



NA -MIC

National Alliance for Medical Image Computing

<http://na-mic.org>

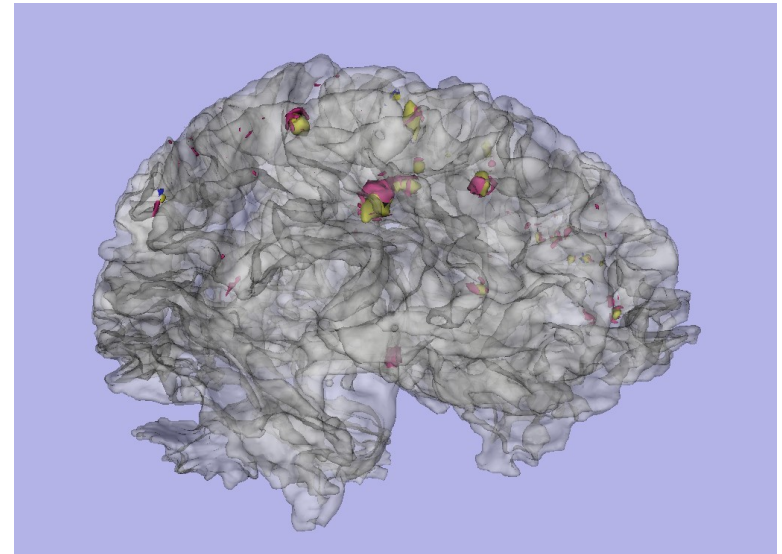
Longitudinal Lesion Comparison

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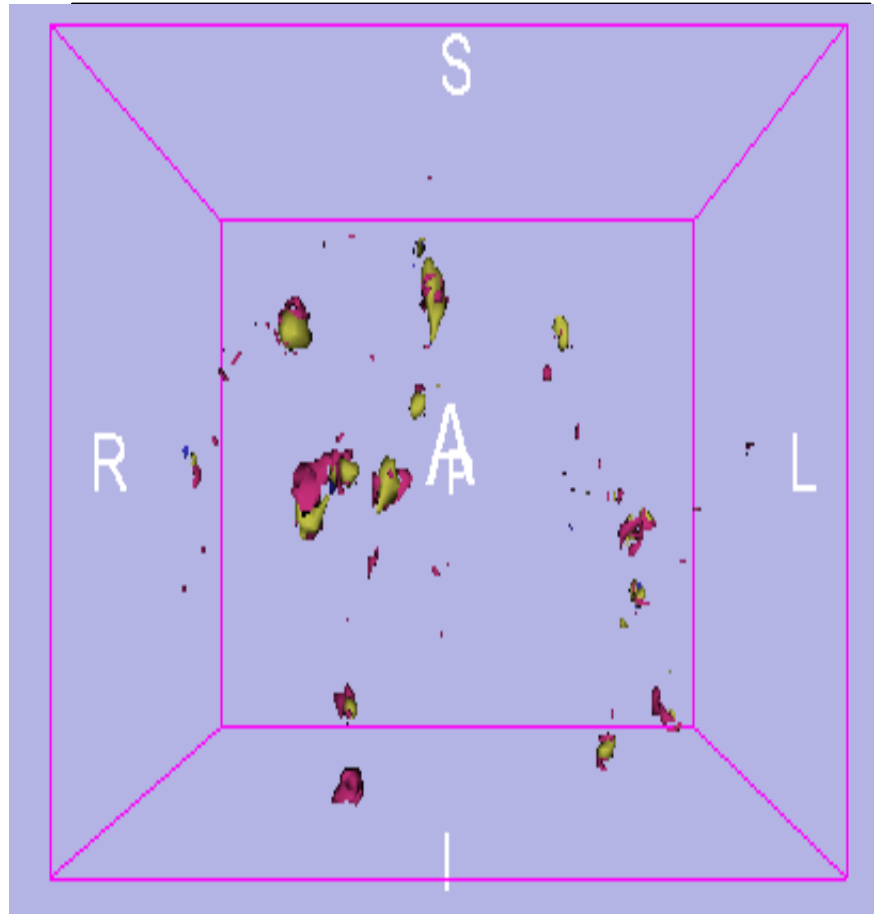


NA-MIC Tutorial Contest:
Summer 2010



Learning Objective

After following this tutorial, you will be able to use Slicer3 to create models that allow you to analyze the changes in white matter lesions between two time points.





Pre-requisite

• This tutorial assumes the user is familiar with loading image datasets and creating basic label maps in Slicer. Please consult the following prerequisite material if you want to brush up on these skills first:

- Data Loading & Visualization tutorial
SoniaPujol, Ph.D., Harvard/SPL
 - http://www.slicer.org/slicerWiki/images/c/c9/3DDataLoadingAndVisualization_Slicer3.6_SoniaPujol.pdf
- User documentation for the Slicer3 Editor module
StevePieper, Ph.D, Harvard/SPL, Isomics
 - <http://www.slicer.org/slicerWiki/index.php/Modules:Editor-Documentation-3.6>



About the Tutorial Data

- This tutorial provides data that has had a time1 and time 2 white matter lesion detection and co-registration performed on the raw images on your behalf. Please consult the following prerequisite material if you want to brush up on these steps first; however, these steps are not required in order to perform the steps in this tutorial:
 - White Matter Lesion Segmentation tutorial, H. Jeremy Bockholt:
 - http://www.na-mic.org/Wiki/index.php/File:Slicer3Training_WhiteMatterLesions_v2.2.1.pdf



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:

[Longitudinal_Lesion_Comparison_TutorialContestSummer2010.zip](#)

Disclaimer: It is the responsibility of the user of Slicer to comply with both the terms of the license and with the applicable laws, regulations, and rules.



Material

- Additionally, you need to use the extensions manager to install the Lesion Comparison module to 3D Slicer. To do accomplish this:
 - Select the Extension Manager from the **View** Menu.
 - Select the **LesionSegmentationApplications**,
 - Click **Download & Install**.
 - After the extension downloads, click **Next**, in the following dialog
 - click **Restart 3D Slicer Now** button.

Select	Status	Name	Category	Description	Home
<input type="checkbox"/>	<input checked="" type="checkbox"/>	ABC			
<input type="checkbox"/>	<input checked="" type="checkbox"/>	EMFiberClusteringModule	Tractography	An EM approach	
<input type="checkbox"/>	<input checked="" type="checkbox"/>	ExampleLoadableGuiLessModule	Examples	An example of i	
<input type="checkbox"/>	<input checked="" type="checkbox"/>	ExampleLoadableModule	Examples	An example of i	
<input type="checkbox"/>	<input checked="" type="checkbox"/>	FuzzySegmentationModule	Segmentation	Segmentation r	
<input type="checkbox"/>	<input checked="" type="checkbox"/>	LabelDiameterEstimation	Statistics		
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	LesionSegmentationApplications			
<input type="checkbox"/>	<input checked="" type="checkbox"/>	plastimatch-slicer			
<input type="checkbox"/>	<input checked="" type="checkbox"/>	PythonSampleScriptedModule	Developer Tools	This is an exam	
<input type="checkbox"/>	<input checked="" type="checkbox"/>	ShellSegmentationModule	Segmentation		



Platform

- The Longitudinal Lesion Comparison Module was developed using both Linux (32 and 64 bit) and Mac (OS X 10.4 – 10.6)
- The module has been tested on both Linux 64-bit and Mac (OS X 10.6)



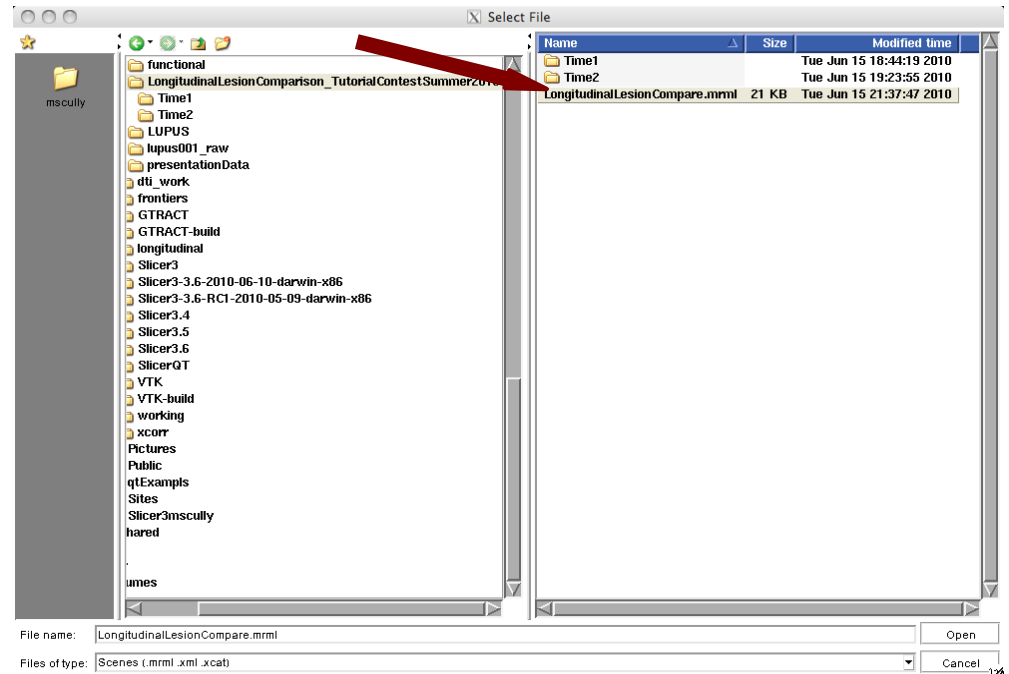
Overview

- Loading the data.
- Creating the image showing lesion changes
- Creating models of the changed lesions
- Examining lesion changes



Loading The Data - I

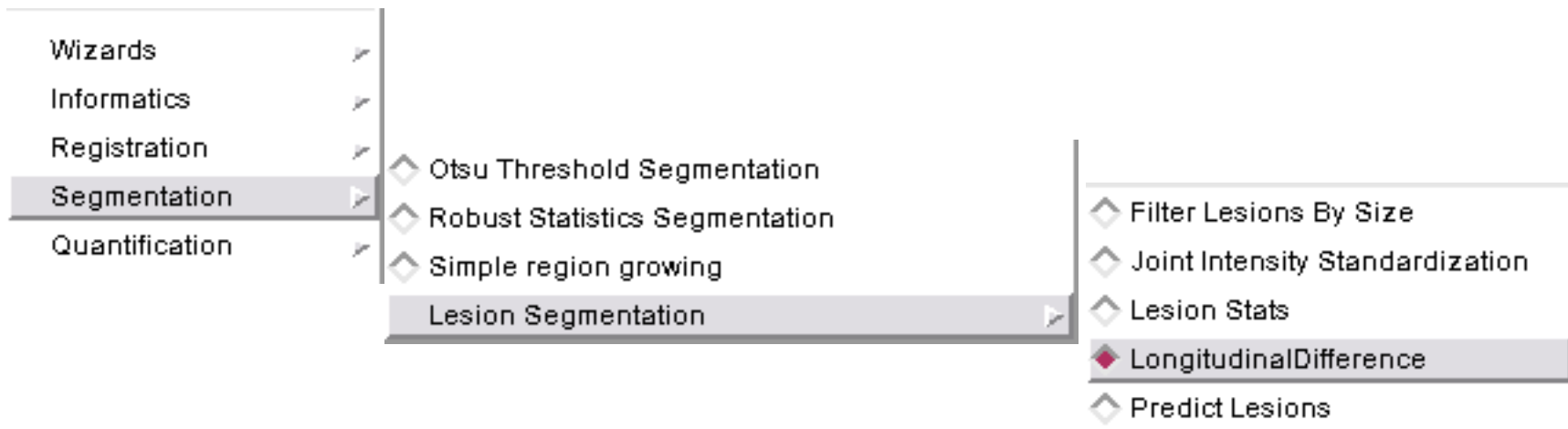
- After downloading the tutorial data, unzip it to a local directory on the computer where 3d Slicer has been installed.
- From the 3d Slicer Menu,
 - select **File**,
 - select **Load Scene**
 - Open the included mrml scene from the tutorial data set.





Lesion Changes Image - I

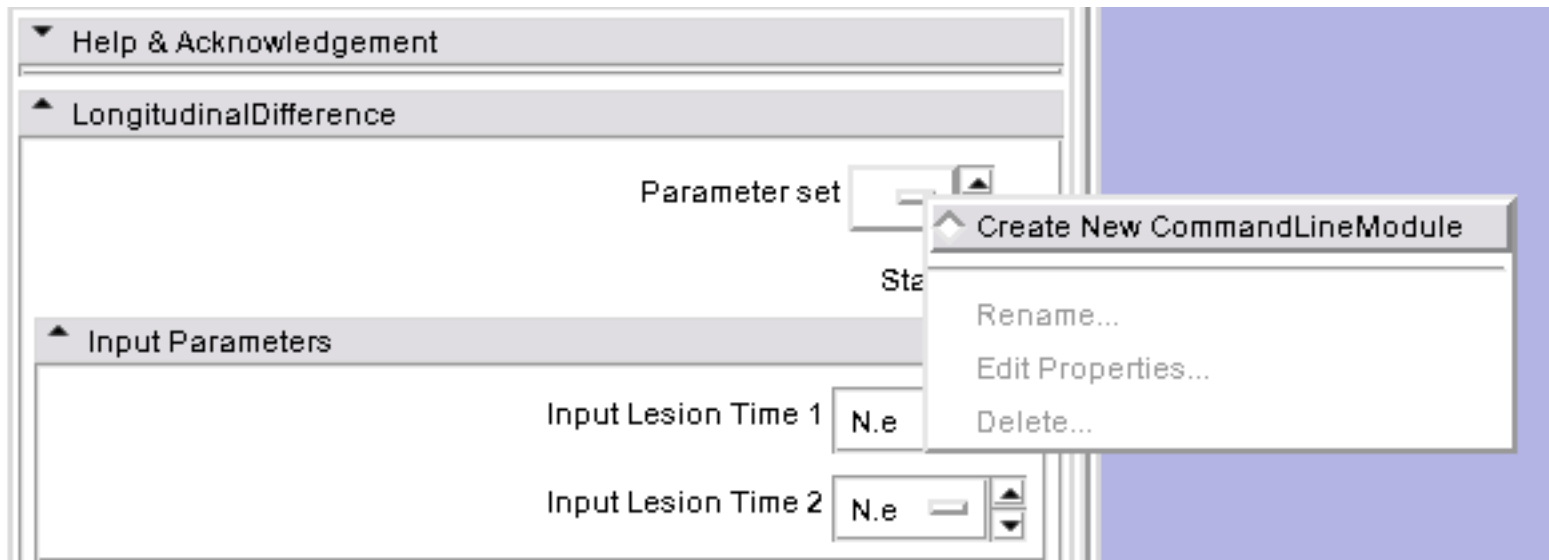
The first step to creating an image showing longitudinal lesion changes is to load the **LongitudinalDifference** module.





Lesion Changes Image - II

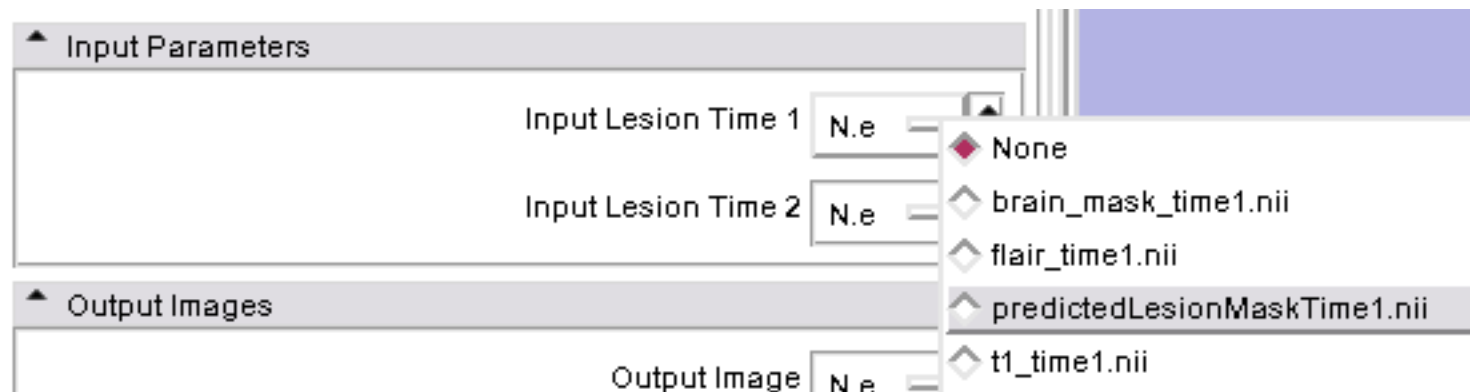
Now choose to **Create New Command Line Module** option.





Lesion Changes Image - III

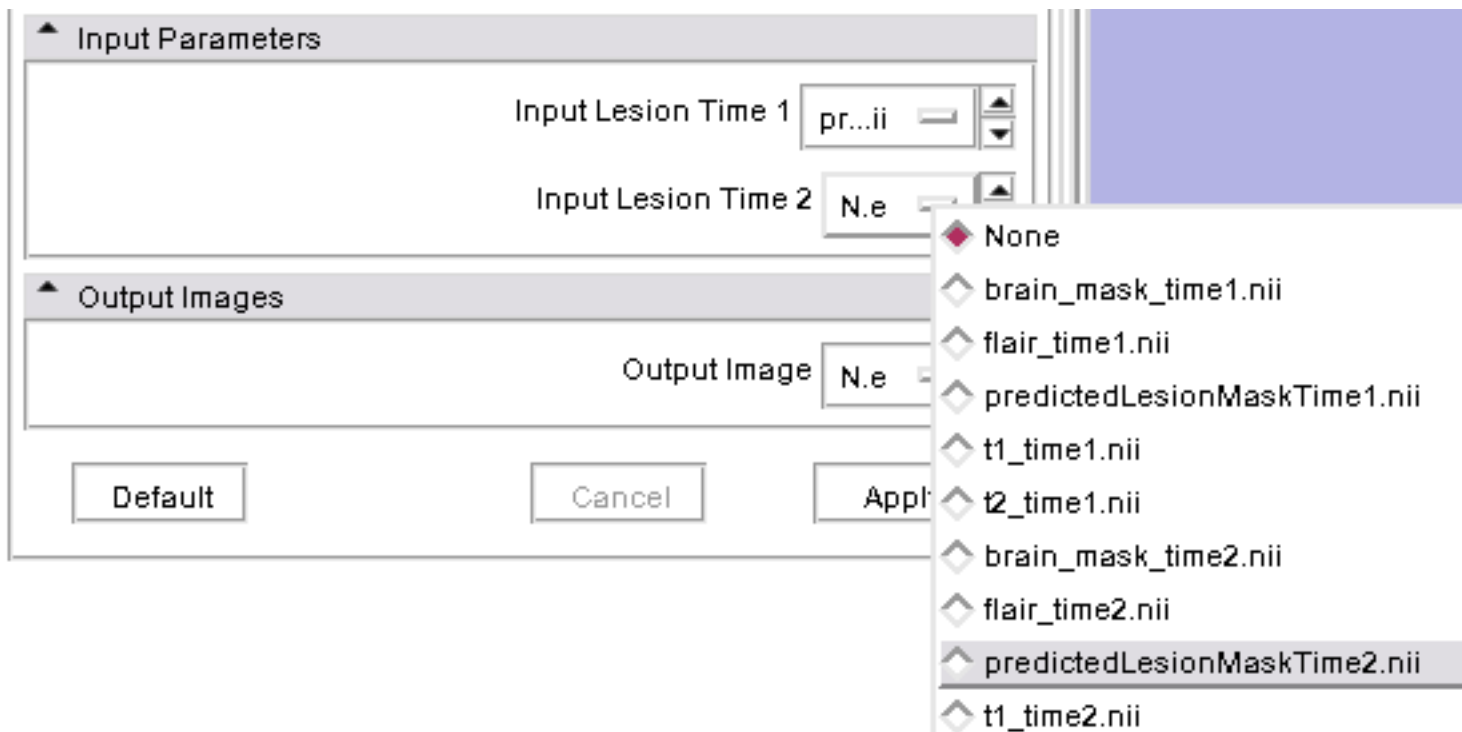
Select '**predictedLesionsTime1.nii.gz**'
for '**Input Lesion Time 1**'





Lesion Changes Image - IV

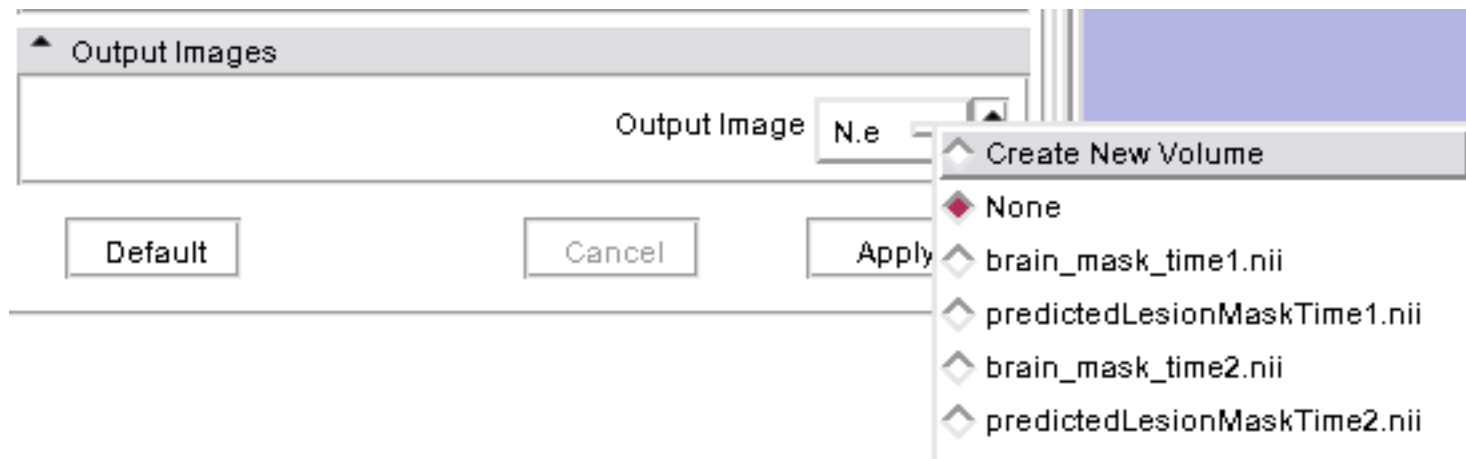
Select '**predictedLesionsTime2.nii.gz**' for '**Input Lesion Time 2**'





Lesion Changes Image - V

Select 'Create New Volume' for 'Output Image'





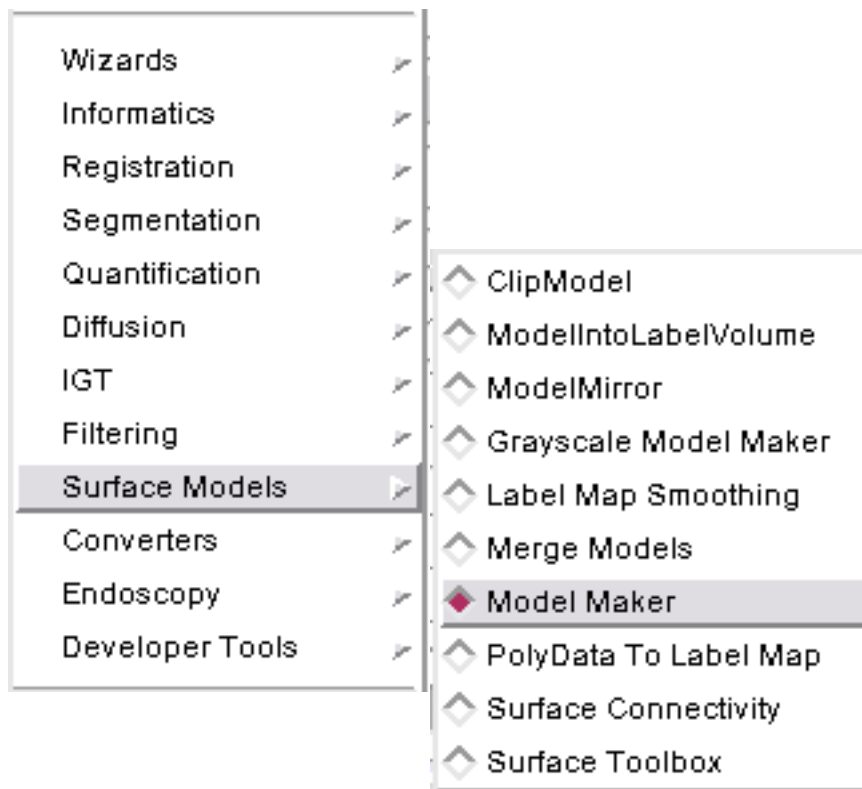
Lesion Changes Image - VI

Click '**Apply**' and wait a few seconds for the module to finish running. When it is completed there will be a new image “**Output Volume**” that represents the changes in lesion between time 1 and time 2. Next we'll generate models from this image.



Lesion Models - I

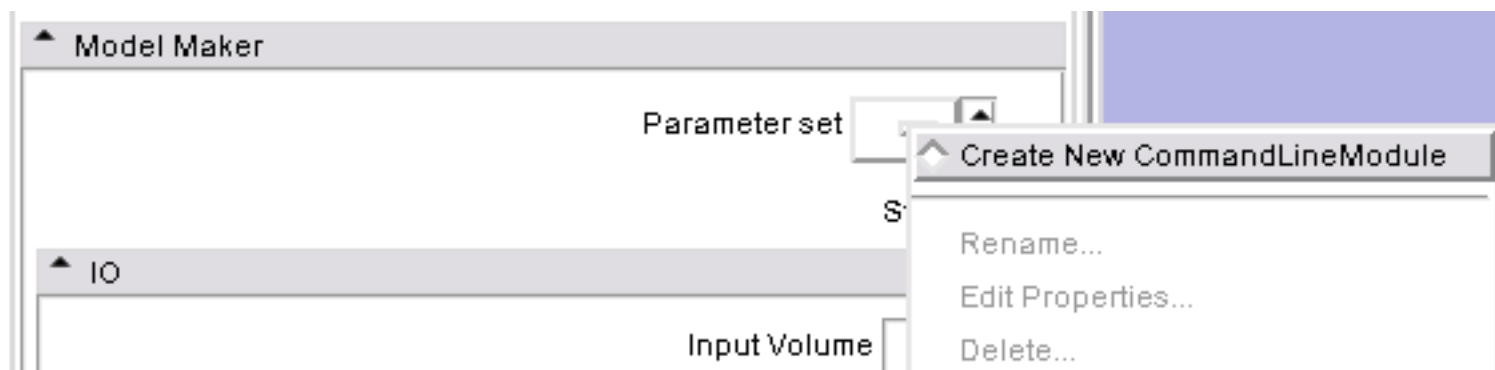
Select the 'Model Maker' module.





Lesion Models - II

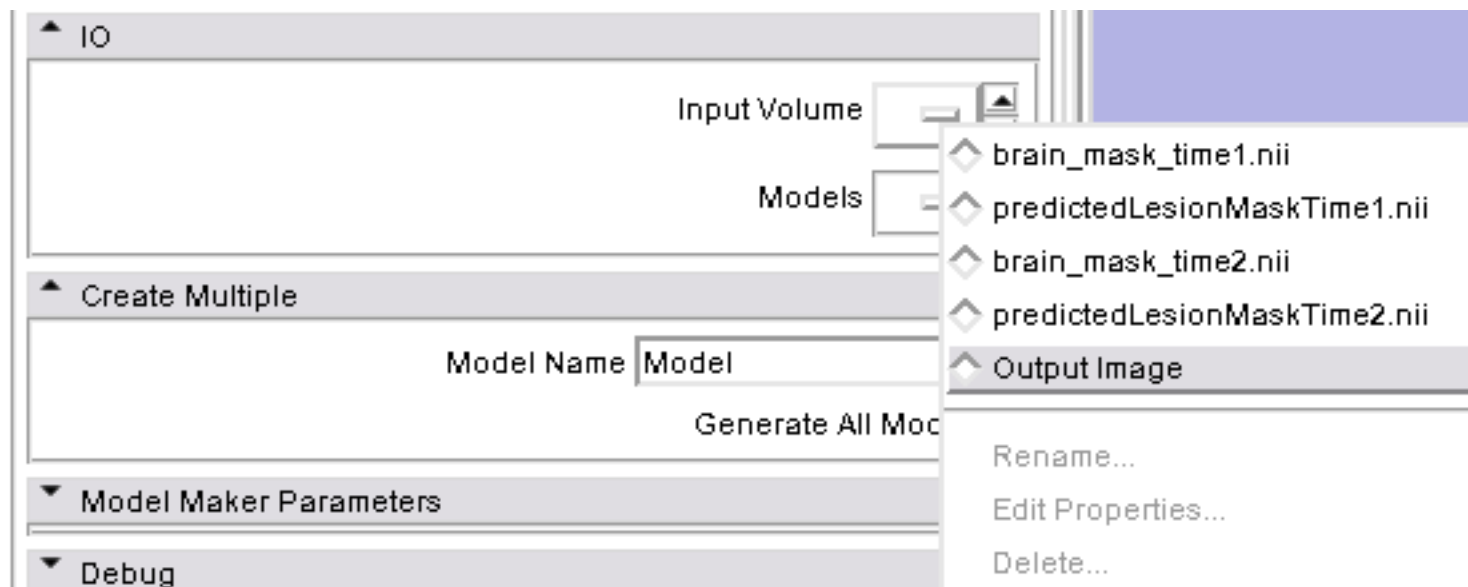
Select 'Create New
CommandLineModule' for 'Parameter
Set'





Lesion Models - III

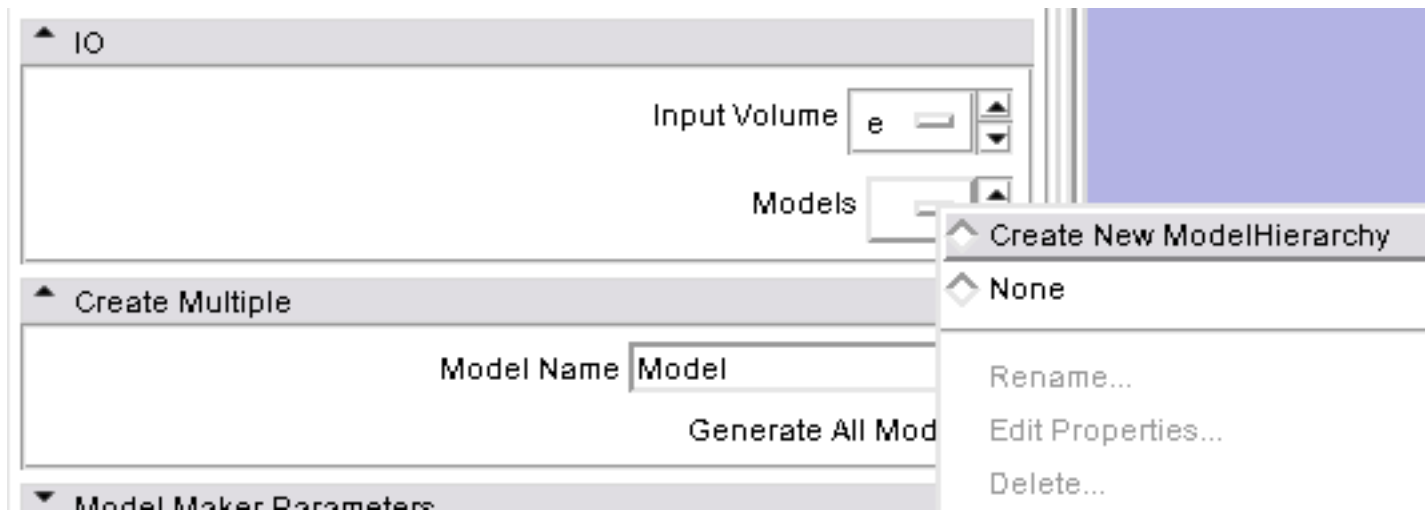
Select '**Ouput Image**' as the '**Input Volume**'





Lesion Models - IV

Select 'Create New Model Hierarchy'
for 'Models'





Lesion Models - V

Change the 'Model Name' to
'LesionChanges'

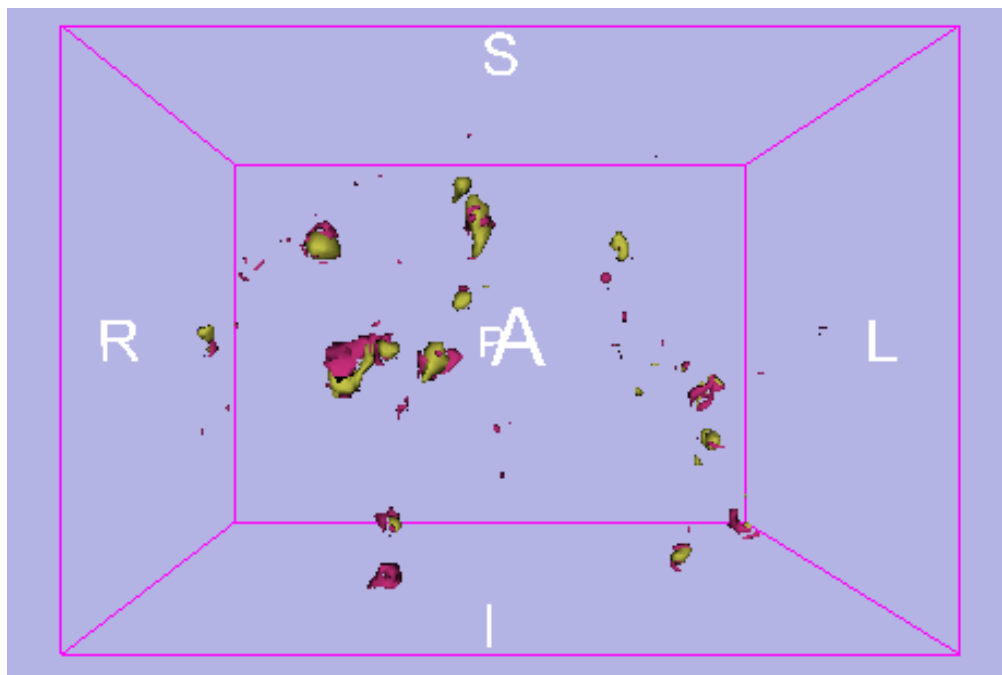
The screenshot shows a software interface with the following components:

- IO**: A section with two input fields: "Input Volume" containing the letter 'e' and "Models" containing the number '1'. Both fields have up and down arrow buttons.
- Create Multiple**: A section with a "Model Name" field containing the text "LesionChanges". A yellow tooltip box is overlaid on this field, containing the text: "Name to use for this model. If making multiple models, use this as a prefix to the label and color name".
- Model Maker Parameters**: A section that is currently collapsed, indicated by a downward-pointing arrow.



Lesion Models - VI

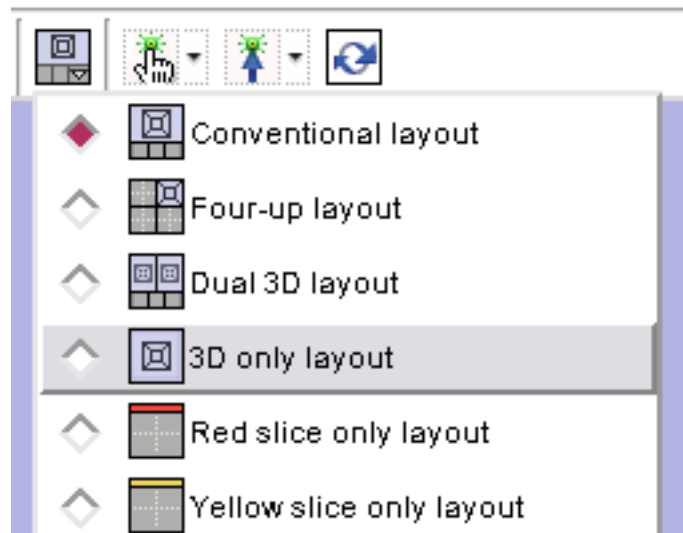
Click '**Apply**' and wait a few seconds for the module to complete.





Examining Changes - I

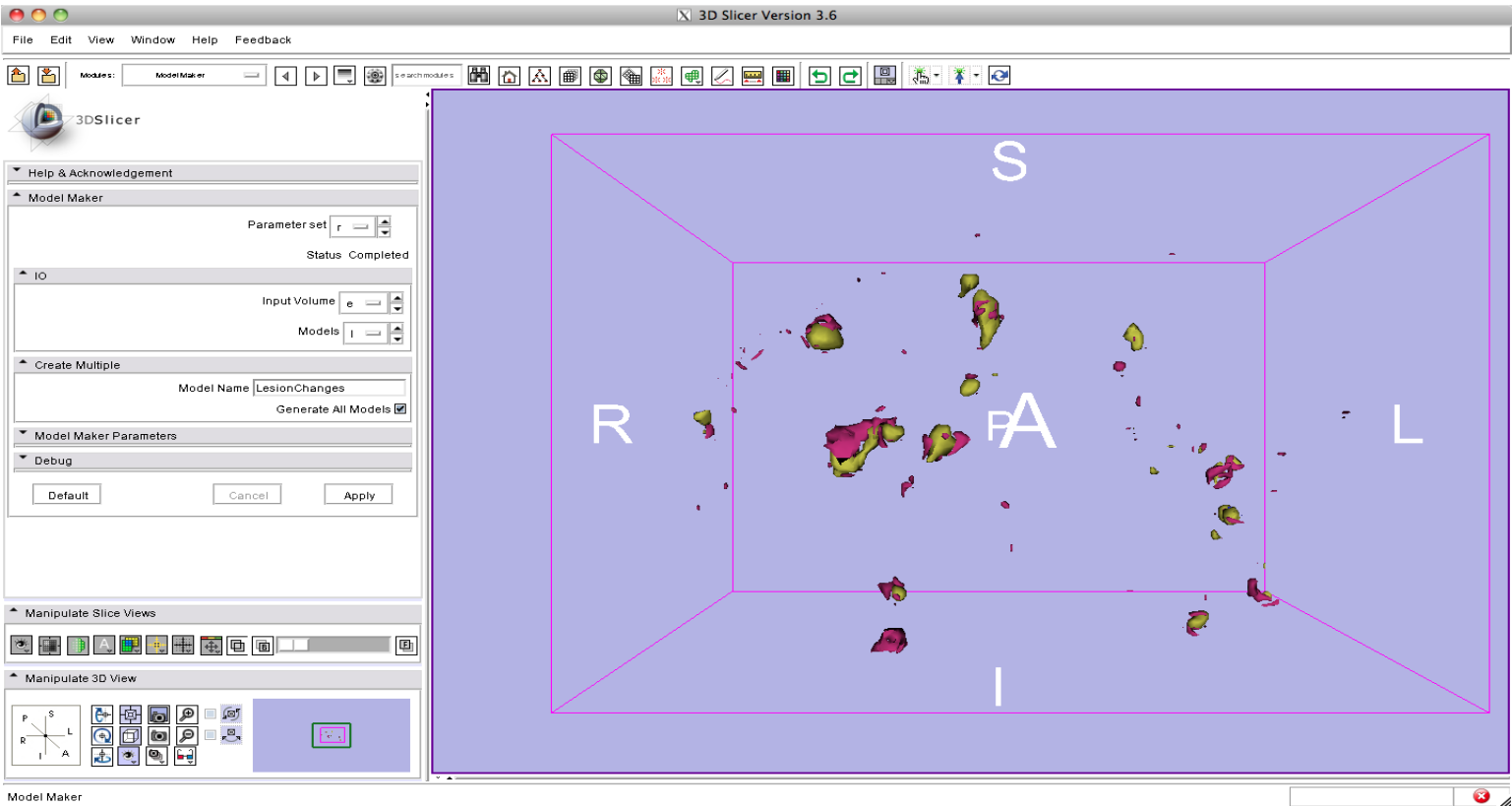
Switch to 3D layout to make visually examining the lesion models easier.





Examining Changes - II

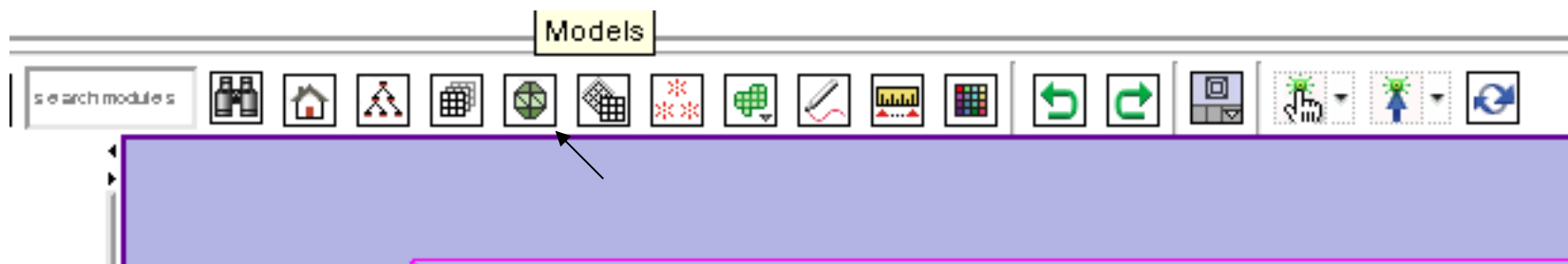
Zoom in





Examining Changes - III

Bring up the **Models** module.





Examining Changes - IV

From the models module you can see there are three different model types:

- LesionChanges_247_monk
- LesionChanges_248_forest
- LesionChanges_245_avery



Examining Changes - V

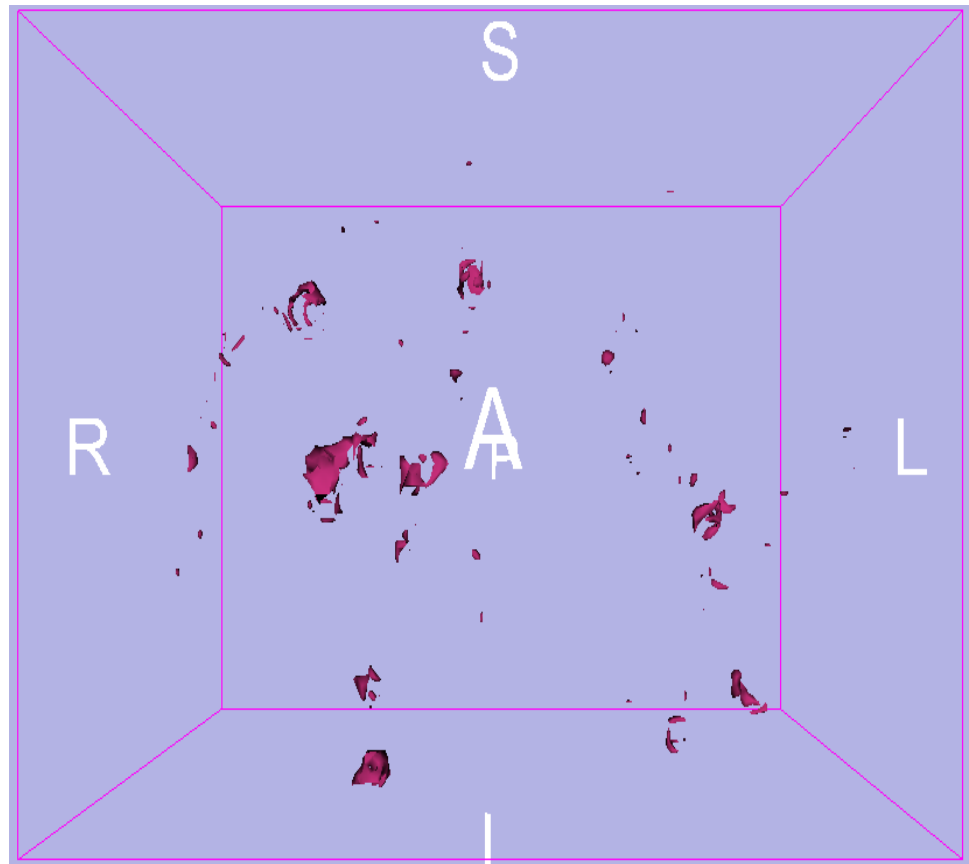
From the Models interface you can adjust the visibility of models.

- Monk is Blue and represents lesion lost between time 1 and 2
- Forest is yellow and represents unchanged lesion
- Avery is red and represents new lesions



Examining Changes - VI

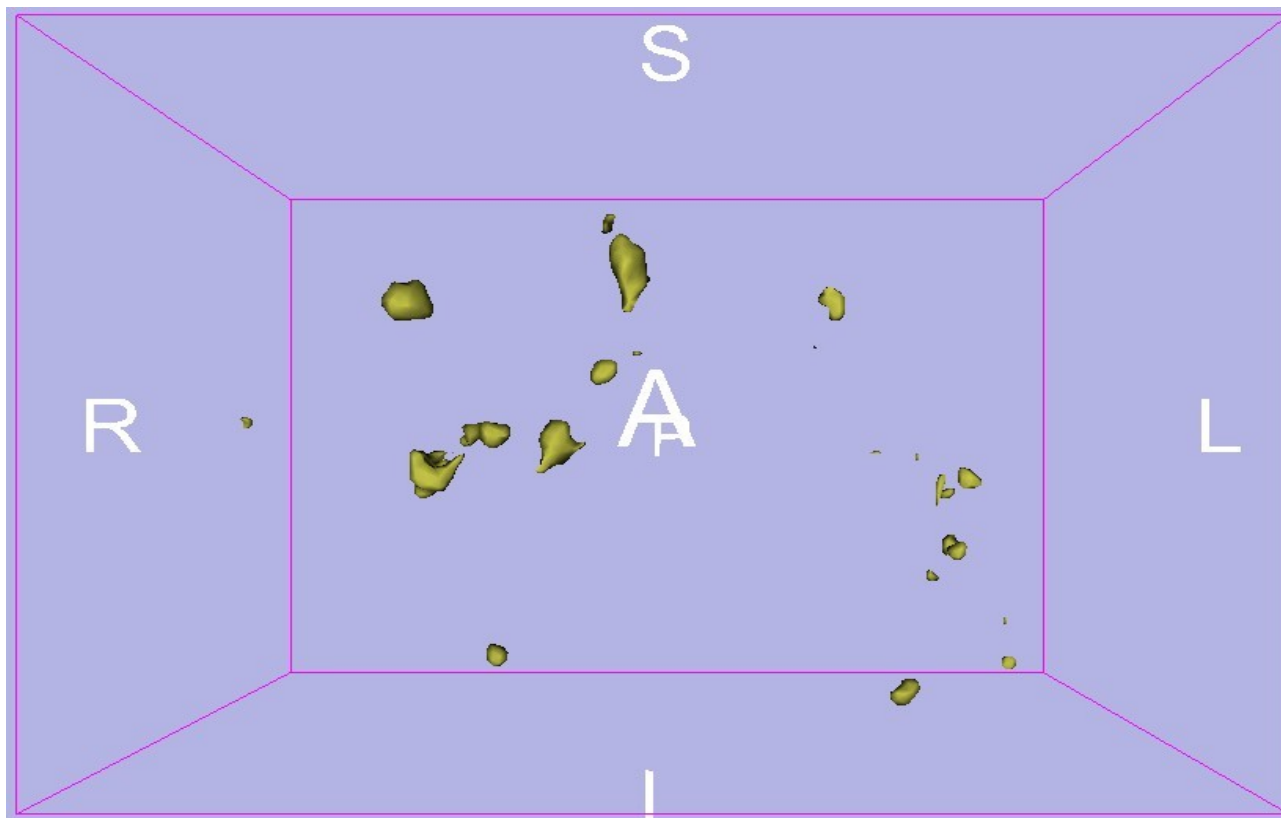
Each model's visibility can be independently adjusted. Here is just the new lesion (a very) with lost and unchanged lesion's visibility turned off.





Examining Changes - VII

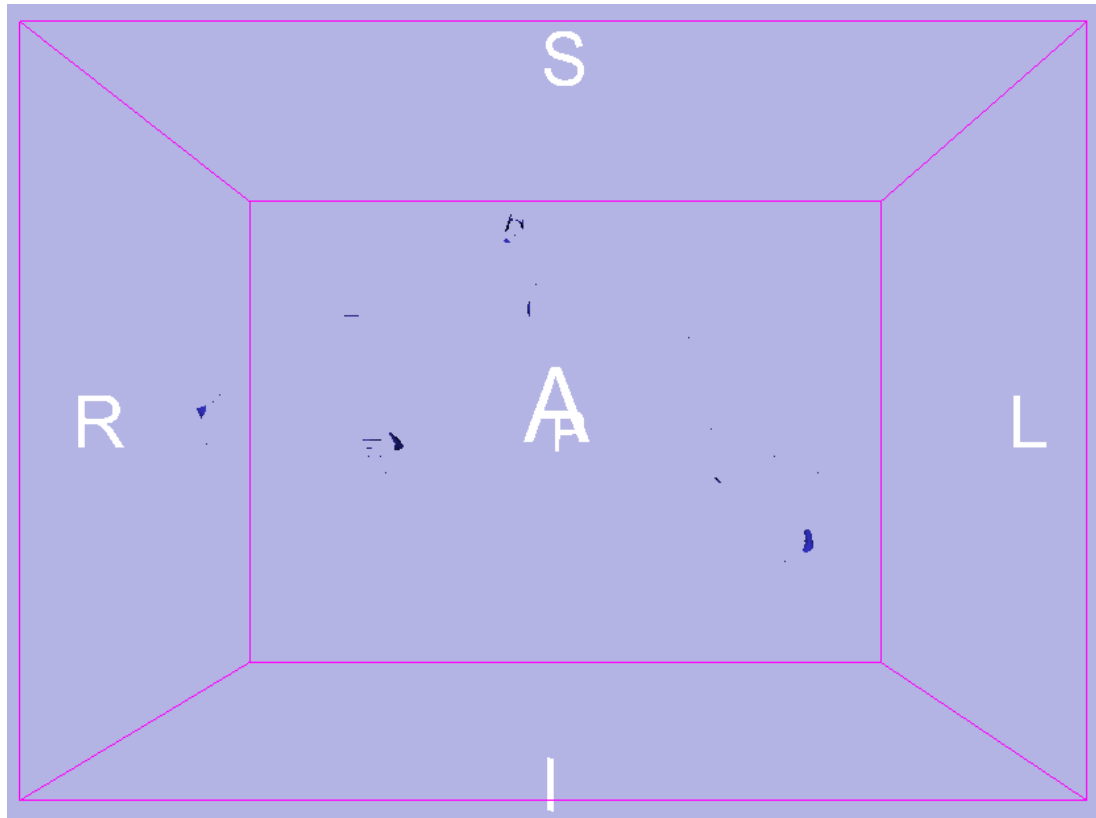
Here are the unchanged lesions.





Examining Changes - VIII

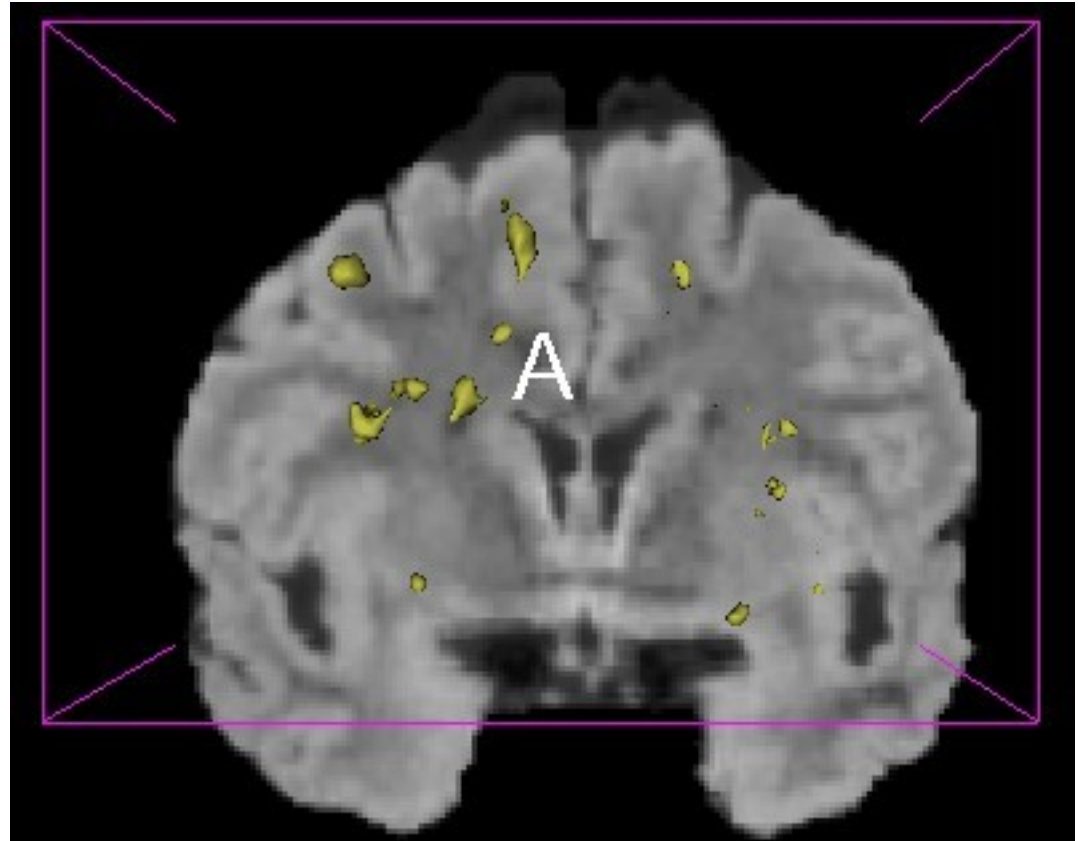
Here are the lost lesions.





Examining Changes - IX

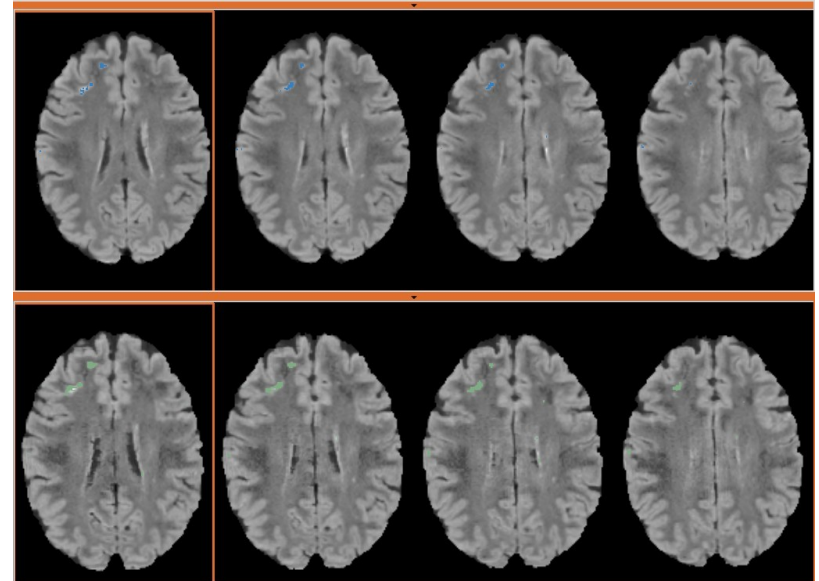
You can also show models with brain slices. Here is a coronal slice of the time 2 FLAIR along with the unchanged lesions.





Conclusion

You should now be able to generate models that demonstrate the changes in lesions in a single subject. These models can be examined on their own, or combined with other models generated from anatomy in order to better understand lesion changes. Using this approach permits the user to analyze longitudinal changes in white matter lesions.





Acknowledgments



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