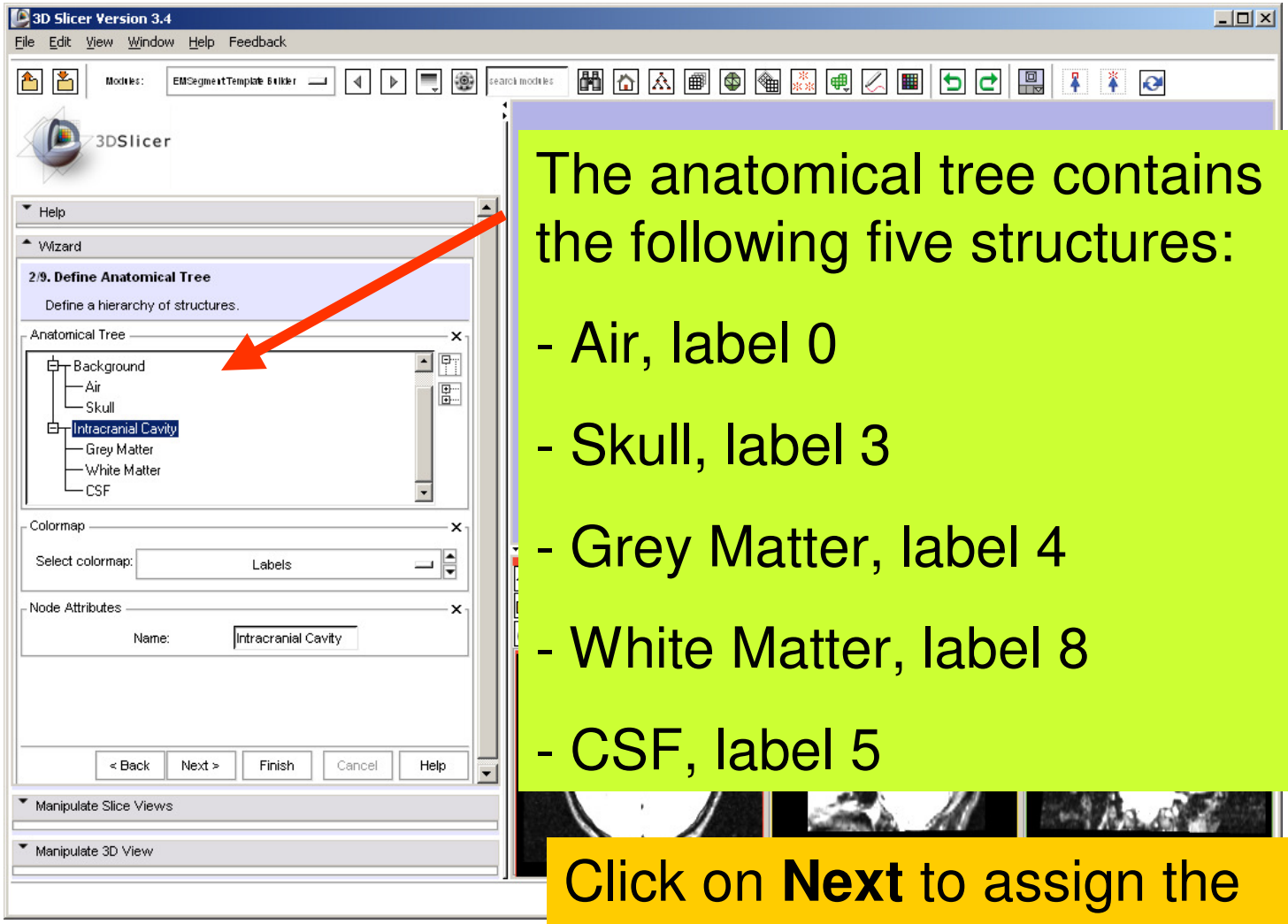
Anatomical Tree



Using the same process, right-click on **Intracranial Cavity**, and add the three following subclasses:

- **Grey Matter, label 4**
- **White Matter, label 8**
- **CSF, label 5**

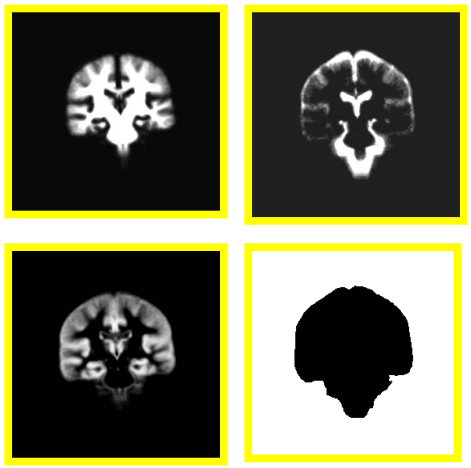
Anatomical Tree



The anatomical tree contains the following five structures:

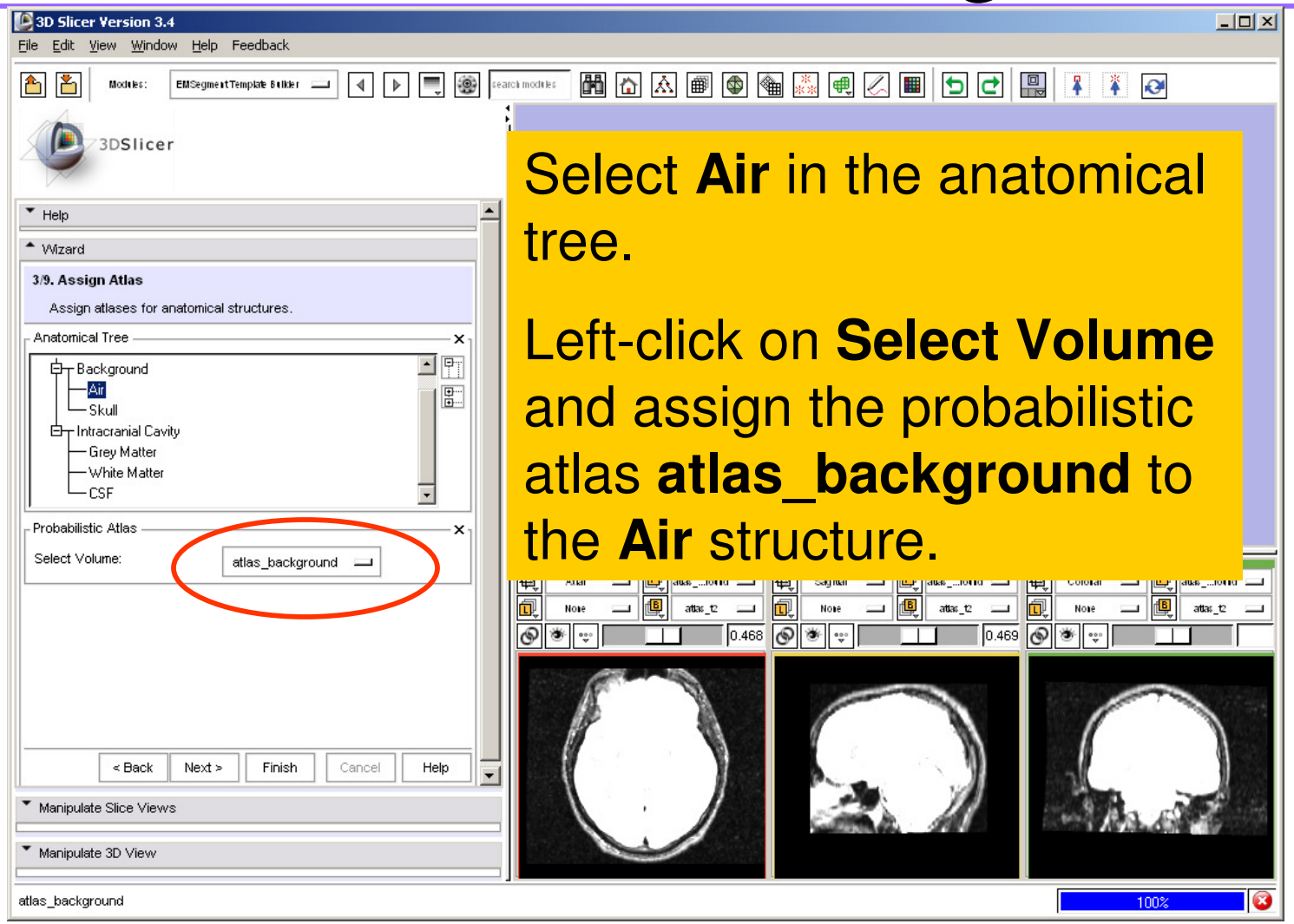
- Air, label 0
- Skull, label 3
- Grey Matter, label 4
- White Matter, label 8
- CSF, label 5

Click on **Next** to assign the atlas to the structures



Atlas Assignment

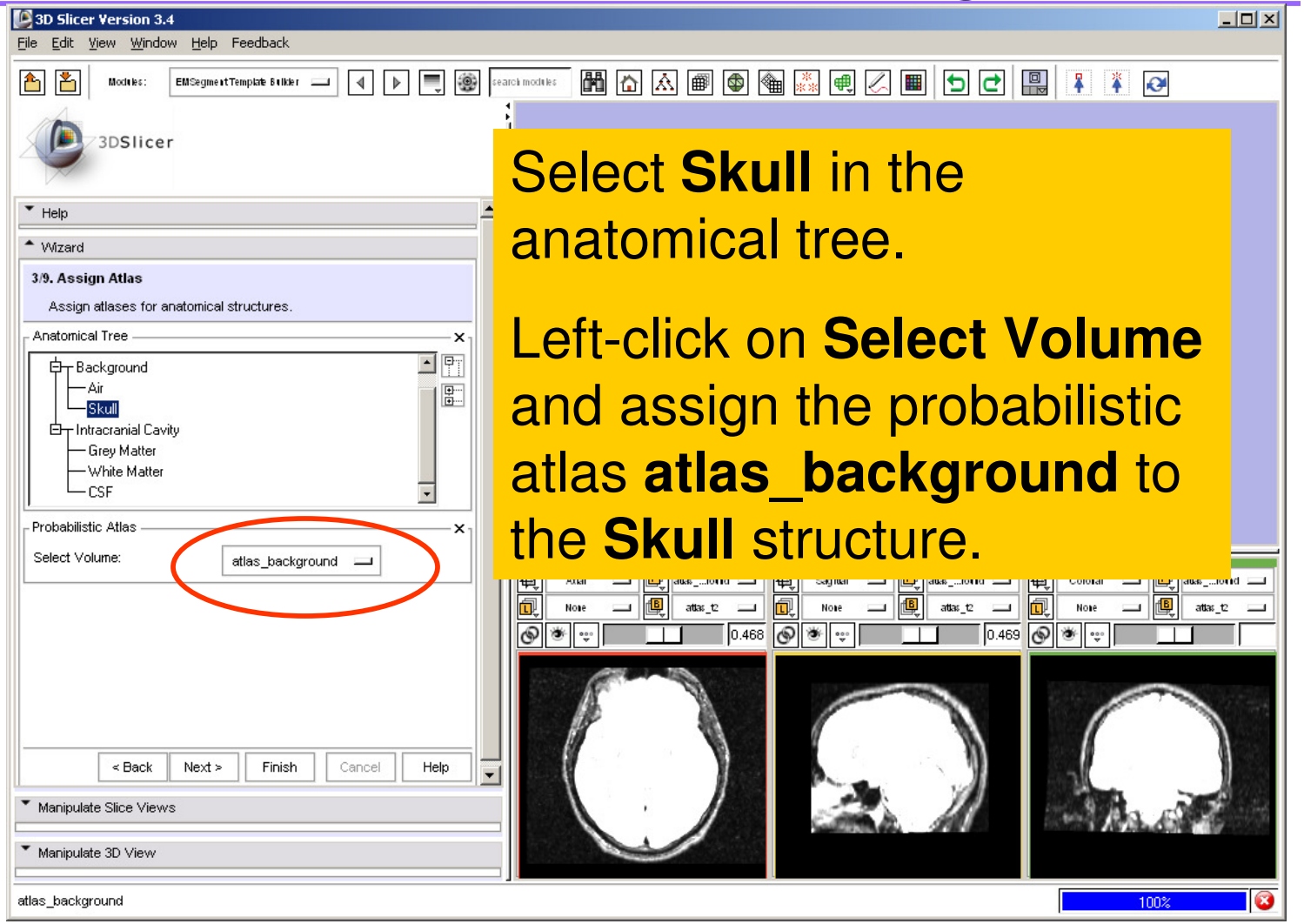
Atlas Assignment



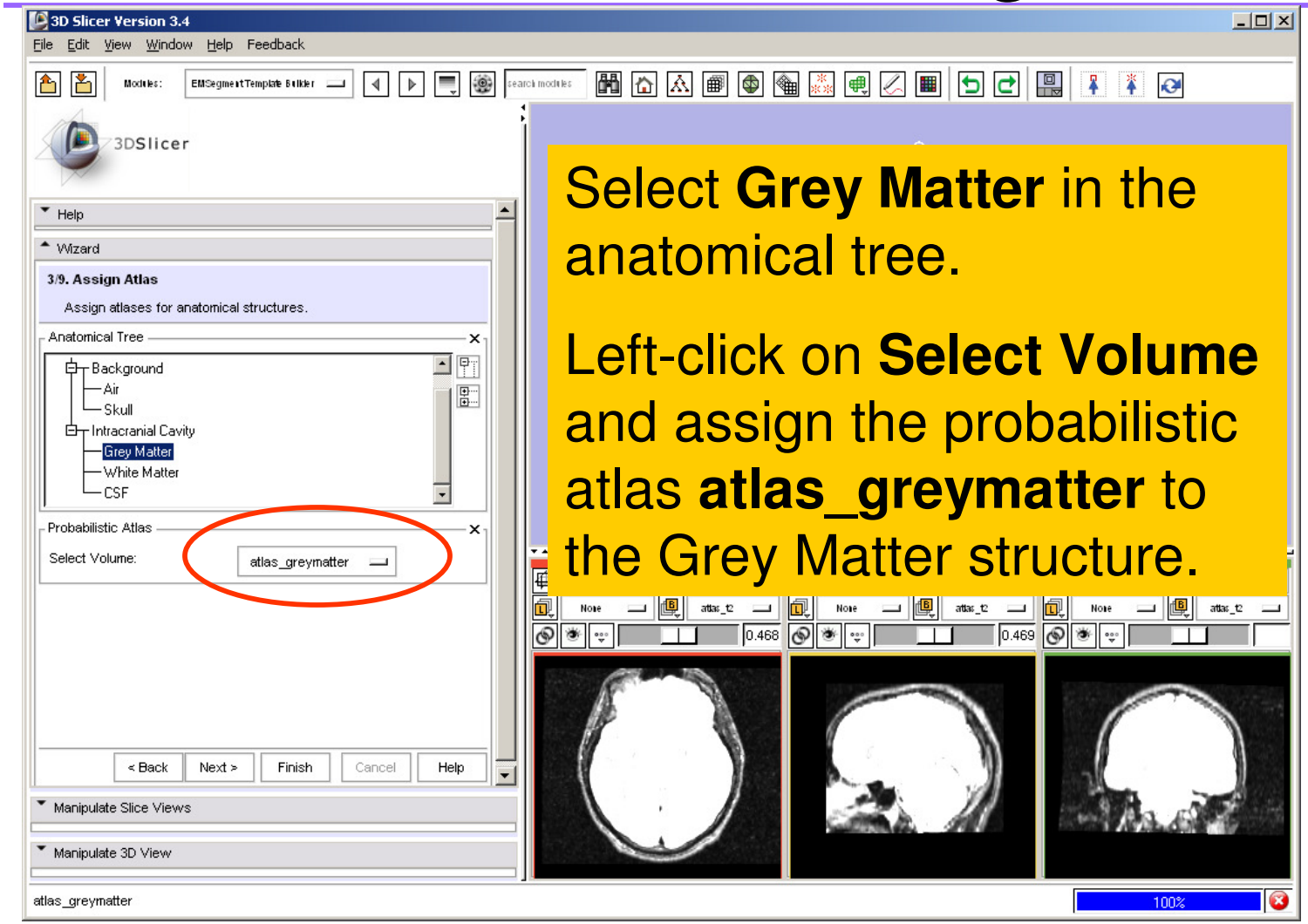
Select **Air** in the anatomical tree.

Left-click on **Select Volume** and assign the probabilistic atlas **atlas_background** to the **Air** structure.

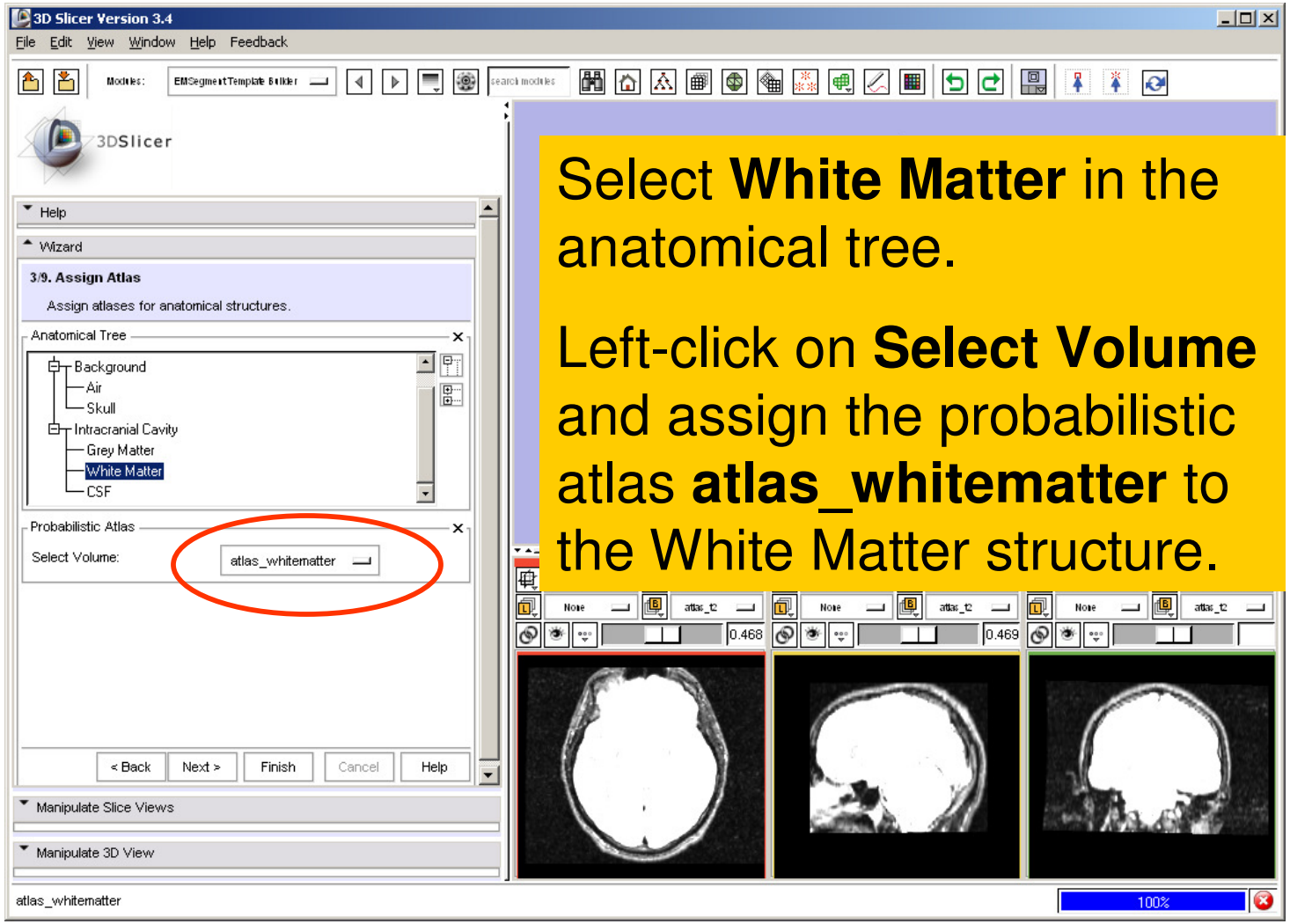
Atlas Assignment



Atlas Assignment



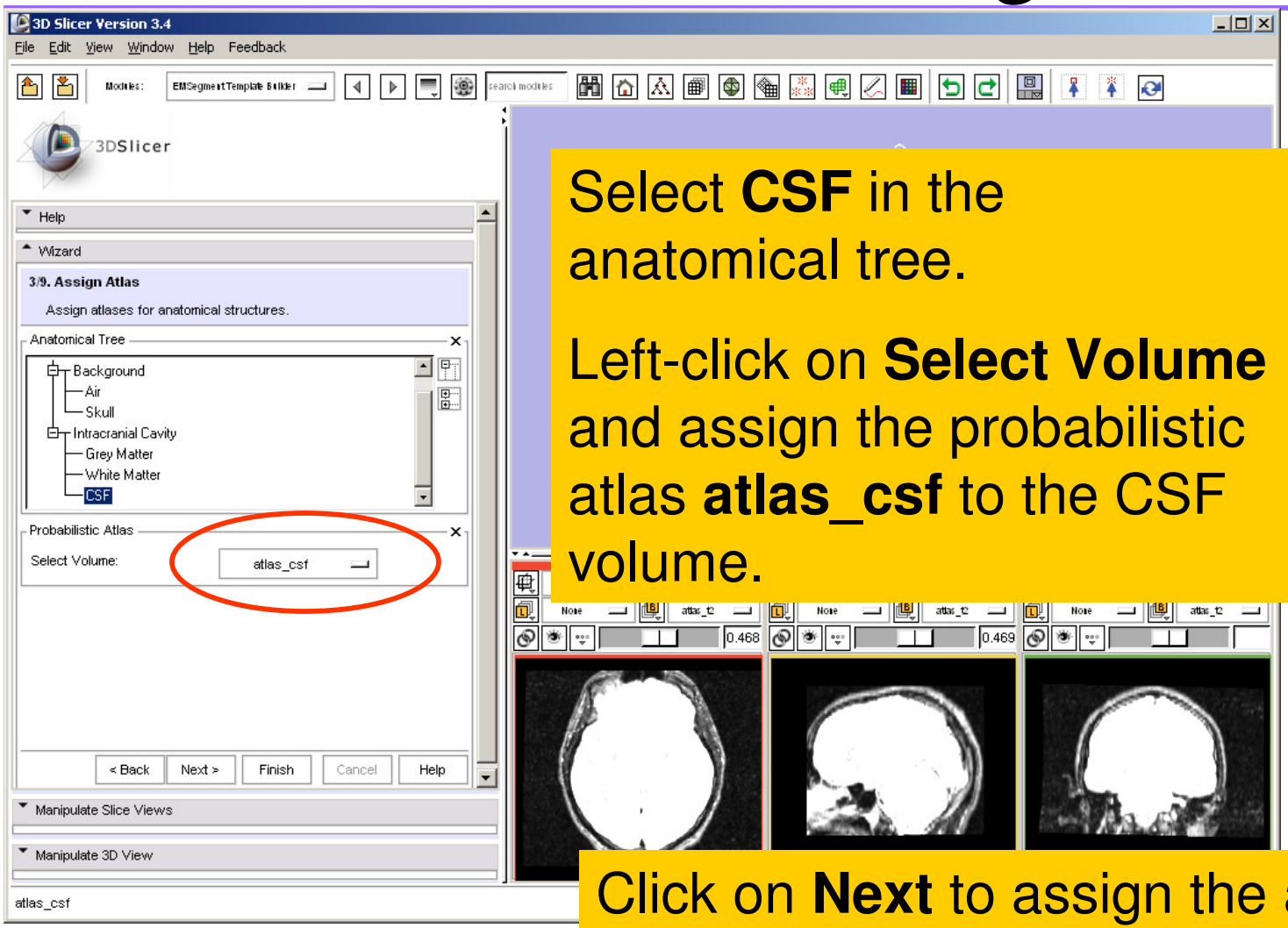
Atlas Assignment



Select **White Matter** in the anatomical tree.

Left-click on **Select Volume** and assign the probabilistic atlas **atlas_whitematter** to the White Matter structure.

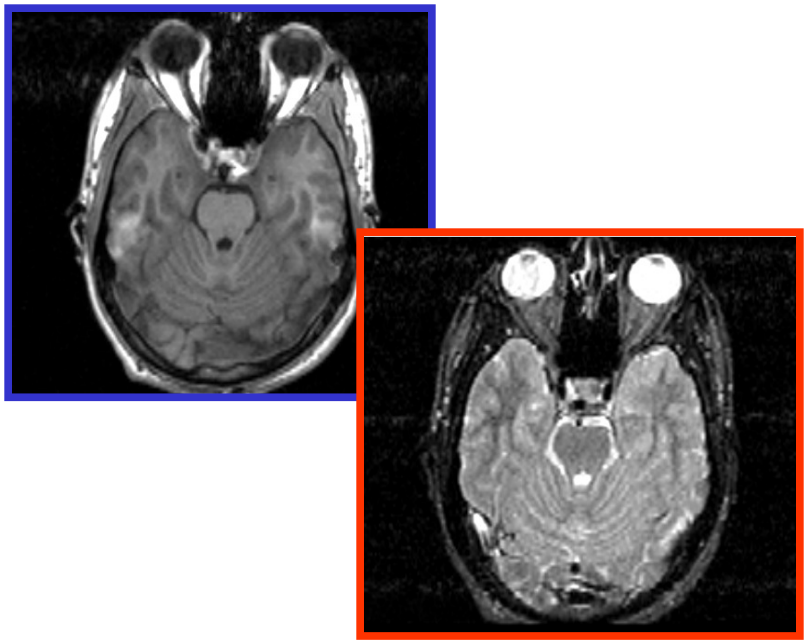
Atlas Assignment



Select **CSF** in the anatomical tree.

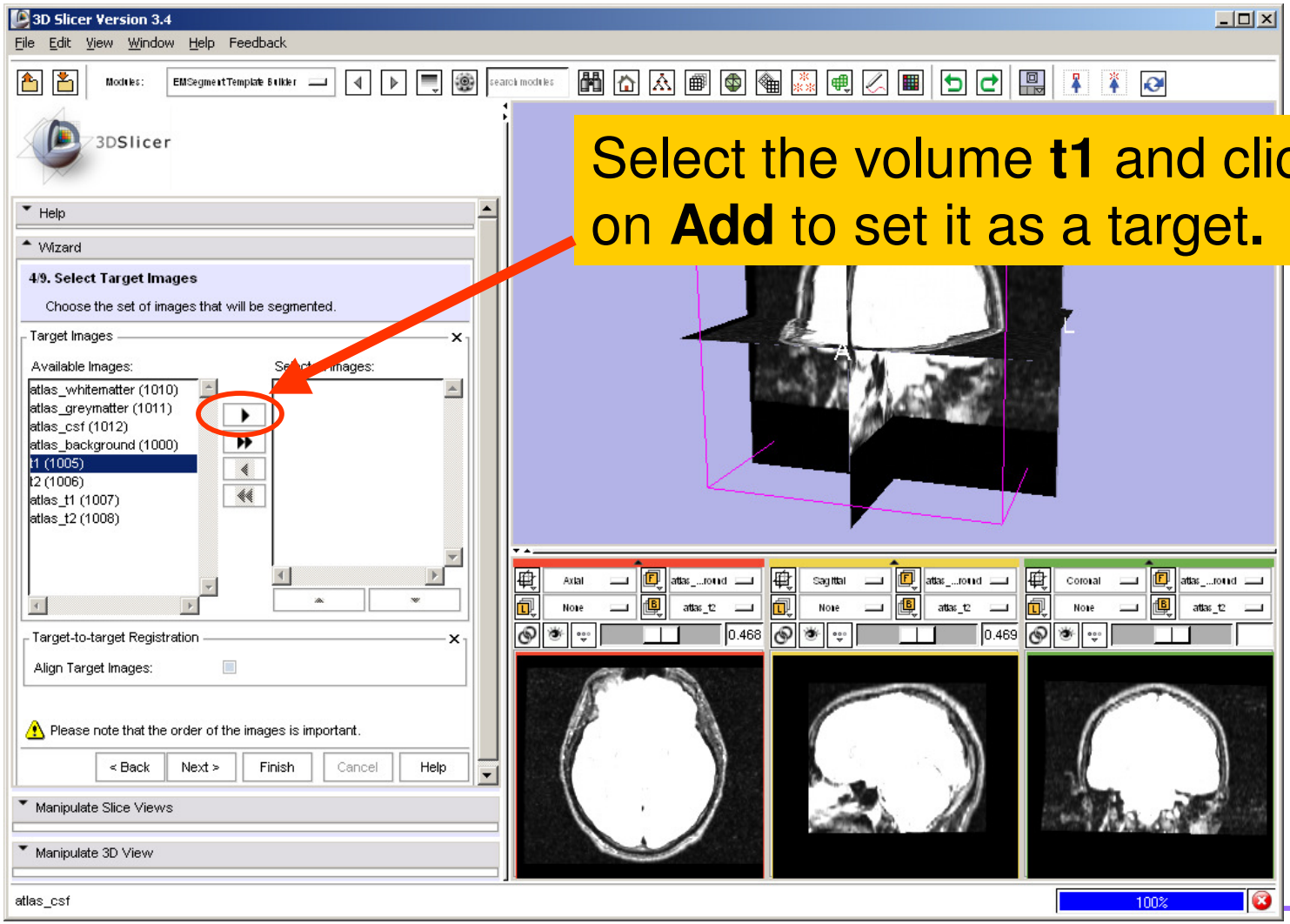
Left-click on **Select Volume** and assign the probabilistic atlas **atlas_csf** to the CSF volume.

Click on **Next** to assign the atlas to select the target images.

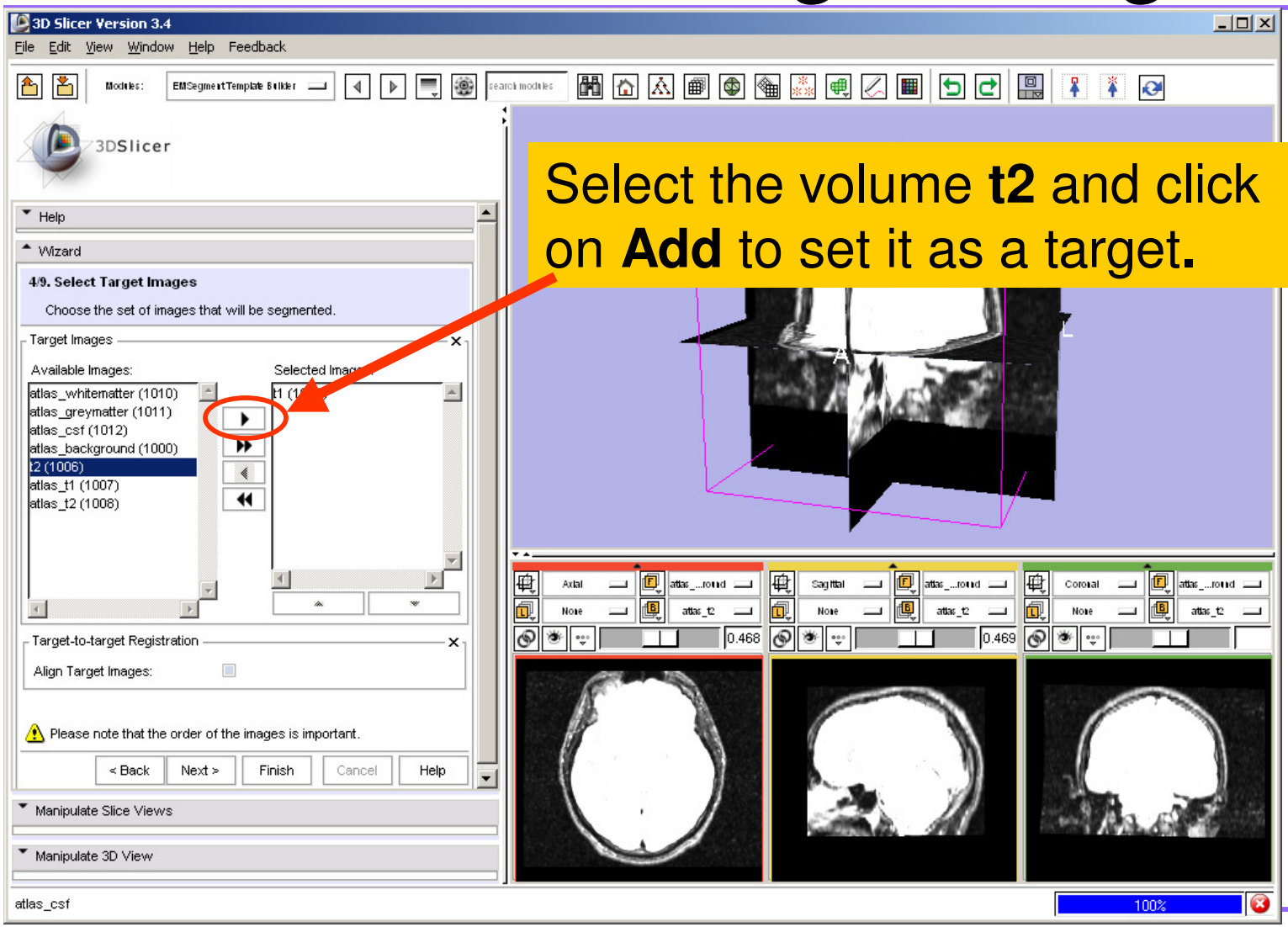


Target Images

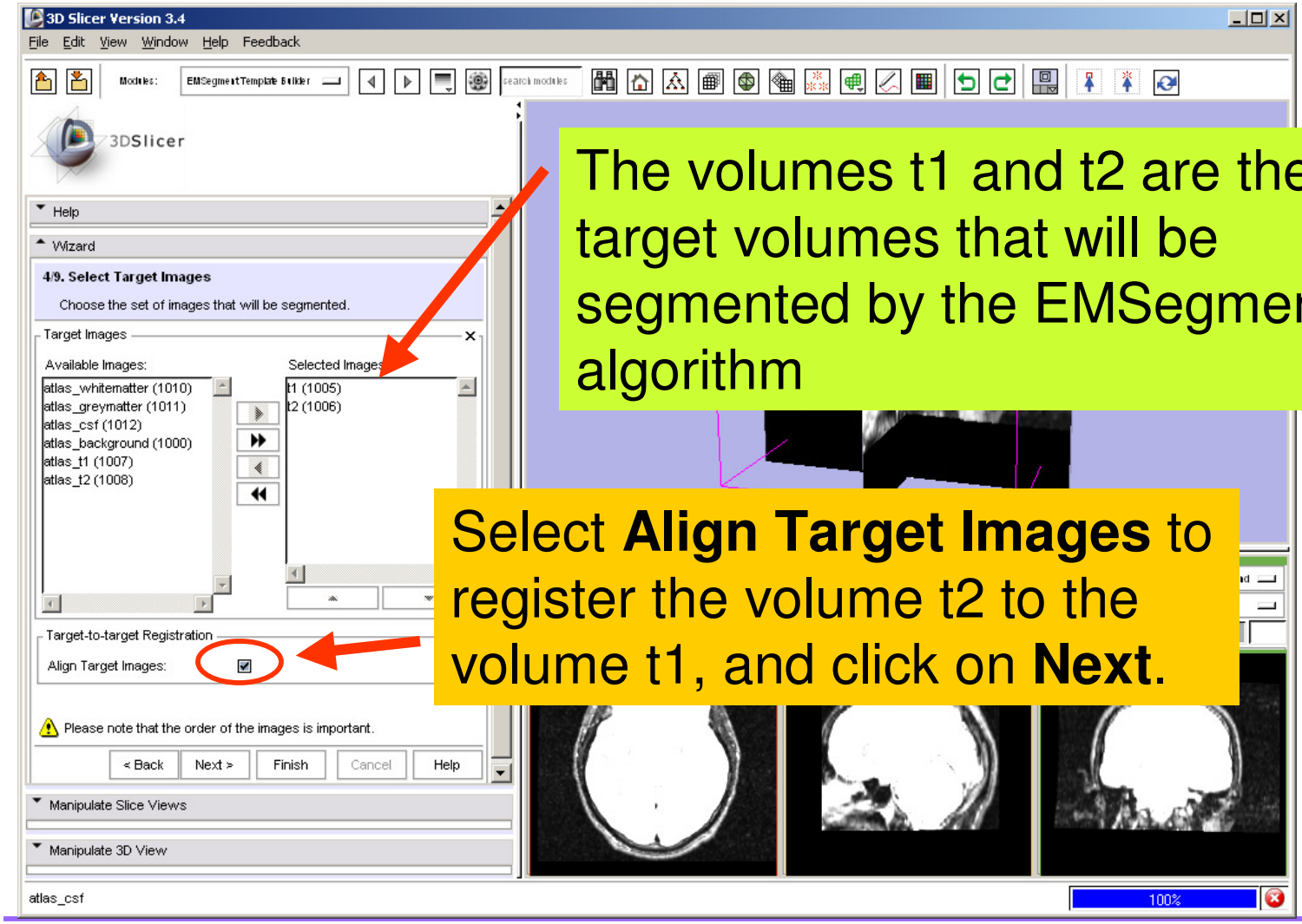
Target Images



Target Images



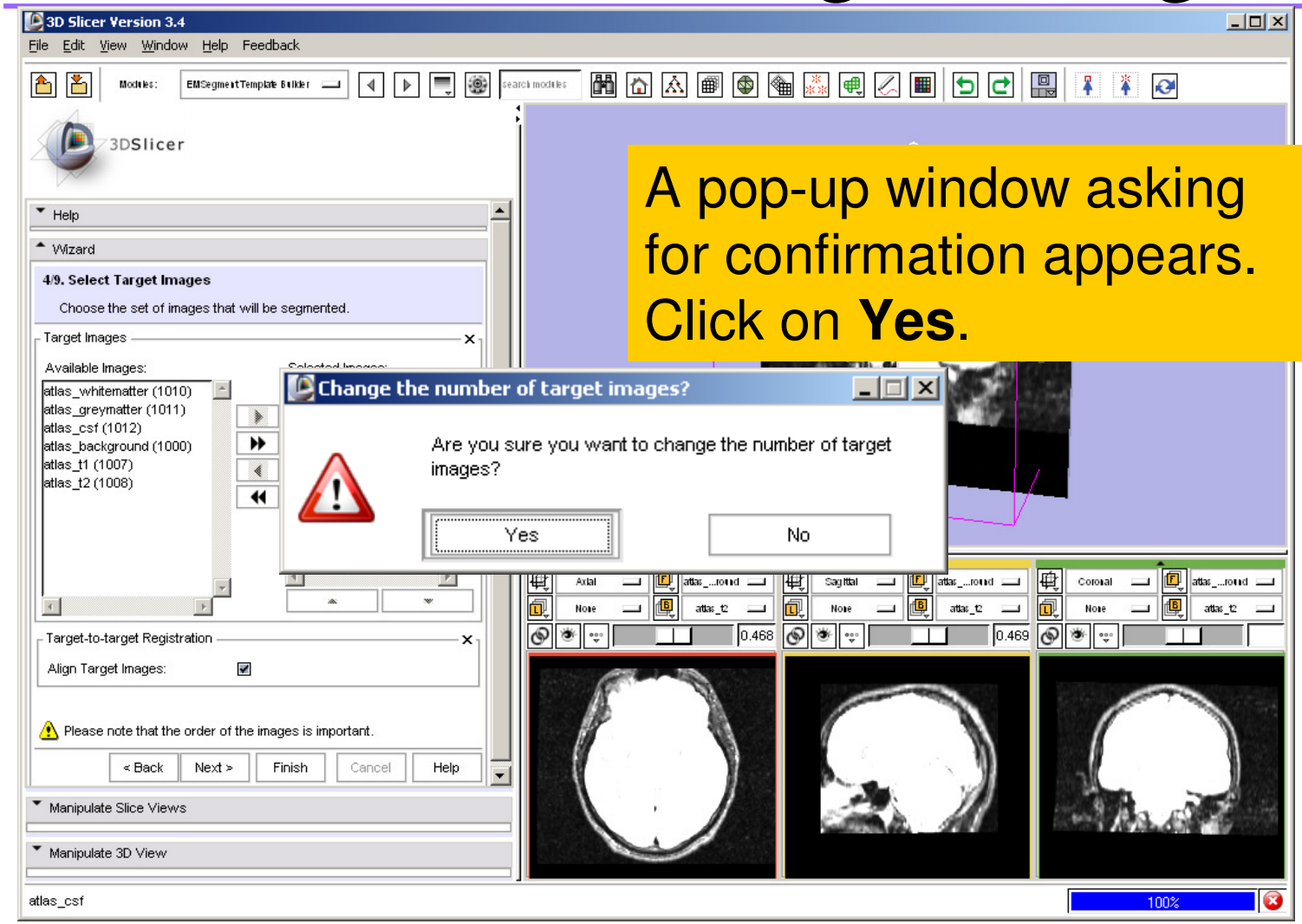
Target Images



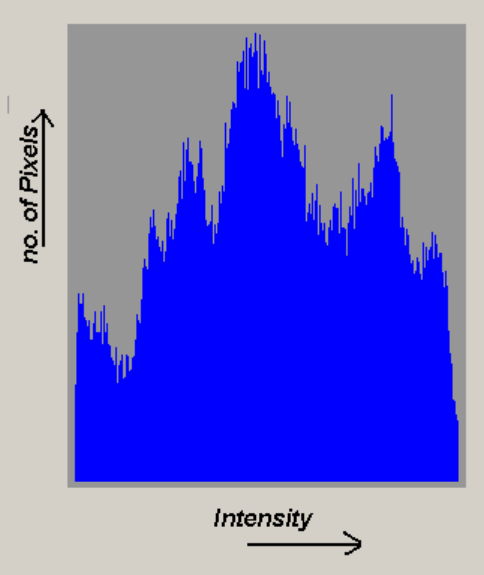
The volumes t1 and t2 are the target volumes that will be segmented by the EMSegmenter algorithm

Select **Align Target Images** to register the volume t2 to the volume t1, and click on **Next**.

Target Images

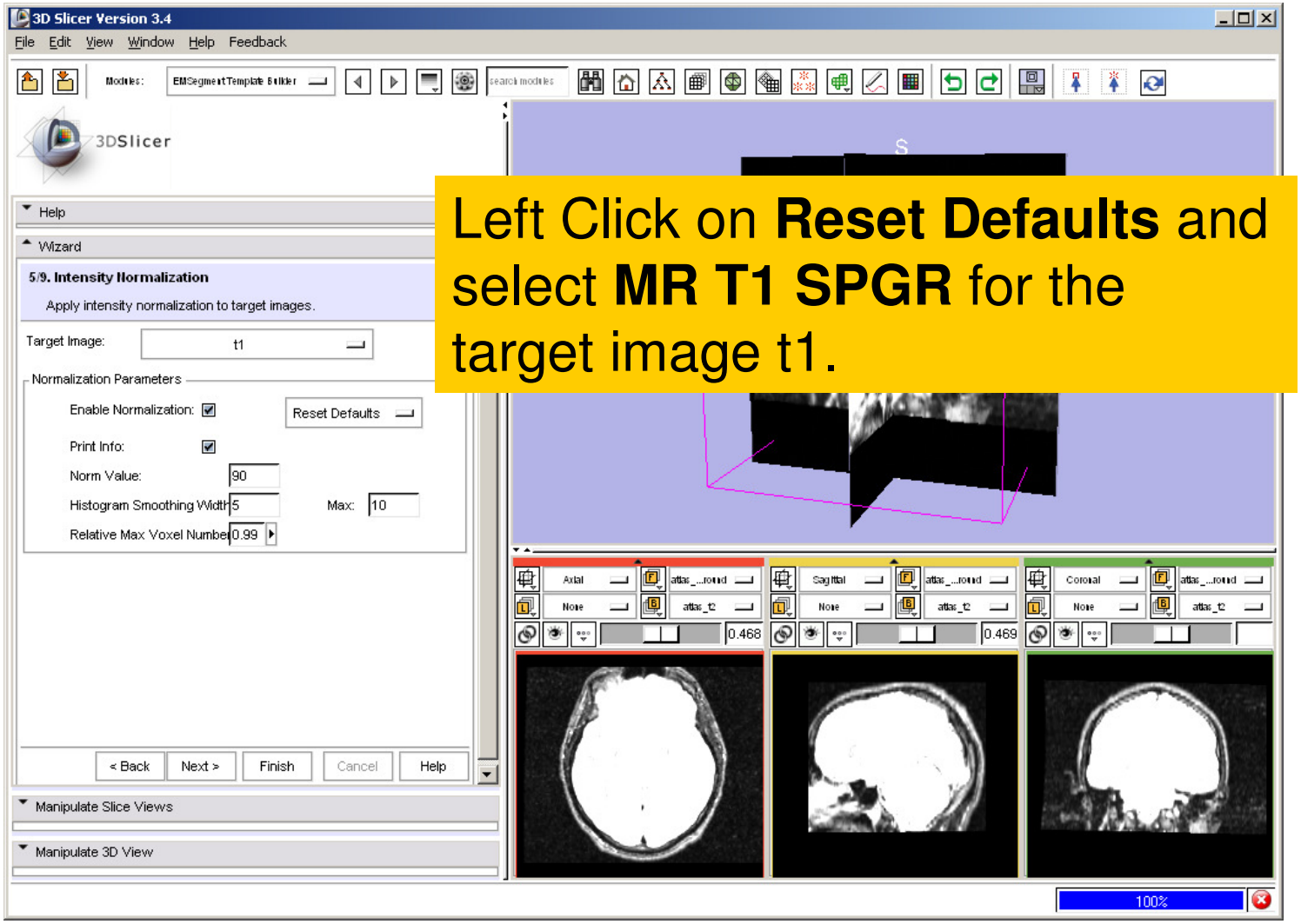


A pop-up window asking for confirmation appears. Click on **Yes**.



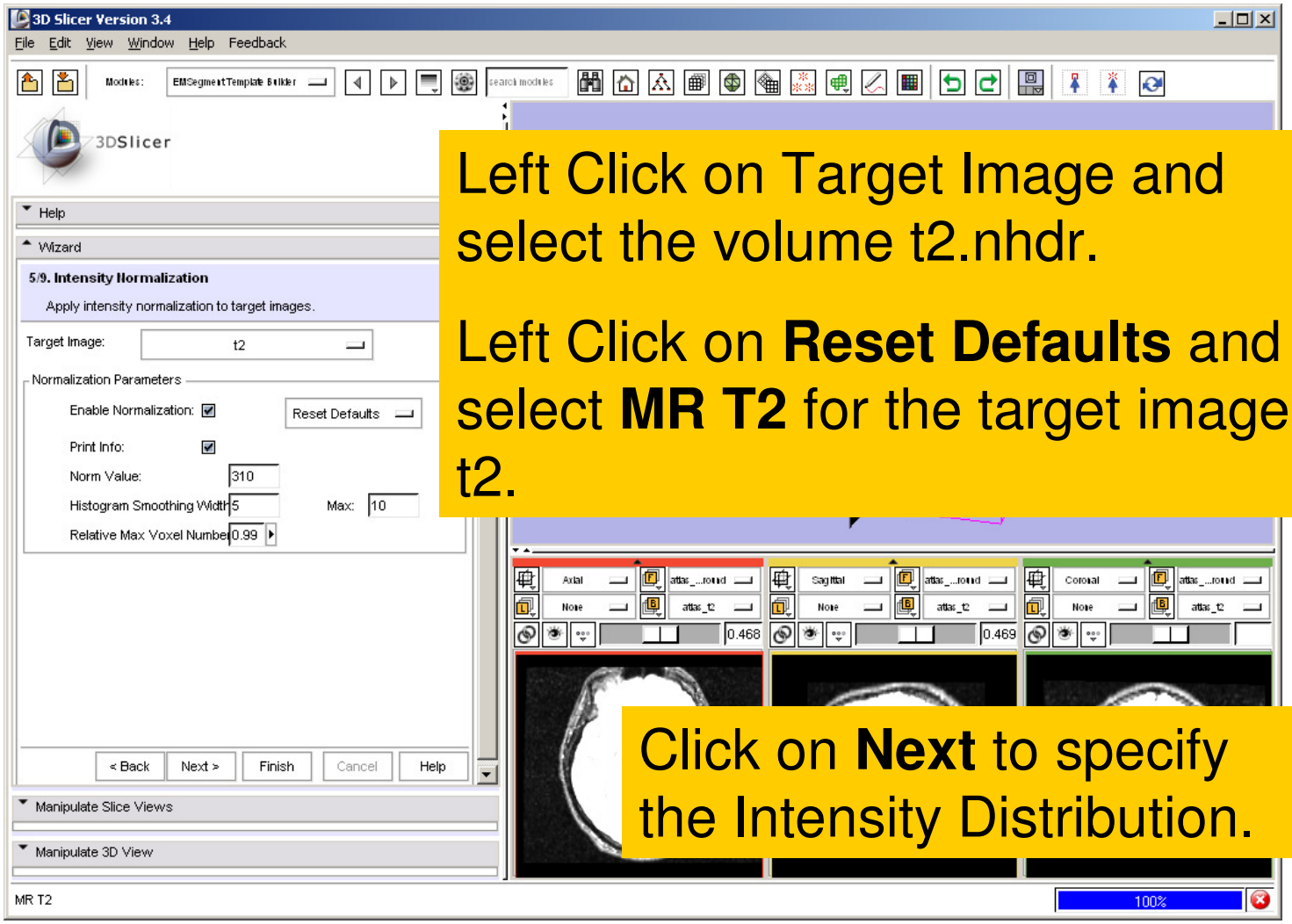
Intensity Normalization

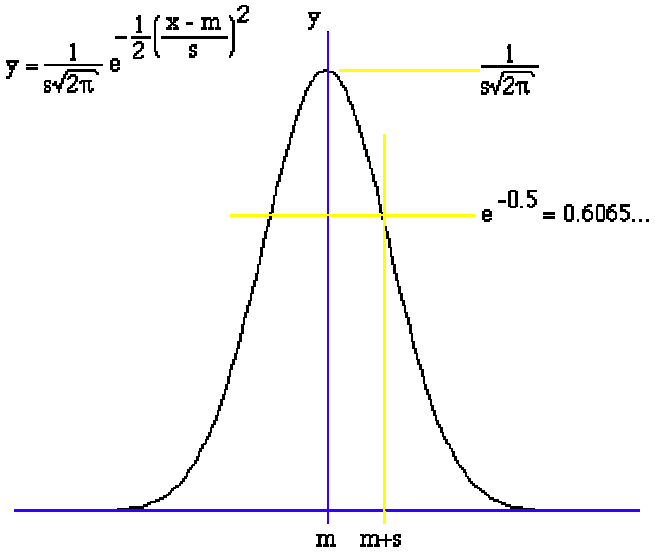
Intensity Normalization



Left Click on **Reset Defaults** and select **MR T1 SPGR** for the target image t1.

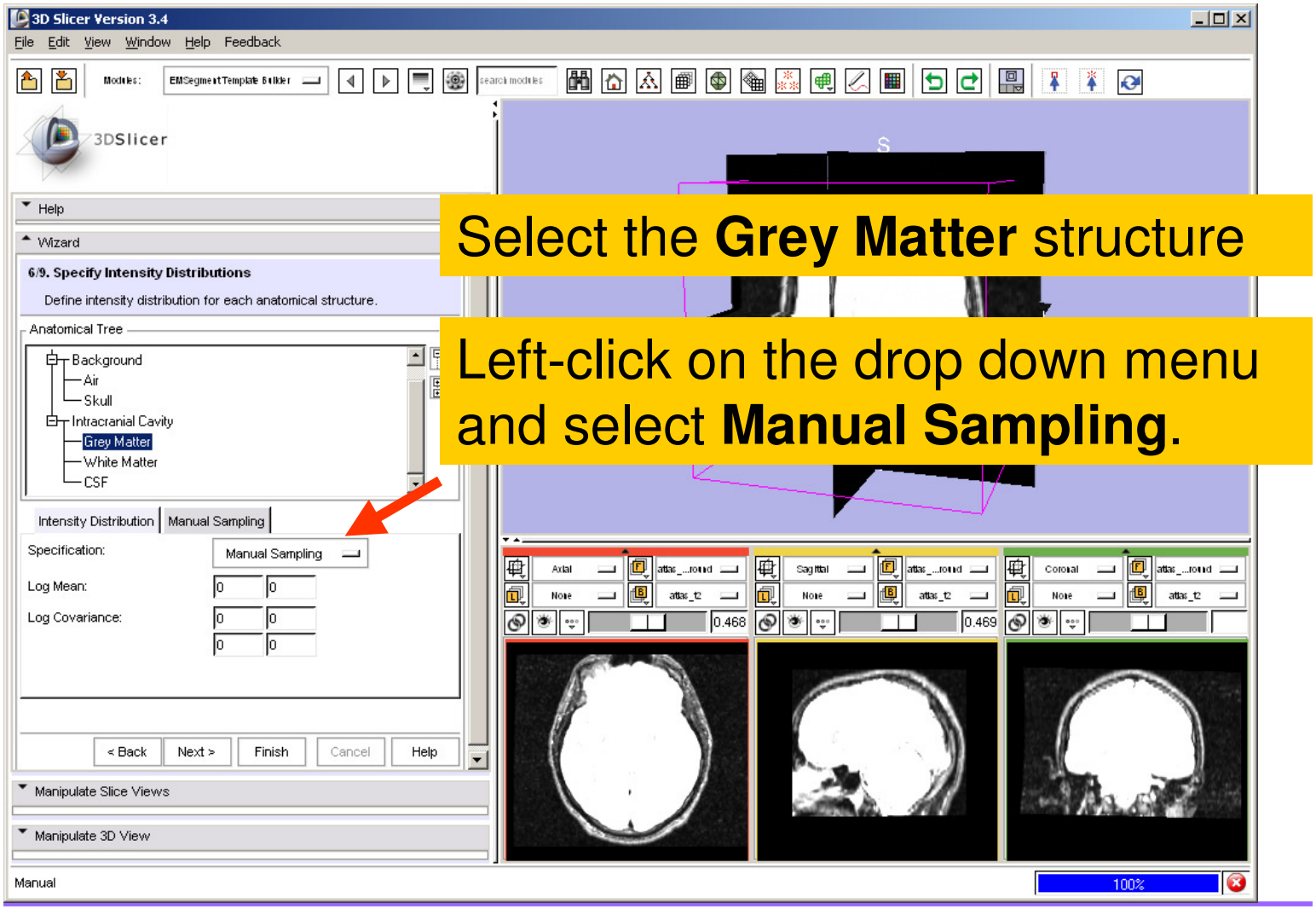
Intensity Normalization



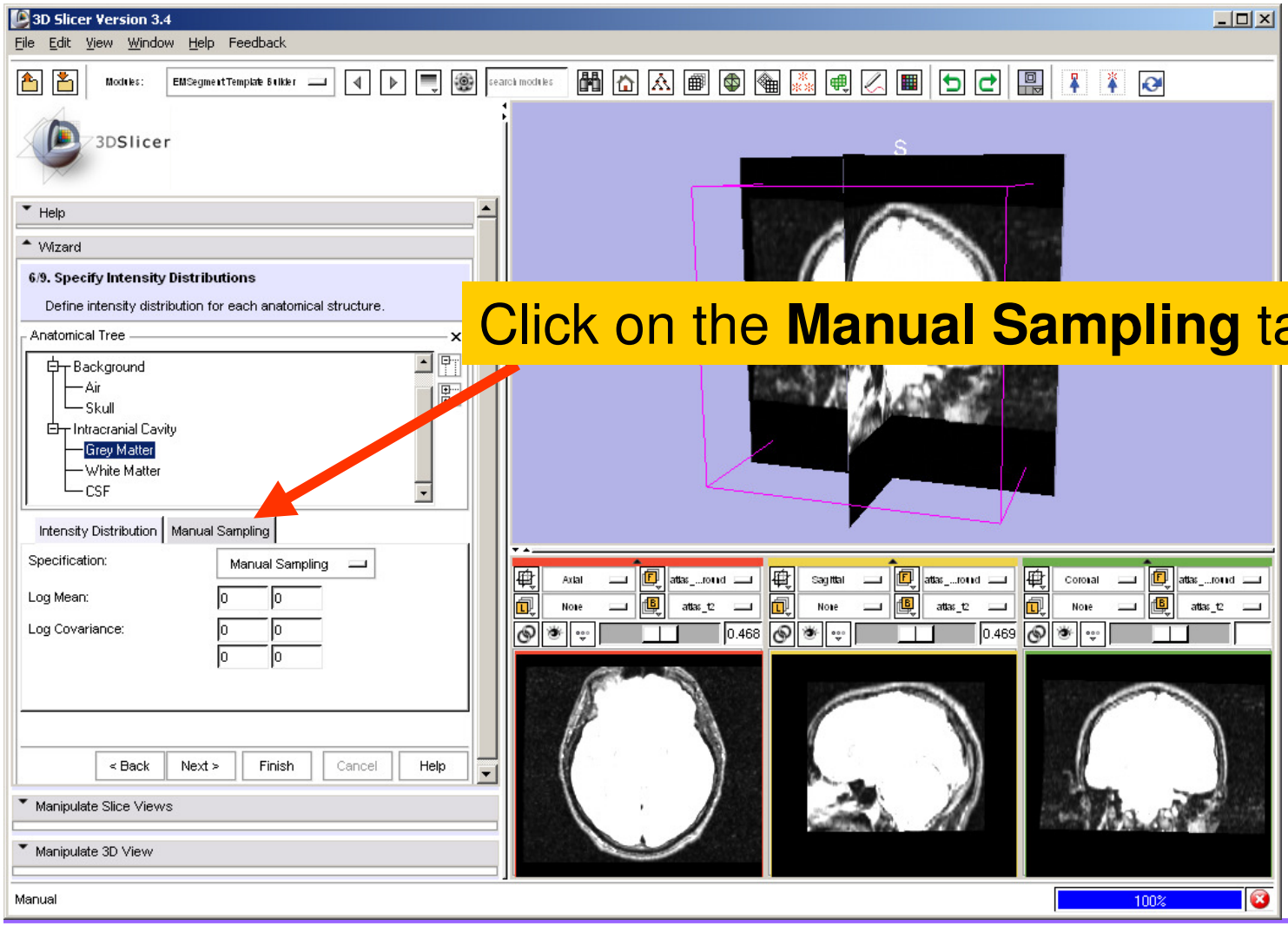


Intensity Distribution

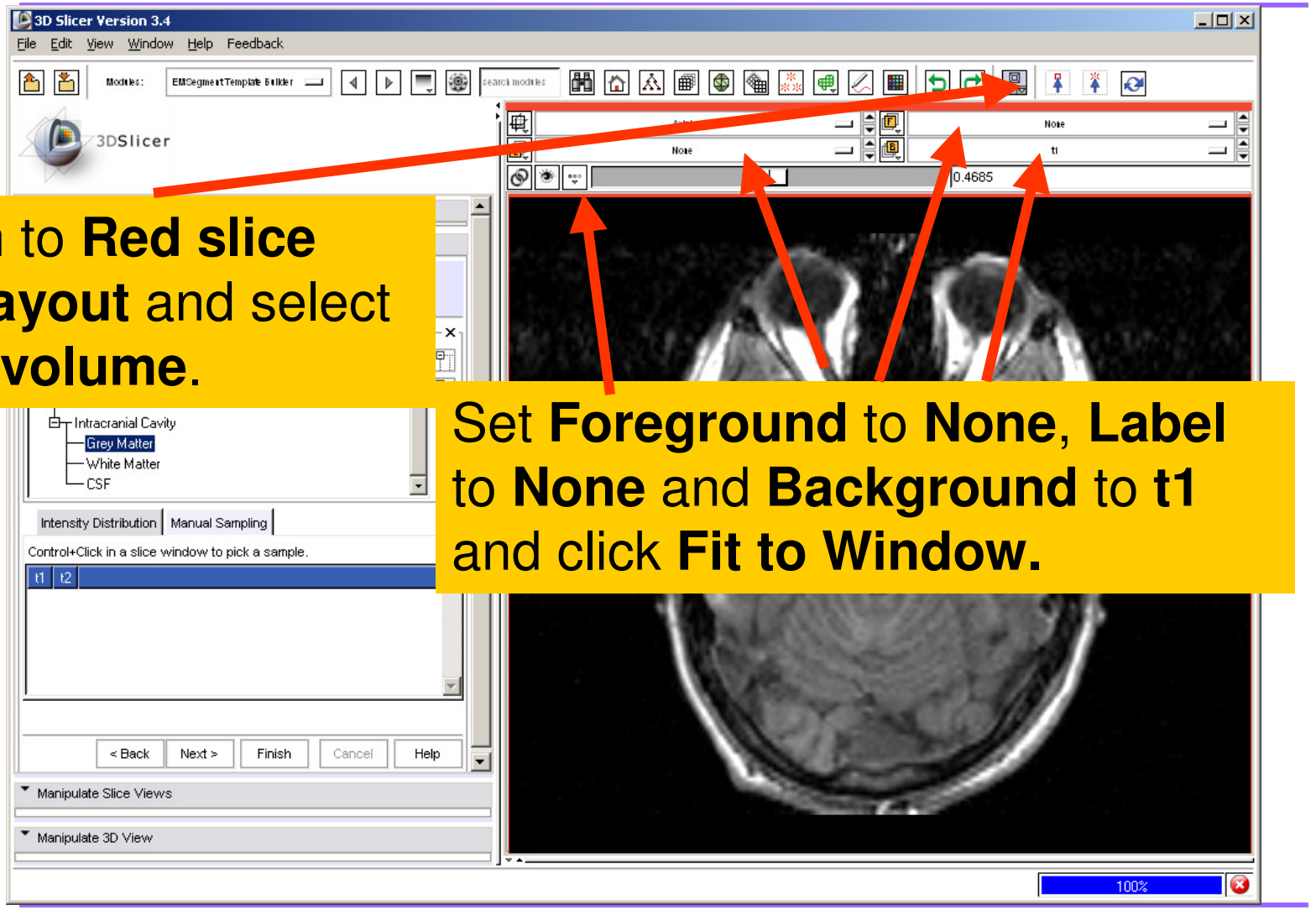
Gaussian Intensity Distribution



Gaussian Intensity Distribution



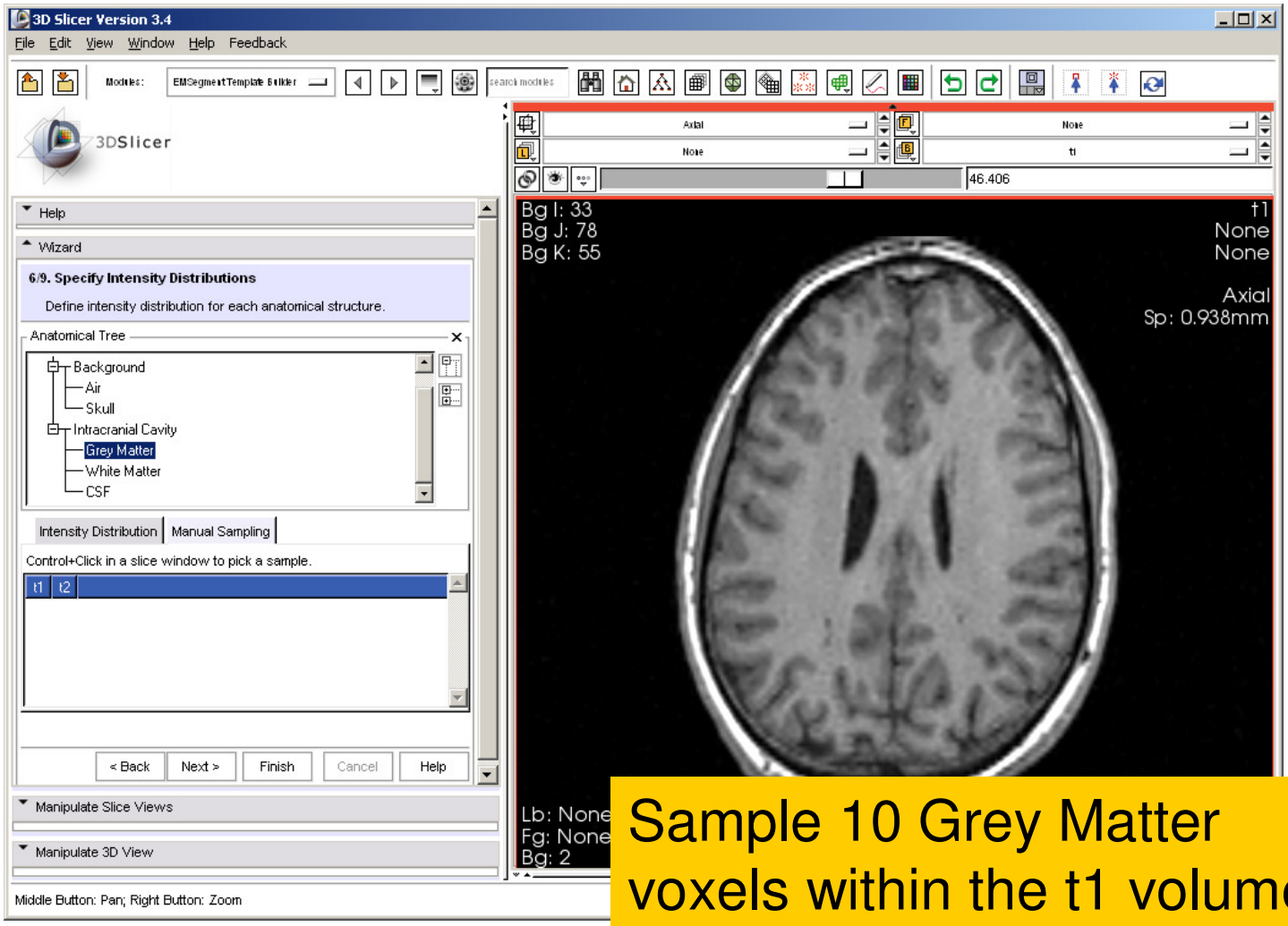
Gaussian Intensity Distribution



Switch to **Red slice only layout** and select the **t1 volume**.

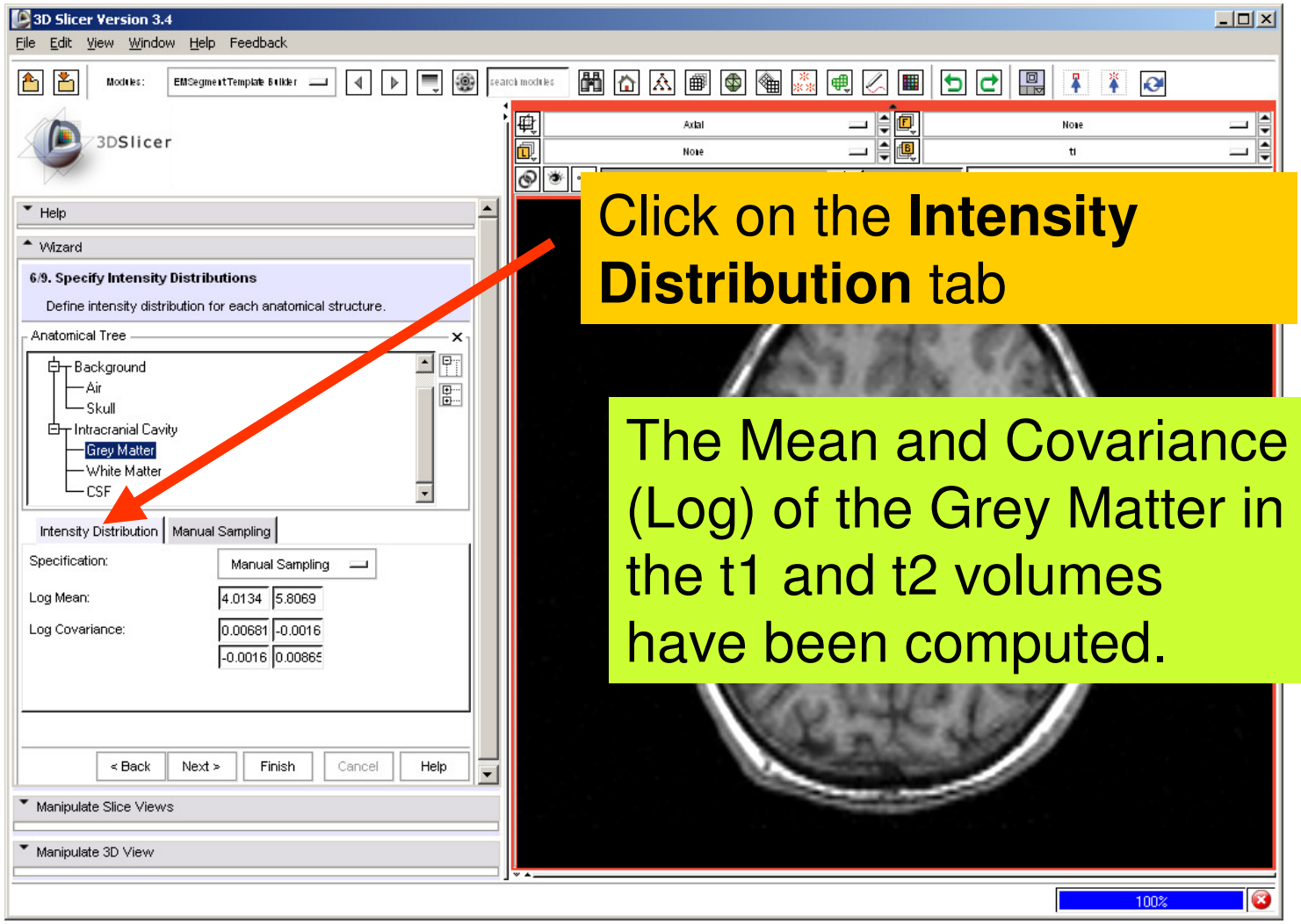
Set **Foreground** to **None**, **Label** to **None** and **Background** to **t1** and click **Fit to Window.**

Gaussian Intensity Distribution

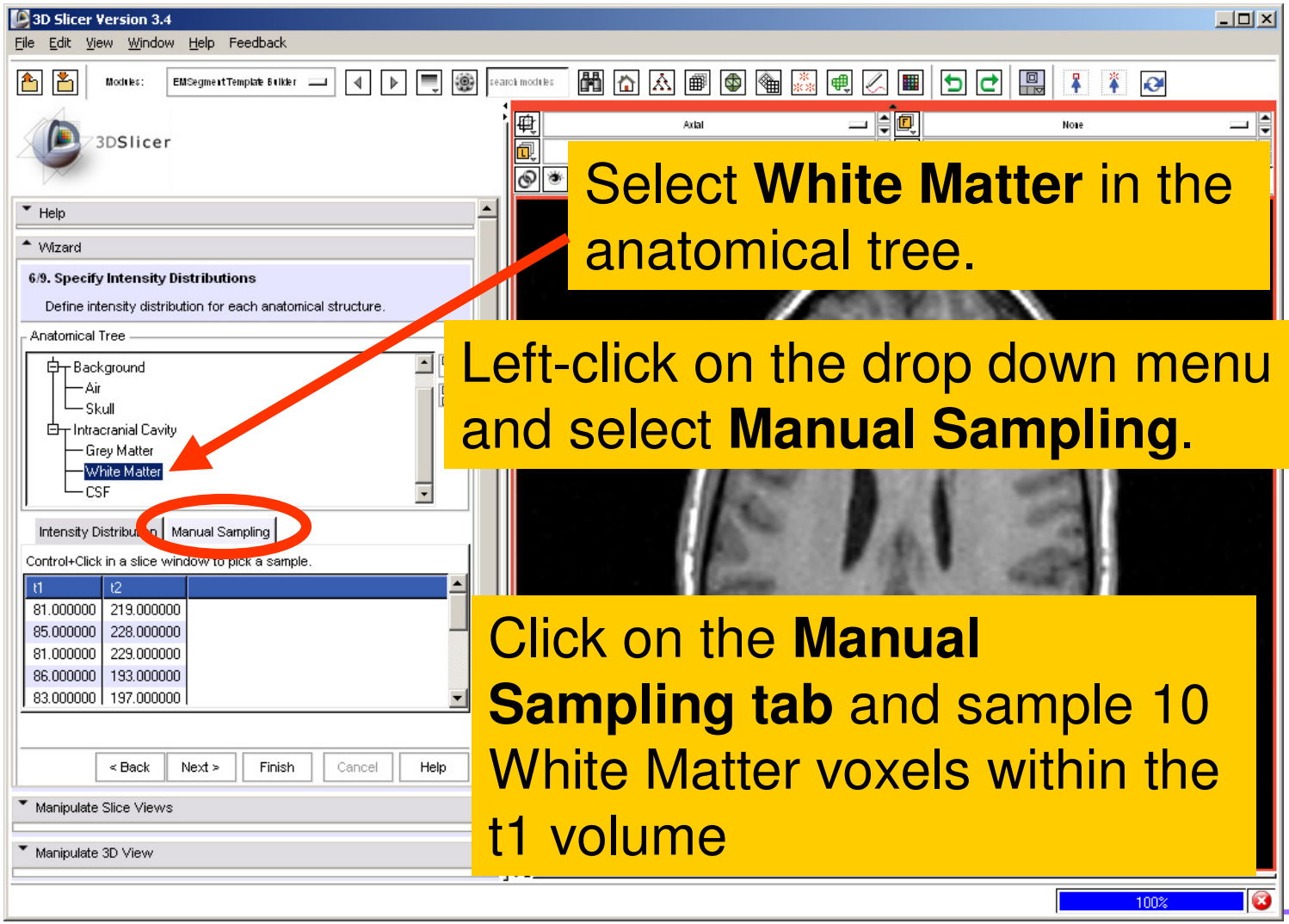


Sample 10 Grey Matter voxels within the t1 volume (**Ctrl + Left Click**)

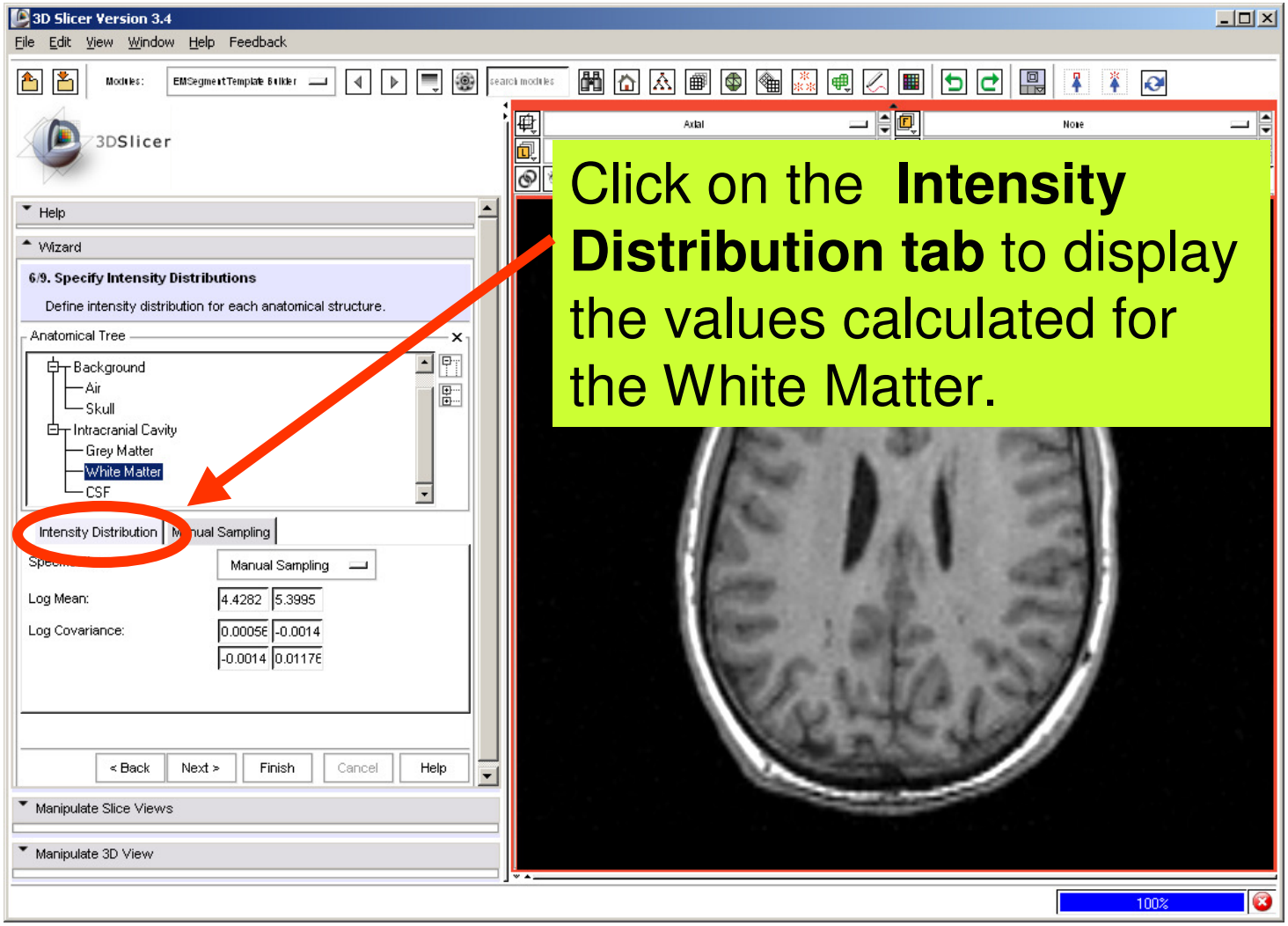
Gaussian Intensity Distribution



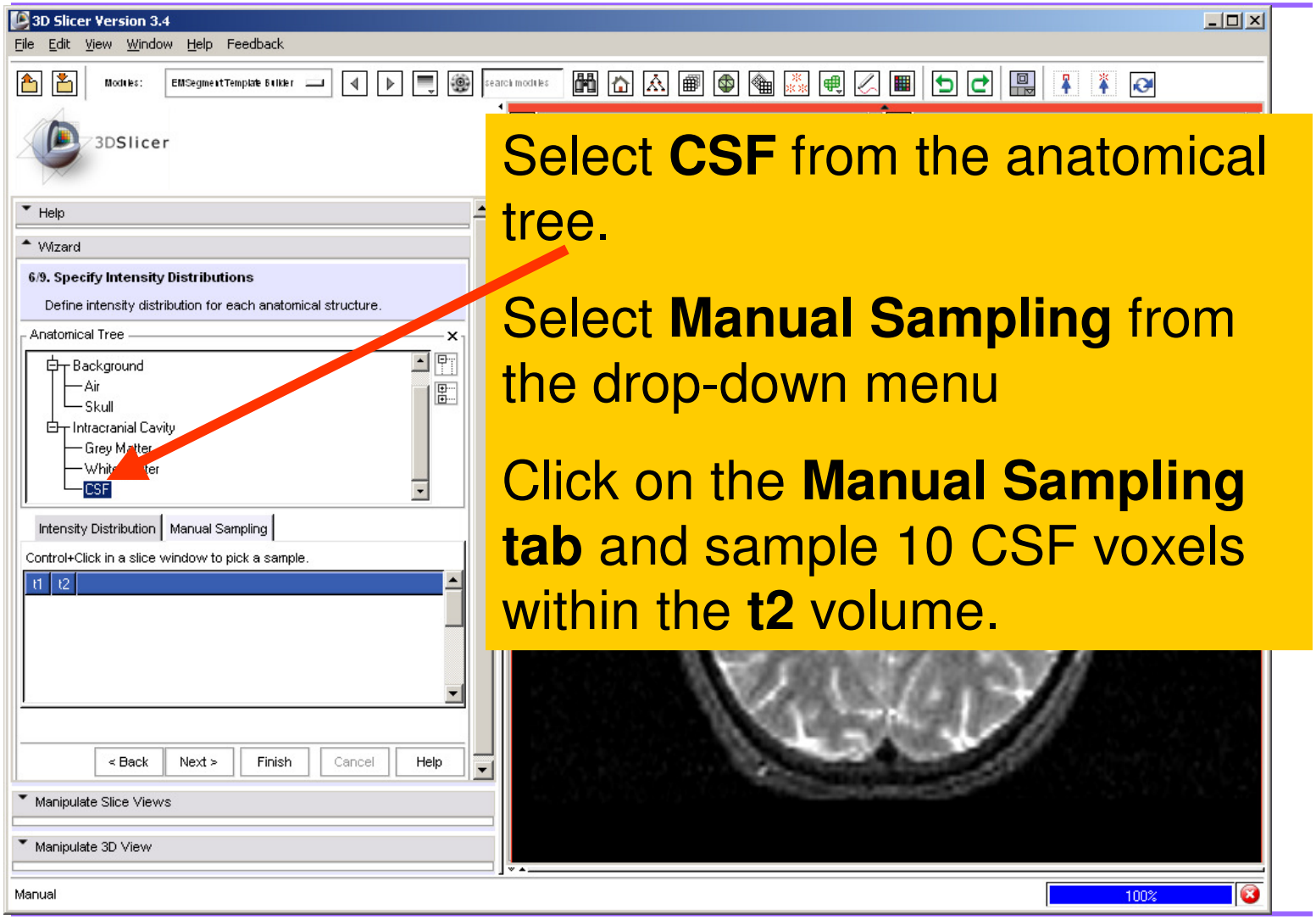
Gaussian Intensity Distribution



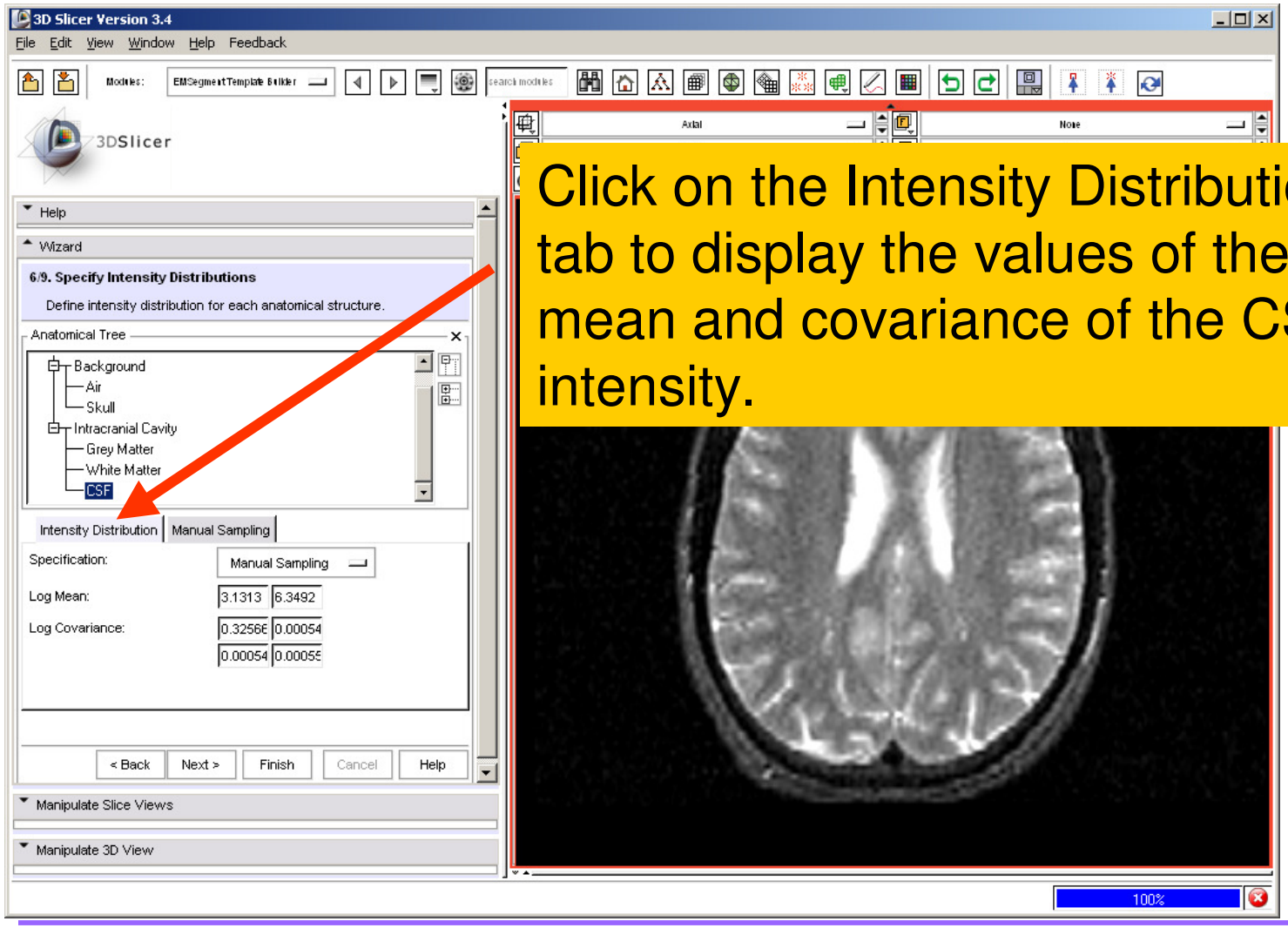
Gaussian Intensity Distribution



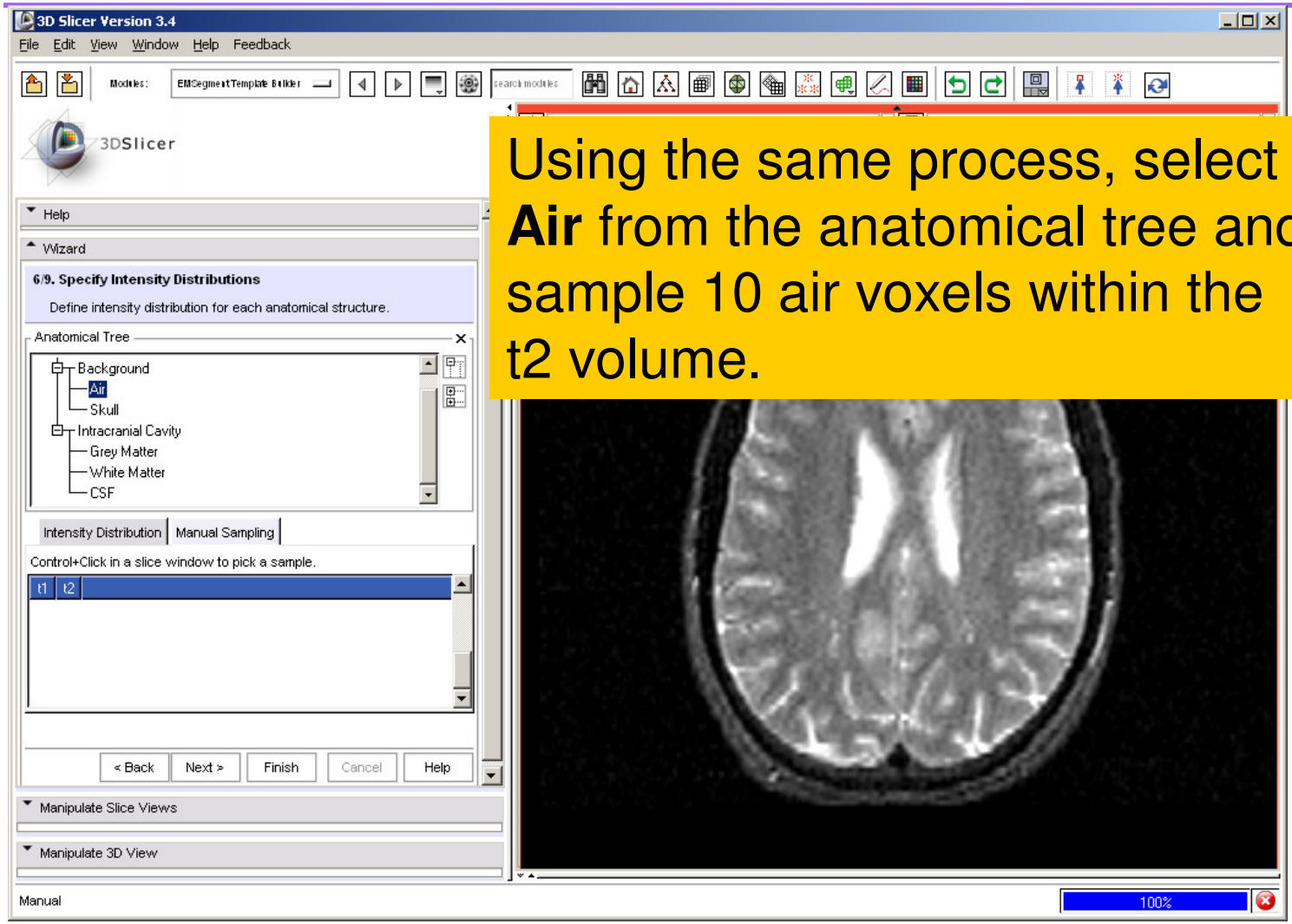
Gaussian Intensity Distribution



Gaussian Intensity Distribution

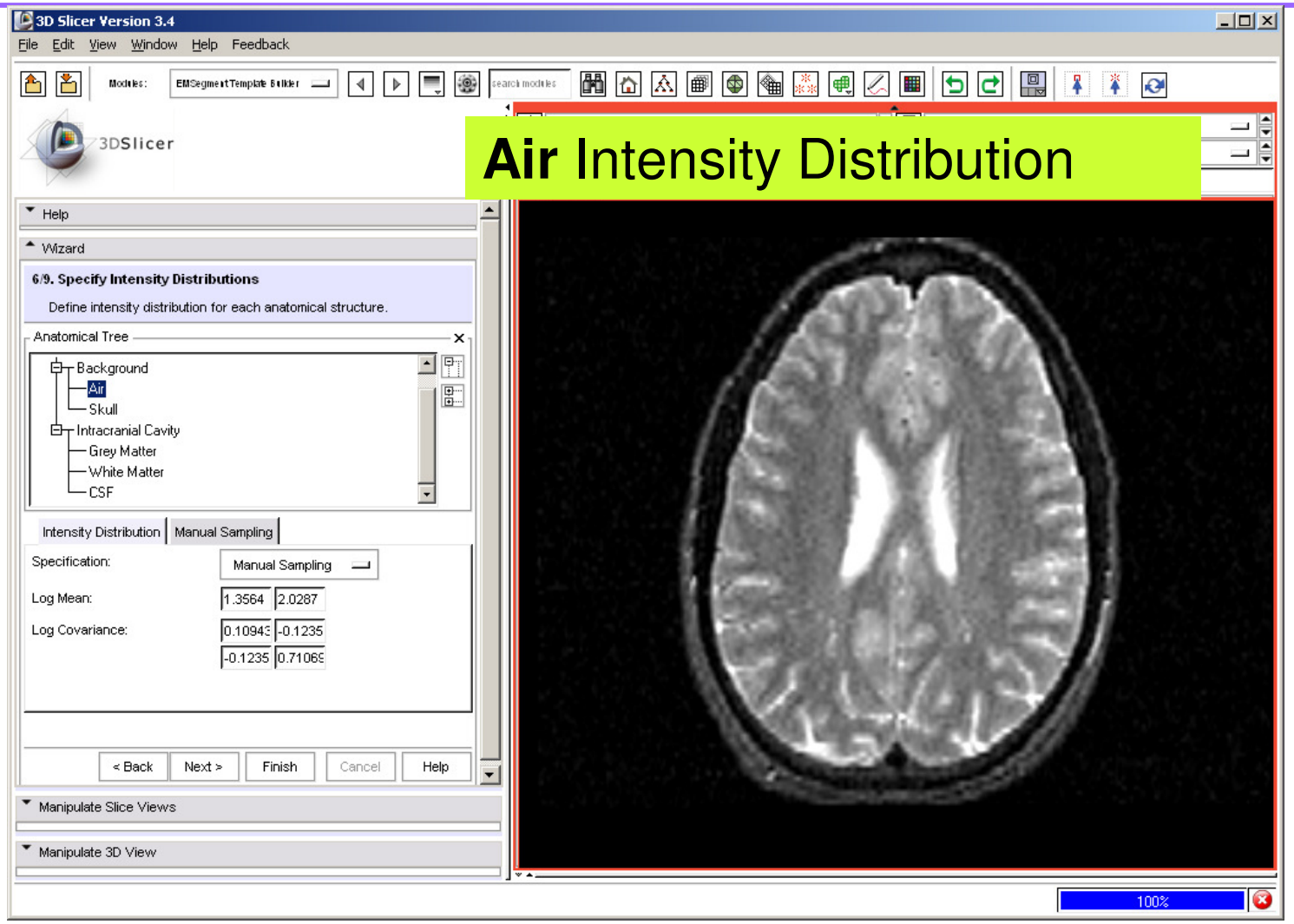


Gaussian Intensity Distribution

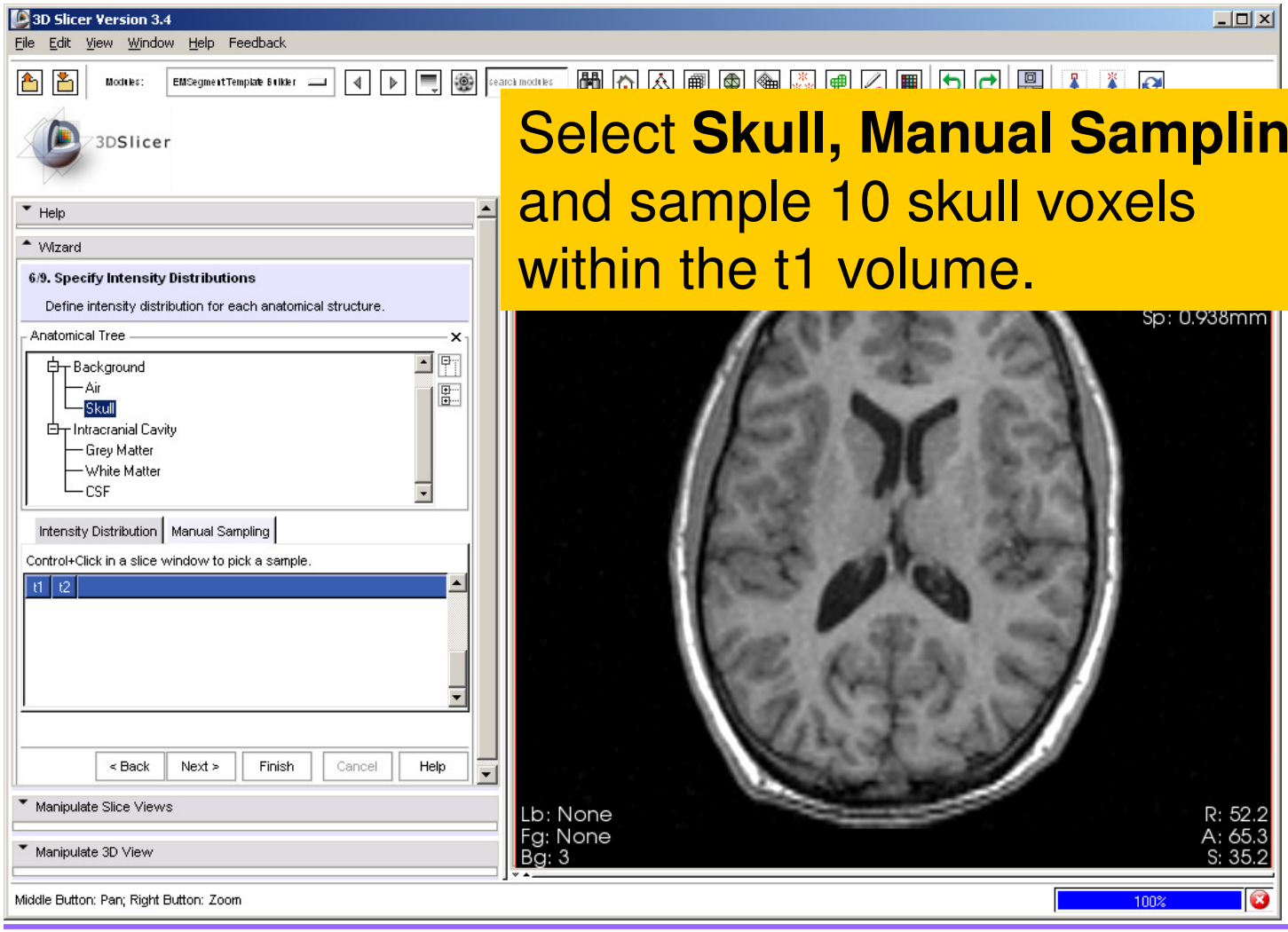


Using the same process, select **Air** from the anatomical tree and sample 10 air voxels within the t2 volume.

Gaussian Intensity Distribution

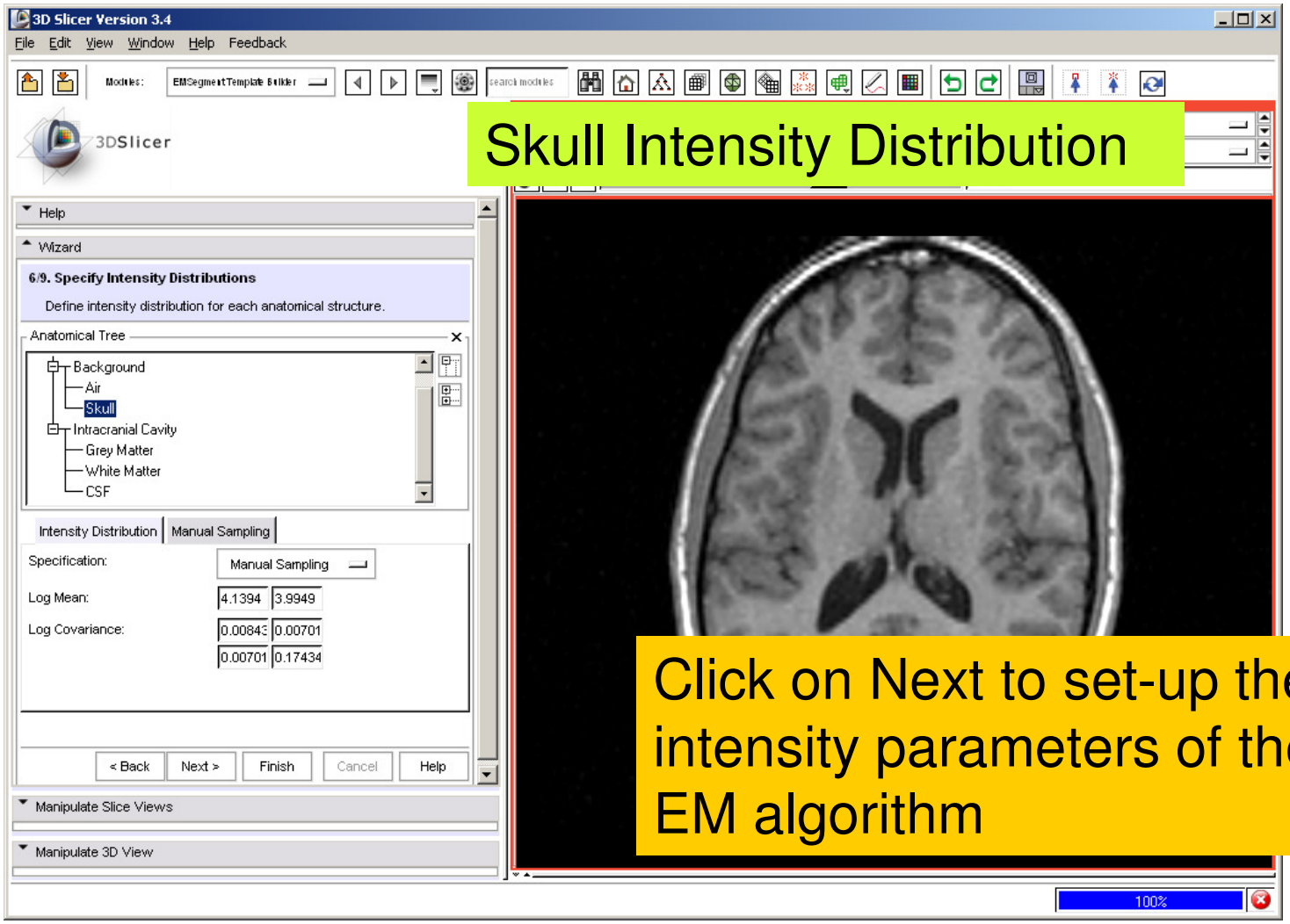


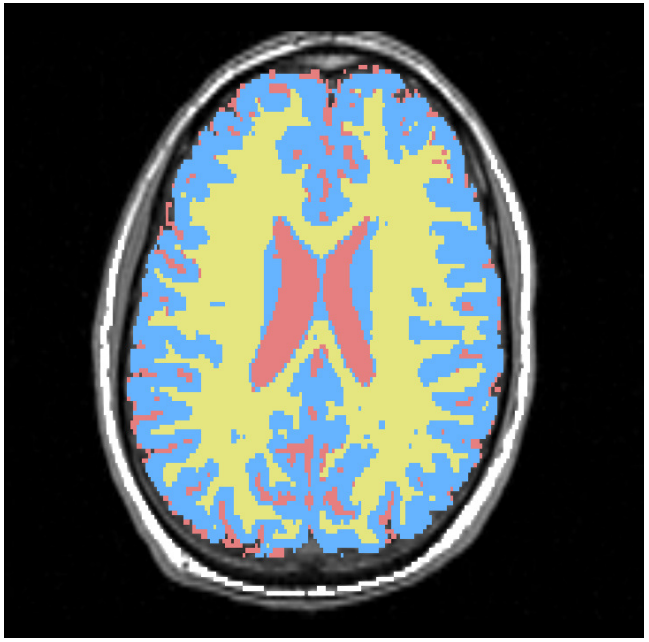
Gaussian Intensity Distribution



Select **Skull, Manual Sampling** and sample 10 skull voxels within the t1 volume.

Gaussian Intensity Distribution



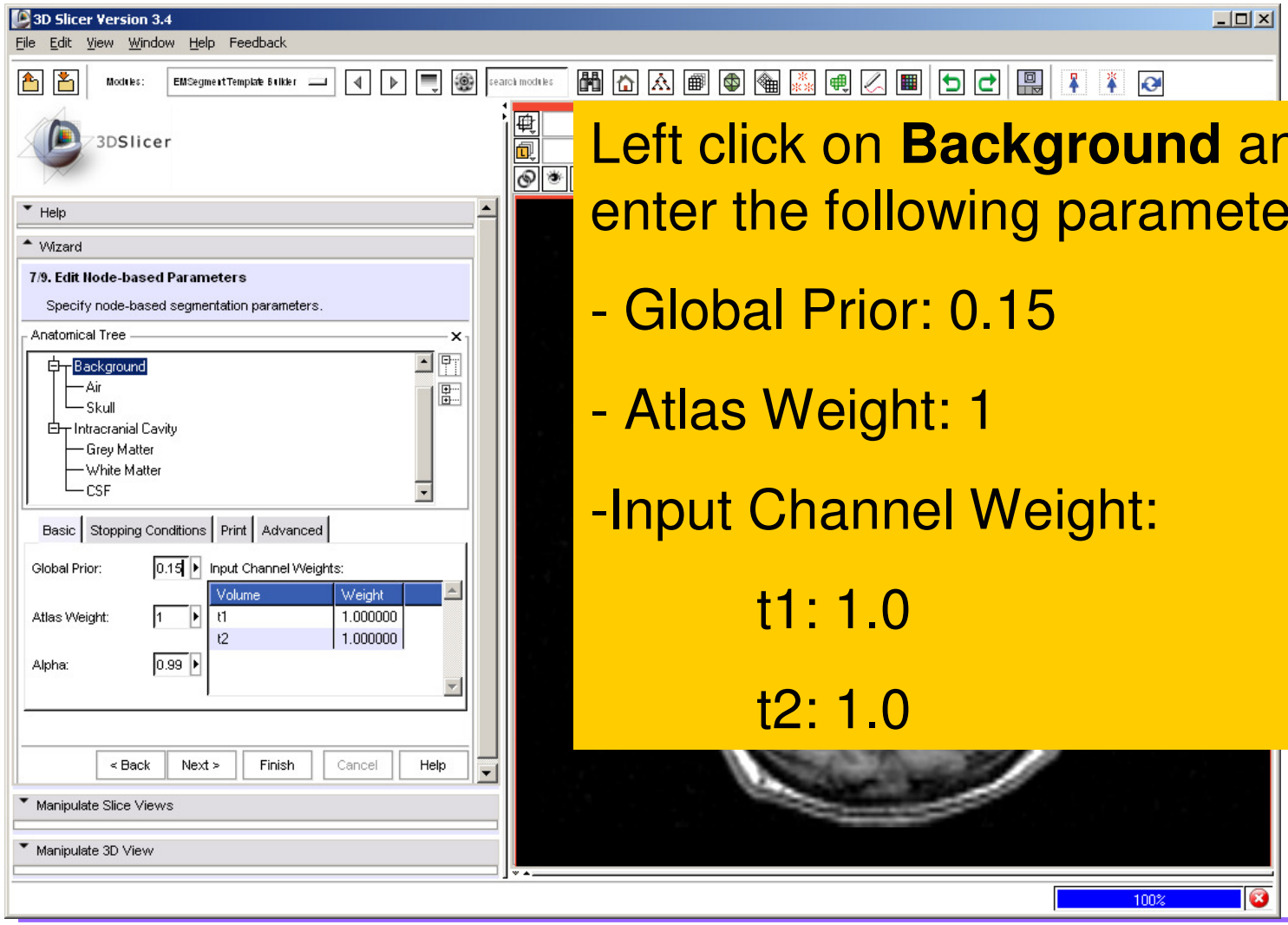


EM Input Parameters

EM Segmentation parameters

- Global Prior p(L) → Global Prior Weight
- Gaussian Intensity Distribution p(L|I) → Input Channel Weight
- Probabilistic Atlas p(L|X) → Atlas Weight

Background Settings



Left click on **Background** and enter the following parameters:

- Global Prior: 0.15

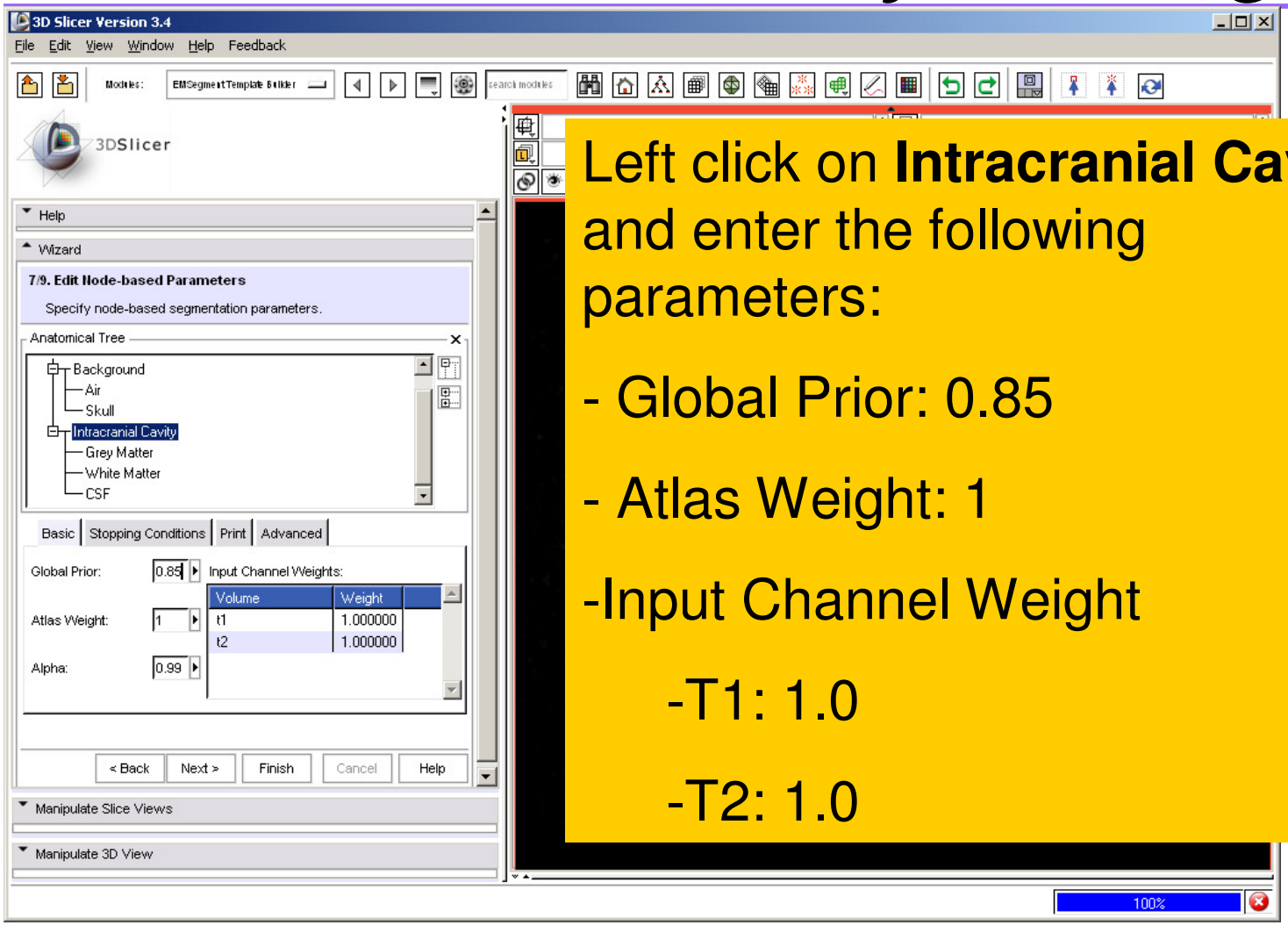
- Atlas Weight: 1

-Input Channel Weight:

t1: 1.0

t2: 1.0

Intracranial Cavity Settings



Left click on **Intracranial Cavity** and enter the following parameters:

- Global Prior: 0.85
- Atlas Weight: 1
- Input Channel Weight
  - -T1: 1.0
  - -T2: 1.0

Air and Skull settings

Enter the following parameters for Air and Skull

Air

Global Prior: p(L) = 0.7
Atlas Weight: p(L|X) = 1
Input Channel Weight: t1, p(L|I) = 1.0 t2, p(L|I) = 1.0

Skull

Global Prior: p(L) = 0.3
Atlas Weight: p(L|X) = 1
Input Channel Weight: t1, p(L|I) = 1.0 t2, p(L|I) = 1.0

Intracranial Cavity

GM

Global Prior: p(L) = 0.45
Atlas Weight: p(L|X) = 0.01
Input Channel Weight: t1, p(L|I) = 1.0 t2, p(L|I) = 0.1

Enter the following parameters for GM, WM and CSF.

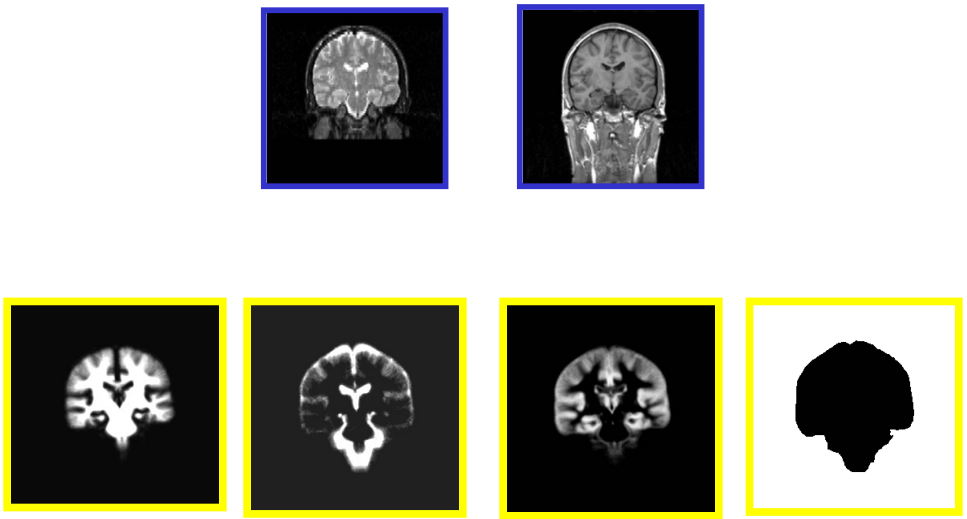
WM

Global Prior: p(L) = 0.3
Atlas Weight: p(L|X) = 0.7
Input Channel Weight: t1, p(L|I) = 0.95 t2, p(L|I) = 0.05

CSF

Global Prior: p(L) = 0.25
Atlas Weight: p(L|X) = 0.01
Input Channel Weight: t1, p(L|I) = 0.1 t2, p(L|I) = 1.0

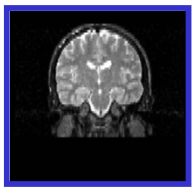
Click on **Next.**



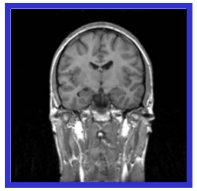
Atlas To Target Registration

EM Pipeline: Patient-Specific Atlas Generation

Registered Normalized Patient data

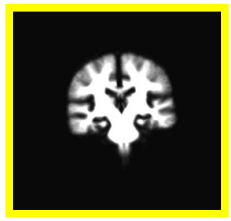


T(t2n)

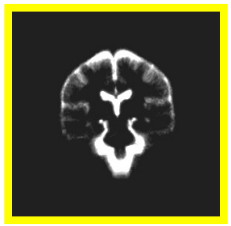


t1n

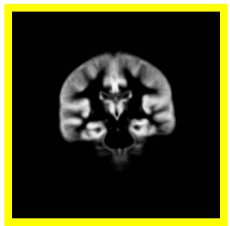
Generic atlas



white matter



csf

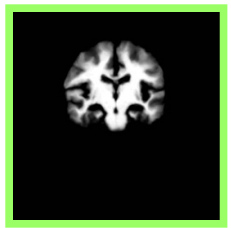


grey matter

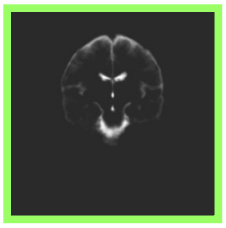
background

Atlas to target registration
Register the generic atlas to the images to create the patient-specific atlas

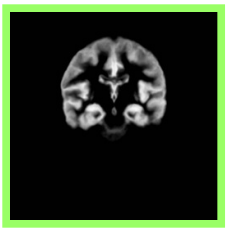
Patient-specific atlas



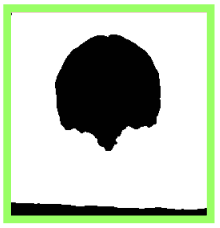
white matter



csf



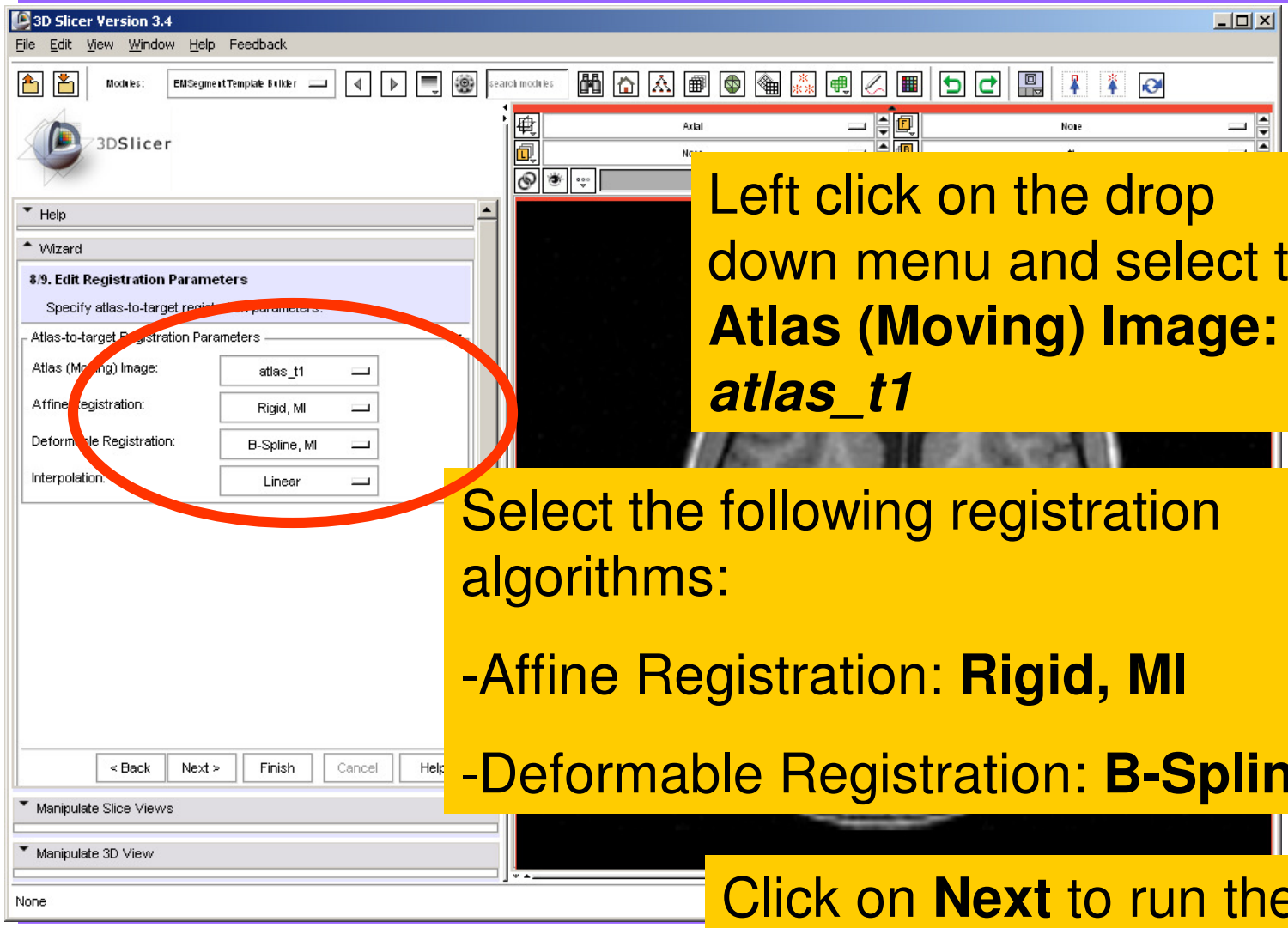
grey matter



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

Atlas To Target Registration



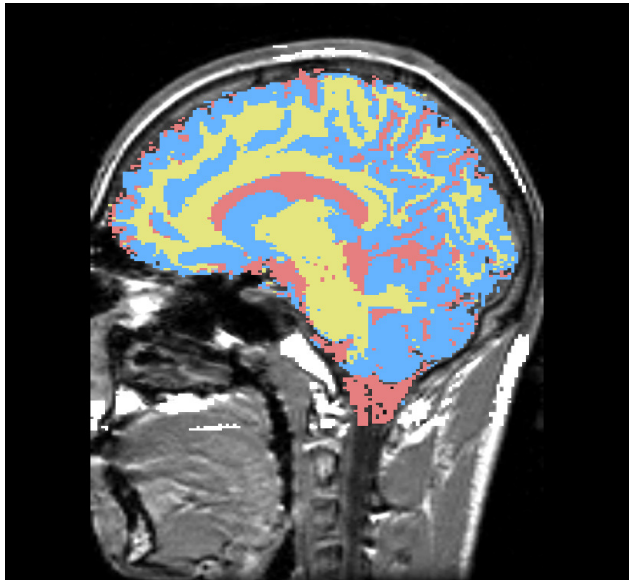
Left click on the drop down menu and select the **Atlas (Moving) Image: *atlas_t1***

Select the following registration algorithms:

-Affine Registration: **Rigid, MI**

-Deformable Registration: **B-Spline, MI**

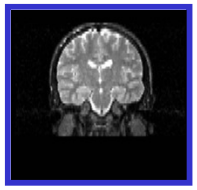
Click on **Next** to run the Segmentation



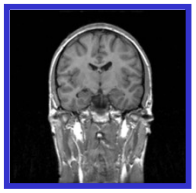
Segmentation

EM Pipeline: Segmentation

Normalized Patient data

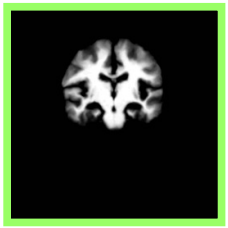


T(t2) normalized

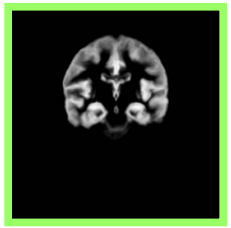


T1 normalized

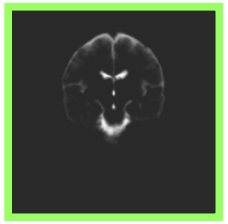
Patient-specific atlas



white matter

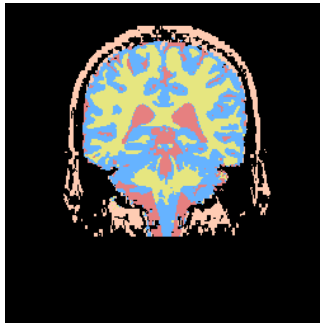


csf



grey matter

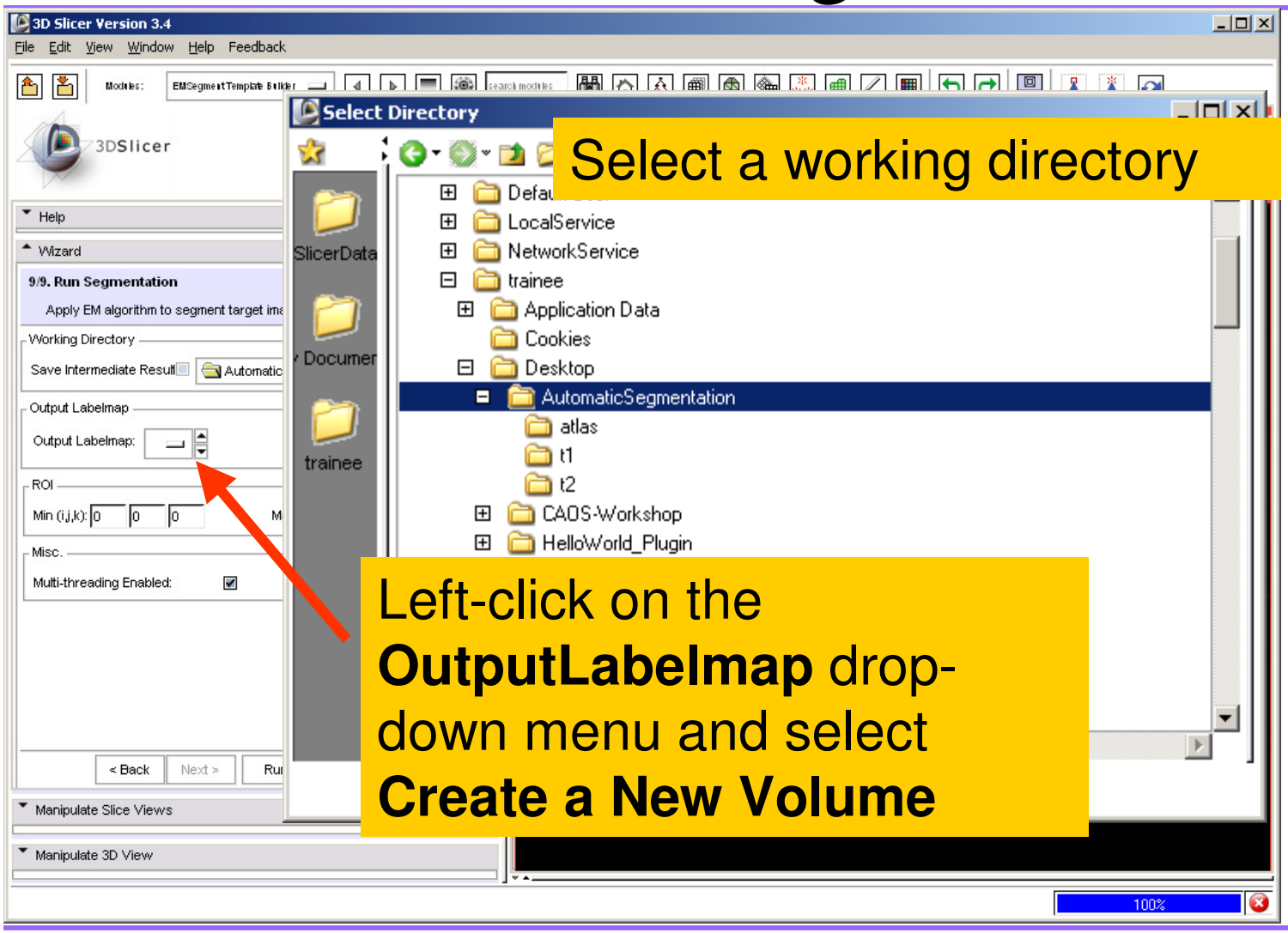
background



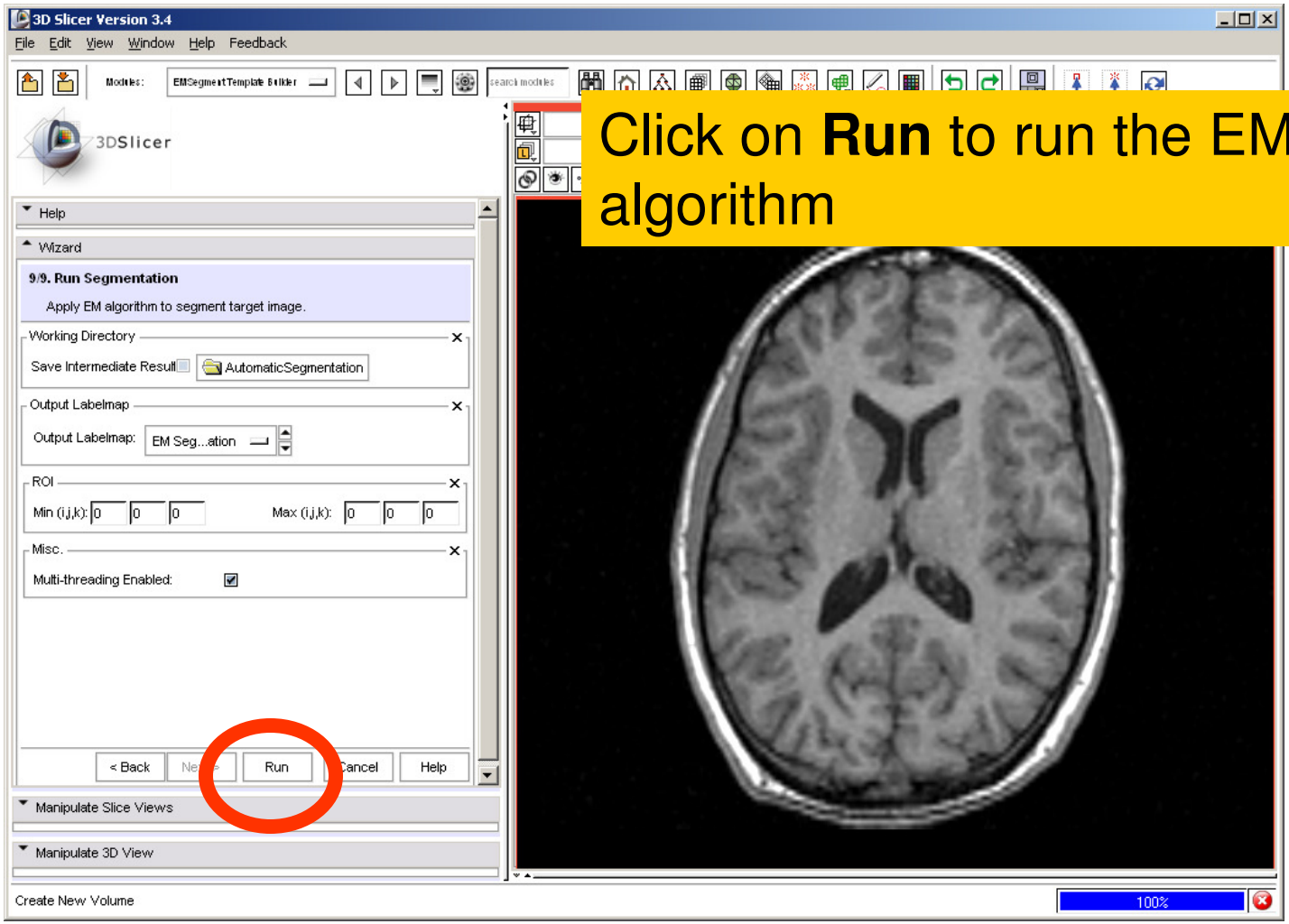
Segment using the Expectation Maximization algorithm

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

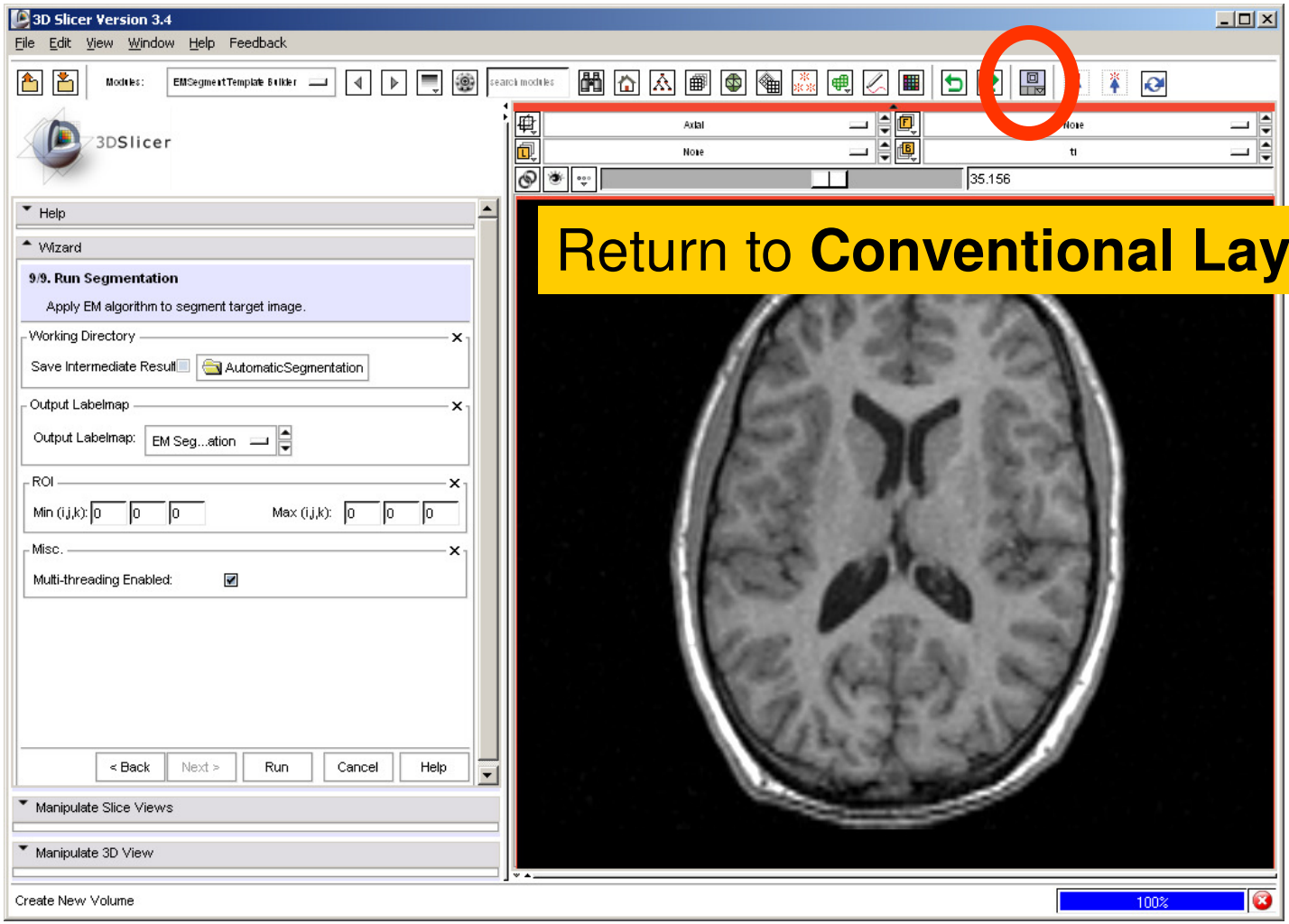
Segmentation



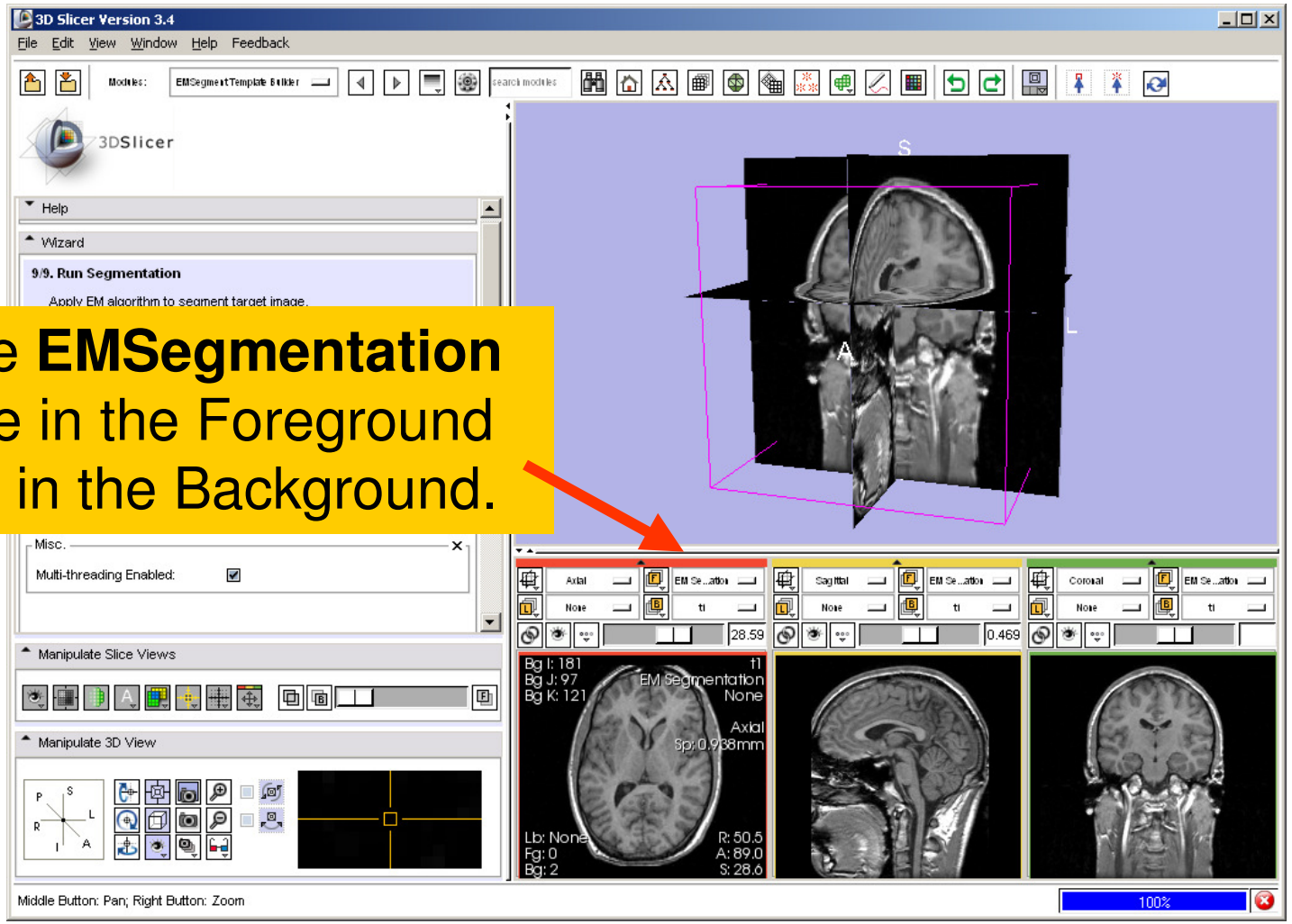
Segmentation



Segmentation



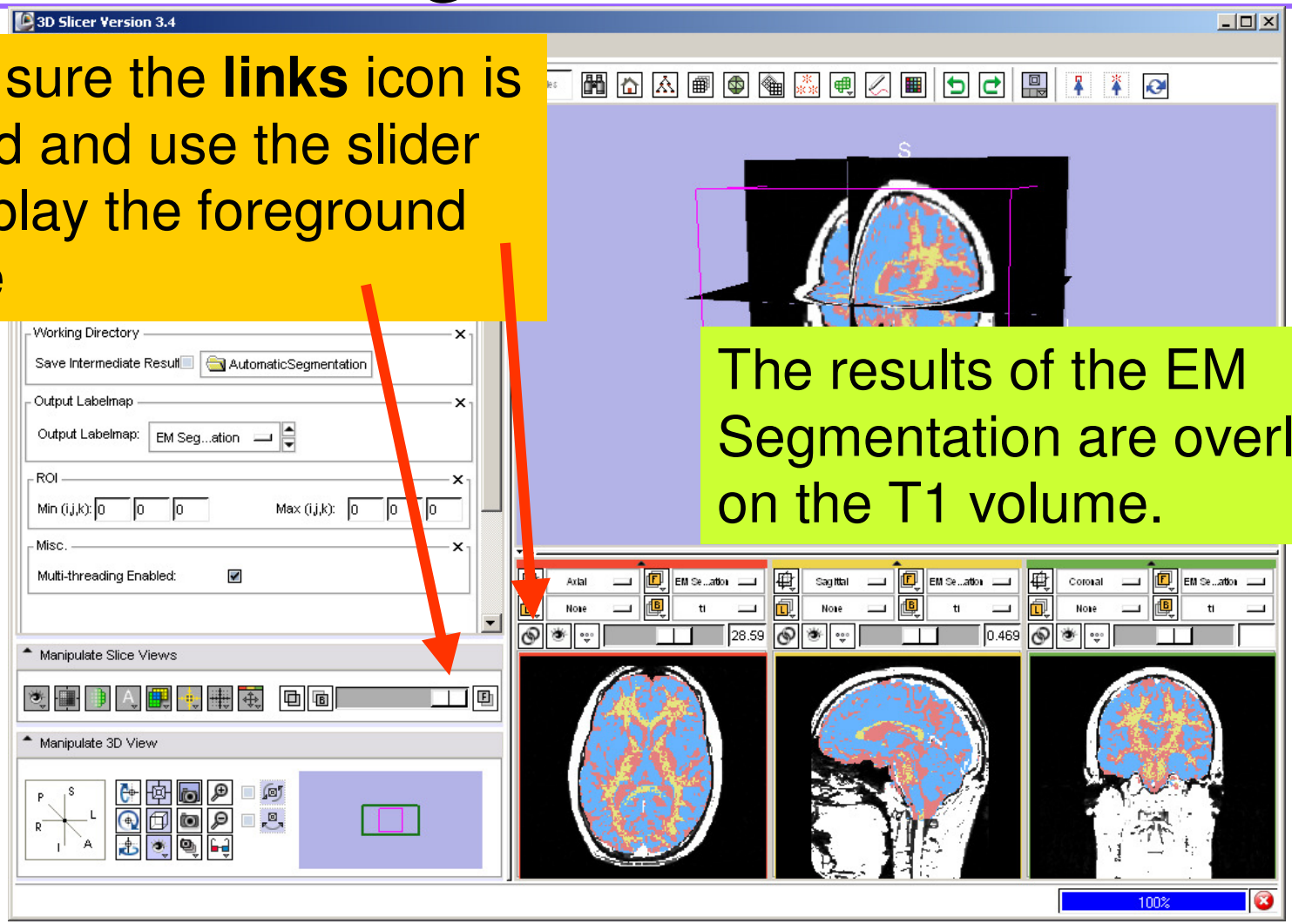
Segmentation Results



Set the **EMSegmentation** volume in the Foreground and **t1** in the Background.

Segmentation Results

Make sure the **links** icon is clicked and use the slider to display the foreground image



The results of the EM Segmentation are overlaid on the T1 volume.

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Neuroimage Analysis Center
NIH P41RR013218

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