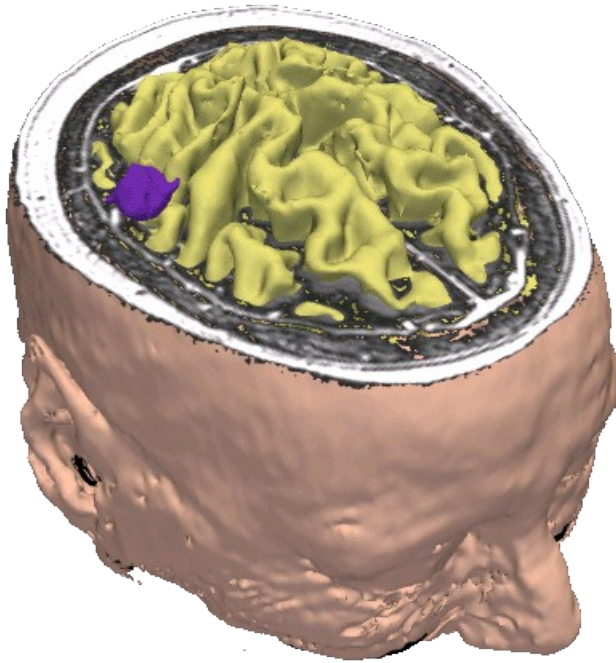


## Measuring Volume Change in Tumors



Kilian M Pohl, PhD  
Ender Konugolu, PhD  
Andriy Fedorov, PhD

This course requires the following installation:

- 3DSlicer version 3.4.1 Software, which can be installed from <http://www.slicer.org/pages/Special:SlicerDownloads>
- A reliable internet connection for downloading the data

***Disclaimer***

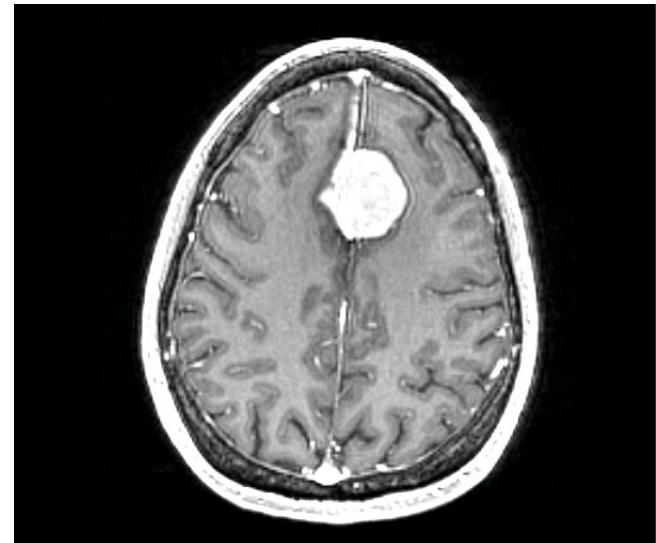
*It is the responsibility of the user of 3DSlicer to comply with both the terms of the license and with the applicable laws, regulations and rules.*

*The module described in this tutorial was tested on Axial 3D SPGR T1 post Gadolinium scans (Voxel dimension: 0.94mm x 0.94mm x 1.20mm, FOV: 240mm, Matrix: 256 x 256)*

This course is built upon two scans of a patient with meningioma:



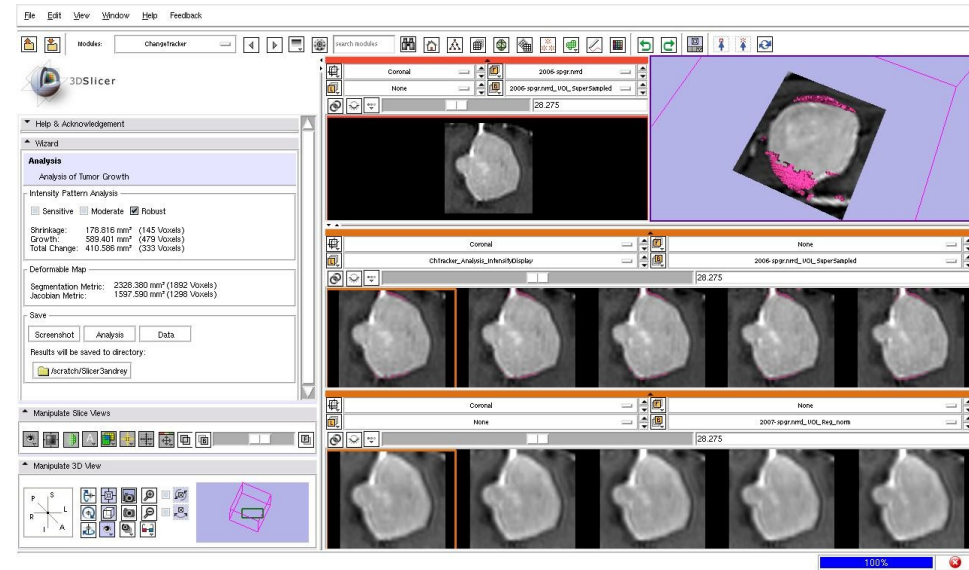
MR Scan 1

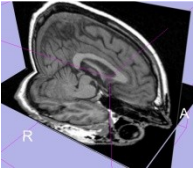


MR Scan 2

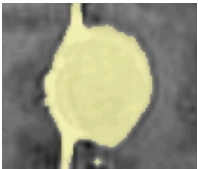
# Learning objective

Following this tutorial, you'll be able to **load two scans** into Slicer3, and **measure and visualize the change in volume** of the meningioma between the two scans.

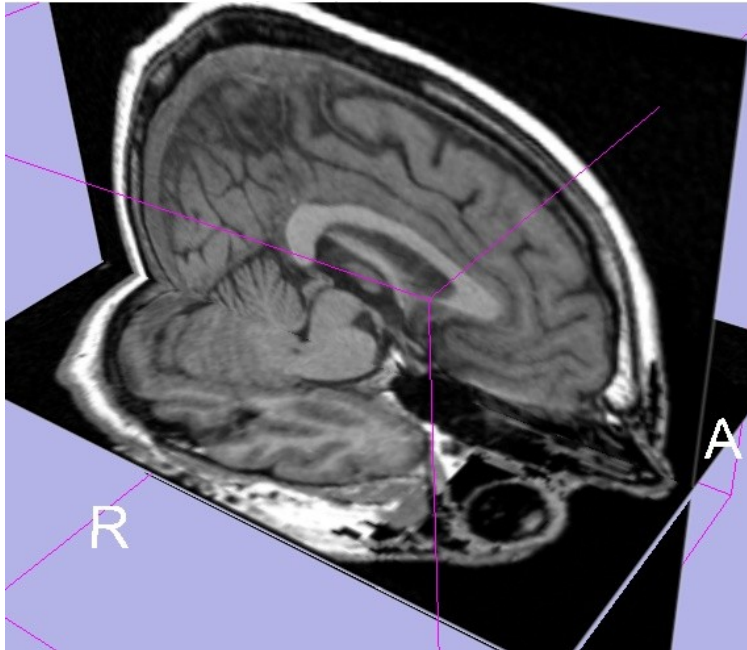




Loading tutorial data



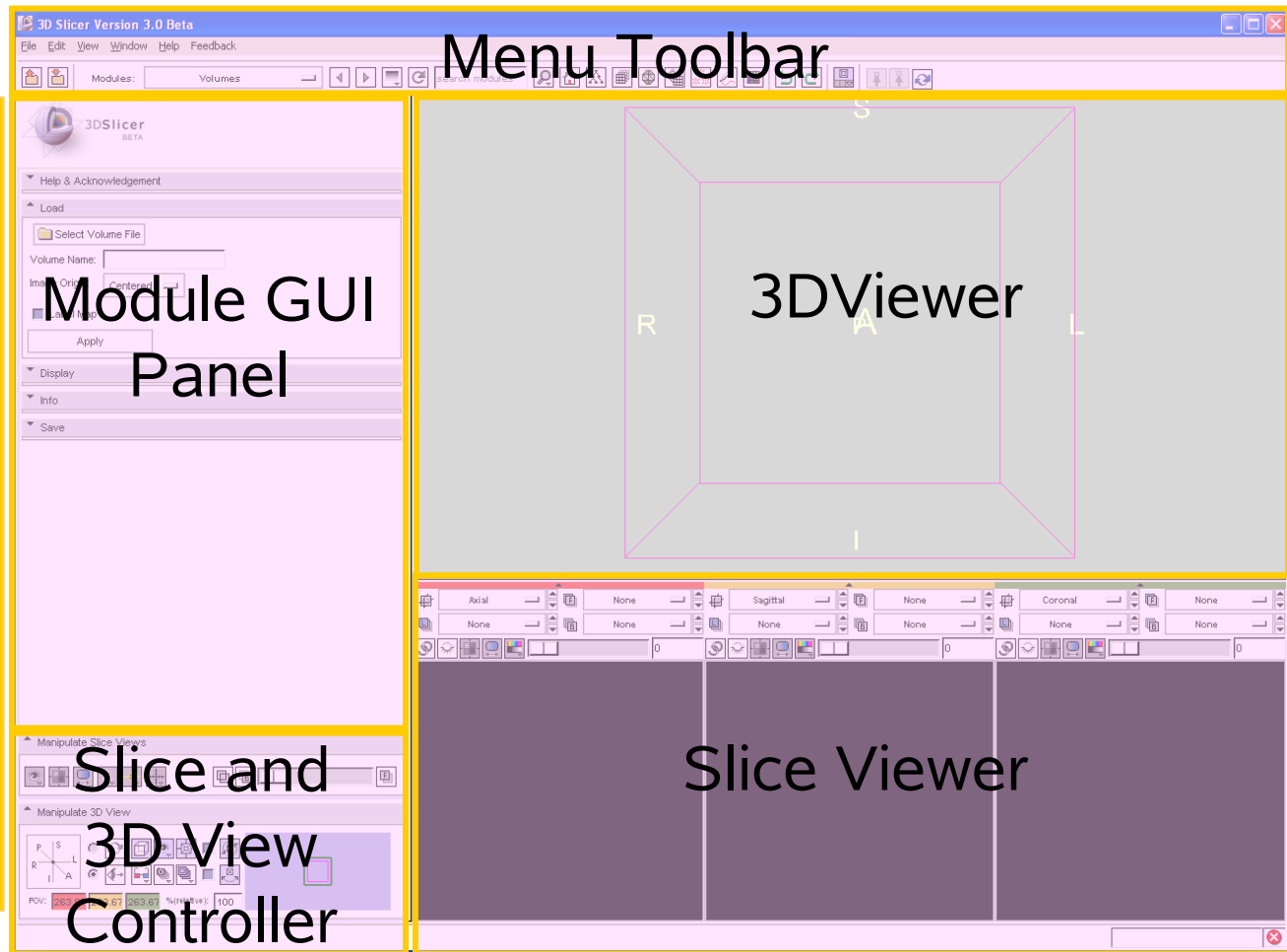
Measuring volume change in tumors



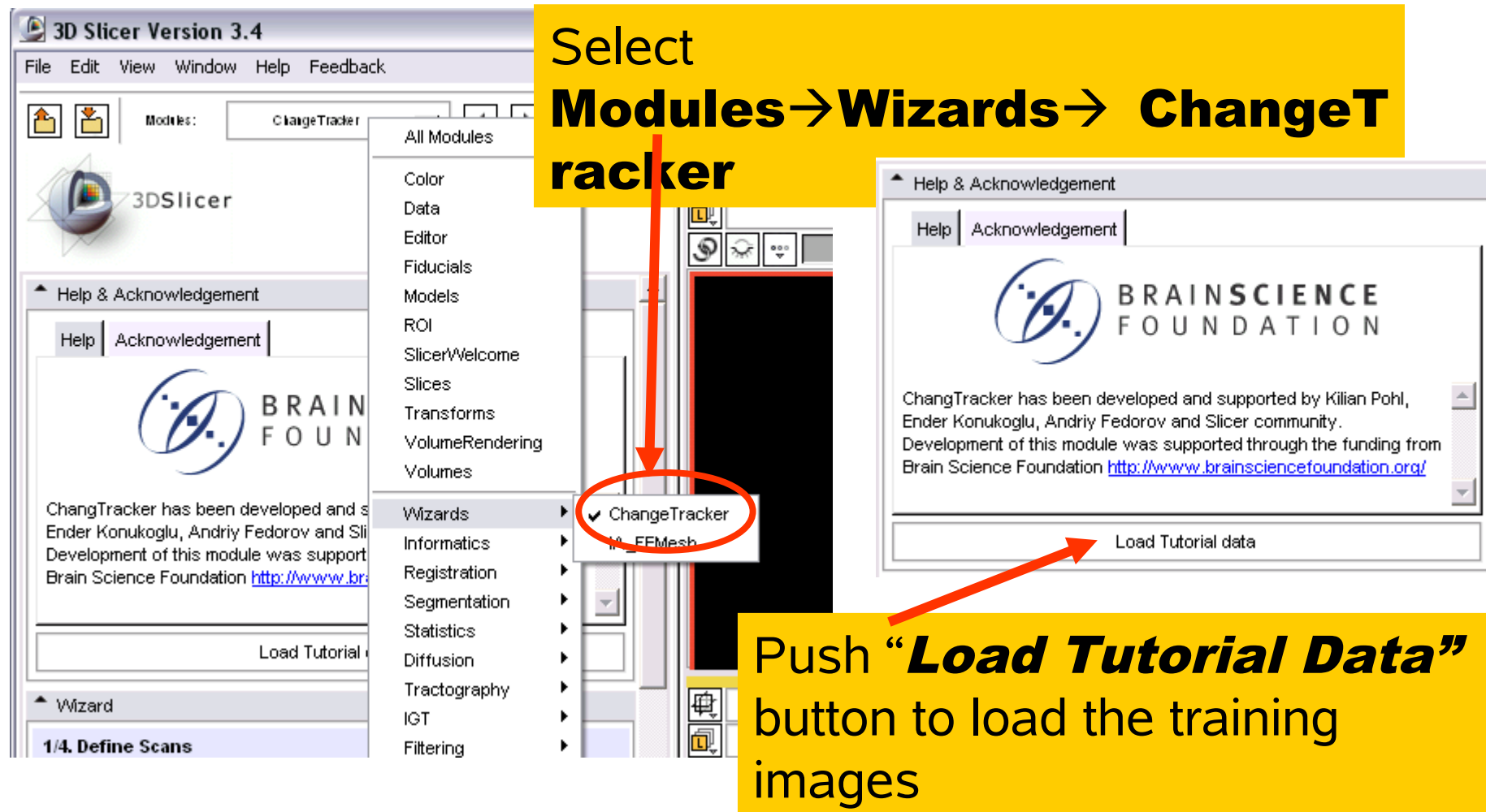
## Part 1: Loading the tutorial data

The Graphical User Interface (GUI) of Slicer3 integrates five components:

- the Menu Toolbar
- the Module GUI Panel
- the 3D Viewer
- the Slice Viewer
- the Slice and 3D View Controller



# Loading training dataset



**Select Modules → Wizards → ChangeTracker**

**Push “Load Tutorial Data” button to load the training images**

3D Slicer Version 3.4

File Edit View Window Help Feedback

Modules: ChangeTracker

3DSlicer

Help & Acknowledgement

Help Acknowledgement

BRAIN SCIENCE FOUNDATION

ChangTracker has been developed and supported by Kilian Pohl, Ender Konukoglu, Andriy Fedorov and Slicer community. Development of this module was supported through the funding from Brain Science Foundation <http://www.brainsciencefoundation.org/>

Load Tutorial data

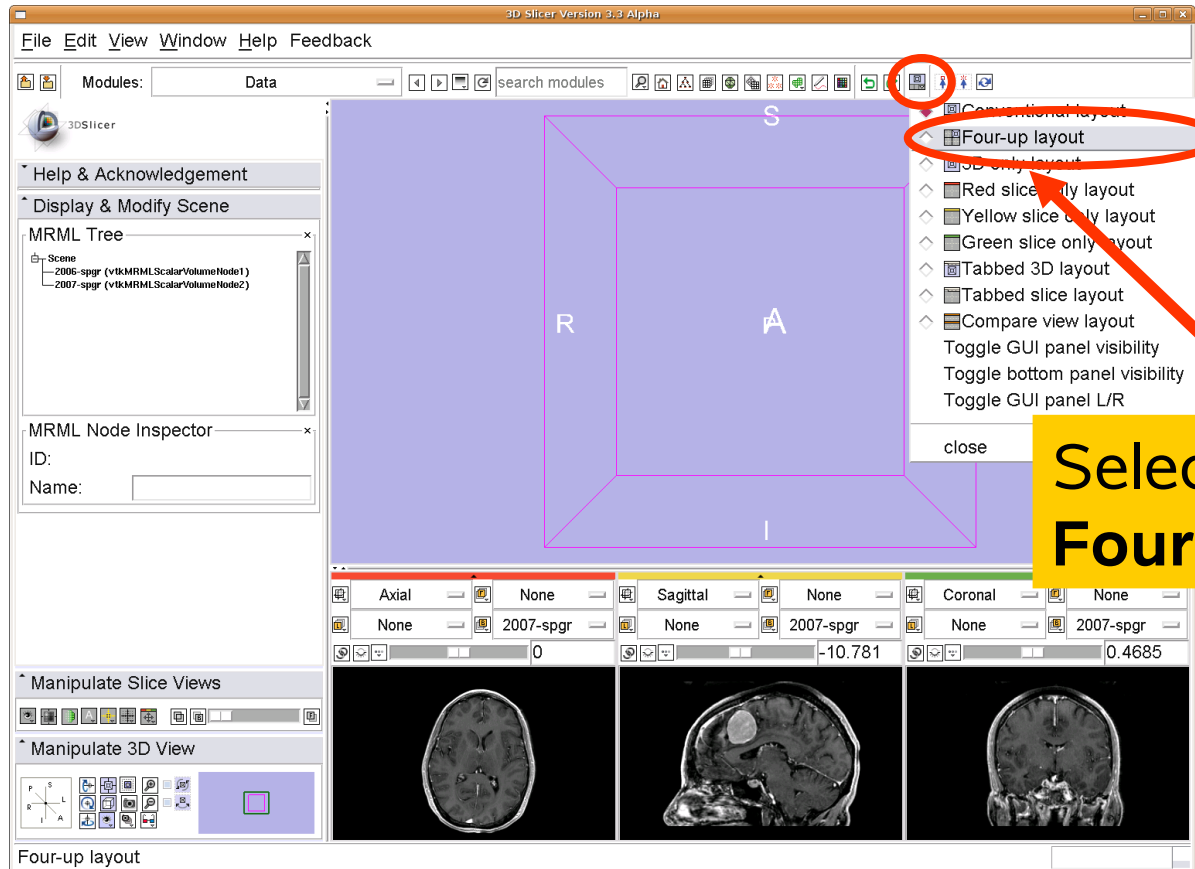
All Modules


- Color
- Data
- Editor
- Fiducials
- Models
- ROI
- SlicerWelcome
- Slices
- Transforms
- VolumeRendering
- Volumes
- Wizards
  - ✓ ChangeTracker
  - FFMesh
- Informatics
- Registration
- Segmentation
- Statistics
- Diffusion
- Tractography
- IGT
- Filtering

1/4. Define Scans

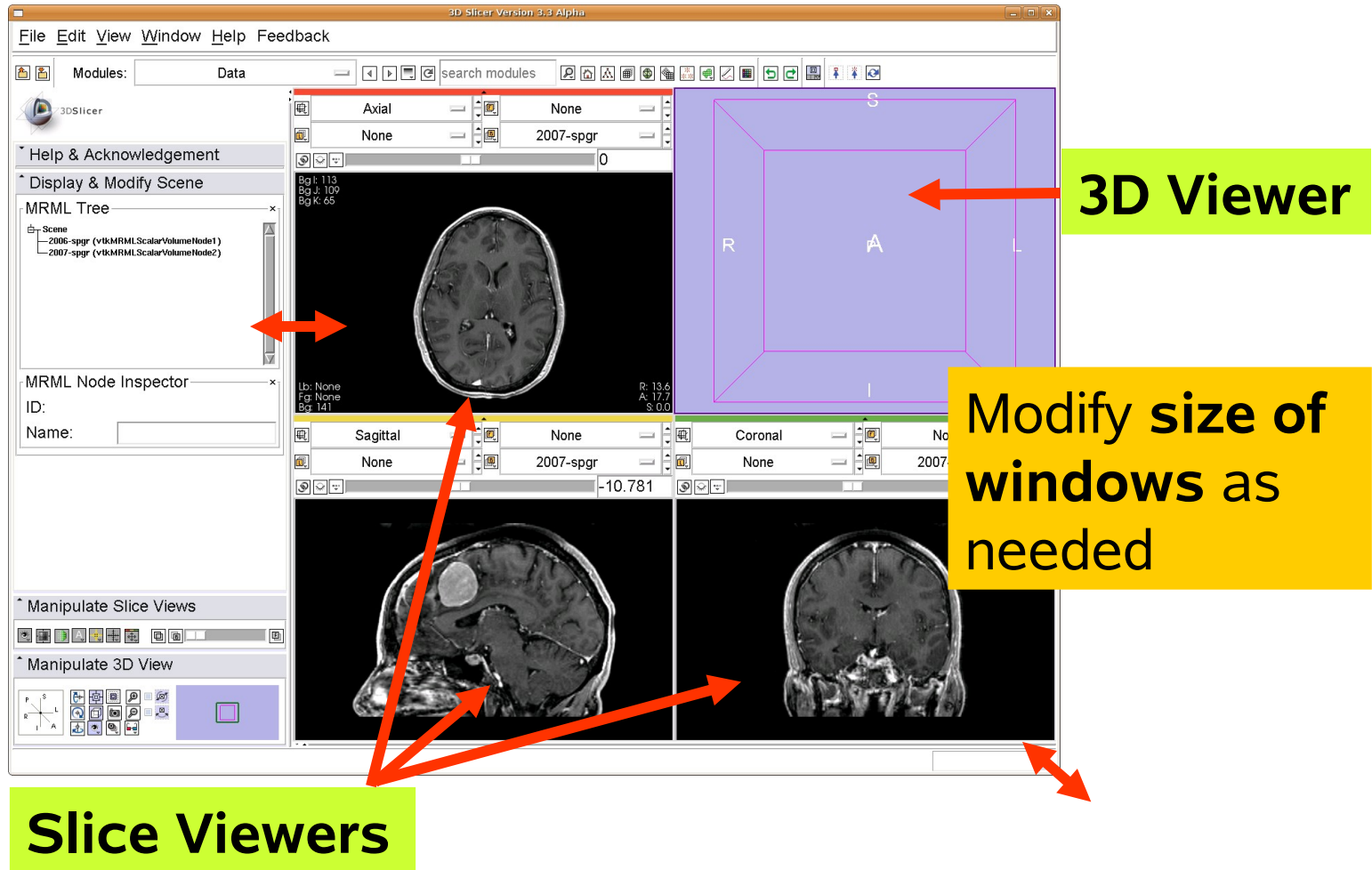


# Modifying Layout of Viewer



Select  and **Four-up layout.**

# New Layout of Viewer



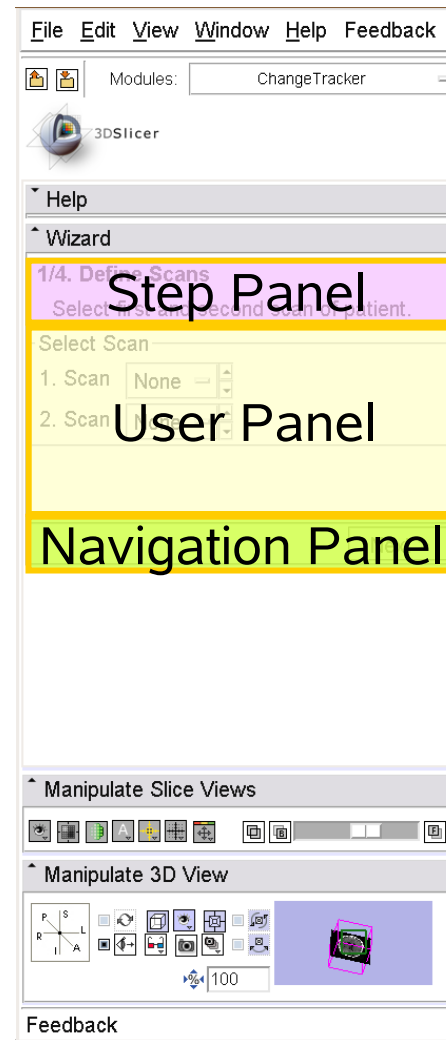


## Part 2: Measuring Volume Change

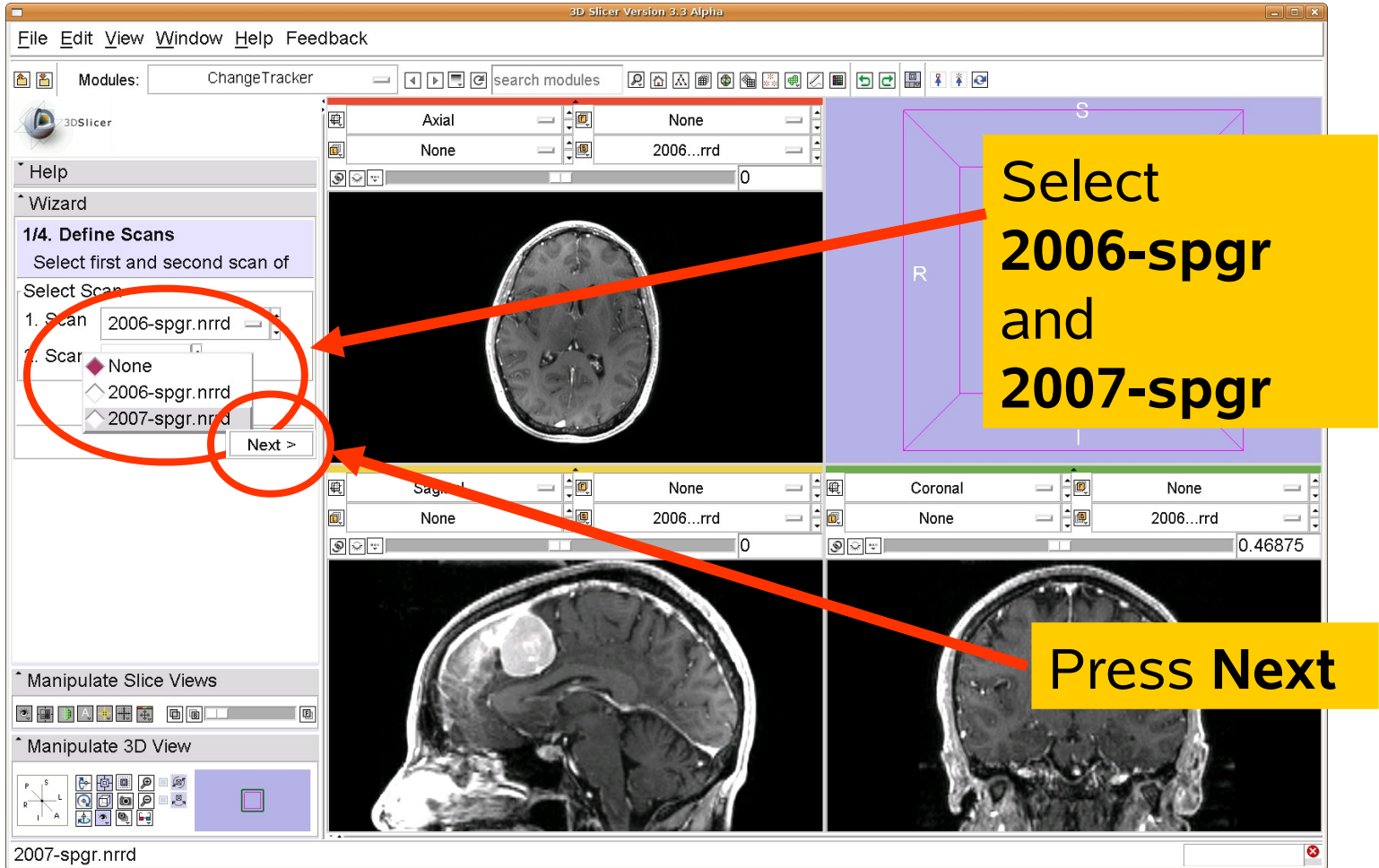
# Workflow Wizard

The Workflow Wizard of Slicer3 guides the user through a sequence of steps and is defined by the following components:

- the Step Panel
- the User Panel
- the Navigation Panel



# Select Scans



3D Slicer Version 3.3 Alpha

File Edit View Window Help Feedback

Modules: ChangeTracker search modules

3DSlicer

Help

Wizard

**1/4. Define Scans**

Select first and second scan of

Select Scan

1. Scan 2006-spgr.nrrd

2. Scan

None

2006-spgr.nrrd

2007-spgr.nrrd

Next >

Manipulate Slice Views

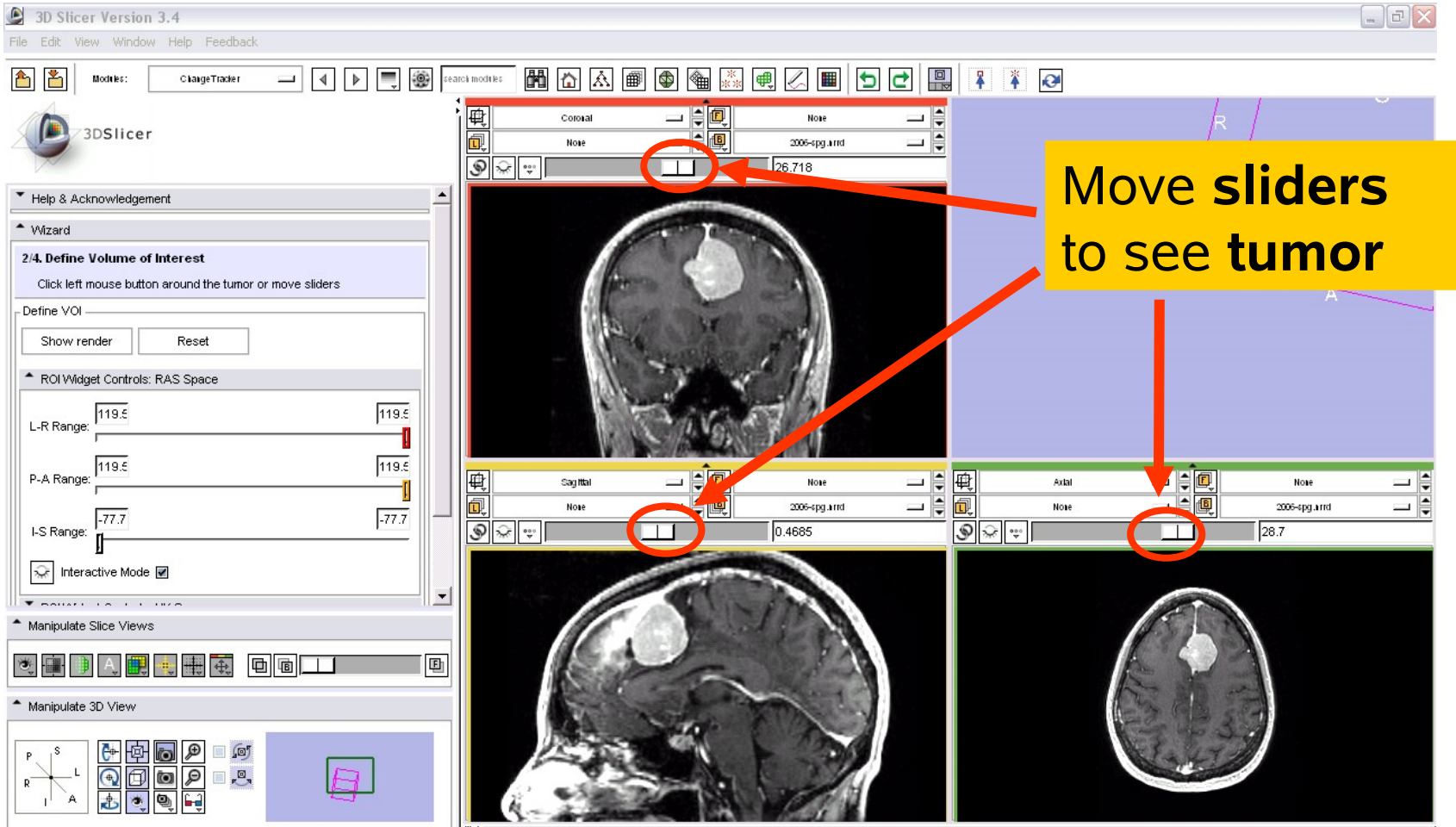
Manipulate 3D View

2007-spgr.nrrd

Select 2006-spgr and 2007-spgr

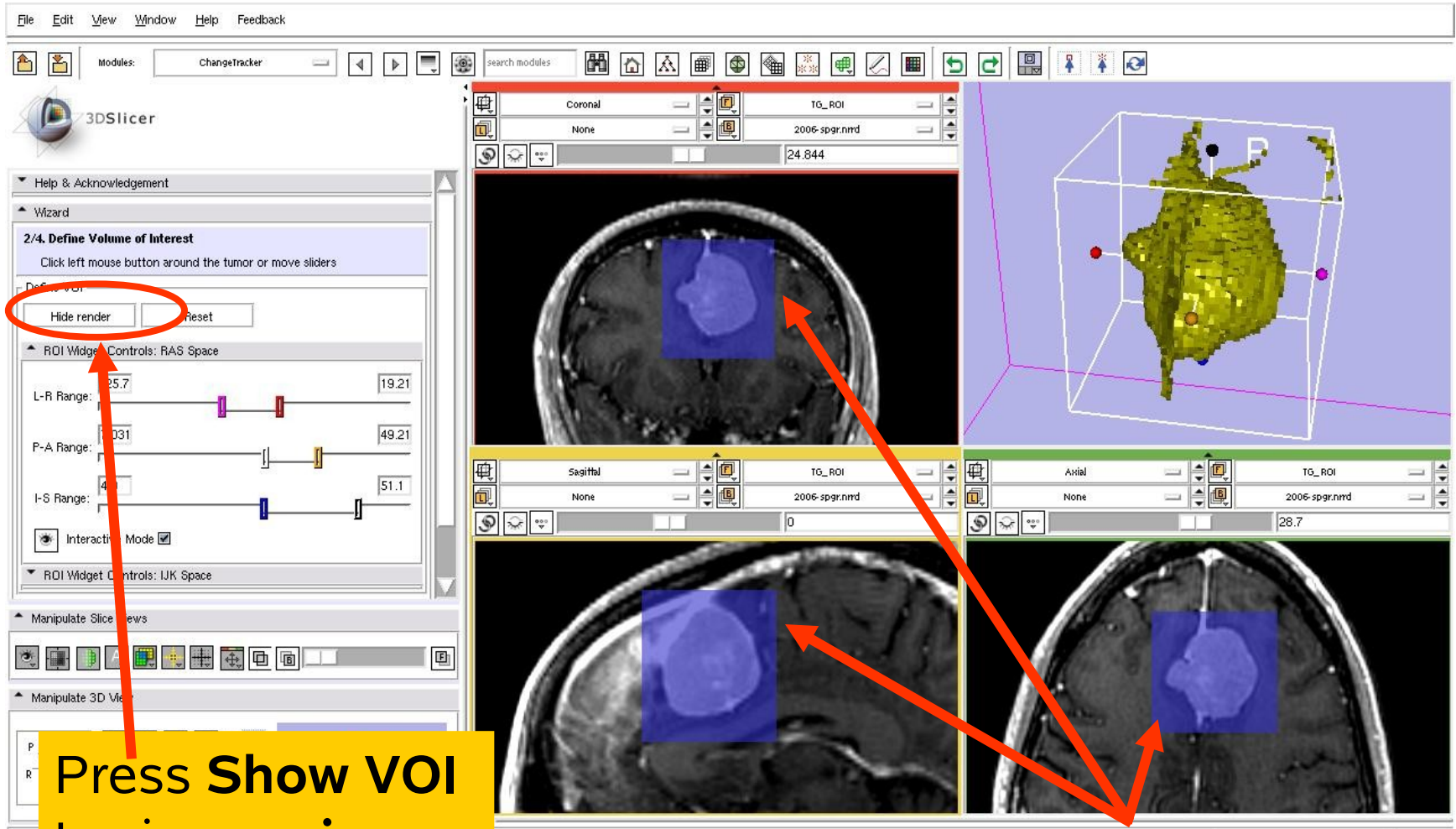
Press Next

# Identify Volume of Interest





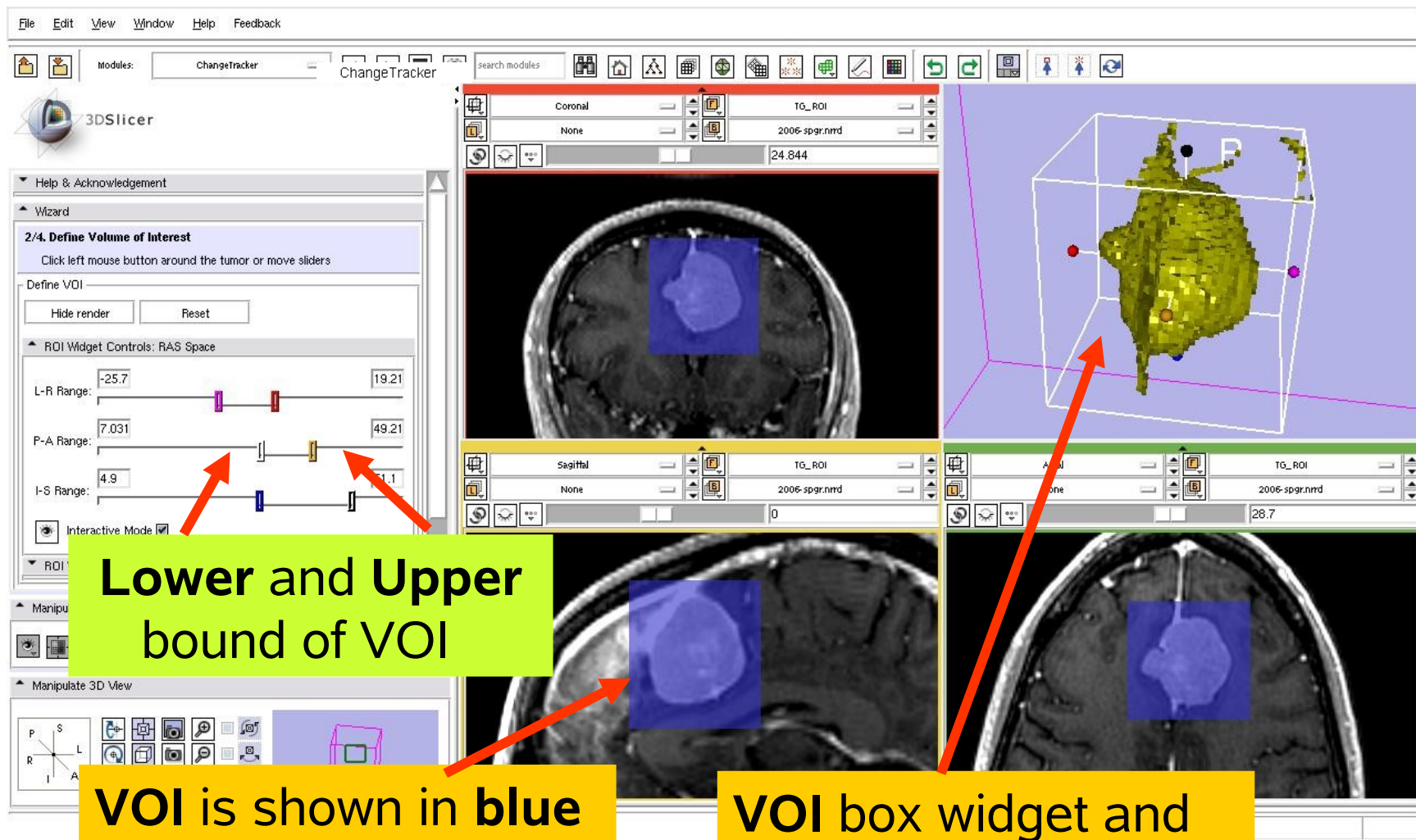
# Identify Volume of Interest



**Press Show VOI  
to view region**

**Identify VOI by clicking left  
mouse button around tumor**

# Identify Volume of Interest

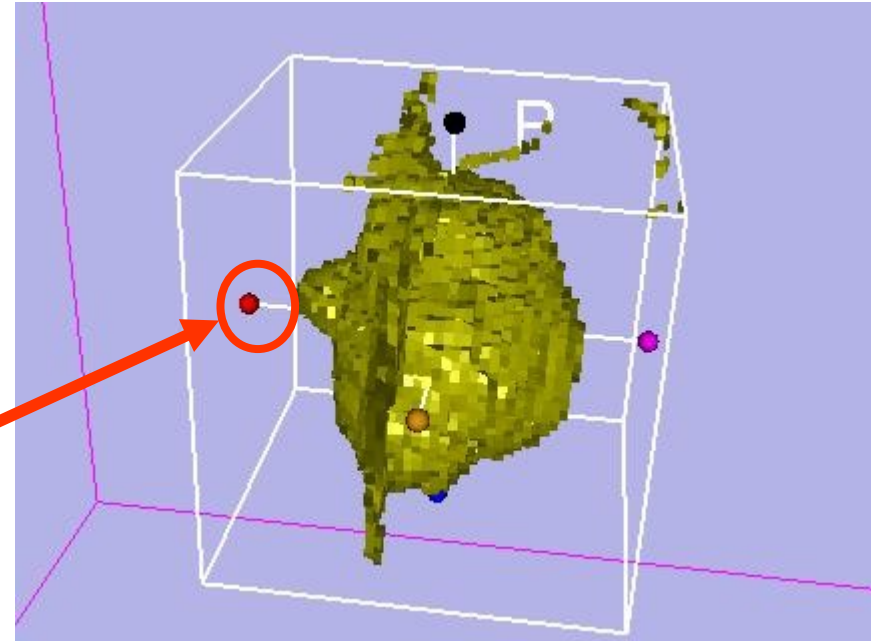
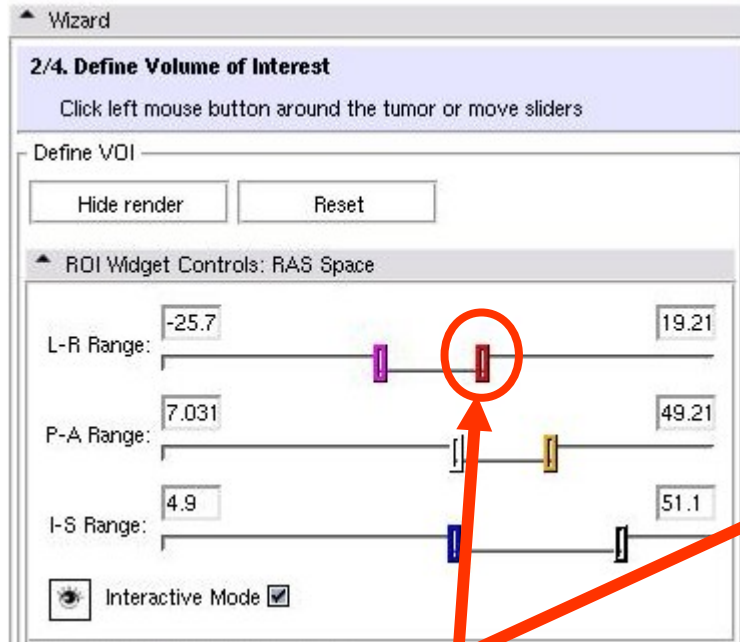


Pohl K, Konukoglu E, Fedorov A  
National Alliance for Medical Image Computing



# Identify Volume of Interest

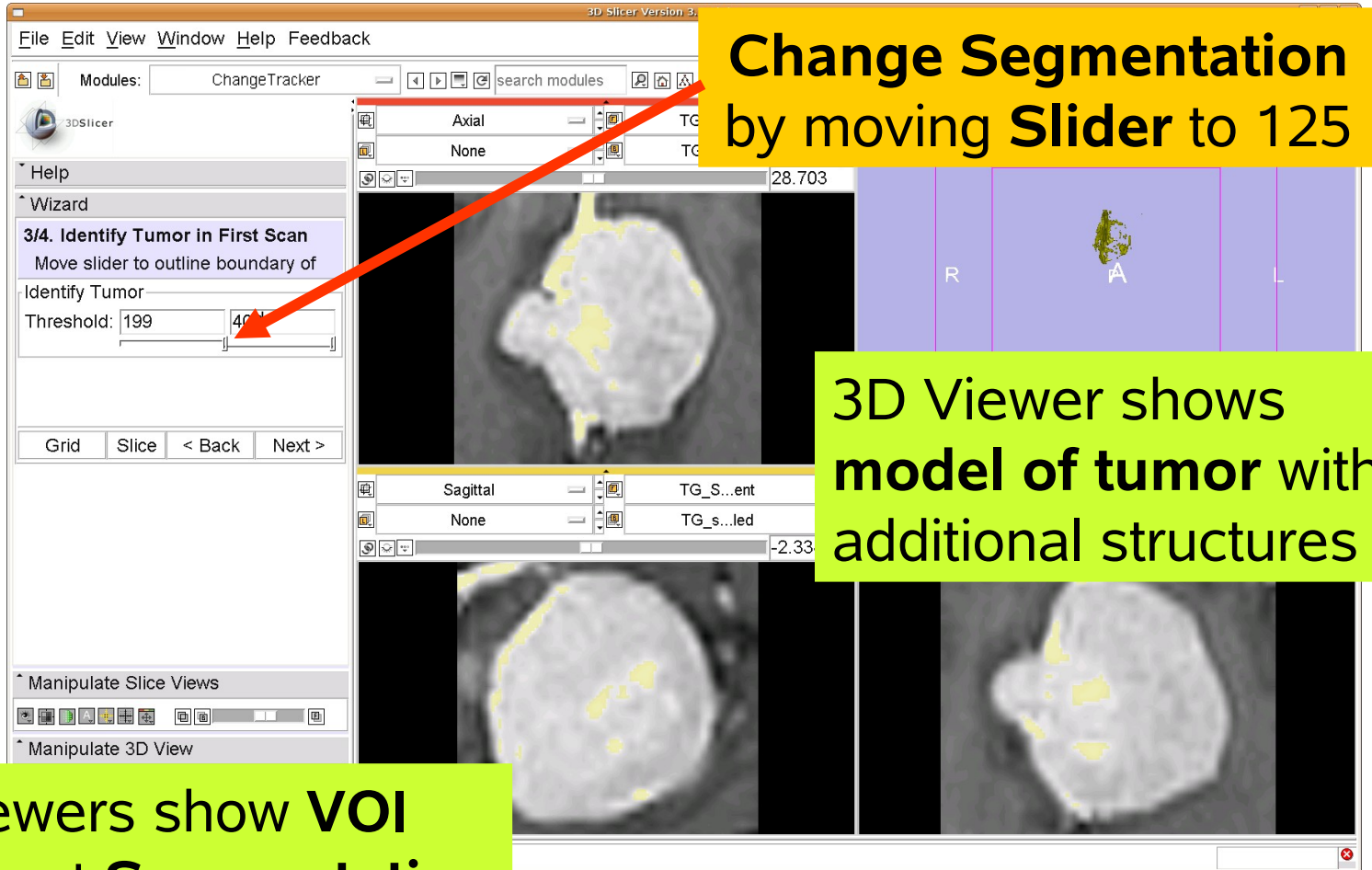
Adjust ROI by moving the ROI Widget Control sliders in the Step panel, or by moving the ROI Widget handles in 3D view



ROI Widget Control sliders are color-coded to match ROI Widget handles in 3D Viewer

Press Next

# Segment Tumor



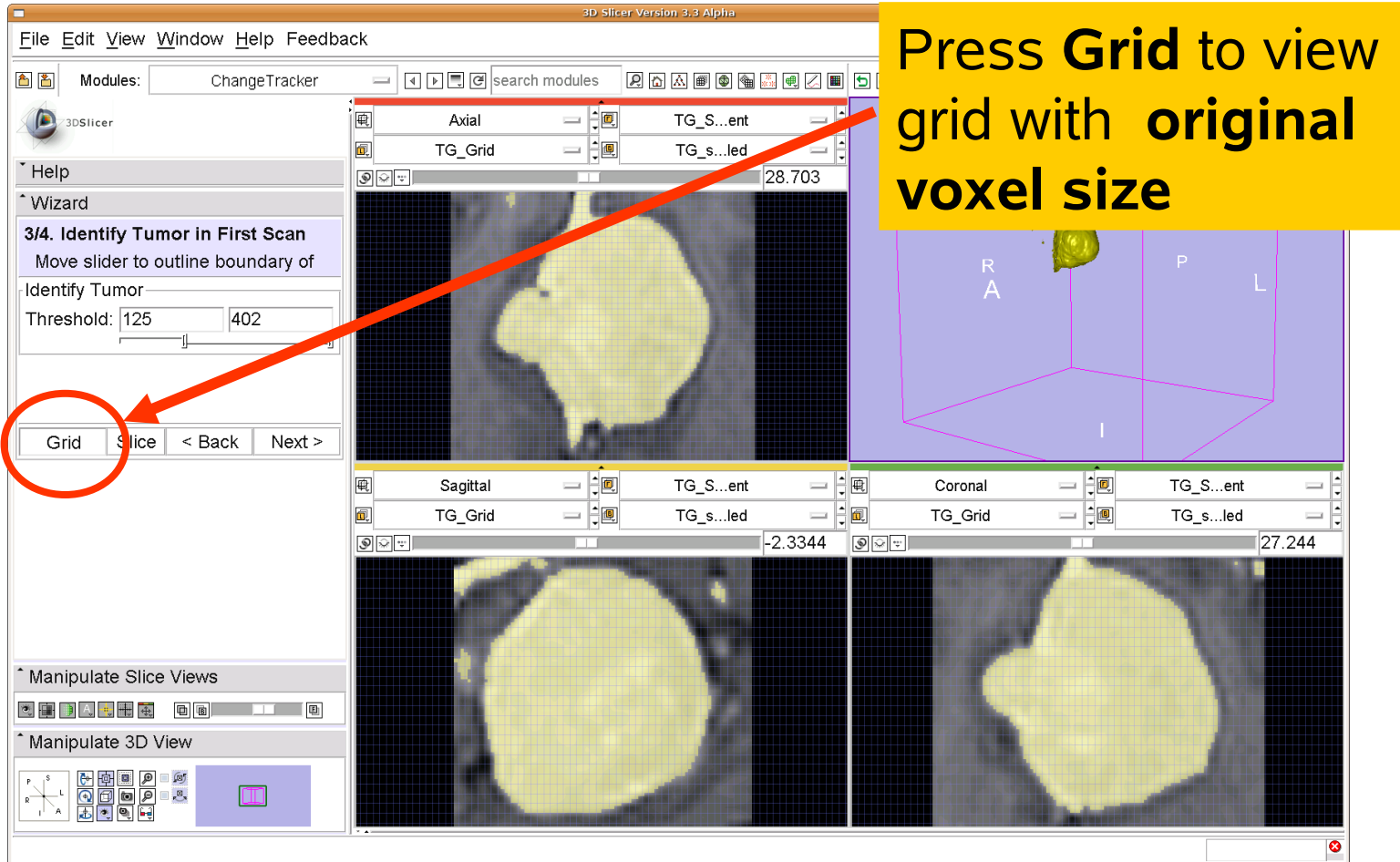
The screenshot shows the 3D Slicer Version 3.0 interface. On the left, the 'Wizard' panel is active, showing step '3/4. Identify Tumor in First Scan' with the instruction 'Move slider to outline boundary of Identify Tumor'. The 'Threshold' slider is set to 199, and a red arrow points to the slider handle. The main 3D viewer displays a brain scan with a yellow segmented tumor. The 'Modules' panel shows 'ChangeTracker' selected. The 'Sagittal' view is selected, and the 'None' view is also selected. The '3D Viewer' shows a model of the tumor with additional structures. The 'Slice Viewers' show the current segmentation.

**Change Segmentation by moving Slider to 125**

**3D Viewer shows model of tumor with additional structures**

**Slice Viewers show VOI with current Segmentation**

# Segment Tumor



3D Slicer Version 3.3 Alpha

File Edit View Window Help Feedback

Modules: ChangeTracker search modules

3DSlicer

Help

Wizard

**3/4. Identify Tumor in First Scan**  
Move slider to outline boundary of

Identify Tumor  
Threshold: 125 402

Grid Slice < Back Next >

Manipulate Slice Views

Manipulate 3D View

Press **Grid** to view grid with **original voxel size**

Axial TG\_S...ent TG\_s...led 28.703

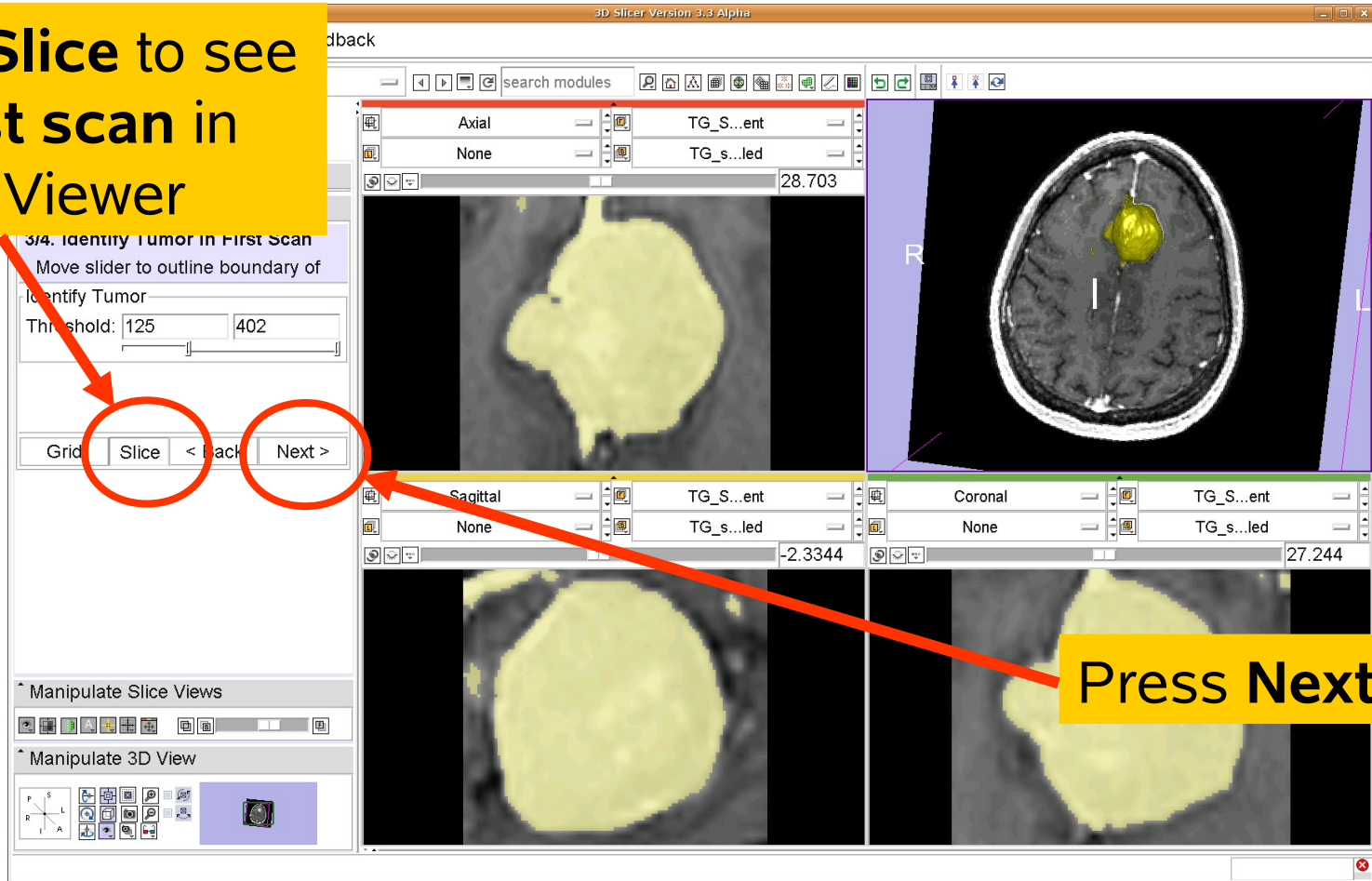
Sagittal TG\_S...ent TG\_s...led -2.3344

Coronal TG\_S...ent TG\_s...led 27.244

TG\_Grid TG\_Grid

# Segment Tumor

Press **Slice** to see the **first scan** in the 3D Viewer

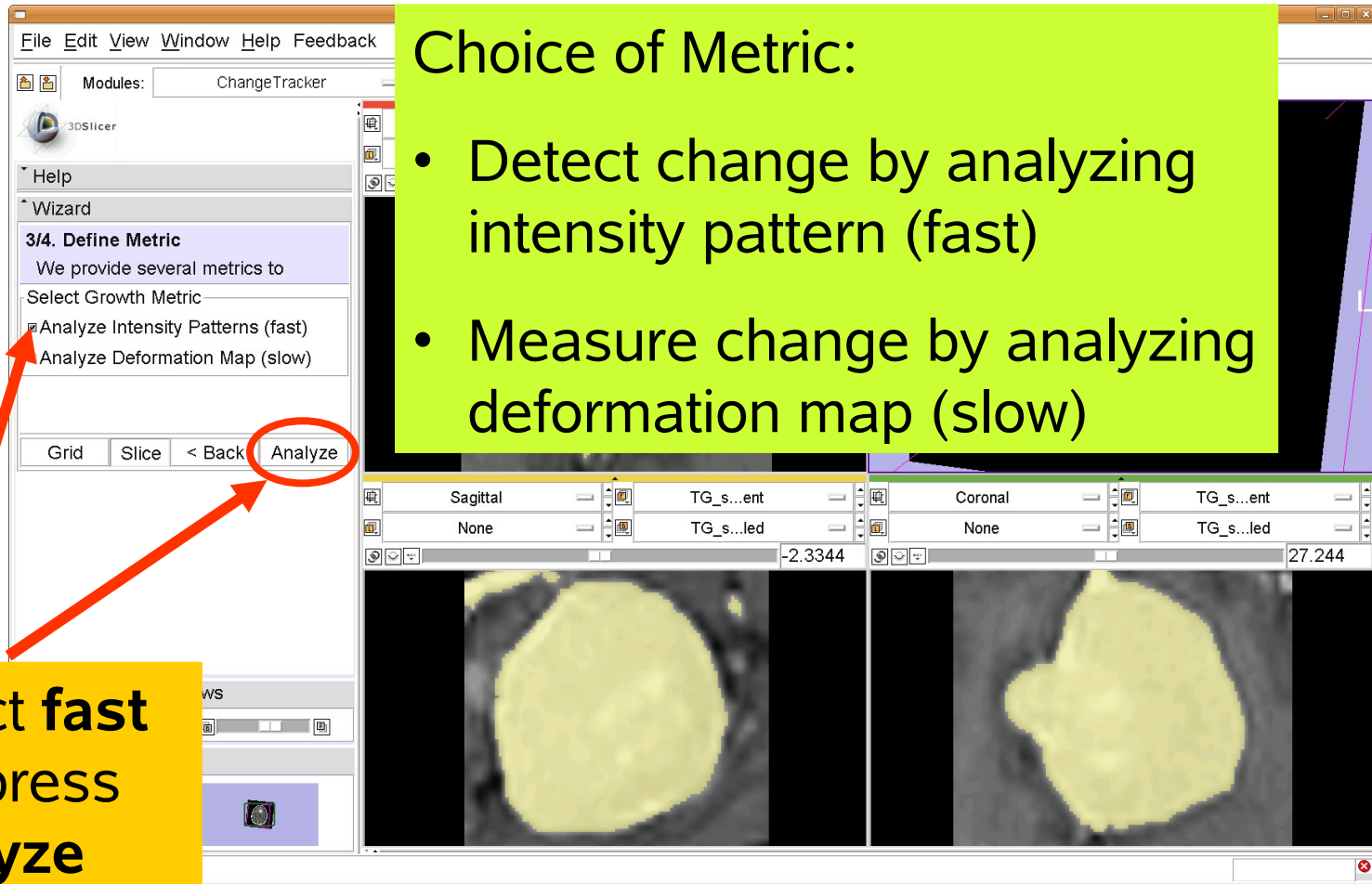


# Choose Metric Type

## Choice of Metric:

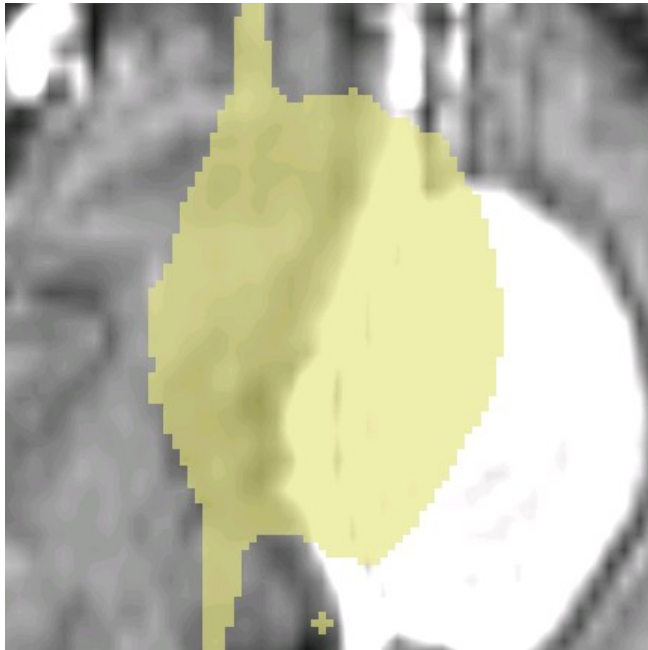
- Detect change by analyzing intensity pattern (fast)
- Measure change by analyzing deformation map (slow)

Select **fast**  
and press  
**Analyze**

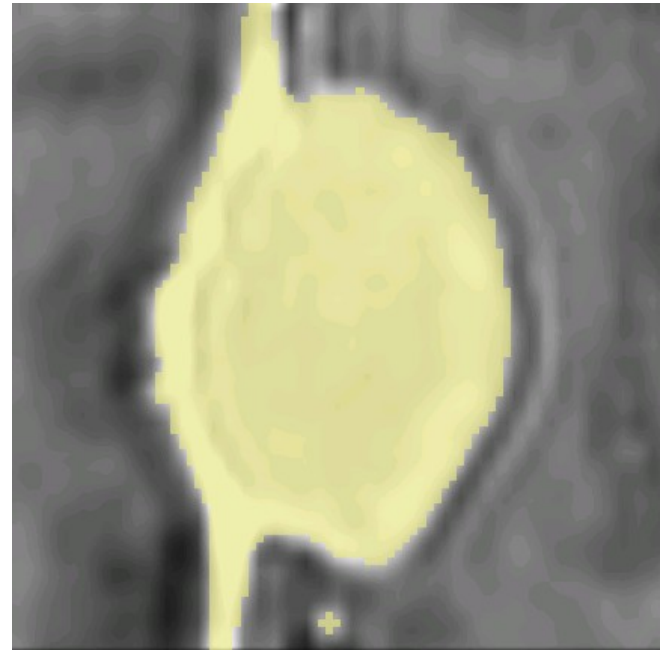


# *Analysis I: Volume Preserving Registration*

---



Before

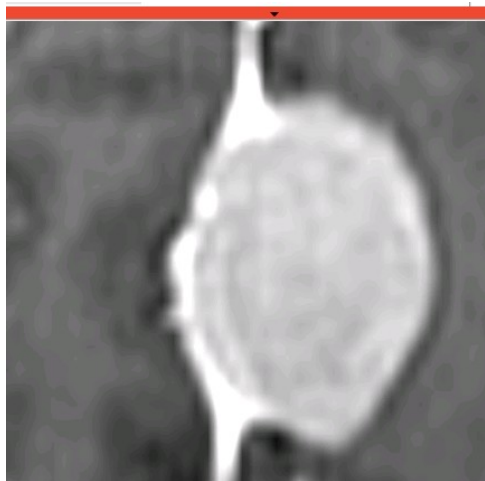


Afterwards

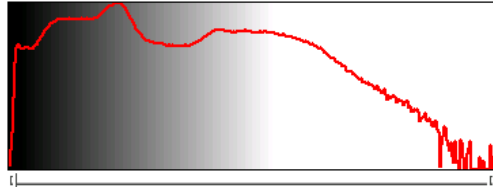


# Analysis II: Normalize Intensities

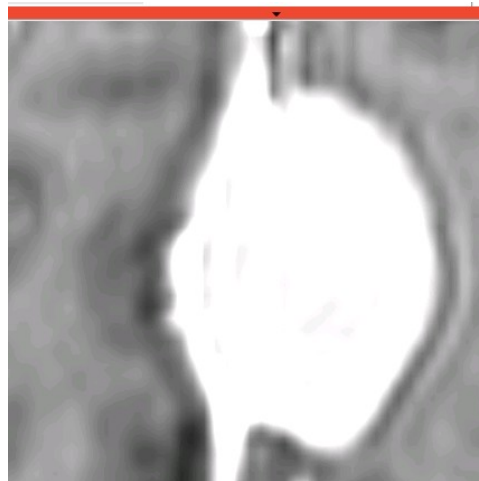
Scan 1



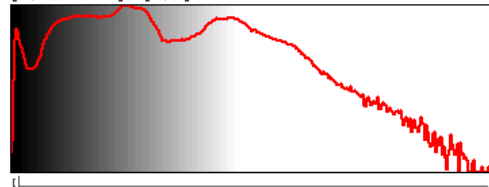
[2, 440.999] x [0, 1]



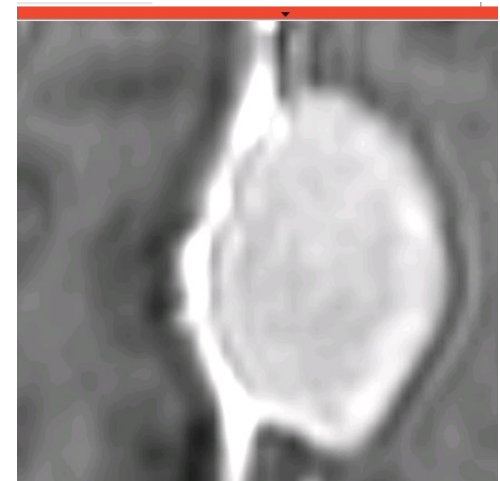
Scan 2



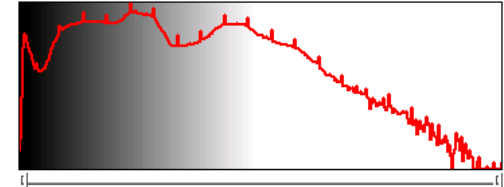
[6, 508.999] x [0, 1]



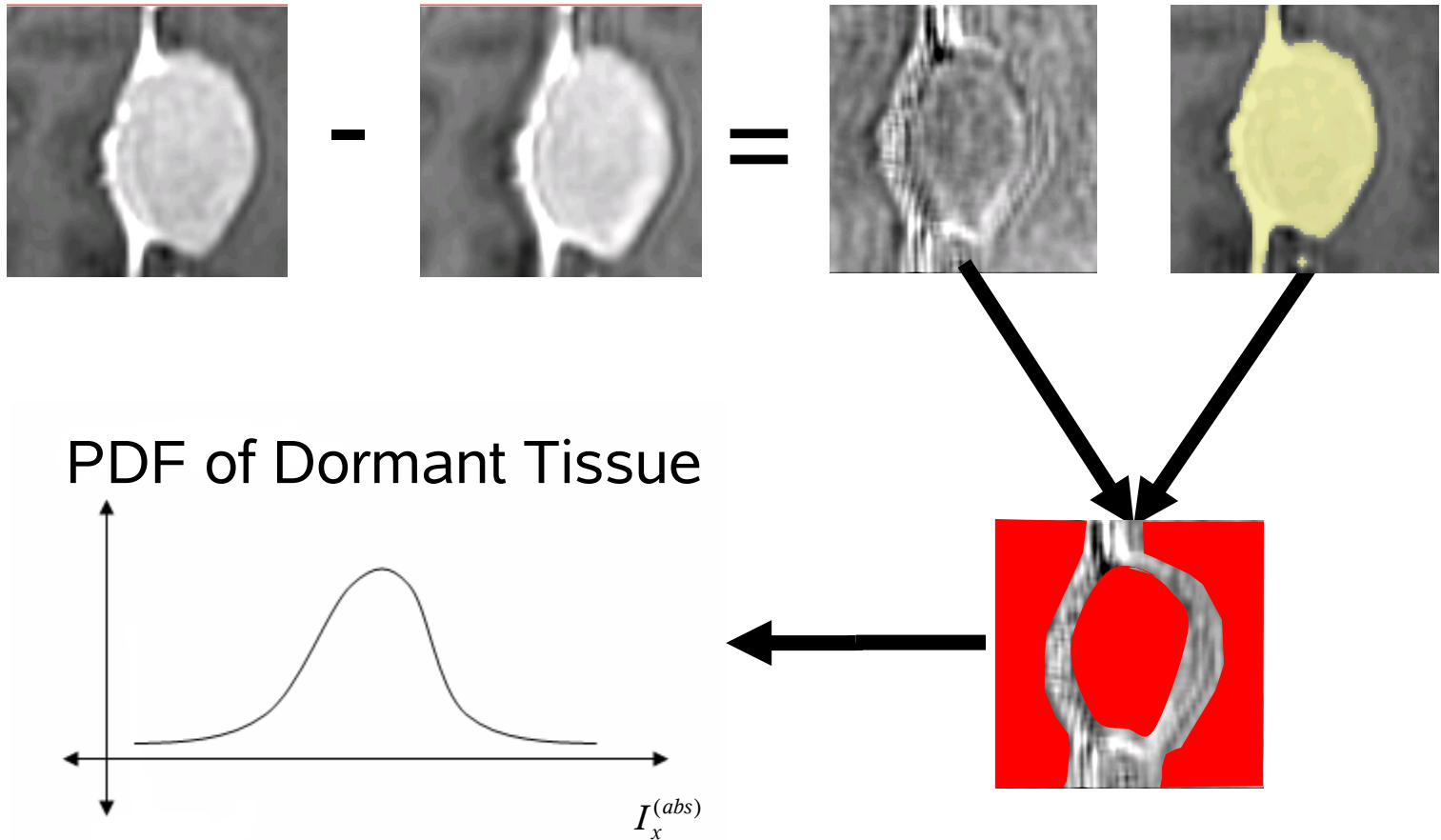
Scan 2 - Norm



[5, 487.999] x [0, 1]



# Analysis III: Detect Change – Intensity Based

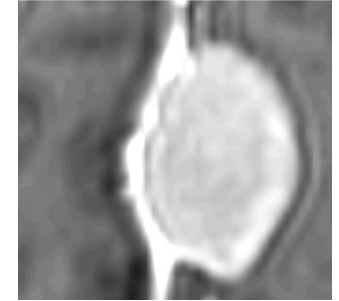
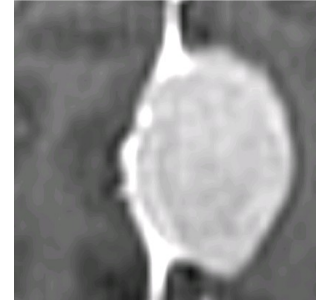
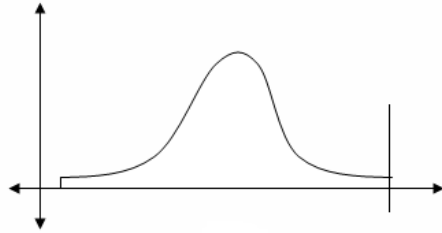


Compute statistics of static tissue:	Subtract Scan2 from Scan1	Define region of static tissue	Determine probability density function
--------------------------------------	---------------------------	--------------------------------	--

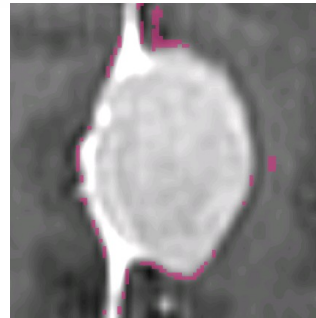


## Analysis III: Detect Change – Intensity Based

Data



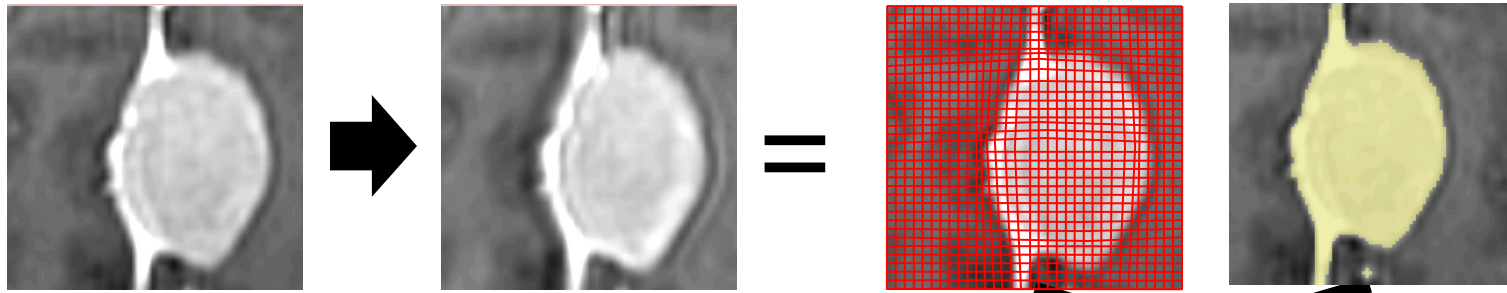
Analysis



Mode :	Sensitive
False Positive Risk:	High
Growth (mm <sup>3</sup> ) :	1301
Growth (voxel):	1057

Konukoglu et al. ,“Monitoring Slowly Evolving Tumors”, ISBI, 2008

# Analysis III: Detect Change–Deformation Map

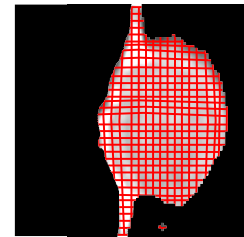


Mode : Segmentation  
Growth (mm<sup>3</sup>) : 1386

Growth (voxels): 1126

Determine change  
via mapping:

Compute diffeomorphic  
mapping between scans



Mode : Jaccobian  
Growth (mm<sup>3</sup>) : 1291

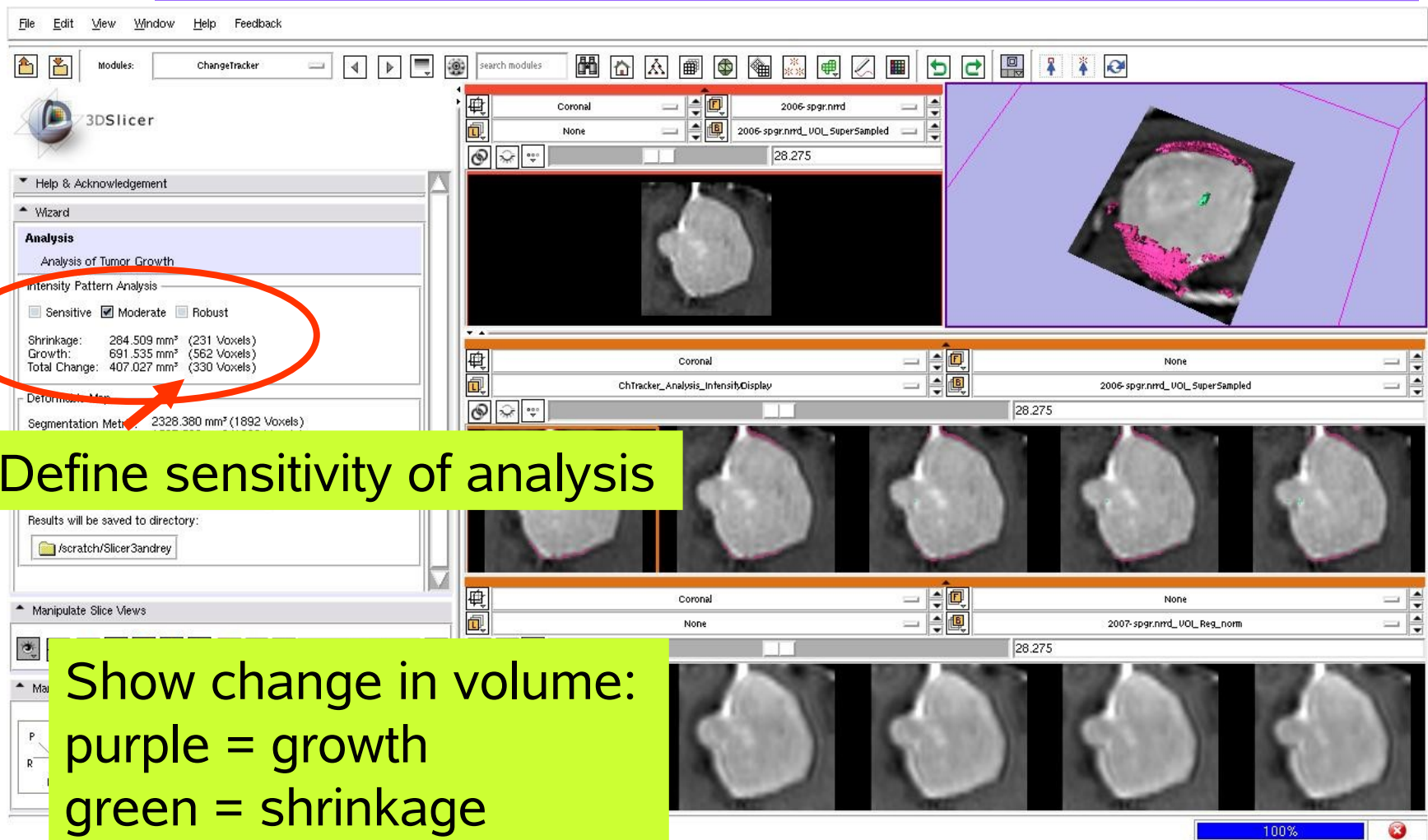
Growth (voxels): 1049

Compute  
Jacobian

or

Apply mapping  
to segmentation

# Show Change in Pathology



The screenshot displays the 3DSlicer interface with the 'ChangeTracker' module active. The 'Analysis' panel on the left shows the 'Analysis of Tumor Growth' section, where 'Intensity Pattern Analysis' is selected. Under this, the 'Moderate' sensitivity option is checked and circled in red. The analysis results are as follows:

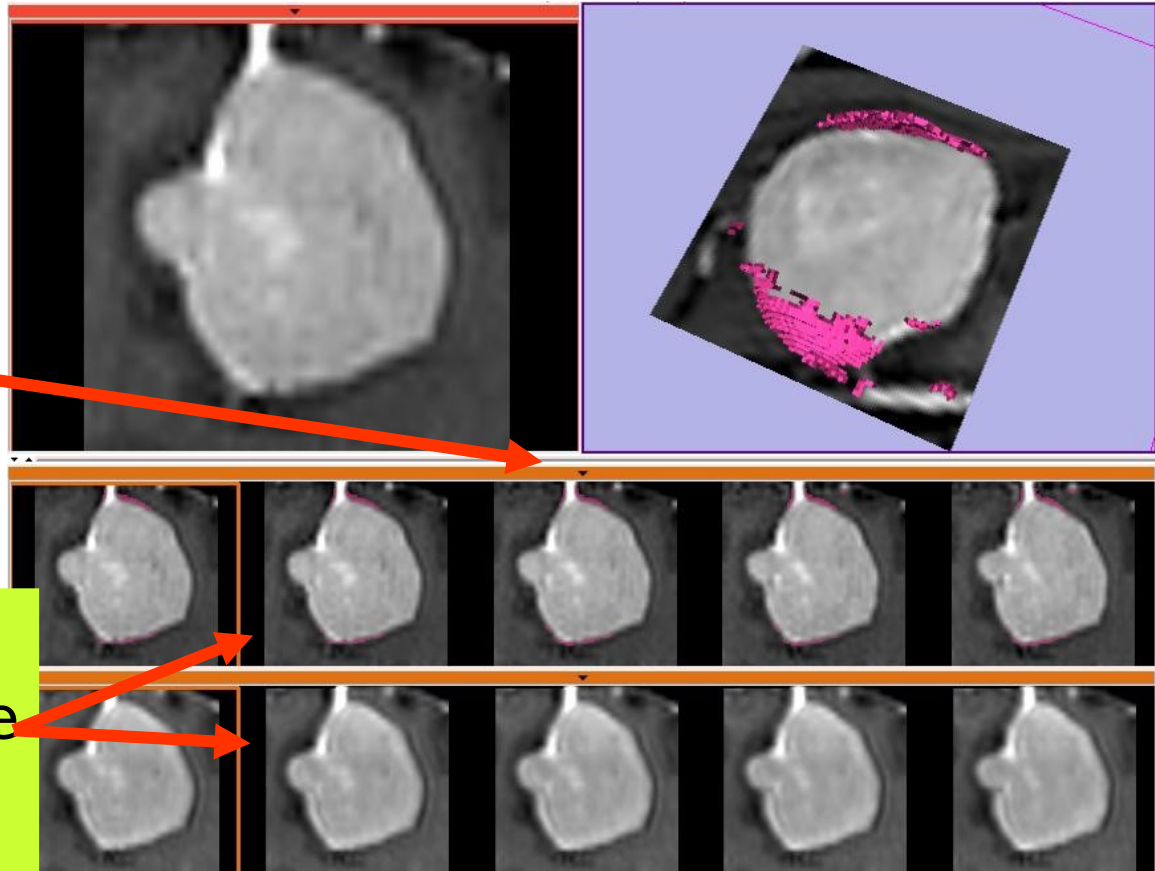
Metric	Value	Voxels
Shrinkage	284.509 mm <sup>3</sup>	(231 Voxels)
Growth	691.535 mm <sup>3</sup>	(562 Voxels)
Total Change	407.027 mm <sup>3</sup>	(330 Voxels)

Below the analysis results, the 'Segmentation Metrics' section shows a total volume of 2328.380 mm<sup>3</sup> (1892 Voxels). A red arrow points from the 'Moderate' checkbox to a yellow callout box that reads: 'Define sensitivity of analysis'.


The main view area shows three panels. The top panel displays a 3D visualization of the tumor volume with growth highlighted in purple and shrinkage in green. The middle panel shows a series of four coronal slices with the tumor volume overlaid. The bottom panel shows another series of four coronal slices, likely representing a different time point or analysis. A yellow callout box at the bottom left of the main view area reads: 'Show change in volume: purple = growth green = shrinkage'.

# Show Change in Pathology

You can hide slice controls to have more screen space for viewing the images

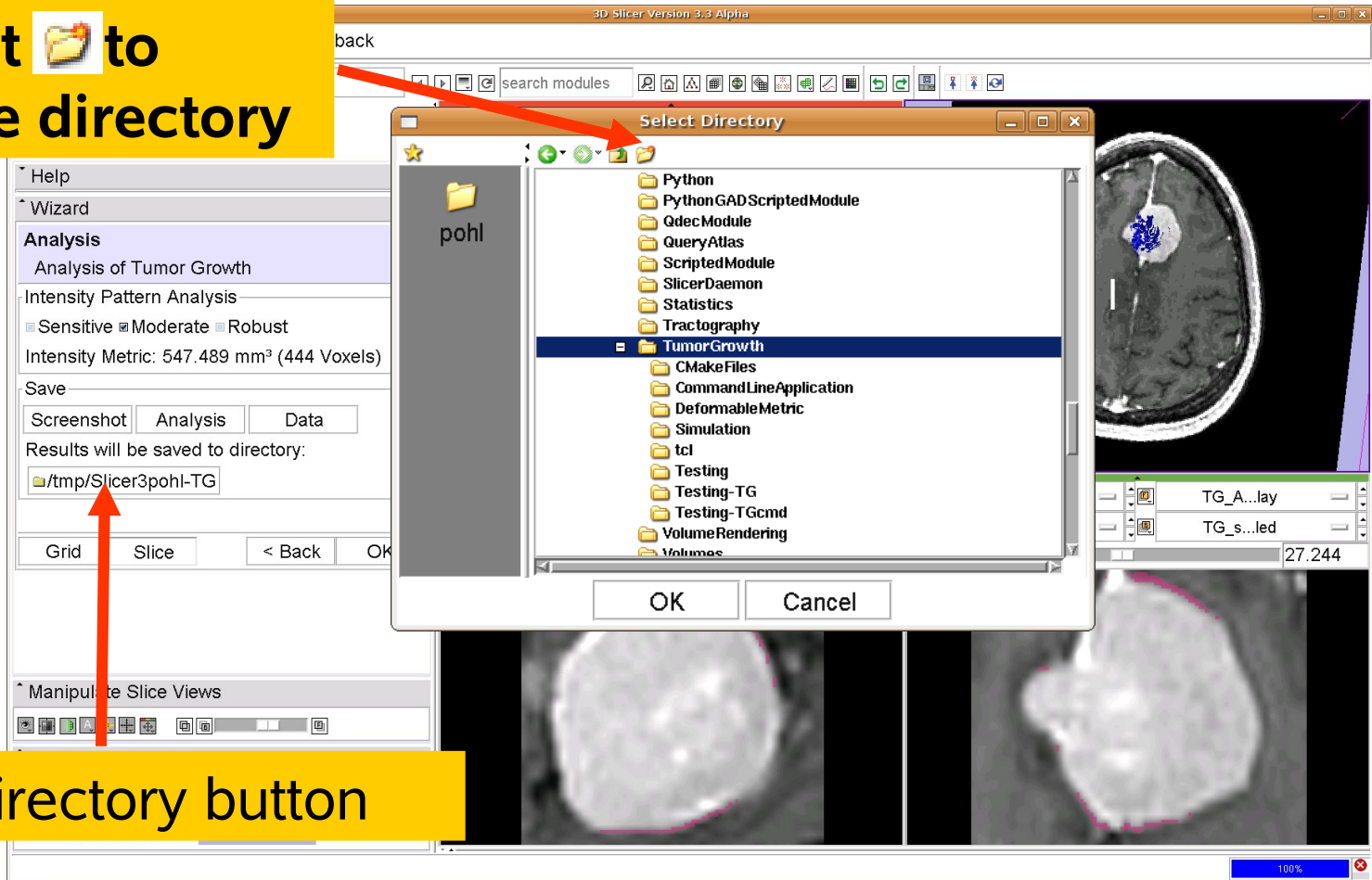


Lightbox View shows 5 consecutive slices for the ROI in the first scan (top), and in the second scan (bottom)

You can switch to  **Four-up** layout or other layout at any time.

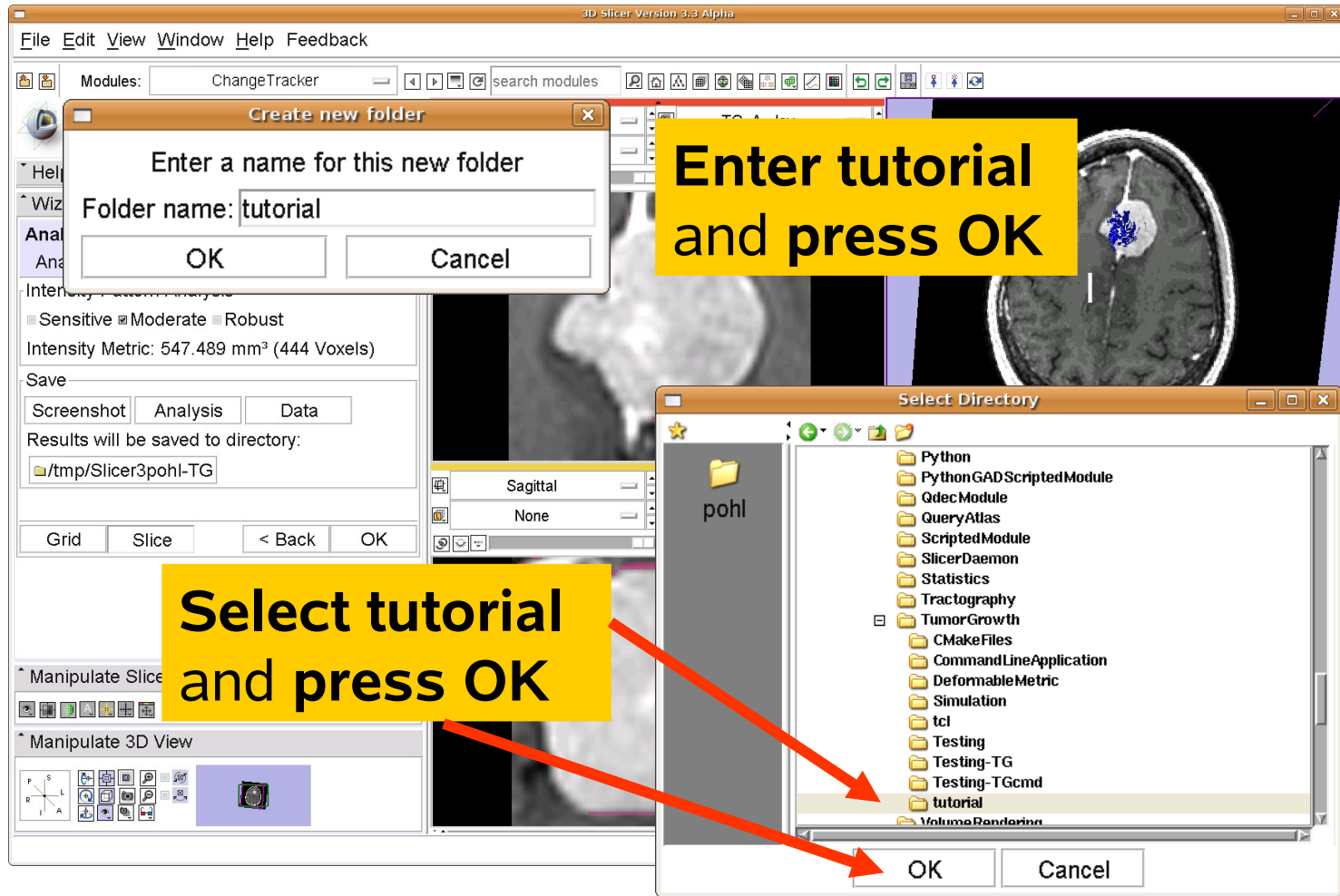
# Define Working Directory

Select  to create directory



Press directory button

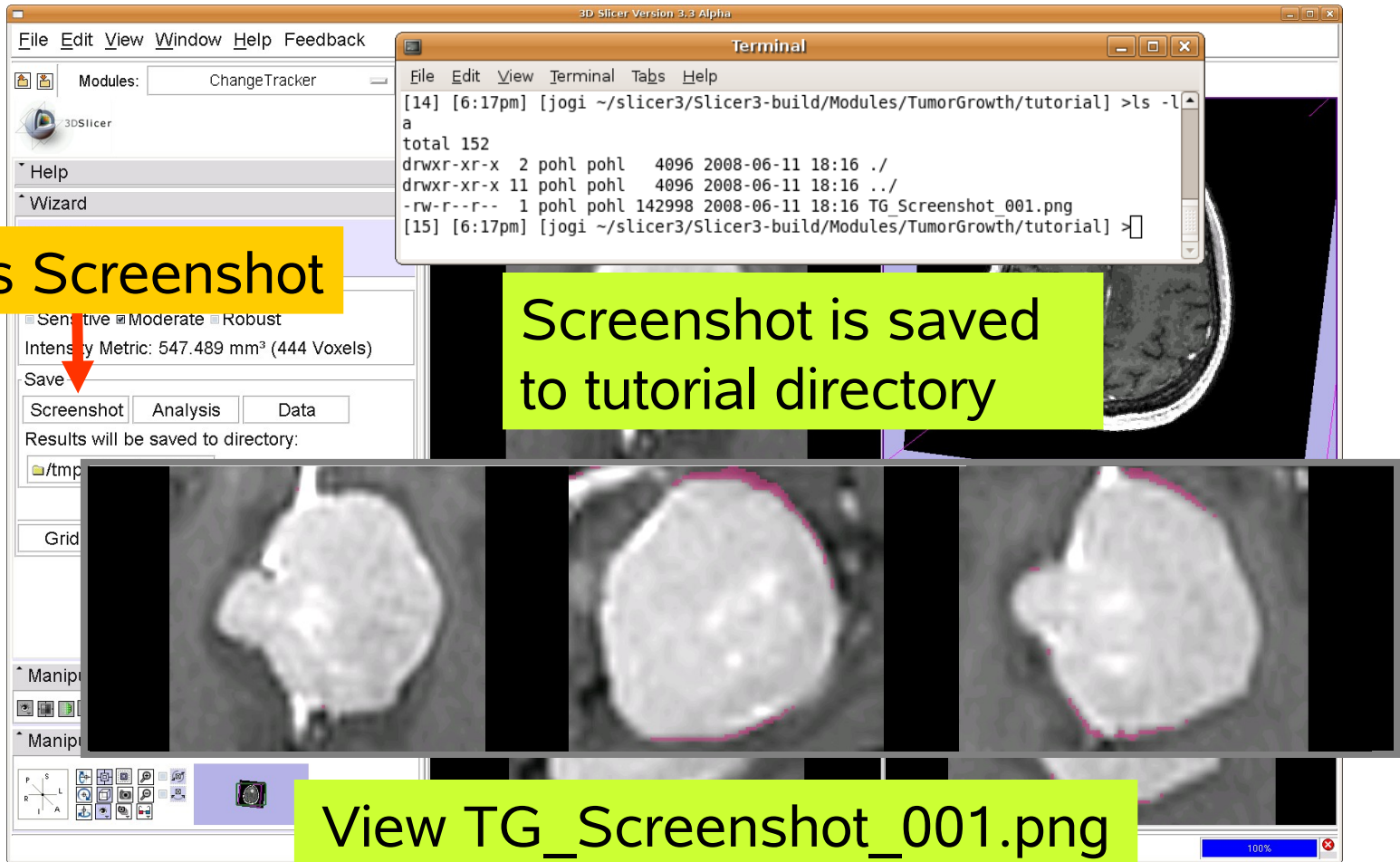
# Define Working Directory





# Save Screenshot

Press Screenshot



The image shows the 3D Slicer interface with a terminal window open. The terminal displays the command `ls -la` and its output, showing a file named `TG_Screenshot_001.png` in the current directory. A yellow box highlights the 'Screenshot' button in the 'Save' section of the 'ChangeTracker' module. A red arrow points from the 'Press Screenshot' text to this button. Another yellow box highlights the terminal output, indicating the screenshot is saved to the tutorial directory. A third yellow box at the bottom highlights the filename `TG_Screenshot_001.png`.

3D Slicer Version 3.3 Alpha

File Edit View Window Help Feedback

Modules: ChangeTracker

Help Wizard

Sensitive Moderate Robust

Intensity Metric: 547.489 mm<sup>3</sup> (444 Voxels)

Save

Screenshot Analysis Data

Results will be saved to directory:

/tmp

Grid

Manip

Manip

100%

Terminal

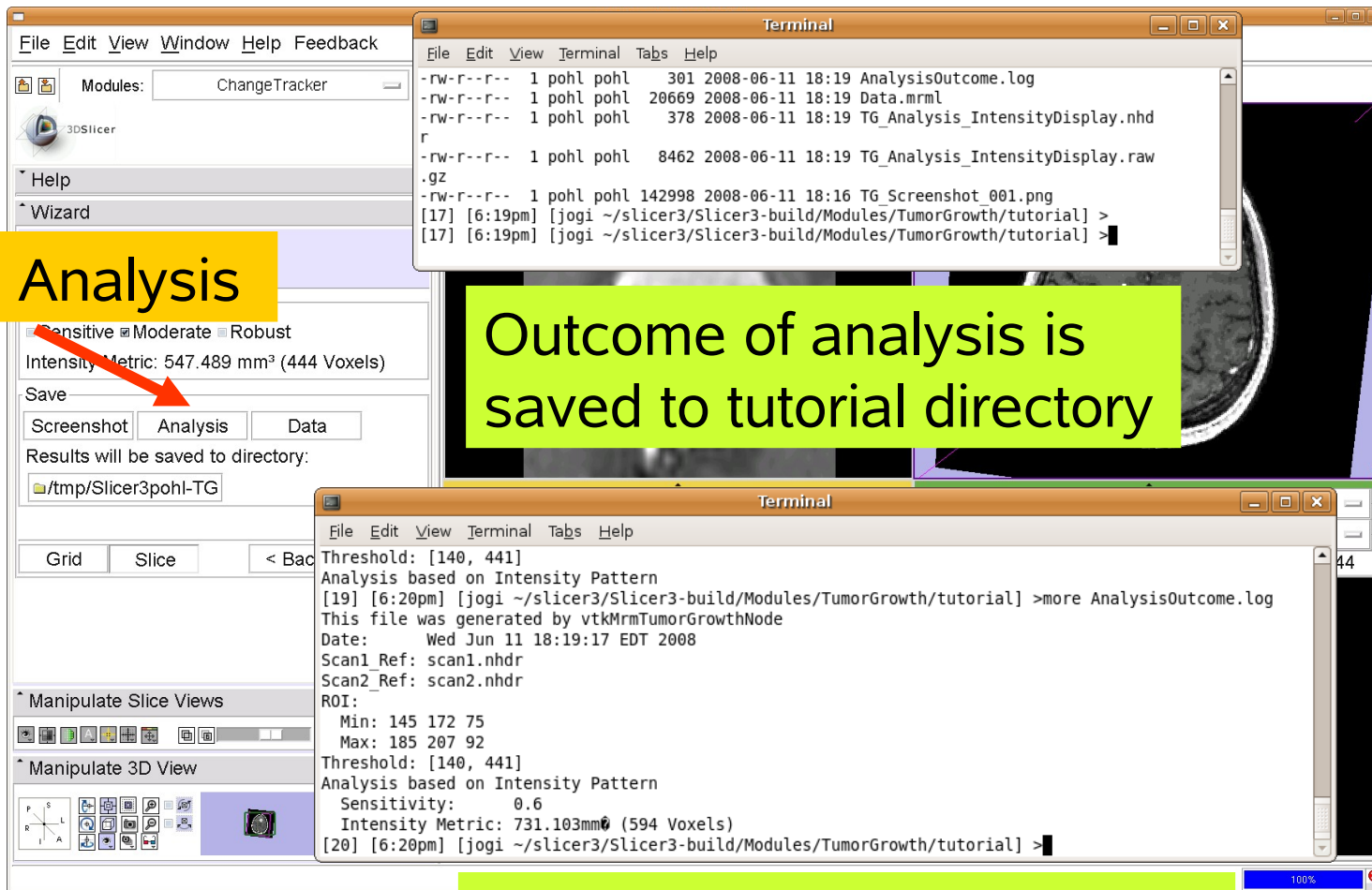
File Edit View Terminal Tabs Help

```
[14] [6:17pm] [jogi ~/slicer3/Slicer3-build/Modules/TumorGrowth/tutorial] >ls -la
total 152
drwxr-xr-x  2 pohl pohl  4096 2008-06-11 18:16 ./
drwxr-xr-x 11 pohl pohl  4096 2008-06-11 18:16 ../
-rw-r--r--  1 pohl pohl 142998 2008-06-11 18:16 TG_Screenshot_001.png
[15] [6:17pm] [jogi ~/slicer3/Slicer3-build/Modules/TumorGrowth/tutorial] >
```

View TG\_Screenshot\_001.png

# Save Analysis Result

Press Analysis



The screenshot shows the 3DSlicer interface with the 'Analysis' button highlighted by a red arrow. A yellow box contains the text 'Outcome of analysis is saved to tutorial directory'. A terminal window shows the command prompt and the output of the analysis, including the file 'AnalysisOutcome.log' and the directory path '/tmp/Slicer3pohl-TG'.

Terminal Output:

```
File Edit View Terminal Tabs Help
-rw-r--r-- 1 pohl pohl 301 2008-06-11 18:19 AnalysisOutcome.log
-rw-r--r-- 1 pohl pohl 20669 2008-06-11 18:19 Data.mrml
-rw-r--r-- 1 pohl pohl 378 2008-06-11 18:19 TG_Analysis_IntensityDisplay.nhd
-rw-r--r-- 1 pohl pohl 8462 2008-06-11 18:19 TG_Analysis_IntensityDisplay.raw
.gz
-rw-r--r-- 1 pohl pohl 142998 2008-06-11 18:16 TG_Screenshot_001.png
[17] [6:19pm] [jogi ~/slicer3/Slicer3-build/Modules/TumorGrowth/tutorial] >
[17] [6:19pm] [jogi ~/slicer3/Slicer3-build/Modules/TumorGrowth/tutorial] >
```

Terminal Output (continued):

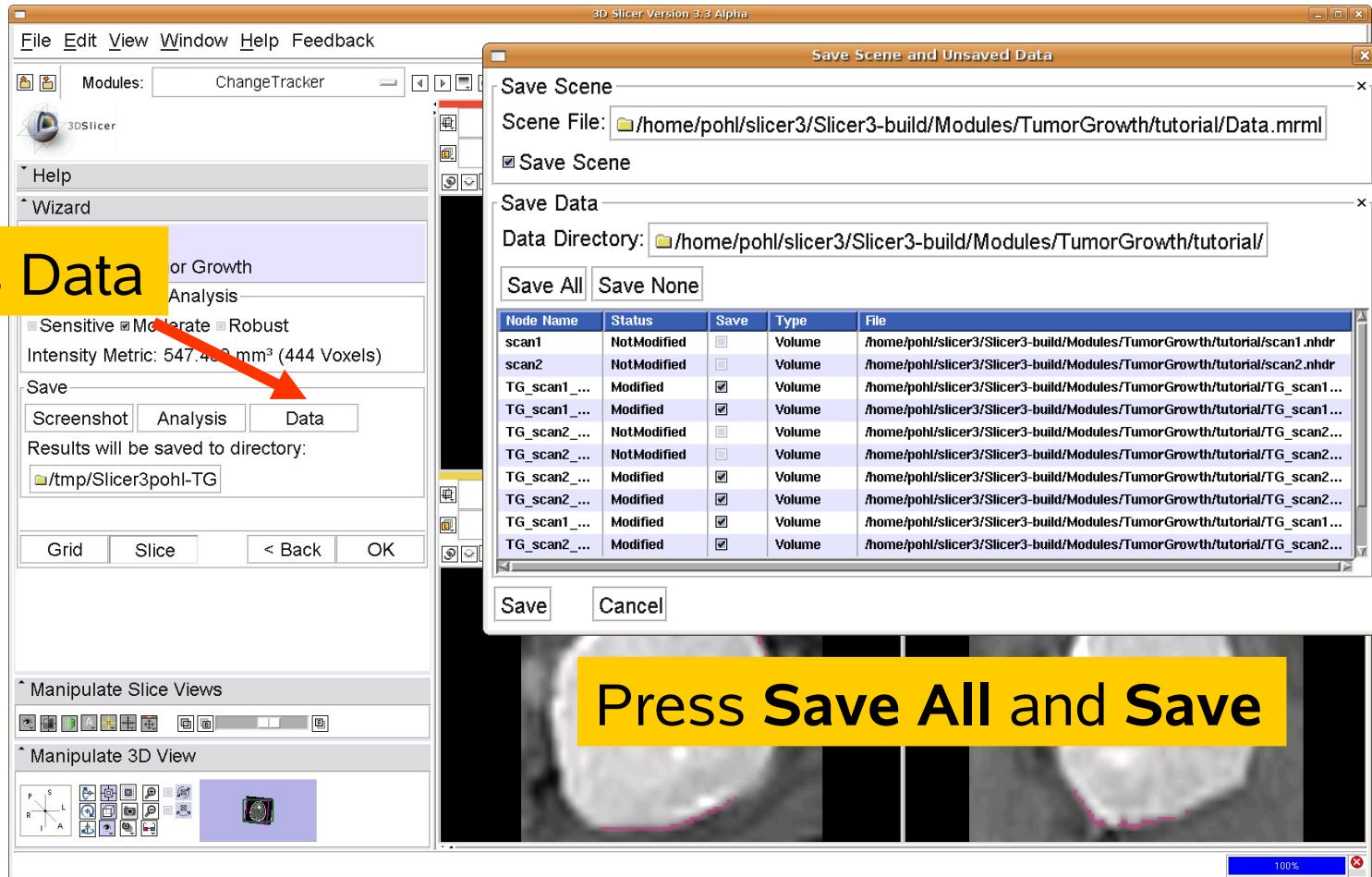
```
File Edit View Terminal Tabs Help
Threshold: [140, 441]
Analysis based on Intensity Pattern
[19] [6:20pm] [jogi ~/slicer3/Slicer3-build/Modules/TumorGrowth/tutorial] >more AnalysisOutcome.log
This file was generated by vtkMrmTumorGrowthNode
Date: Wed Jun 11 18:19:17 EDT 2008
Scan1 Ref: scan1.nhdr
Scan2 Ref: scan2.nhdr
ROI:
Min: 145 172 75
Max: 185 207 92
Threshold: [140, 441]
Analysis based on Intensity Pattern
Sensitivity: 0.6
Intensity Metric: 731.103mm³ (594 Voxels)
[20] [6:20pm] [jogi ~/slicer3/Slicer3-build/Modules/TumorGrowth/tutorial] >
```

View AnalysisOutcome.log

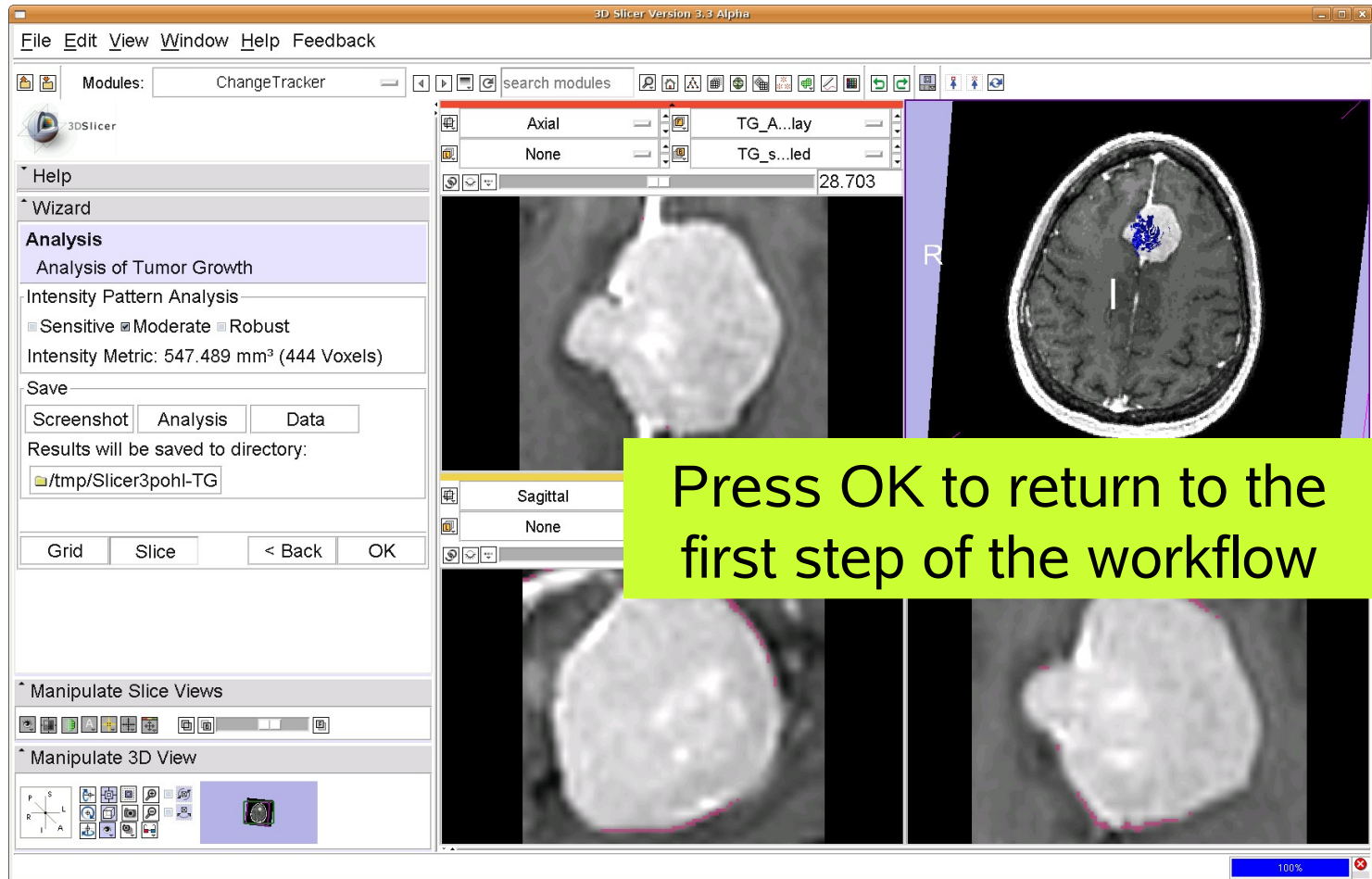


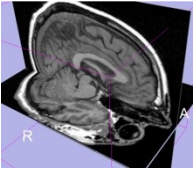
# Save Intermediate Results

Press Data

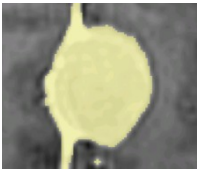


# Finish Workflow





Loading a scene



Measuring volume change in tumors

- We tested the tool on Axial 3D SPGR T1 post Gadolinium scans  
(Voxel dimension: 0.94mm x 0.94mm x 1.20mm, FOV: 240mm, Matrix: 256 x 256)
- We expect the tool to work also on set of scans that fulfill the following requirements:
  - same patient was scanned
  - scans were acquired with the same acquisition protocol
  - scans have isotropic resolution
  - pathology appearance is hyper-intense



# Acknowledgments

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NIH U54EB005149

add nac, ncigt and spl acknowledgements



Brain Science Foundation



INRIA, France