

An Introduction to Image Phenotyping

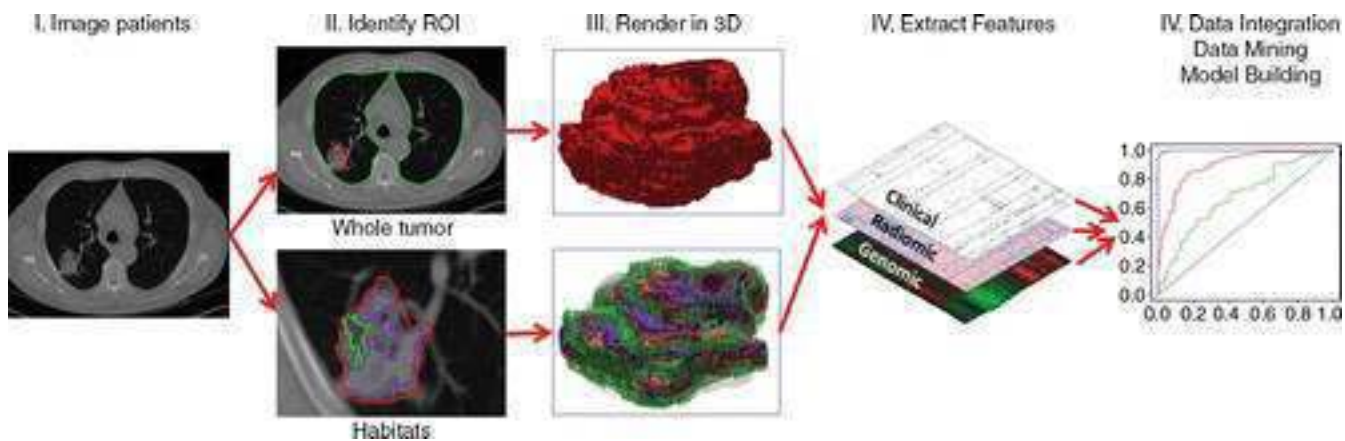
Sonia Pujol, Ph.D.

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Director of Training & Dissemination
Neuroimaging Analysis Center

Brigham and Women's Hospital
Harvard Medical School

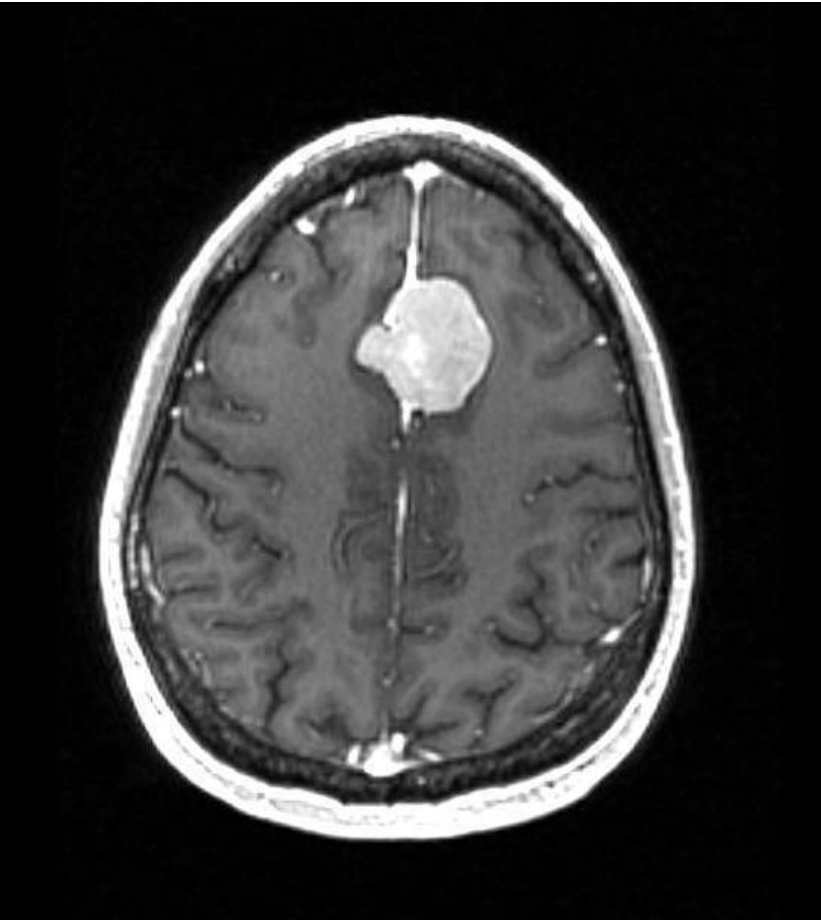
Imaging Phenotypes

- Imaging phenotypes describe features of disease that can be detected through medical imaging combined with feature detection, machine learning and statistical analysis, and correlated with other indicators of disease.



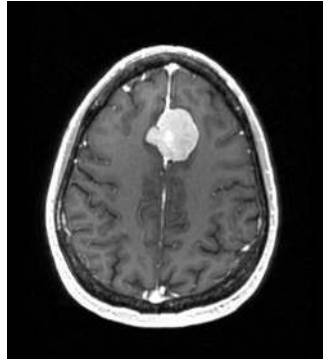
Gillies et al. Radiology 2015

Clinical Case: Meningioma



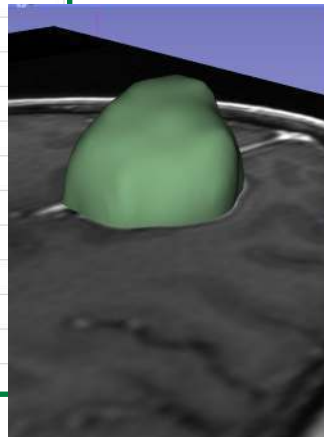
- Meningiomas are slow-growing extra axial brain tumor arising from arachnoidal cells
- Treatment options include observation, surgery and radiation therapy
- Image-based predictors of tumor grades have the potential to enhance clinical decision-making

Overall Goal

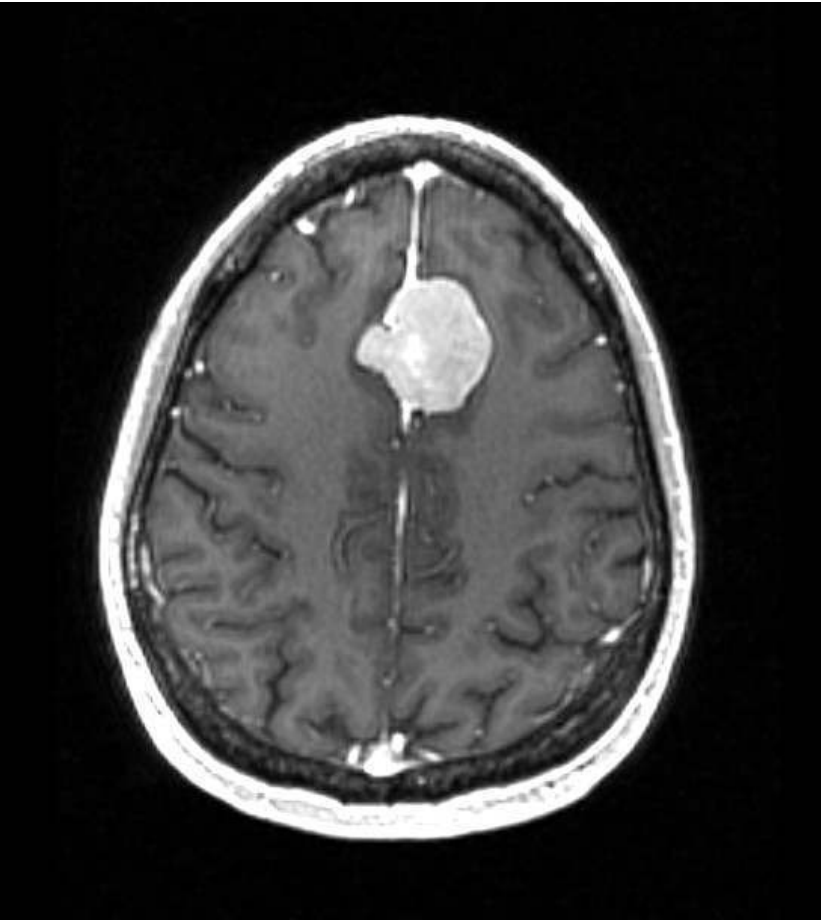


This tutorial is an introduction to the basics of image phenotyping for tumor characterization using the 3D Slicer platform.

Kurtosis	12.4315749384
Mean	179.297568367
GrayLevelVariance	1.00567651545
HighGrayLevelEmphasis	45.873151021
DependenceEntropy	6.16459662954
DependenceNonUniformity	548.562883325
GrayLevelNonUniformity	4972.61959737
SmallDependenceEmphasis	0.0389261318031
SmallDependenceHighGrayLe...	1.92568883112
DependenceNonUniformityNor...	0.0395817074338
LargeDependenceEmphasis	237.650263367
LargeDependenceLowGrayLev...	5.58612453125
DependenceVariance	51.1747739691



Imaging Features



- Quantitative features derived from imaging data have the potential to provide clinically relevant information for predicting tumor grade and evaluating response treatment

Tutorial materials

- 3D Slicer release version 4.10.1
- Slicer Radiomics Extension
- Meningioma dataset



3D Slicer installation

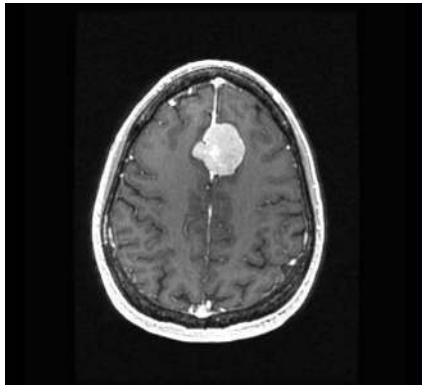
- To install and start the 3D Slicer software on your computer, follow the instructions of the **Quick Start Guide tutorial** available at <https://www.slicer.org/wiki/Documentation/4.10/Training>

	Windows	Mac OS X	Linux
Stable Release <i>older releases</i>	version 4.10.1 revision 27931 built 2019-01-16	version 4.10.1 revision 27931 built 2019-01-18	version 4.10.1 revision 27931 built 2019-01-16
Nightly Build	version 4.11.0 revision 28040 built 2019-03-18	version 4.11.0 revision 28040 built 2019-03-18	version 4.11.0 revision 28040 built 2019-03-18

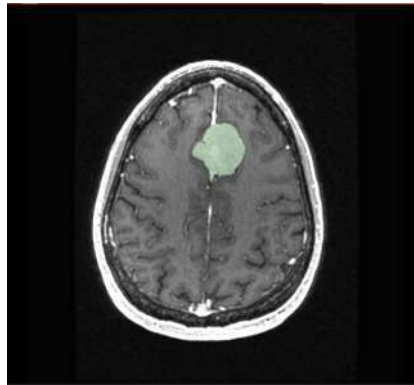
Disclaimer

- 3D Slicer is a free open source software for medical image computing research distributed under a BDS style license.
- The software is not FDA approved or CE-Marked, and is for research use only.

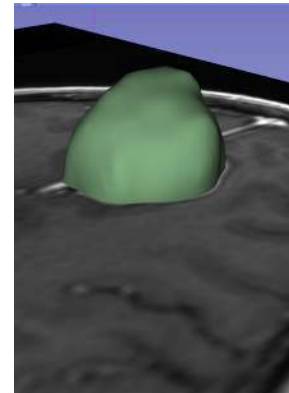
Workflow Overview



Step 1: Data
Loading



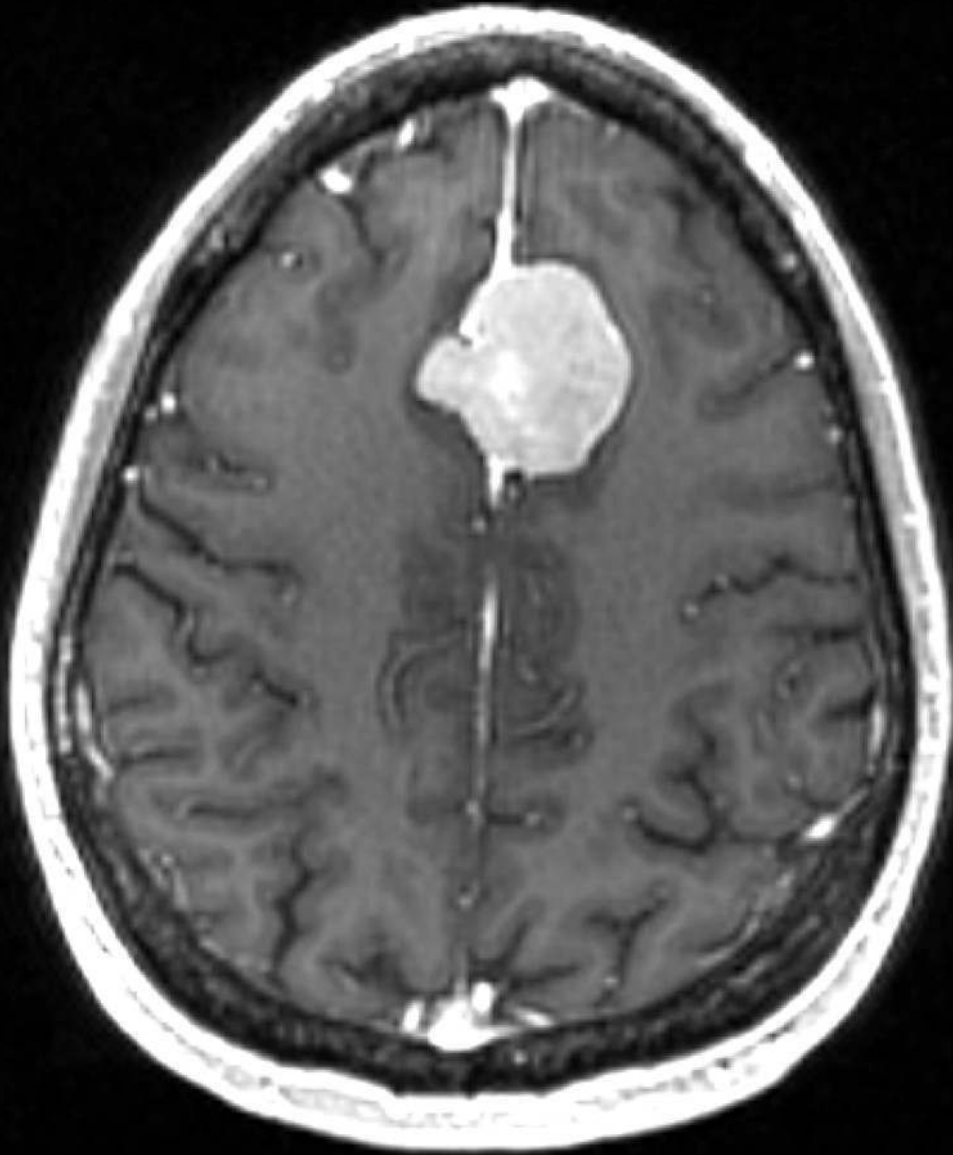
Step 2: Tumor
Segmentation



Step 3: Tumor
Volume Calculation

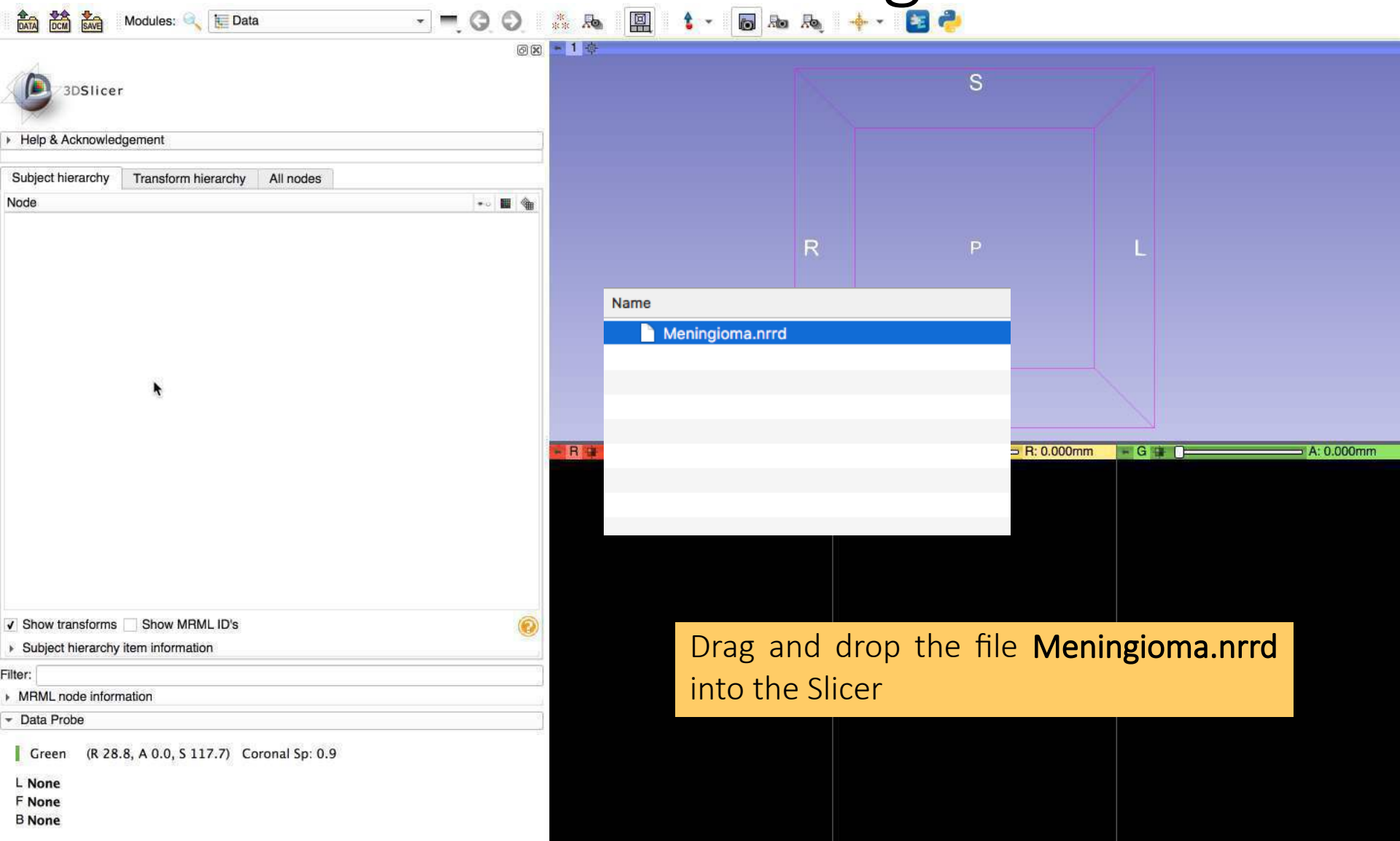
Kurtosis	12.4315749384
Mean	179.297568367
GrayLevelVariance	1.00567651545
HighGrayLevelEmphasis	45.873151021
DependenceEntropy	6.16459662954
DependenceNonUniformity	548.562883325
GrayLevelNonUniformity	4972.61959737
SmallDependenceEmphasis	0.0389261318031
SmallDependenceHighGrayLe...	1.92568883112
DependenceNonUniformityNor...	0.0395817074338
LargeDependenceEmphasis	237.650263367
LargeDependenceLowGrayLev...	5.58612453125
DependenceVariance	51.1747739691

Step 4: Imaging Features
Extraction

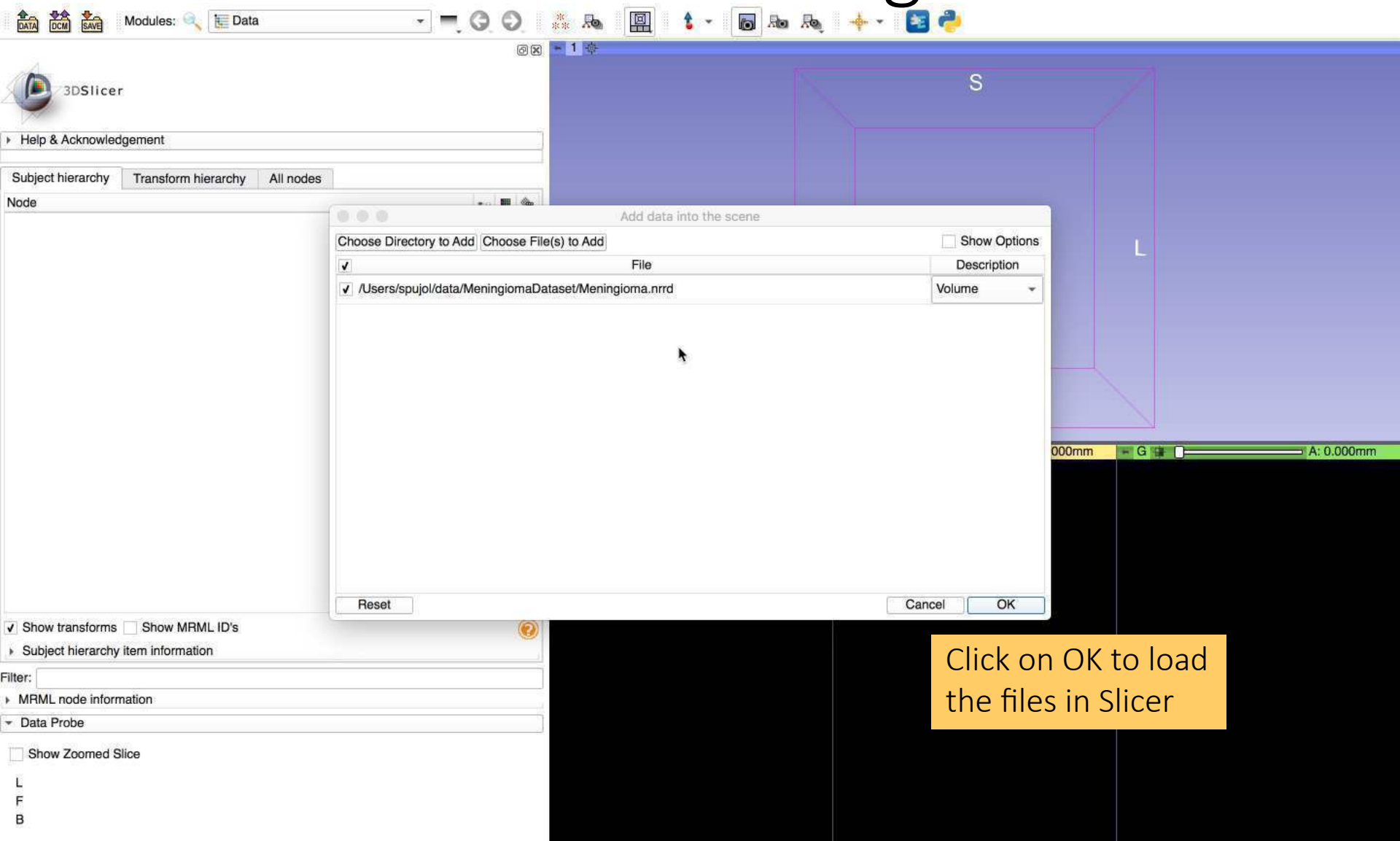


Part 1: Data
Loading and tumor
diameter
measurements

Data Loading



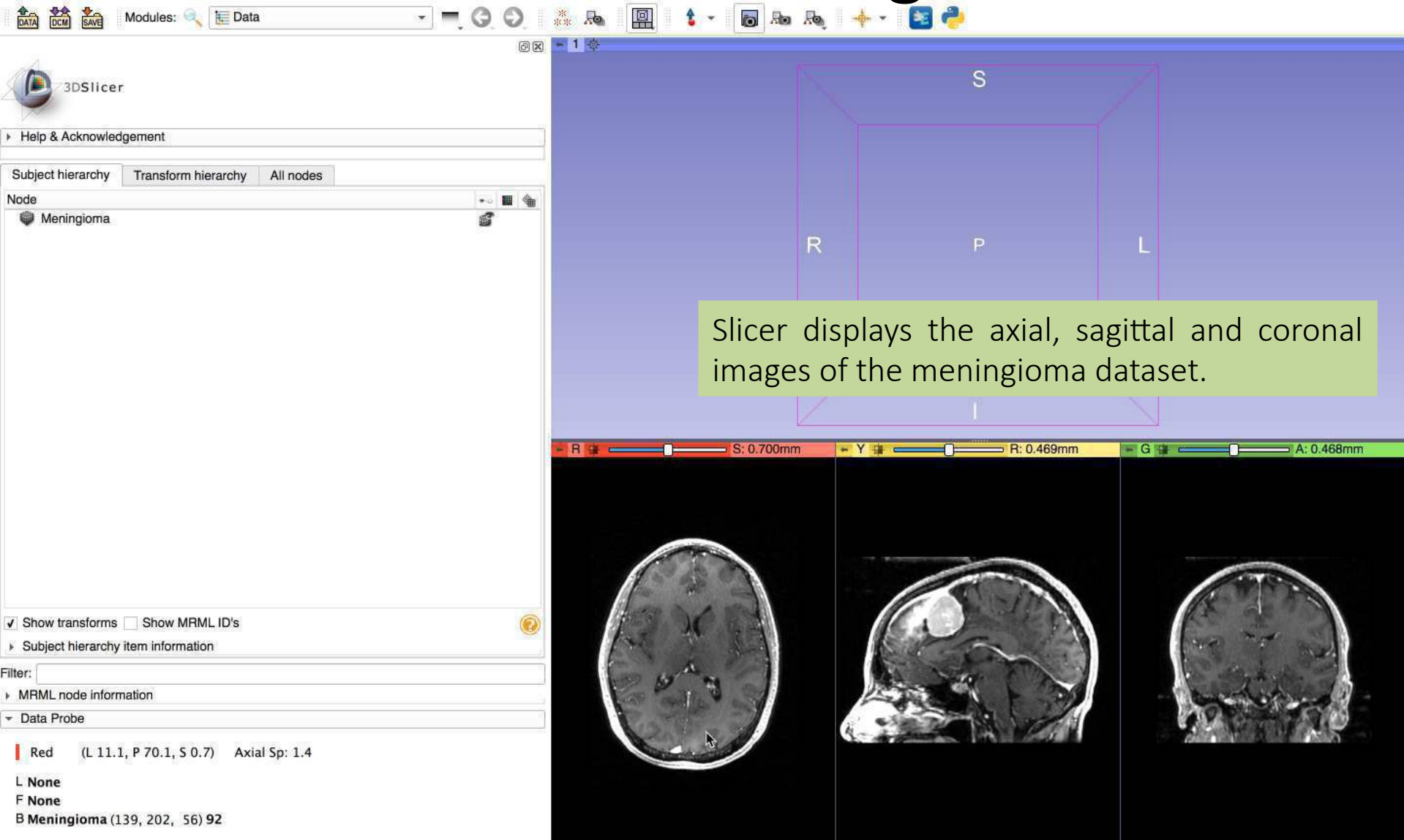
Data Loading



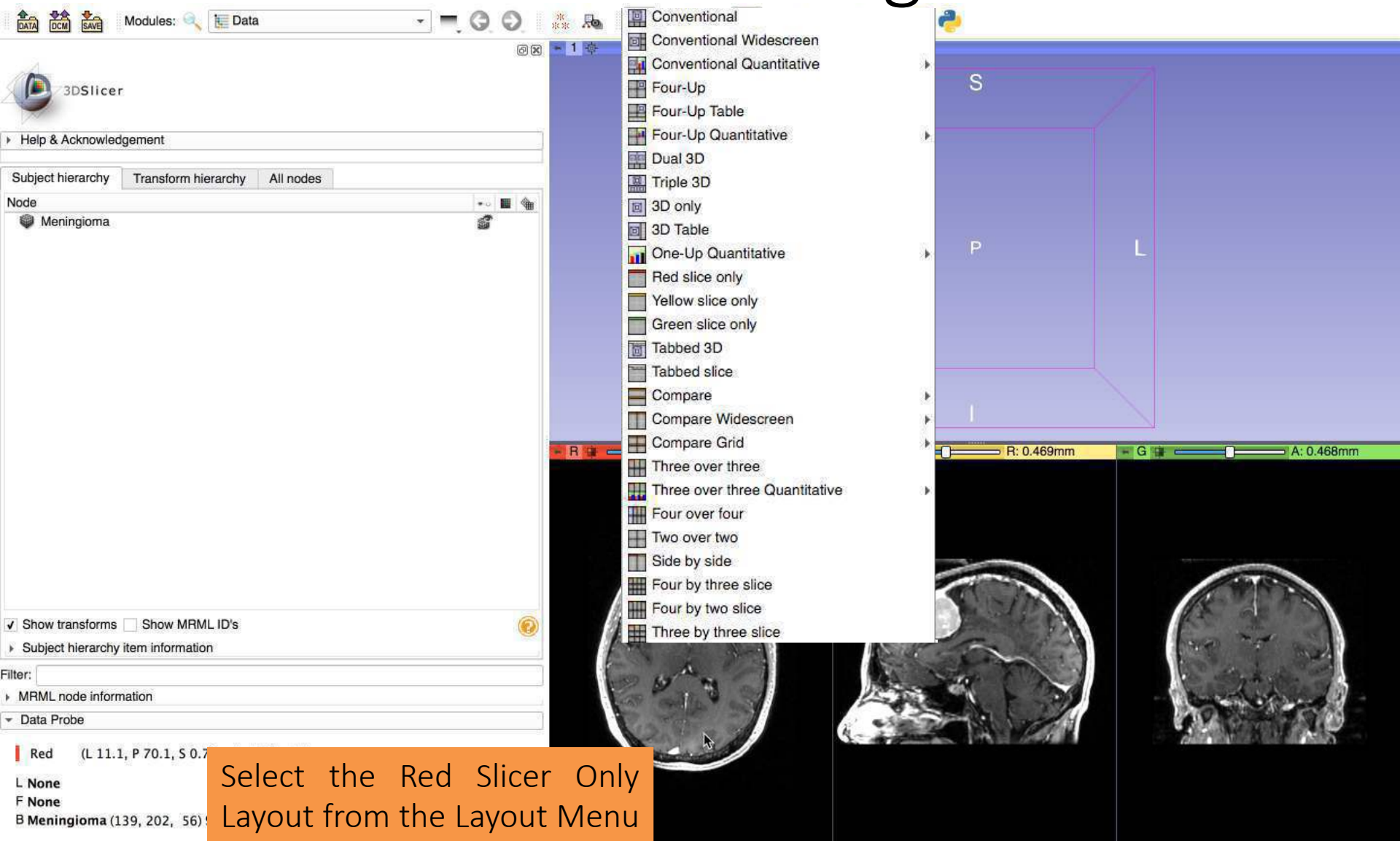
Click on OK to load the files in Slicer



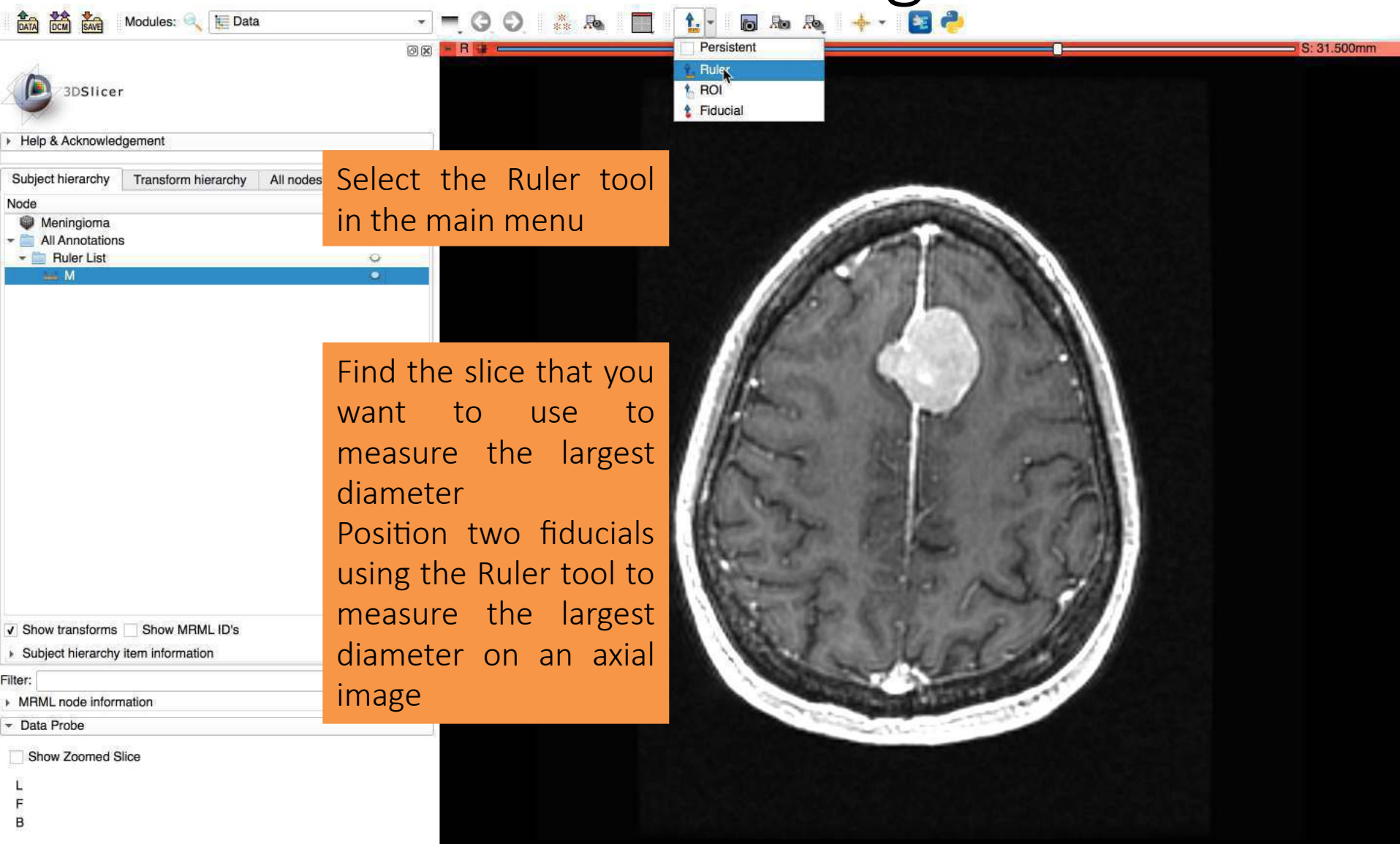
Data Loading



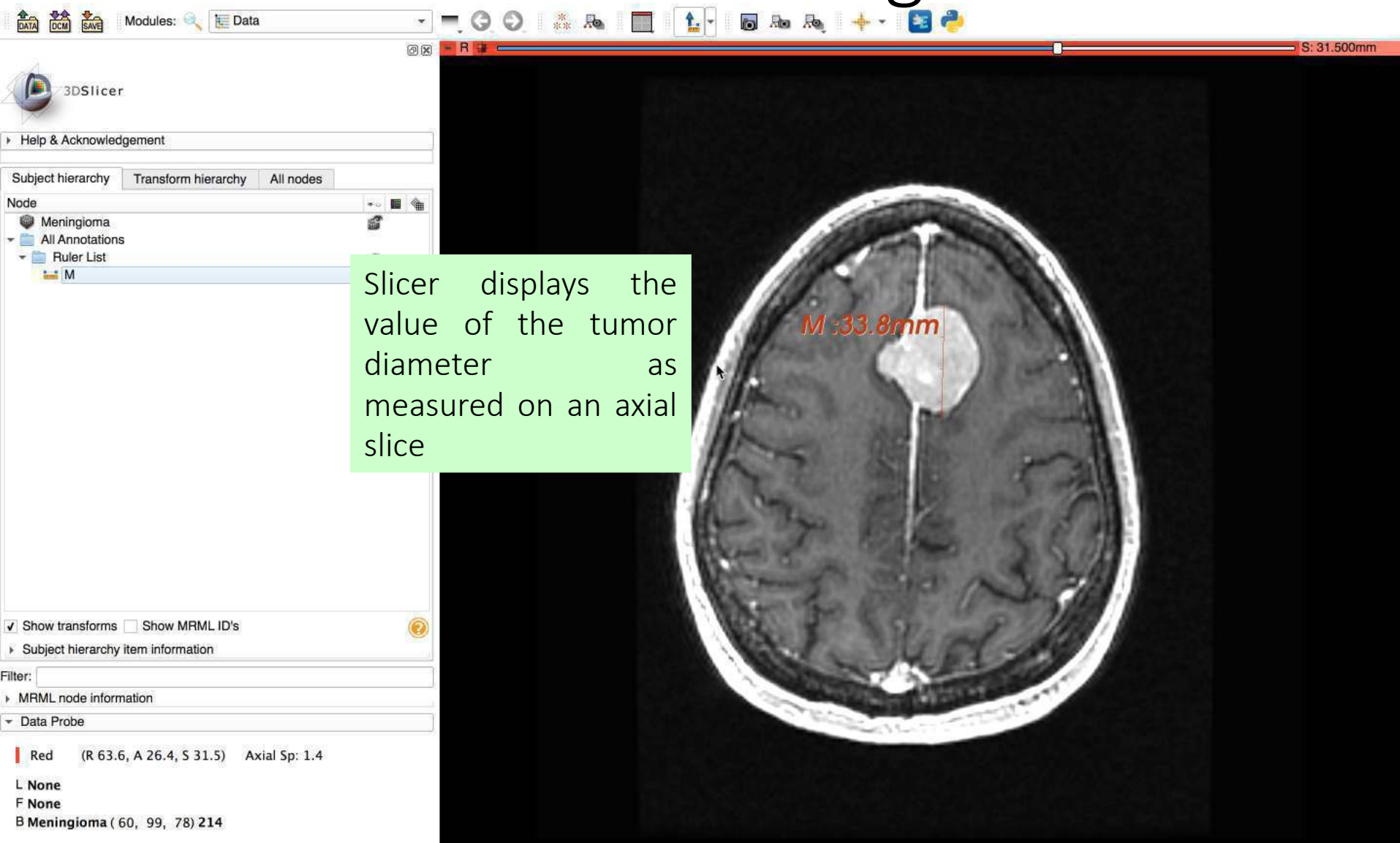
Data Loading

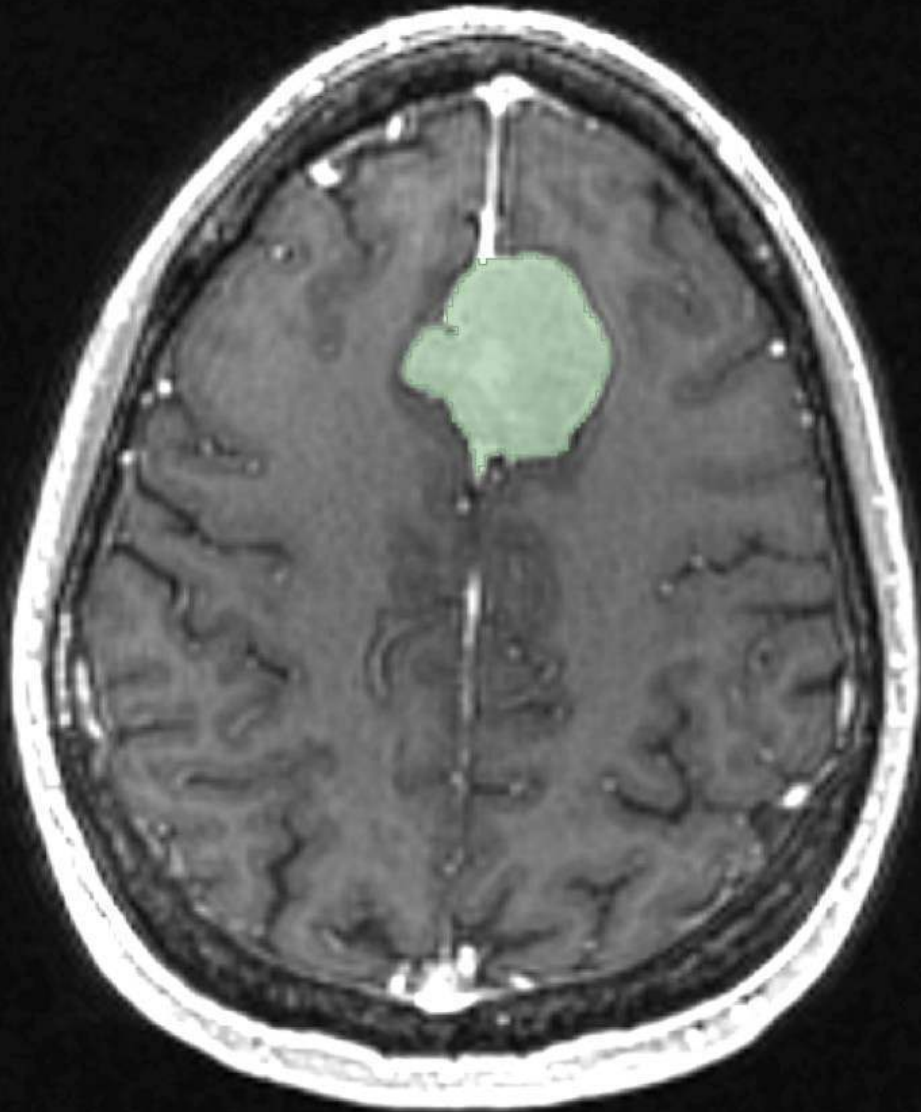


Data Loading



Data Loading





Part
Seg

Part 2: Tumor Segmentation

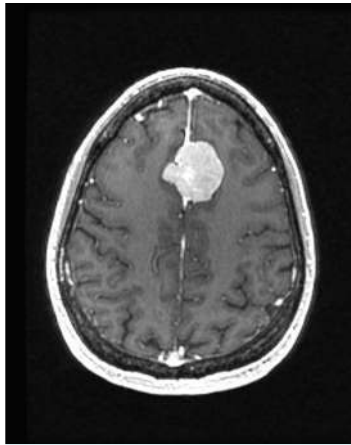
Image Segmentation

- Image Segmentation is the process of identifying the contours of structures of interest in imaging data
- Image Segmentation can be performed by manual contouring or by using automated segmentation algorithms

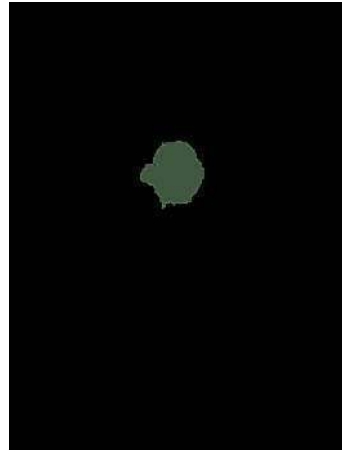
Image Segmentation

- The Segment Editor module of 3D Slicer provides powerful tools for manual and semi-automated segmentation
- The module takes a reference image (**Master Volume**) as input and produces a segmented image (**Segmentation**) in output

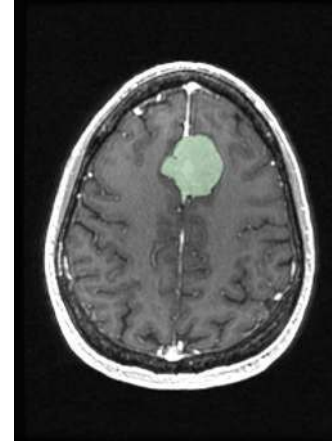
Terminology



Master Volume



Segmentation

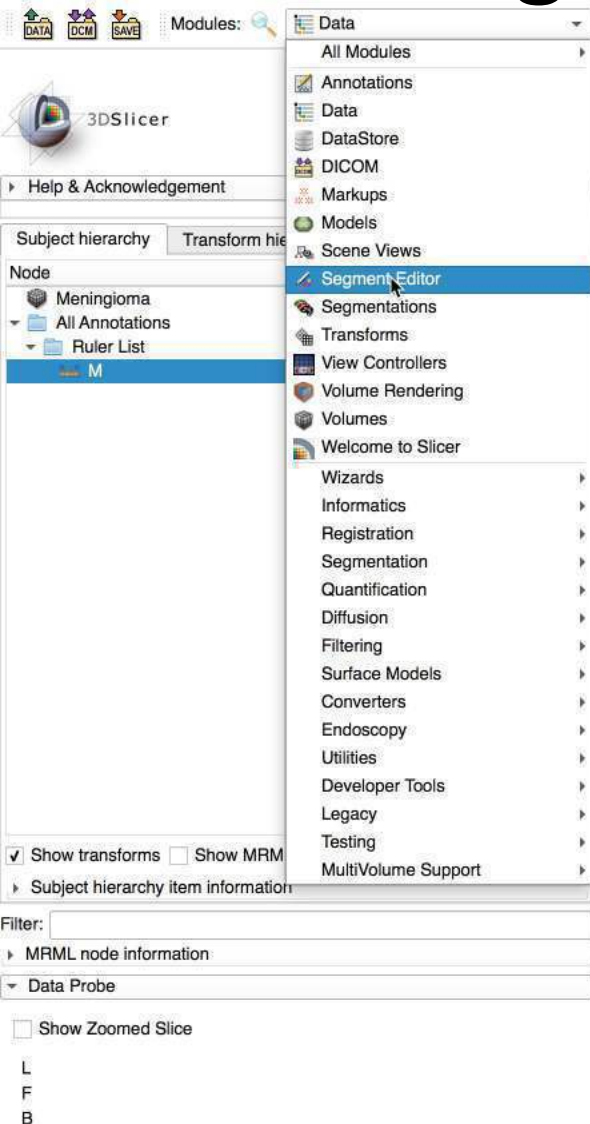


Master Volume
&
Segmentation

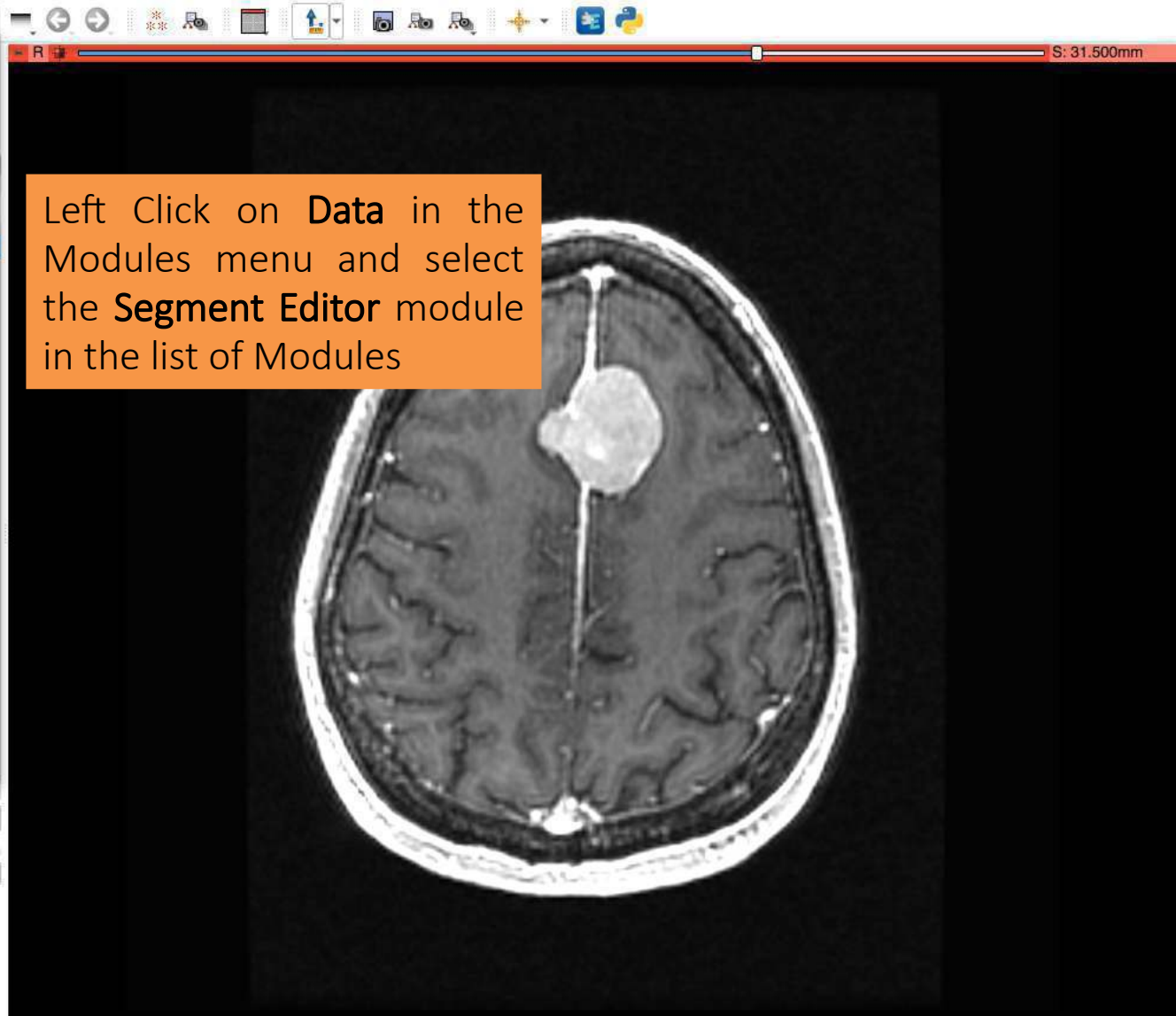
In this tutorial,

- The Master Volume **Meningioma** is the initial brain MRI dataset
- The Segmentation Volume **Segmentation** is a segmentation object with the same dimensions and origin as the Master Volume

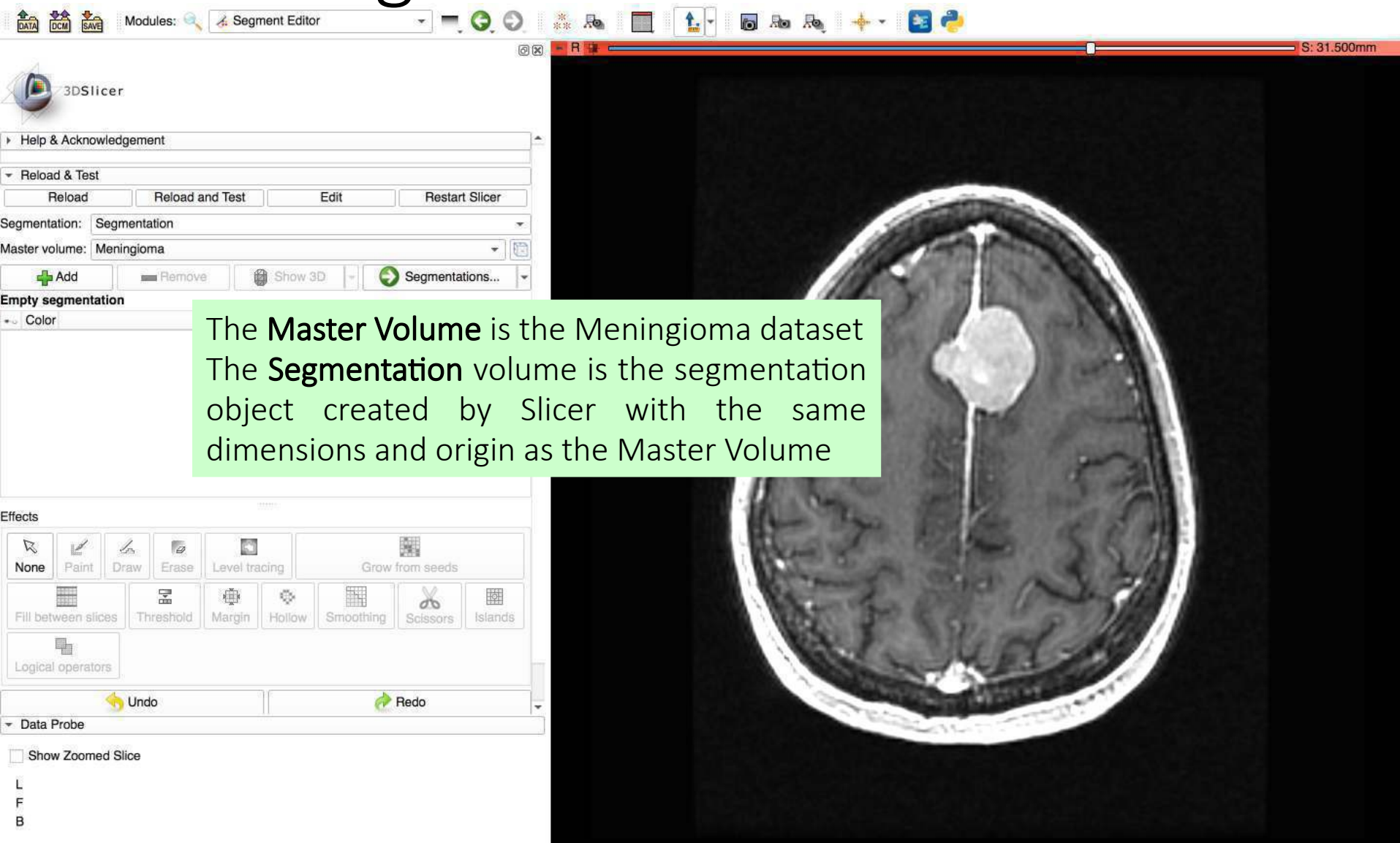
Segment Editor Module



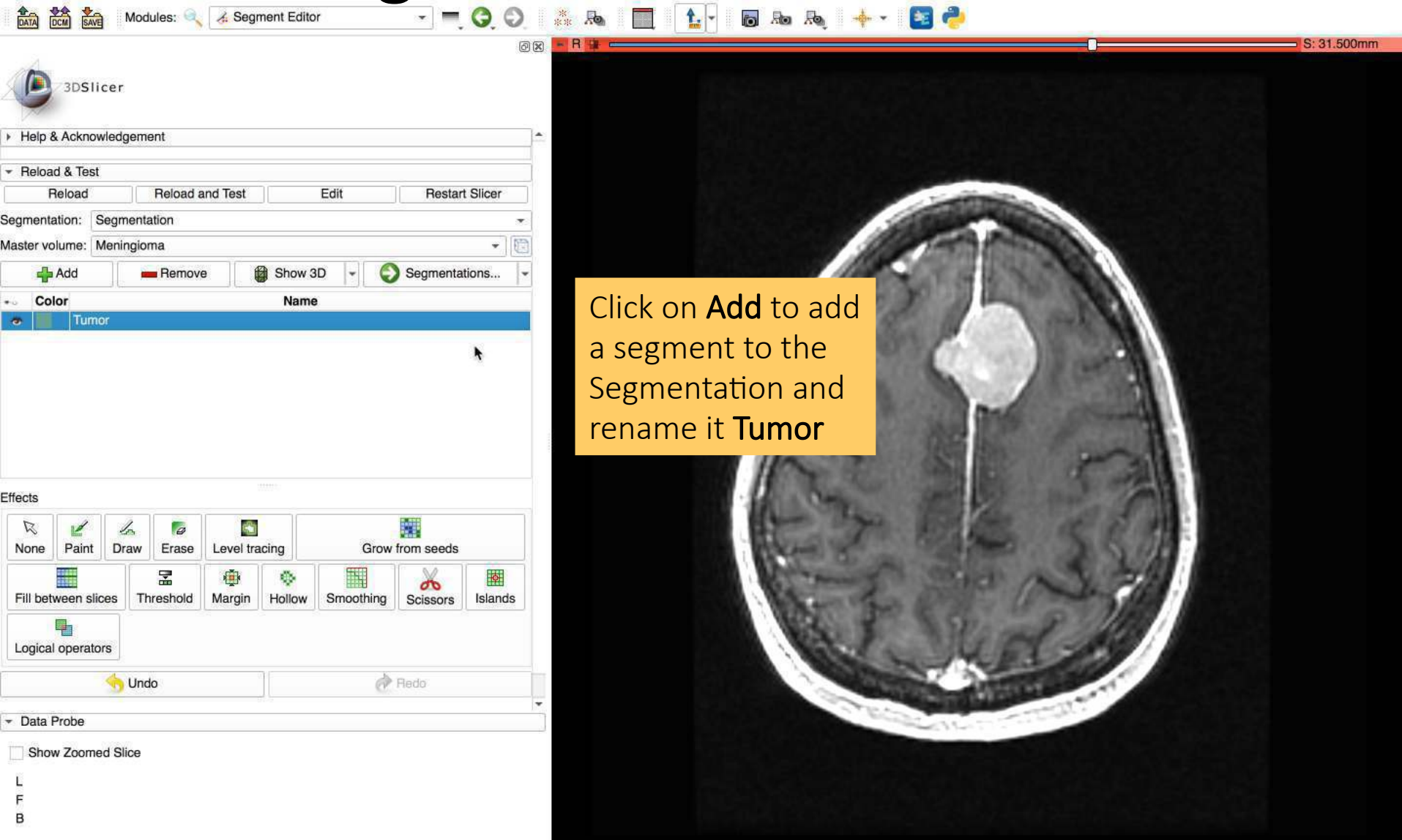
Left Click on **Data** in the Modules menu and select the **Segment Editor** module in the list of Modules



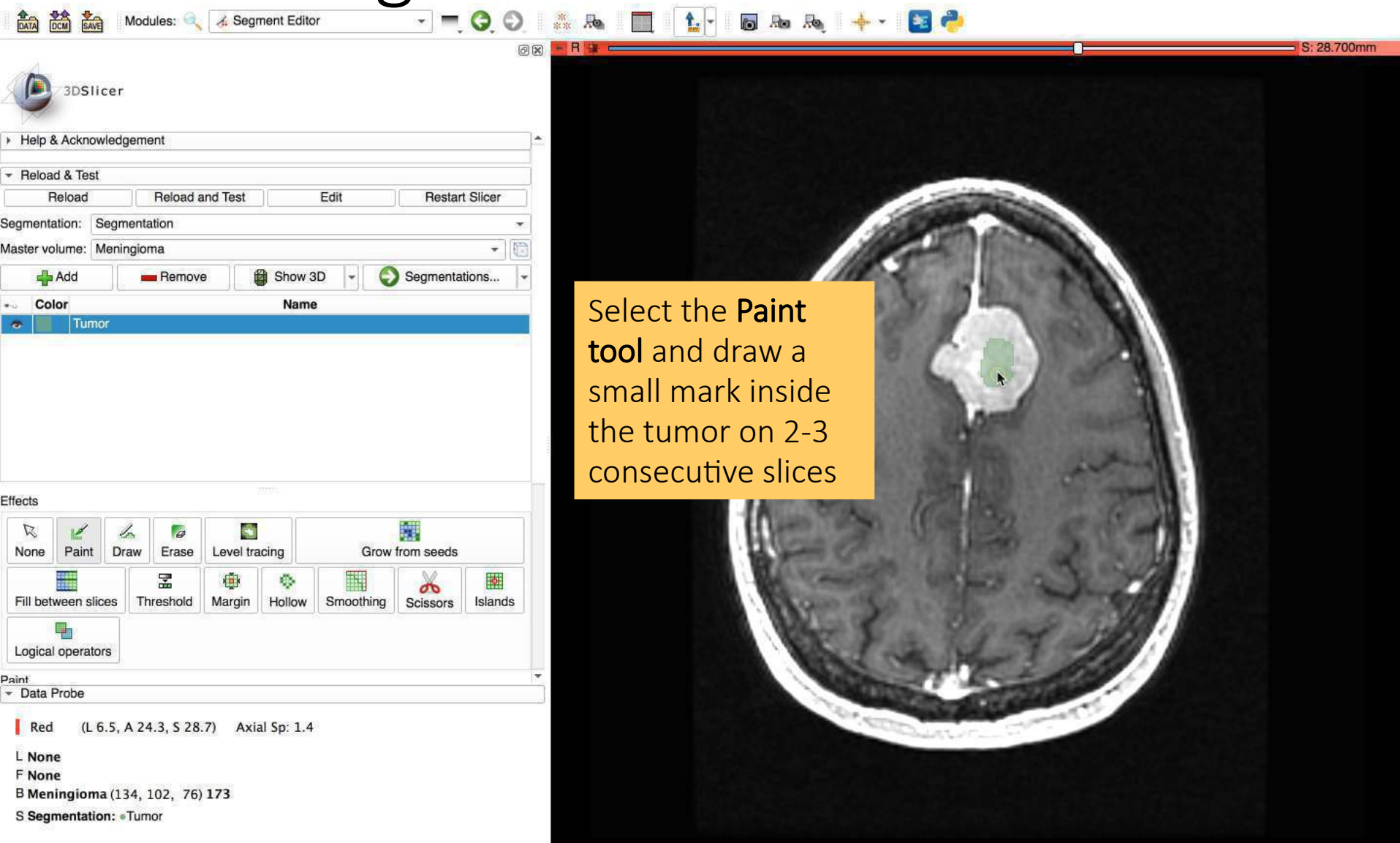
Segment Editor Module



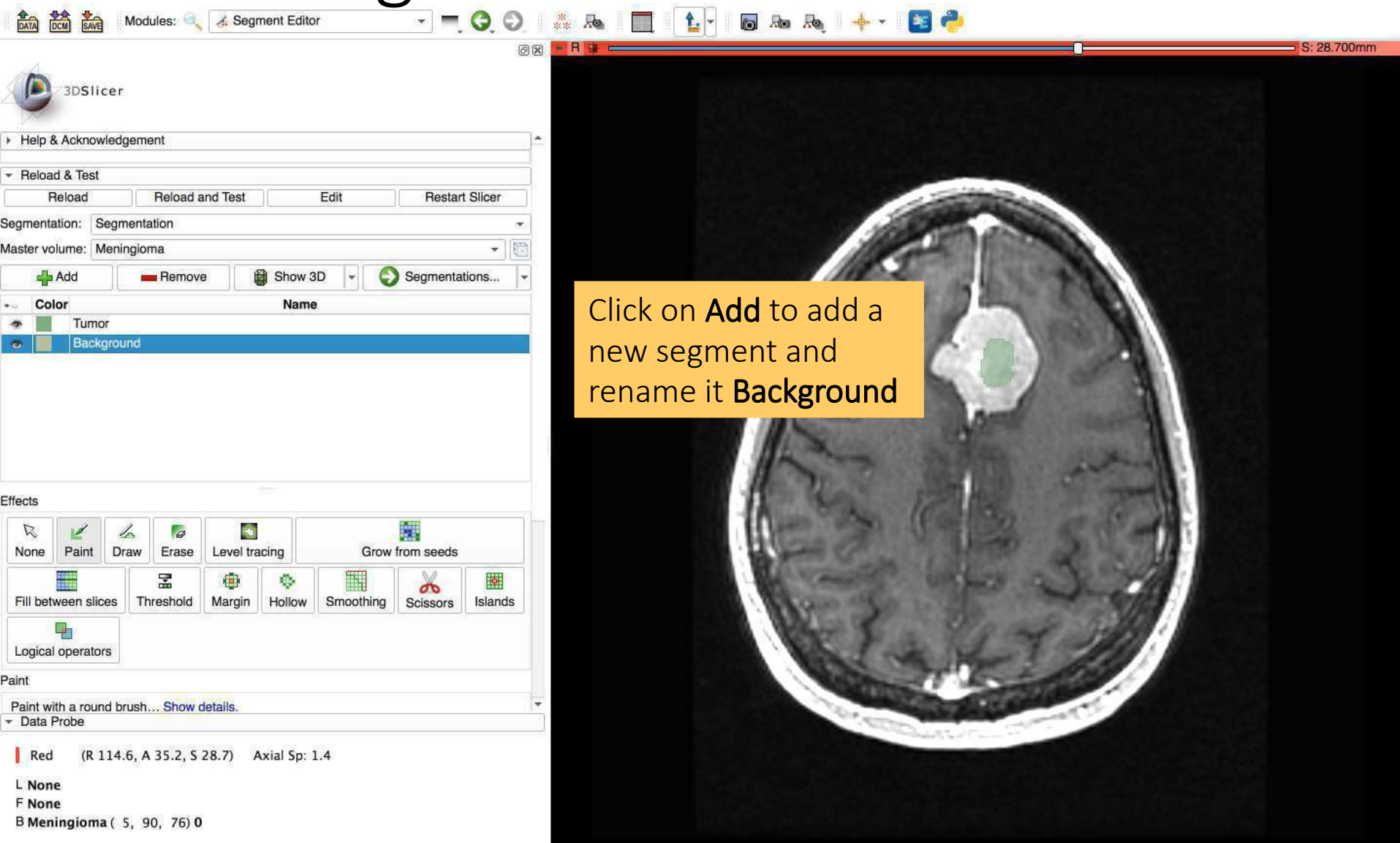
Segment Editor Module



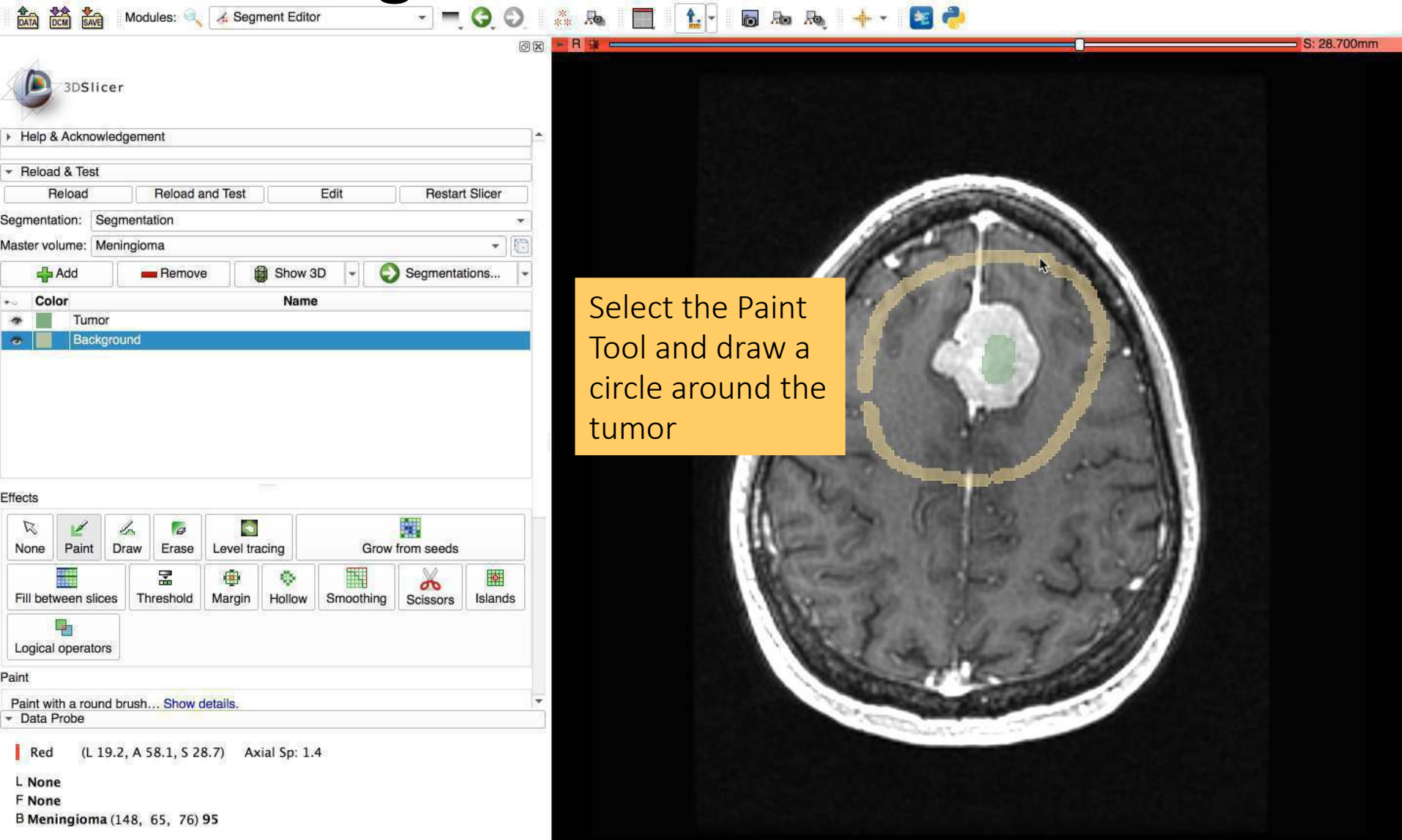
Segment Editor Module



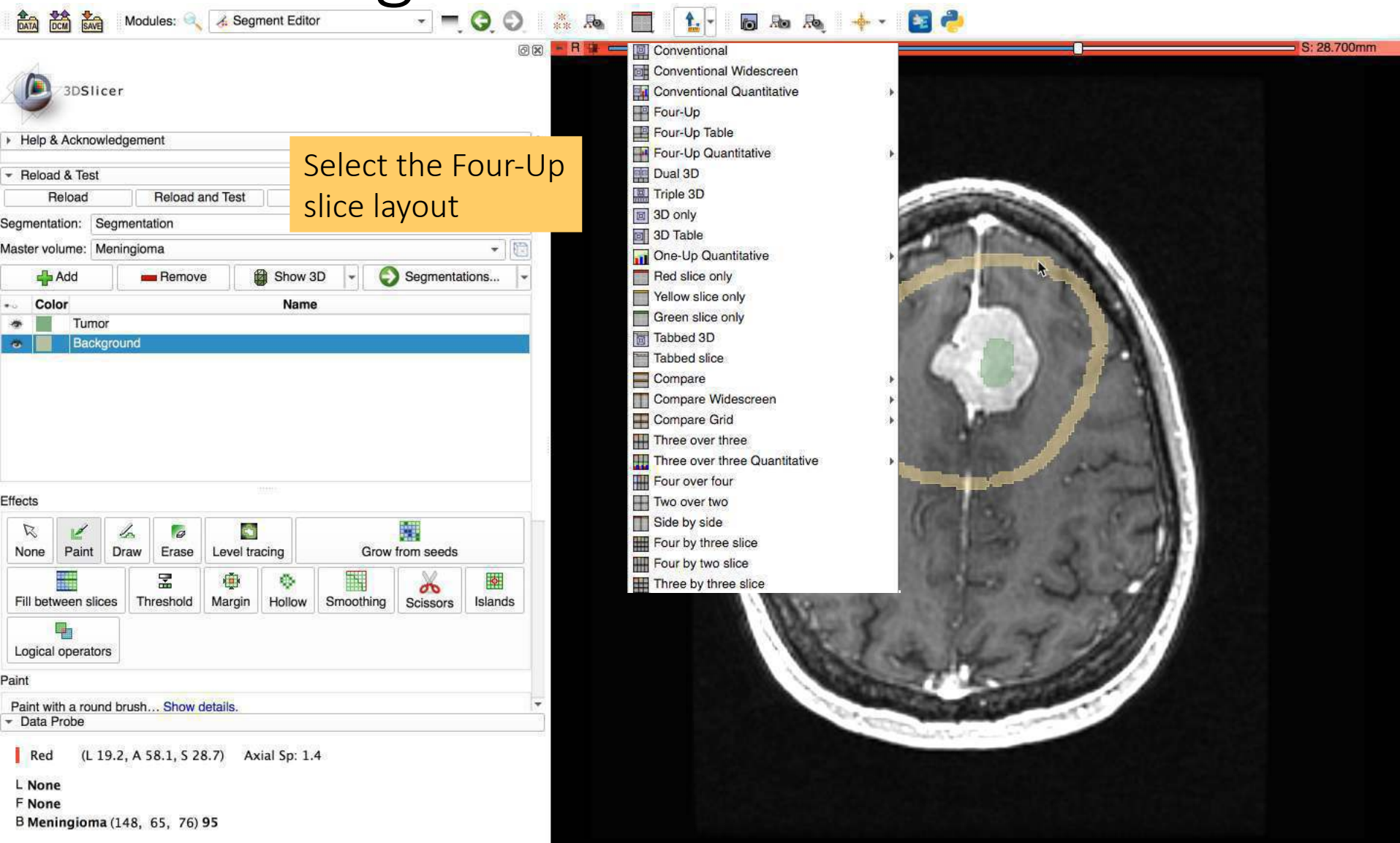
Segment Editor Module



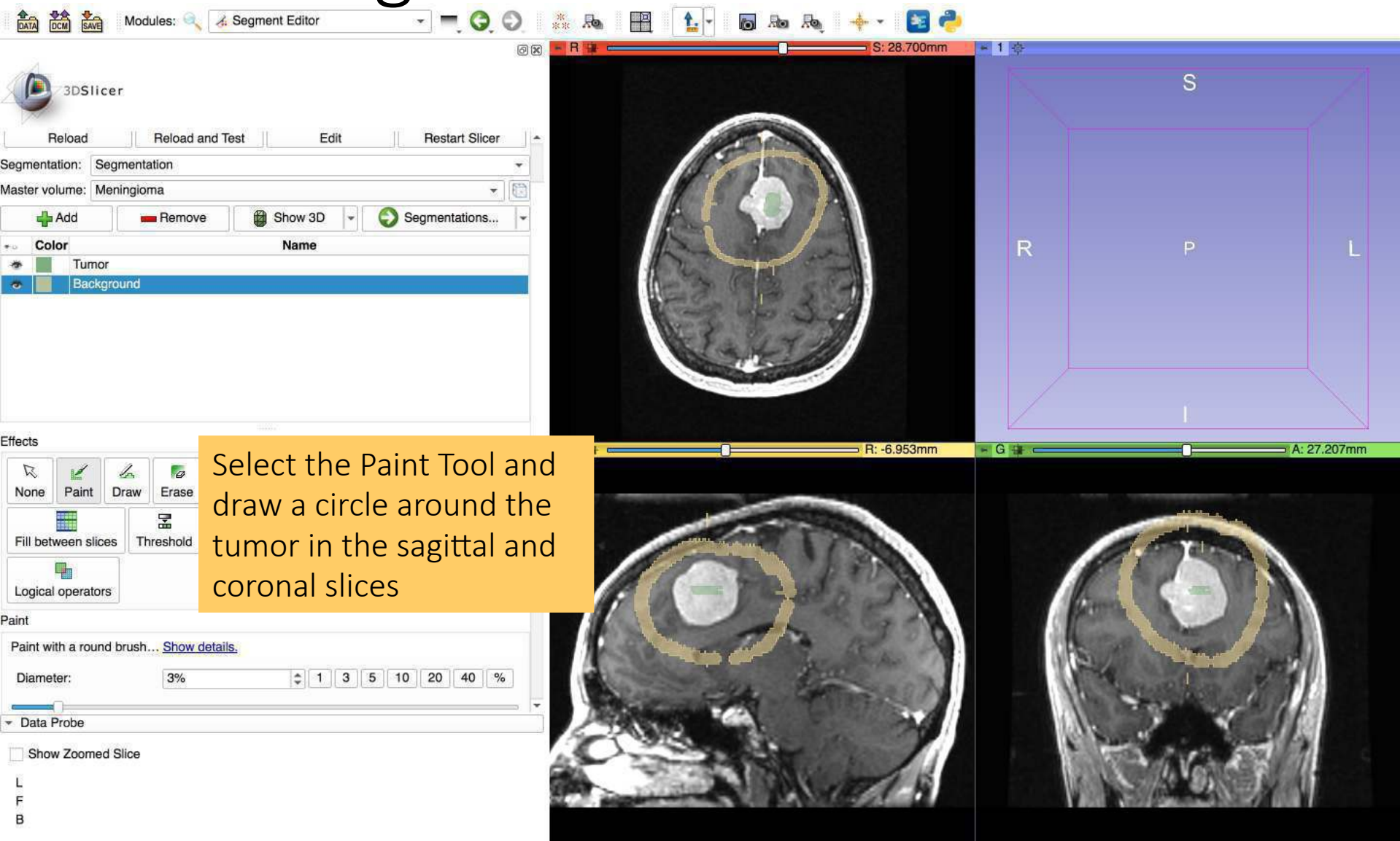
Segment Editor Module



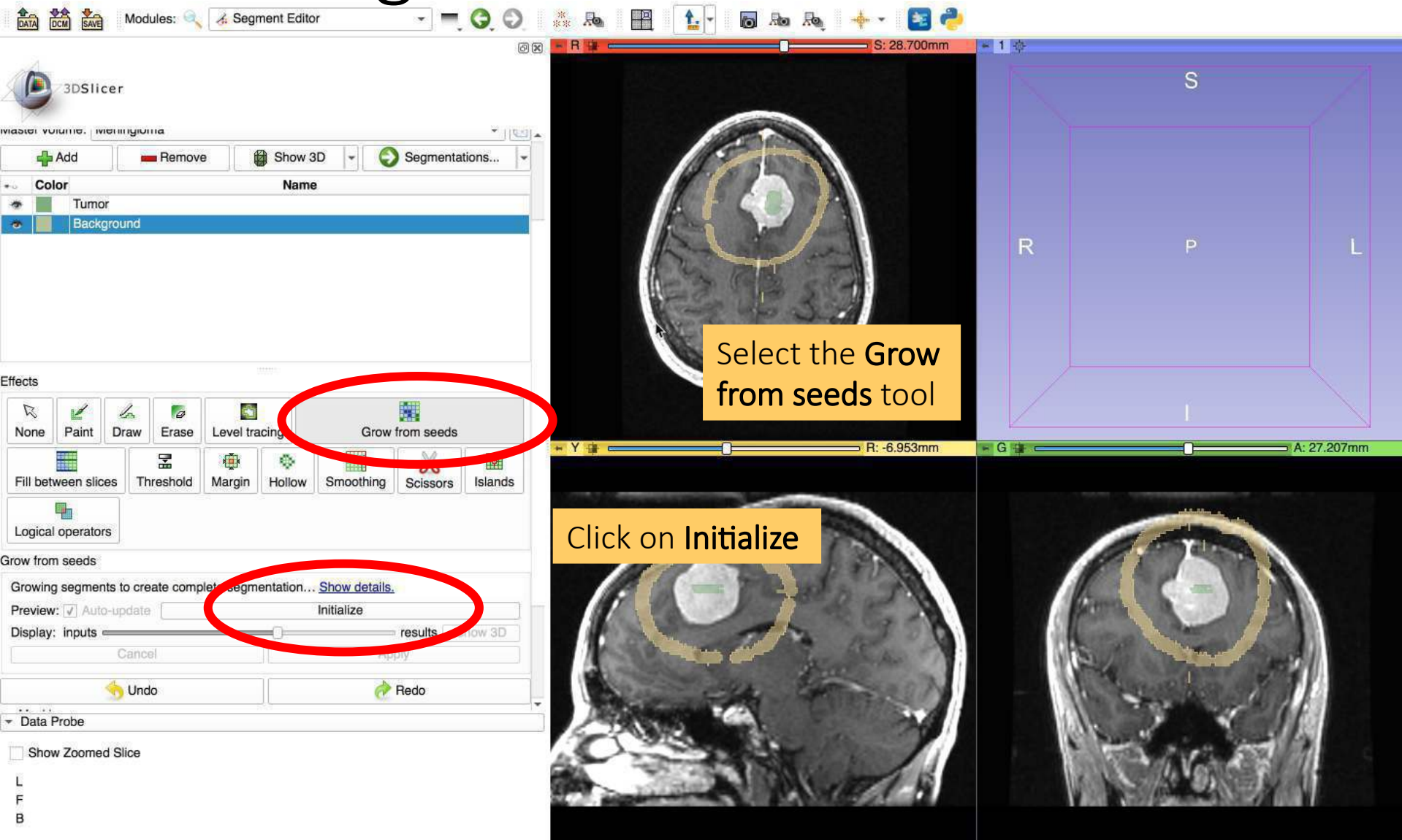
Segment Editor Module



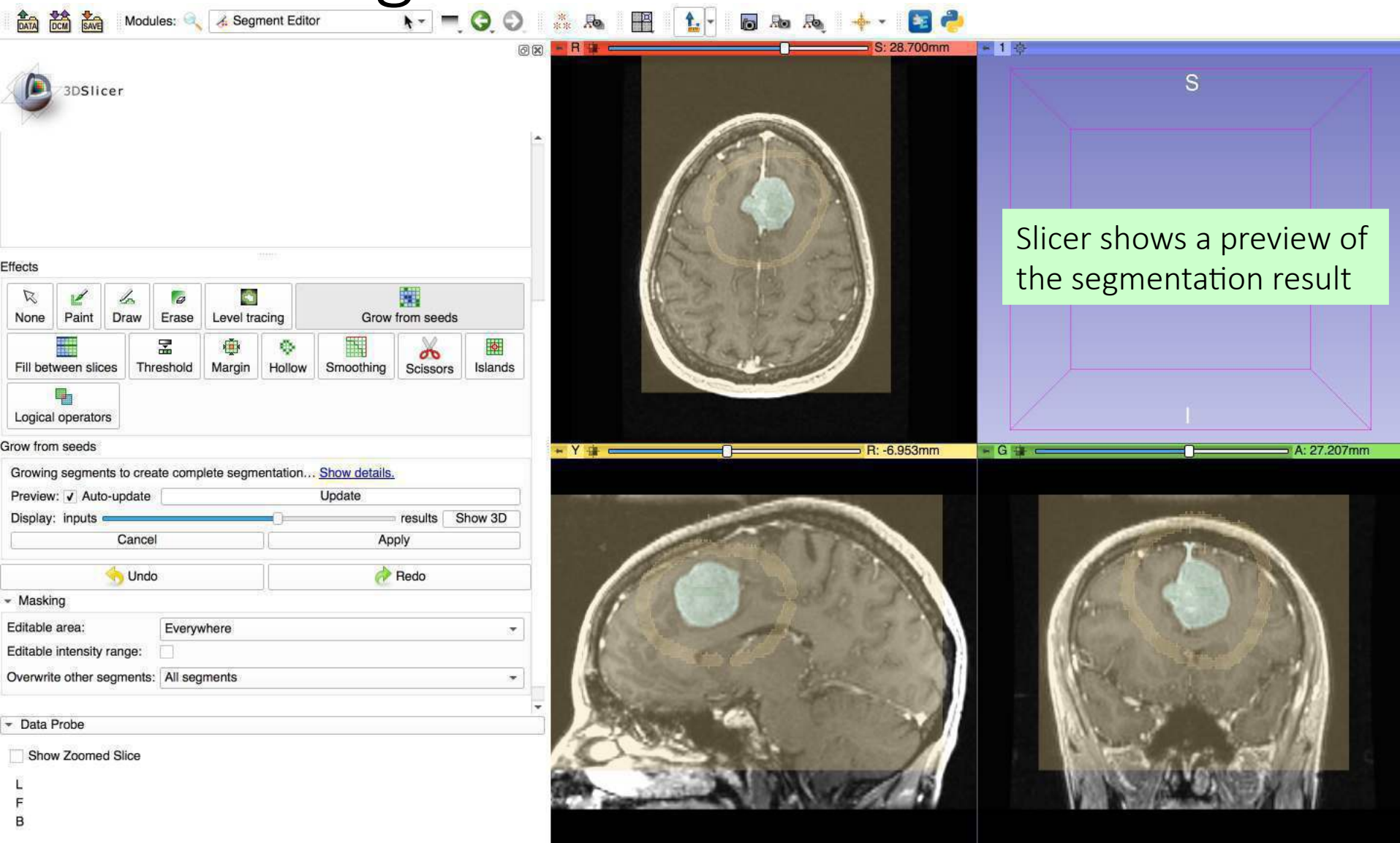
Segment Editor Module



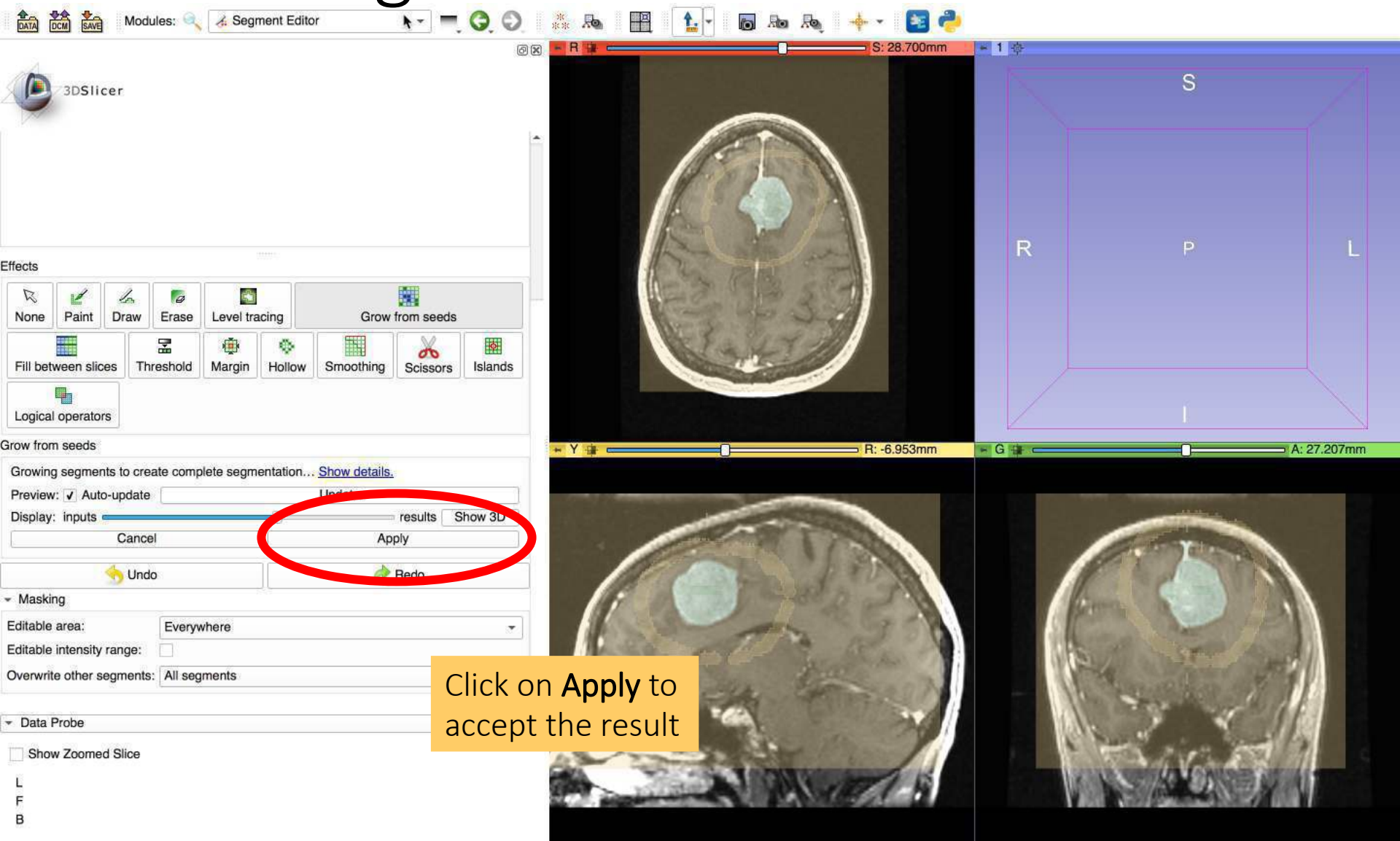
Segment Editor Module



Segment Editor Module



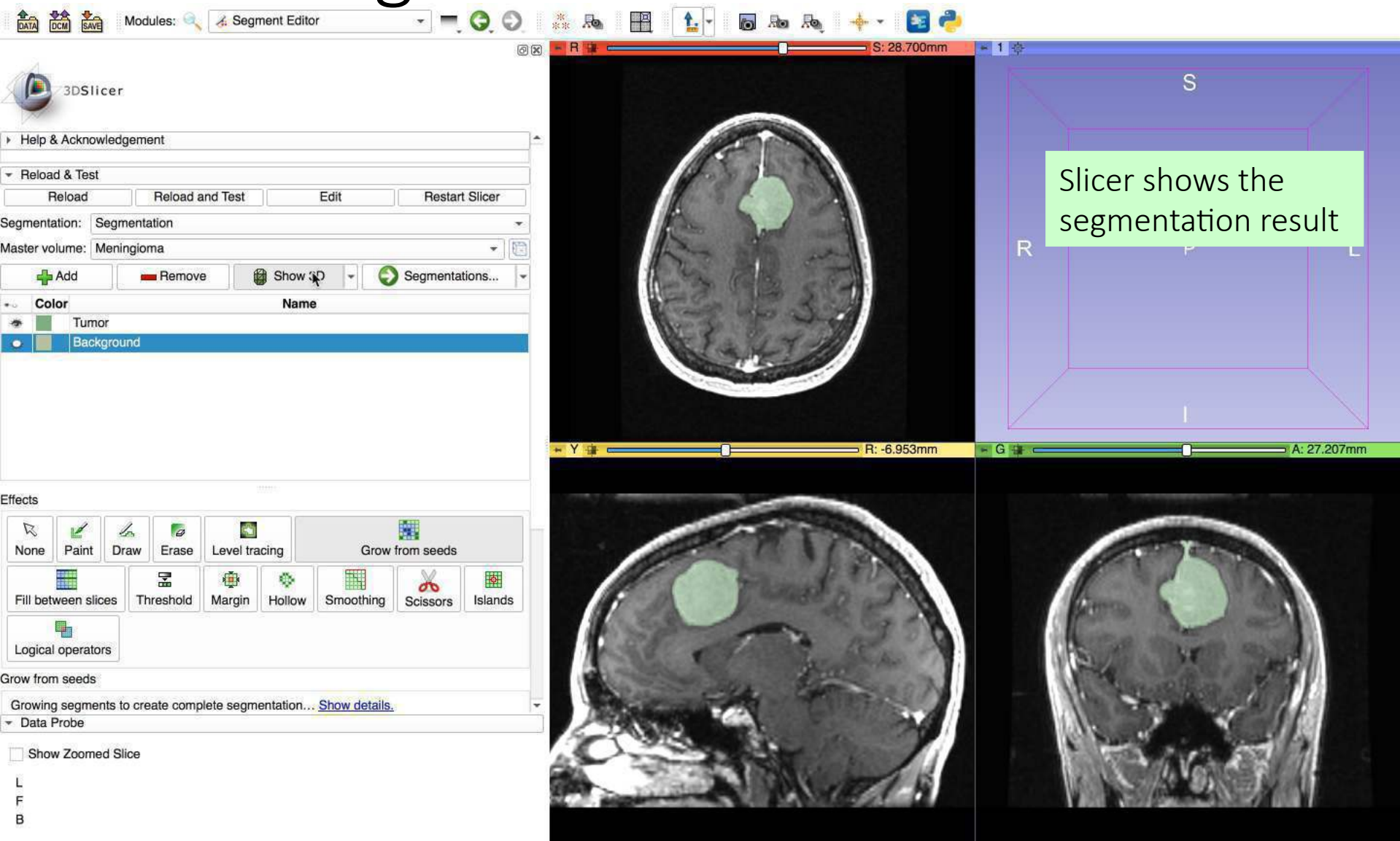
Segment Editor Module



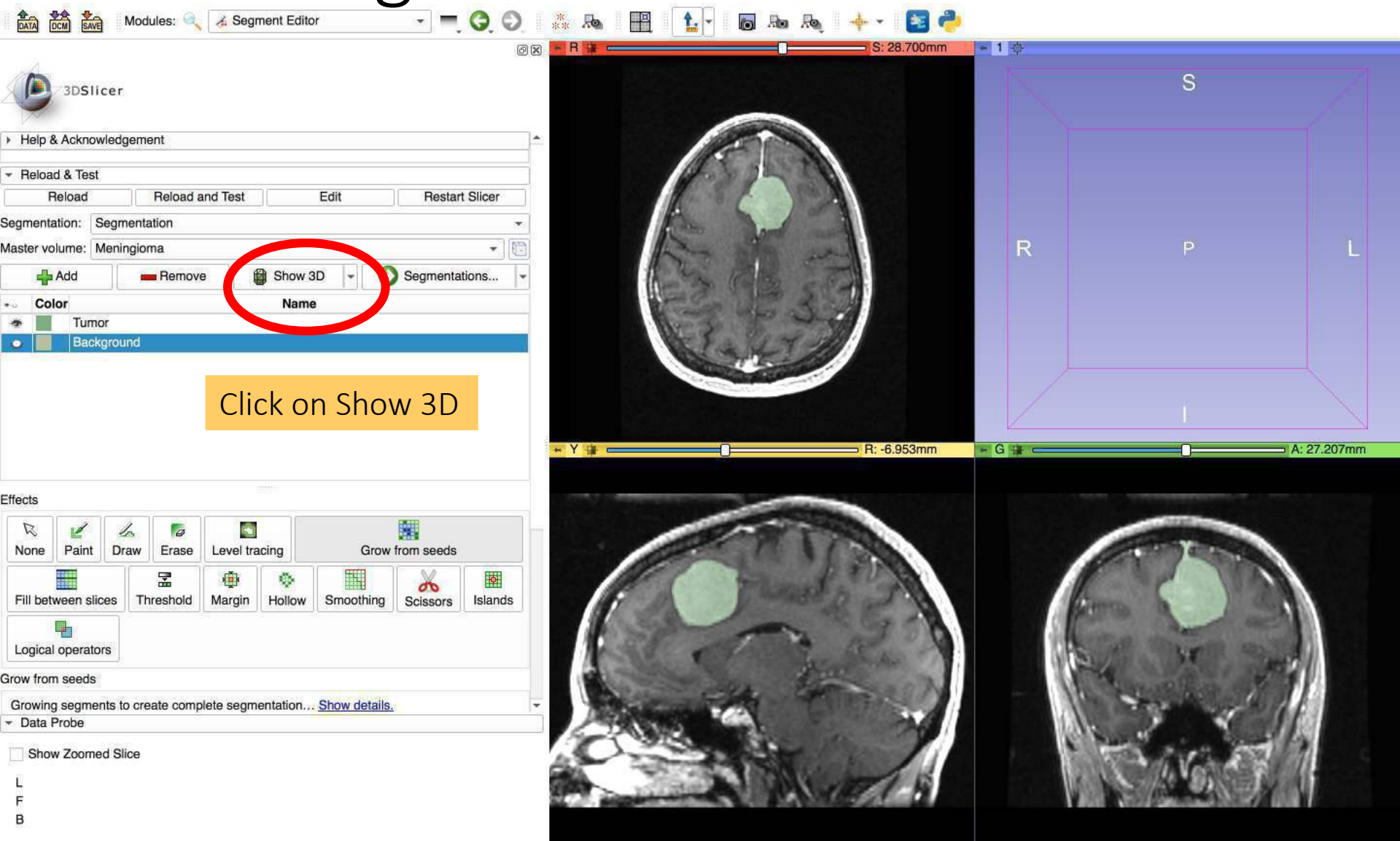
Click on **Apply** to accept the result



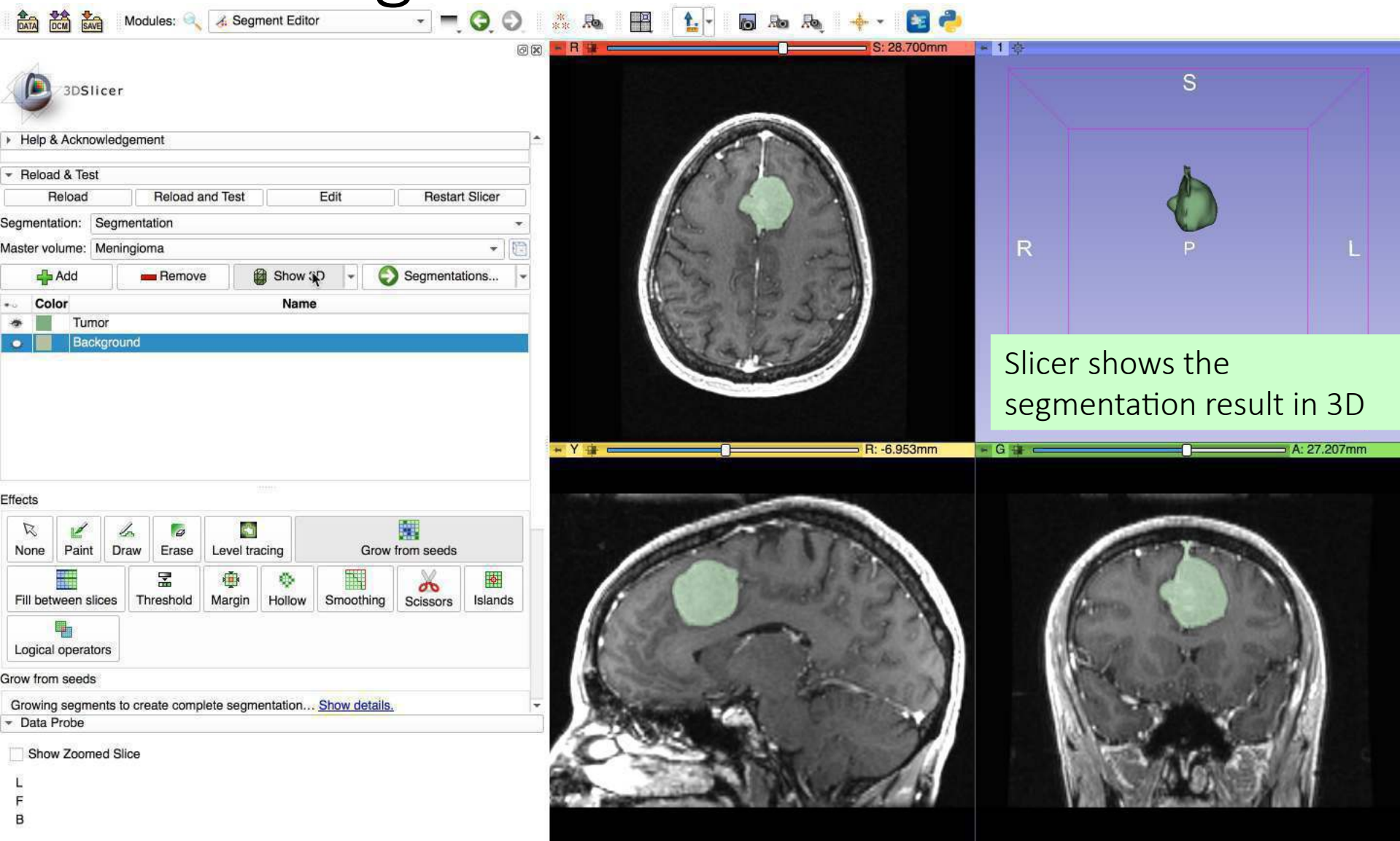
Segment Editor Module



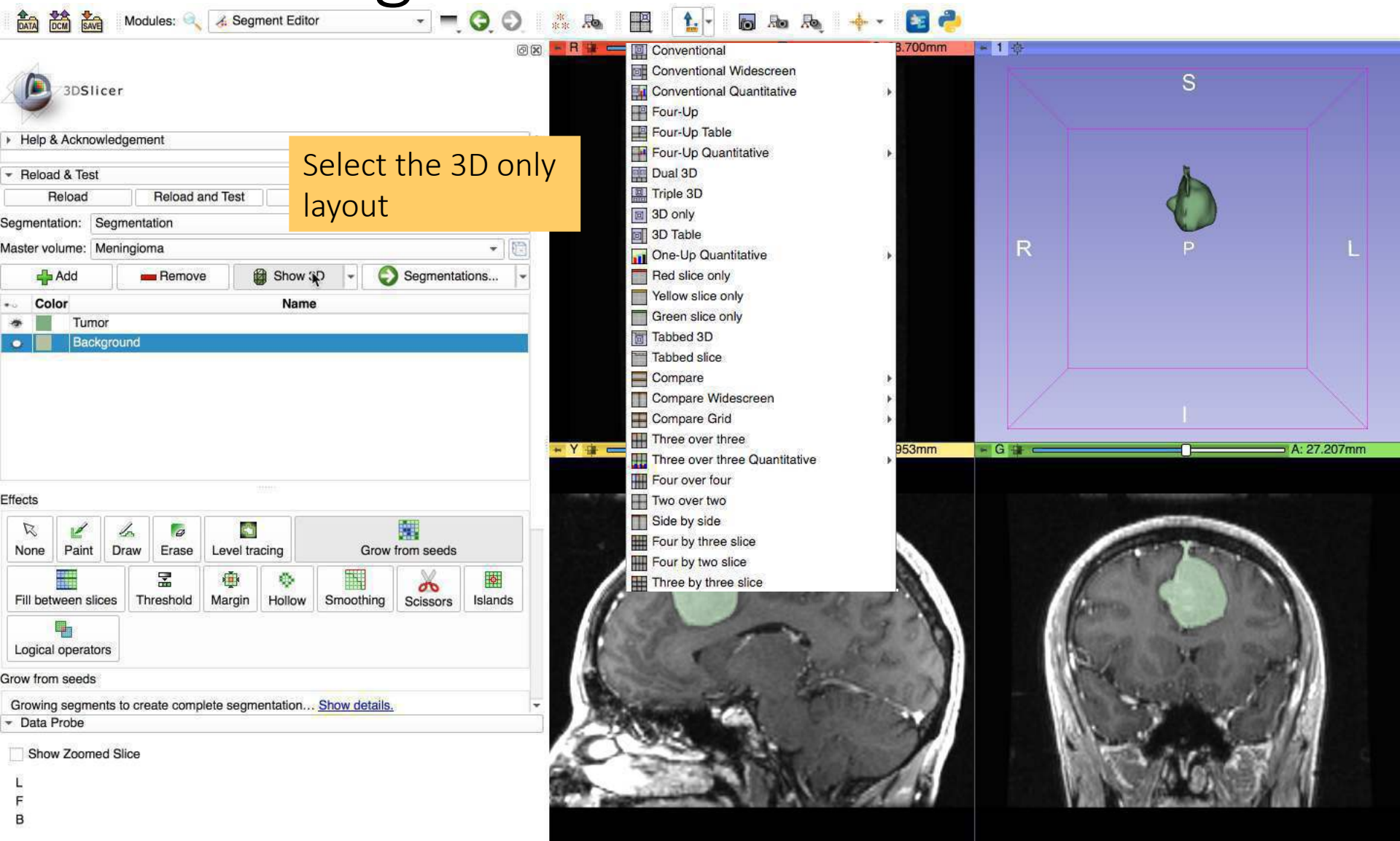
Segment Editor Module



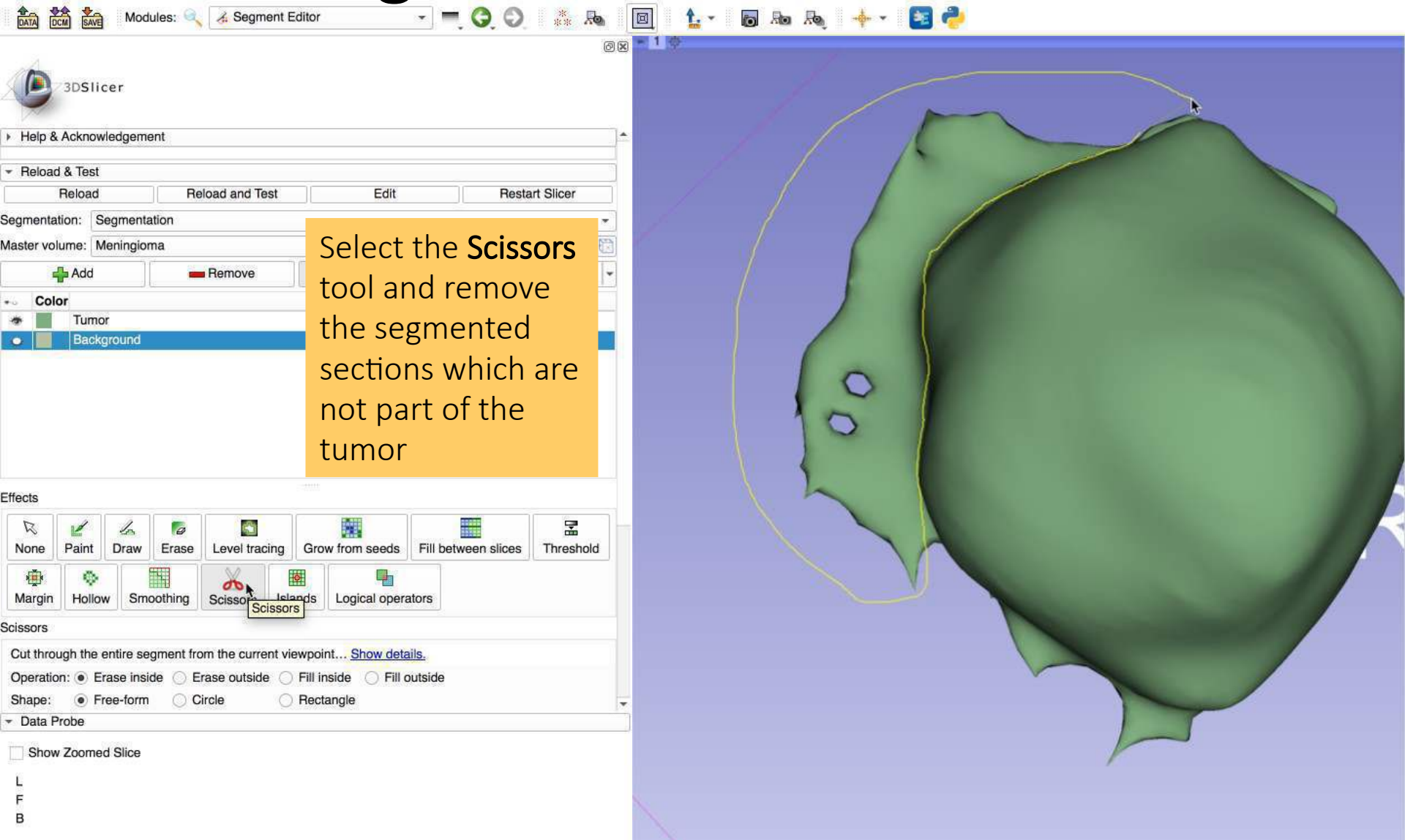
Segment Editor Module



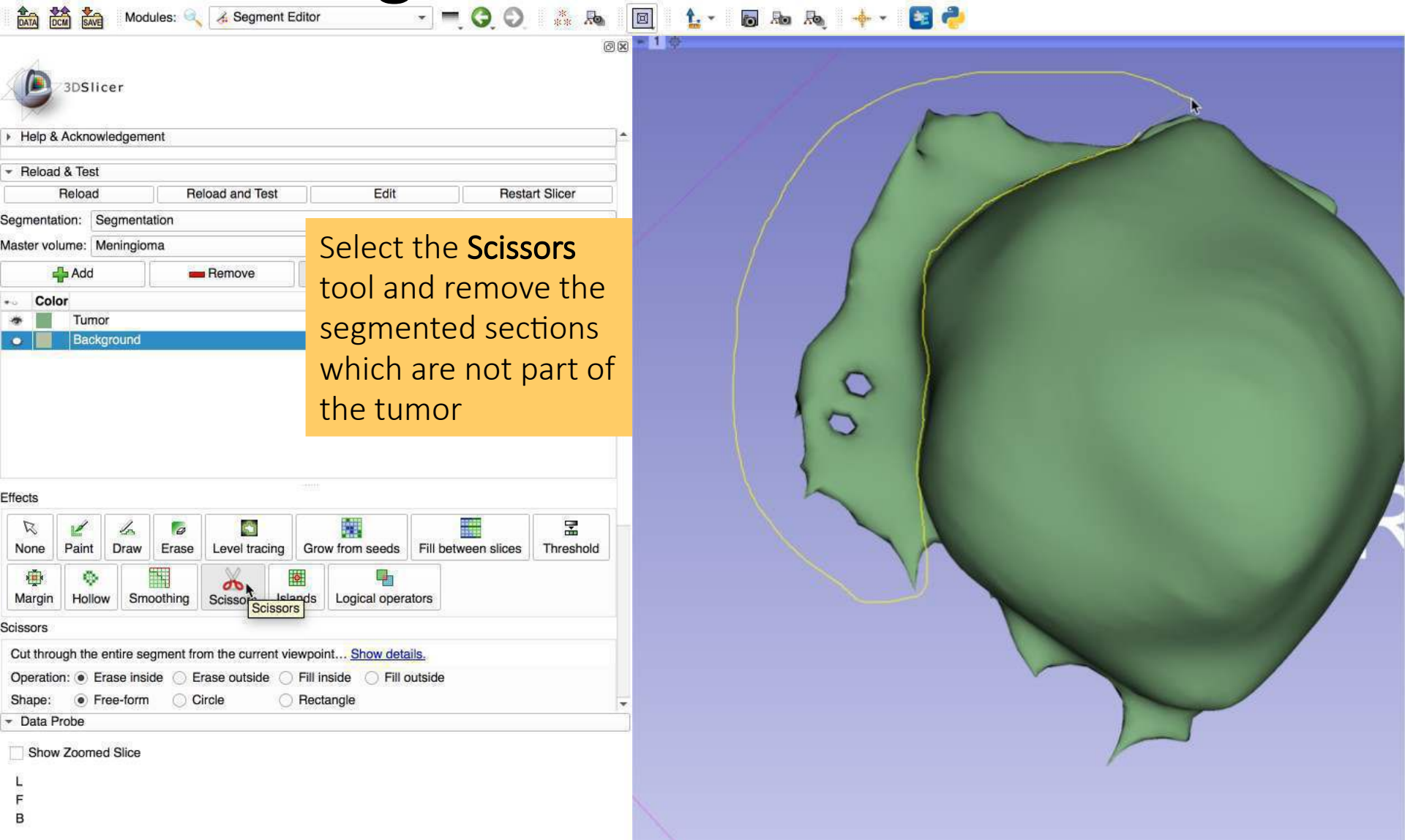
Segment Editor Module



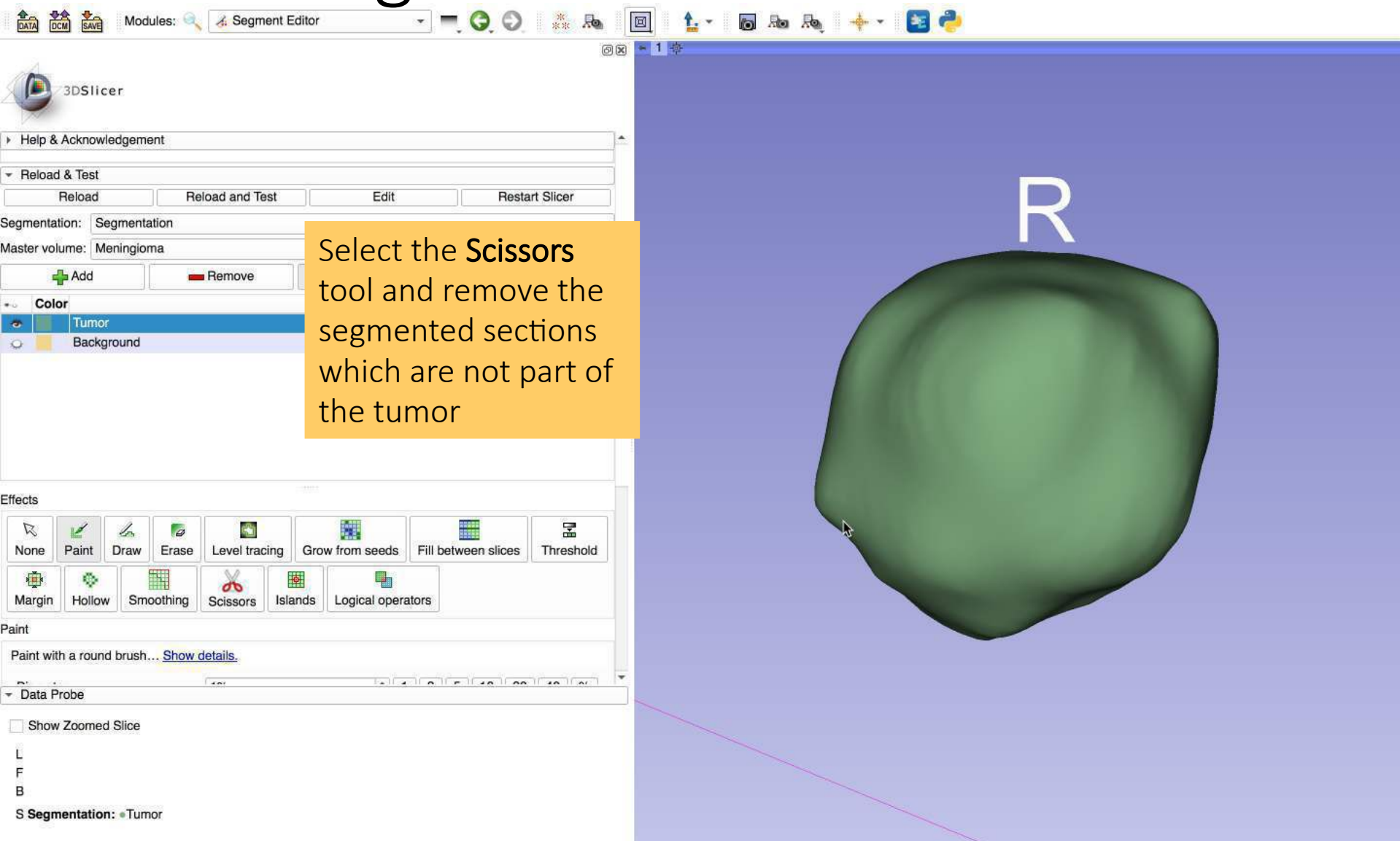
Segment Editor Module

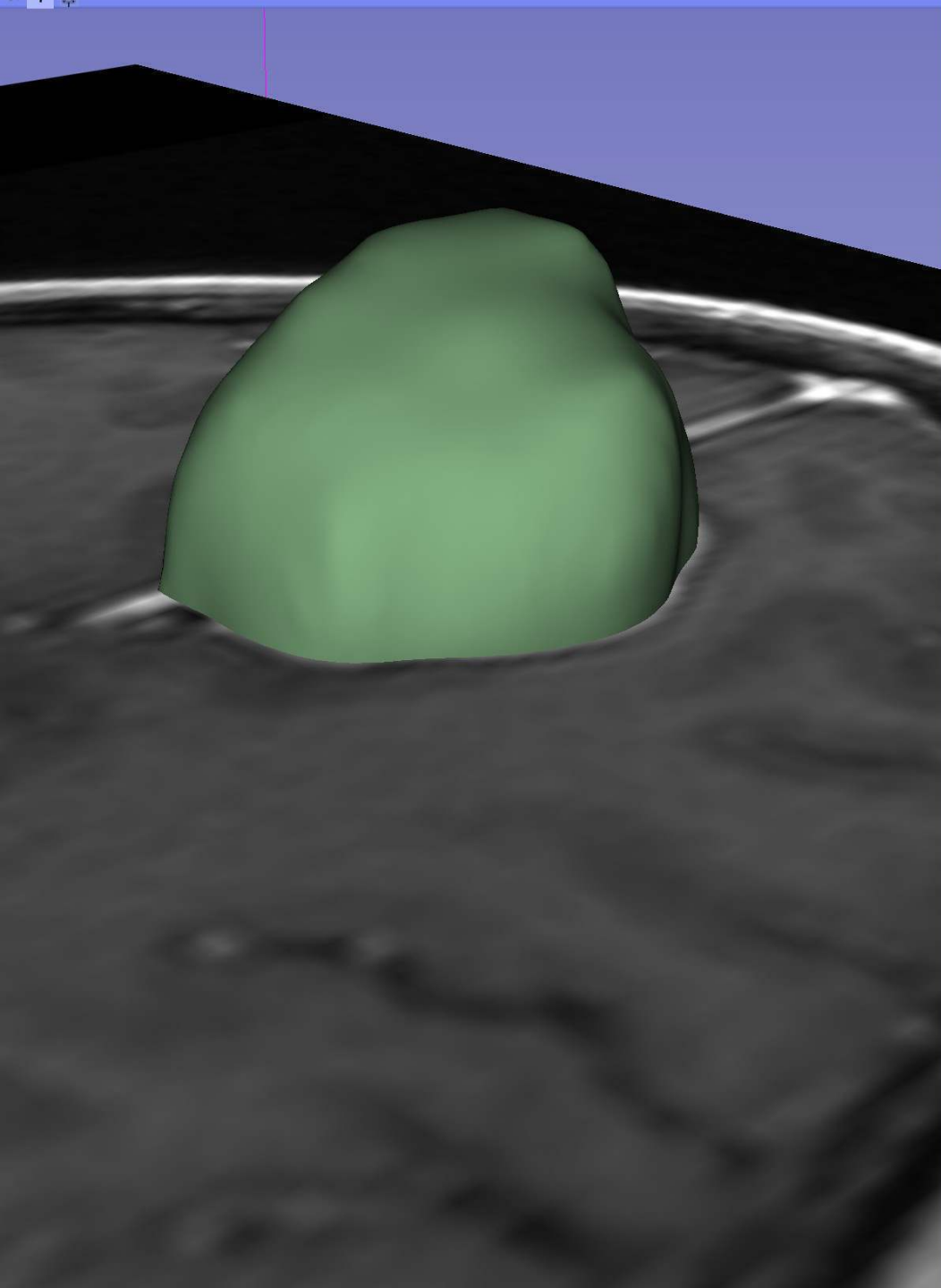


Segment Editor Module



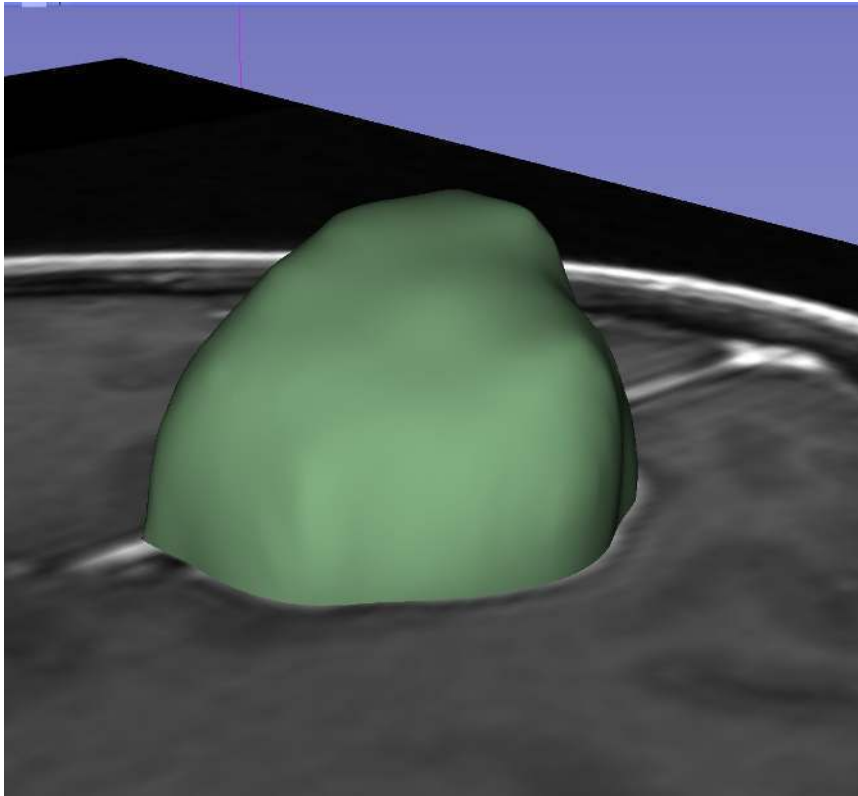
Segment Editor Module





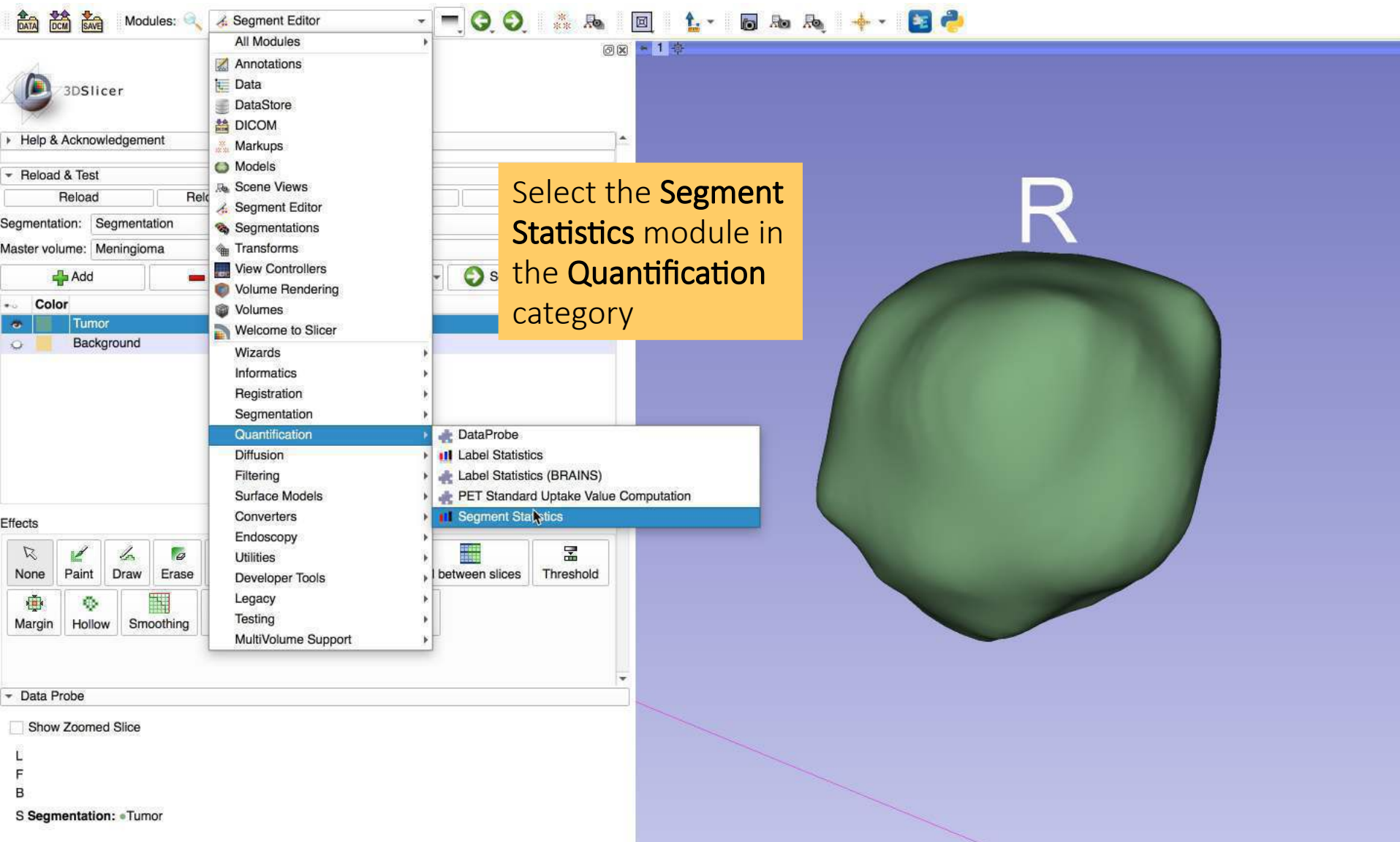
Part 3: Tumor Volume Calculation

3D Measurements

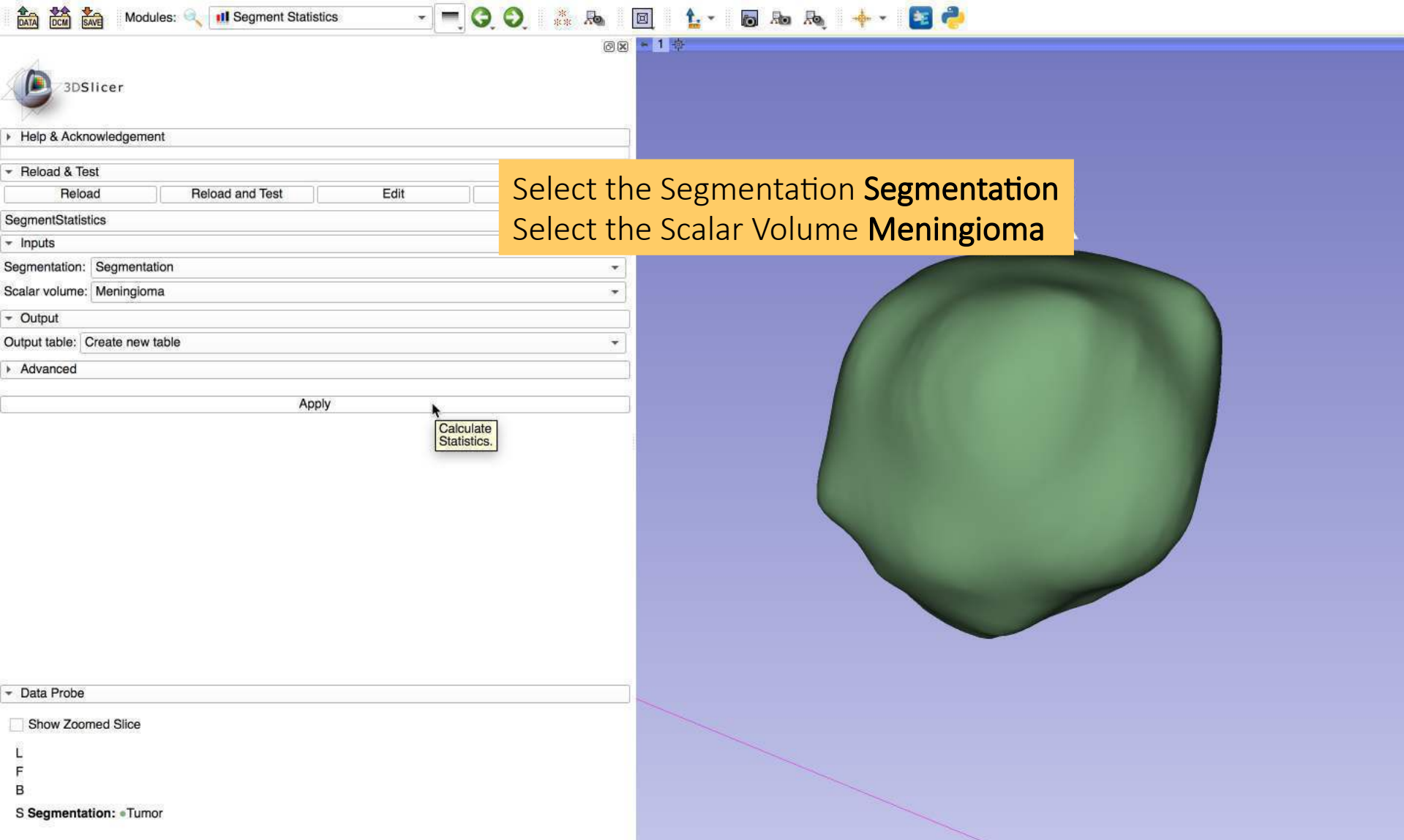


This section shows how to compute the volume of the segmented tumor using the Segment Statistics module

Tumor Measurements



Tumor Measurements



Tumor Measurements

The screenshot displays the 3D Slicer software interface. The top toolbar contains icons for DATA, DCM, SAVE, and a Modules dropdown menu. The Modules dropdown is open, showing a list of modules. A red arrow points to the 'Conventional' module. The 'SegmentStatistics' module is selected in the Modules dropdown. The left sidebar shows the 'SegmentStatistics' module's settings. The 'Inputs' section shows 'Segmentation: Segmentation' and 'Scalar volume: Meningioma'. The 'Output' section shows 'Output table: Table'. The 'Apply' button is circled in red. The main 3D view shows a green tumor model labeled 'R'. The bottom status bar displays 'Y', 'R: 0.469mm', 'G', and 'A: 27.481mm'. The bottom right corner shows three axial, sagittal, and coronal views of the tumor.

3DSlicer

Help & Acknowledgement

Reload & Test

Reload Reload and Test Edit Restart Slicer

SegmentStatistics

Inputs

Segmentation: Segmentation

Scalar volume: Meningioma

Output

Output table: Table

Advanced

Apply

Select the **Conventional layout** and click on Apply

Conventional

Conventional Widescreen

Conventional Quantitative

Four-Up

Four-Up Table

Four-Up Quantitative

Dual 3D

Triple 3D

3D only

3D Table

One-Up Quantitative

Red slice only

Yellow slice only

Green slice only

Tabbed 3D

Tabbed slice

Compare

Compare Widescreen

Compare Grid

Three over three

Three over three Quantitative

Four over four

Two over two

Side by side

Four by three slice

Four by two slice

Three by three slice

Y R: 0.469mm G A: 27.481mm

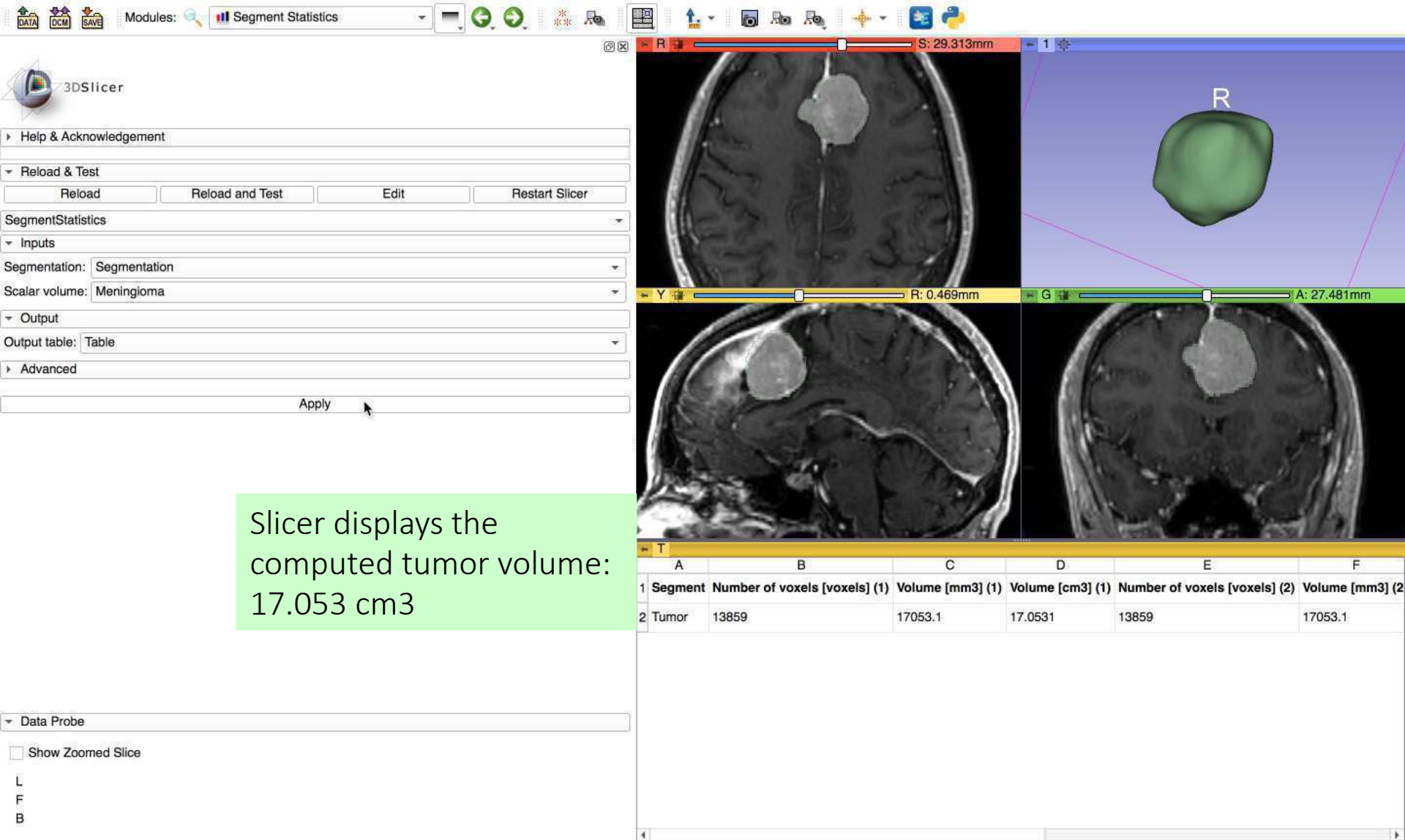
L

F

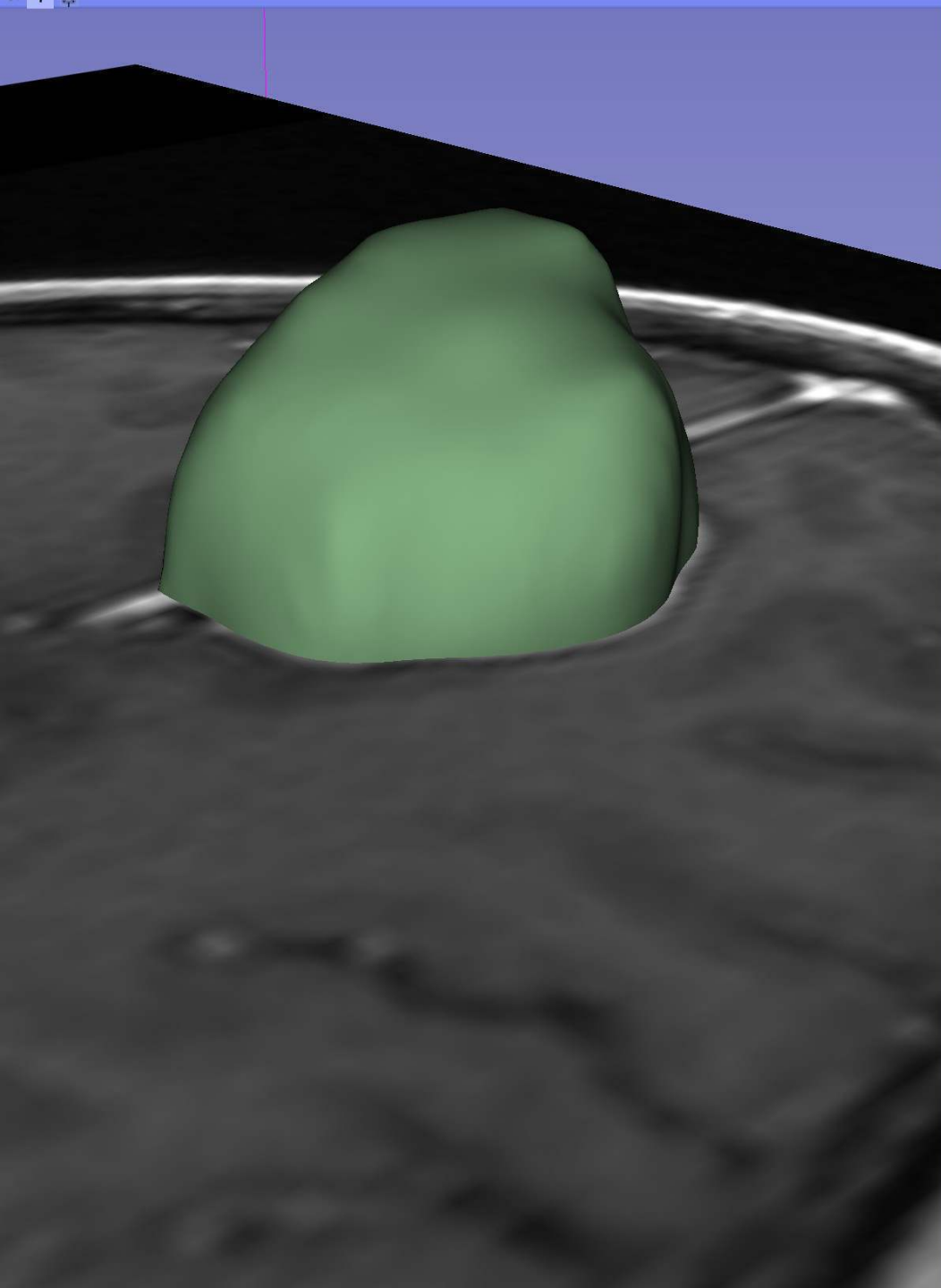
B



Tumor Measurements



Slicer displays the
computed tumor volume:
17.053 cm³



Part 4: Quantitative Imaging features computation



PyRadiomics package

- **Pyradiomics** is an open source python package that enables the automated extraction of over 1,500 quantitative features from medical imaging data.
- The package includes tools for image pre-processing and filtering based on SimpleITK
- Pyradiomics command line tools enable batchprocessing

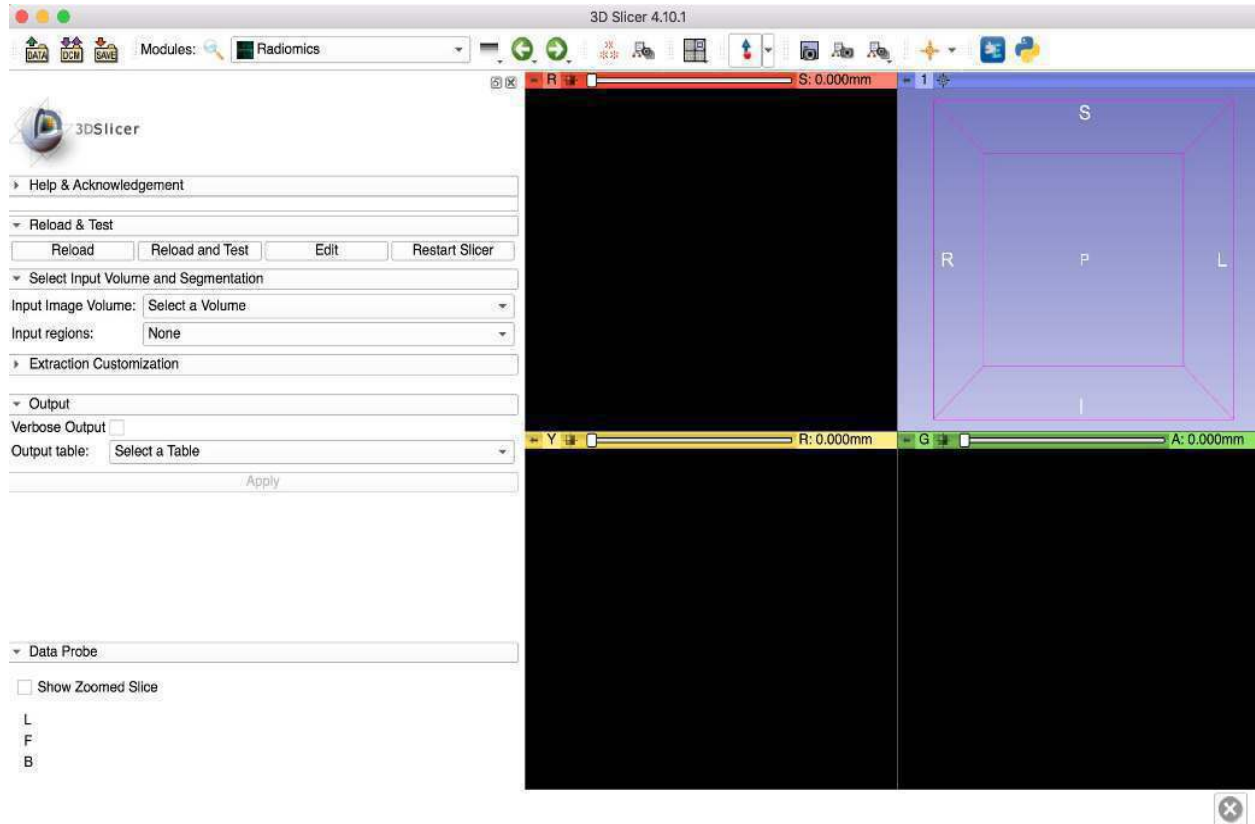
<https://pyradiomics.readthedocs.io>

<http://www.radiomics.io/>

van Griethuysen, J. J. M., Fedorov, A., Parmar, C., Hosny, A., Aucoin, N., Narayan, V., Beets-Tan, R. G. H., Fillon-Robin, J. C., Pieper, S., Aerts, H. J. W. L. (2017). Computational Radiomics System to Decode the Radiographic Phenotype. Cancer Research, 77(21), e104–e107.



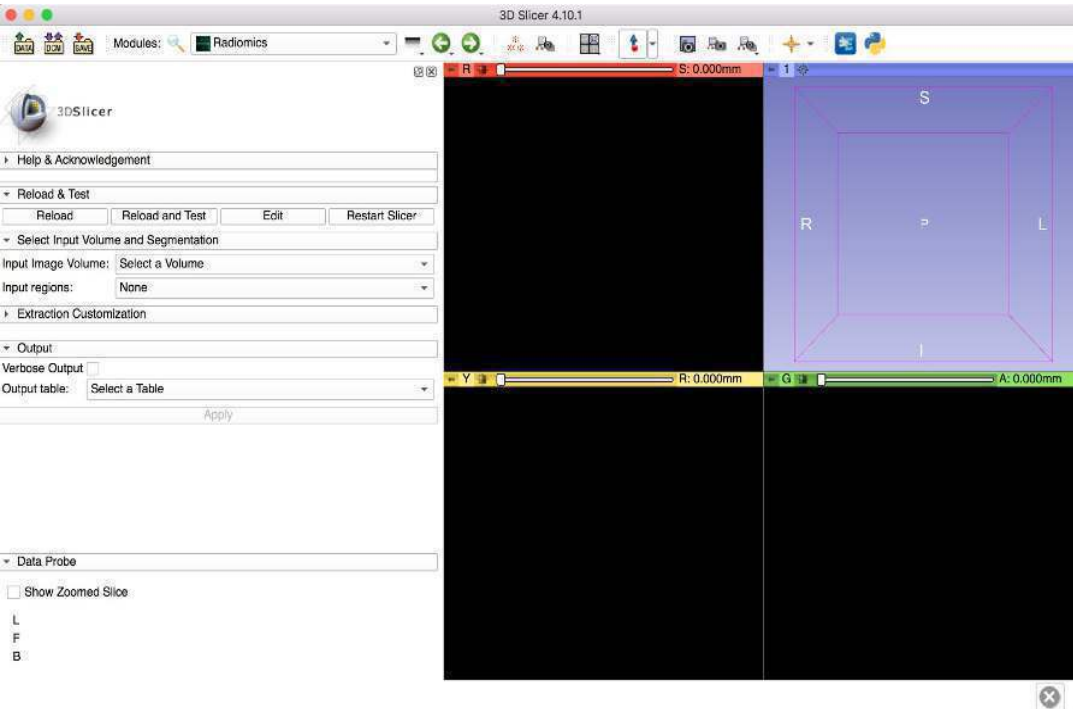
Slicer Radiomics



The **Slicer Radiomics** extension provides a graphical user interface to the pyradiomics library

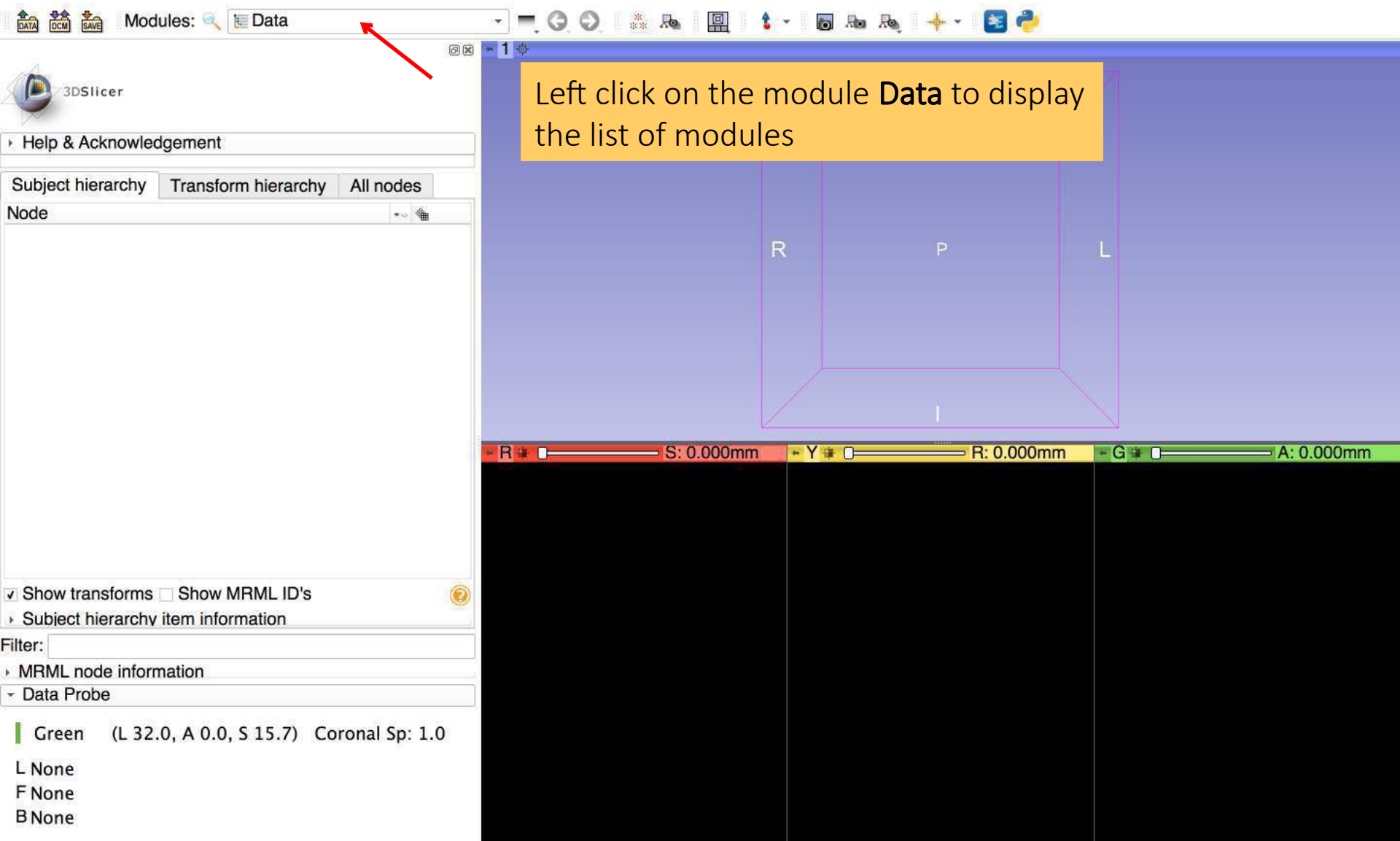


Slicer Radiomics

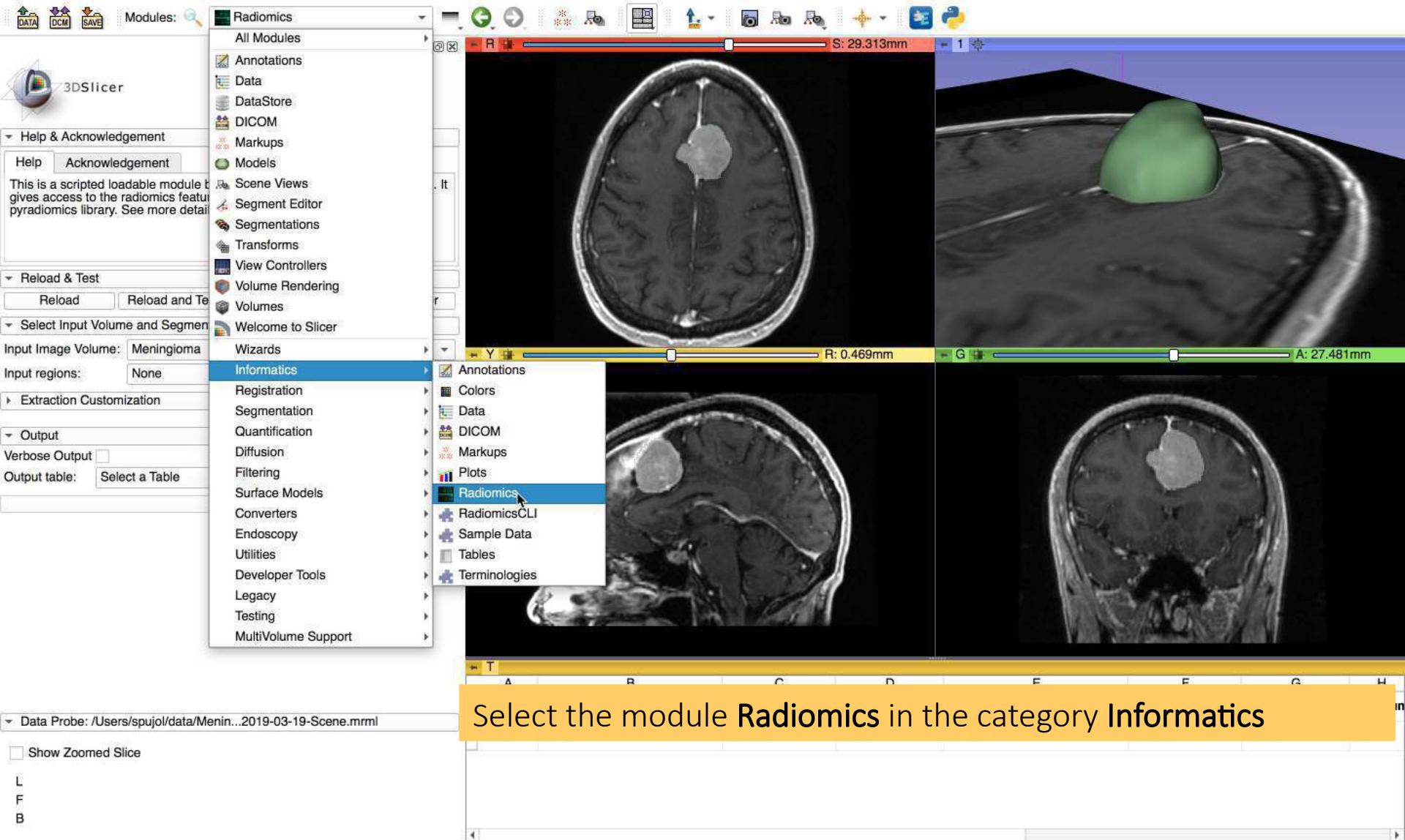


The Slicer Radiomics Extension enables interactive imaging features exploration and configuration of extraction parameters

Radiomics Module



Radiomics Module Installation



Radiomics Module Installation

The screenshot shows the 3DSlicer Radiomics module interface. The top toolbar includes icons for DATA, DCM, SAVE, and a Modules dropdown menu with 'Radiomics' selected. The main window is divided into three panes: a central axial MRI slice, a right-side 3D green model of a meningioma labeled 'R', and a bottom row of two sagittal MRI slices. The left sidebar contains the Radiomics module settings. Three yellow callout boxes provide instructions: the first points to the 'Input Image Volume' (Meningioma) and 'Input regions' (Segmentation) fields; the second points to the 'Feature Classes' section where 'firstorder' and 'glcm' are selected; the third points to the 'Output table' dropdown set to 'Table_1' and the 'Apply' button.

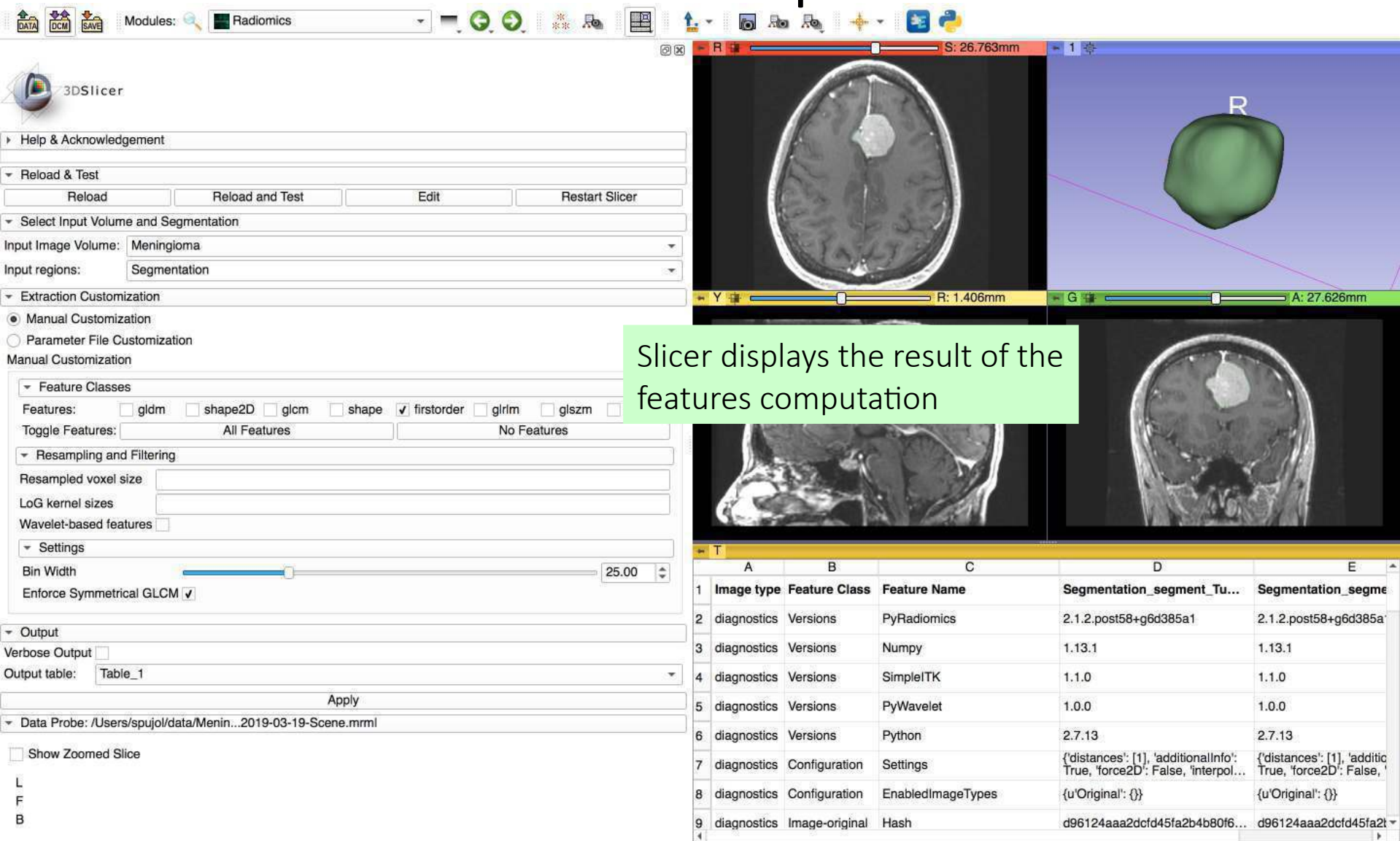
Select the Image Volume **Meningioma**
Select the Input Regions **Segmentation**

Select the feature class First Order
and glcm

Select **Output Table** → Create New
and click on **Apply**



Features Computation



The screenshot displays the 3D Slicer interface with the Radiomics module active. The left sidebar shows the 'Extraction Customization' panel, where 'Manual Customization' is selected. Under 'Feature Classes', 'firstorder' is checked. The 'Output' section shows 'Table_1' as the output table. The main window displays four MRI slices: axial, sagittal, coronal, and a 3D volume rendering of a meningioma. A green text box highlights the text 'Slicer displays the result of the features computation'.

Feature Computation Results Table:

	A	B	C	D	E
	Image type	Feature Class	Feature Name	Segmentation_segment_Tu...	Segmentation_segme
1	diagnostics	Versions	PyRadiomics	2.1.2.post58+g6d385a1	2.1.2.post58+g6d385a1
2	diagnostics	Versions	Numpy	1.13.1	1.13.1
3	diagnostics	Versions	SimpleITK	1.1.0	1.1.0
4	diagnostics	Versions	PyWavelet	1.0.0	1.0.0
5	diagnostics	Versions	Python	2.7.13	2.7.13
6	diagnostics	Configuration	Settings	{'distances': [1], 'additionalInfo': True, 'force2D': False, 'interpol...	{'distances': [1], 'additio...
7	diagnostics	Configuration	EnabledImageTypes	{'u'Original': {}}	{'u'Original': {}}
8	diagnostics	Image-original	Hash	d96124aaa2dcfd45fa2b4b80f6...	d96124aaa2dcfd45fa2b...

Features Computation

Slicer displays the values of the 18 features for the **FirstOrder** class includes 18 features

34	original	firstorder	InterquartileRange	20.0
35	original	firstorder	Skewness	1.99316623652
36	original	firstorder	Uniformity	0.358800750225
37	original	firstorder	Median	177.0
38	original	firstorder	Energy	453513881.0
39	original	firstorder	RobustMeanAbsoluteDeviation	9.02739158026
40	original	firstorder	MeanAbsoluteDeviation	15.6561086211
41	original	firstorder	TotalEnergy	558034658.262
42	original	firstorder	Maximum	370.0
43	original	firstorder	RootMeanSquared	180.8961587
44	original	firstorder	90Percentile	202.0
45	original	firstorder	Minimum	36.0
46	original	firstorder	Entropy	1.83048891173
47	original	firstorder	Range	334.0
48	original	firstorder	Variance	575.802209976
49	original	firstorder	10Percentile	156.0
50	original	firstorder	Kurtosis	12.4315749384
51	original	firstorder	Mean	179.297568367

Conclusion

- This tutorial provides a basic introduction to image phenotyping using the Slicer Radiomics extension.
- The extension enables the computation of feature classes implemented in pyradiomics
- The description of each class is available at <https://pyradiomics.readthedocs.io/>

Acknowledgments

- Neuroimage Analysis Center (NIH P41 EB015902)