



NA-MIC

*National Alliance for Medical Image Computing*

<http://na-mic.org>

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# White Matter Lesion Segmentation

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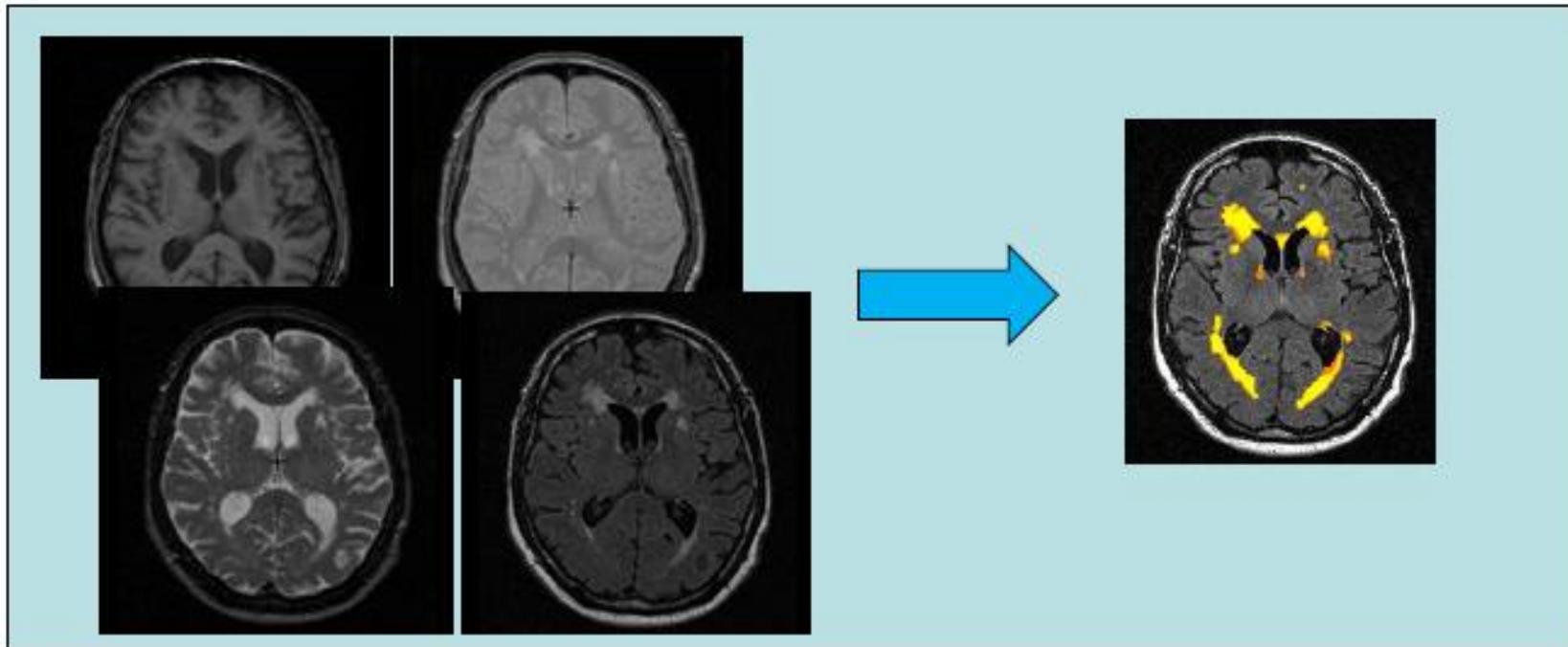
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NA-MIC Tutorial Contest: Summer 2010



# Learning Objective

Learn how to run “White Matter Lesion Segmentation” module in Slicer 3.





# Pre-requisite

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- Data Loading and Visualization (Sonia Pujol, Ph.D.)
  - <http://www.na-mic.org/Wiki/index.php/Slicer3.2:Training>



# Material

- This tutorial requires **Slicer3.6 (release version)** and the tutorial dataset. They are available at the following locations:
- **Slicer3.6** download page  
<http://www.slicer.org/pages/Downloads/>
- **Tutorial dataset:**  
[http://wiki.na-mic.org/Wiki/index.php/File:White\\_Matter\\_Lesion\\_Segmentation\\_TutorialContestSummer2010.zip](http://wiki.na-mic.org/Wiki/index.php/File:White_Matter_Lesion_Segmentation_TutorialContestSummer2010.zip)

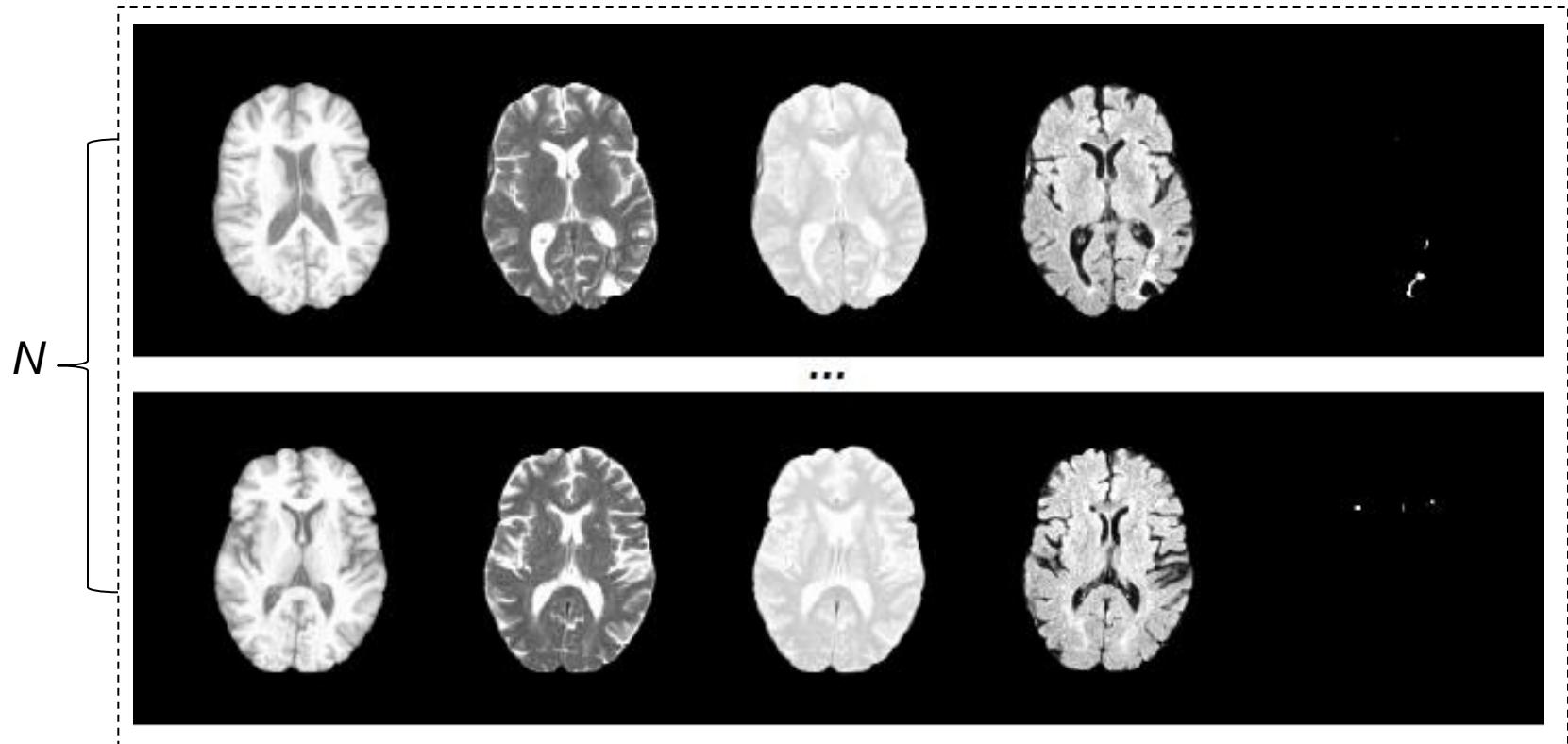
**Disclaimer:** *It is the responsibility of the user of Slicer to comply with both the terms of the license and with the applicable laws, regulations, and rules.*



# Material: Sample Data

- Training data

*Input:  $N$  training images ( $T1$ ,  $T2$ ,  $PD$ ,  $FLAIR$ , lesion ROI)*

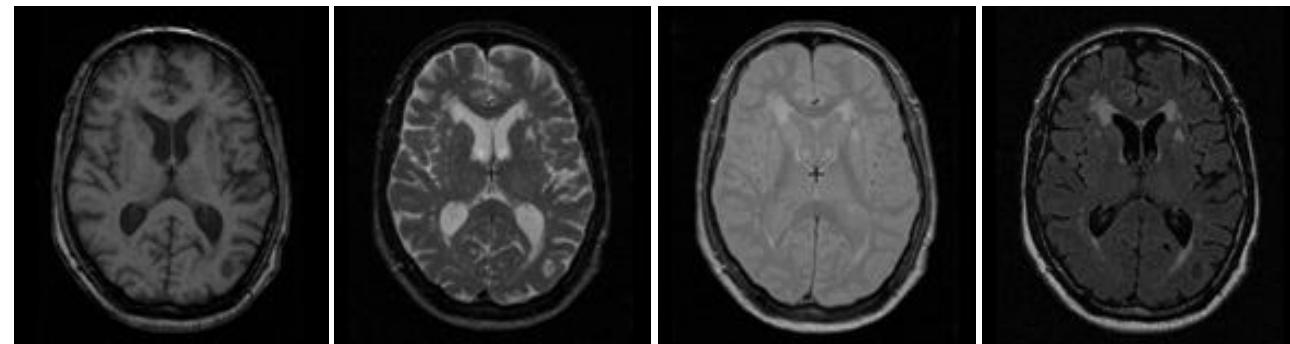




# Material: Sample Data

- Testing data

*Input: testing image (T1, T2, PD, FLAIR)*





# Platform

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- This tutorial has tested on a Linux (64 bit) machine.



# Overview

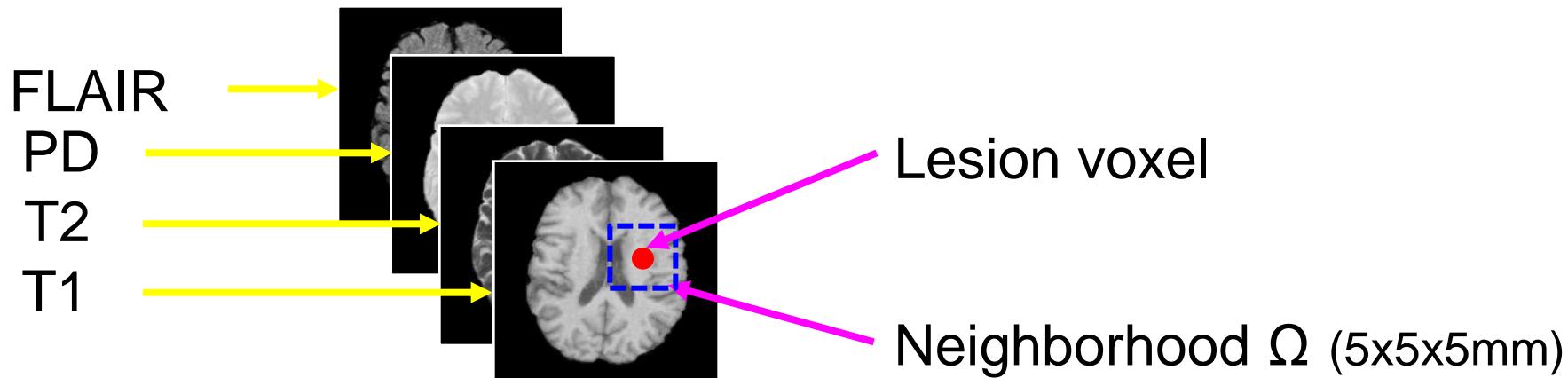
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- **Introduction**
- Getting started
- Pipeline 1 - Training & Segmentation only
- Pipeline 2 - Preprocessing, Training, and Segmentation
- Conclusion



# Introduction

- Learning based WML segmentation



$$F(v) = \{I(t_m) | t_m \in \Omega(v_m), m \in \{T_1, T_2, PD, FLAIR\}\}$$

- SVM → To train a WML segmentation classifier.
- Adaboost → To adaptively weight the training samples and improve the generalization of WML segmentation method.



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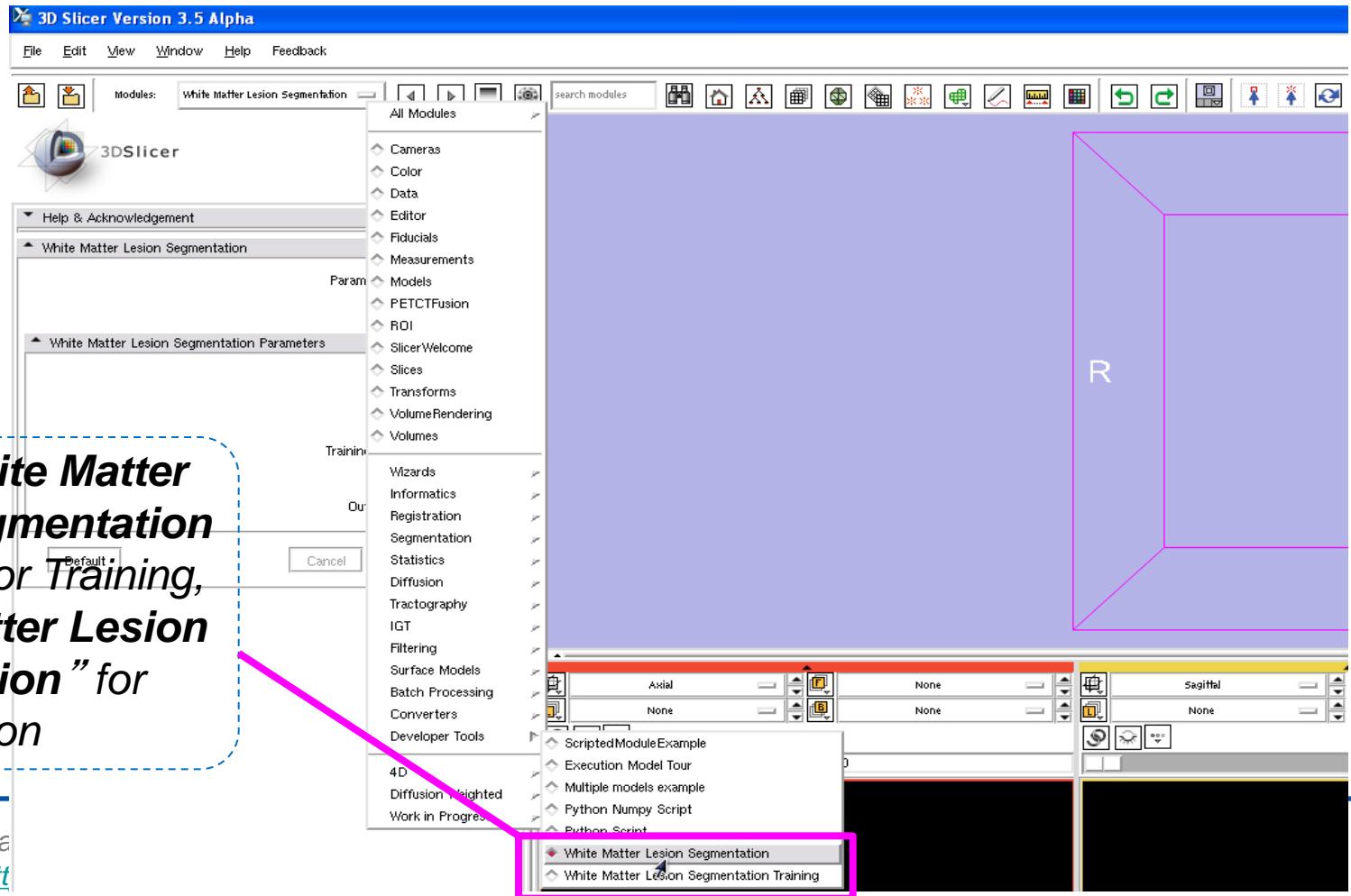
# Getting started

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- Module installation
  - Press F2 or go to View >> Application Settings >> Module Settings on the menu of Slicer3.
  - Click the “add a preset” button.
  - Select the location of the White Matter Lesion Segmentation modules (*wmlstrain* and *wmlstest*).
  - Close Slicer3 and restart.



## • Execution





# Overview

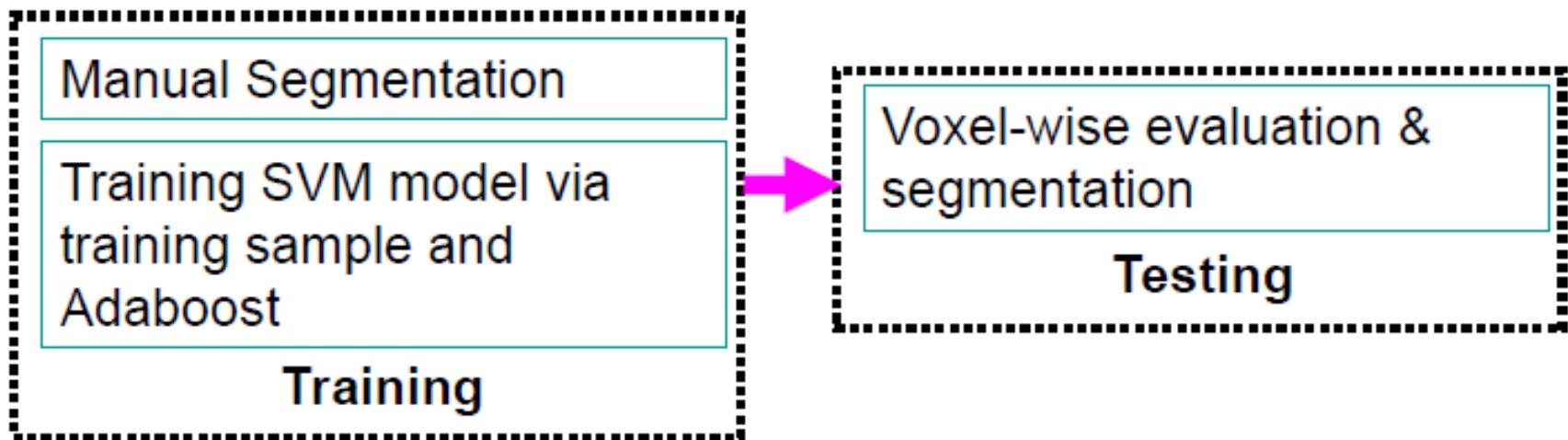
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# Pipeline 1 (w/o Preprocessing)

- In case your images are already preprocessed...



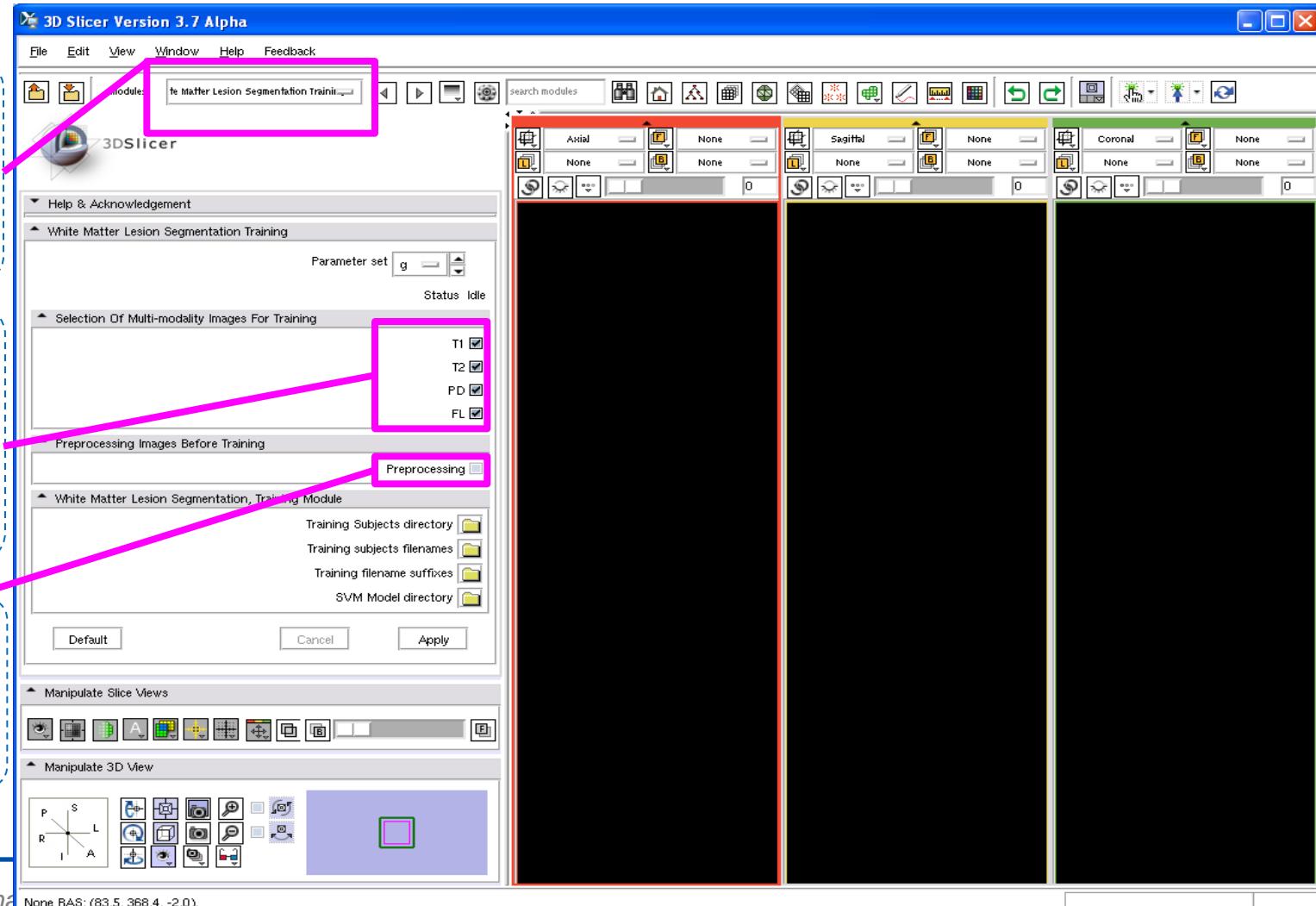


# Training

Select “White Matter Lesion Segmentation Training”

Check image modalities you want to train, e.g. T1, T2, PD, and FLAIR

DO NOT check this box to skip preprocessing





White Matter Lesion Segmentation, Training Module

Training Subjects directory

Training subjects filenames

Training filename suffixes

SVM Model directory

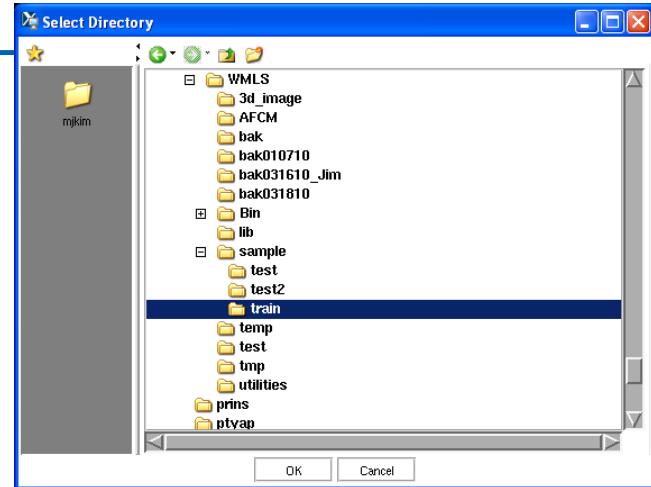
Default      Cancel      Apply

Manipulate Slice Views

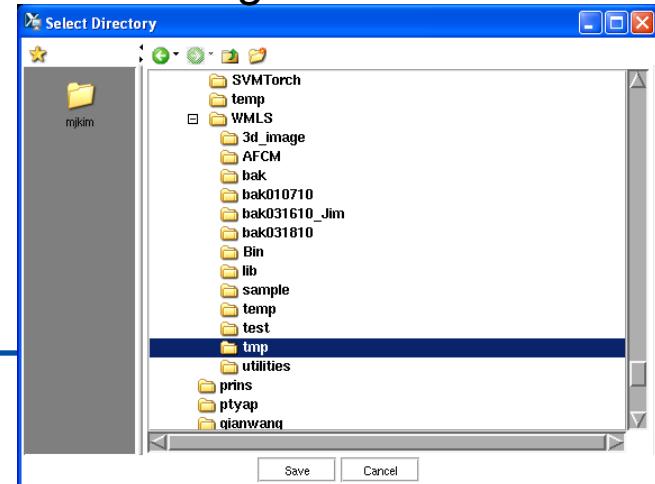
Manipulate 3D View

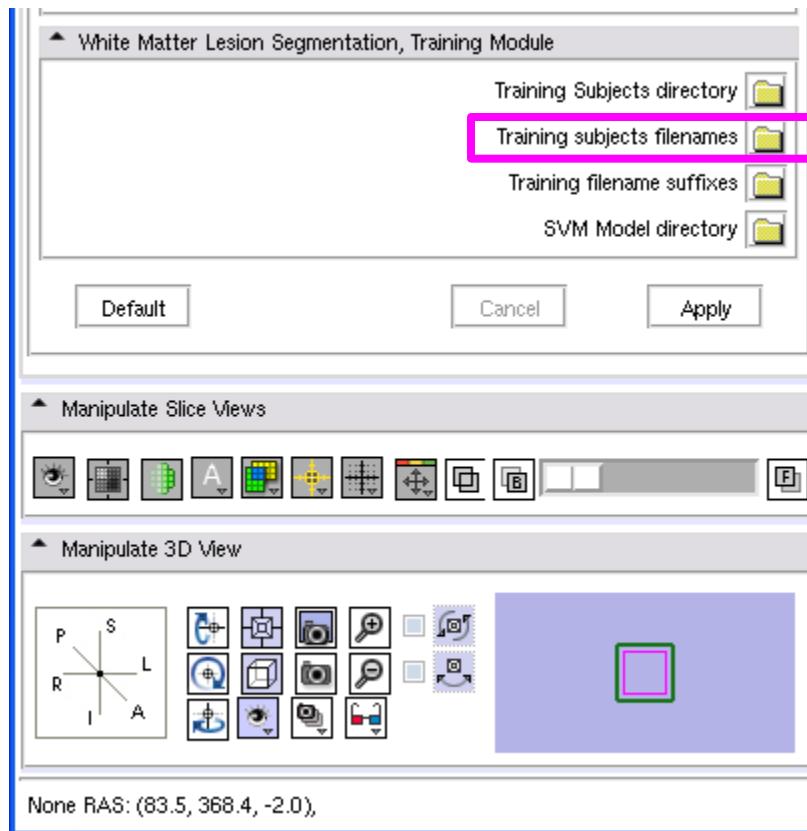
None RAS: (83.5, 368.4, -2.0),

*Click and select the location containing training images*

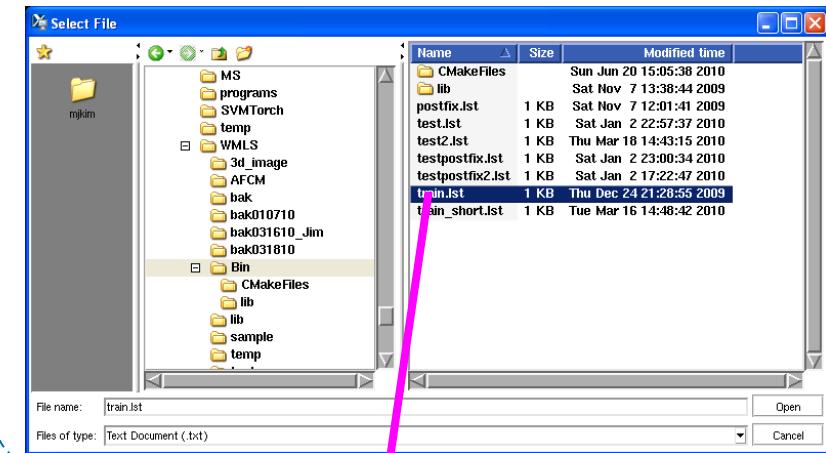


*Click and select the location where SVM model will be saved after training*



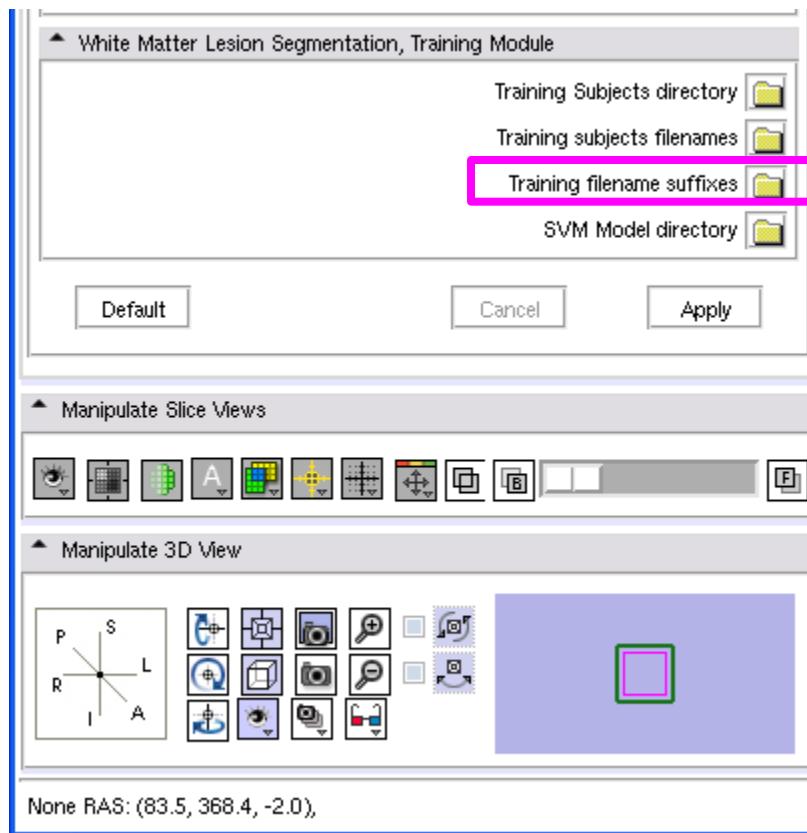


Click and select the text file containing the list of filenames of training images

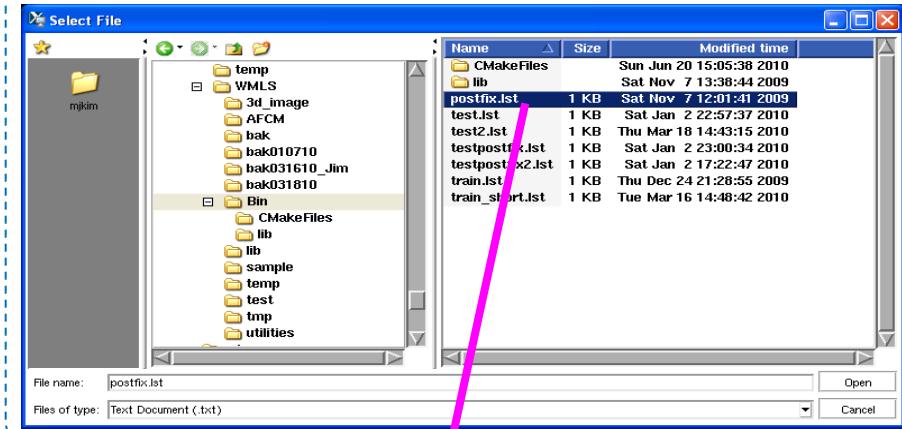


Example)

303D20268
305D40291
301D00368
303D20146
604H30067
303D20258
303D20153
302D10226
303D20114

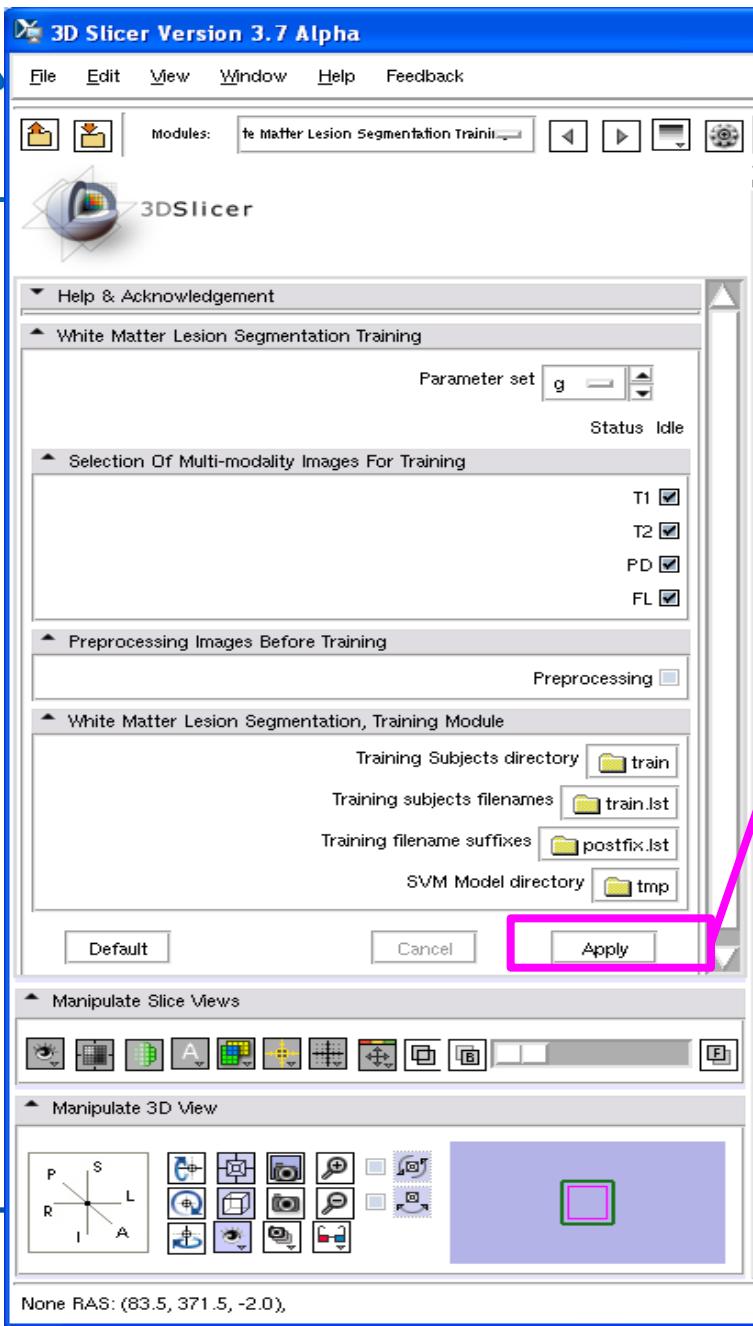


*Click and select the file containing the list of prefixes of training images*



Example)

.T1.byte.cbq.match.smooth.hdr  
.T2.byte.cbq.match.smooth.hdr  
.PD.byte.cbq.match.smooth.hdr  
.FL.byte.cbq.match.smooth.hdr  
.lesion.mask.hdr  
.lesion.mask.open.hdr  
.lesion.premask.hdr



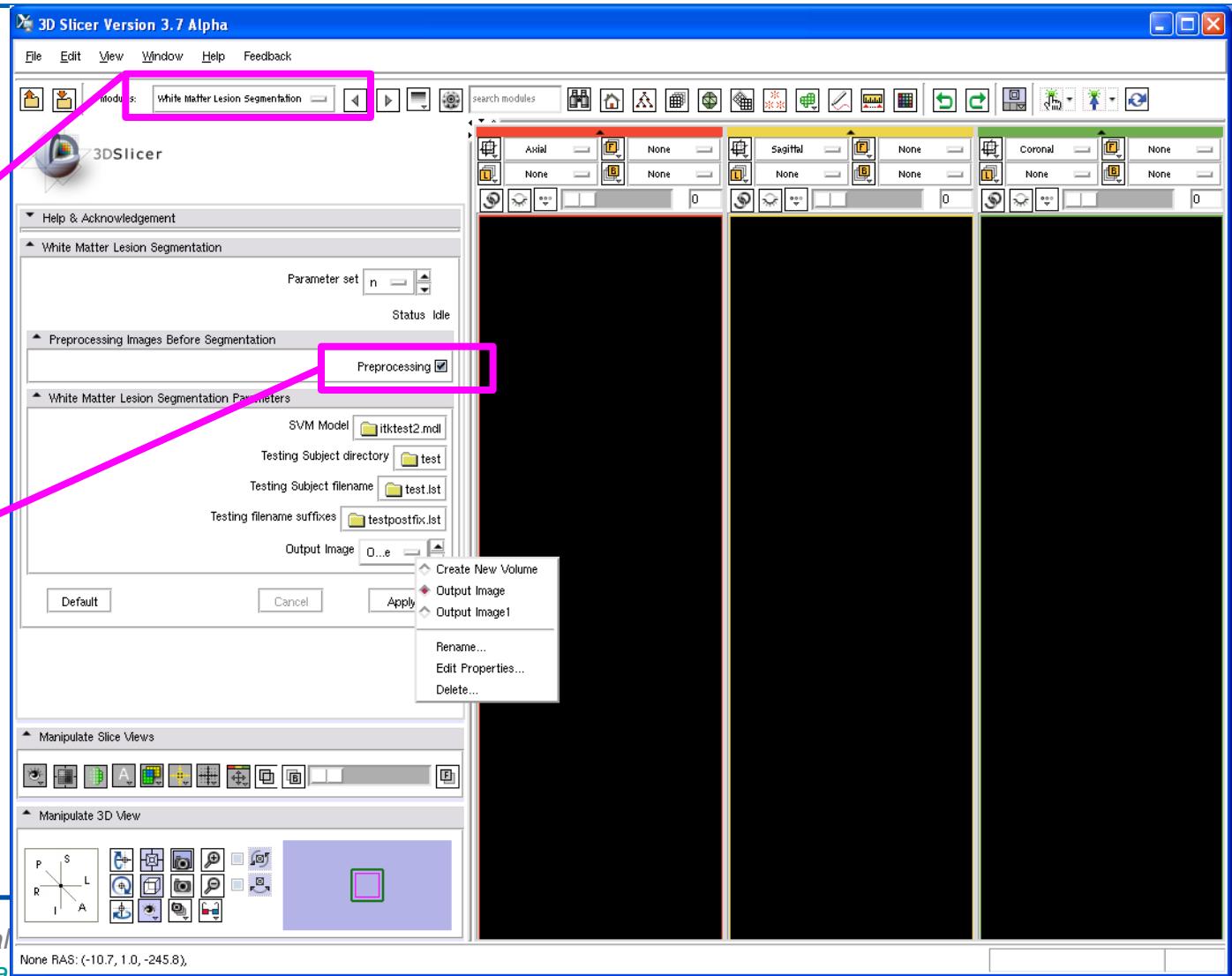
If all parameters are selected, press “Apply”.

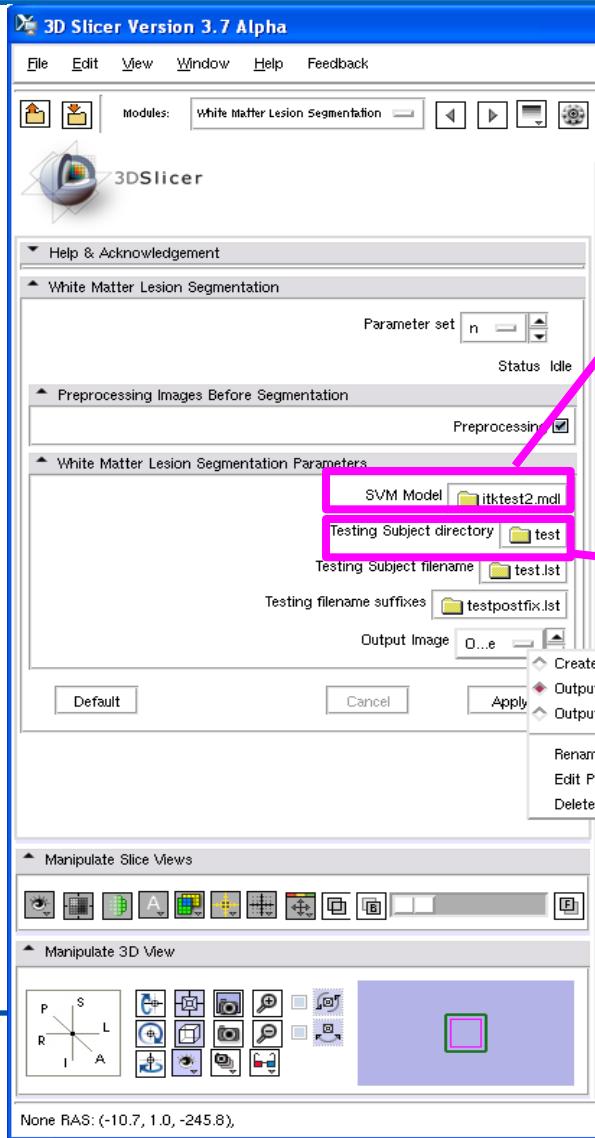


# Testing (Segmentation)

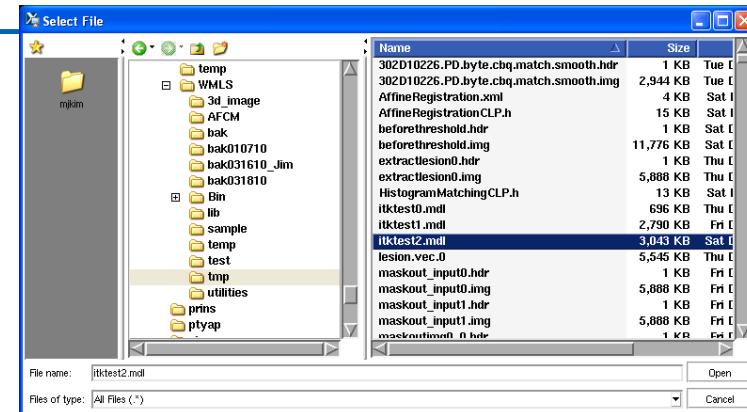
Select “White Matter Lesion Segmentation Training”

DO NOT check this box to skip preprocessing

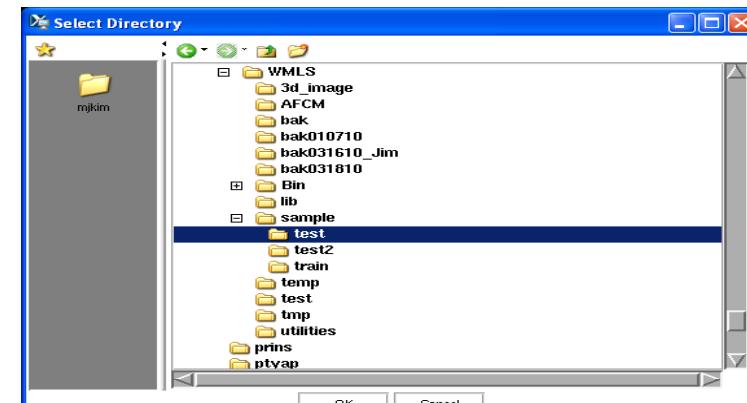




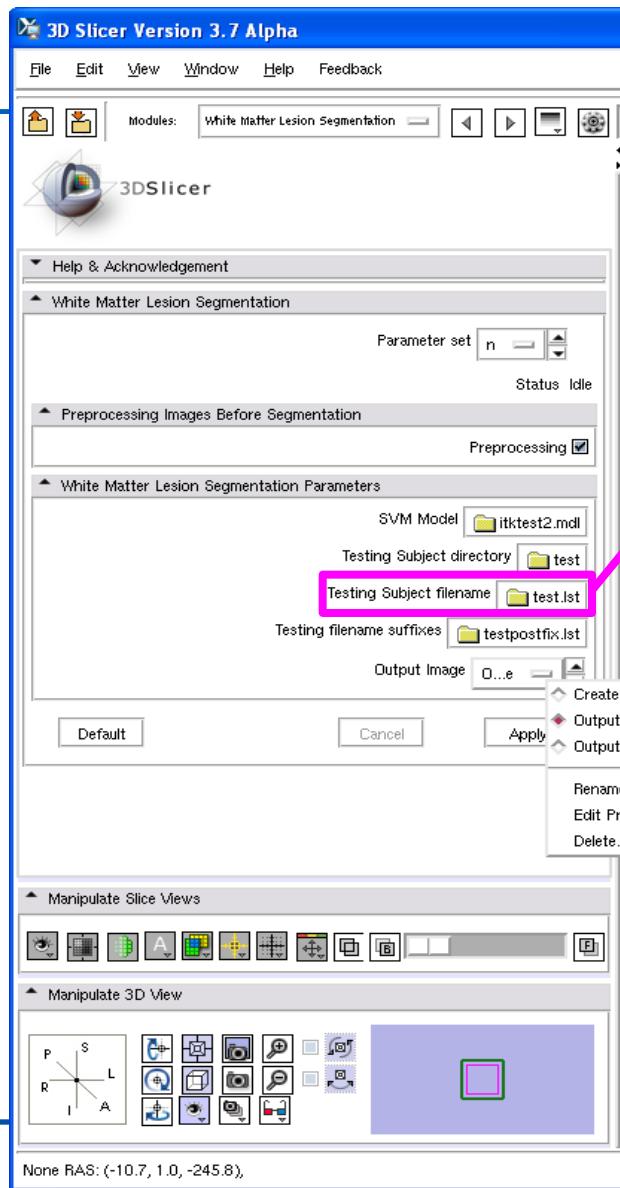
*Click and specify the location containing the saved SVM models in the “Training” stage.*



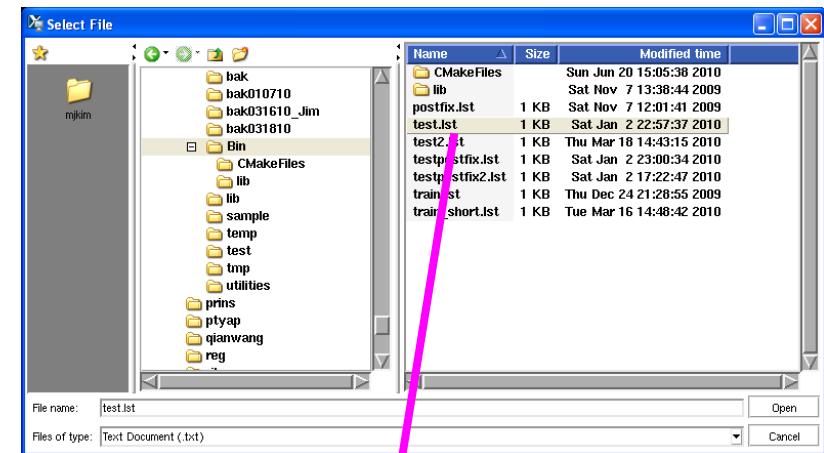
*Click and select the location containing testing images.*



*inputting*



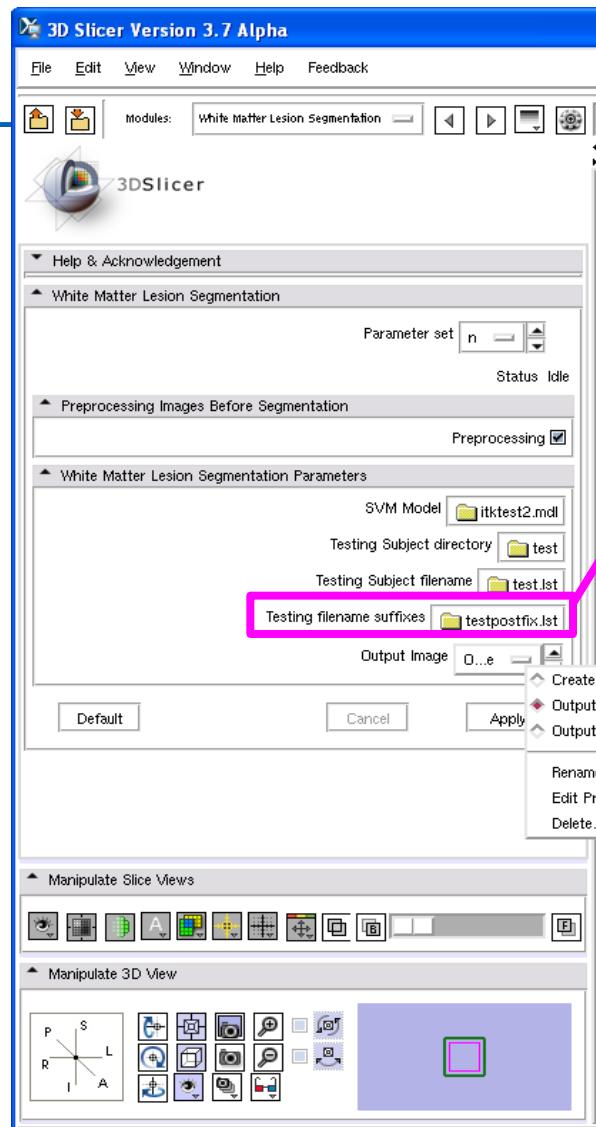
*Click and select the file containing the list of filename of testing image.*



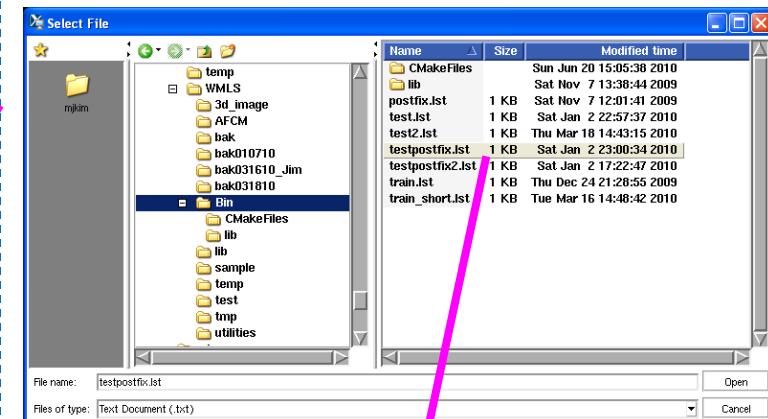
Example:

601H03166

puting



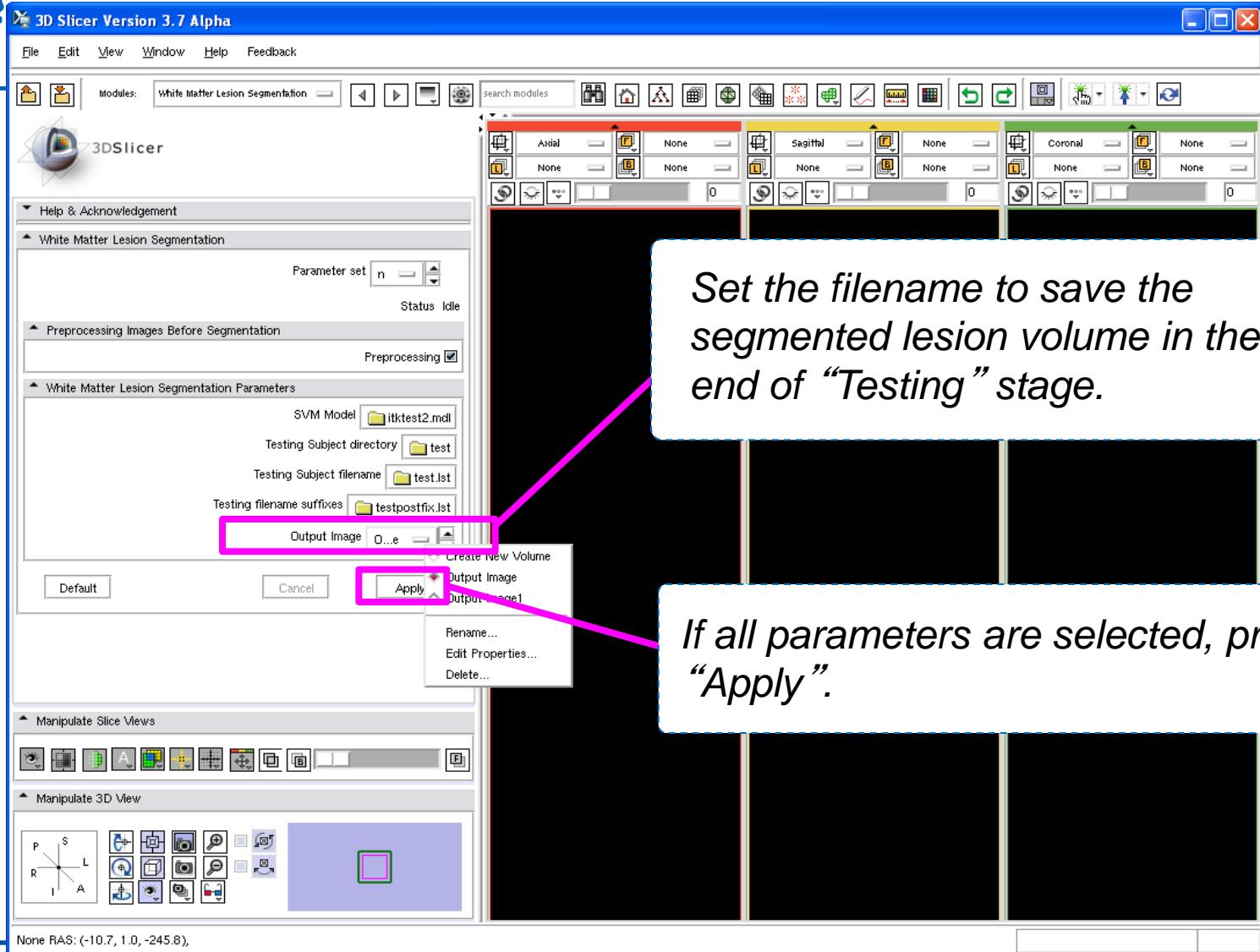
*Click and select the file containing the list of prefixes of testing image.*



Example:

.T1.byte.cbq.match.smooth.hdr  
.T2.byte.cbq.match.smooth.hdr  
.PD.byte.cbq.match.smooth.hdr  
.FL.byte.cbq.match.smooth.hdr

None RAS: (-10.7, 1.0, -245.8),

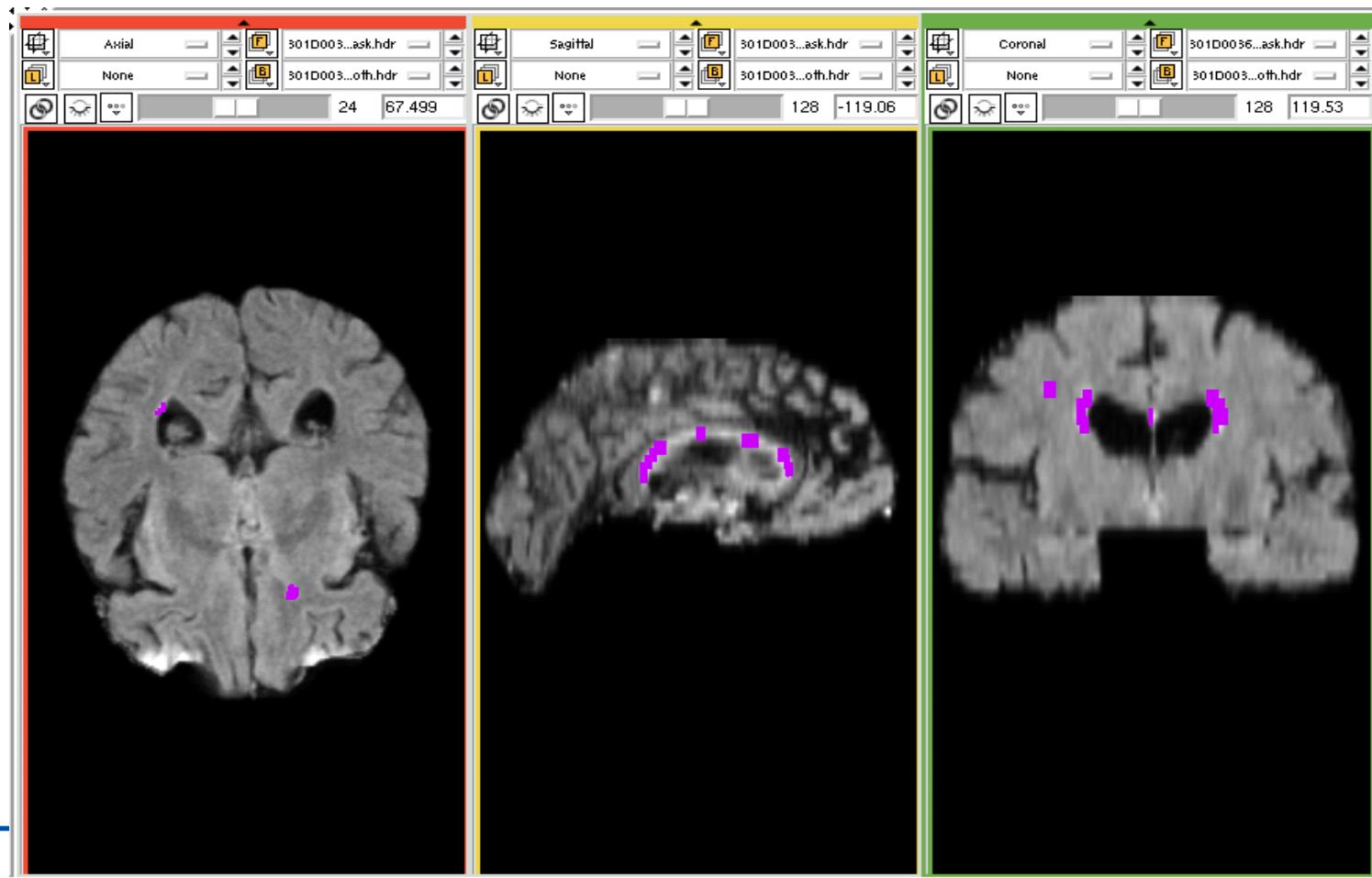


*Set the filename to save the segmented lesion volume in the end of “Testing” stage.*

*If all parameters are selected, press “Apply”.*



- Visualization of the segmented lesion volume



26, 92), Fg: Out of Frame, Bg: Out of Frame,



# Overview

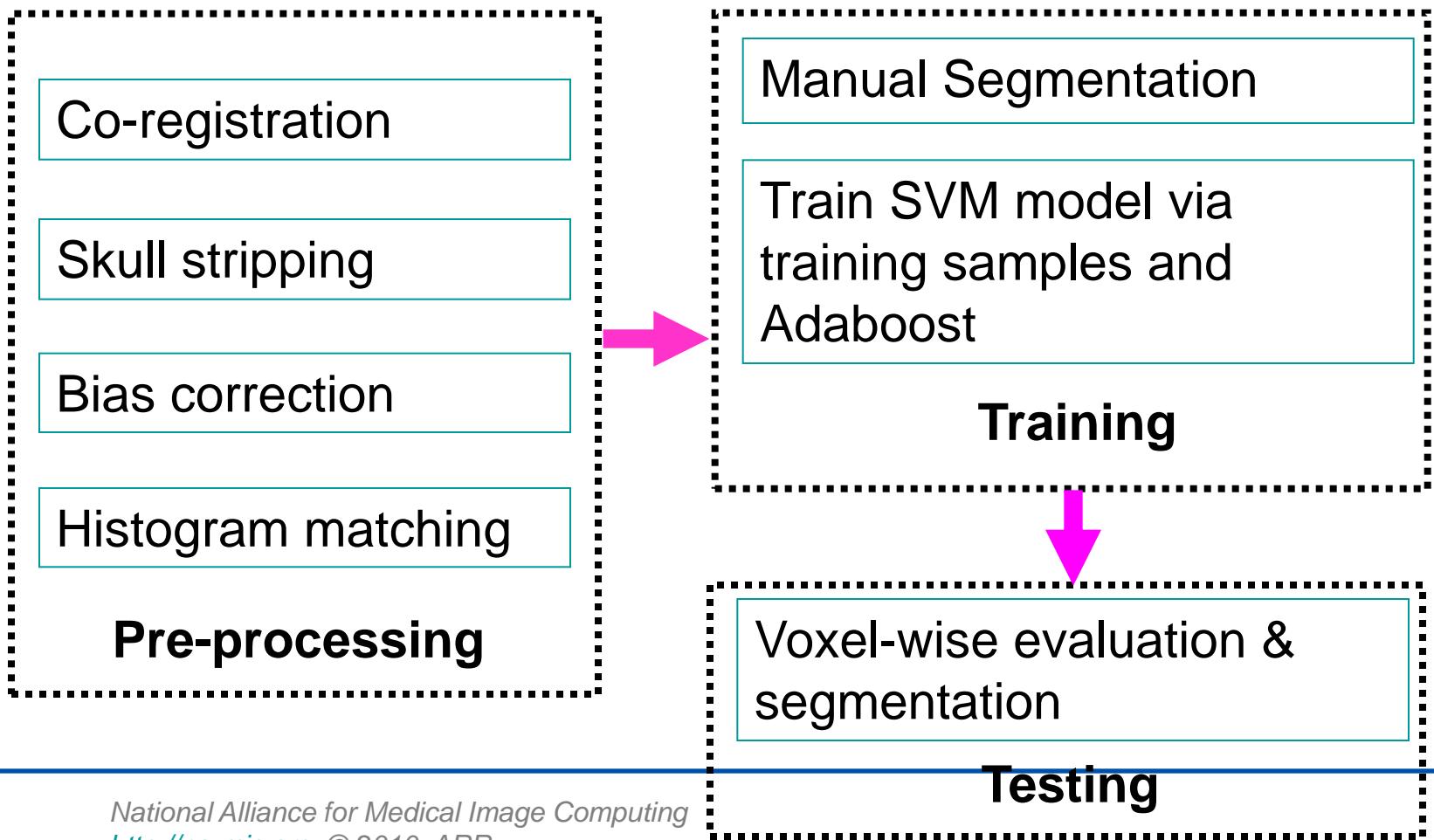
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# Pipeline (w/ Preprocessing)

- If your images are unprocessed...

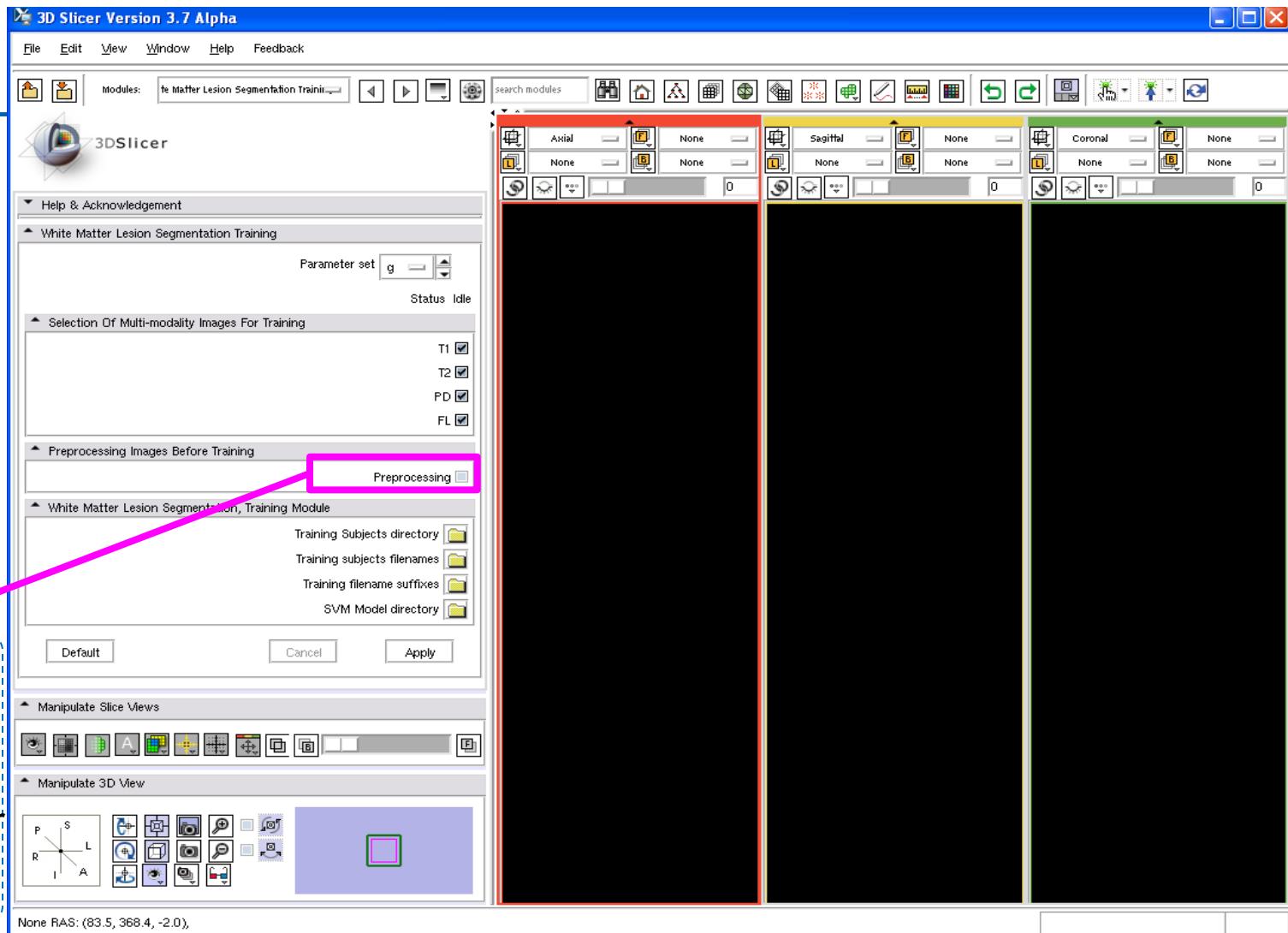




# Training/Testing w/ Preprocessing

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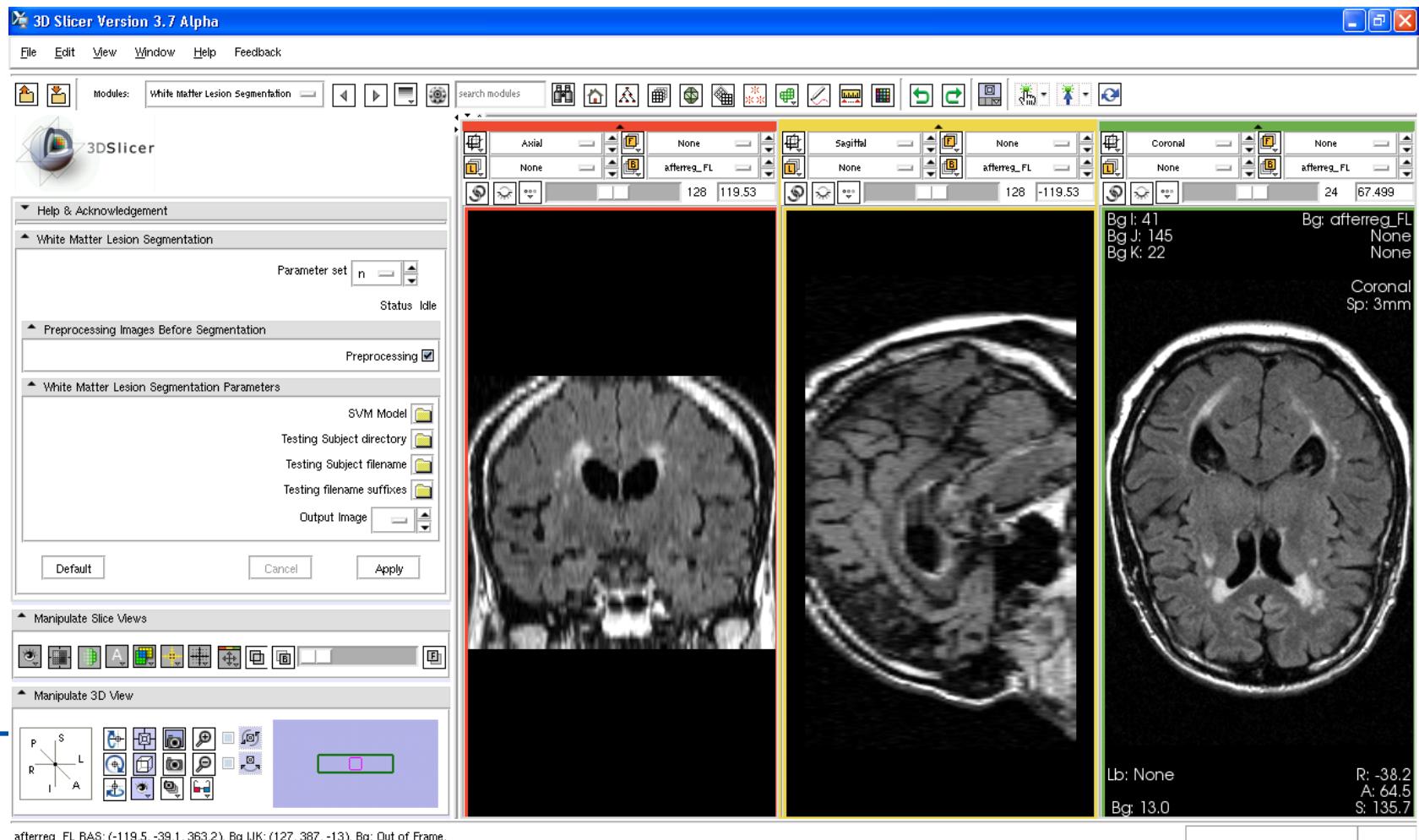
- In the training or testing menu, check the “Preprocessing” option.
- Intermediate files by processing steps are saved in the directory you specified in the training/testing menu.
- For other training and testing options, see page 12-24.



*Check this box  
for preprocessing  
before “training”.  
Do same thing for  
“testing”.*

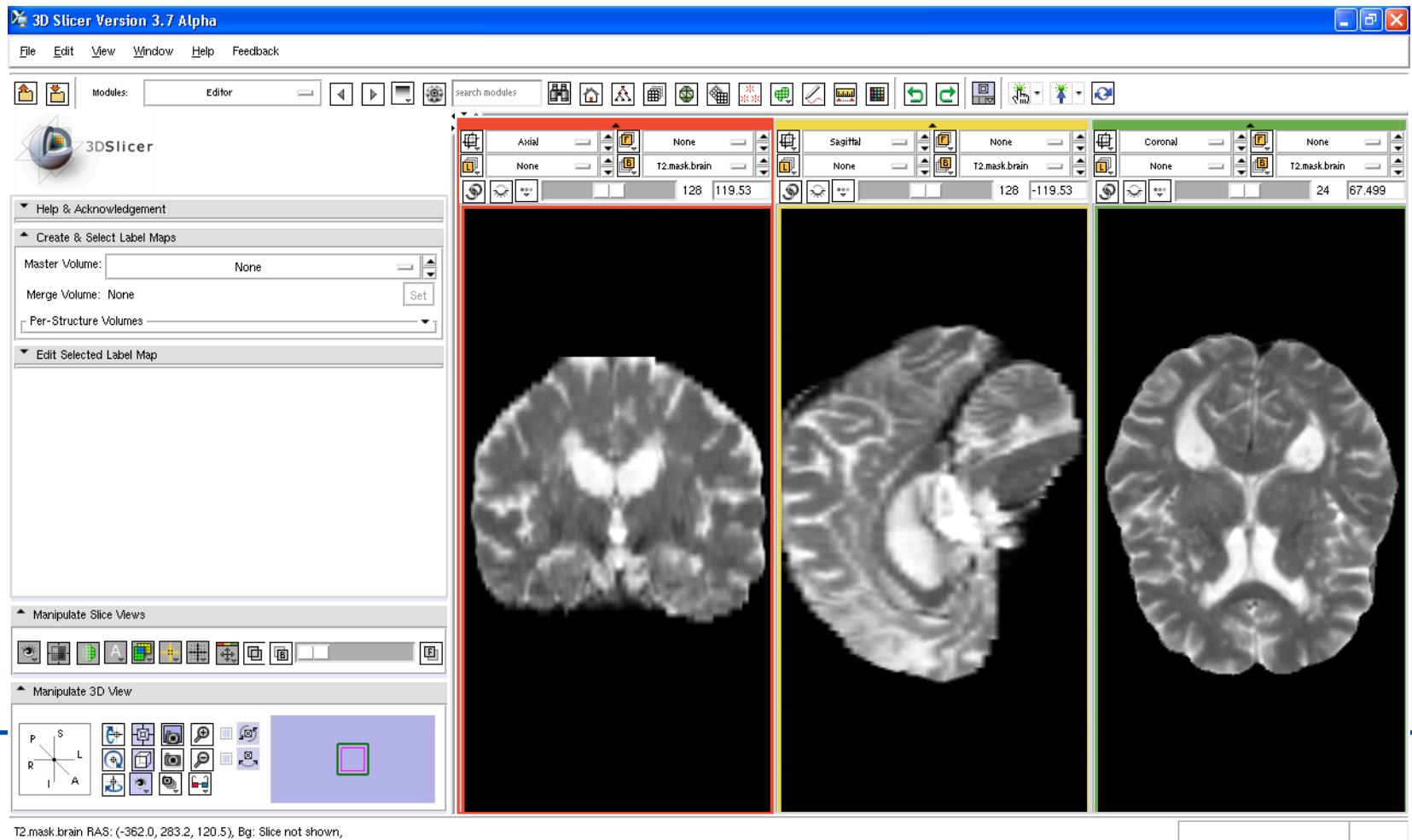


- Example of preprocessing – coregistration (FLAIR)



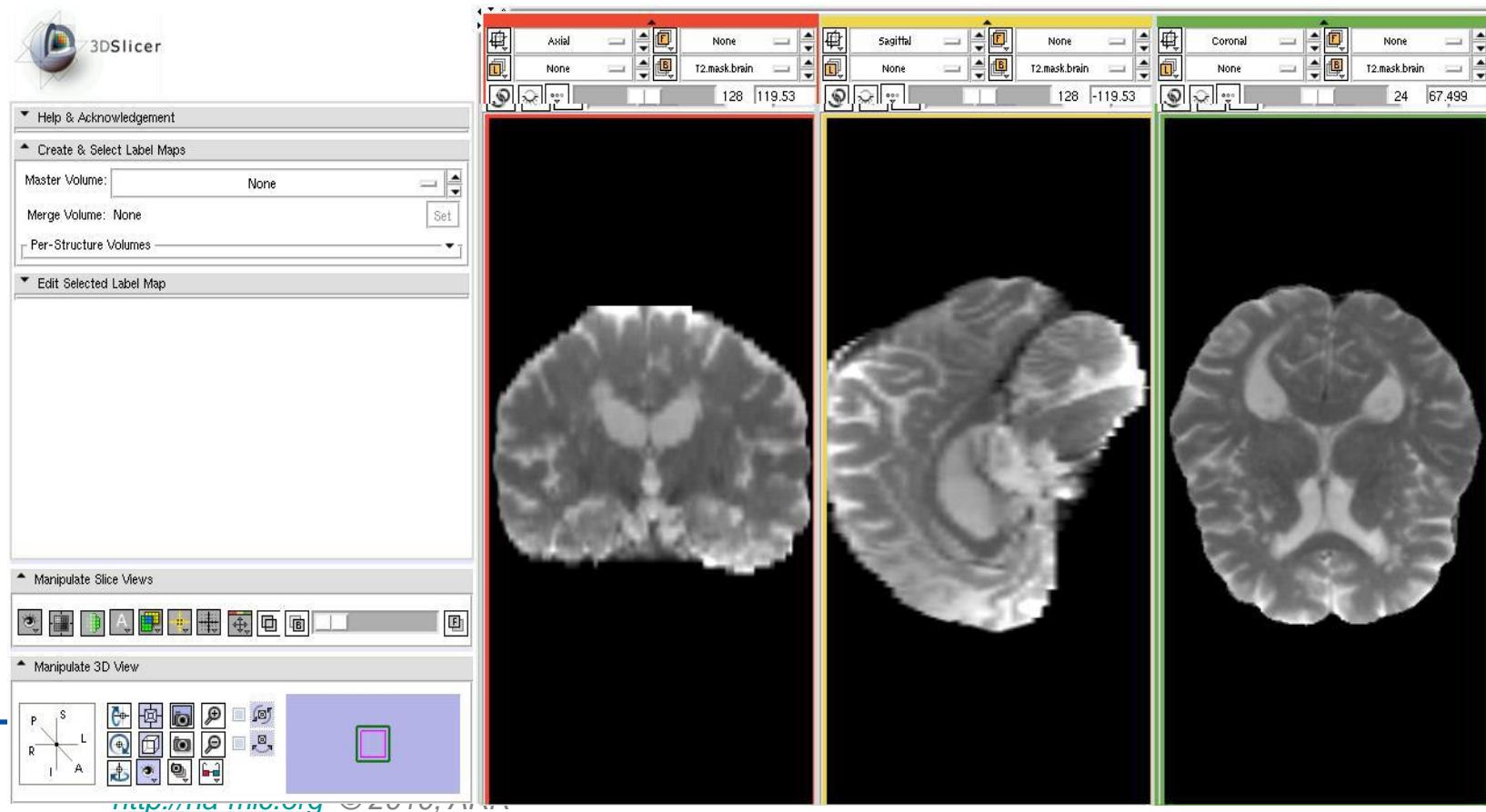


- Example of preprocessing – skull stripping





- Example of preprocessing – bias correction and histogram matching





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# Conclusion

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- A Slicer3 module for automatic segmentation of white matter lesions has been developed.
    - Preprocessing
      - Coregistration, skull stripping, bias correction, and histogram matching
    - Training
      - Build SVM model using multi-protocol MRIs (T1, T2, PD, and FLAIR)
    - Segmentation
      - Test new subject images using the SVM model built in the training stage
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# Acknowledgments

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