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

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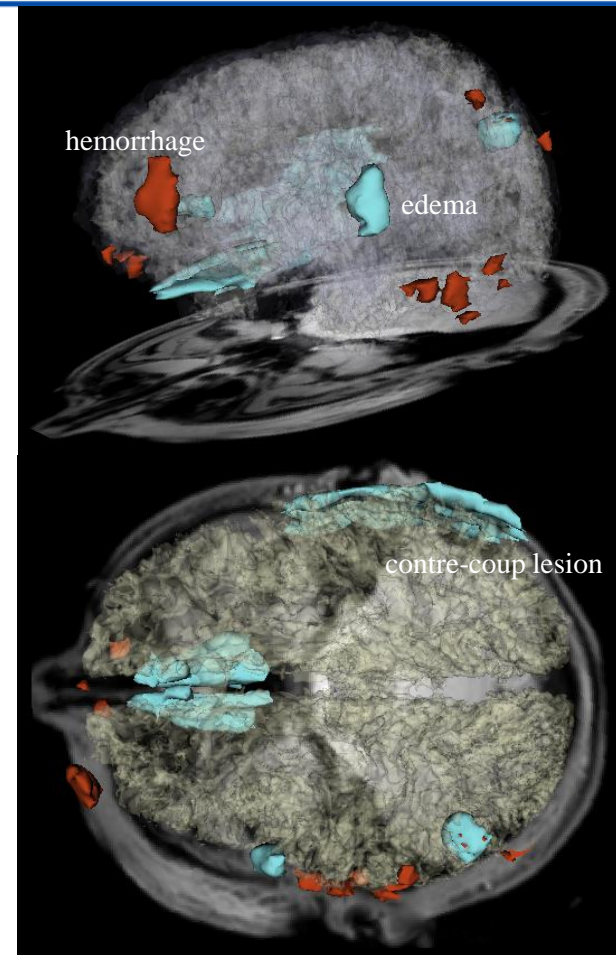
<http://www.na-mic.org>

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NA-MIC Tutorial Contest,
End-to-End Solution contest category**



Learning Objectives

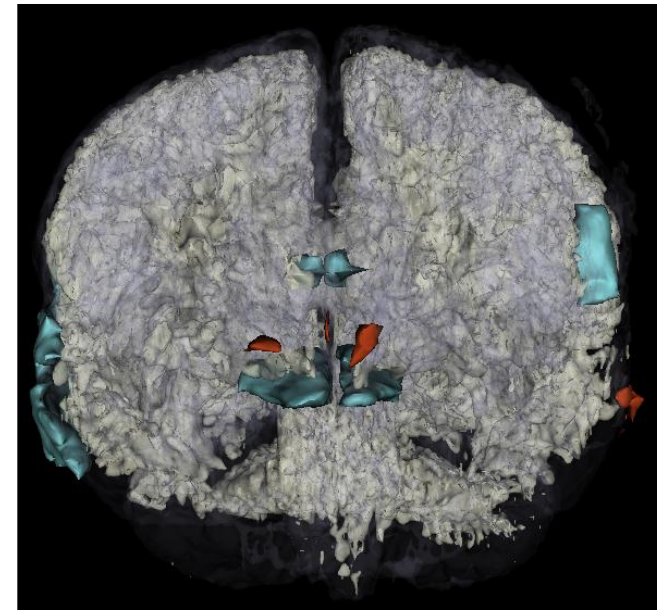
- acquire familiarity with several MR sequences commonly used for TBI imaging
- learn how to apply ABC to perform joint co-registration and automatic segmentation of TBI volumes
- acquire expertise on how to identify and characterize TBI pathology using various MRI sequences
- gain exposure to informed 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_Data>LoadingAndVisualization_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 (cyan) and hemorrhage (red) in a traumatic brain injury patient, with white matter (solid beige) and gray matter (transparent hue) superposed.



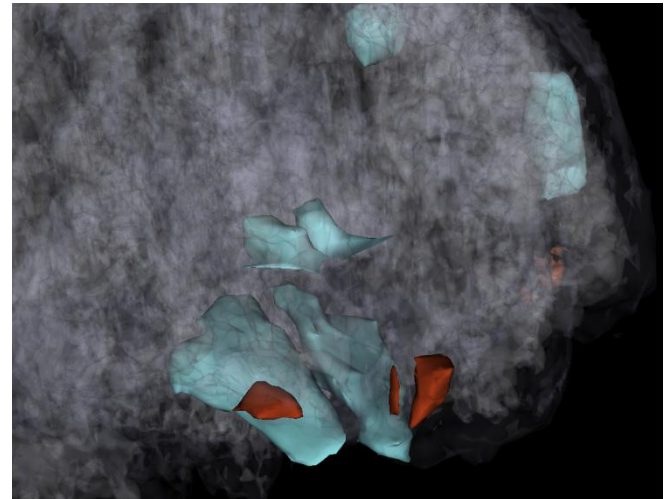
Material

This tutorial requires the installation of the **Slicer4.2.x release** and the tutorial dataset. They are available at the following locations:

Slicer4.2.x download page

<http://download.slicer.org/>

Tutorial dataset: The dataset can be downloaded [here](#).

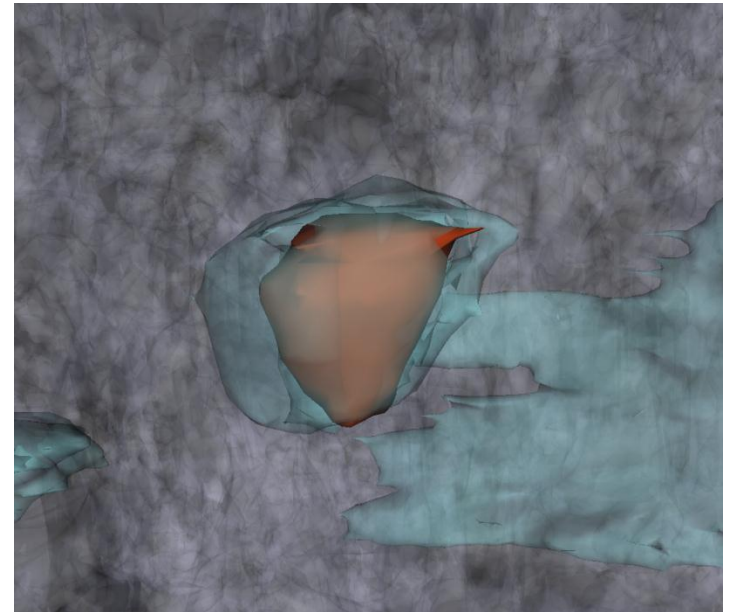


Enhanced view of frontal edema and hemorrhage several days after the insult. This type of pathology is very common in traumatic brain injury.



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

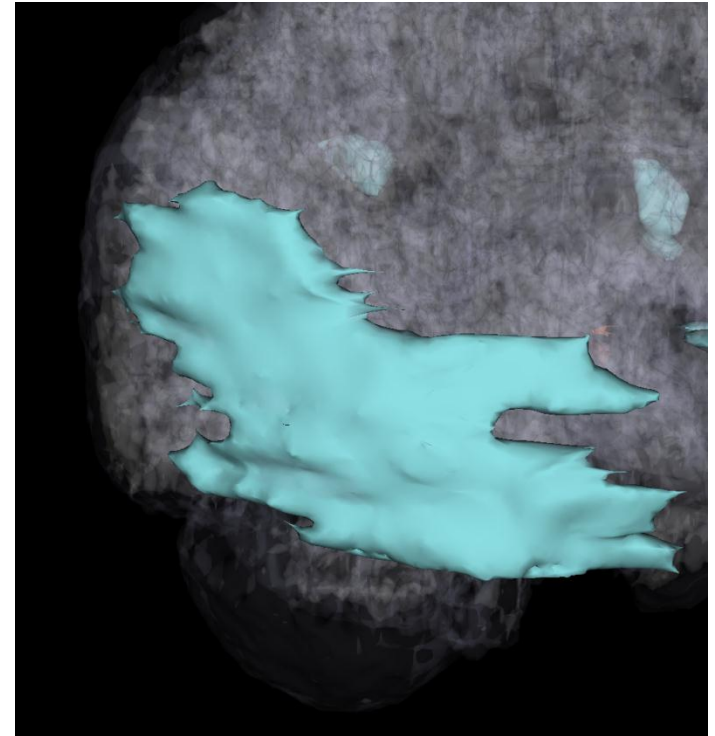


Detailed view of parietal edema (teal) and hemorrhage. It is interesting to note how the non-hemorrhagic edemic region encases the brain portion that is actively bleeding. With recovery, it is expectable for the hemorrhage to shrink in both volume and mass.



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.

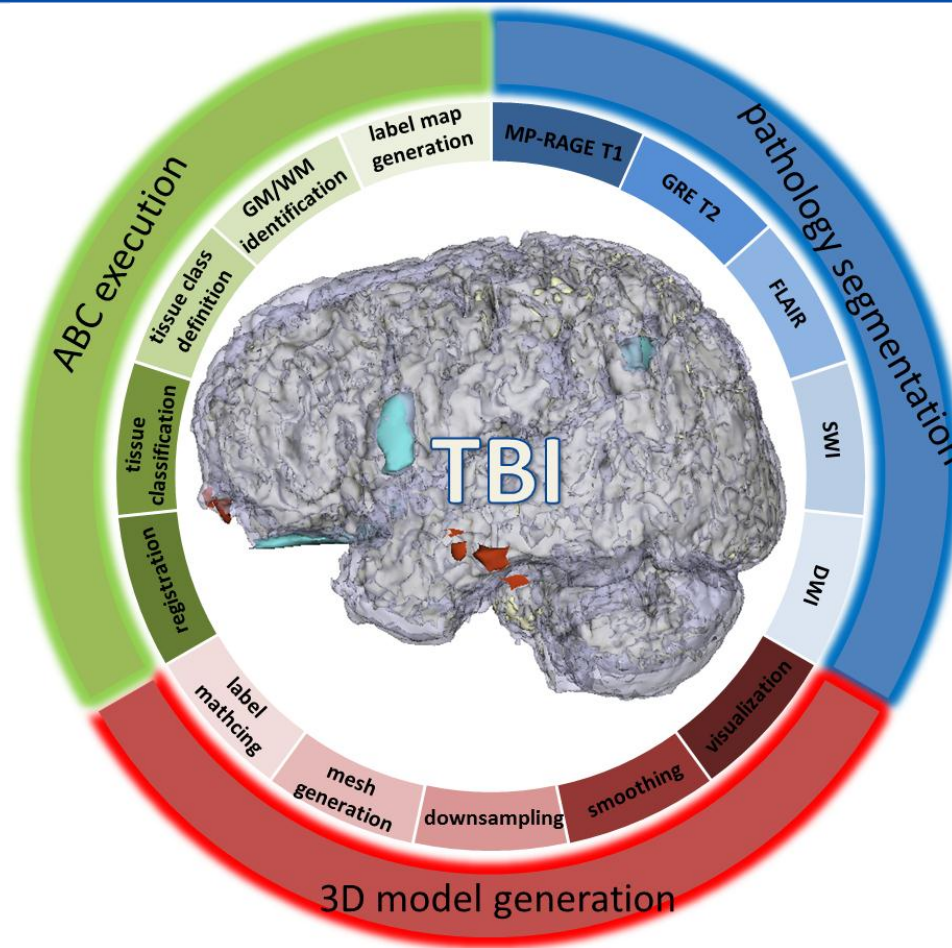


Traumatic Brain Injury (TBI)

- 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



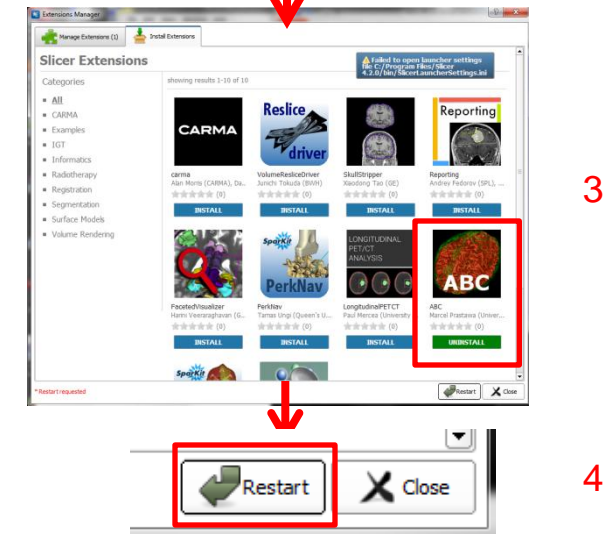
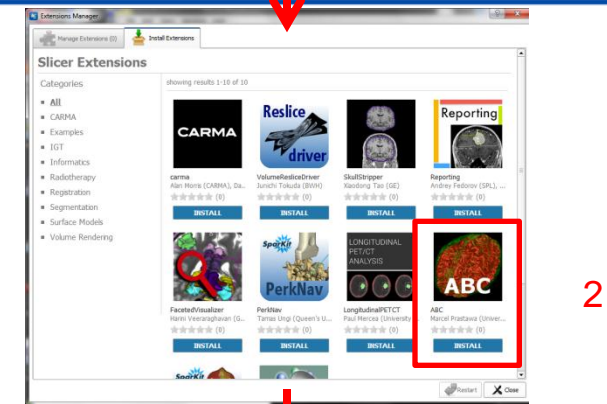
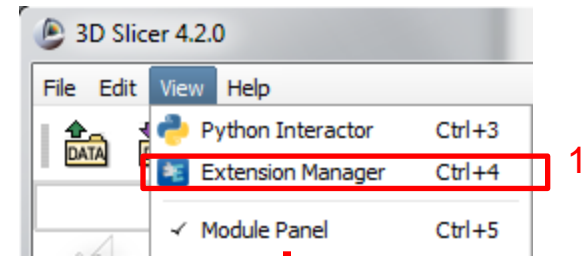
Conceptual Framework





Installing ABC

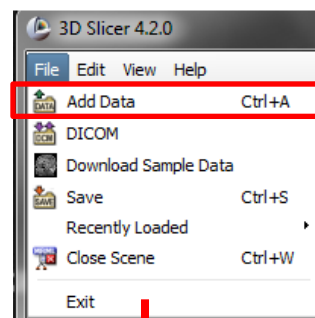
- After Slicer has been loaded, the Welcome window will appear.
- To install the ABC module:
 - 1 – Click on *View* → *Extension Manager*
 - 2 – Click on *ABC* under the *Install Extensions* tab
 - 3 – Click *Install*
 - 4 – Click *Restart* at the bottom right



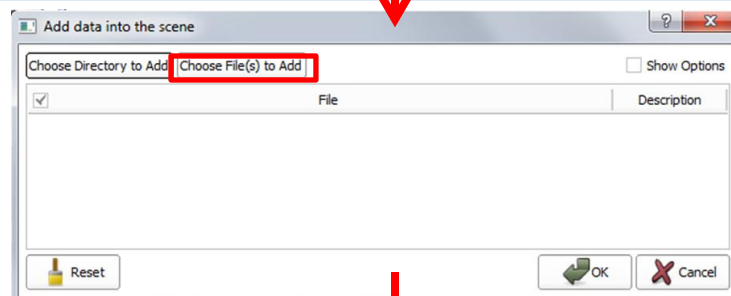


Loading TBI data

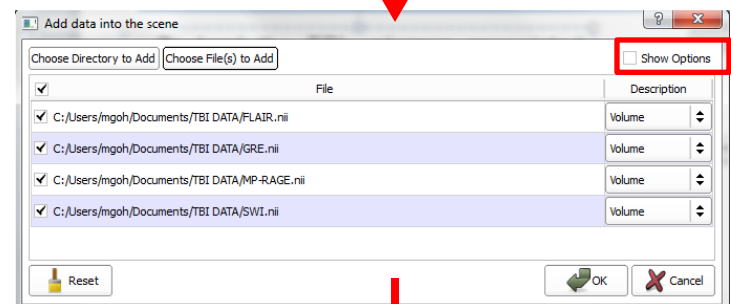
- To load the TBI volumes associated with the case study:
 - 1 – Click on *File* → *Add Data*
 - 2 – Click on *Choose File(s) to add*. Navigate to the data folder and select the desired files to add.
 - 3 – Click on *Show Options*
 - 4 – In the *Add Data* dialog box, check all the boxes that say *Centered*. This will ensure all volumes are centered about the same origin.



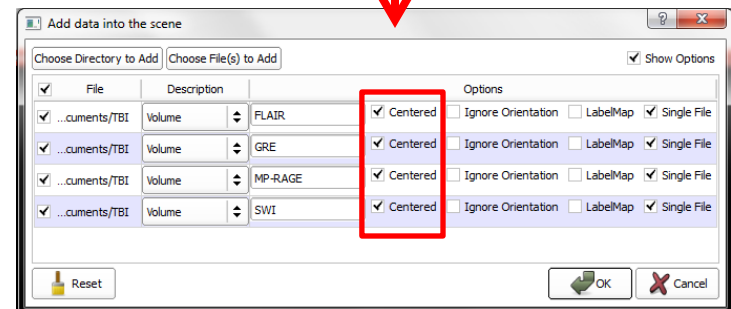
1



2






3

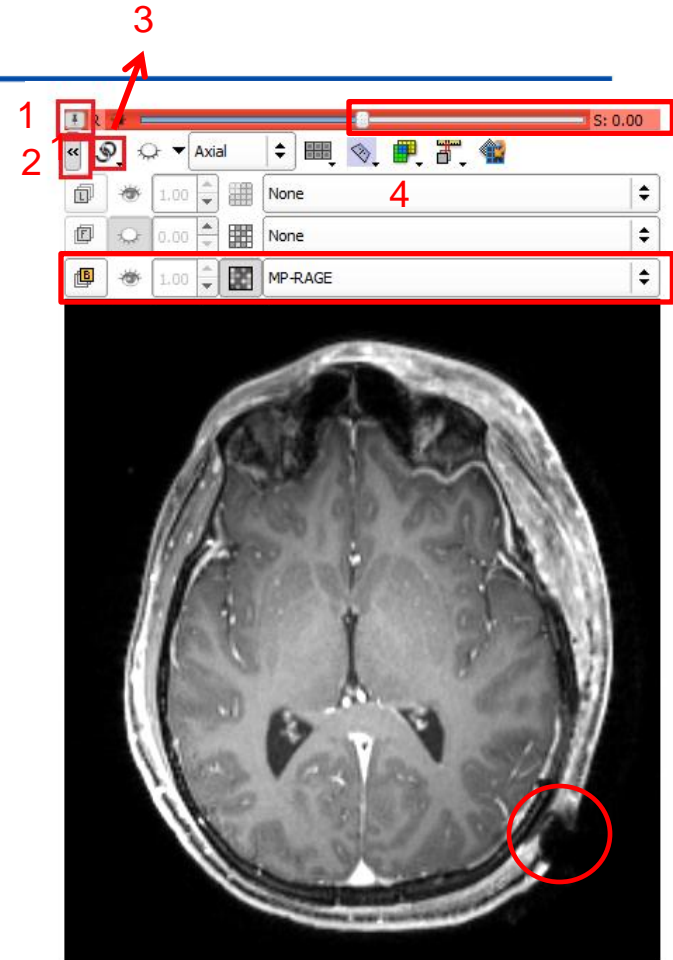


4



Exploring the data

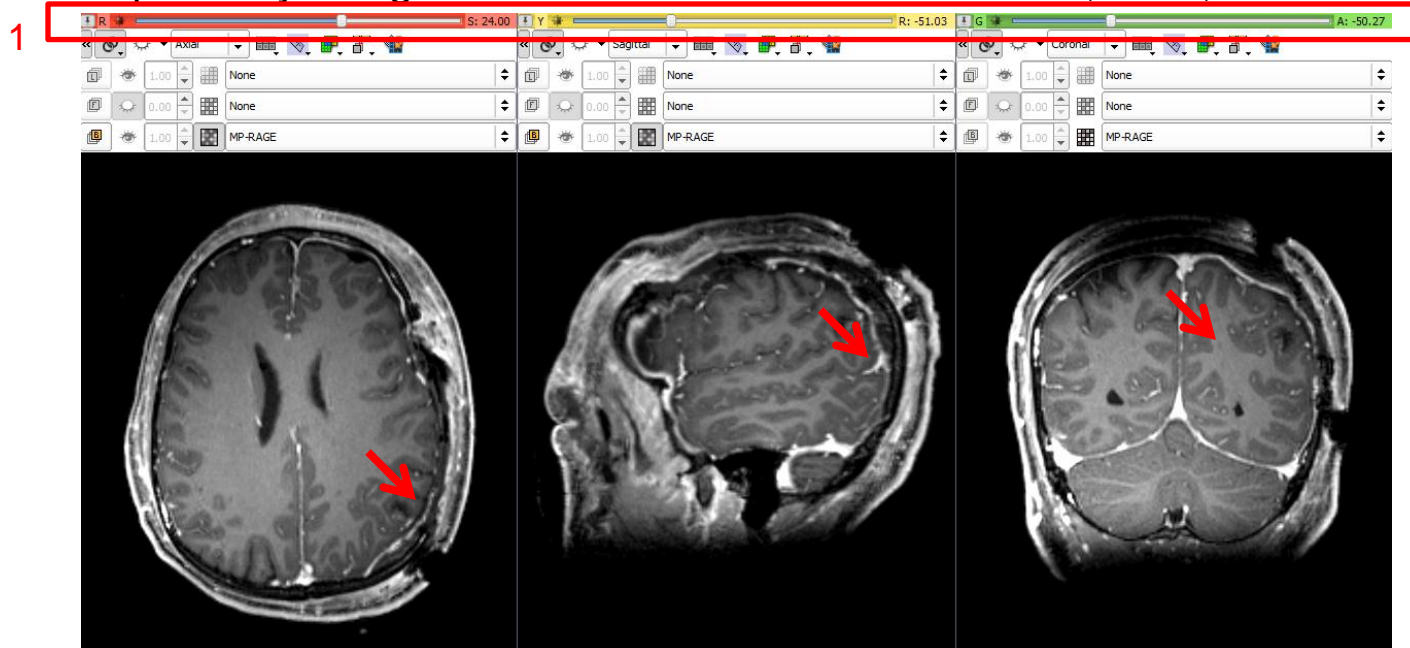
- 4 TBI data volumes are provided for this tutorial: MP-RAGE, FLAIR, GRE, and SWI.
- MP-RAGE: this is an anatomical volume acquired using a T1-weighted sequence, in which white matter has higher intensity than gray matter
 - To explore a TBI-related lesion in this patient:
 - 1 – Hover over  to reveal the dropdown menu. (Click to pin the menu)
 - 2 – Click () to reveal more menu options
 - 3 – Link the views using ()
 - 4 – Select the MP-RAGE.nii volume from the background drop-down menu and navigate to slice 0 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)





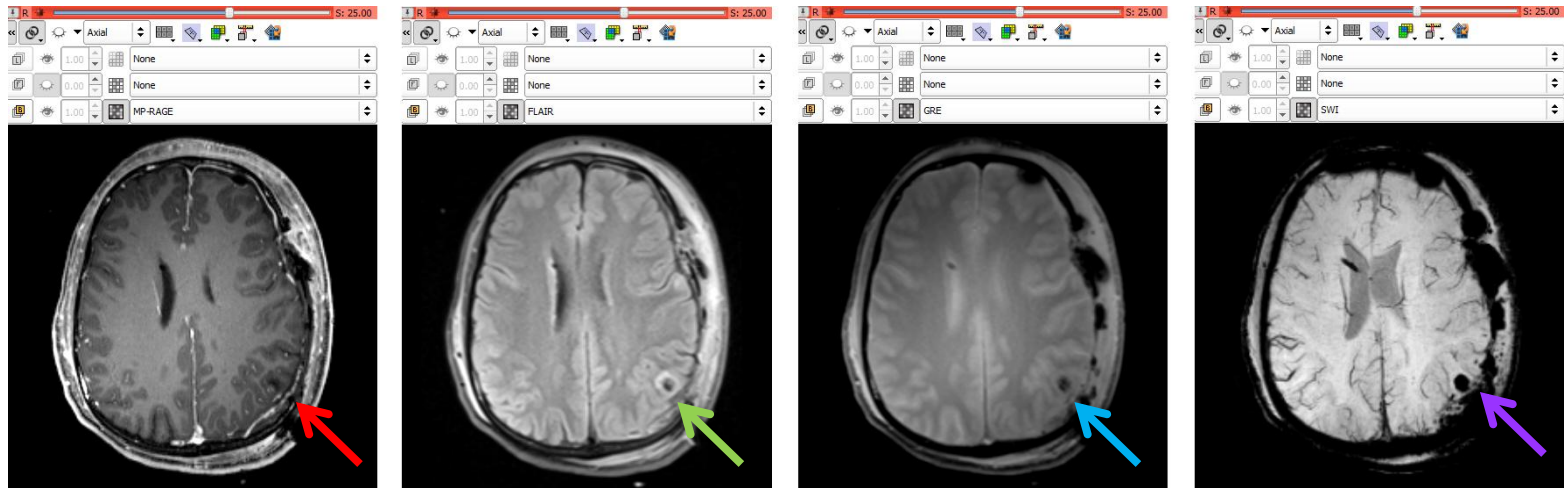
Exploring the data

- To locate the lesion more accurately within the head:
 - 1 – **navigate** to the following slices using the sliders:
 - Slice 24 in the **axial** view, -51 in the **sagittal** view, and 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

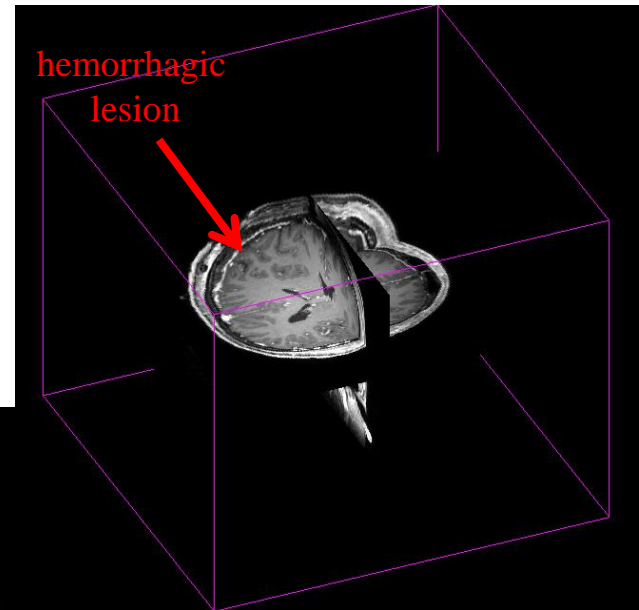
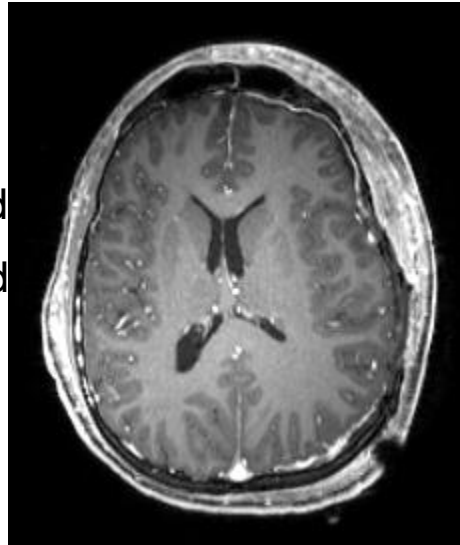
SWI

- 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



Sequence types: **MP-RAGE**

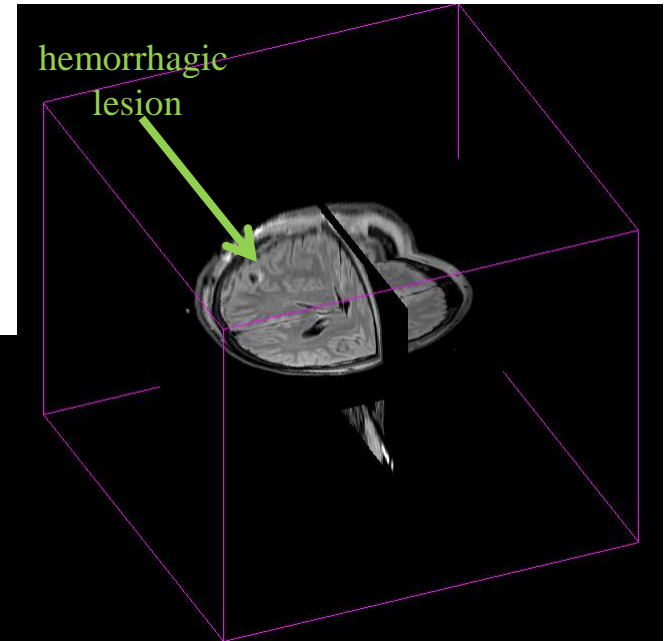
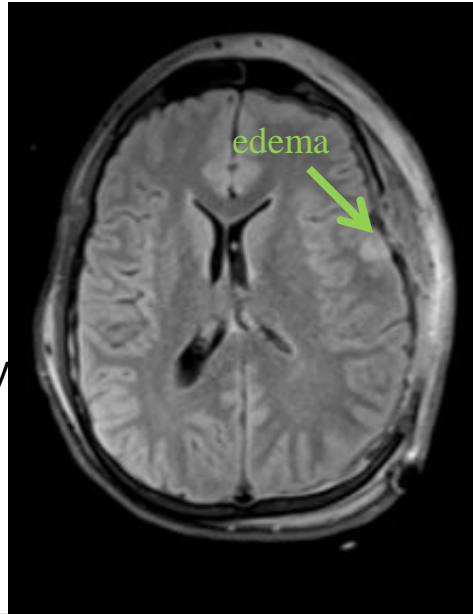
- MP-RAGE = magnetization prepared rapid gradient echo
- This sequence is a fast 3D gradient echo sequence designed for rapid acquisition with T1-weighted dominance, rapid sampling time, high signal intensity and contrast
- Although ideal for the acquisition of anatomical data sets, the abilities of this sequence to detect TBI-related pathology is very limited and its use must usually be complemented by other sequences





Sequence types: FLAIR

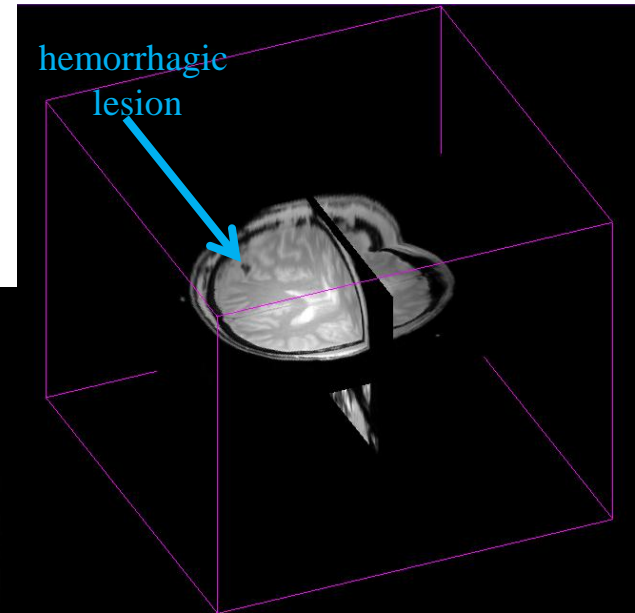
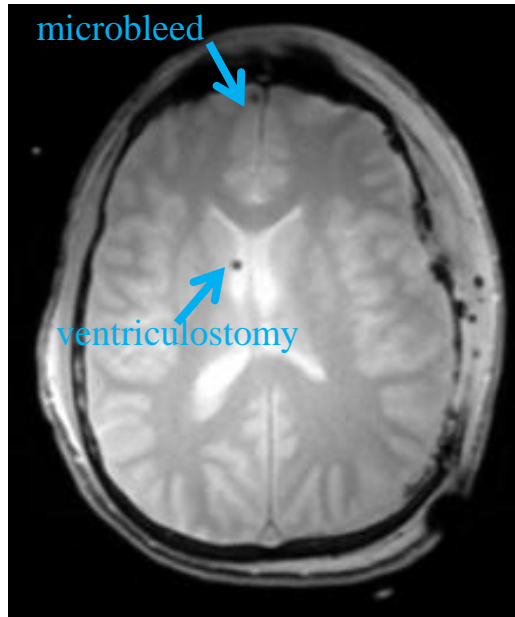
- FLAIR = fluid attenuation inversion recovery
- This sequence is an inversion recovery sequence with long TI adjusted to the TR of a fluid type whose effect is sought to be removed from the result image
- Hyperintensities in FLAIR images are indicative of CSF-perfused, edemic cortical tissue
- Compared to other sequences, FLAIR is not very useful for hemorrhage detection





Sequence types: GRE T2

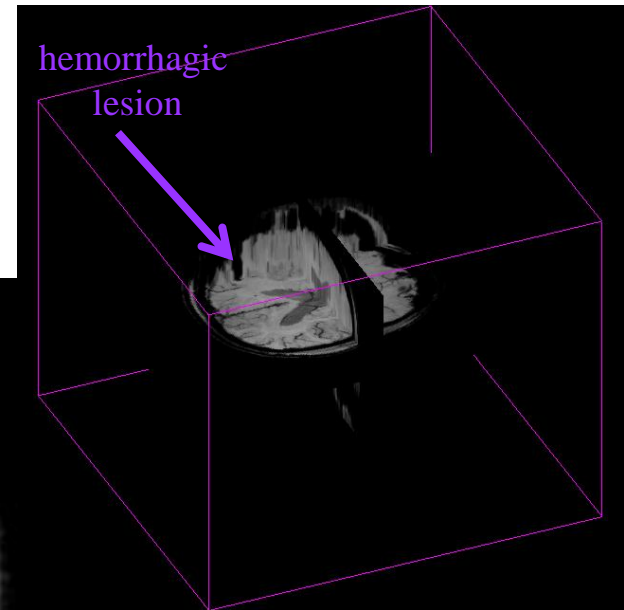
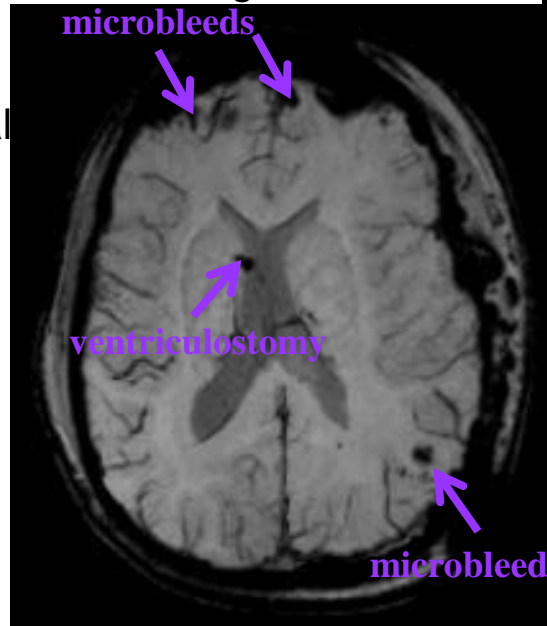
- GRE = gradient recalled echo
- This T2 weighted sequence has some very useful, though rather limited, ability to identify hemorrhage
- In our dataset, it can identify one microbleed in the frontal lobe, as well as the ventriculostomy
- Some studies have proposed that, although useful, GRE T2 sequences are not as sensitive to microbleeds as SWI





Sequence types: SWI

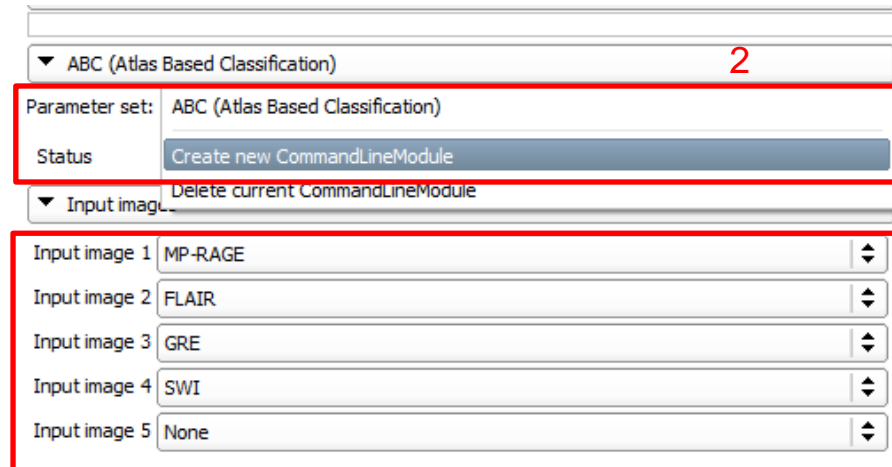
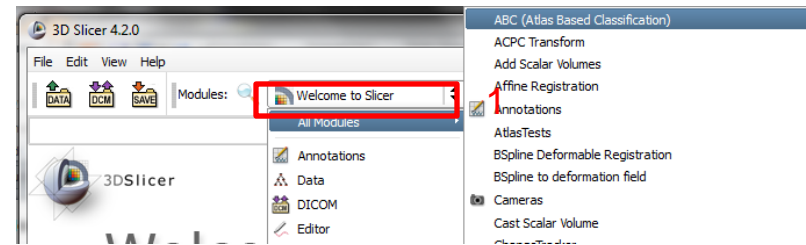
- SWI = susceptibility weighted imaging
- This sequence exploits susceptibility differences between tissues to create an enhanced contrast magnitude image which is exquisitely sensitive to venous blood, bleeds, and iron storage
- In our dataset, this sequence identifies several micro-bleeds as well as the ventriculostomy
- SWI is a classical sequence used for TBI imaging which can reveal the path of the ventriculostomy






Configure ABC

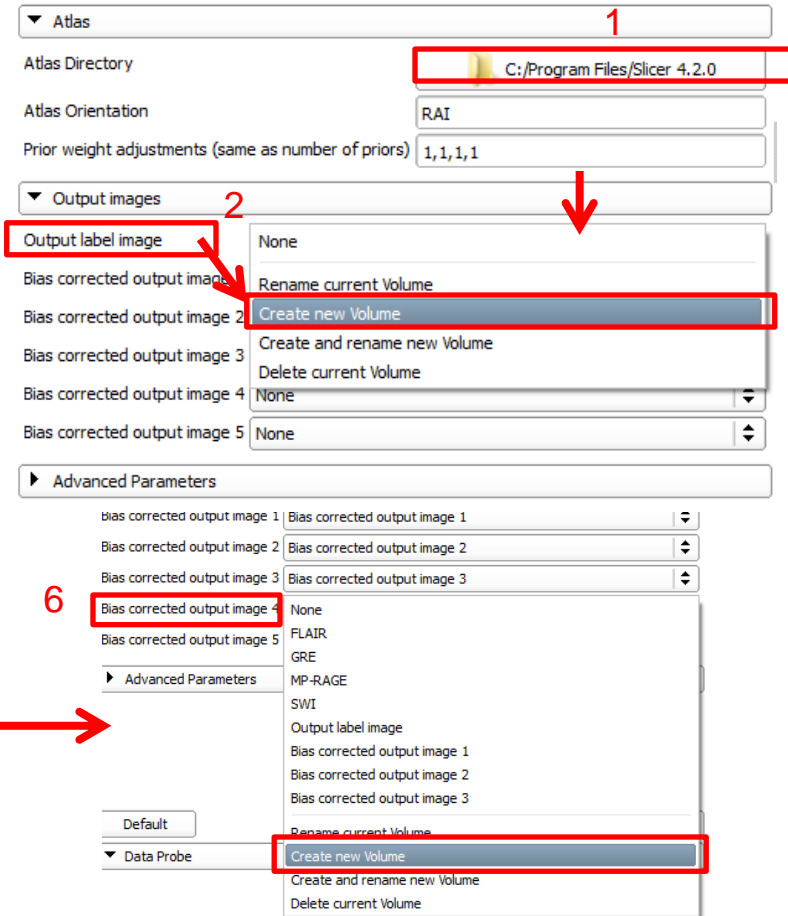
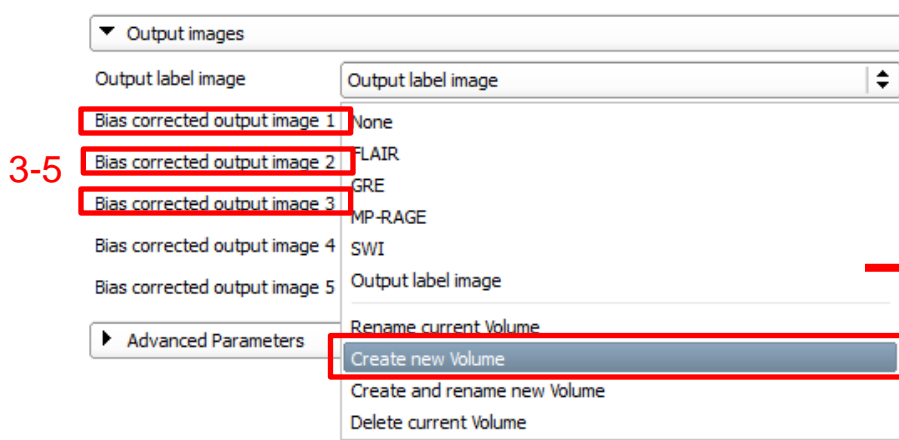
- To load ABC, click on:
 - 1 – *Welcome to Slicer* → *All Modules* → *ABC*
- The ABC interface appears on the left. To specify input data:
 - 2 – click *ABC (Atlas Based Classification)* → *Create New Command Line Module*
 - 3 – click *Input image 1* → *MP-RAGE.nii*
 - 4 – click *Input image 2* → *FLAIR.nii*
 - 5 – click *Input image 3* → *GRE.nii*
 - 6 – click *Input image 4* → *SWI.nii*





Configure ABC

- 1 – click on  to locate and select the *adult-atlas* directory, which was included in the tutorial data set
- 2 – click the dropdown menu under *Output label image*, then *Create New Volume*
- 3 – click *Bias corrected output image 1* → *Create New Volume*
- 4 – click *Bias corrected output image 2* → *Create New Volume*
- 5 – click *Bias corrected output image 3* → *Create New Volume*
- 6 – 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

Advanced Parameters 1

PreFiltering method: Curvature flow Grad aniso diffusion

PreFiltering iterations (0 = off): 1

PreFiltering time steps: 0.01

Bias Field Polynomial Degree (0 = off): 4

Initial distribution estimator: robust standard

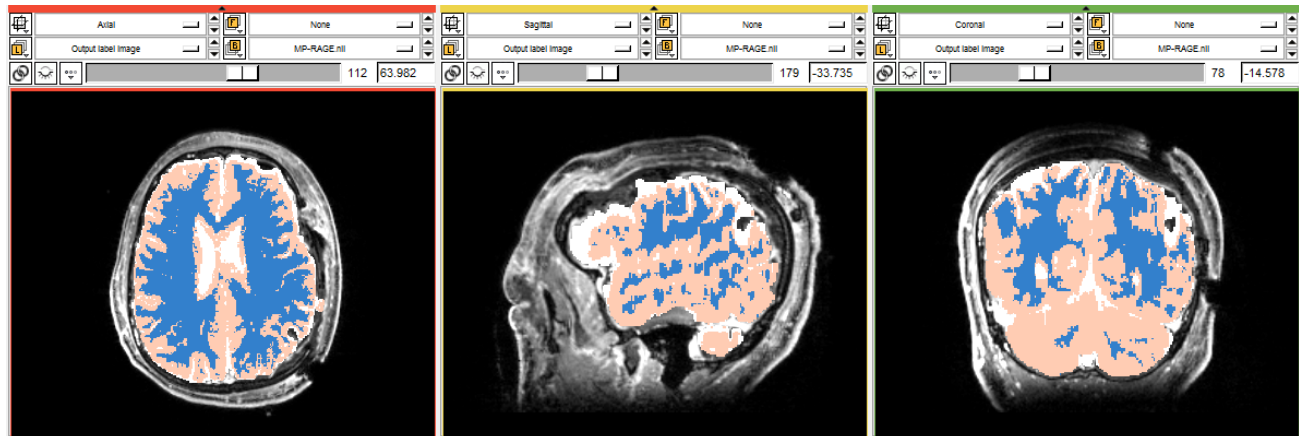
Atlas Transform Type: affine rigid identity

Coregistration Transform Type: affine rigid identity 2

Atlas Warping Fluid Iterations (0 = off): 0

Atlas Warping Fluid Maximum Step: 0.5

Cancel Apply 3



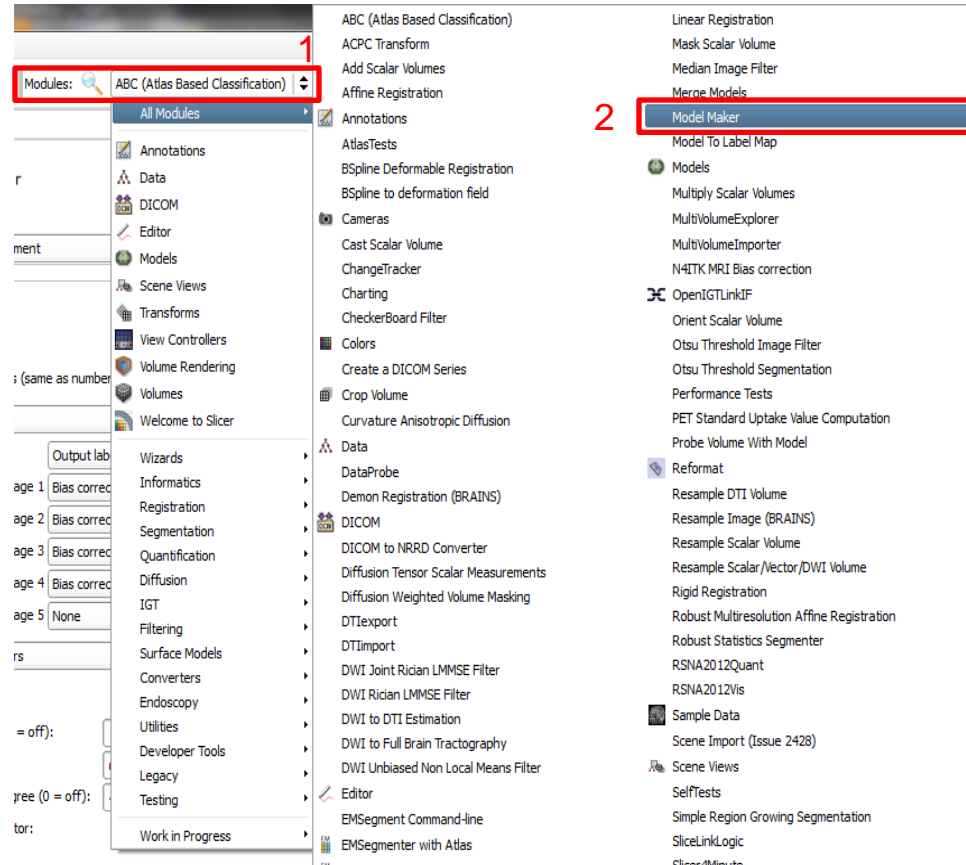


Generate 3D Models

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.



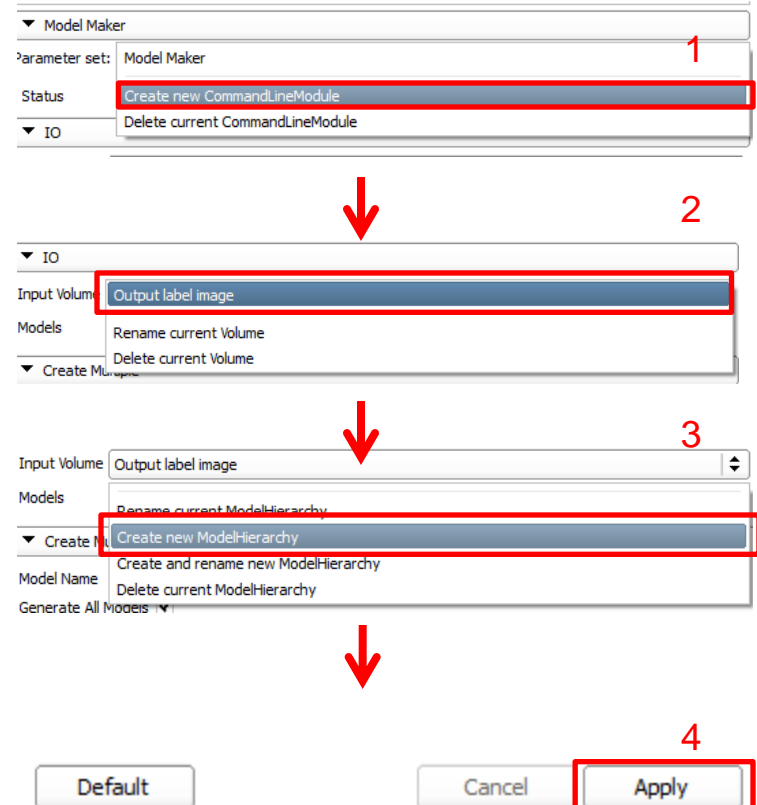


Generate 3D Models

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.

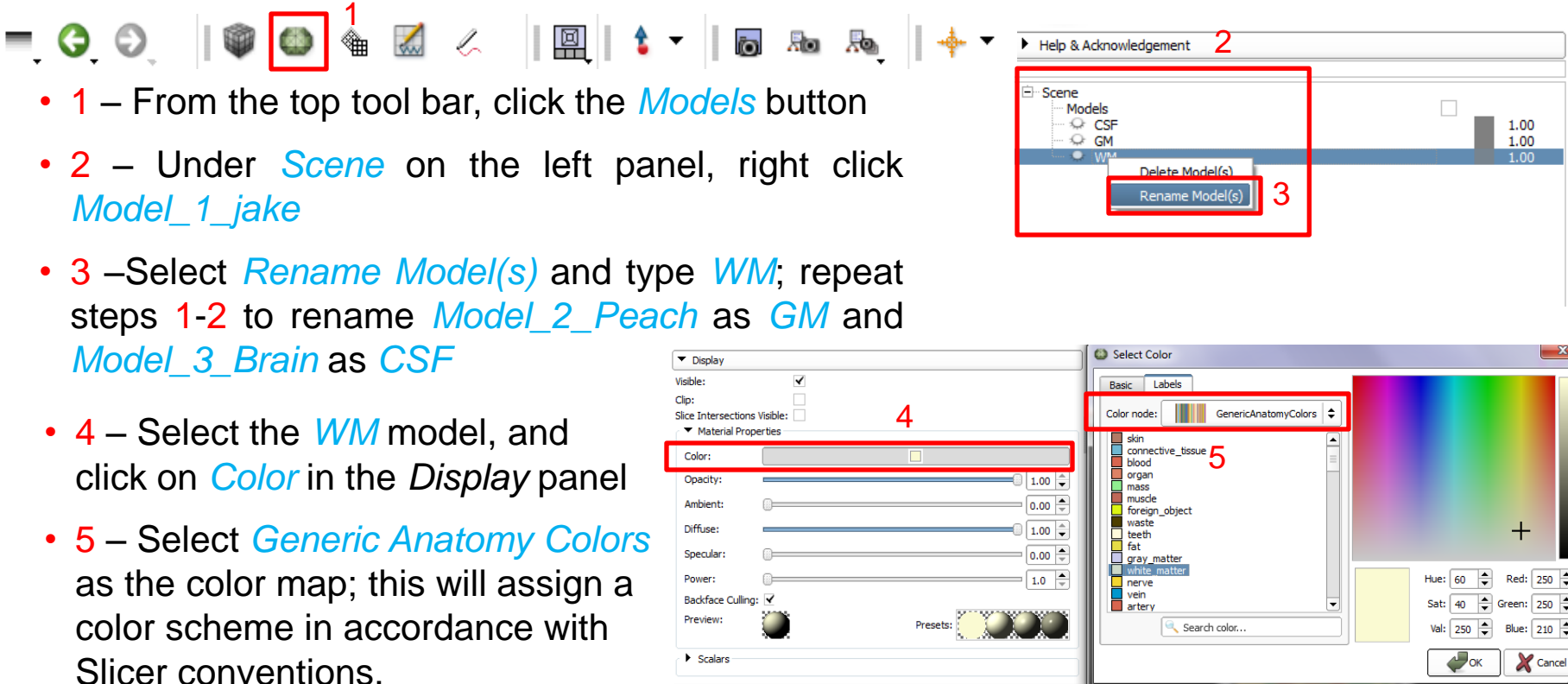




Choose color map scheme

To choose an appropriate color map for the models:

- **1** – From the top tool bar, click the *Models* button
- **2** – Under *Scene* on the left panel, right click *Model_1_jake*
- **3** – Select *Rename Model(s)* and type *WM*; repeat steps **1-2** to rename *Model_2_Peach* as *GM* and *Model_3_Brain* as *CSF*
- **4** – Select the *WM* model, and click on *Color* in the *Display* panel
- **5** – Select *Generic Anatomy Colors* as the color map; this will assign a color scheme in accordance with Slicer conventions.





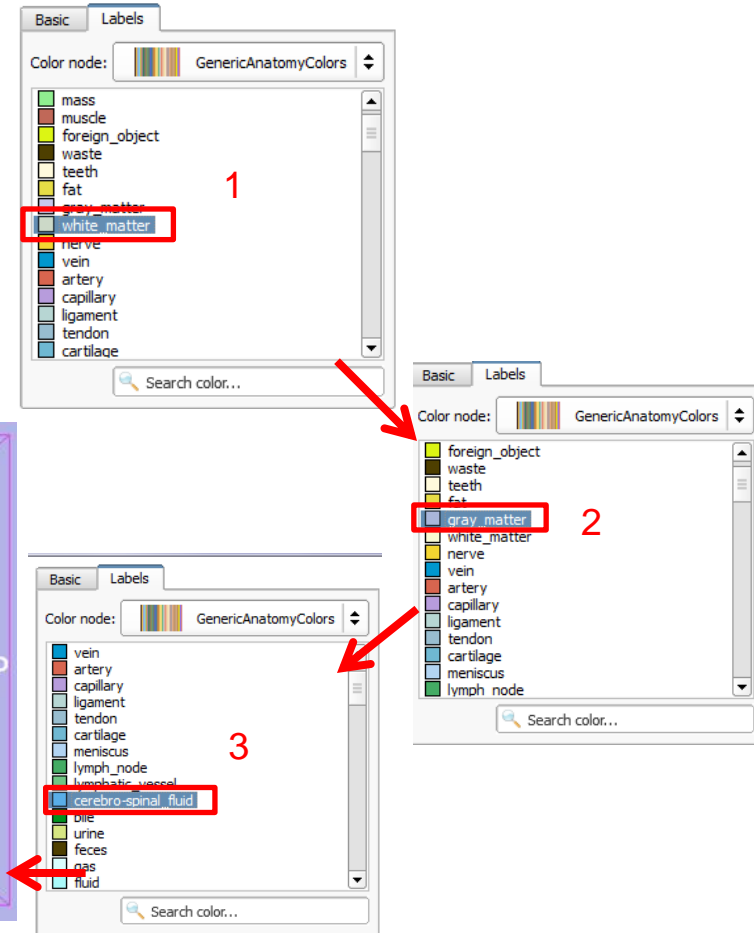
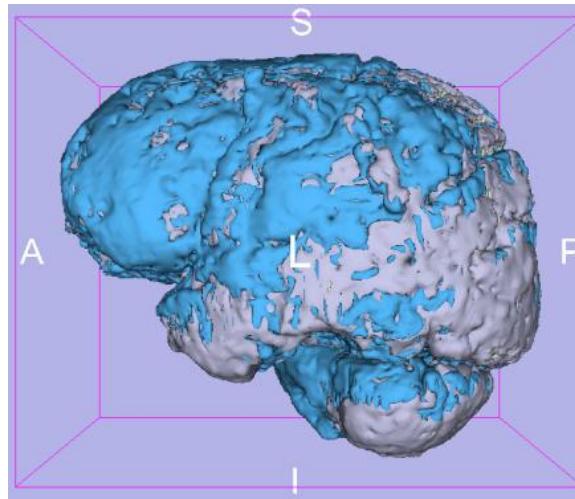
Choose color map scheme

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.





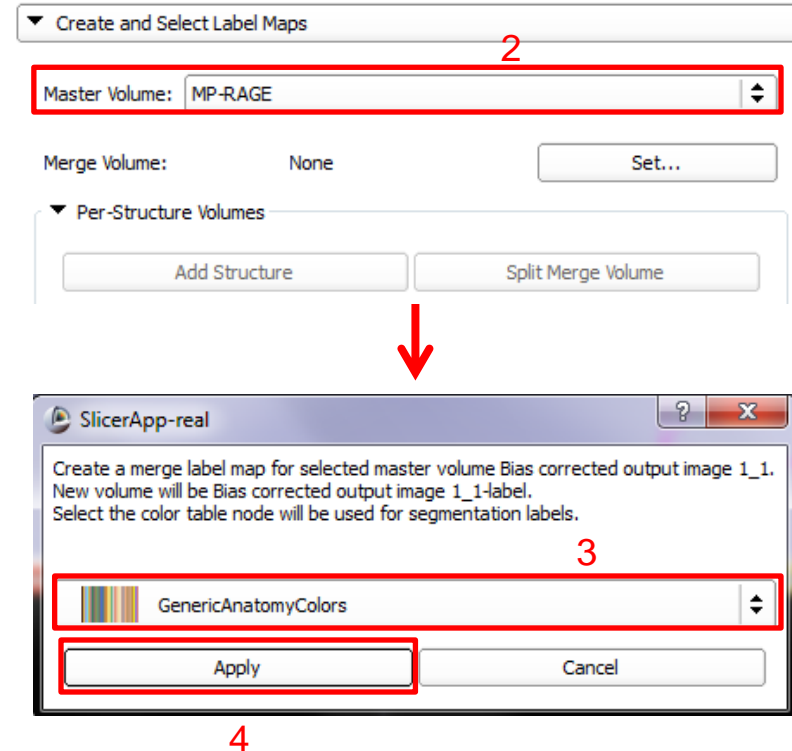
Create labels for pathology

We can now create a label map for pathology:



- 1 – From the tool bar, click on the *Editor* button
- 2 – On the left panel, set *Master Volume* to *MP-RAGE*
- 3 – In the pop up window, select *General Anatomy Colors*
- 4 – Click *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*

The screenshot shows the Slicer software interface. At the top, the 'Edit Selected Label Map' toolbar is visible. A red box labeled '1' highlights the 'Level Tracing' icon (a green square with a white grid). Below the toolbar, the 'Active Tool' is set to 'DefaultTool'. The 'Label:' field shows 'tissue' and '1', with a red box labeled '2' around the color selection area. Below this, the 'Color Box' dialog is open, showing a list of labels. A red box labeled '3' highlights the row for '31: edema'.

Number	Color	Name
...24		lymphatic_vessel
...25		cerebro-spinal_fluid
...26		bile
...27		urine
...28		feces
...29		gas
...30		fluid
31		edema
...32		bleeding
...33		necrosis
...34		clot
...35		embolism
...36		head
...37		central_nervous_system



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 16-18. The hypointense region in the middle is actually hemorrhage, but it will be segmented separately in following steps

The screenshot shows the Slicer software interface. The volume list on the left has 'FLAIR' selected and highlighted with a red box (1). The toolbar on the right has a menu icon highlighted with a red box (2). The layout menu on the right has 'Red slice only' selected and highlighted with a red box (3). The main image window shows an axial FLAIR MRI slice with a yellow level tracing tool applied to a hyperintense region (4). A red arrow points from the toolbar menu icon to the layout menu.



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, mouse over the arrows (a) on the *label map* (b) bar.
- 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.

The screenshot shows the 3D Slicer interface. At the top, the 'MP-RAGE-label_1' bar is visible, with arrows (a) and a slider (b) highlighted. A red arrow (1) points to the 'MP-RAGE-label_1' bar. A red arrow (2) points to the slider. A red arrow (3) points to the 'Color Box' dialog box. The 'Color Box' dialog box shows a table of labels with '32: bleeding' selected.

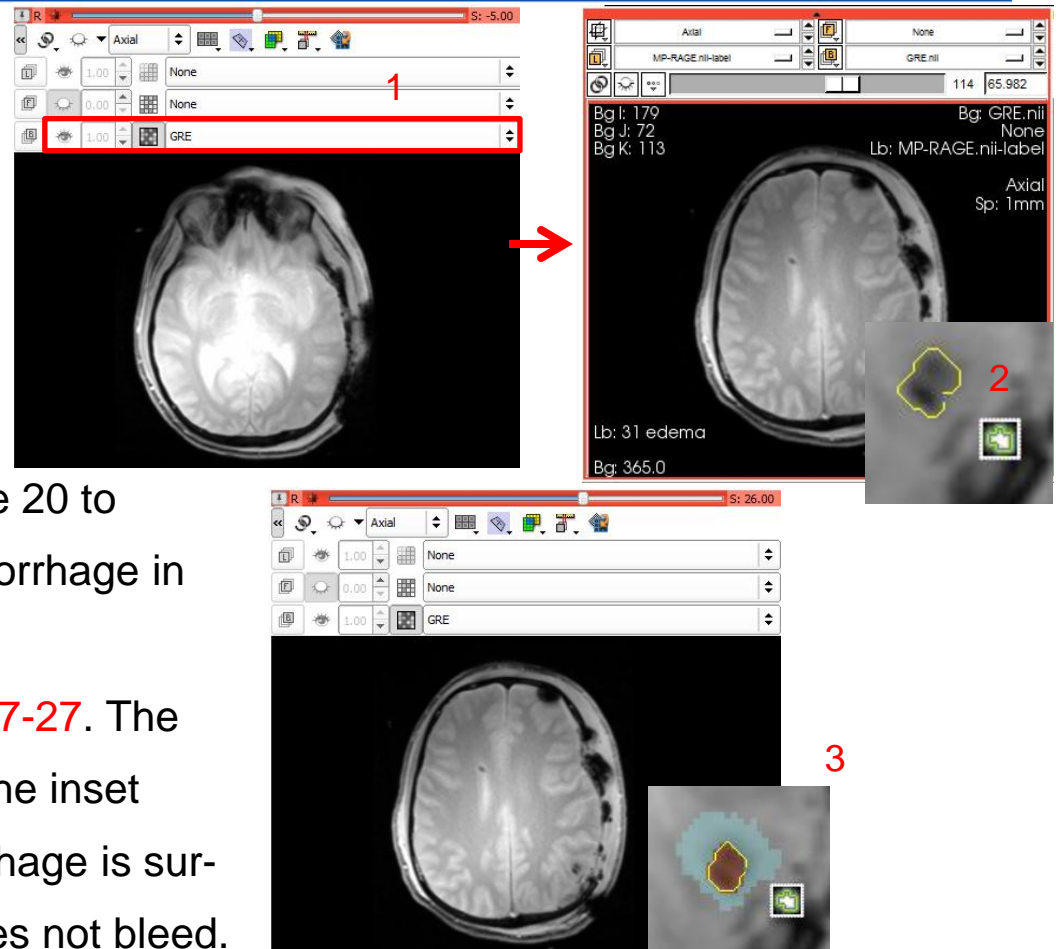
Number	Color	Name
28	dark green	feces
29	light blue	gas
30	light blue	fluid
31	light blue	edema
32	red	bleeding
33	dark red	necrosis
34	dark red	clot
35	dark red	embolism
36	dark red	head
37	yellow	central_nervous_system
38	yellow	brain
39	gray	gray_matter_of_brain
40	green	telencephalon
41	green	cerebral_cortex



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 17-27. 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*
- 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*

The screenshot displays the software interface for creating 3D models. The interface is divided into several panels. Panel 1 (left) shows a menu with 'Conventional' selected. Panel 2 (top right) shows the 'Input Volume' dropdown set to 'MP-RAGE.nii-label'. Panel 3 (middle right) shows the 'Models' dropdown with 'Create new ModelHierarchy' selected. Panel 4 (bottom right) shows the 'Model Maker Parameters' section with 'Labels' set to '31,32'. Red arrows and numbers 1-5 indicate the sequence of actions.



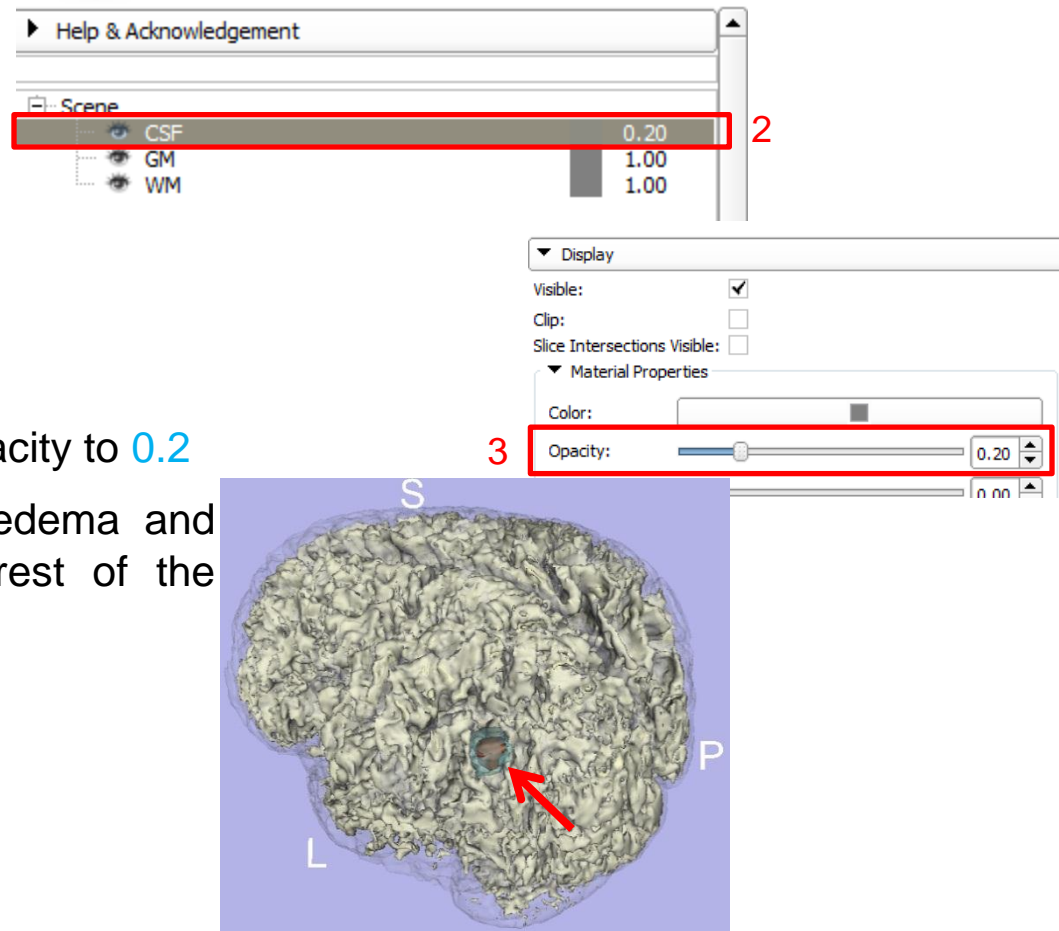
Visualize full 3D model

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



- 1 – On the tool bar, click Models
- 2 – Under *Scene*, select *CSF*
- 3 – Under *Display*, 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.





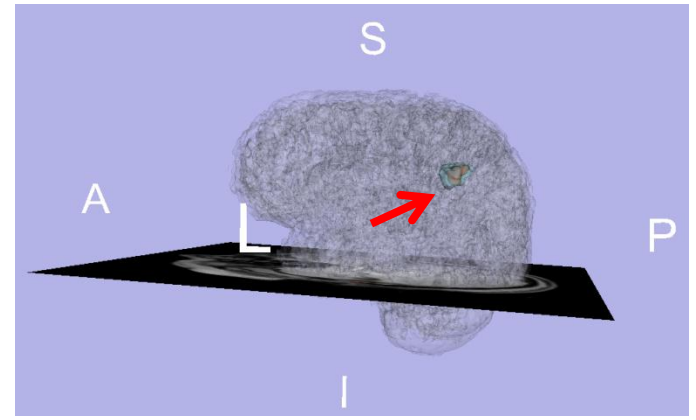
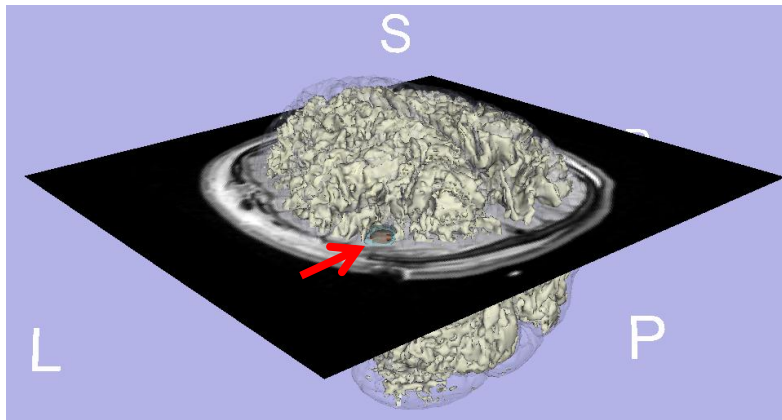
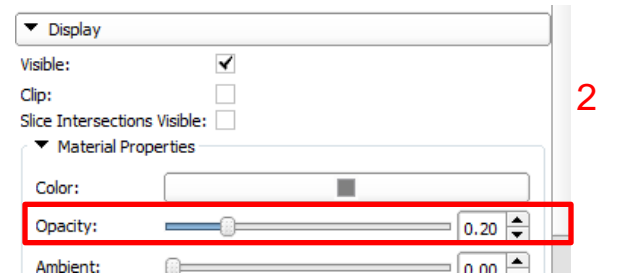
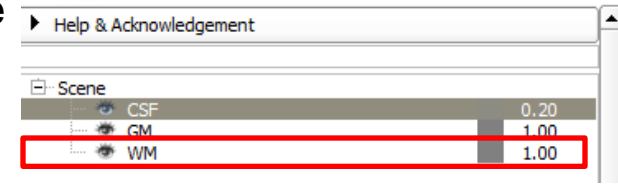
Exploring the results

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)

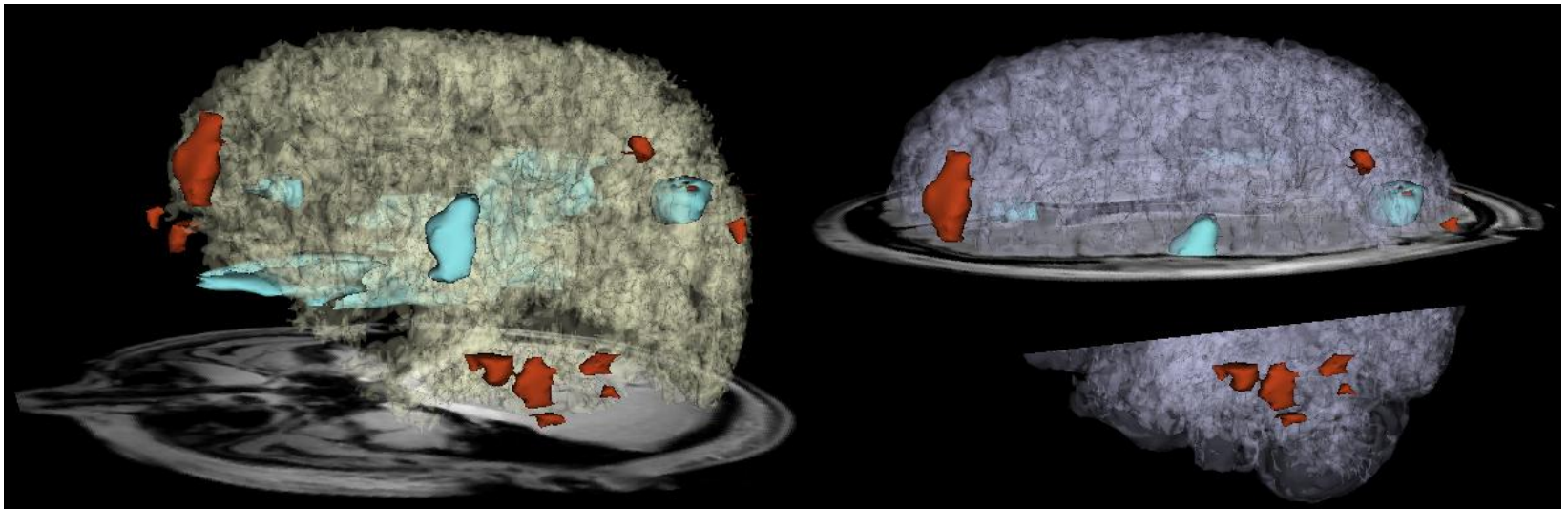
- 2 – Under *Hierarchy and Display*, set *WM* opacity to 0.2





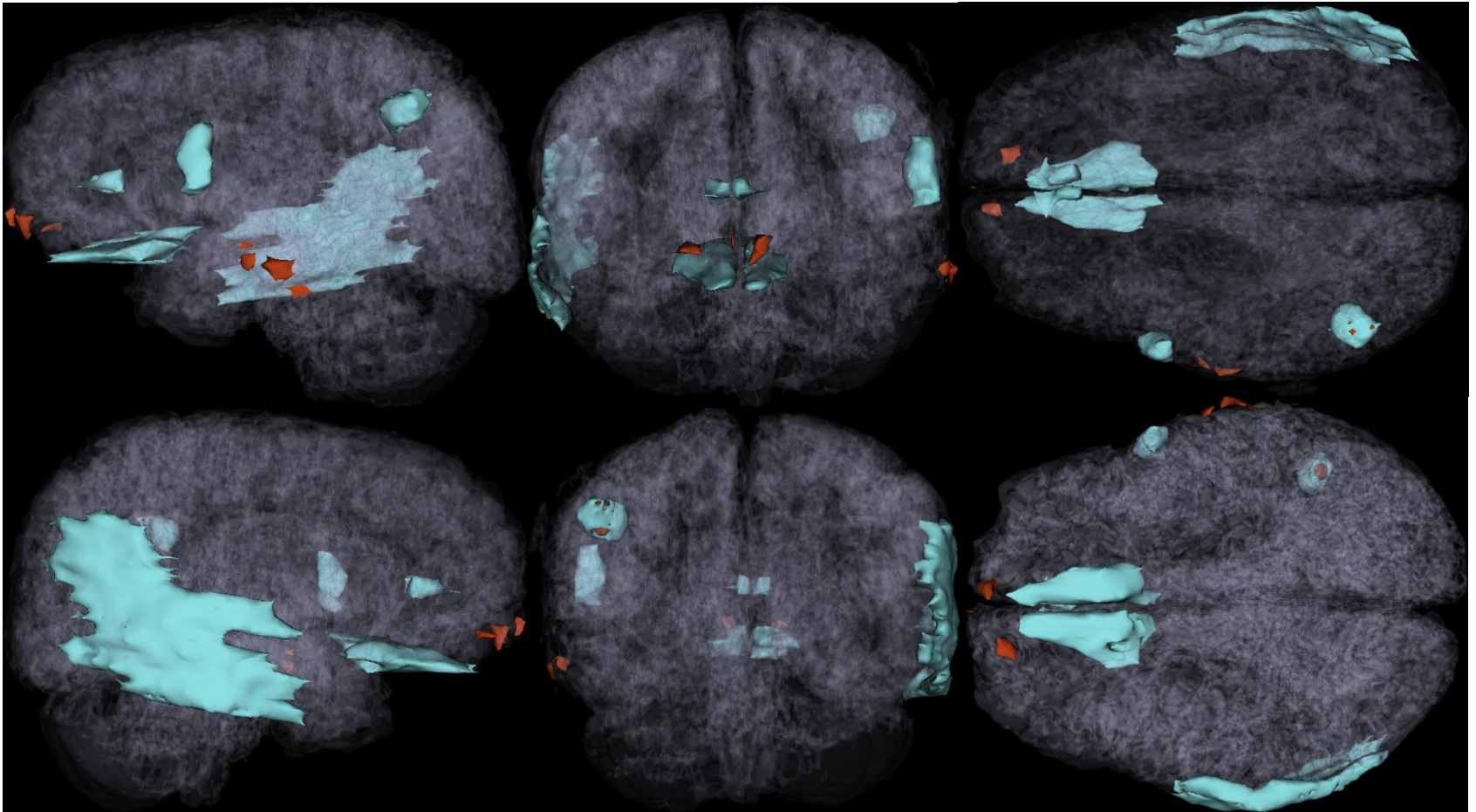
The complete model

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.



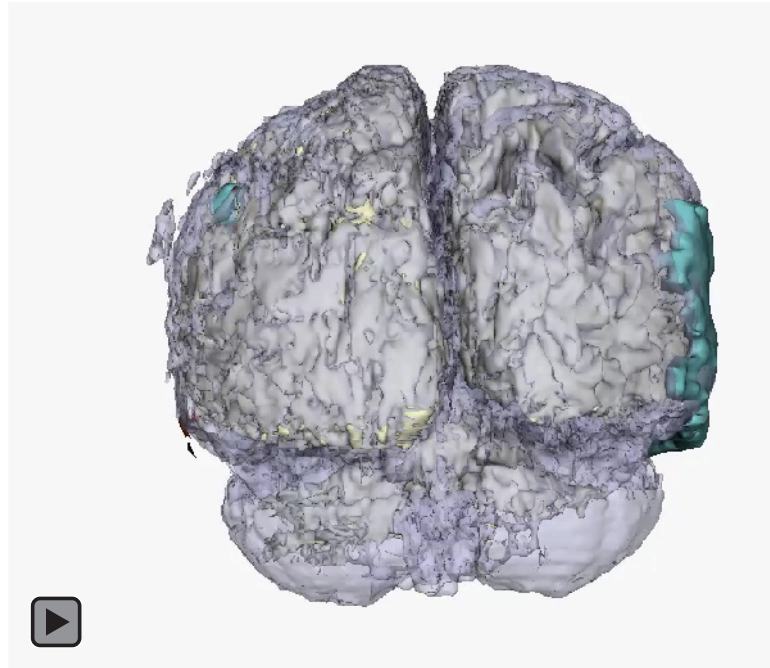


The complete model





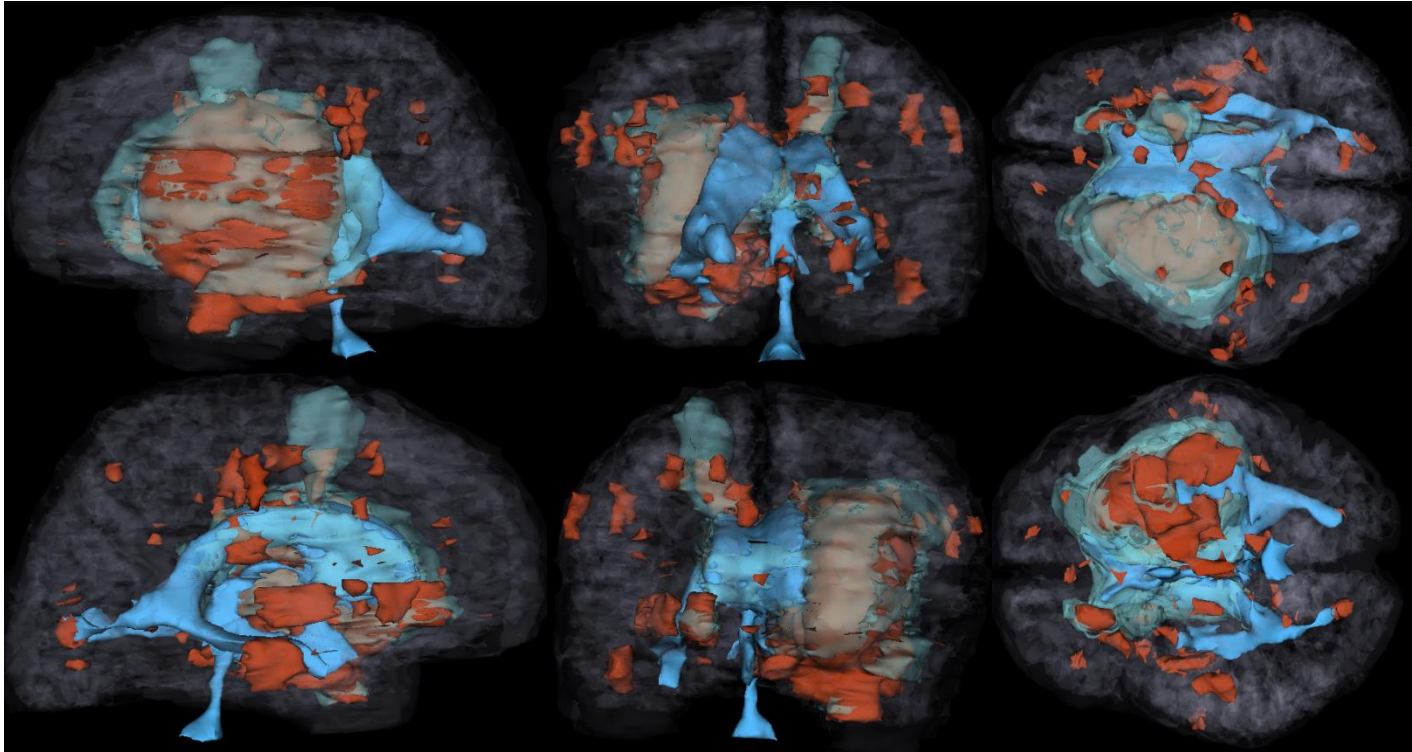
Complete model animation



Click on image to play



Example of severe TBI segmentation



Download movie of this subject's segmentation from link below:

<http://wiki.na-mic.org/Wiki/index.php/File:TBIsegmentation-Subject2.avi>



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
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