Automatic Segmentation of Traumatic Brain Injury MRI volumes using Atlas Based Classification and 3D Slicer

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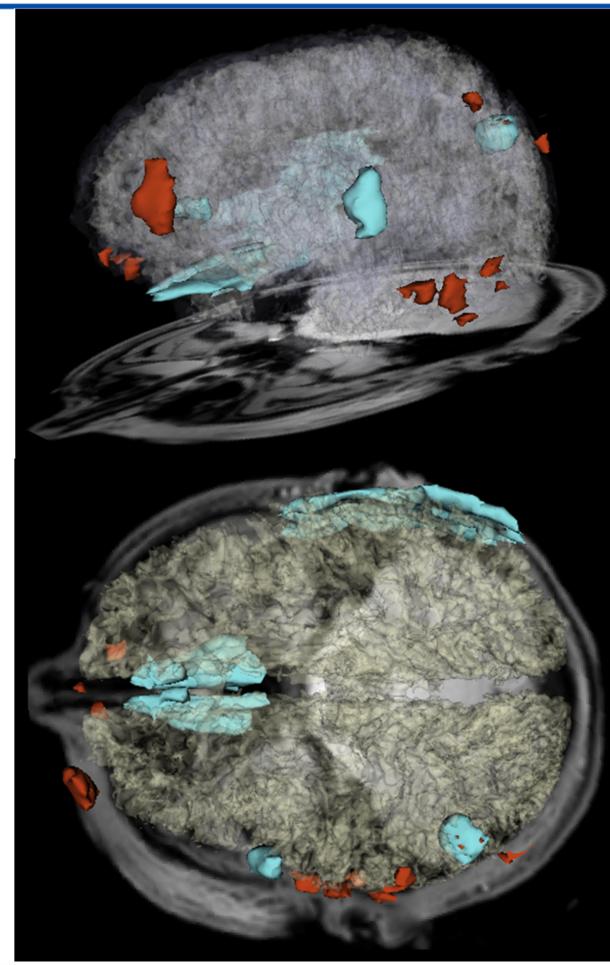
Learning Objectives

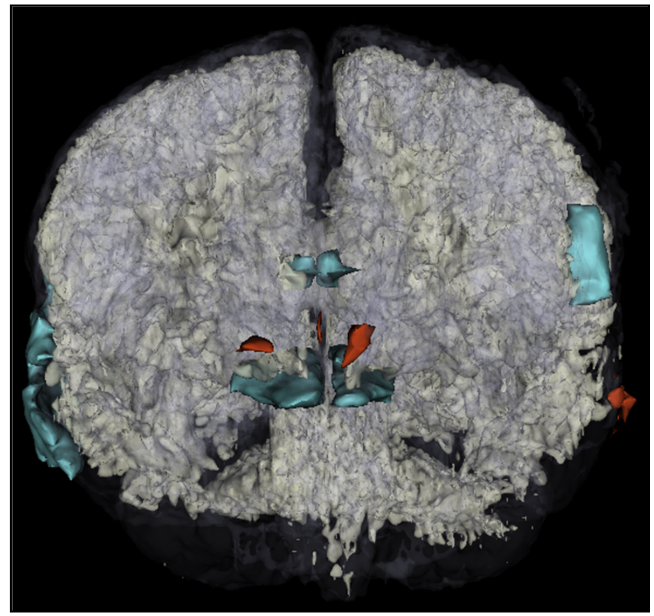
- acquire familiarity with several MR sequences commonly used for TBI imaging
- learn how to apply ABC to perform joint co-registration and automatic segmentation of TBI volumes
- acquire expertise on how to identify and characterize TBI pathology using various MRI sequences
- gain exposure to informed strategies for quantification of TBI-related edema or hemorrhage



Pre-requisites

- This tutorial assumes that you have already completed the following tutorials:

  - **Slicer 3 Visualization Tutorial** by Sonia Pujol, available at
    - http://www.slicer.org/slicerWiki/images/2/2e/Slicer3_DataLoadingAndVisualization_UCSF2010_SoniaPujol.pdf
  - **Interactive Editor Tutorial** by Sonia Pujol, available at
    - http://www.slicer.org/slicerWiki/images/6/69/InteractiveEditorTutorial_Slicer3.6-SoniaPujol.pdf



Edema (teal) and hemorrhage (red) in a traumatic brain injury patient, with white matter (solid beige) and gray matter (transparent hue) superposed.

Material

This tutorial requires the installation of the **Slicer3.6 release** and the tutorial dataset. They are available at the following locations:

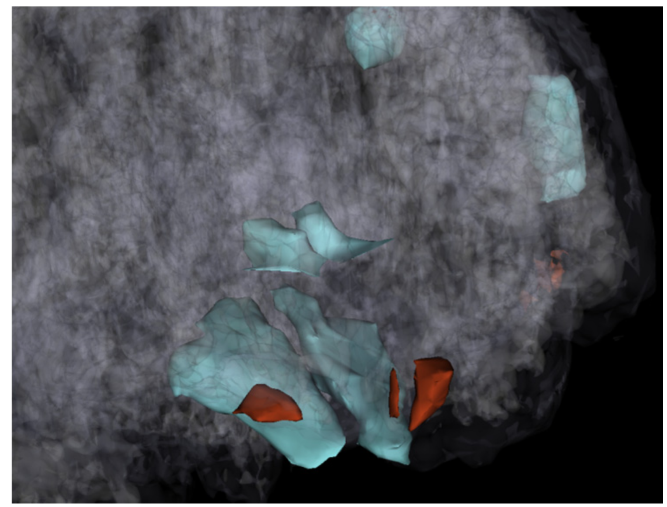
Slicer3.6 download page

http://www.slicer.org/pages/Downloads/

Tutorial dataset:

TBISegmentationData_TutorialContestSummer2011.zip

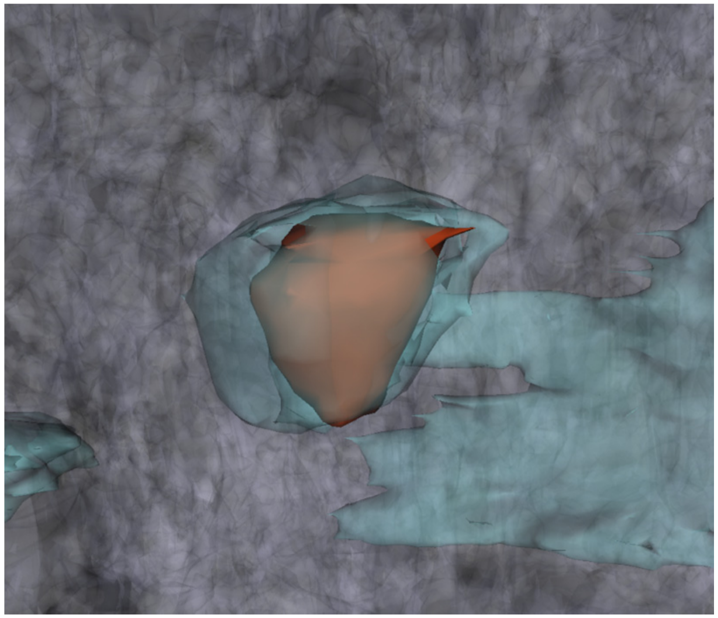
http://www.na-mic.org/Wiki/images/7/74/TBISegmentationData_TutorialContestSummer2011.zip



Enhanced view of frontal edema and hemorrhage several days after the insult. This type of pathology is very common in traumatic brain injury.

Platform

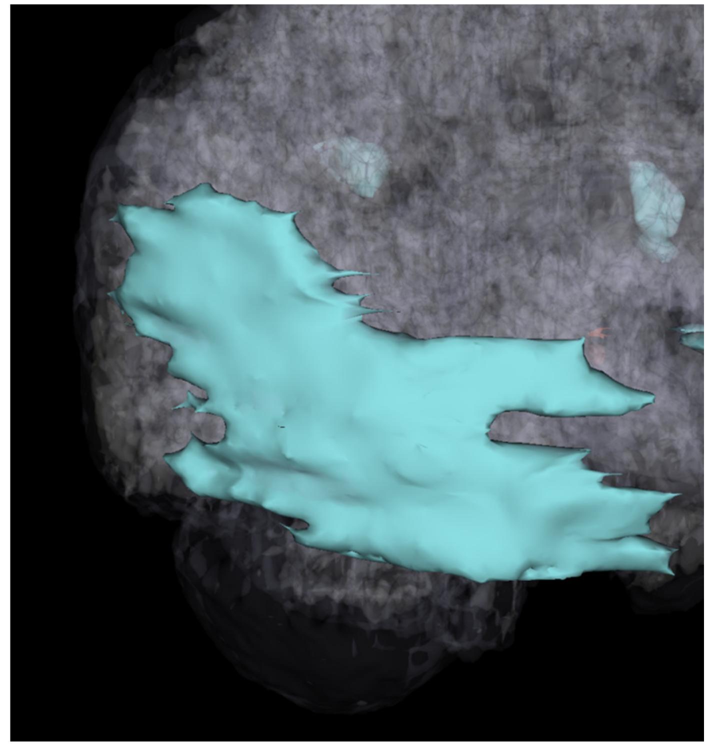
- This tutorial has been developed on Windows 7. It is compatible with the following platforms:
  - Windows XP, Windows 7
  - Linux 32, Linux 64
  - Mac/Darwin



Detailed view of parietal edema (teal) and hemorrhage. It is interesting to note how the non-hemorrhagic edemic region encases the brain portion that is actively bleeding. With recovery, it is expectable for the hemorrhage to shrink in both volume and mass.

Overview

- Clinical background
- Clinical workflow
  - installation of the ABC module
  - loading and exploration of TBI data
  - understanding common MR sequences for TBI
  - automatic segmentation of TBI using ABC
  - generation of 3D models
  - lesion segmentation and model generation
- Conclusions

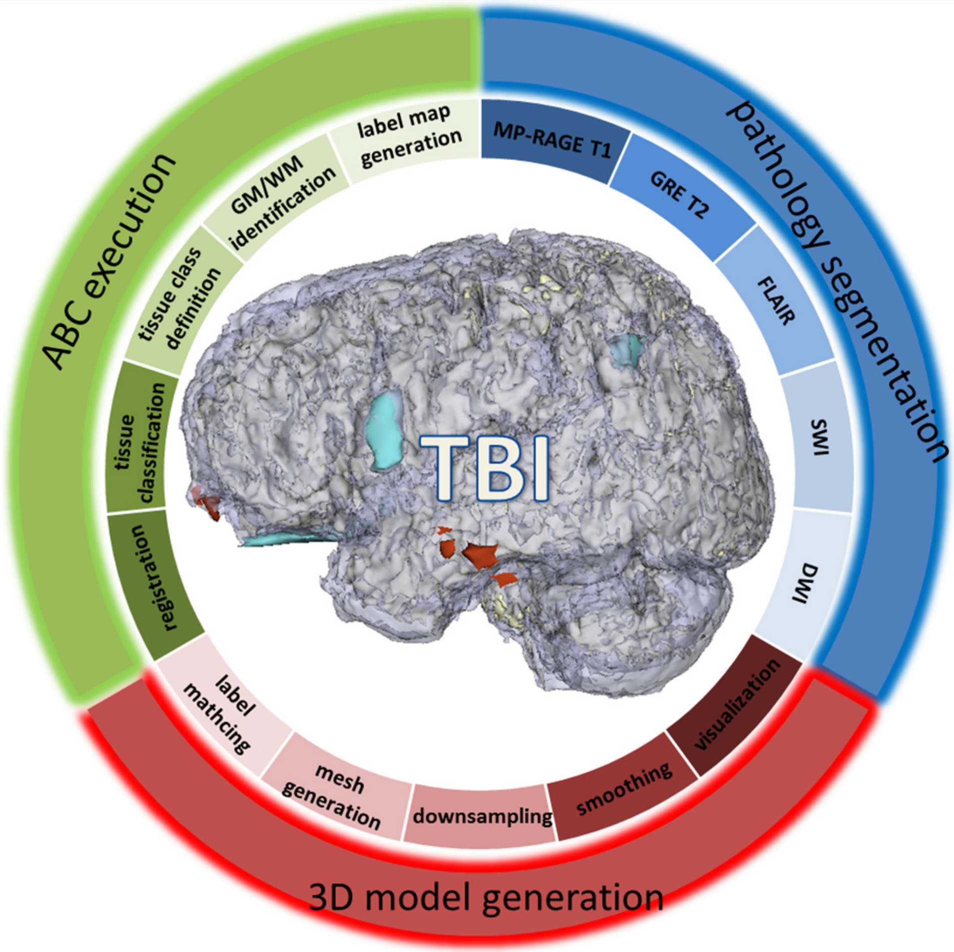


Contre-coup edema due to acceleration/deceleration forces at work during traumatic brain injury. Although contralateral with respect to the primary injury, the spatial extent of this edemic region is notable.

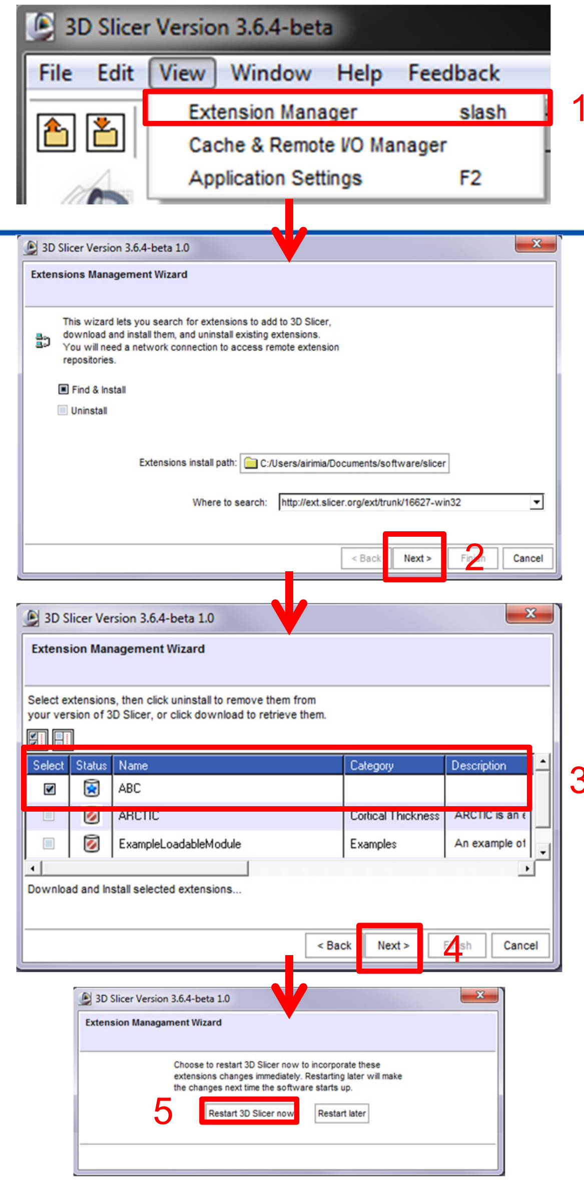
Traumatic Brain Injury (TBI)

- With traumatic brain injury (TBI), there are an estimated 1.7 million cases in the United States alone every year, with an estimated 1.2 million ER visits and over 50,000 deaths.
- Over 5.3 million cases of required long-term daily assistance exist as a result of TBI, which results in health care costs of over $60 billion/year
- Despite many innovations, progress towards patient-tailored characterization of the structural and functional substrates associated with TBI-related neural and cognitive impairment remains dissatisfactory and the relationship between neurophysiological markers of cognitive dysfunction and TBI structural damage has not been acceptably elucidated
- 3D Slicer offers a powerful and unparalleled set of tools for the exploration and quantification of TBI

Conceptual Framework



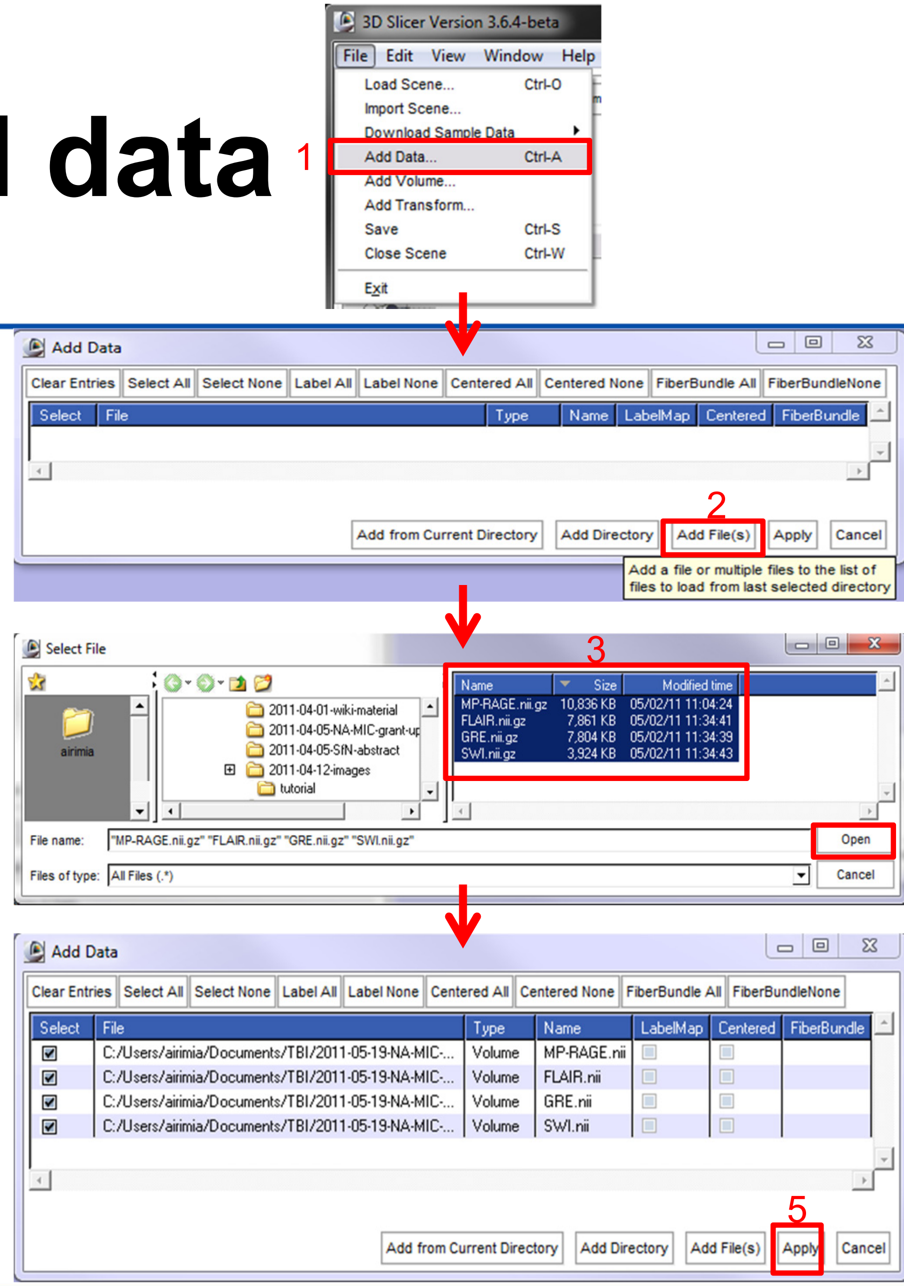
Installing ABC



- After Slicer has been loaded, the Welcome window will appear.
- To install the ABC module:
  - 1 – Click on *View* → *Extension Manager*
  - 2 – Click on *Next*
  - 3 – *Select* ABC from the list of modules
  - 4 – Click on *Next*; you will be prompted to specify the local hard drive location for ABC
  - 5 – After installation, you must select *Restart 3D Slicer now* for the changes to take effect

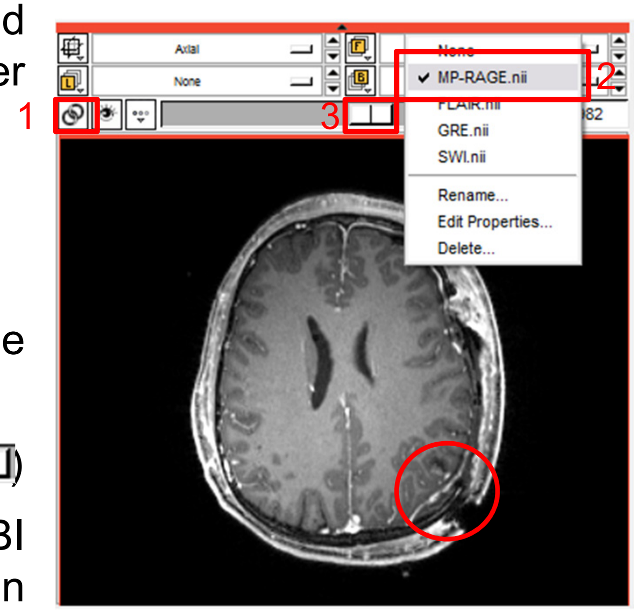
Loading TBI data

- After Slicer has been loaded, the Welcome window will appear.
- To load the TBI volumes associated with the case study:
  - 1 – Click on *File → Add Data*
  - 2 – Click on *Add File(s)*
  - 3 – Navigate to the data folder and sort the volume files in descending order by size. This will ensure that all files are later processed in proper order.
  - 4 – Click on *Open*
  - 5 – In the *Add Data* dialog box, click on *Apply*



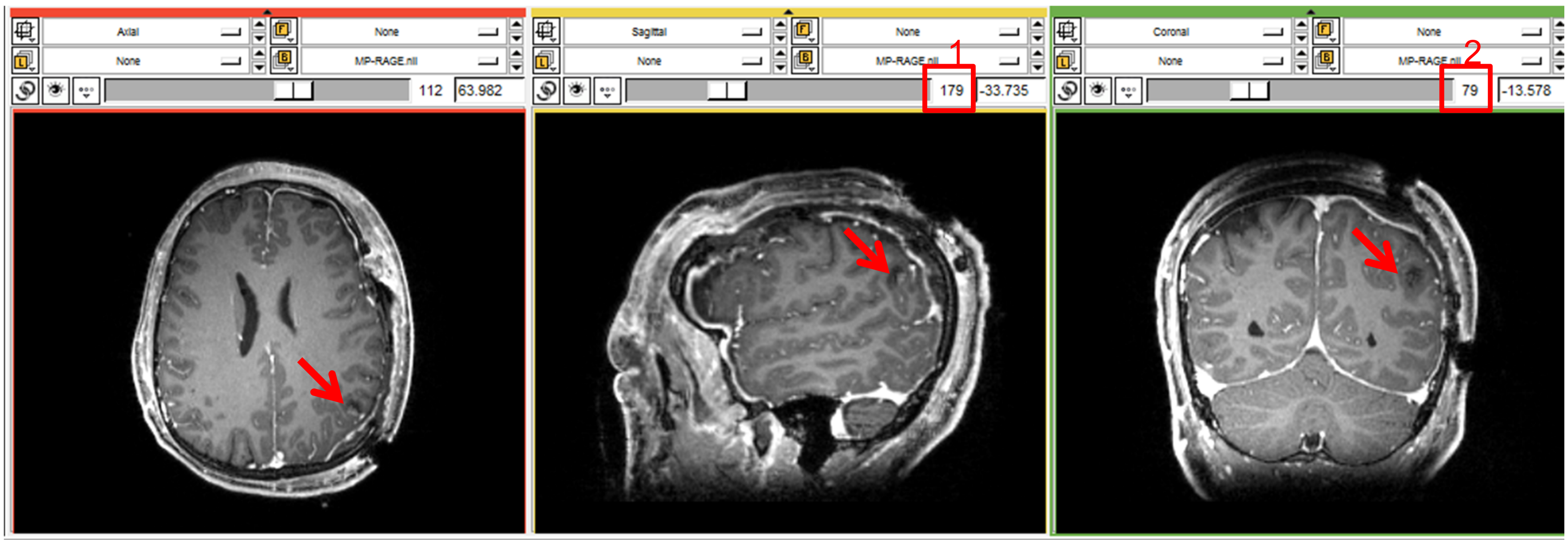
Exploring the data

- 4 TBI data volumes are provided for this tutorial: MP-RAGE, FLAIR, GRE, and SWI.
- MP-RAGE: this is an anatomical volume acquired using a T1-weighted sequence, in which white matter has higher intensity than gray matter
    - To explore a TBI-related lesion in this patient:
        - 1 – link the views using
        - 2 – select the MP-RAGE.nii volume from the background drop-down menu ( )
        - 3 – navigate to slice 112 using the slider ( )
    - The lesion associated with open-head TBI becomes apparent as a hypo-intensity located in the parieto-occipital region (see circle to the right)

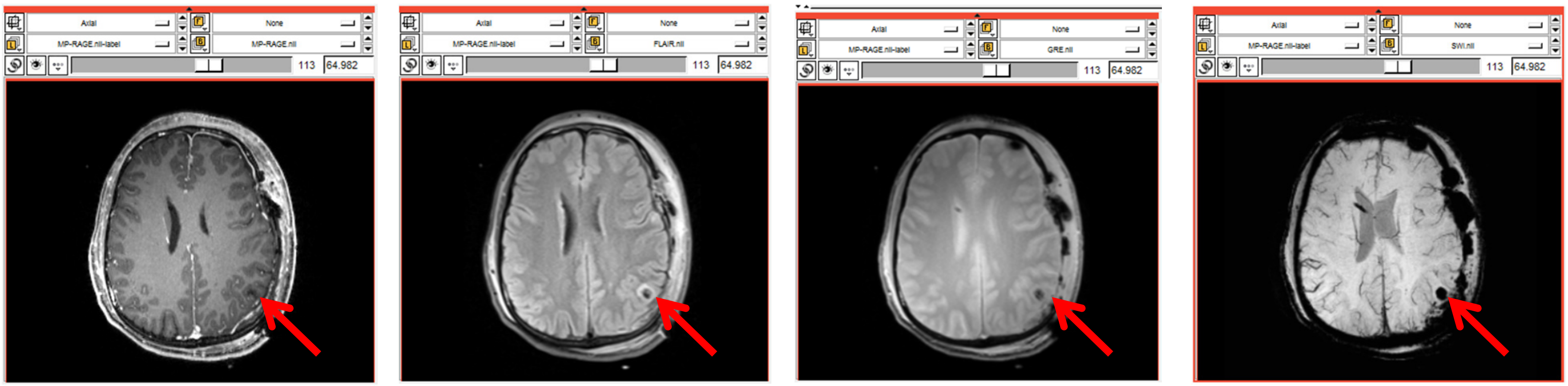


Exploring the data

- To locate the lesion more accurately within the head:
  - 1 – navigate to slice 179 in the sagittal view
  - 2 – navigate to slice 79 in the coronal view
- The lesion and open head injuries are now apparent on all three views
- Similar exploratory navigation can reveal the lesion in FLAIR, GRE, and SWI volumes



Exploring the data



MP-RAGE T1 | FLAIR | GRE T2 | SWI

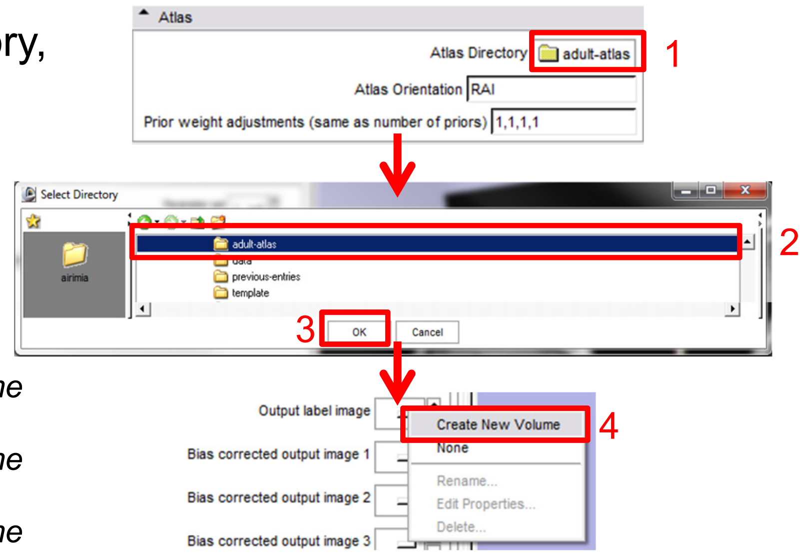
- Use of multiple image channels provides complementary information on pathologies
- T1 is a standard volume, with good anatomical resolution and high WM/GM contrast
- FLAIR is excellent for revealing CSF-perfused lesions as image hyper-intensities
- T2 GRE is useful for discerning areas associated with hemorrhages
- SWI is suitable for the detection of micro-bleeds and is superior to GRE in this respect

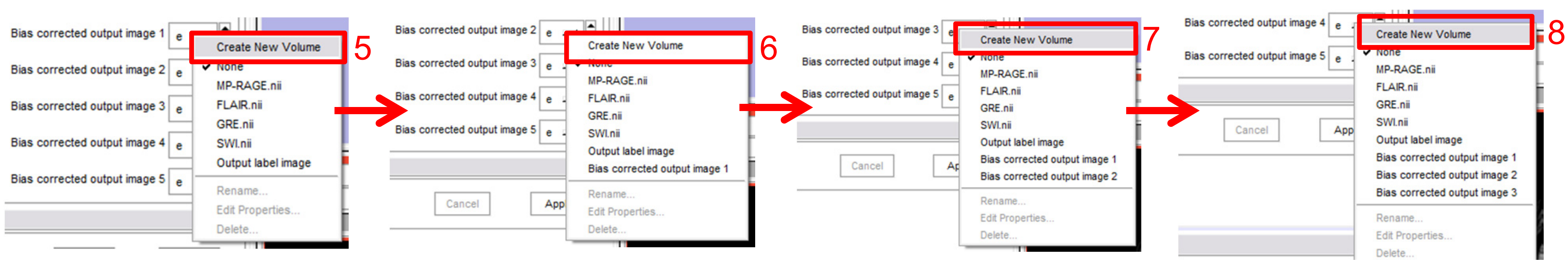
Configure ABC

- To load ABC, click on:
  - 1 –*Modules → All Modules → ABC*
- The ABC interface appears. To specify input data:
  - 2 – click *Parameter Set → Create New Command Line Module*
  - 3 – click *Input image 1 → MP-RAGE.nii*
  - 4 – click *Input image 2 → FLAIR.nii*
  - 5 – click *Input image 3 → GRE.nii*
  - 6 – click *Input image 4 → SWI.nii*

Configure ABC

- 1 – click on [folder icon] and locate the *adult-atlas* directory, which was included in the tutorial data set
- 2 – select *adult-atlas* from its location
- 3 – click OK to select the atlas template
- 4 – click *Output label image→ Create New Volume*
- 5 – click *Bias corrected output image 1 → Create New Volume*
- 6 – click *Bias corrected output image 2 → Create New Volume*
- 7 – click *Bias corrected output image 3 → Create New Volume*
- 8 – click *Bias corrected output image 4 → Create New Volume*



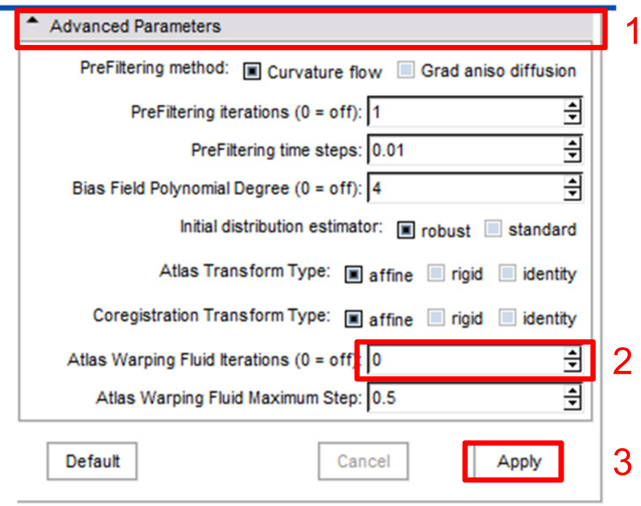


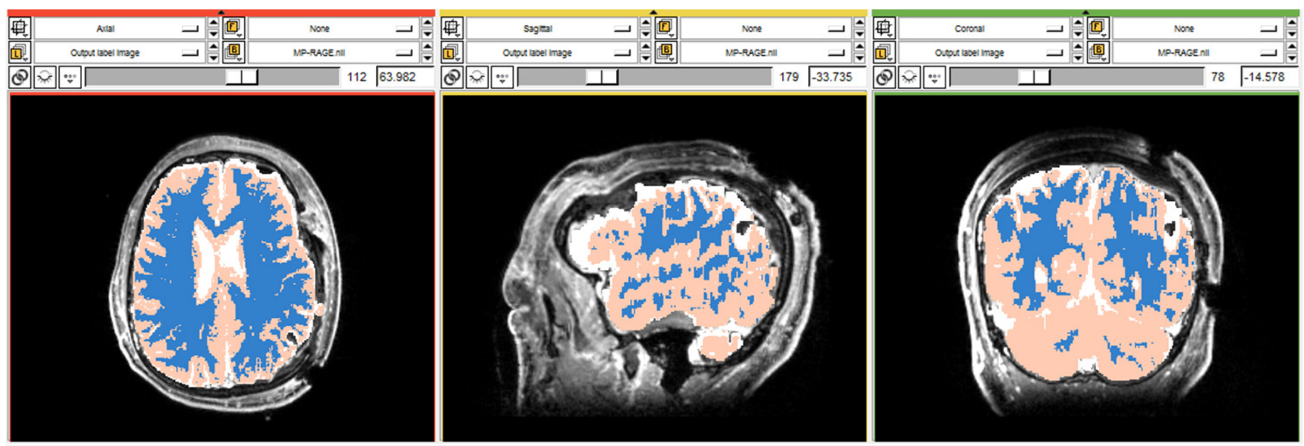
Execute ABC

- 1 – click on the *Advanced Parameters* arrow
- 2 – enter 0 (off) for the number of fluid iterations
- 3 – click *Apply* to run ABC on the dataset
- ABC will now co-register the FLAIR, GRE and SWI images to the MP-RAGE image, and perform the tissue classification
- Allow up to several hours for ABC execution
- ABC produces 3

tissue categories:

- gray matter
- white matter
- CSF



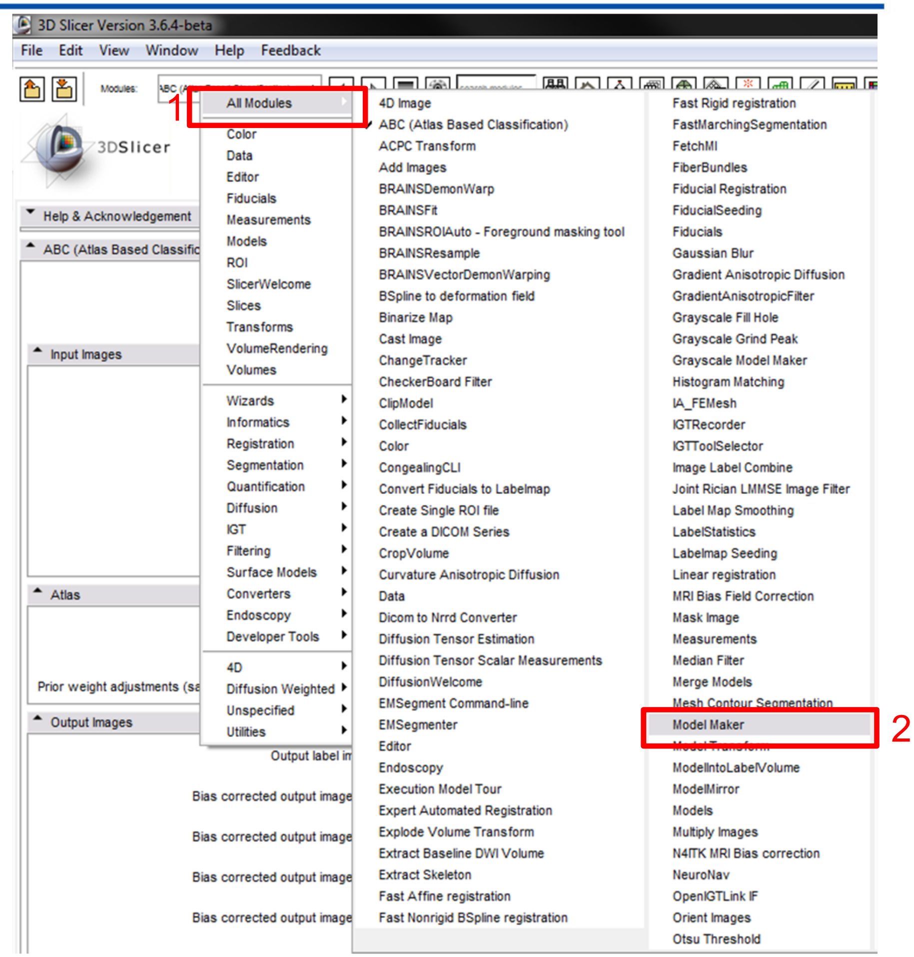


Generate 3D Models

Now that we have obtained the label map of GM, WM and CSF using ABC, we can generate the 3D models associated with each of these three tissue types.

- 1 – From the *Modules* drop-down menu, select *All Modules*
- 2 – From the second column, select *Model Maker*

This will display the interface of the *Model Maker* module, which allows one to create 3D models in Slicer.

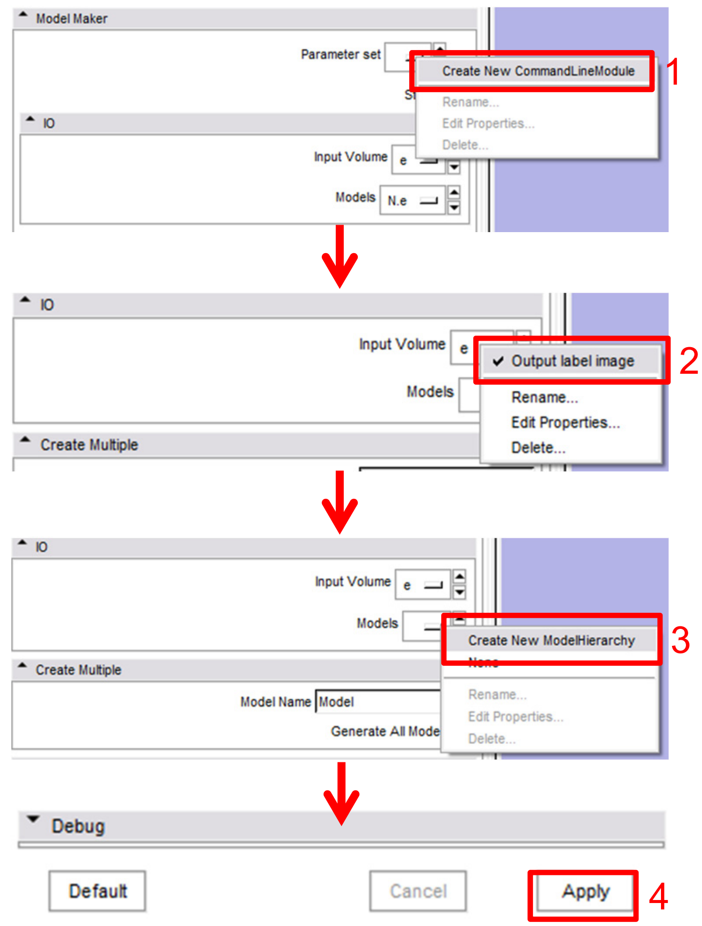


Generate 3D Models

To generate the 3D models:

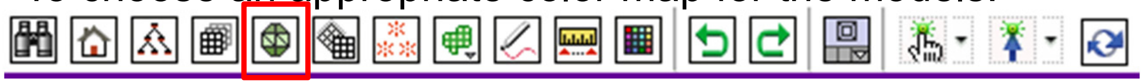
- 1 – From the *Parameter Set* drop-down menu, select *Create New Command Line Module*
- 2 – From the *Input Volume* drop-down menu, select *Output label image*
- 3 – From the *Models* drop-down menu, select *Create New Model Hierarchy*
- 4 – Click *Apply*

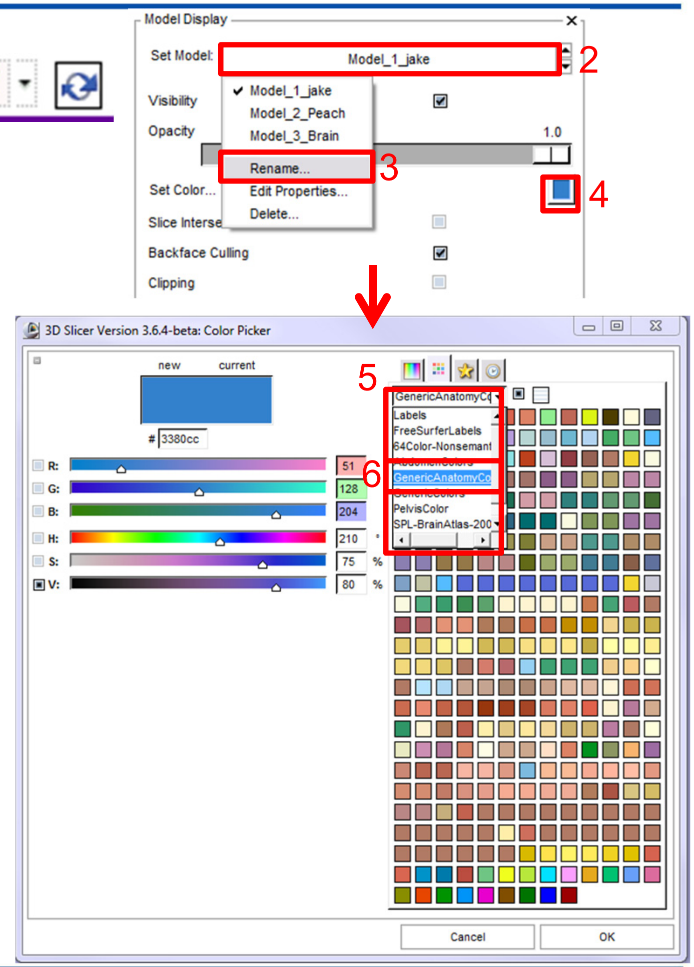
These steps will create 3D models for WM, GM and CSF.



Choose color map scheme

To choose an appropriate color map for the models:





- 1 – From the tool bar, click on the Models button
- 2 – From the *Set Model* drop-down menu, select *Model_1_jake*
- 3 – From the *Set Model* drop-down menu, select *Rename* and type *WM*; repeat steps 1-2 to rename *Model_2_Peach* as *GM* and *Model_3_Brain* as *CSF*
- 4 – Set the model to *WM* as in step 2, and click on the color box;
- 5 – In the *Color Picker* dialog box, click on the color drop down menu
- 5 – Select *Generic Anatomy Colors* as the color map; this will assign a color scheme in accordance with Slicer conventions.

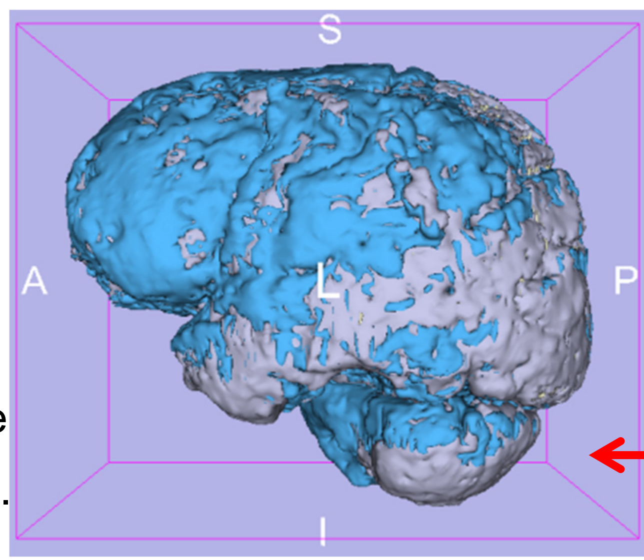
Choose color map scheme

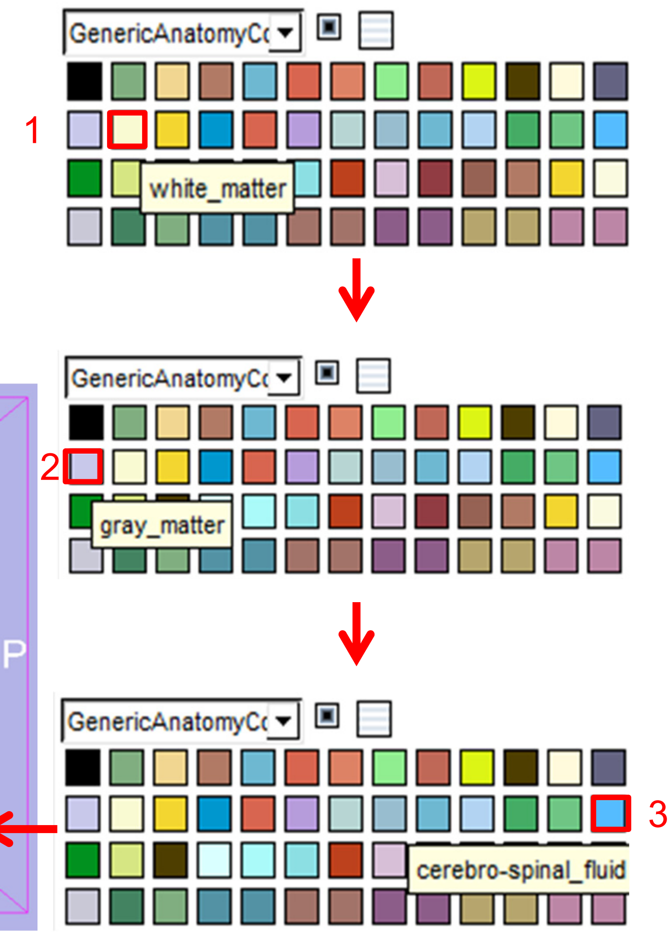
Now that we have selected an appropriate color scheme, we need to assign suitable colors to each tissue type.

- 1 – In the *Color Picker* dialog box, select beige for WM

Repeat steps 2-5 on the previous slide for *GM* and *CSF*

- 2 – For *GM,* click on purple as shown
- 3 – For *CSF,* click on blue as shown. The 3D model should now look as to the right. Note the variable CSF thickness.



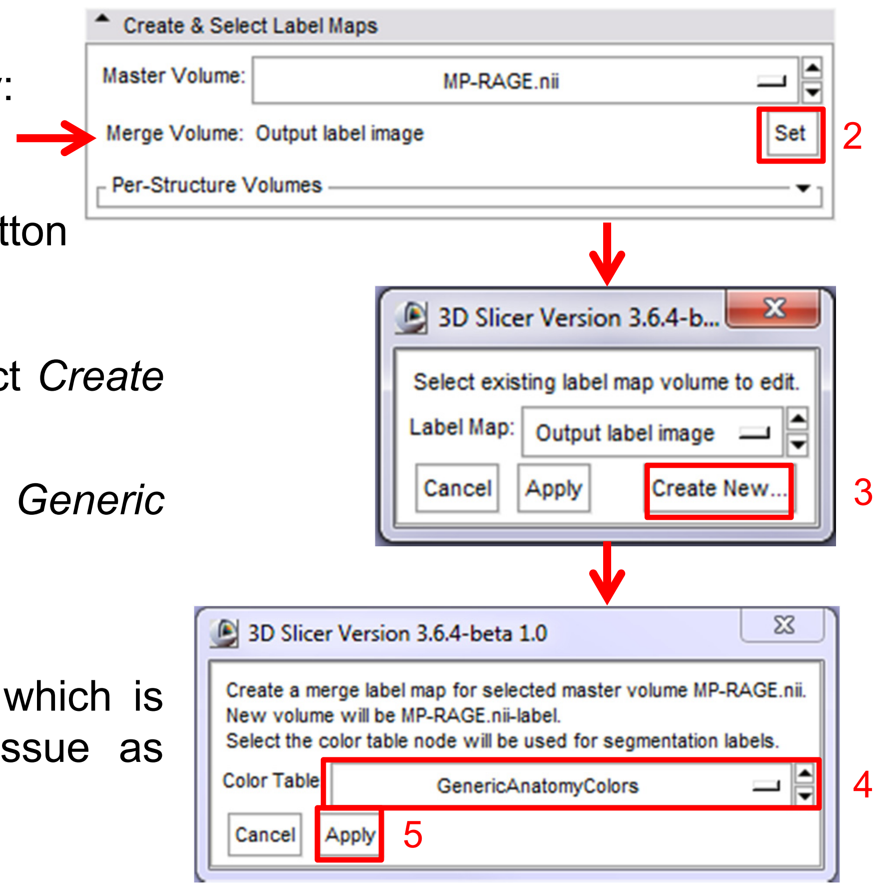


Create labels for pathology

We can now create a label map for pathology:

- 1 – From the tool bar, click on the Editor button
- 2 – Click on the *Set* button
- 3 – In the *Set Label Map* dialog box, select *Create New*
- 4 – In the *Color Table* dialog box, select *Generic Anatomy Colors*
- 5 – Click on *Apply*

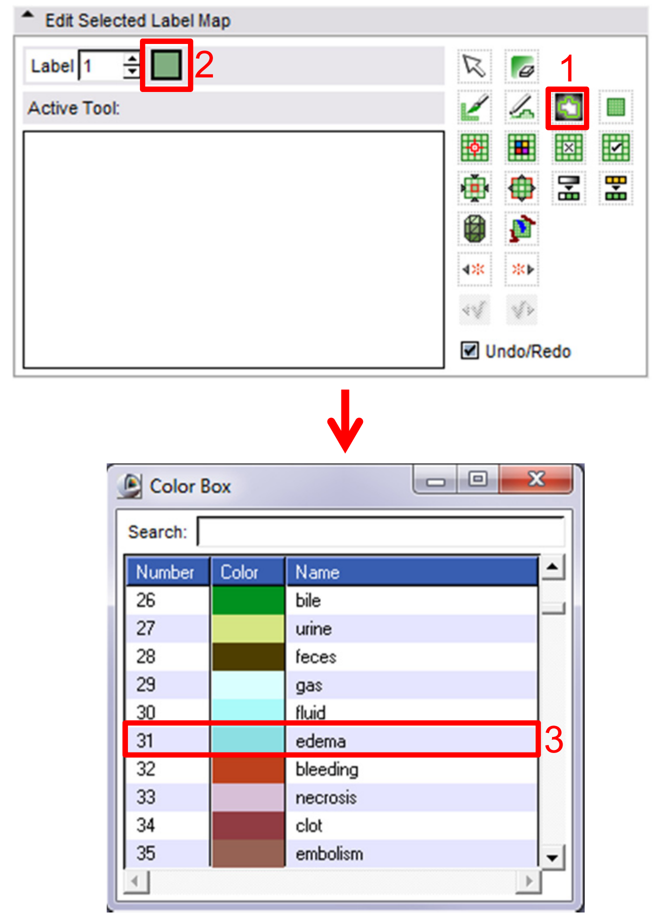
This will create a label map for pathology which is distinct from the label map for normal tissue as created by ABC.



Assign label for edema

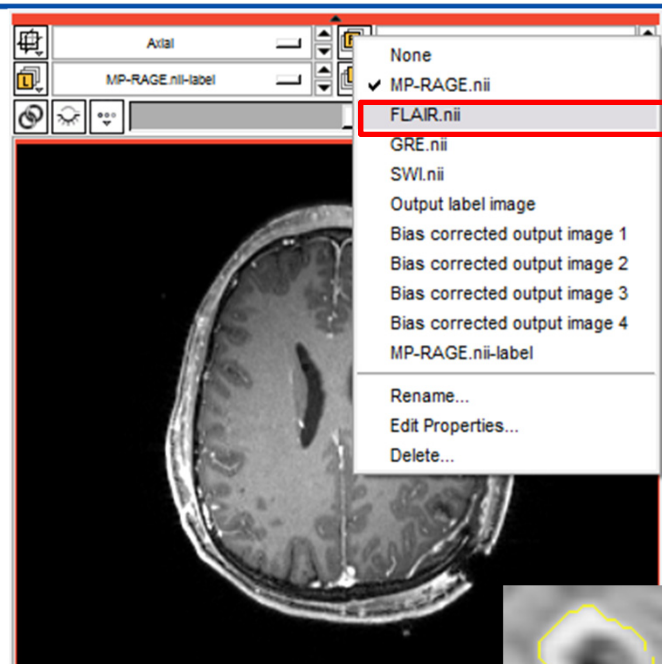
Now we can assign labels for the two pathology types, namely edema and bleeding:

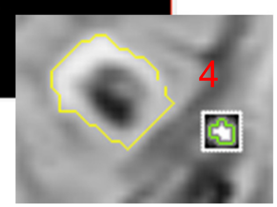
- 1 – From the label edit bar, click on *Level Tracing*
- 2 – Click on the color button next to the *Label*
- 3 – In the *Color Box* dialog box, select *31: edema*

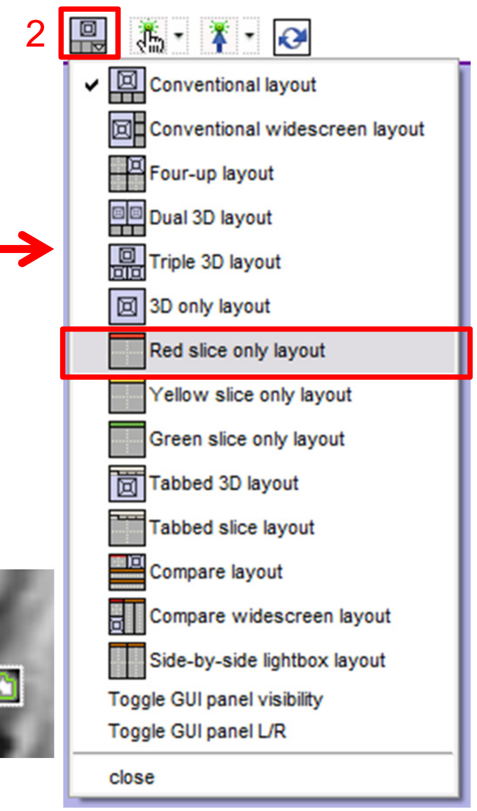


Segment edema from FLAIR

- 1 – In the *Foreground* menu, select *FLAIR.nii*
- 2 – Click on *the* tool bar menu
- 3 – select *Red slice only Layout*
- 4 – Use the level tracing tool to segment the edema using the FLAIR volume.



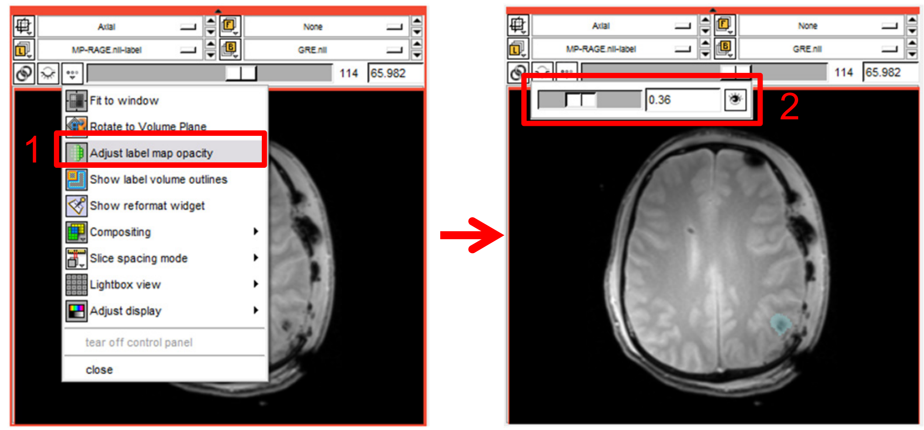




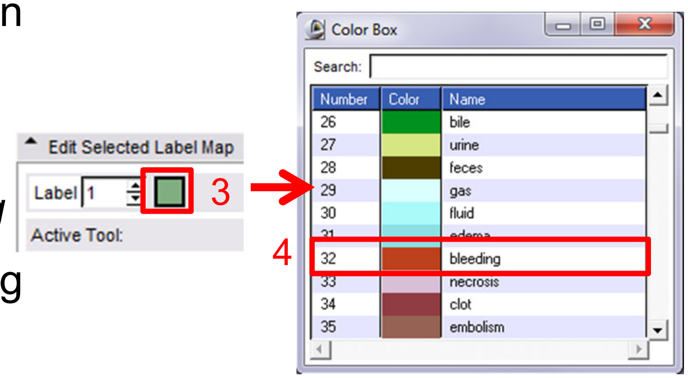
Recall that edema is hyperintense in this sequence modality, and that it appears in slices 105-117. The hypointense region in the middle is actually hemorrhage, but it will be segmented separately in following steps so we need not worry about it for now.

Assign label for bleeding

Once the edema has been segmented, we can proceed to the segmentation of hemorrhage. Viewing the label map and the underlying image at the same time can be accomplished by adjusting label map opacity.



- 1 – From the red slice image options menu, click on *Adjust label map opacity*
- 2 – Use the slider to select a convenient opacity
- 3 – In the *Color Box* dialog box, select *32: bleeding*



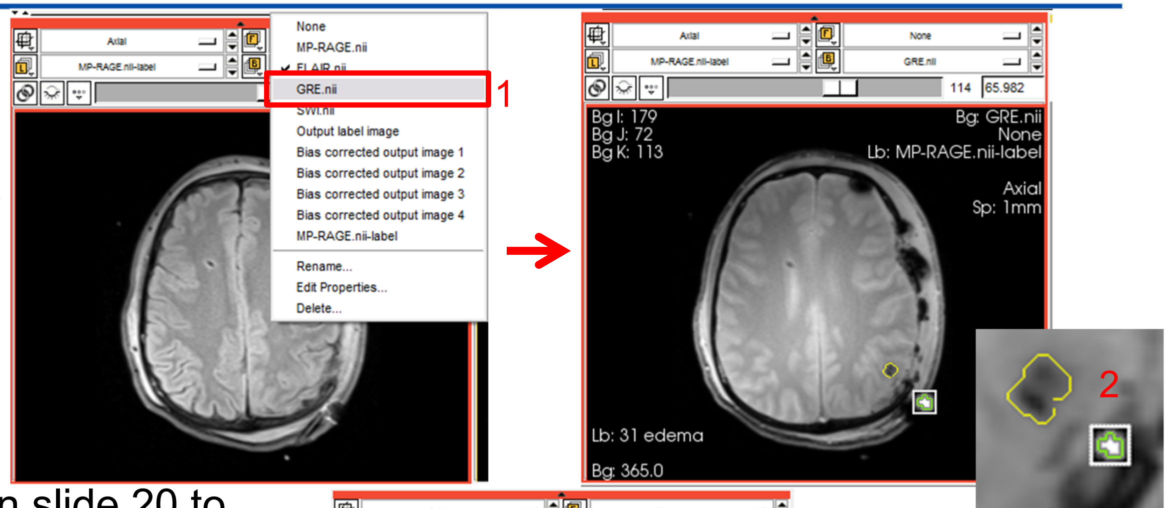
This step ensures that 3D Slicer color labeling conventions are respected.

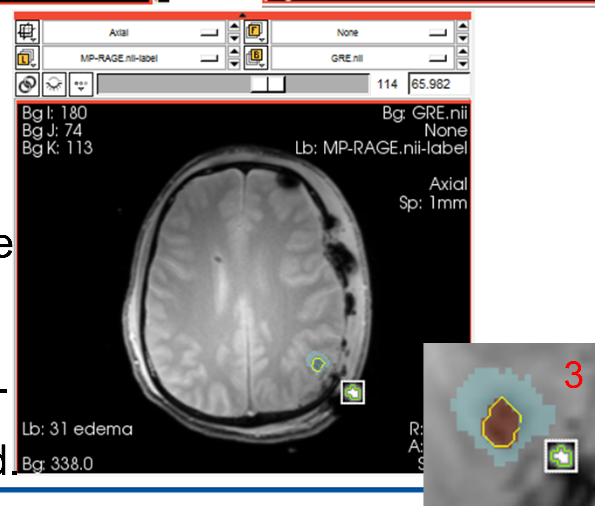
Segment bleeding from GRE

We can now segment bleeds.

- 1 – From the red slice background menu, click on *GRE.nii*
- 2 – Use the label map opacity slider as shown on the previous slide as well as the level tracing tool as demonstrated on slide 20 to obtain a convenient view of the hemorrhage in relation to the surrounding edema.

3 – Segment the bleeding in slices 106-116. The label map should now be similar to the inset shown to the right. Note that hemorrhage is surrounded by edemic region which does not bleed.

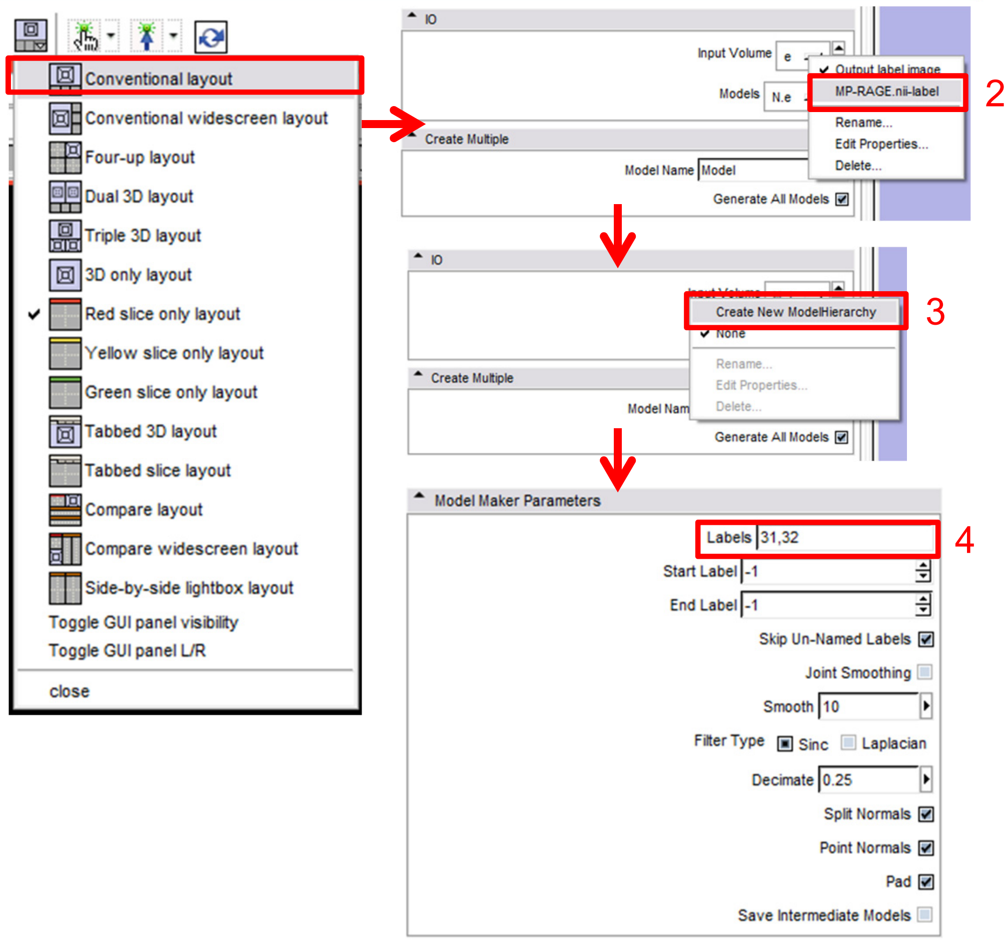




Create pathology 3D models

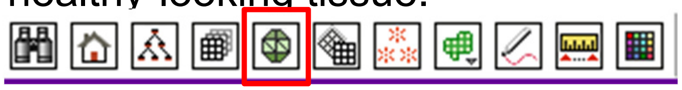
Once pathology has been segmented, their 3D models can be created.

- 1 – From the tool bar menu, select the *Conventional layout*
- 2 – For *Input Volume,* select *MP-RAGE.nii-label.* This is the label map for the pathology.
- 3 – Under *Models*, select *Create New Model Hierarchy*
- 4 – Under *Model Maker Parameters*, type “31,32” in the *Label* input box.
- 5 – Click on *Apply*

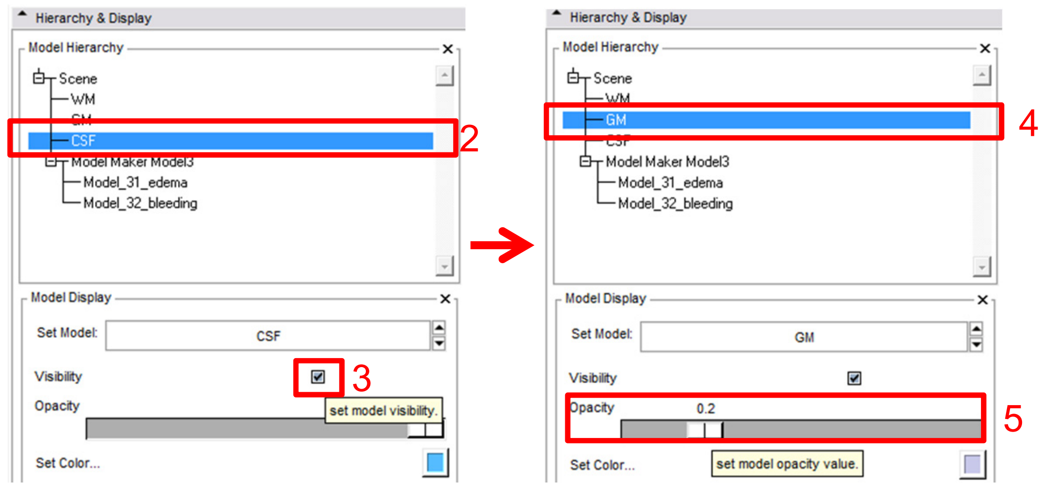


Visualize full 3D model

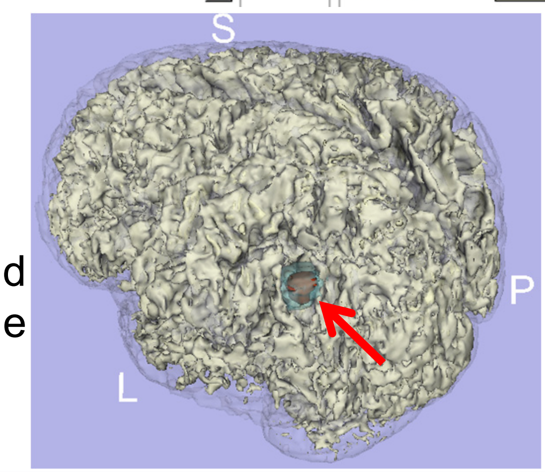
We can now visualize the full model, which includes both pathology and healthy-looking tissue.



- 1 – On the tool bar, click Models
- 2 – Under *Hierarchy and Display,* select *CSF*
- 3 – Under *Visibility*, uncheck the toggle box
- 4 – Under *Hierarchy and Display,* select *GM*
- 5 – Decrease the opacity to 0.2



This will allow us to visualize the edema and hemorrhage in relationship to the rest of the brain, as shown to the right.



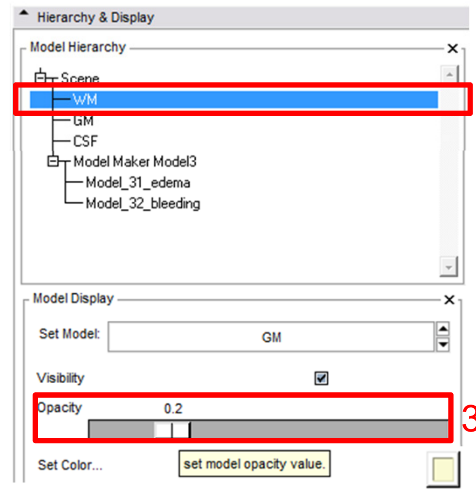
Exploring the results

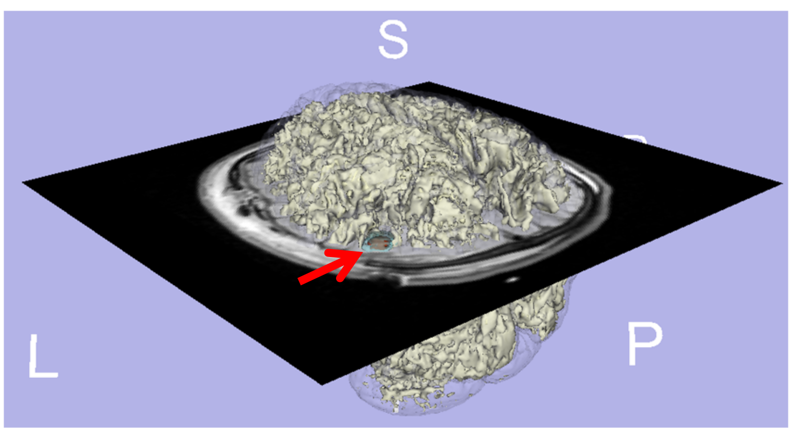
Further exploration of these results might include simultaneous overlay of a desirable slice:

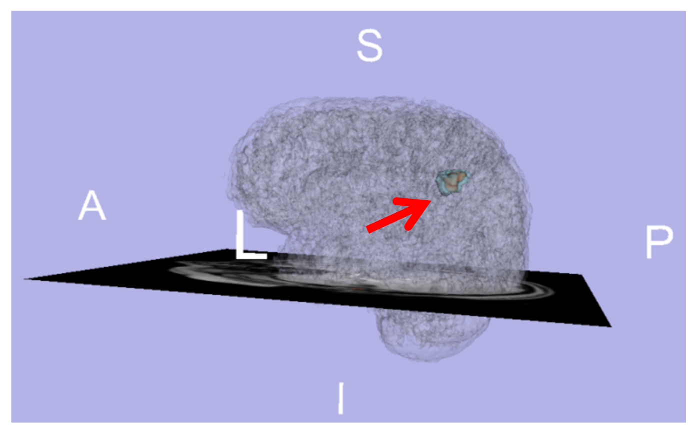
- 1 – On the red box tool bar, toggle slice visibility (left below)

One can also display the pathology with GM/WM transparency (see figure to the right below)

- 2 – Under *Hierarchy and Display,* set *WM* opacity to 0.2

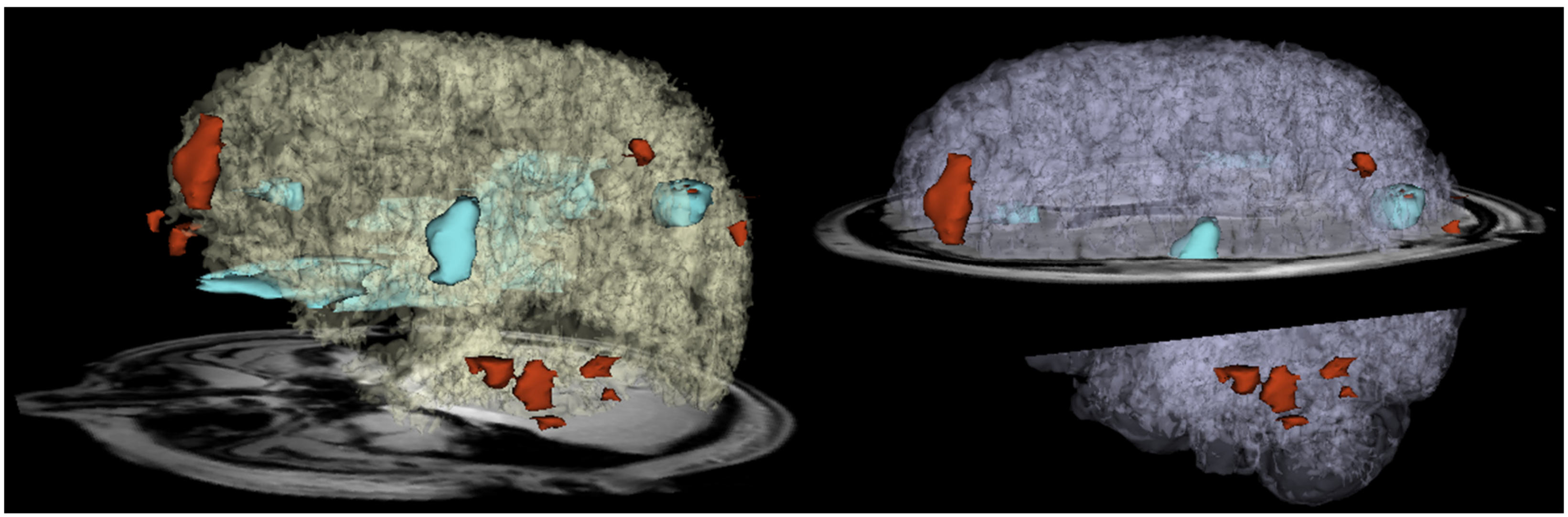




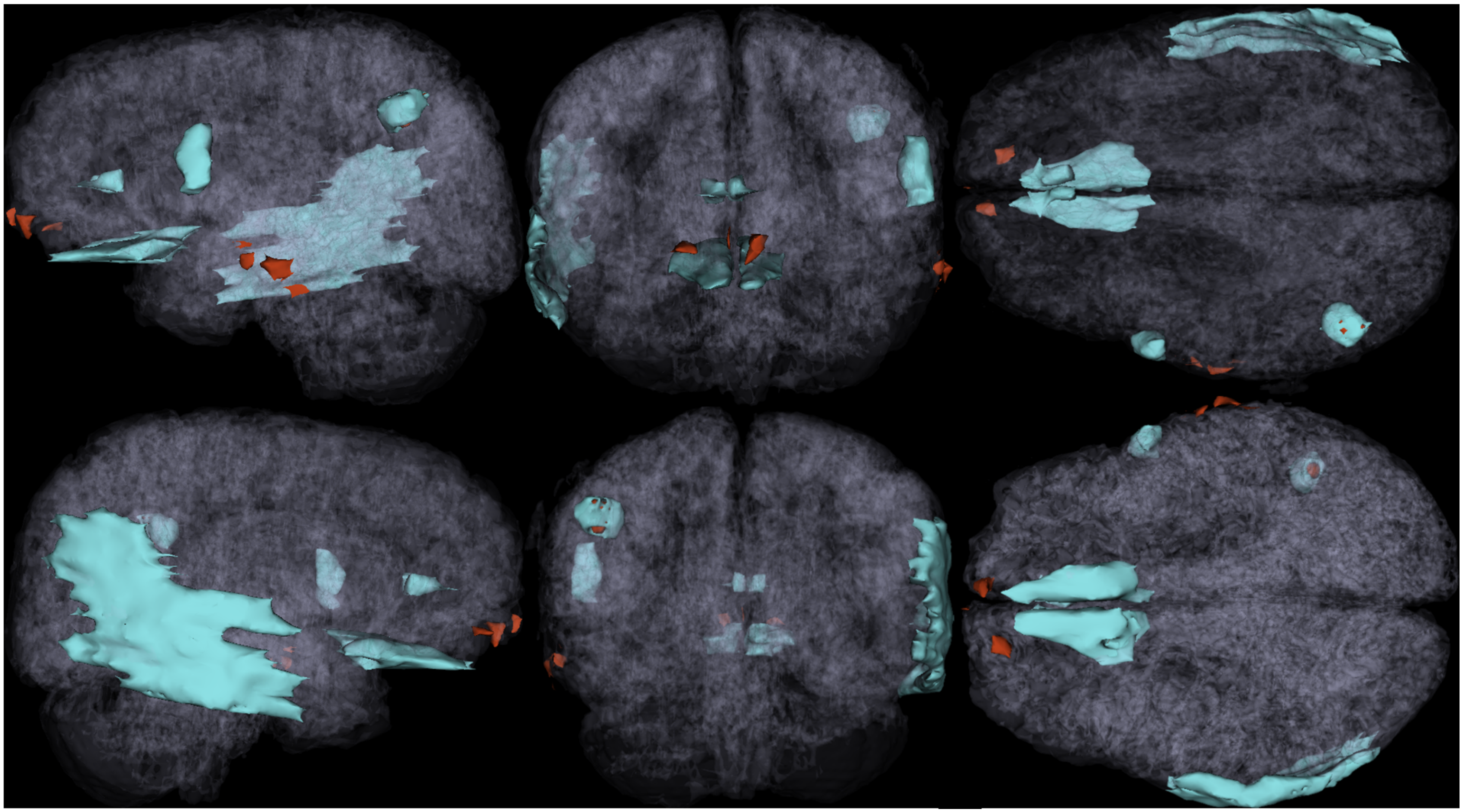


The complete model

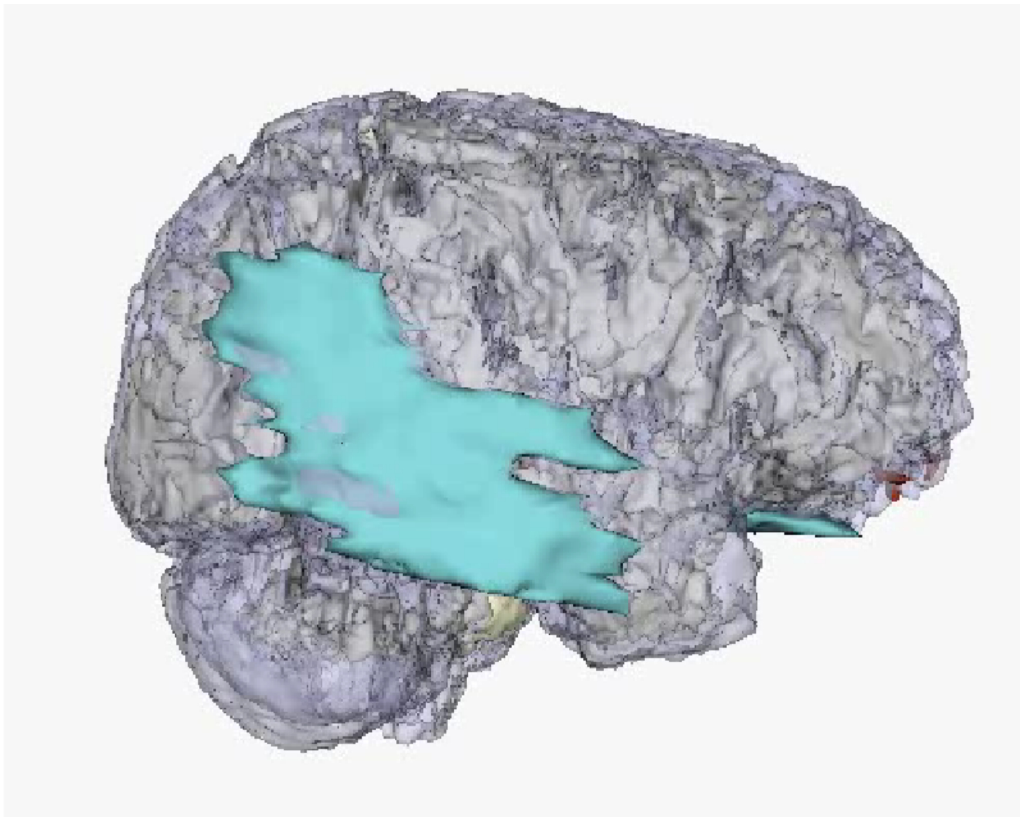
Segmentation of remaining lesions and hemorrhages in this subject can be accomplished using the tools and workflows demonstrated in this tutorial. Sample images of this undertaking are illustrated below.



The complete model



Complete model animation



Conclusion

- 3D Slicer offers powerful methodologies for the visualization of pathology due to traumatic brain injury
- Use of multiple MR image channels greatly enhances the ability to study and understand TBI structure/extent
- ABC is a robust algorithm to perform joint co-registration and automatic segmentation of TBI
- Completion of this tutorial allows one to acquire useful expertise on how to identify and characterize TBI
- Use of 3D Slicer can offer informed strategies for quantification of TBI-related edema or hemorrhage and for improved insight of clinical relevance

Acknowledgments

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National Institutes of Health

National Institute of Neurological Disorders and Stroke

NIH P01NS058489 (PI: Paul Vespa MD, FAAN, FCCN)

Laboratory of Neuro Imaging

University of California, Los Angeles

Director: Arthur W. Toga PhD

Bibliography

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A Irimia, MC Chambers, M Filippou, JR Alger, MW Prastawa, B Wang, S Gouttard, SMA Pujol, SR Aylward, DA Hovda, G Gerig, AW Toga, R Kikinis, PM Vespa, JD van Horn (2011) Three-dimensional calculation and quantification of morphometric and volumetric cortical atrophy indices of widespread clinical use from MRI volumes of traumatic brain injury using 3D Slicer *Proceedings of the 41st Annual Meeting of the Society for Neuroscience (SfN 2011), Washington, DC (this work was honored with the 1st Prize in the Fine Science Tools Research Contest of the Brain Research Institute at UCLA)*

A Irimia, JD van Horn, MC Chambers, MW Prastawa, S Gouttard, PM Vespa, DA Hovda, JR Algers, SMA Pujol, G Gerig, SR Aylward, AW Toga, R Kikinis (2011) Automatic multimodal MR image segmentation for the clinical assessment of traumatic brain injury in 3D Slicer *Proceedings of the 17th Annual Meeting of the Organization on Human Brain Mapping (OHBM 2011), Quebec City, Canada*

Further reading

On TBI:

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