


# An Introduction to Image Phenotyping

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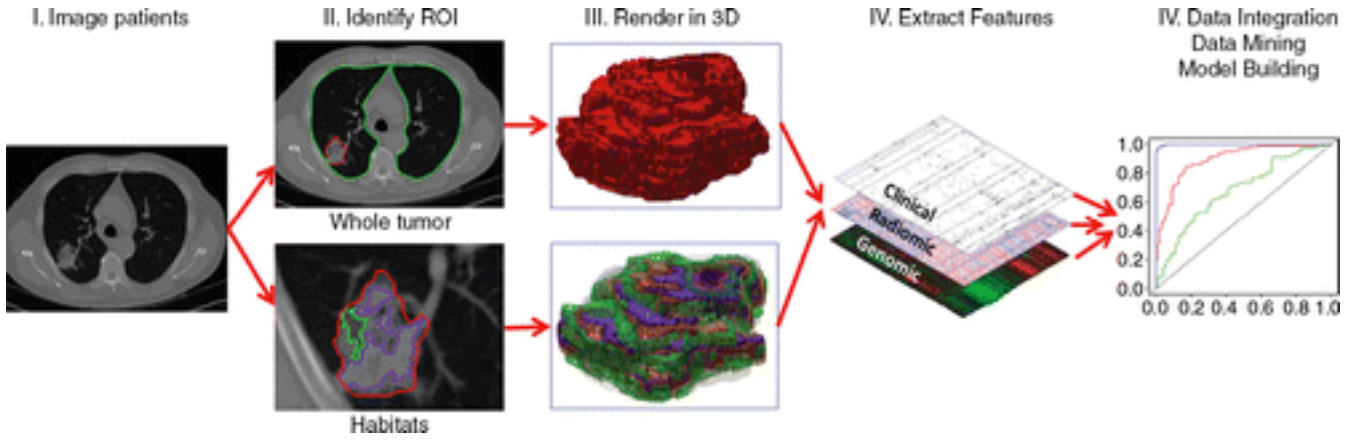
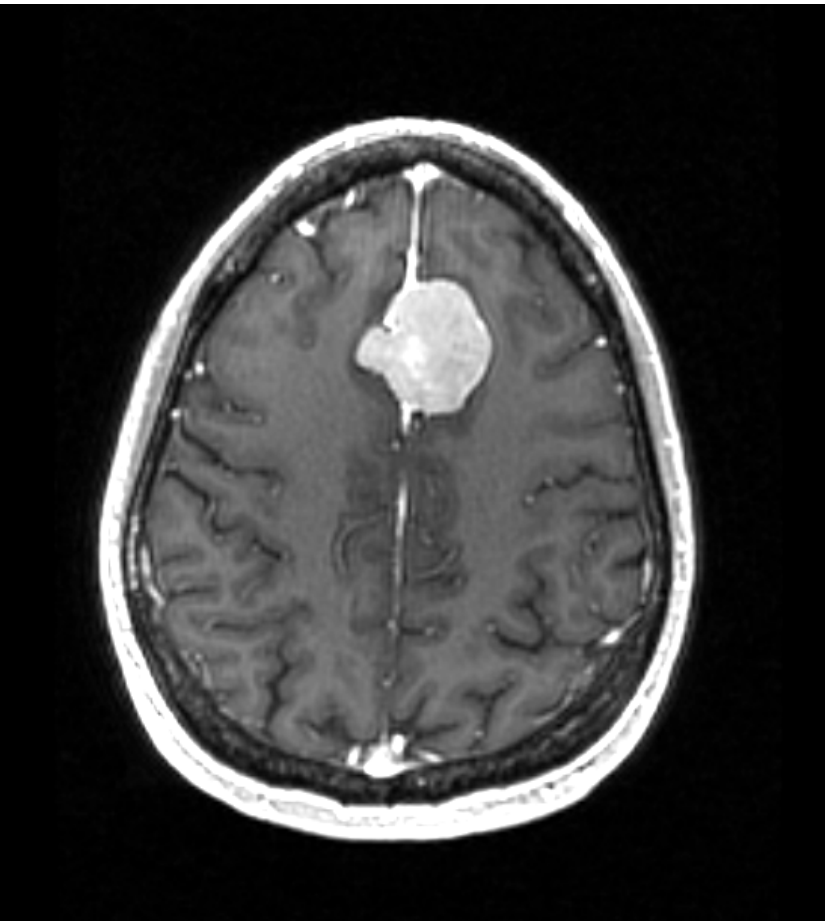
# Imaging Phenotypes

- 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.



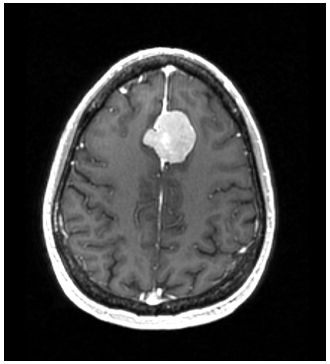

Gillies et al. Radiology 2015

# Clinical Case: Meningioma

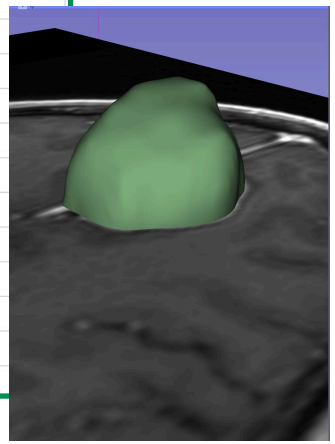


- Meningiomas are slow-growing extra axial brain tumor arising from arachnoidal cells
- Treatment options include observation, surgery and radiation therapy
- Image-based predictors of tumor grades have the potential to enhance clinical decision-making

# Overall Goal

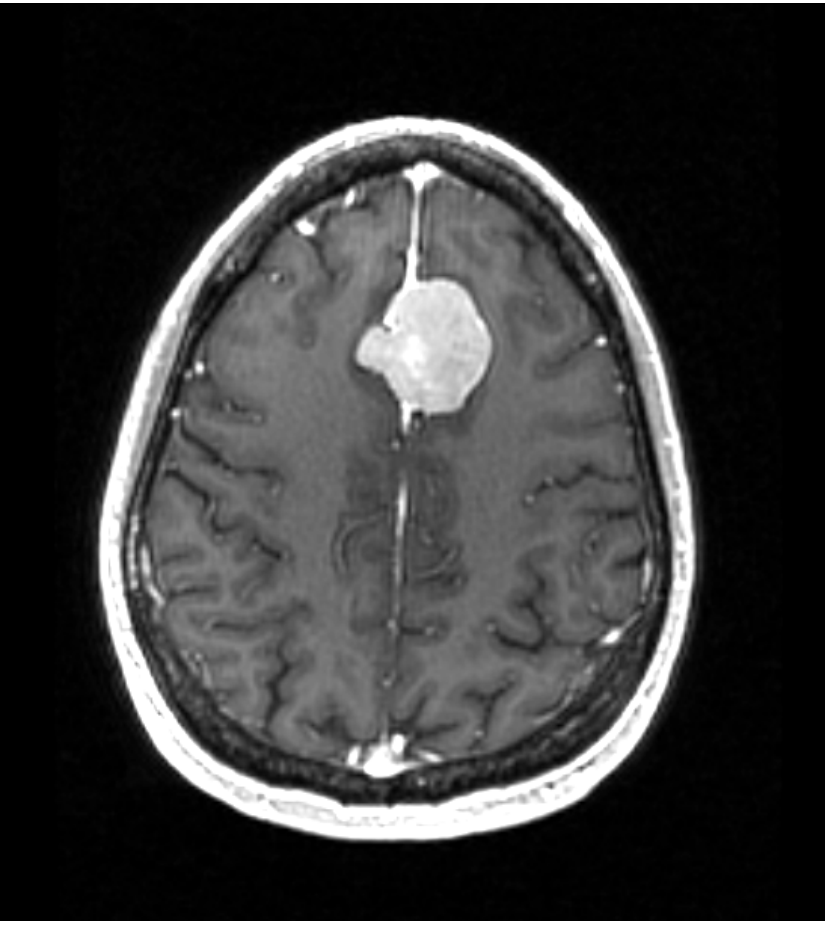



| | |
|---|---|
| Kurtosis | 12.4315749384 |
| Mean | 179.297568367 |
| GrayLevelVariance | 1.00567651545 |
| HighGrayLevelEmphasis | 45.873151021 |
| DependenceEntropy | 6.16459662954 |
| DependenceNonUniformity | 548.562883325 |
| GrayLevelNonUniformity | 4972.61959737 |
| SmallDependenceEmphasis |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



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

# Imaging Features



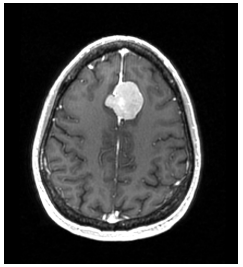
Quantitative features derived from imaging data have the potential to provide clinically relevant information for predicting tumor grade and evaluating response treatment

# Tutorial materials

- 3D Slicer release version 4.10.1

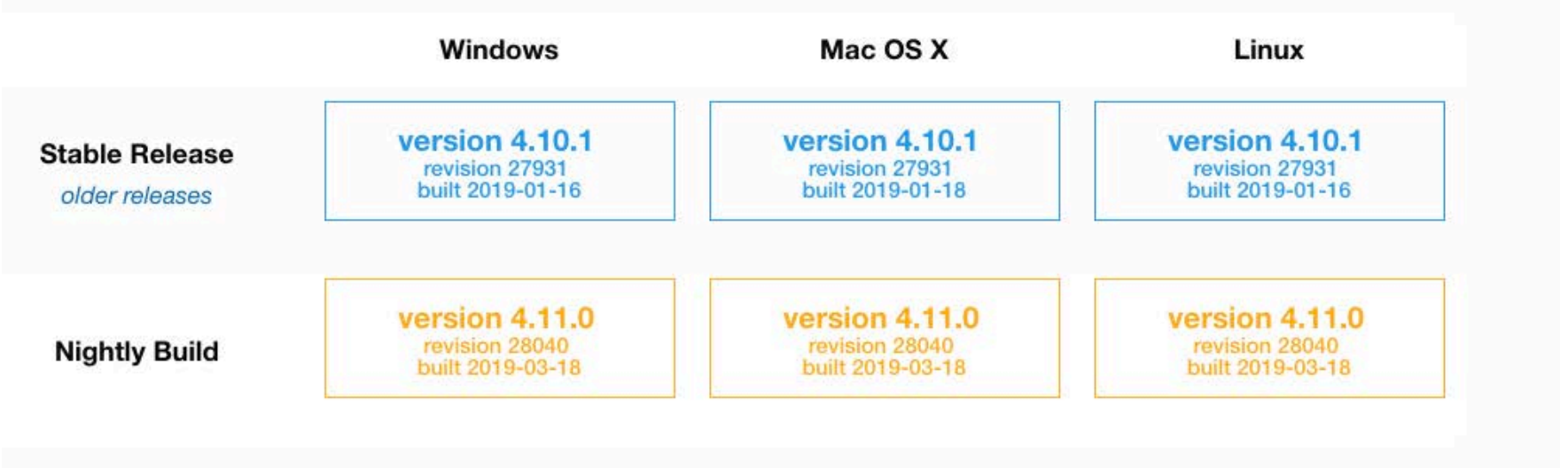

- Slicer Radiomics Extension


- 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

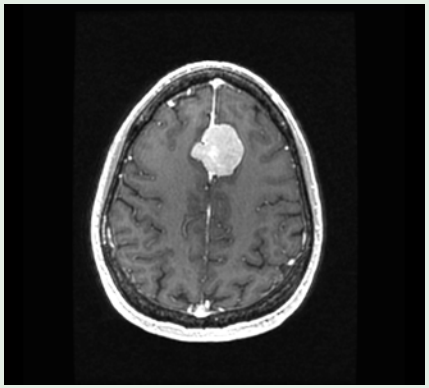


# Disclaimer

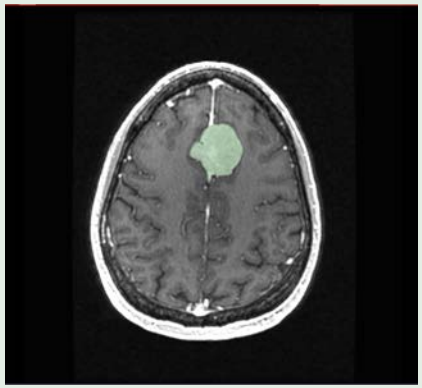
- 3D Slicer is a free open source software for medical image computing research distributed under a BDS style license.

- The software is not FDA approved or CE-Marked, and is for research use only.

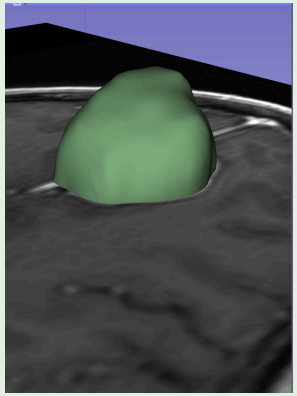
# Workflow Overiew



Step 1: Data Loading



Step 2: Tumor Segmentation



Step 3: Tumor Volume Calculation

| | |
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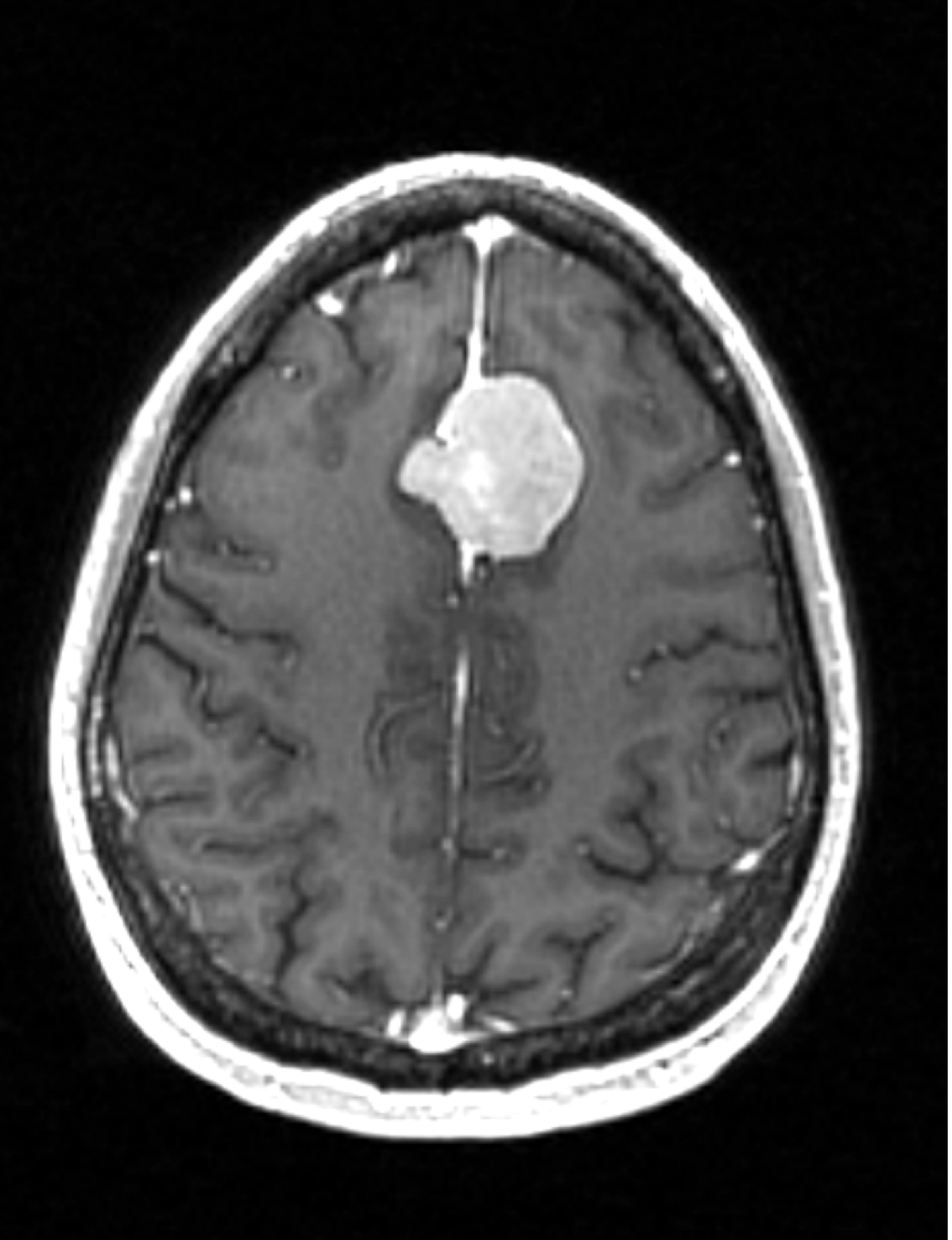
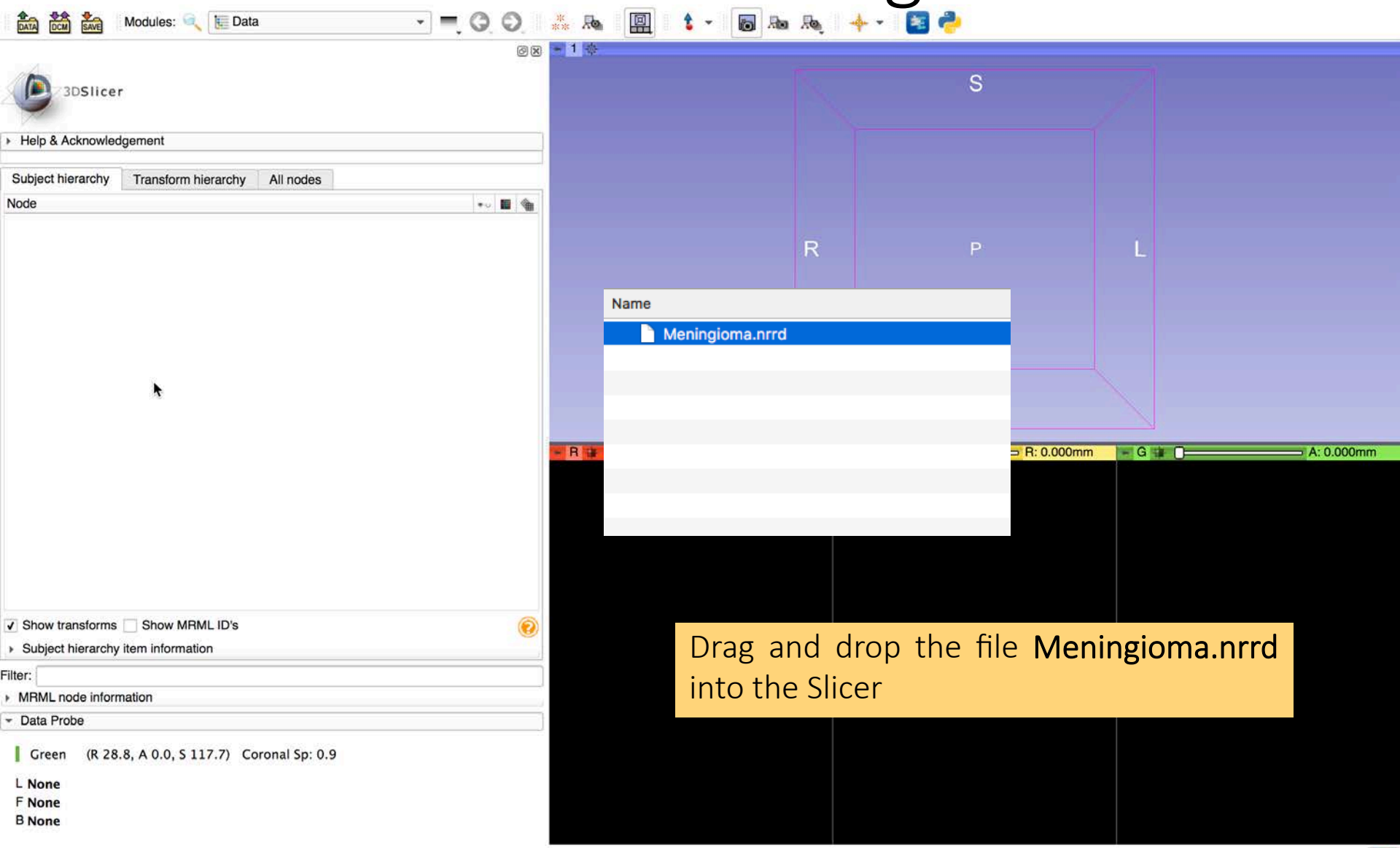
| LargeDependenceEmphasis | 237.650263367 |
| LargeDependenceLowGrayLev… | 5.58612453125 |
| DependenceVariance | 51.1747739691 |

Step 4: Imaging Features Extraction



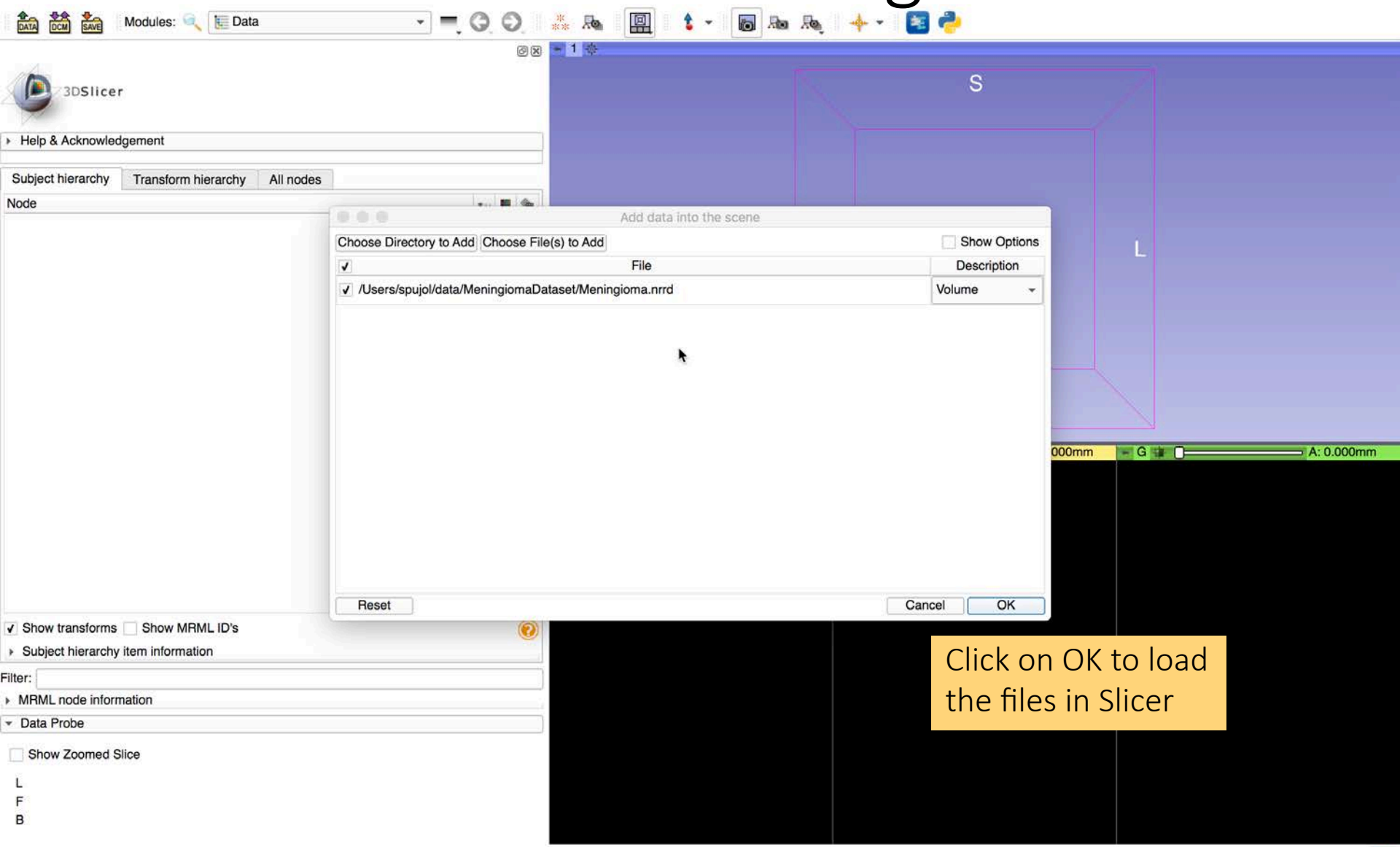
# Part 1: Data Loading and tumor diameter measurements

# Data Loading



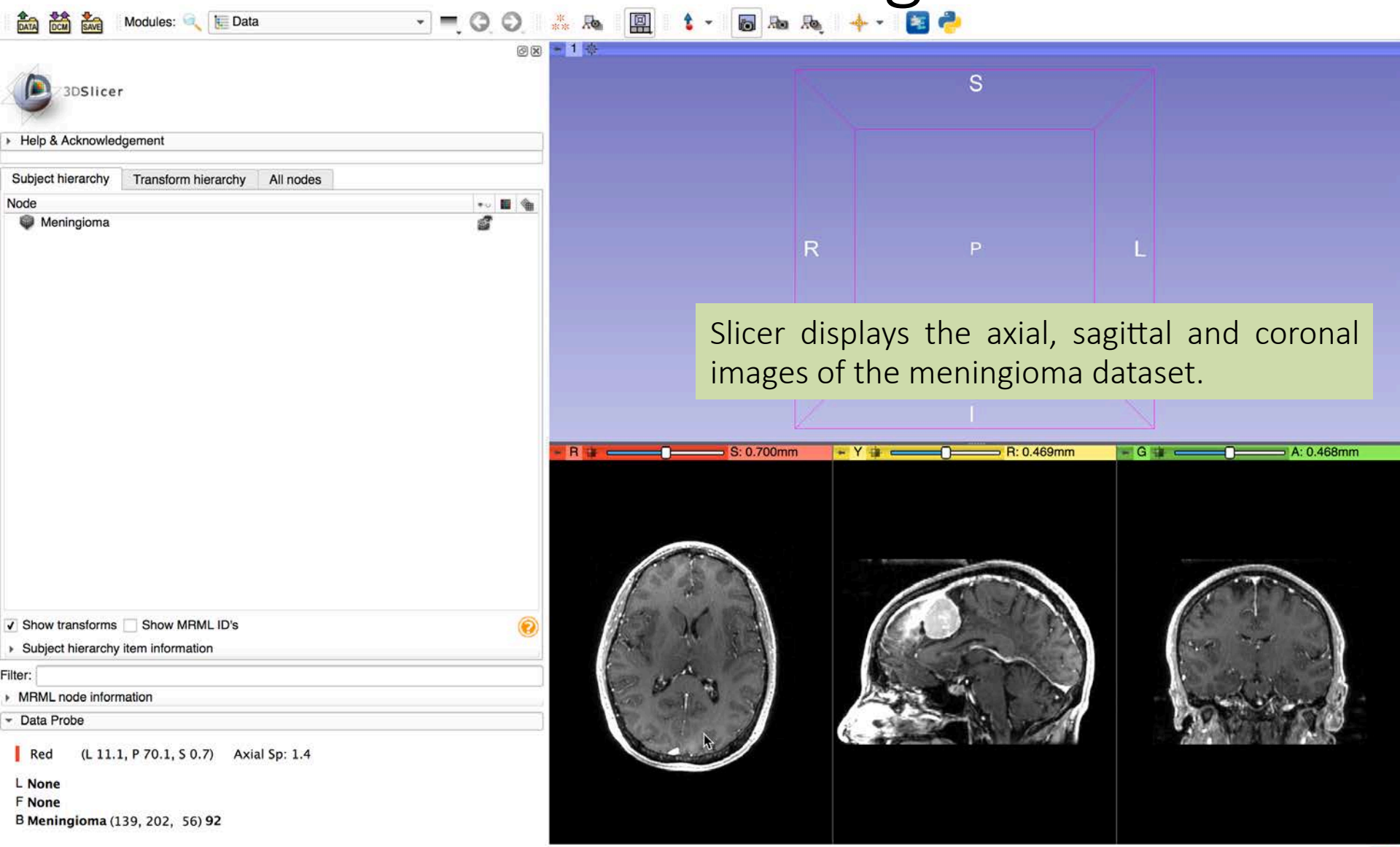

Drag and drop the file **Meningioma.nrrd** into the Slicer

# Data Loading



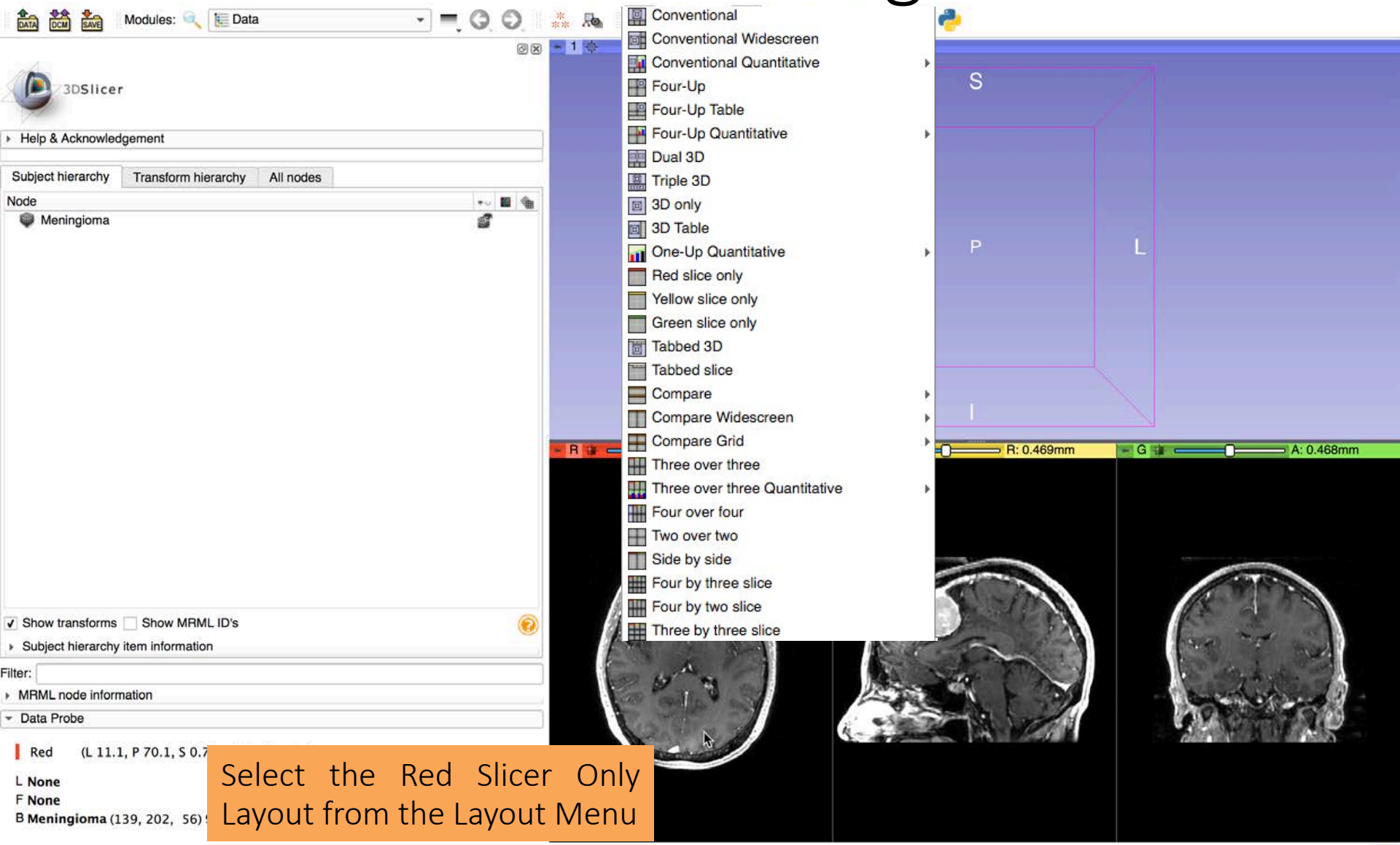

Click on OK to load the files in Slicer

# Data Loading



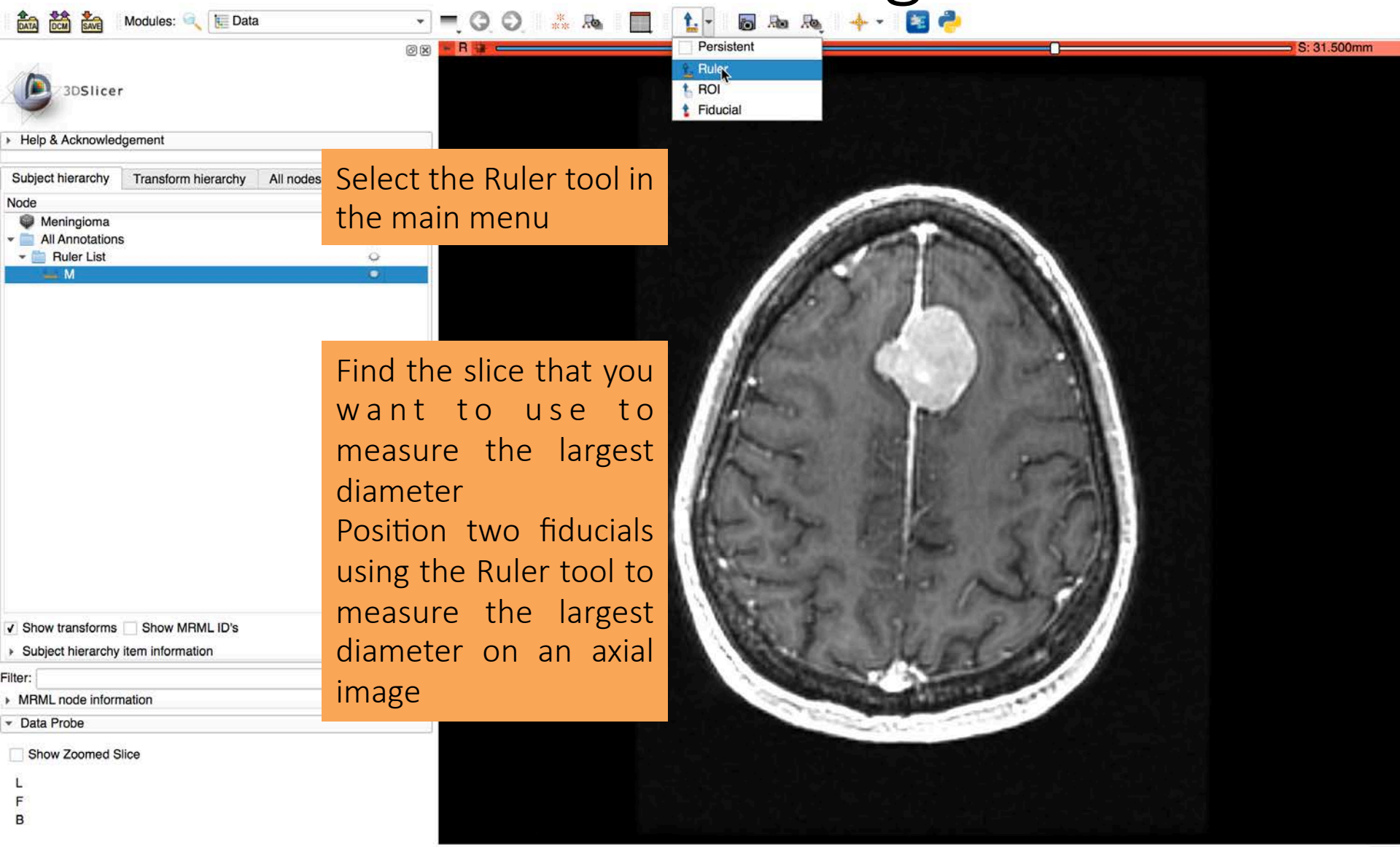

Slicer displays the axial, sagittal and coronal images of the meningioma dataset.

# Data Loading




Select the Red Slicer Only Layout from the Layout Menu

# Data Loading

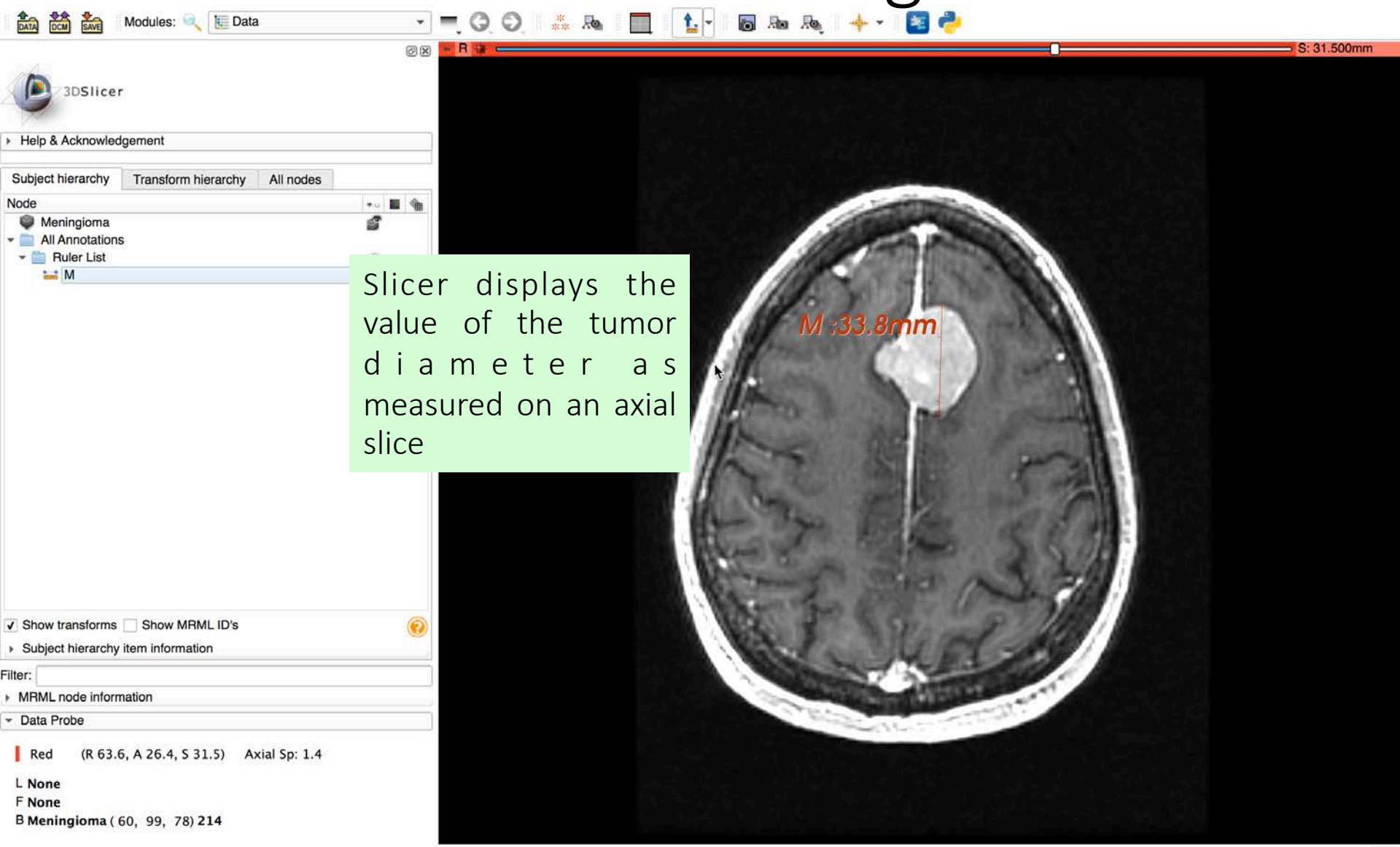



Select the Ruler tool in the main menu

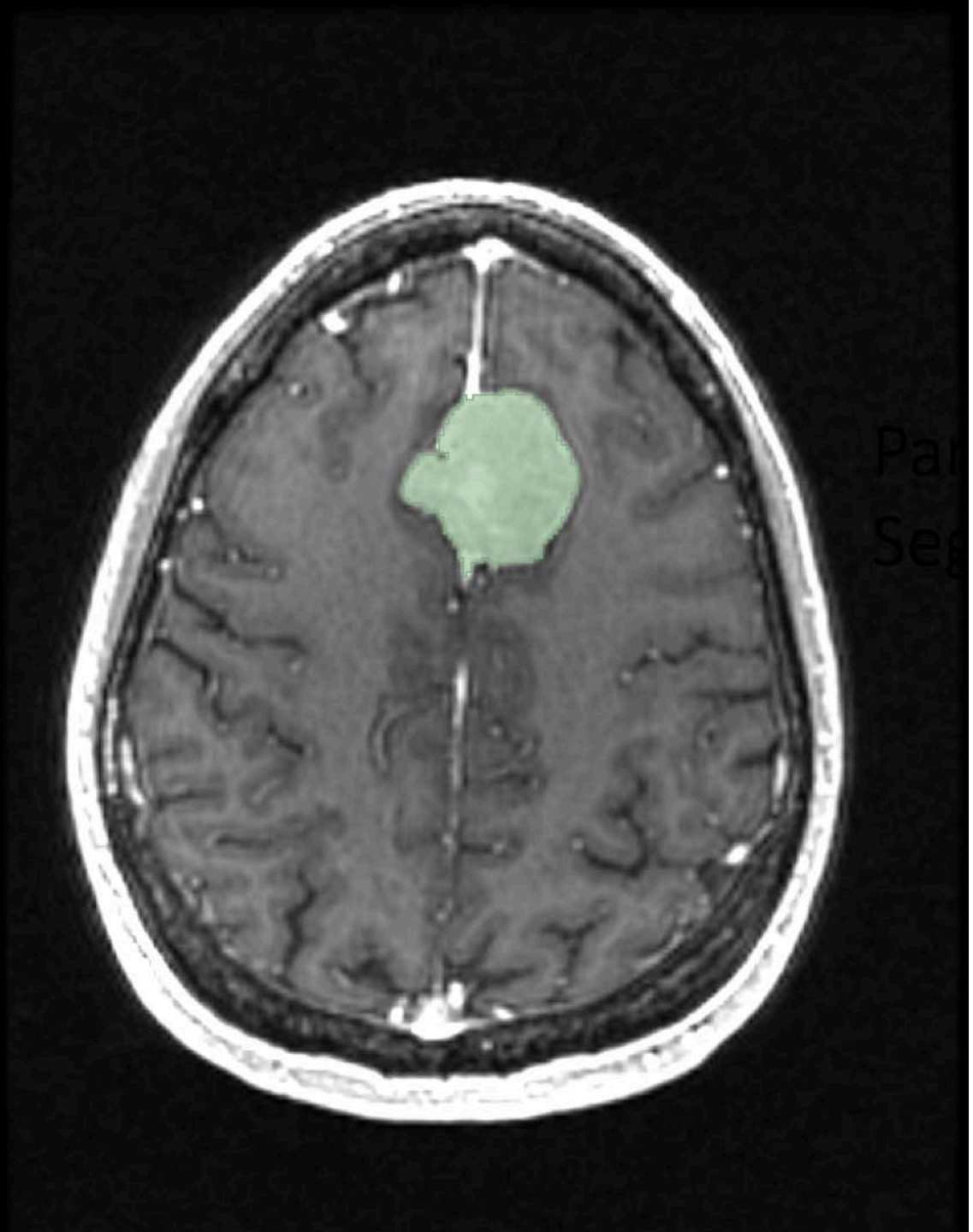
Find the slice that you want to use to measure the largest diameter

Position two fiducials using the Ruler tool to measure the largest diameter on an axial image

# Data Loading




Slicer displays the value of the tumor diameter as measured on an axial slice



# Part 2: Tumor Segmentation

# Image Segmentation

- Image Segmentation is the process of identifying the contours of structures of interest in imaging data

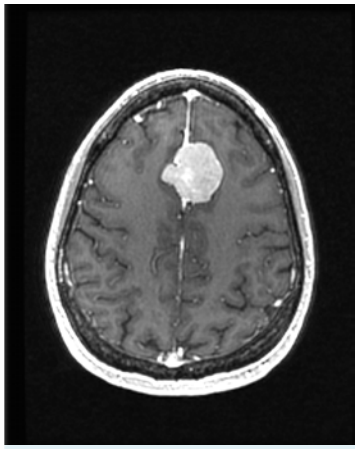
- Image Segmentation can be performed by manual contouring or by using automated segmentation algorithms

# Image Segmentation

- The Segment Editor module of 3D Slicer provides powerful tools for manual and semi-automated segmentation

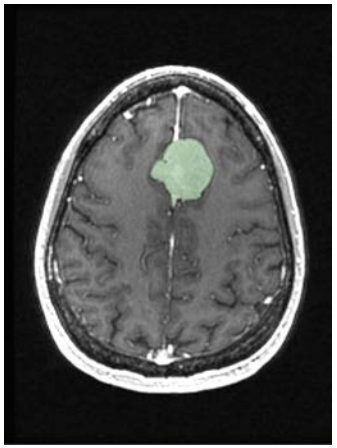
- The module takes a reference image (**Master Volume**) as input and produces a segmented image (**Segmentation)** in output

# Terminology



Master Volume

Segmentation

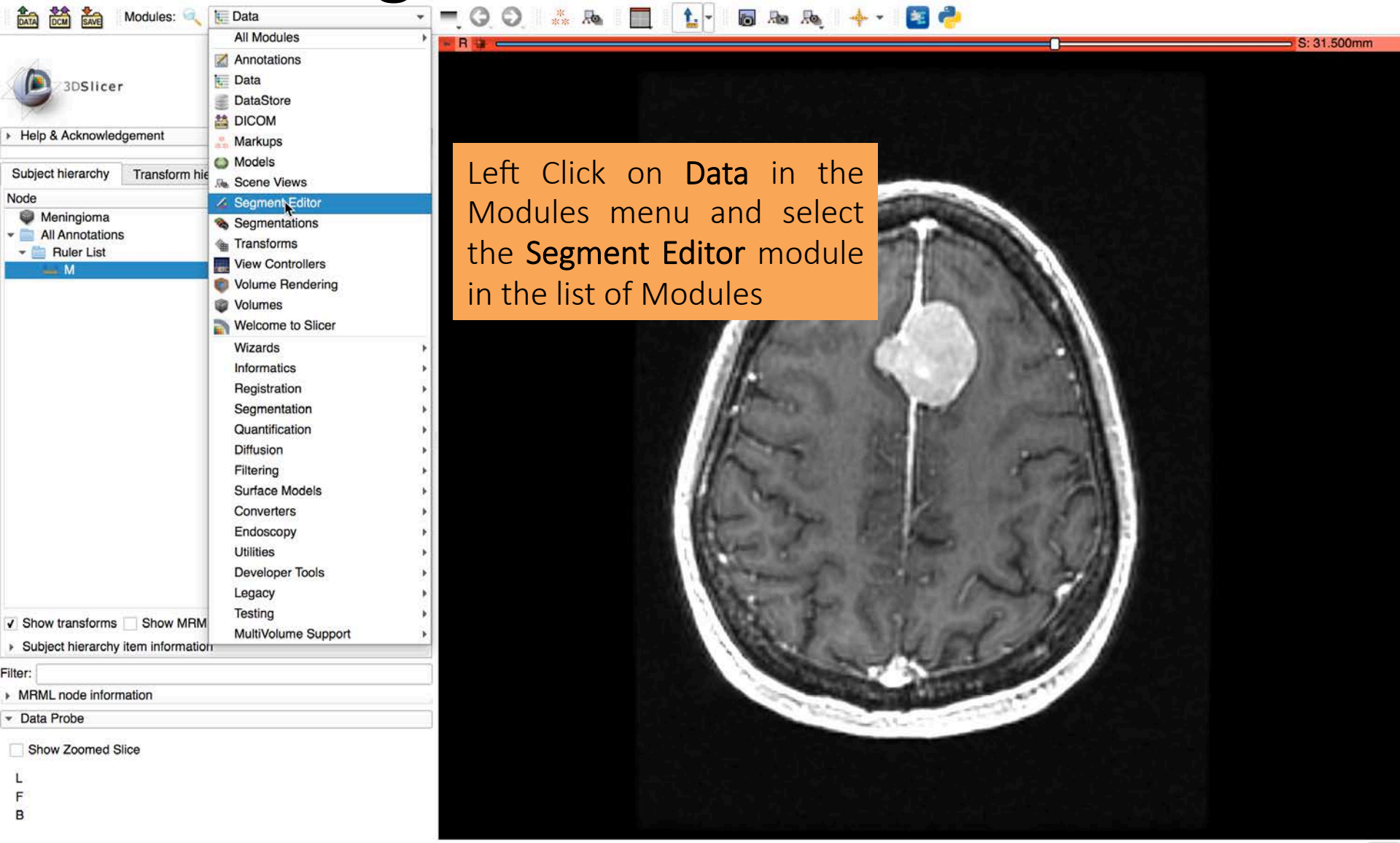


Master Volume
&
Segmentation

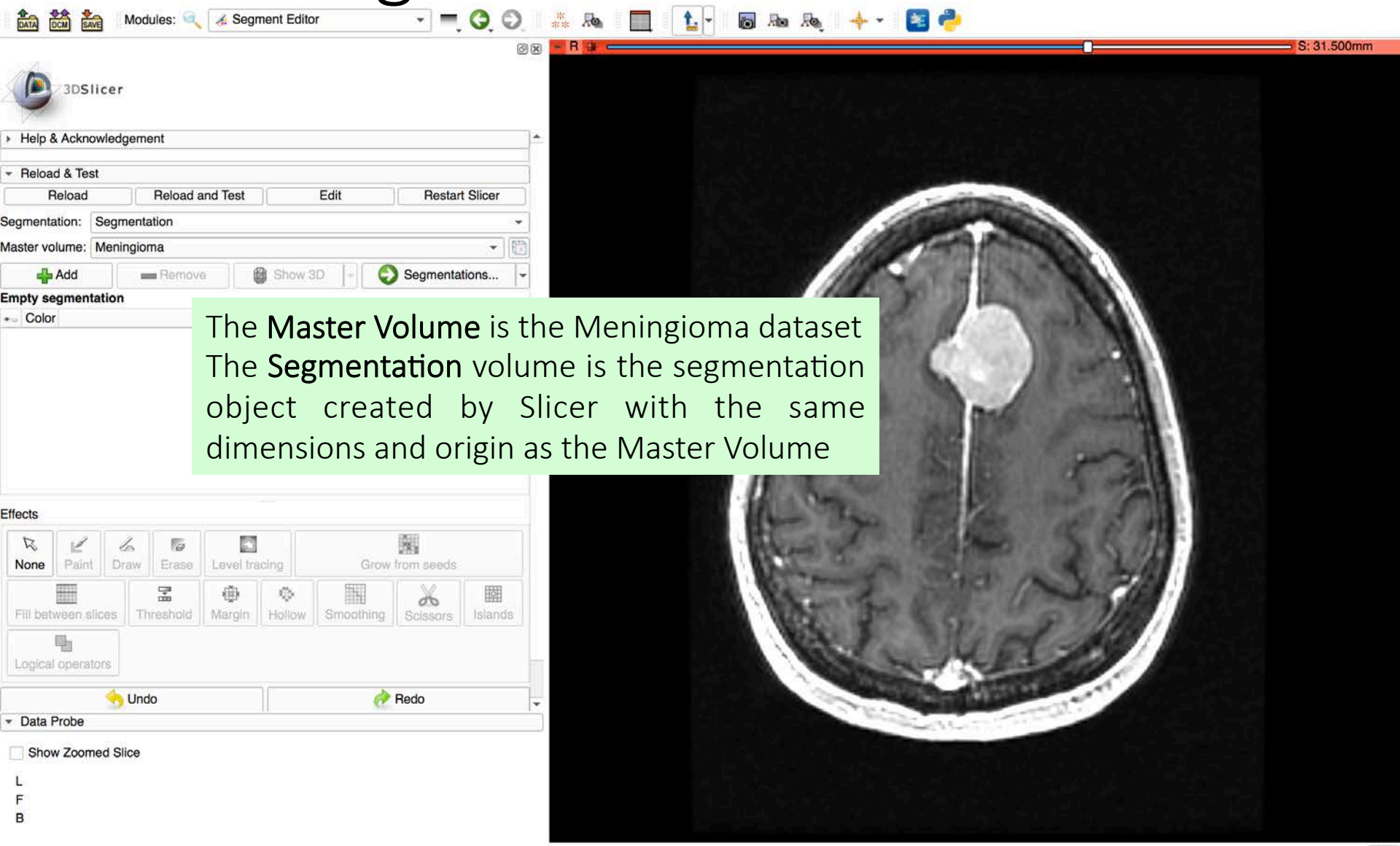
In this tutorial,

- 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

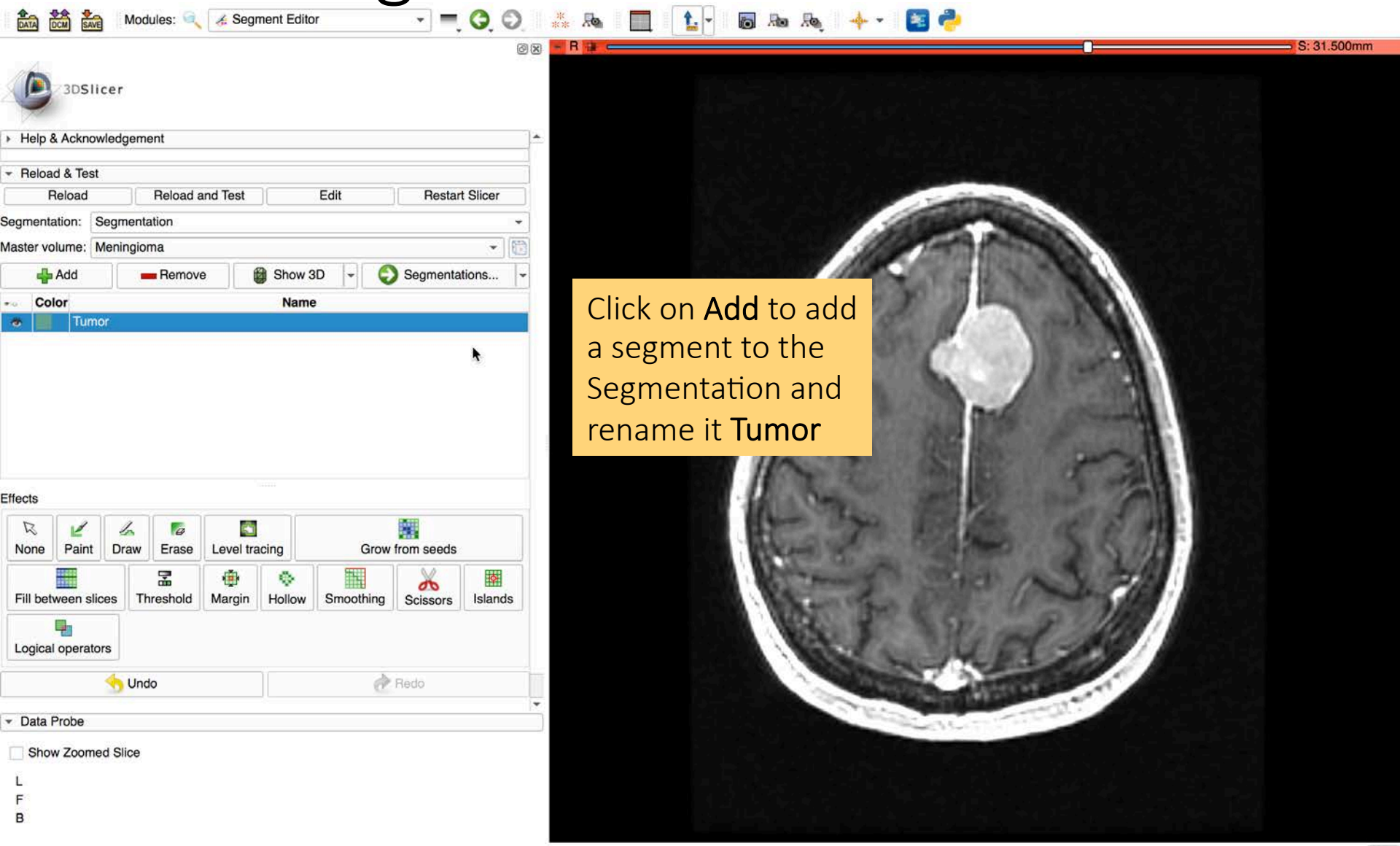


# Segment Editor Module

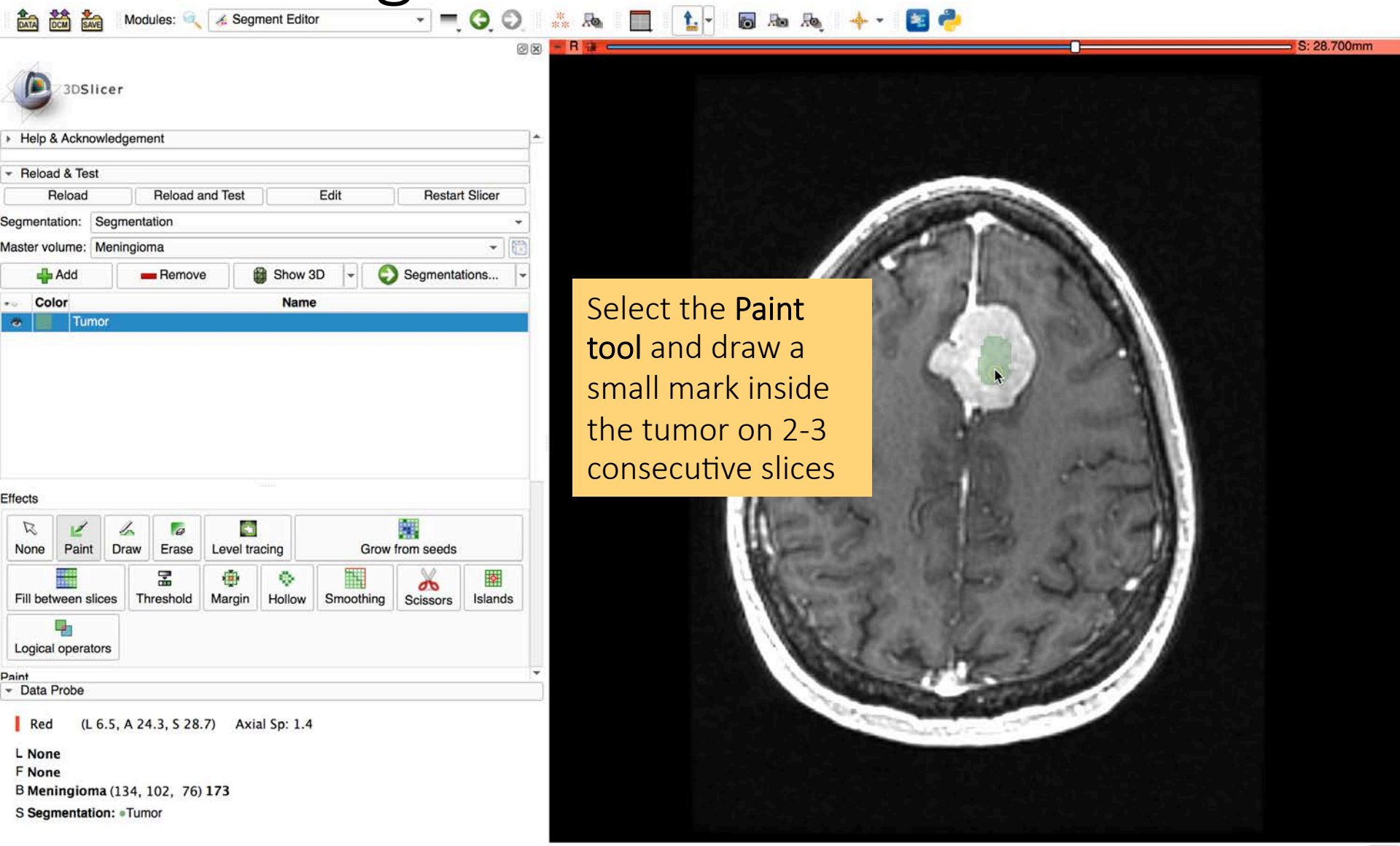



The **Master Volume** is the Meningioma dataset
The **Segmentation** volume is the segmentation object created by Slicer with the same dimensions and origin as the Master Volume

# Segment Editor Module

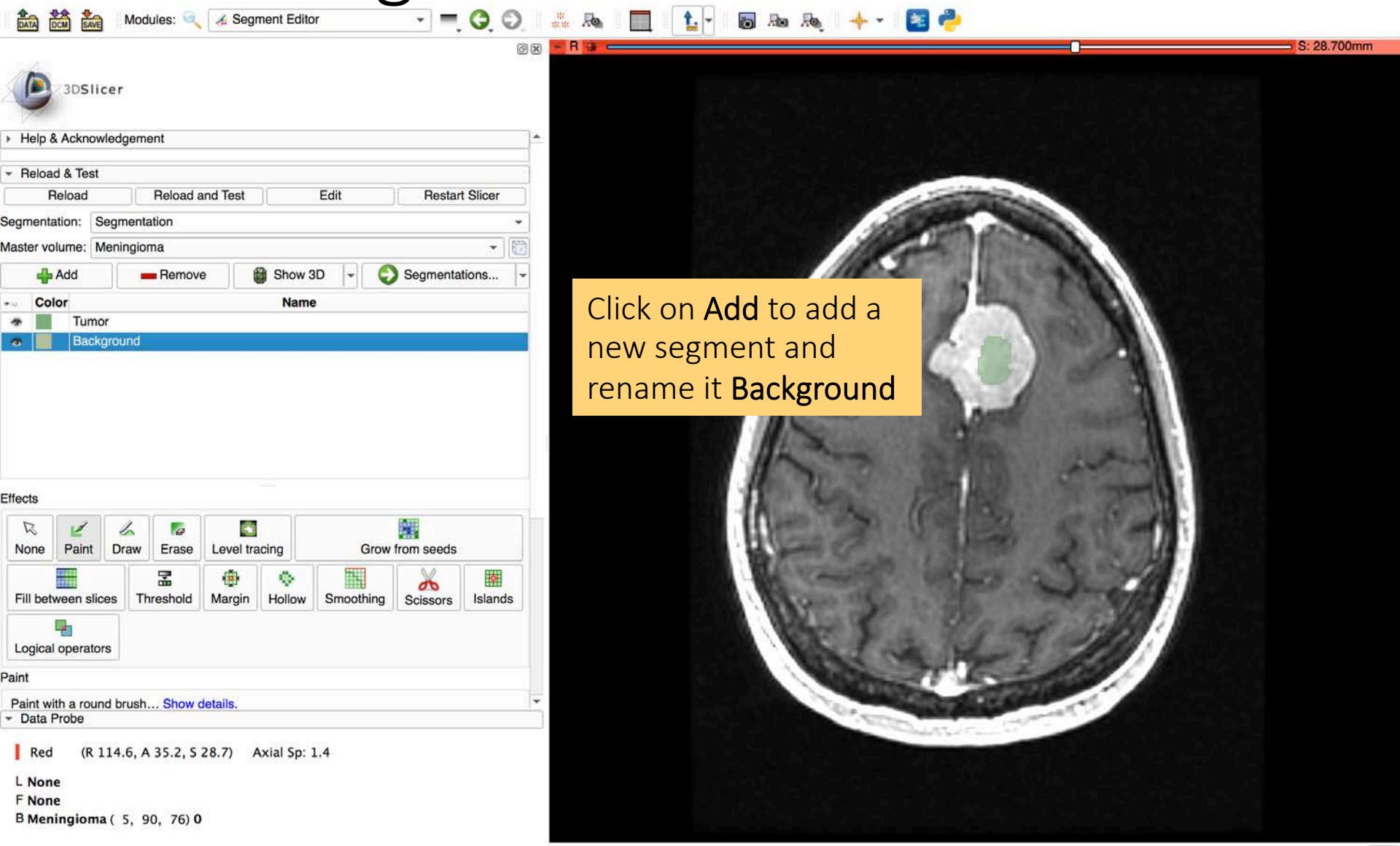


# Segment Editor Module

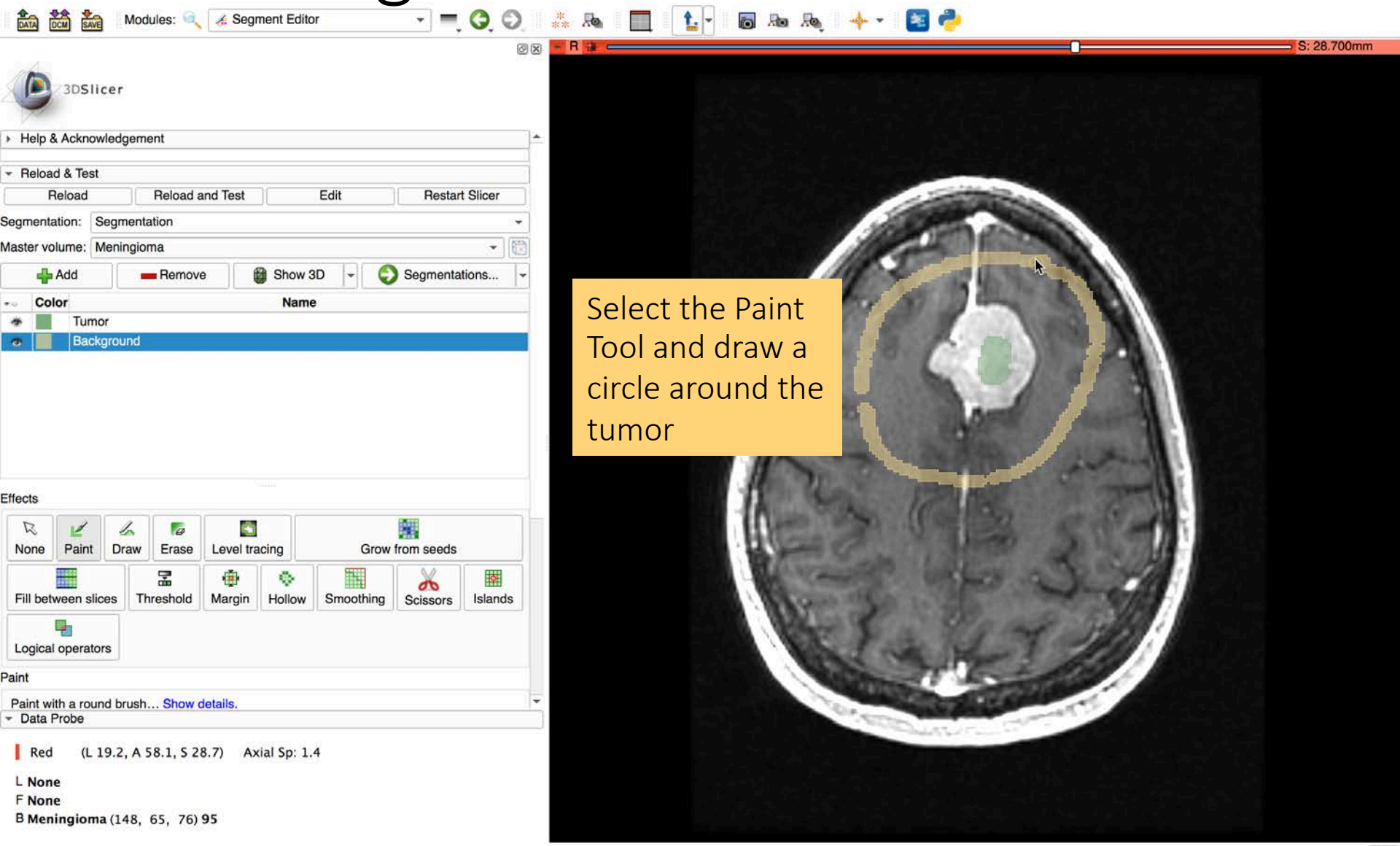



Select the **Paint tool** and draw a small mark inside the tumor on 2-3 consecutive slices

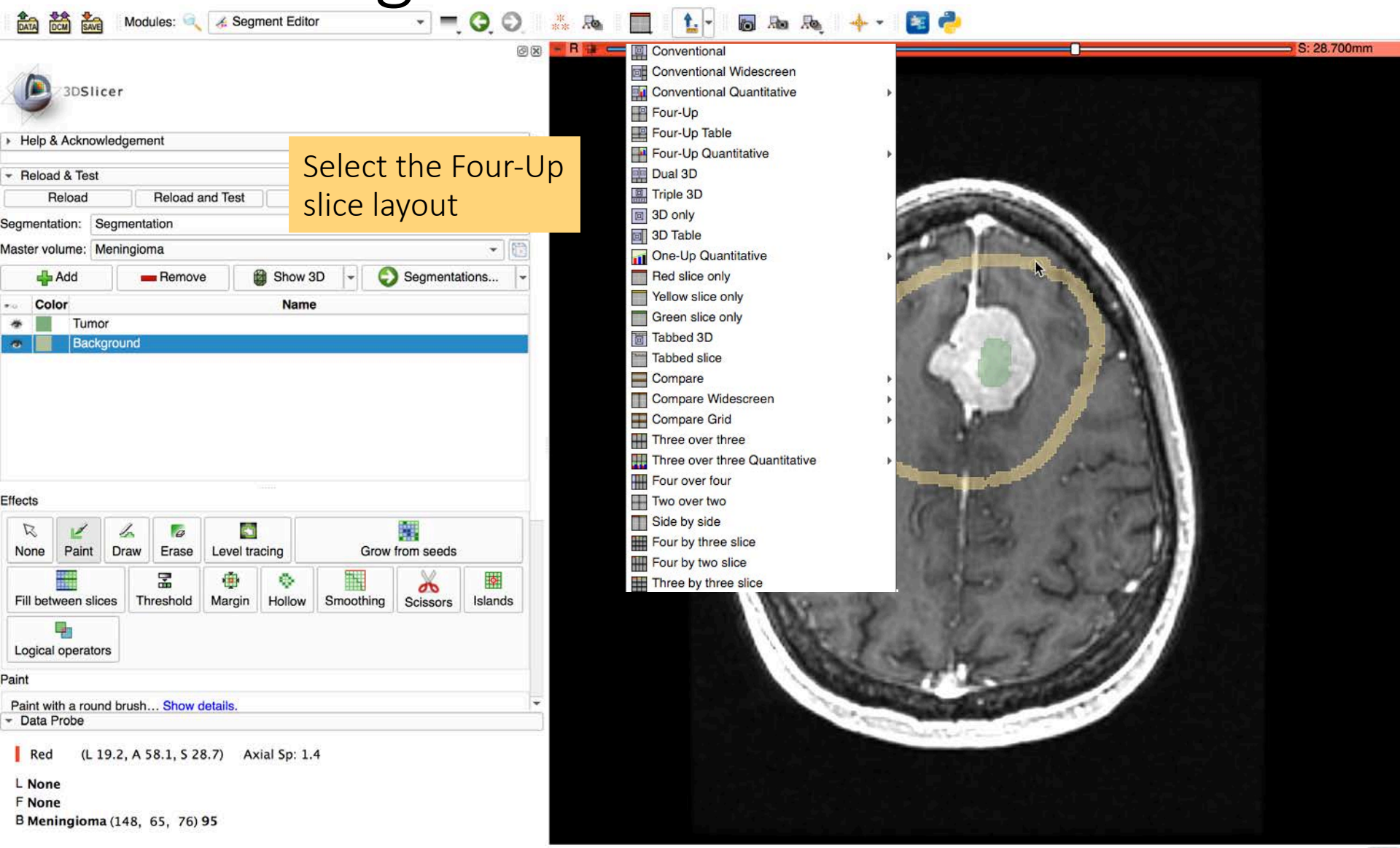
# Segment Editor Module



# Segment Editor Module

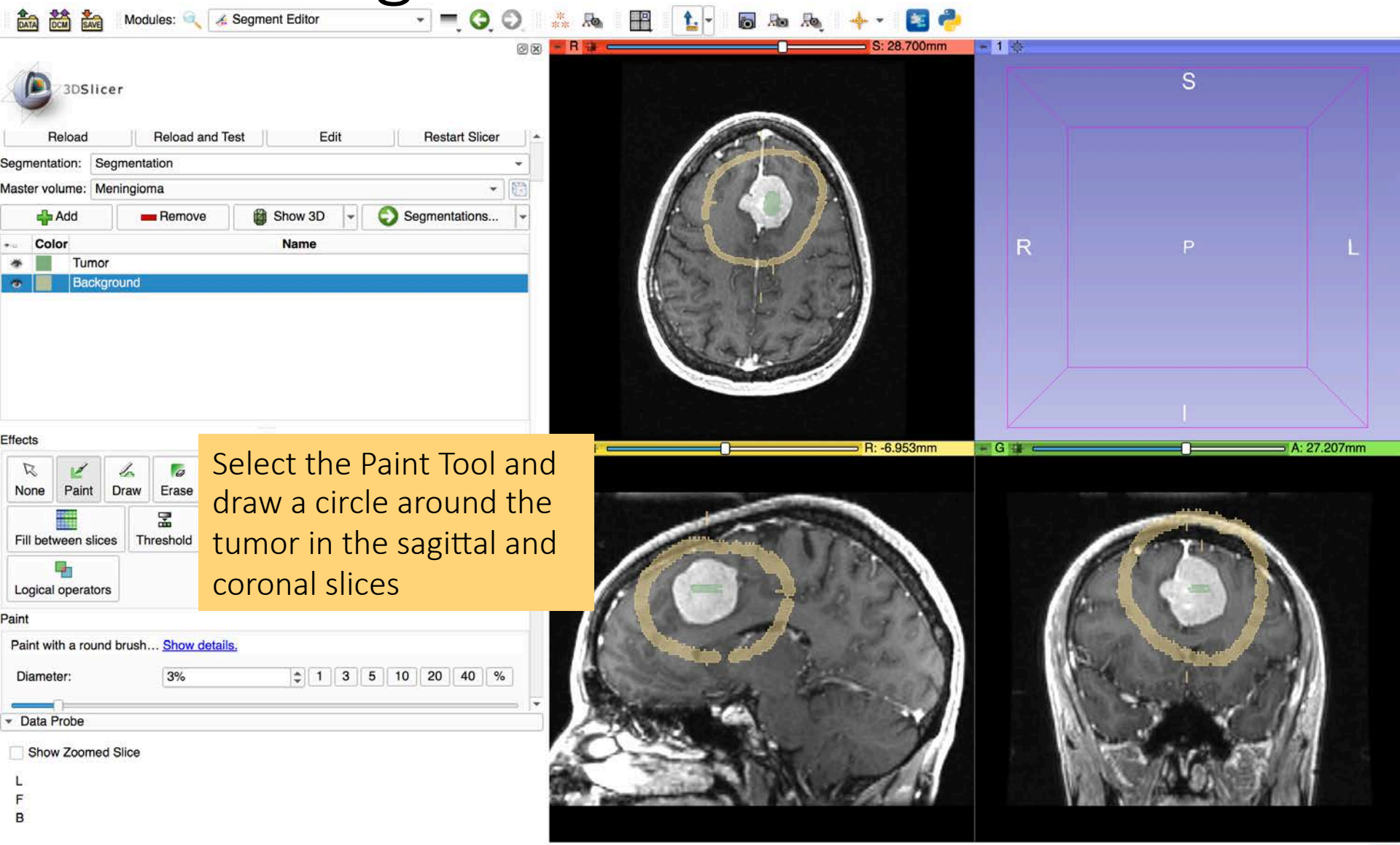


# Segment Editor Module



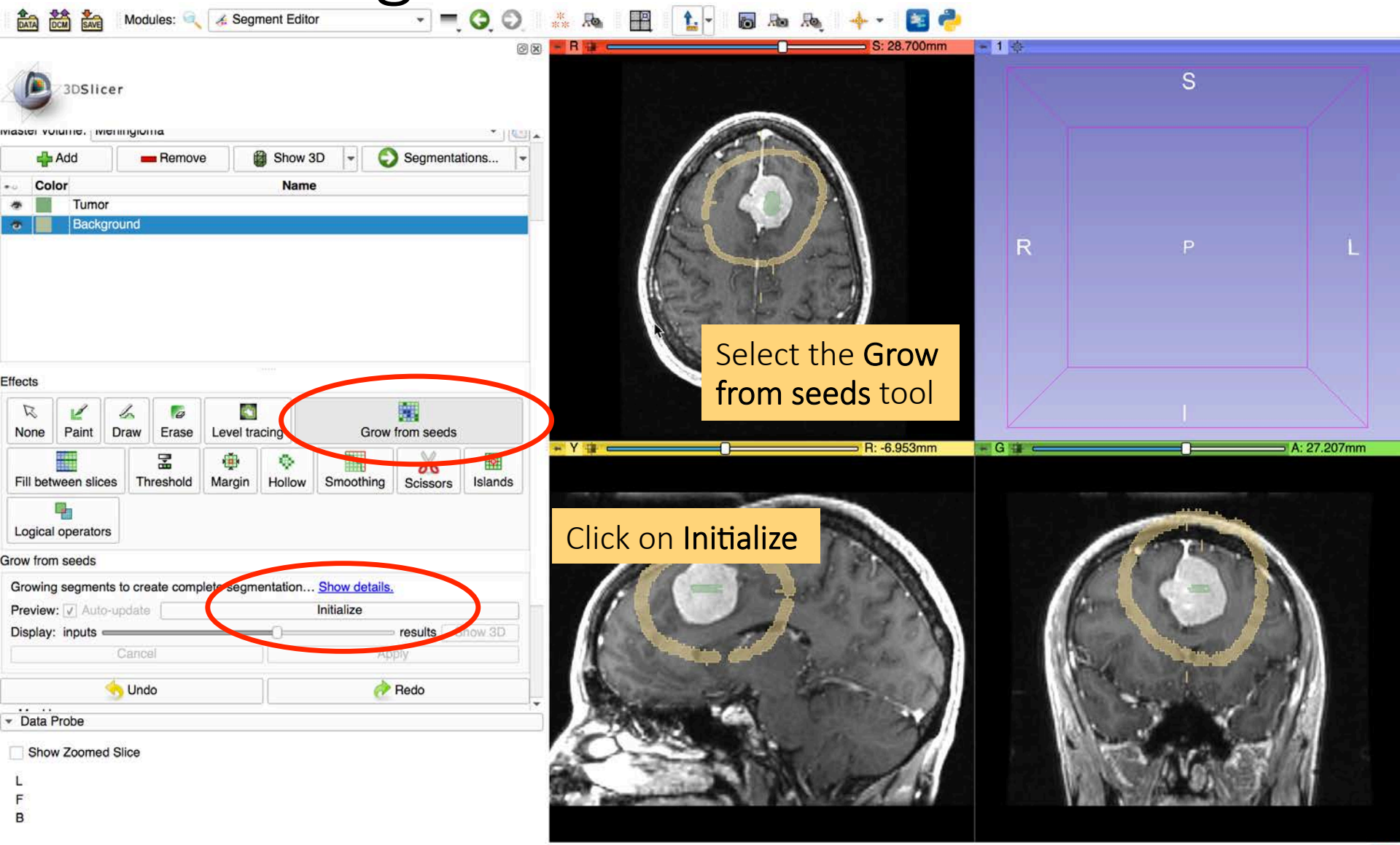

Select the Four-Up slice layout

# Segment Editor Module

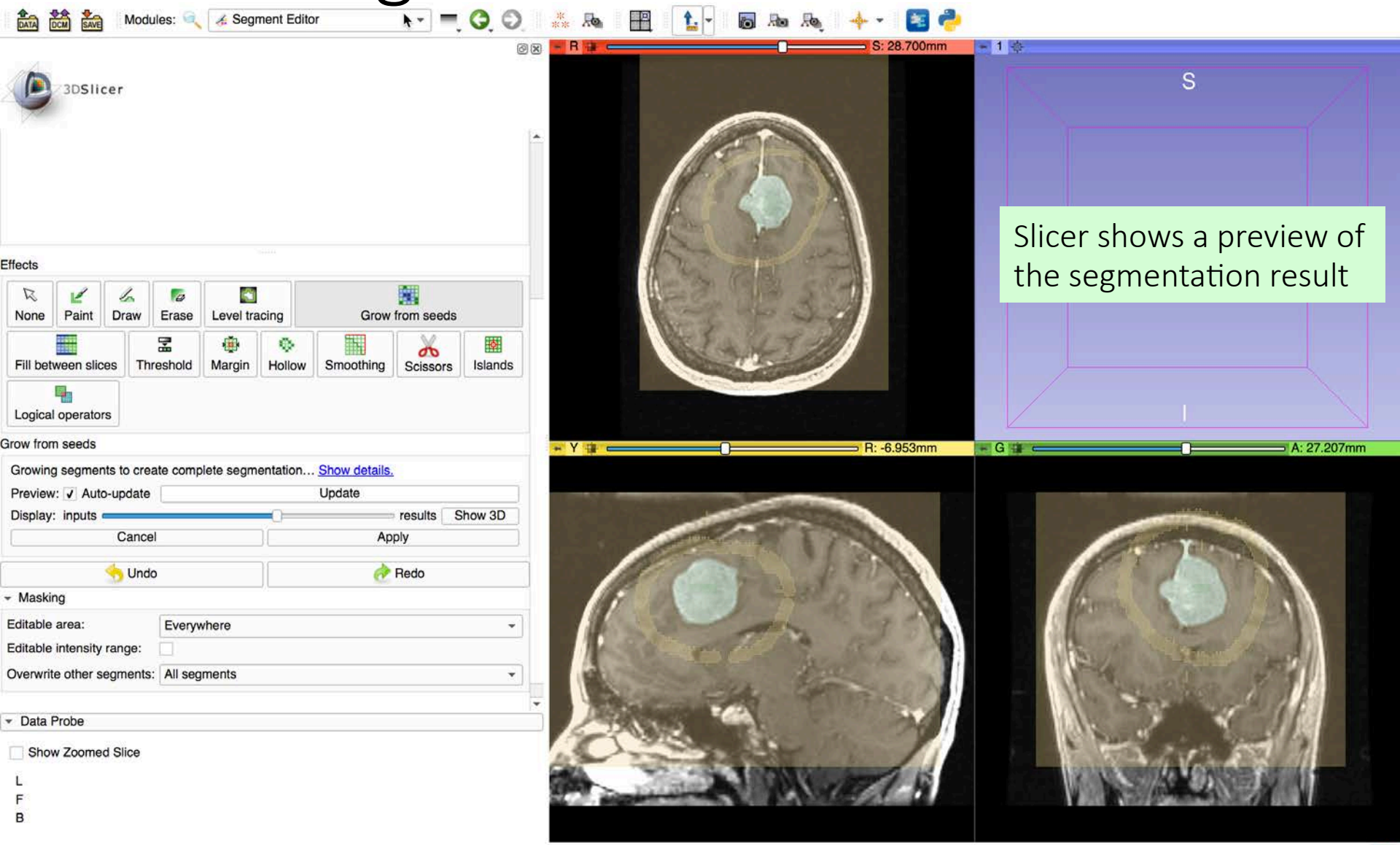



Select the Paint Tool and draw a circle around the tumor in the sagittal and coronal slices

# Segment Editor Module

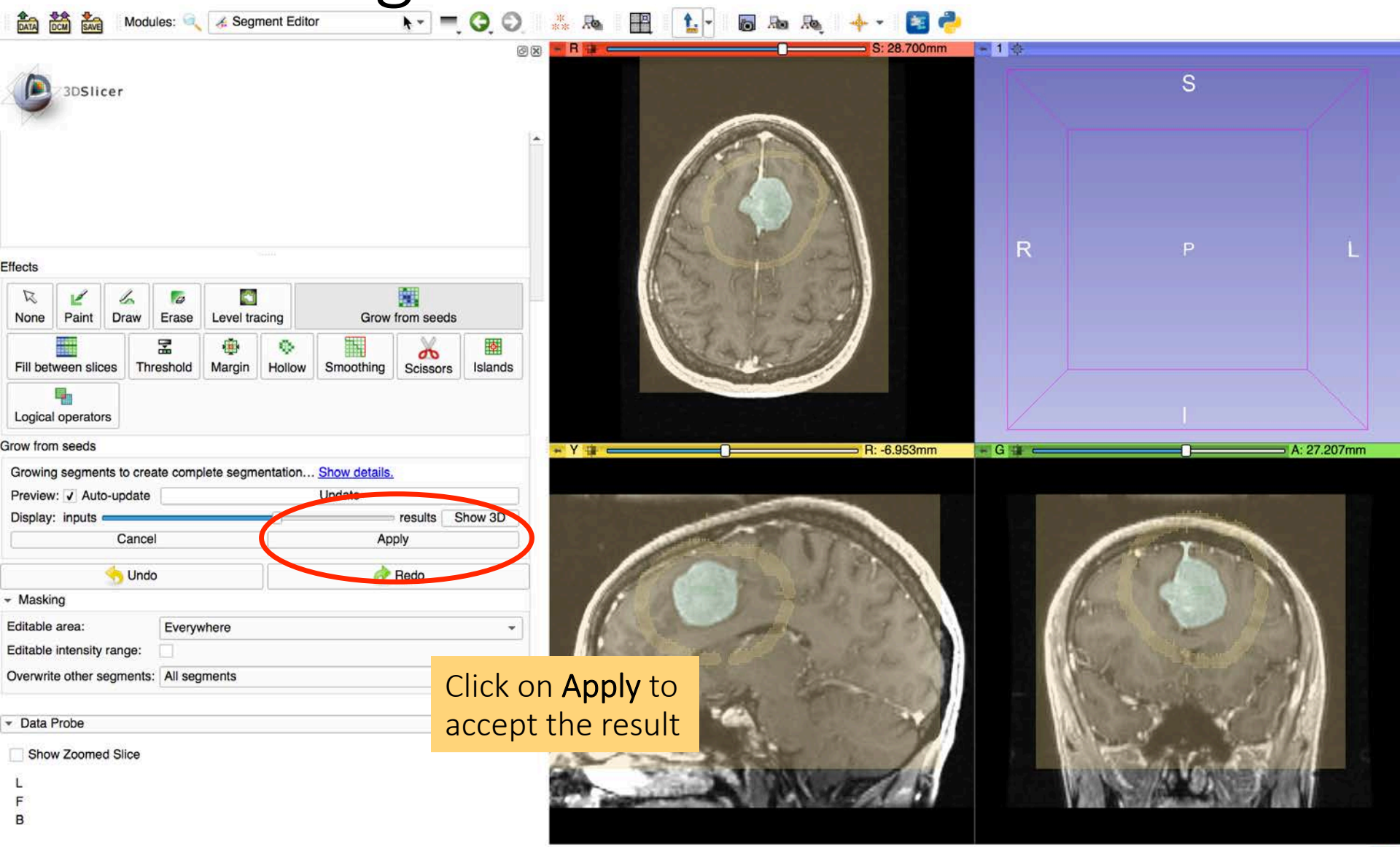


# Segment Editor Module



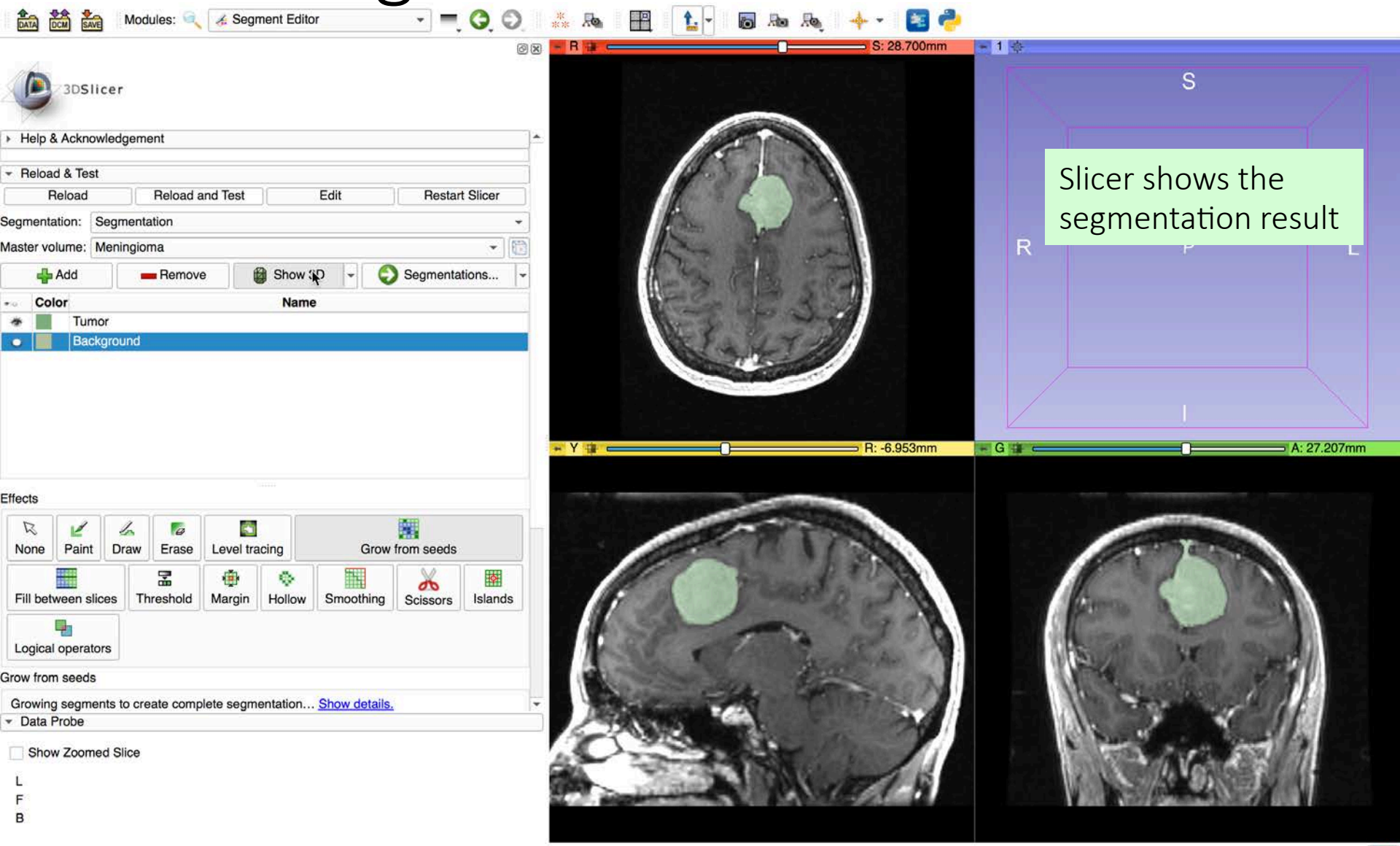

Slicer shows a preview of the segmentation result

# Segment Editor Module




Click on **Apply** to accept the result

# Segment Editor Module



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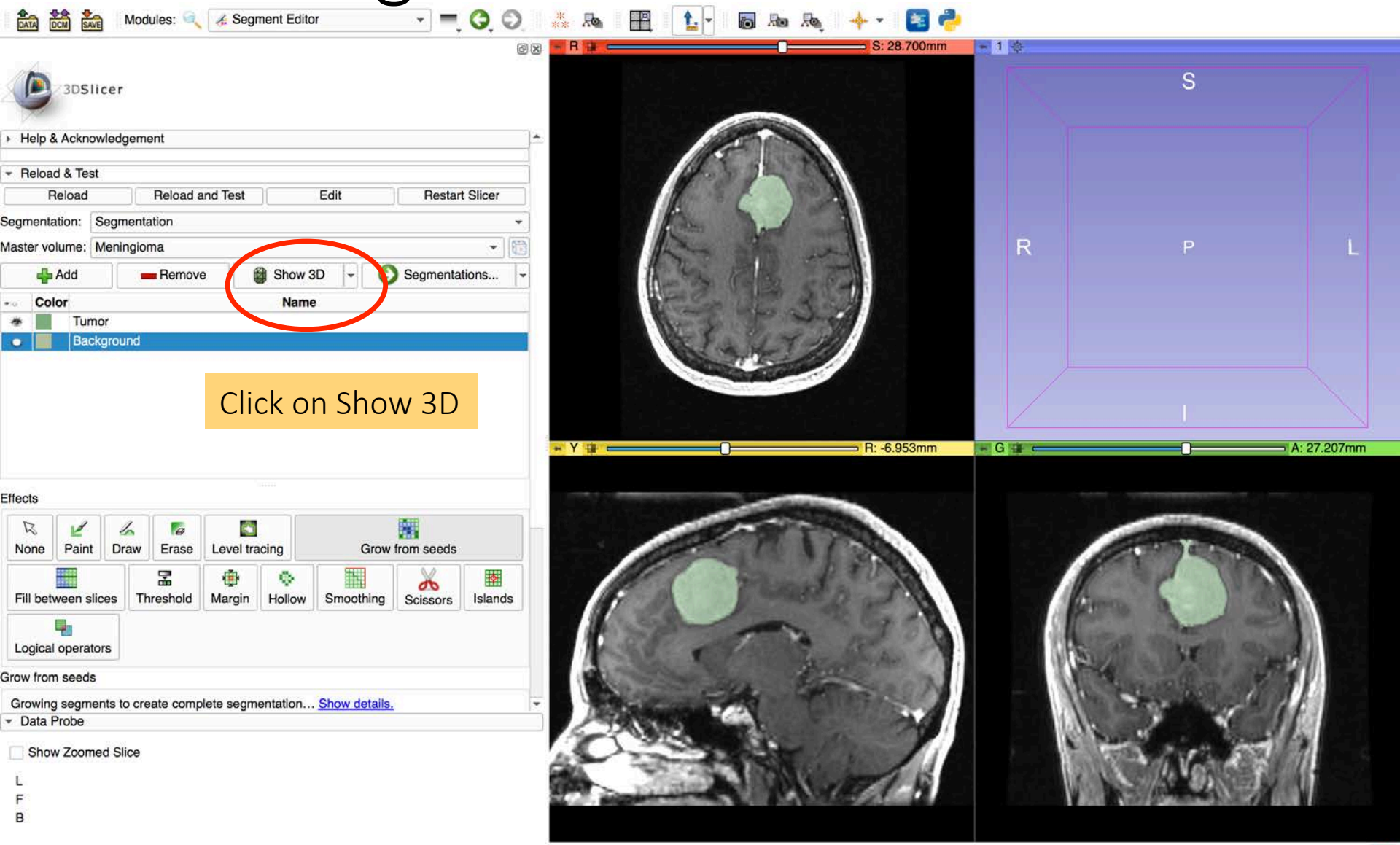

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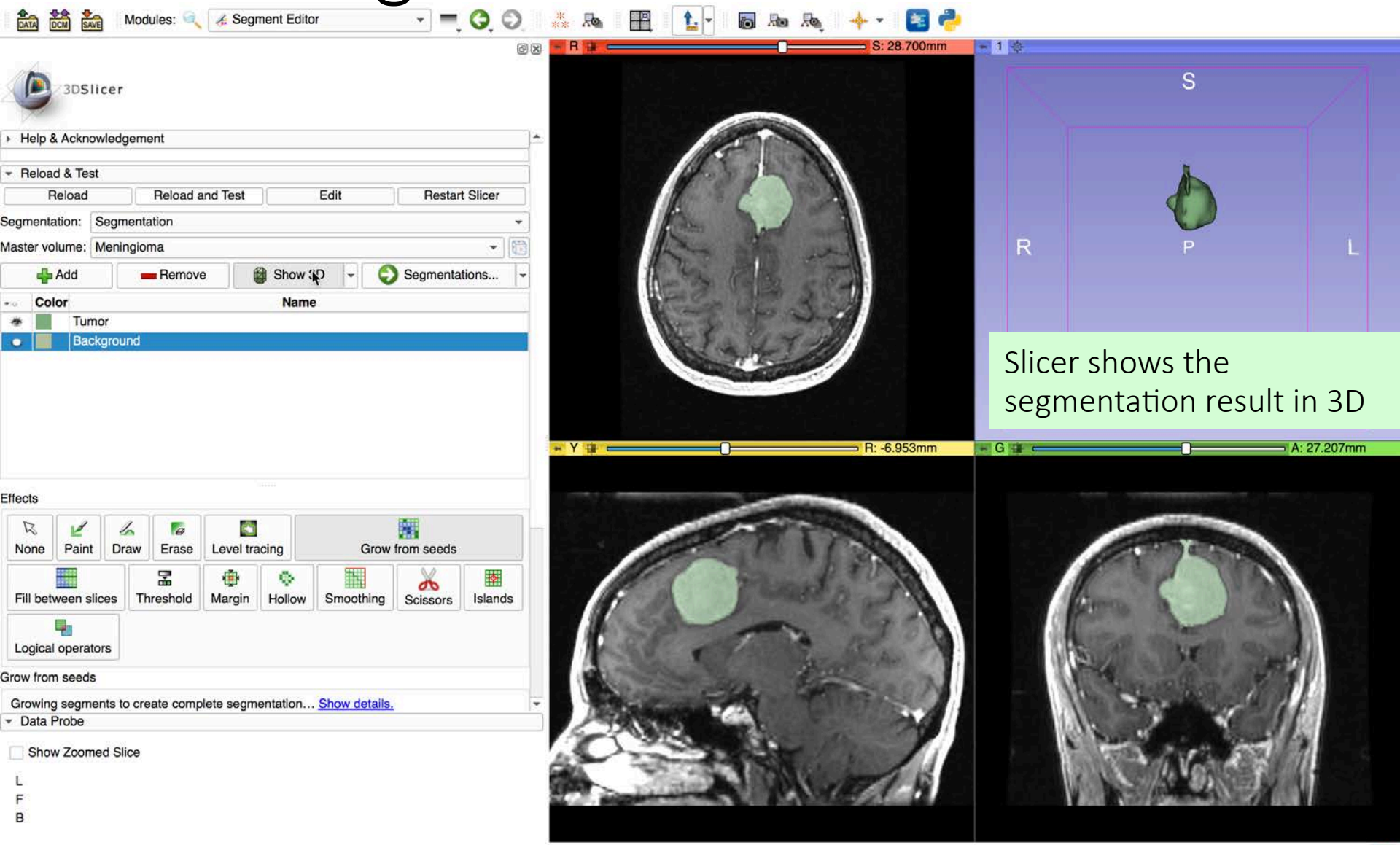
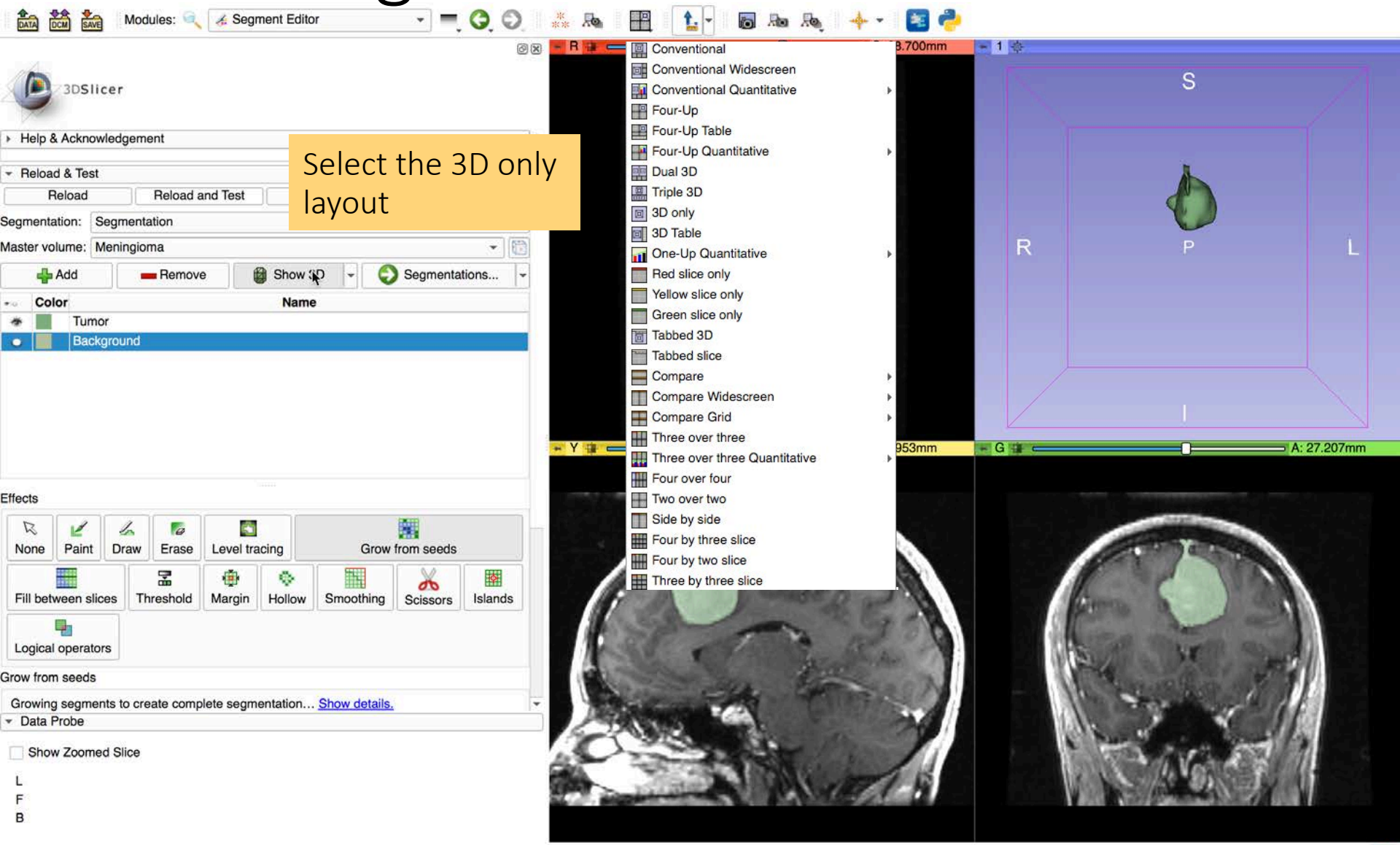


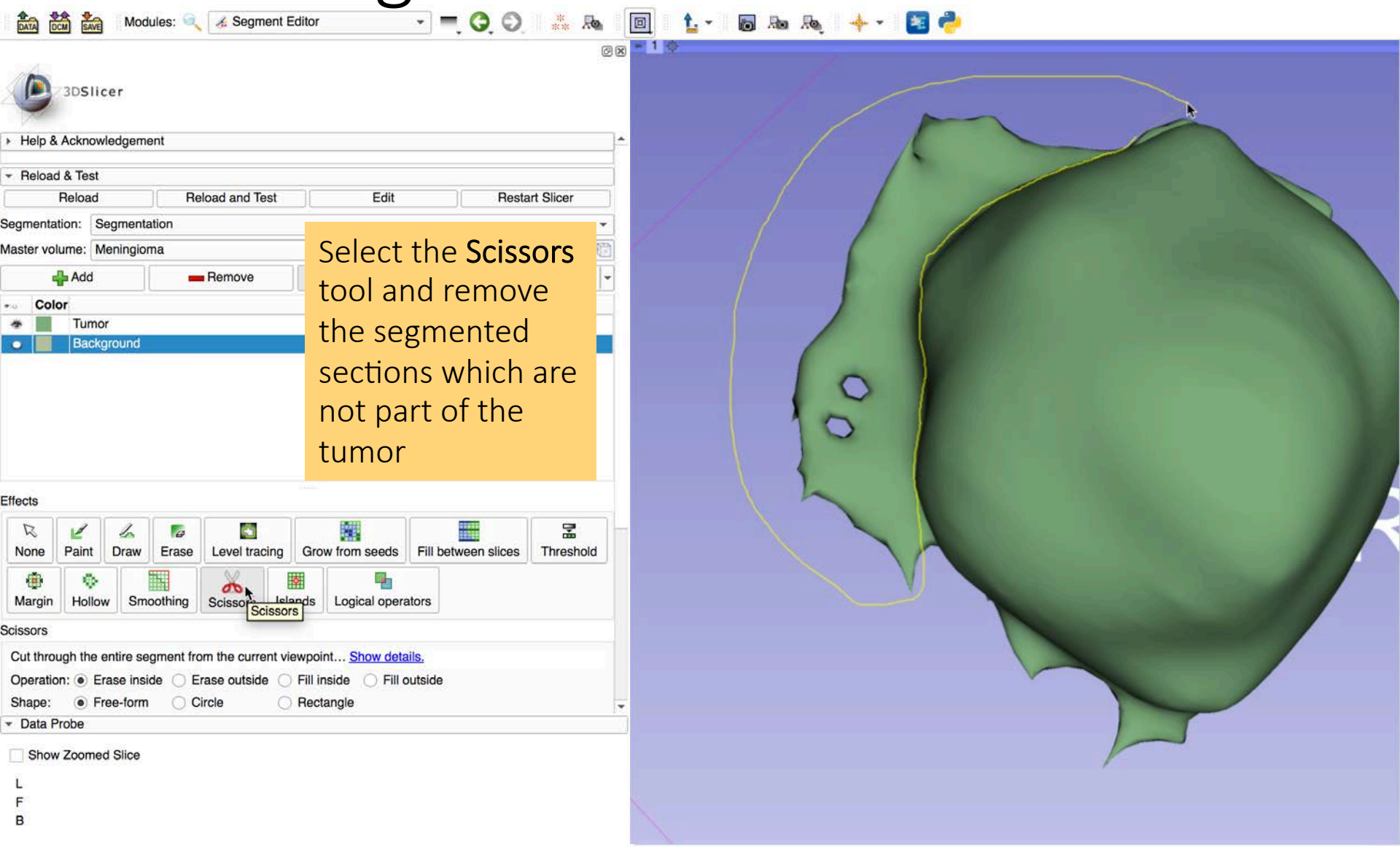

Slicer shows the segmentation result in 3D

# Segment Editor Module




Select the 3D only layout

# Segment Editor Module



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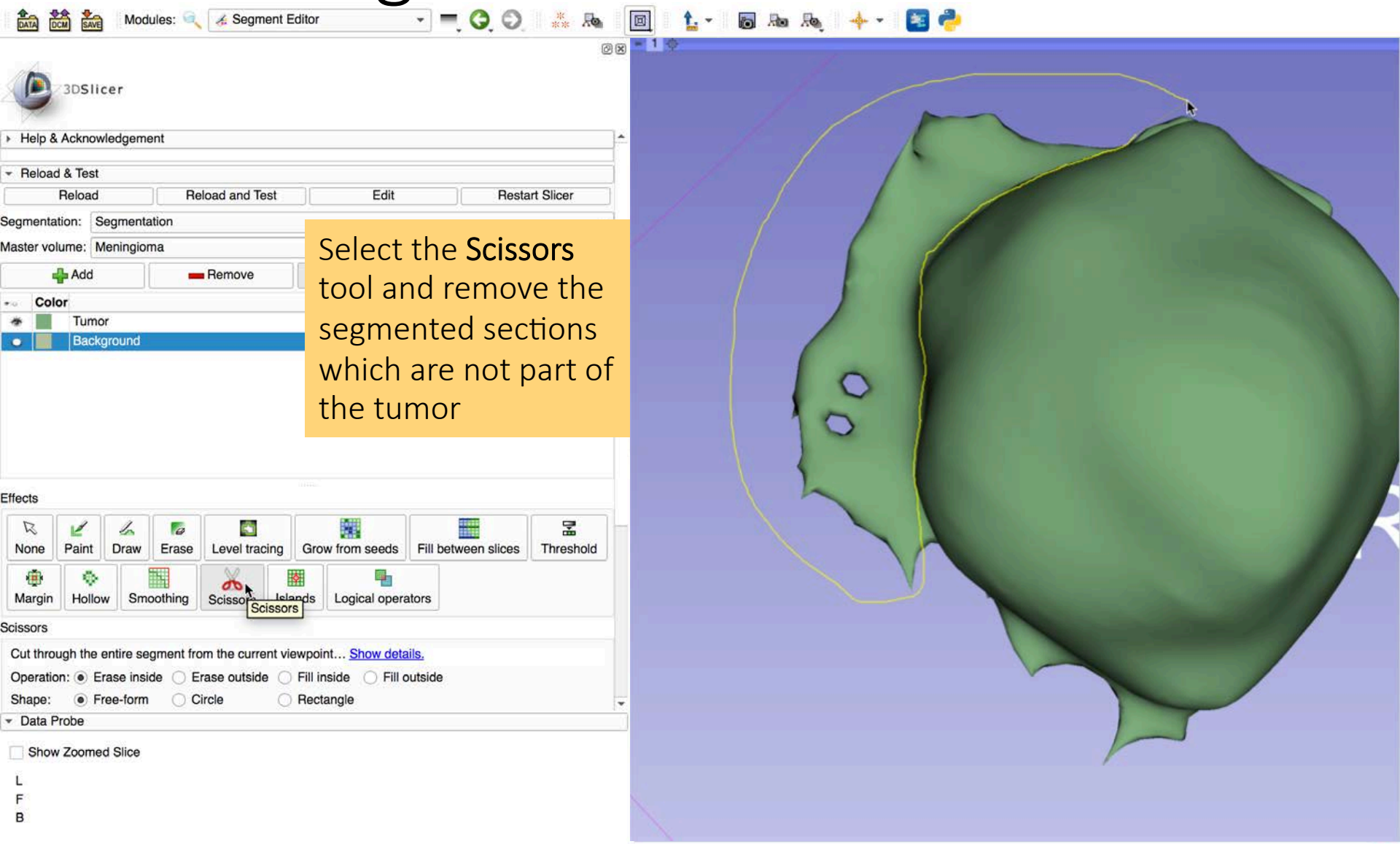

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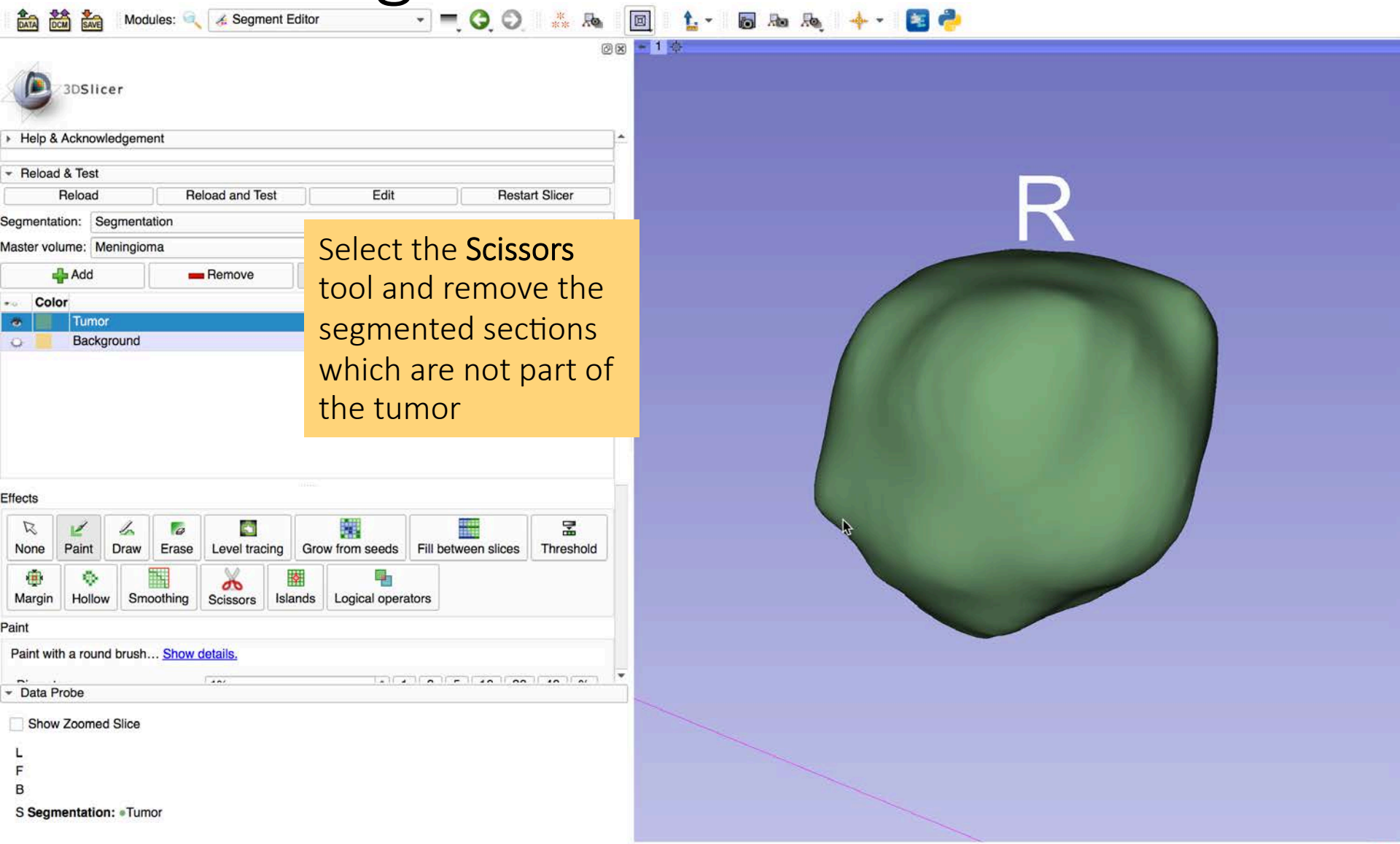
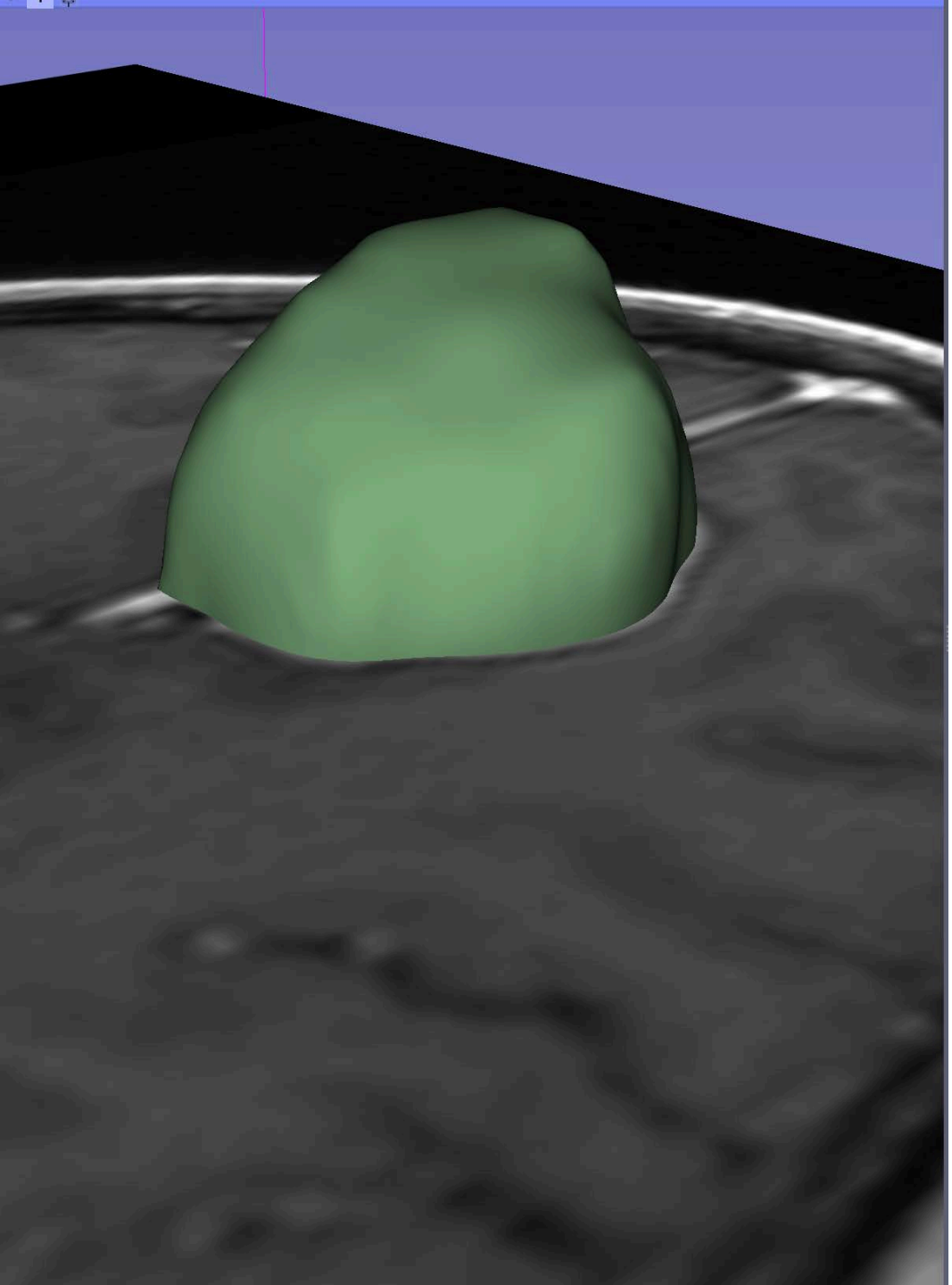
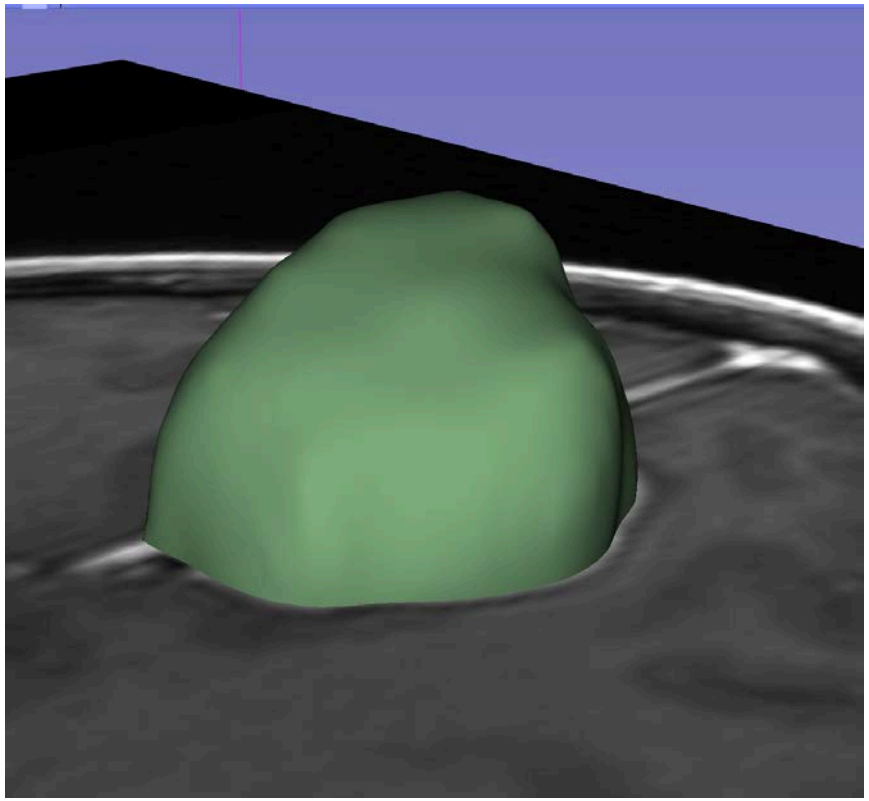



Select the **Scissors** tool and remove the segmented sections which are not part of the tumor



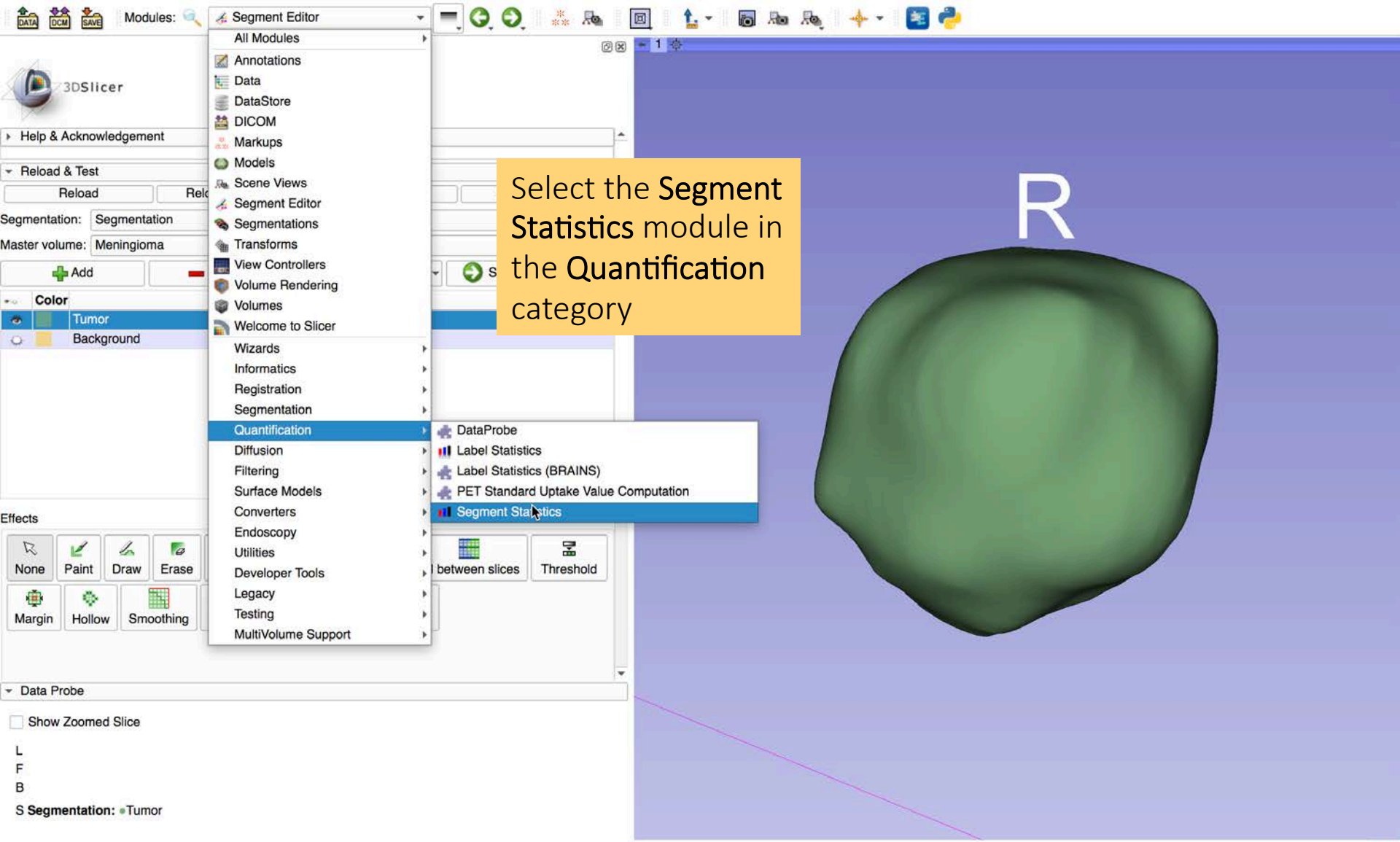
# Part 3: Tumor Volume Calculation

# 3D Measurements



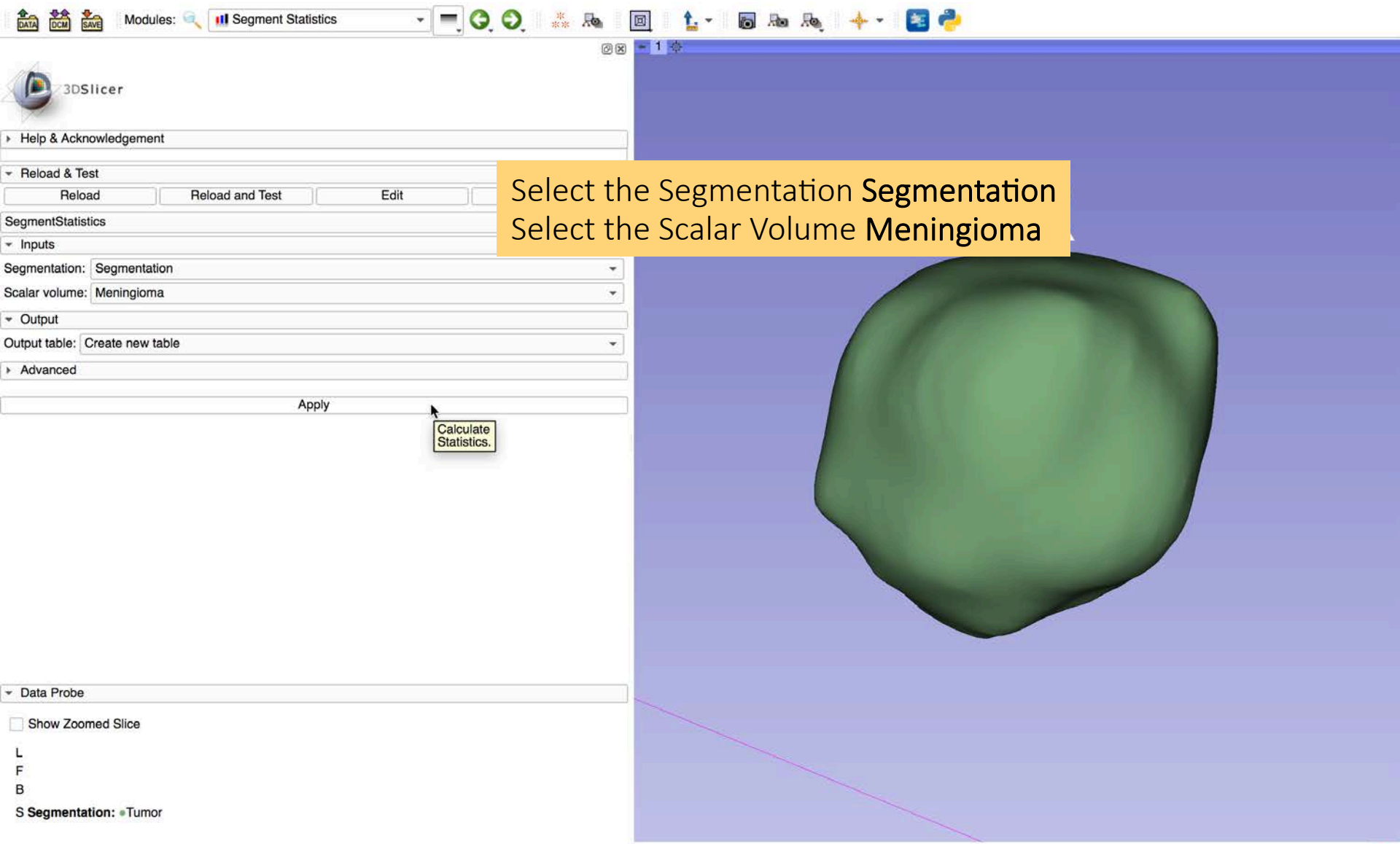
This section shows how to compute the volume of the segmented tumor using the Segment Statistics module

# Tumor Measurements




Select the **Segment Statistics** module in the **Quantification** category

# Tumor Measurements



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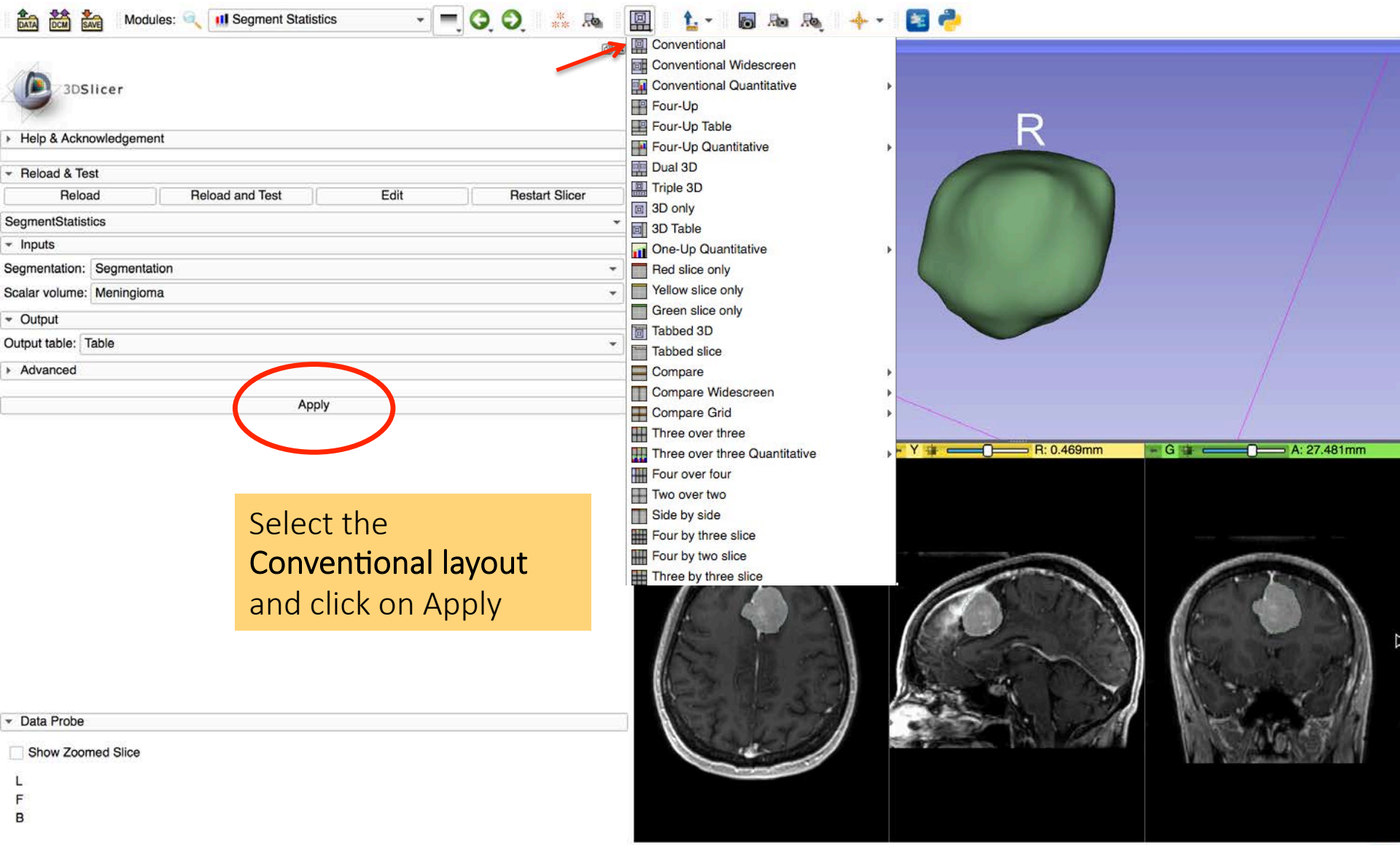
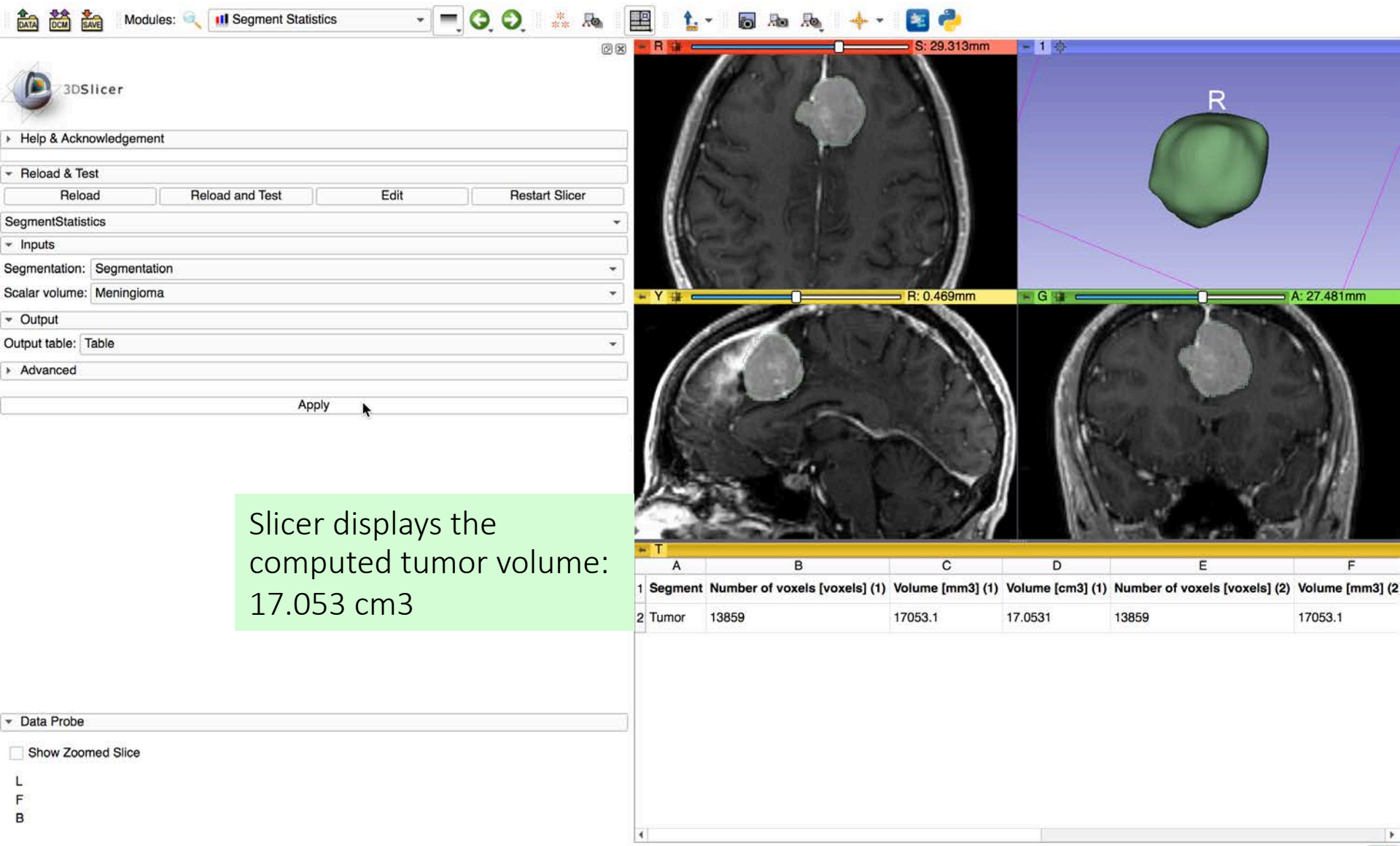
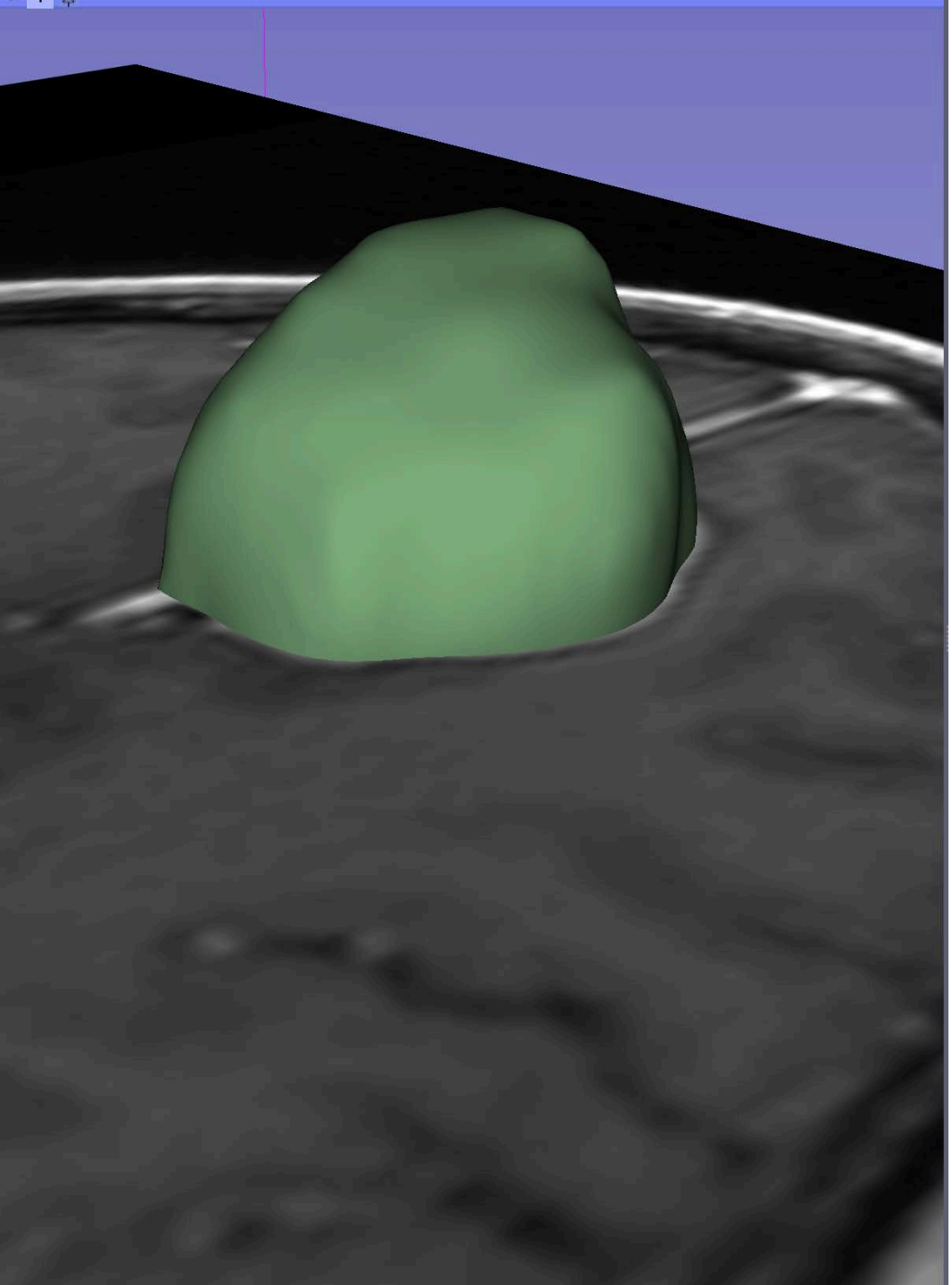



Select the **Conventional layout** and click on Apply

# 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

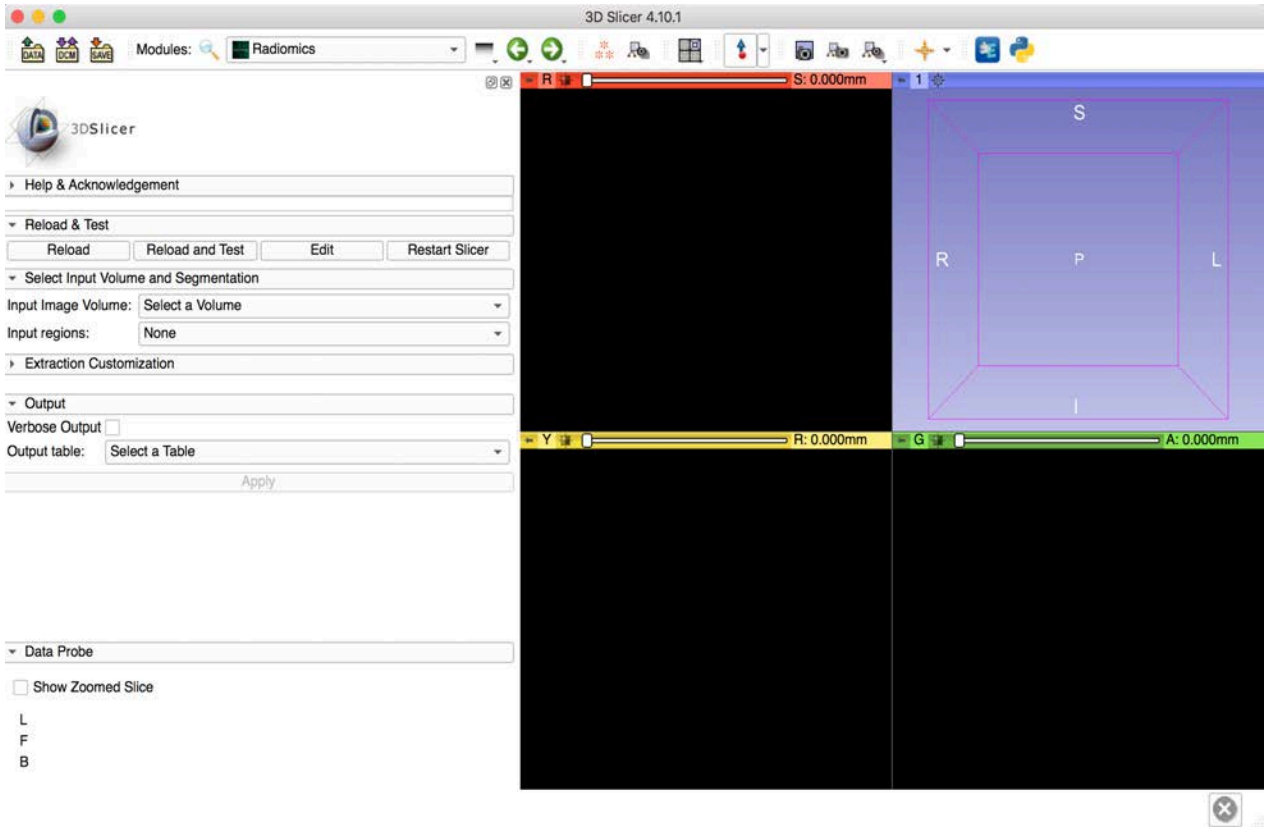
https://pyradiomics.readthedocs.io

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.*



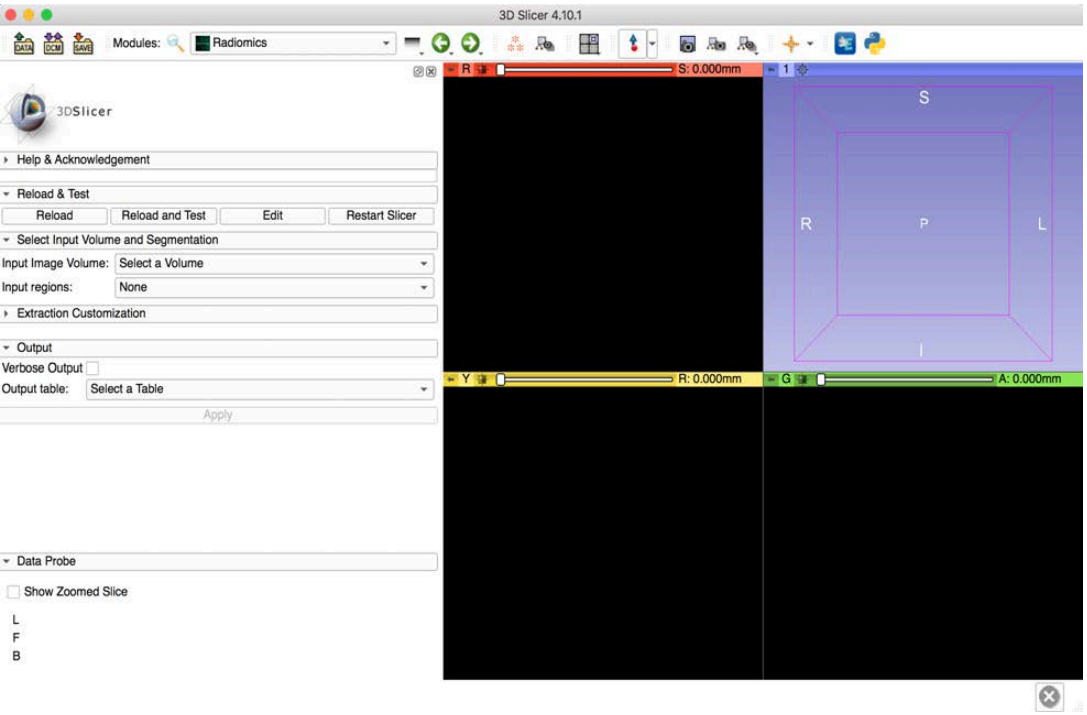
# Slicer Radiomics




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

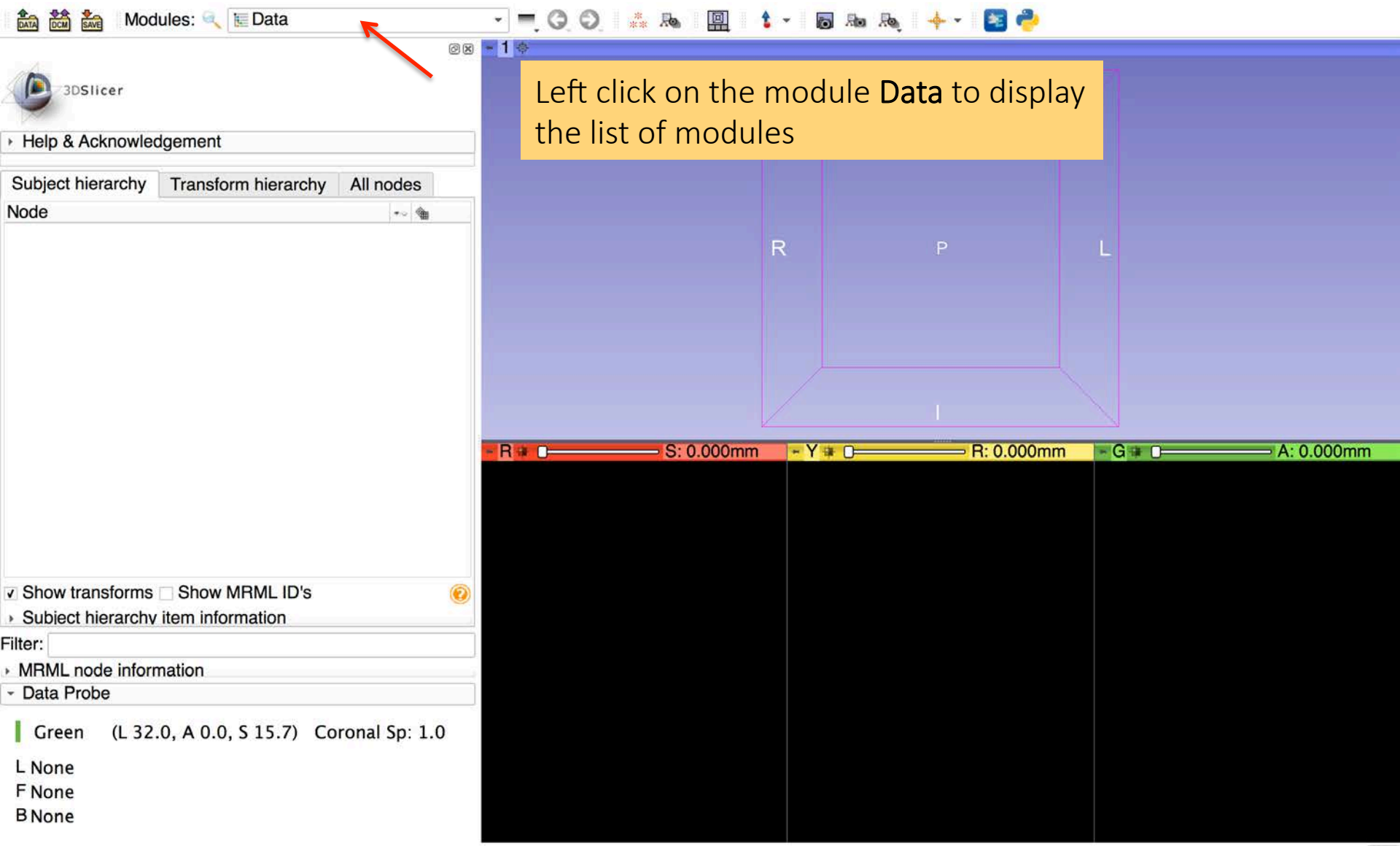


# Slicer Radiomics

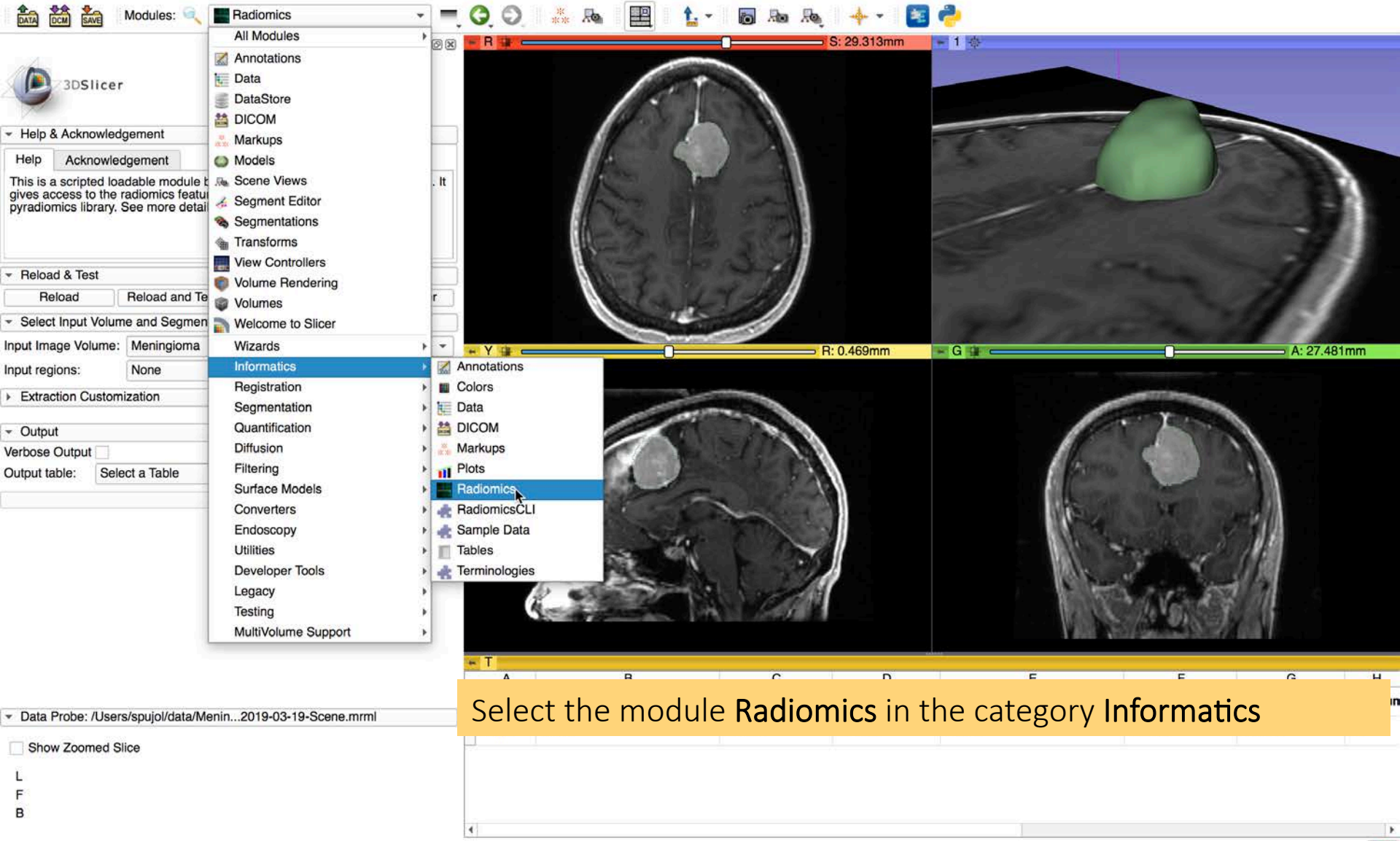



The Slicer Radiomics Extension enables interactive imaging features exploration and configuration of extraction parameters

# Radiomics Module

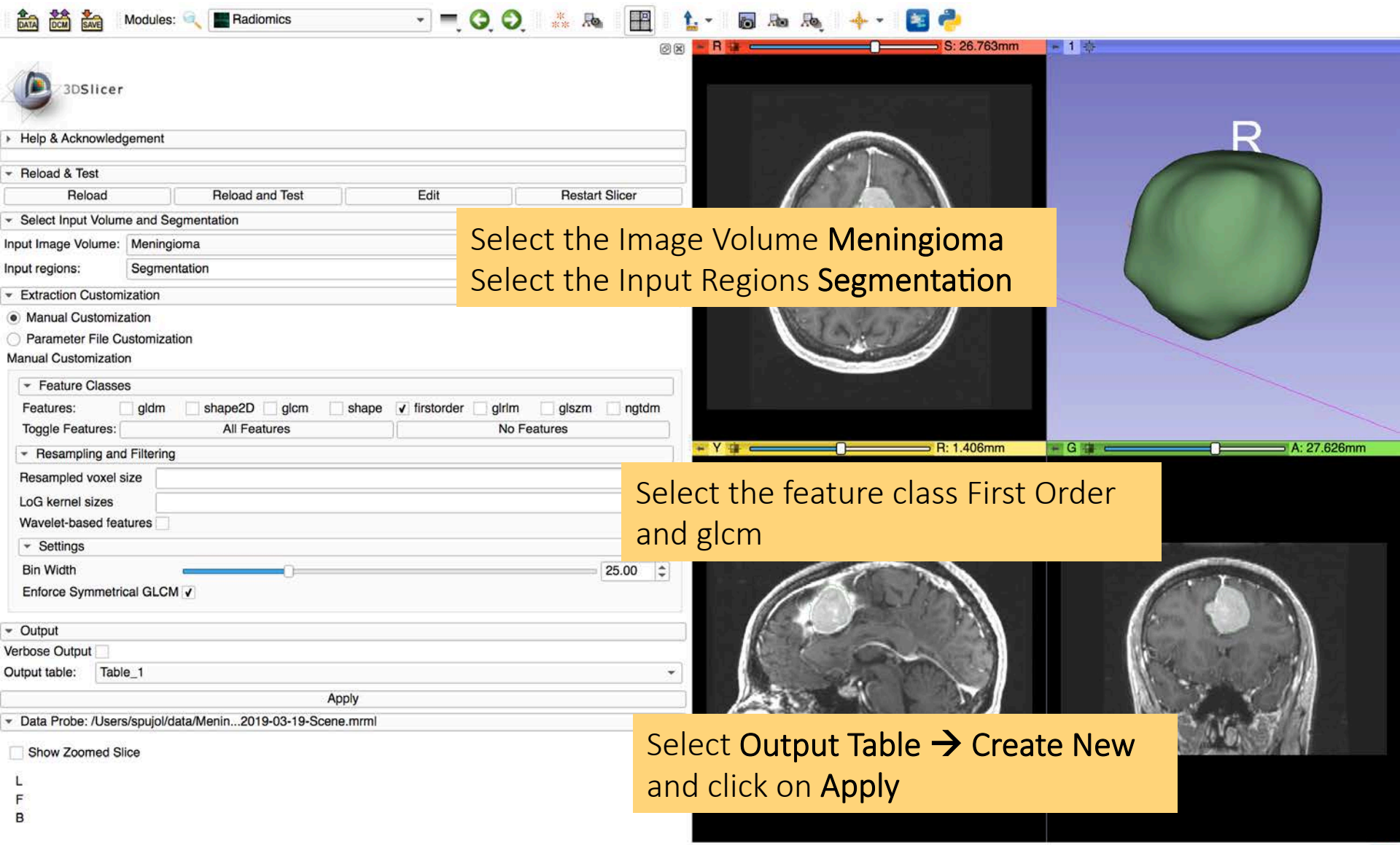


# Radiomics Module Installation

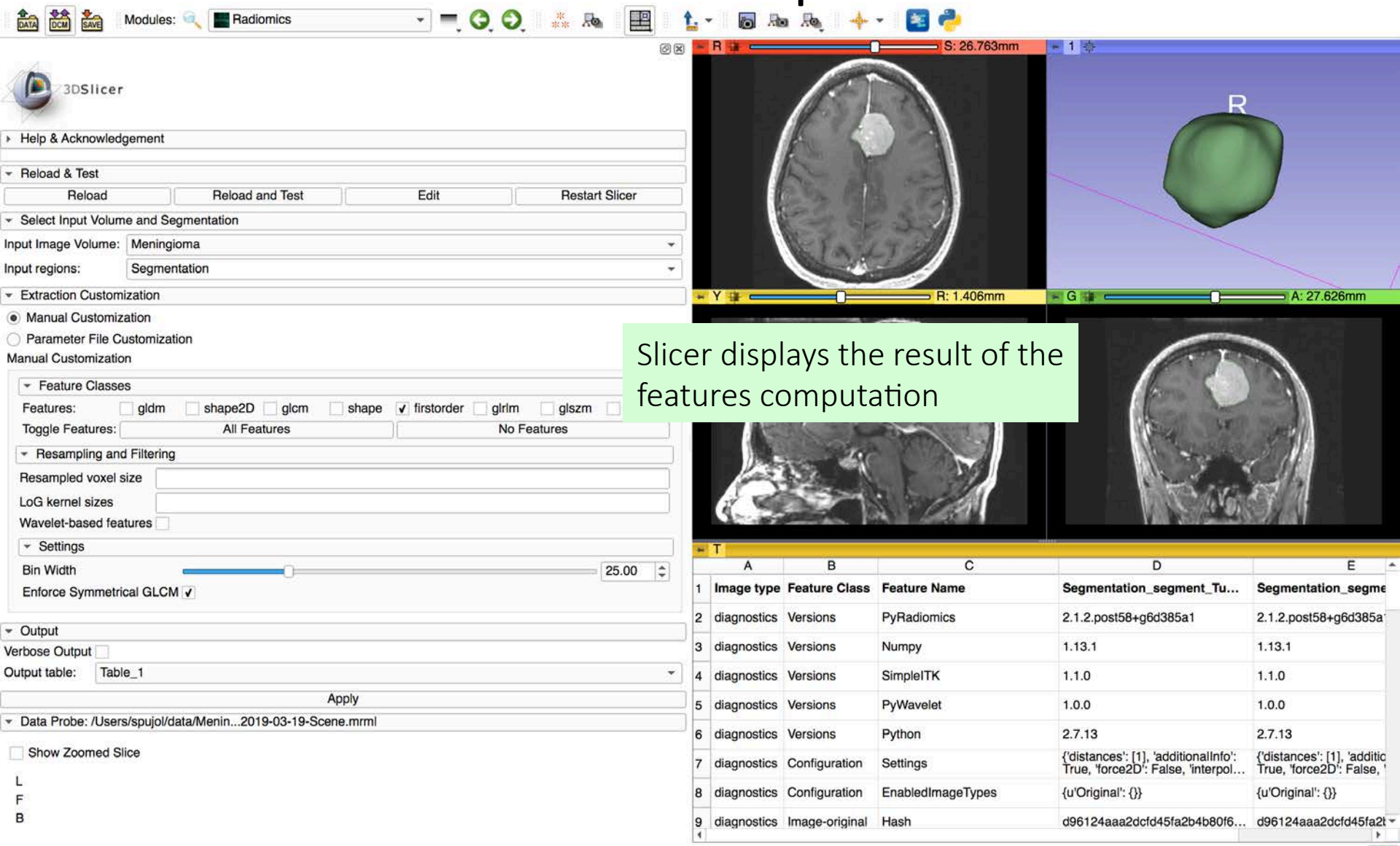



Select the module **Radiomics** in the category **Informatics**

# Radiomics Module Installation



# Features Computation




Slicer displays the result of the features computation

| | A | B | C | D | E |
|---|---|---|---|---|---|
| 1 | Image type | Feature Class | Feature Name | Segmentation_segment_Tu... | Segmentation_segme |
| 2 | diagnostics | Versions | PyRadiomics | 2.1.2.post58+g6d385a1 | 2.1.2.post58+g6d385a |
| 3 | diagnostics | Versions | Numpy | 1.13.1 | 1.13.1 |
| 4 | diagnostics | Versions | SimpleITK | 1.1.0 | 1.1.0 |
| 5 | diagnostics | Versions | PyWavelet | 1.0.0 | 1.0.0 |
| 6 | diagnostics | Versions | Python | 2.7.13 | 2.7.13 |
| 7 | diagnostics | Configuration | Settings | {'distances': [1], 'additionalInfo': True, 'force2D': False, 'interpol... | {'distances': [1], 'additic True, 'force2D': False, ' |
| 8 | diagnostics | Configuration | EnabledImageTypes | {u'Original': {}} | {u'Original': {}} |
| 9 | diagnostics | Image-original | Hash | d96124aaa2dcfd45fa2b4b80f6... | d96124aaa2dcfd45fa2b |

# Features Computation

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

| | | | | |
|---|---|---|---|---|
| 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/

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The mission of the Neuroimage Analysis Center (NAC) (NIH P41 EB015902)

is to advance the role of neuroimaging in health care.