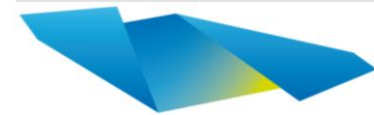




# 3D Slicer for DCE-MRI Image Analysis

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# Installers

	Windows	Mac OS X	Linux
<b>Stable Release</b> <i>older releases</i>	<b>version 4.10.2</b> revision 28257 built 2019-05-22	<b>version 4.10.2</b> revision 28257 built 2019-05-30	<b>version 4.10.2</b> revision 28257 built 2019-05-22
<b>Preview Release</b>	<b>version 4.11.0</b> revision 28431 built 2019-08-11	<b>version 4.11.0</b> revision 28431 built 2019-08-11	<b>version 4.11.0</b> revision 28431 built 2019-08-11

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

# Installations

\*Stable version required currently to access the required modules.

- Require 2 main Extensions to be installed:
- View → Extension Manager → Install Extensions → Search:



### PkModeling

PkModeling is a Slicer4 Extension that provides pharmacokinetic modeling for dynamic contrast enhanced MRI (DCE MRI). [More](#)

Disable

Uninstall



### T1Mapping

T1 mapping estimates effective tissue parameter maps (T1) from multi-spectral FLASH MRI scans with different flip angles. [More](#)

Disable






Uninstall

- Then restart Slicer.

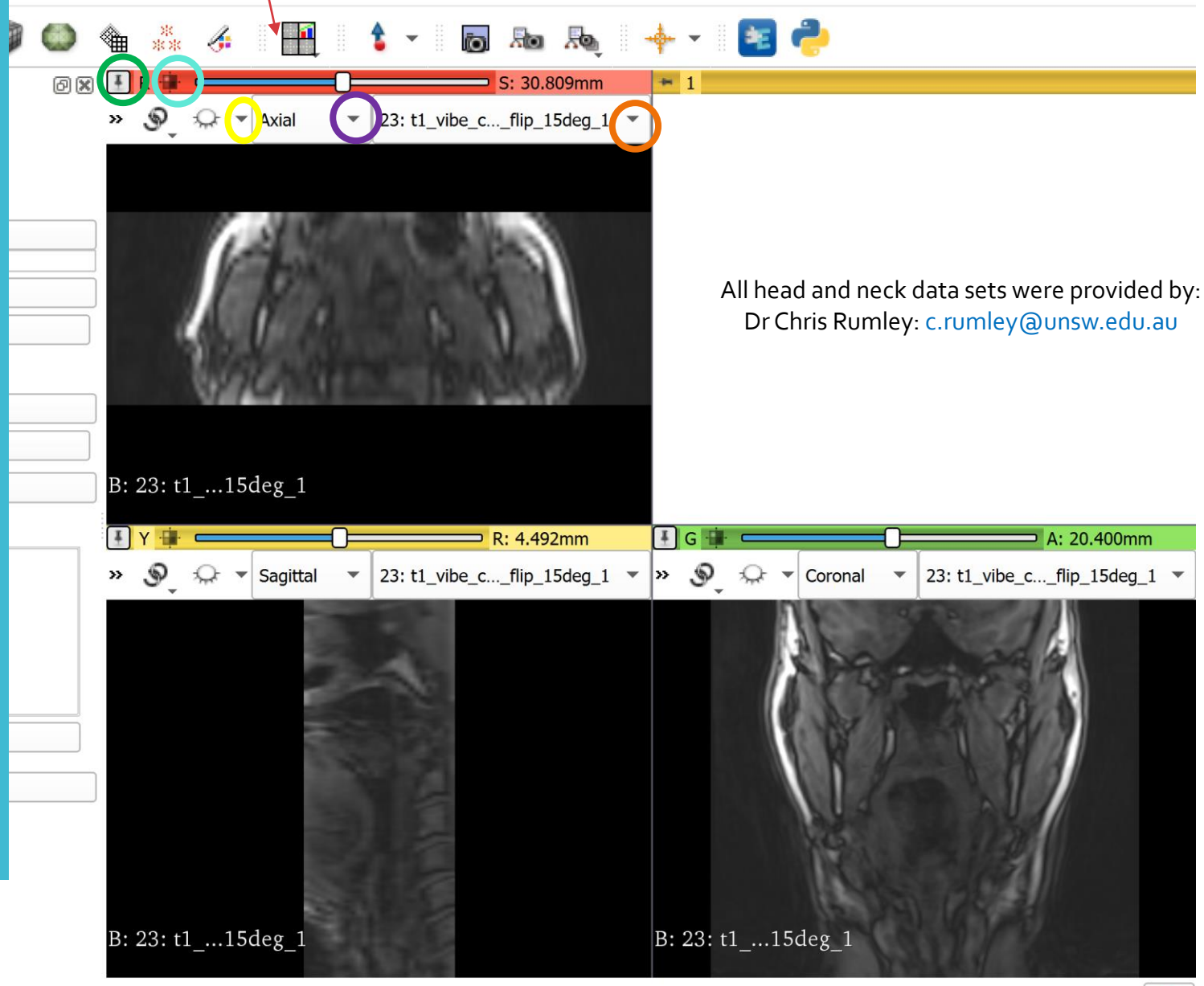
# Installations

# Navigating

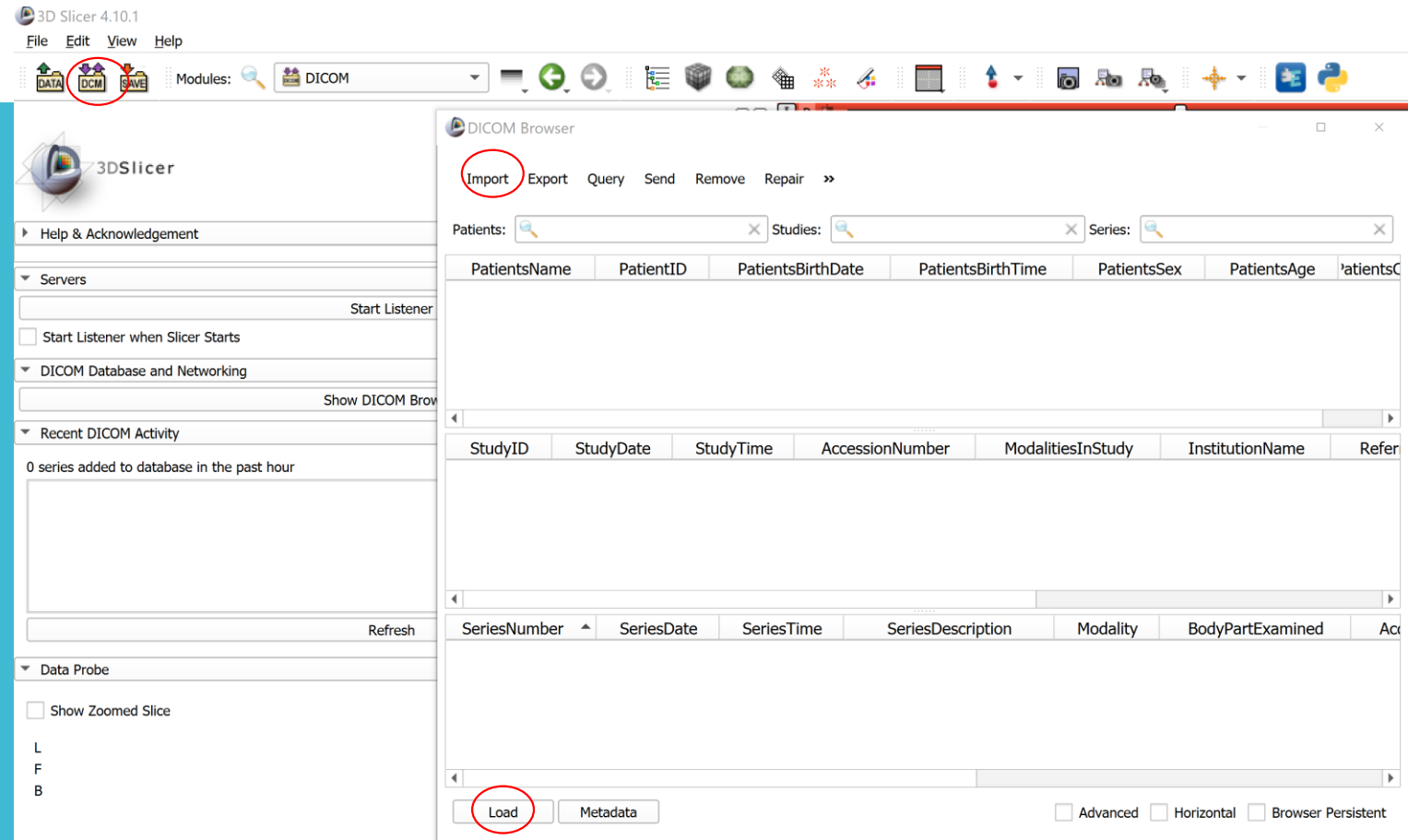
To change views below: E.g. Single or quad windows

-  To see image viewing options
-  Change plane of observation
-  Change image data set observing
-  Centre image
-  Set background and foreground preferences

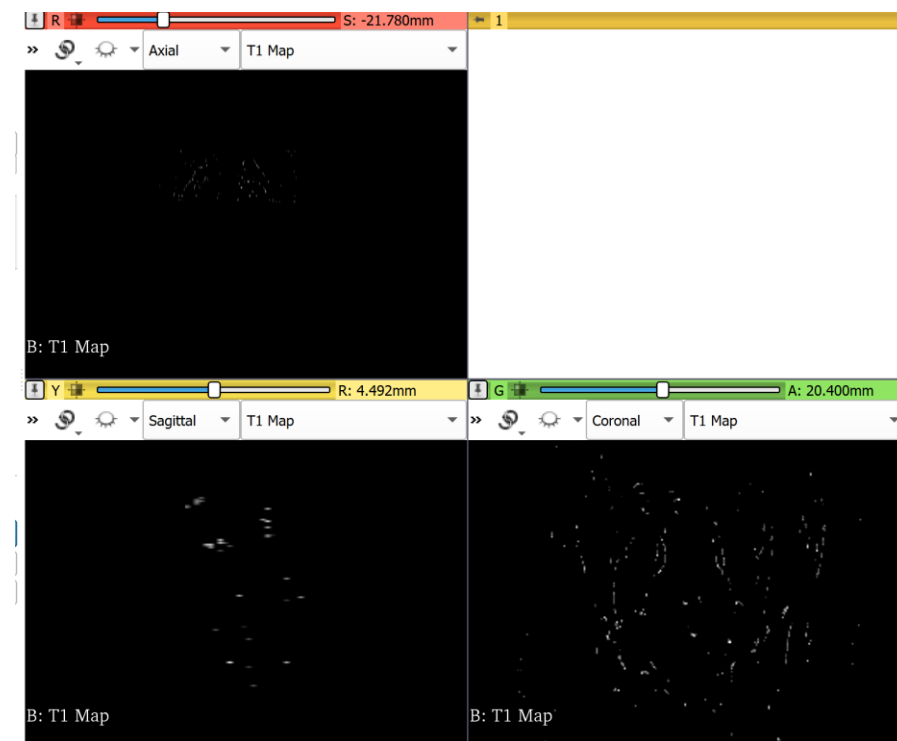
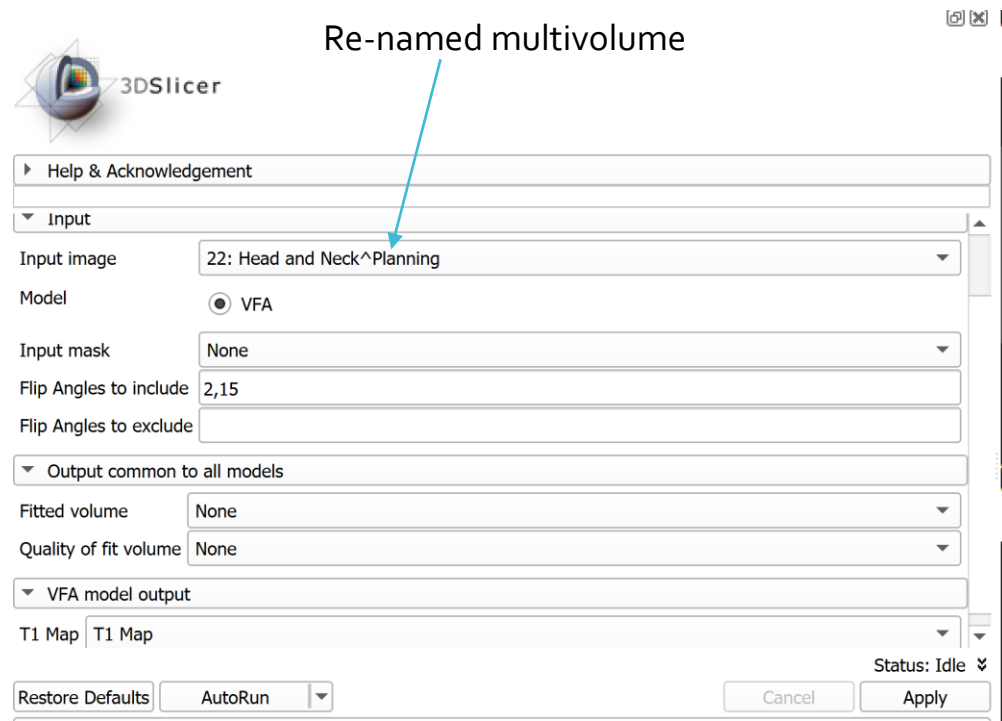
- Scroll over image to browse through slices
- Right click and scroll to zoom centrally on image
- Left click and scroll to change brightness of all images



# T<sub>1</sub>-Mapping using VFA Method



- DICOM Browser → Import: to load in VFA scan images
- Load in both flip angle scan data at the same time (select both folders)
  - This registers them together as a multi-volume; required for the T<sub>1</sub>-mapping module
  - Slicer will generally re-name the volume for you after the 'study name' in the DICOM header of the VFA scans



- Too see **theory** behind how this map was generated:
  - *Sung et al., 2013, Transmit B<sub>1</sub> + Field Inhomogeneity and T<sub>1</sub> Estimation Errors in Breast DCE-MRI at 3T*

- Input image: Must be in multi-volume format
- Model: VFA
- Type in FA's used, commas to separate
- Don't enter any in exclude box
- Output T1 Map → New Volume → T1 Map
- This will generate T1 map in 3D

# T<sub>1</sub>-Mapping

# Handling DCE-MRI Data Sets



## Exploration and Study of MultiVolume Image Data using 3D Slicer

Meysam Torabi and Andriy Fedorov  
[torabi@bwh.harvard.edu](mailto:torabi@bwh.harvard.edu), [fedorov@bwh.harvard.edu](mailto:fedorov@bwh.harvard.edu)

Surgical Navigation and Robotics Lab and Surgical Planning Lab,  
Brigham and Women's Hospital and Harvard Medical School, April 2013.

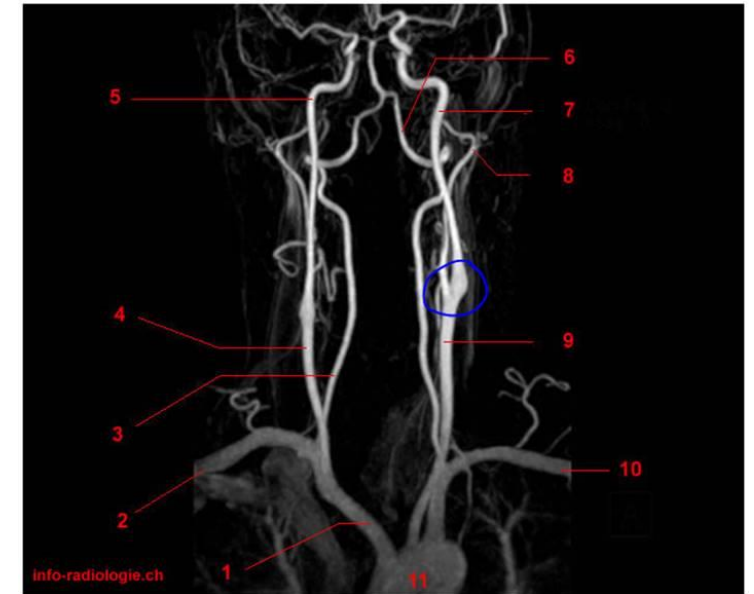
Surgical Planning Laboratory

[https://www.slicer.org/w/images/2/2c/MultiVolumeExplorer\\_Meysam\\_SNR-April2013-v3.pdf](https://www.slicer.org/w/images/2/2c/MultiVolumeExplorer_Meysam_SNR-April2013-v3.pdf)

- Loaded in as multi-volumes.
- To work with these, **see above slides**.

# Generating an AIF

- By now, you should have:
  - Loaded in your DCE image data set
  - Made them easier to observe in appearance
  - Selected a frame for analysis in coronal plane (can do any plane though)
  - Generated a T1 Map
- The next step is generating an AIF:
  - My example will be using the carotid carotid bulb/ carotid sinus for the head and neck.
  - Need location to have rapid uptake of contrast.



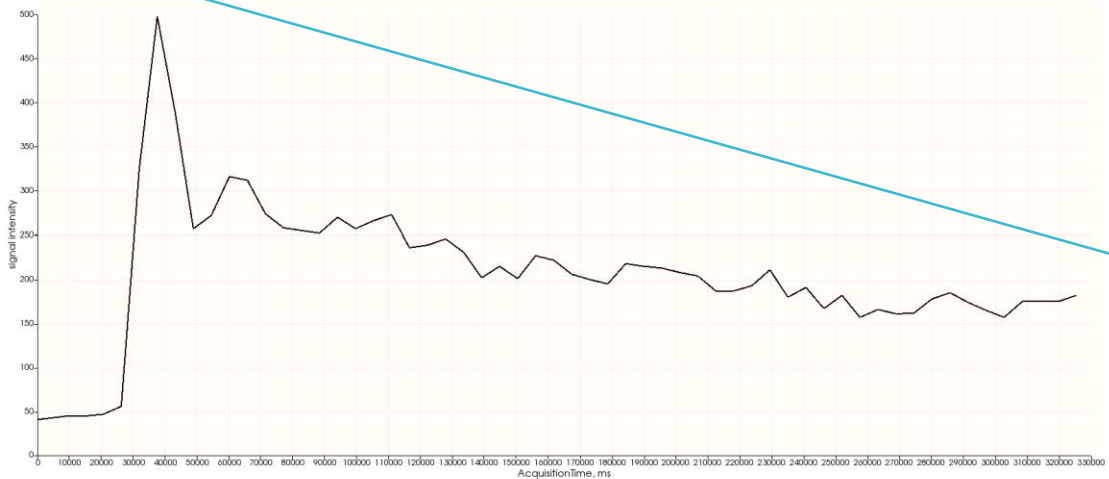




3DSlicer

Plotting Settings

Plotting



Undock chart

Data Probe

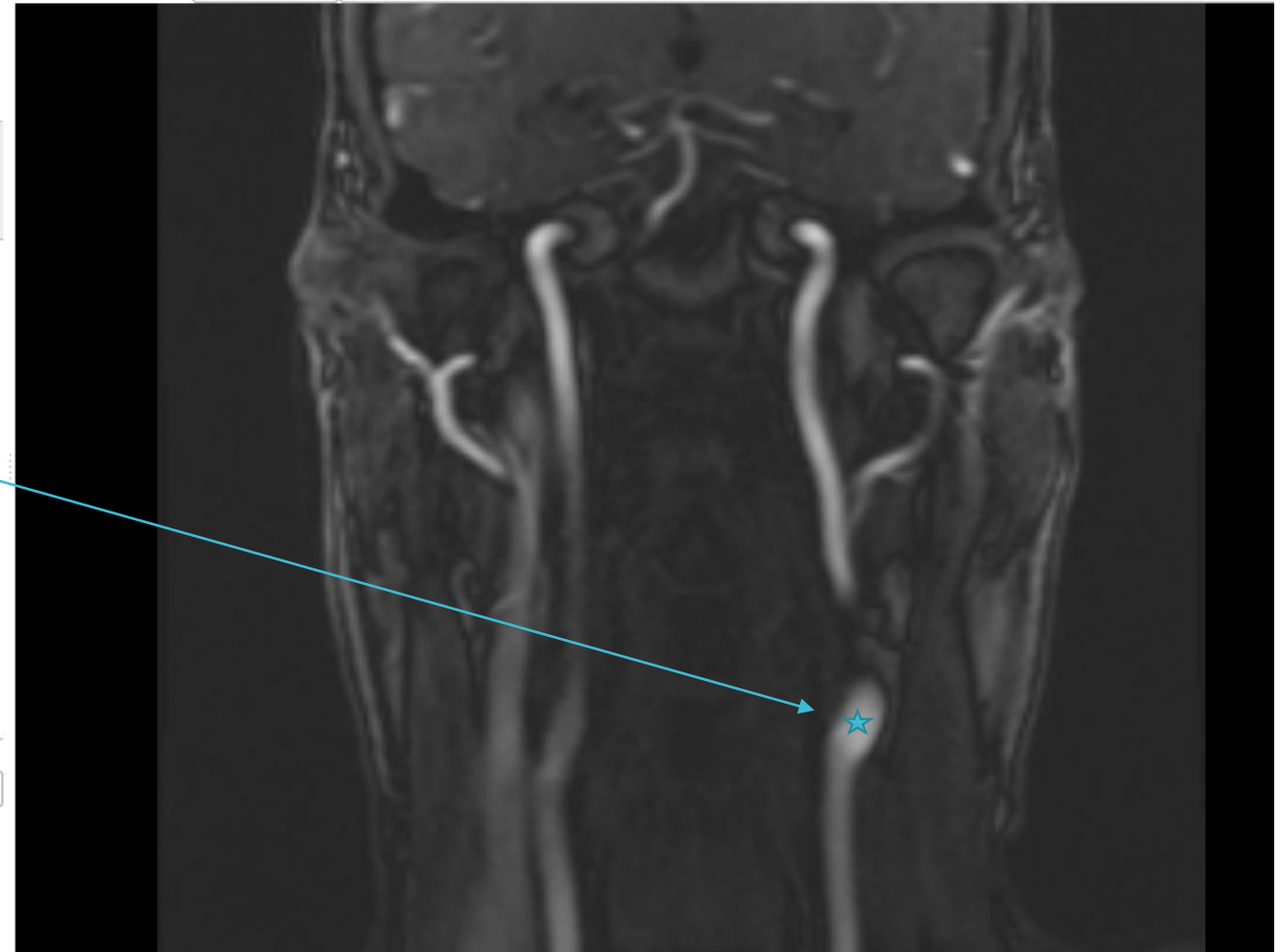
Green (L 34.8, P 0.6, I 19.9) Coronal Sp: 3.0

L None

F None

Still viewing original DCE image series

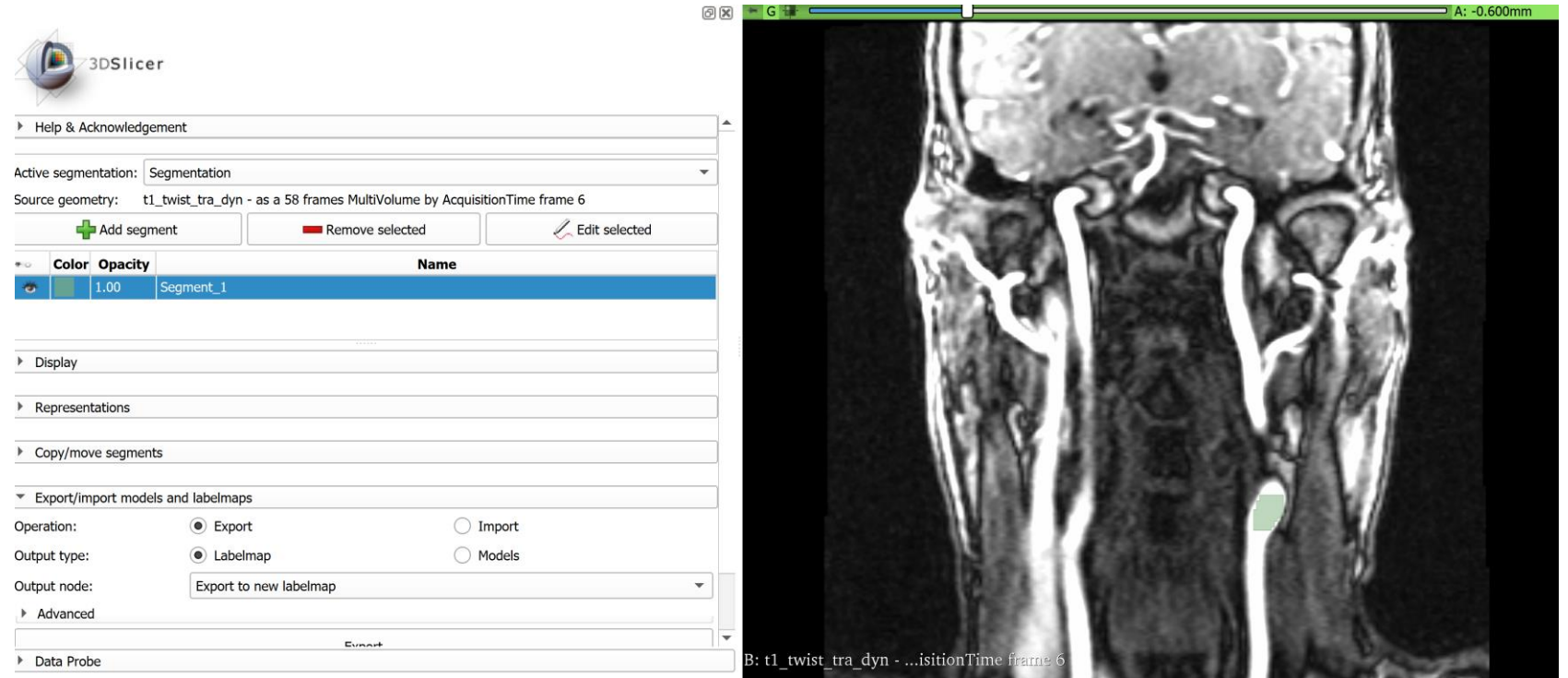
t1\_twist\_tra\_dyn - as a 58 frames MultiVolume by AcquisitionTime

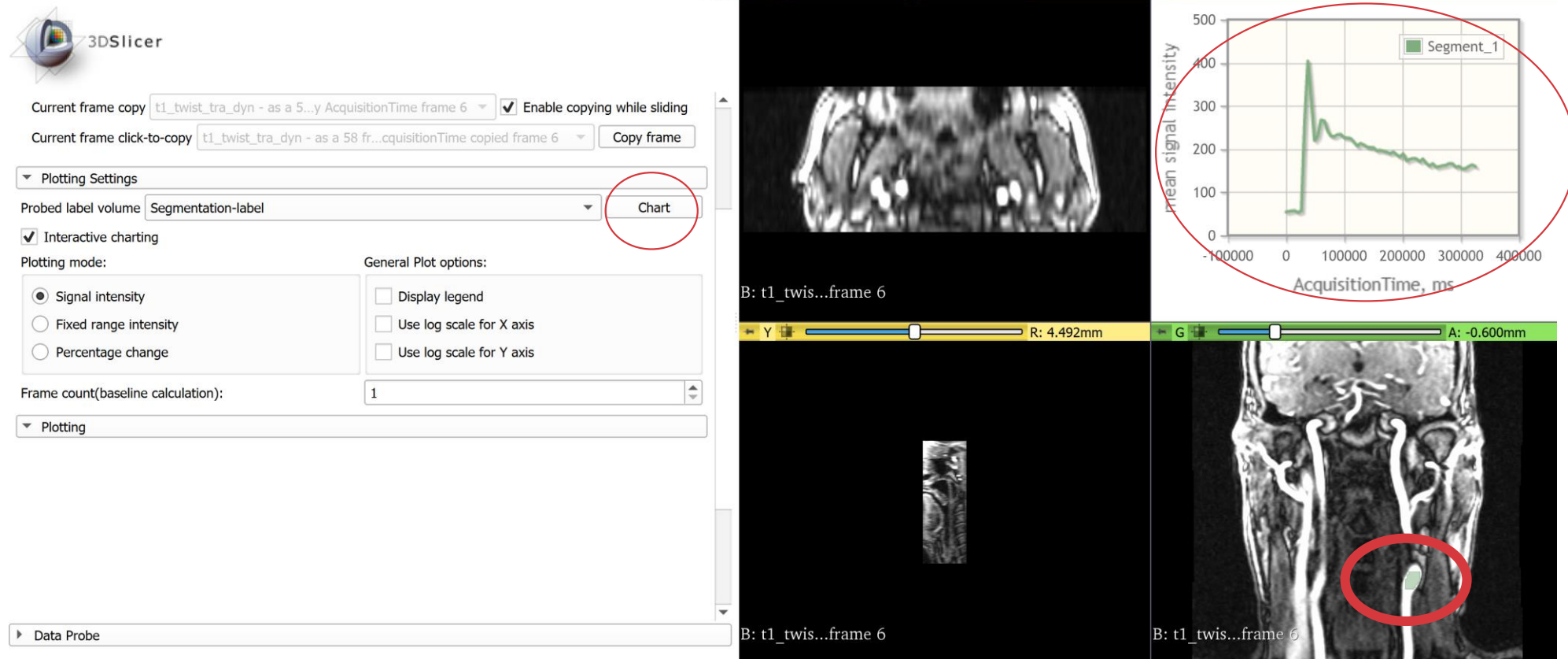


- MultiVolume Exporter → Select DCE series at desired spatial location as Input → Select frame (should be copied already) → Observe plot to see signal uptake vs time.

# AIF Generation

- Segment Editor Module → Select desired frame from series → Add segment
- Use any drawing tool of choice (e.g. paint) over approx. uniform ROI that highlighted good uptake.
- *Export to new label map*





## AIF Generation

- Multivolume Exporter → Use desired frame → Plotting Settings
- Select your exported segmentation to be the probed label volume
- Chart
  - Easiest observation: Set viewing to 4-Up Quantitative
  - The shape of the uptake will be used as your AIF.

# PK-Modeling Module

Now to combine all previous steps

- **PKModeling Module:**

- Parameters will be auto-set to standardised prostate DCE-MRI parameters.
- Alter accordingly for your particular body region and contrast media.
- T<sub>1</sub> overall tissue value will have to be estimated from your T<sub>1</sub> Map or assumed from literature\*.
- Can get individual patient haematocrit values- but generally okay to use a population standard.

The screenshot displays the PKModeling module interface. At the top, a dropdown menu is set to 'PkModeling'. Below it, the 'Parameter set:' dropdown is also set to 'PkModeling'. The 'PkModeling Parameters' section contains several input fields: 'T1 Blood Value' (1600.00), 'T1 Tissue Value' (1597.00), 'Relaxivity Value' (0.0039), 'Hematocrit Value' (0.4), and 'AUC Time Interval Value' (90.00). There is a checkbox for 'Compute fpv (3-parameter model)' which is currently unchecked. The 'AIF Mode' section has three radio buttons: 'AverageUnderAIFMask' (selected), 'Population', and 'Prescribed'. At the bottom, there is a dropdown menu set to 'IO'.

- **For AIF Mode:**

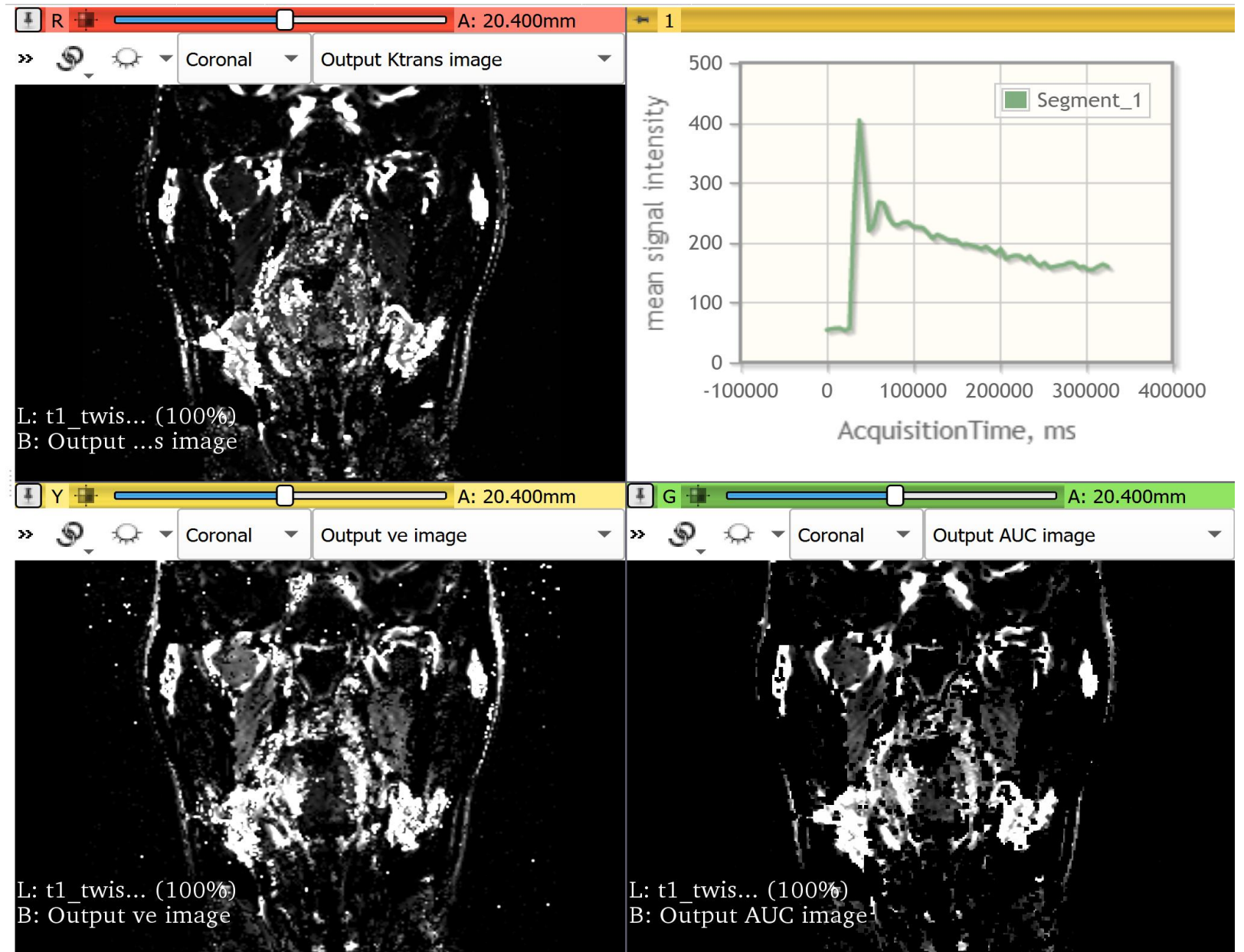
- Select **AverageUnderAIFMask** if last step completed for segment map
- Can use Population based for estimate but not as accurate for individual.
- *Cont.*

# PK-Modelling Module

▼ IO	
Input 4D Image	t1_twist_tra_dyn - as a 58 frames MultiVolume by AcquisitionTime ▼
ROI Mask Image	None ▼
T1 Map Image	T1 Map ▼
AIF Mask Image	Segmentation-label ▼
Prescribed AIF	None ▼
Output Ktrans image	Output Ktrans image ▼
Output ve image	Output ve image ▼
Output fpv image	None ▼
Output maximum slope image	None ▼
Output AUC image	Output AUC image ▼
▶ Advanced options ▼	

- **Input** as above:
  - Input 4D image is your DCE-Data set
  - ROI Mask Image if you have your known ROI already (not included above)
  - Input your T1 map and Segment-label generated prior
    - If using a population based AIF, leave the AIF Mask field blank.
- **Output:** The parameter maps you desire (save each as new volume maps).

# The Output

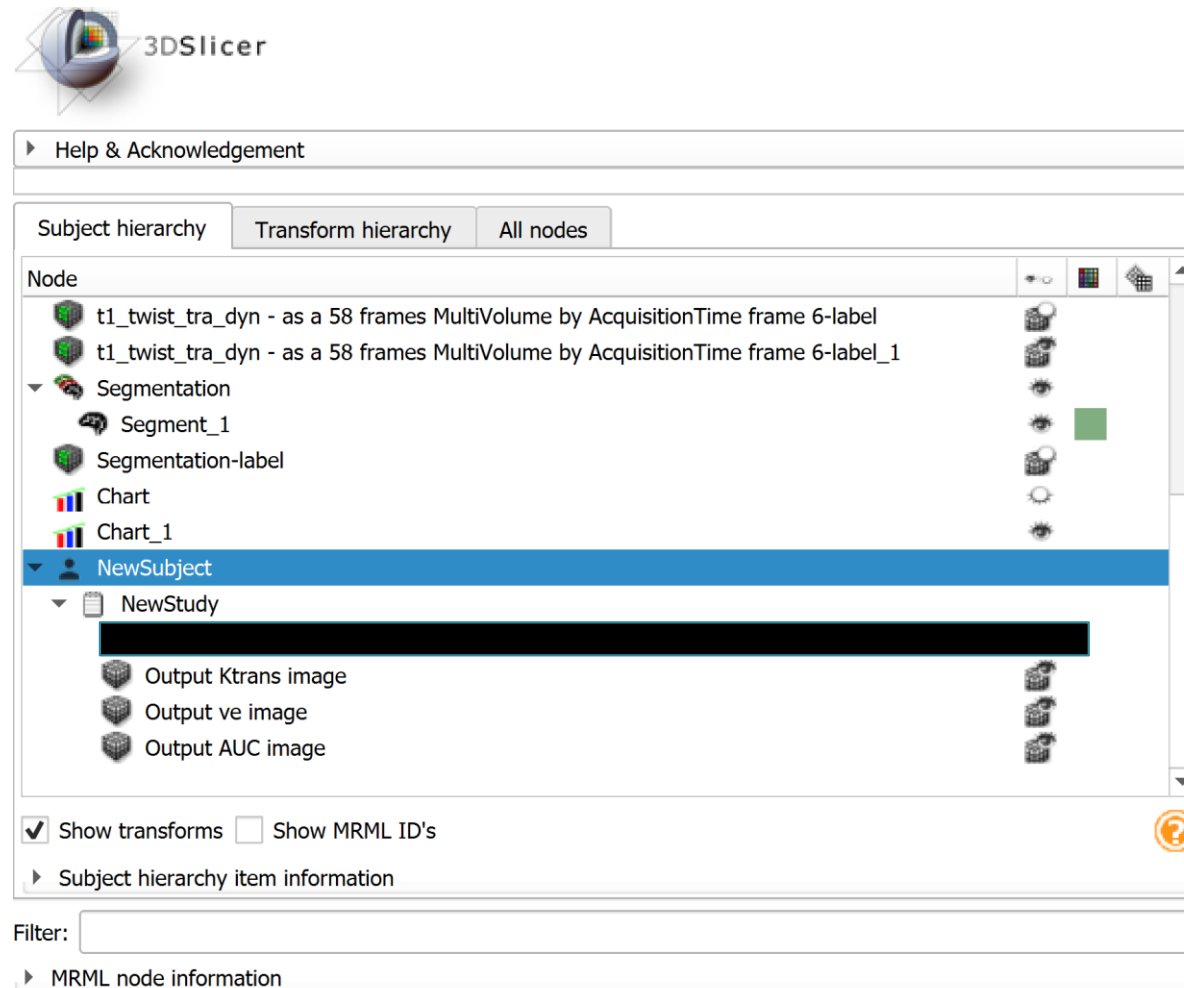


# Exporting

- There are several exporting methods for the PK Maps:
  - Direct DICOM Export
    - Requires the Quantitative Reporting extension installed or to apply a scaling filter beforehand: Want float-point values to be conserved.
  - Nrrd (standard- recommended)
    - E.g. Using nrrd reader on MATLAB or Python for analysis.
  - MatlabBridge extension
    - MATLAB only based analysis.



# Export to DICOM



- Open: **Data Module**
- Create 'New Subject' (right click in blank space)
  - Create new 'Child Study'
  - Drag maps into 'New Study'
- Right click on the New Study → Export to DICOM

\*T1-map can require a different subject → See next 2 slides.



# Export

DICOM Export

☒ Export series ☐ Export entire scene

1. Select node

Node

- PlotChart
- bgChartTable
- t1\_twist\_tra\_dyn - as a 58 fra...
- t1\_twist\_tra\_dyn - as a 58 fra...
- t1\_twist\_tra\_dyn - as a 58 fra...
- t1\_twist\_tra\_dyn - as a 58 fra...
- Segmentation
  - Segment\_1
- Segmentation-label
- Chart

2. Select export type

Scalar Volume (50%, 4 series) (DICOMScalarVolu

3. Edit DICOM tags

Patient tag name	Value
PatientBirthDate	
PatientComments	
PatientID	PK Maps
PatientName	
PatientSex	

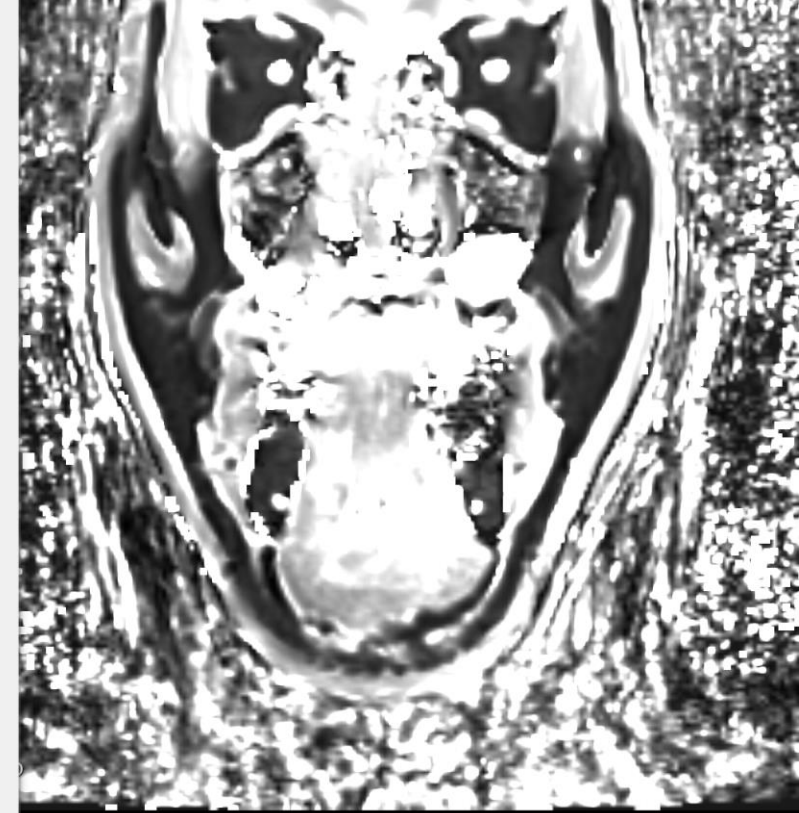
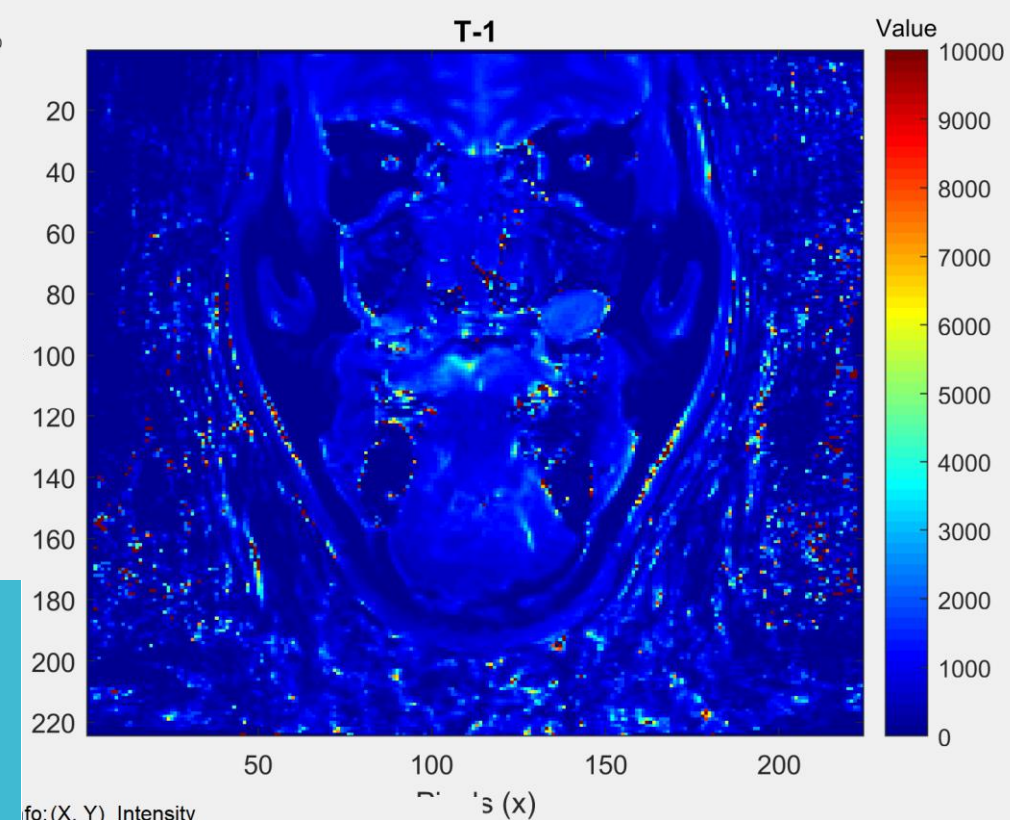
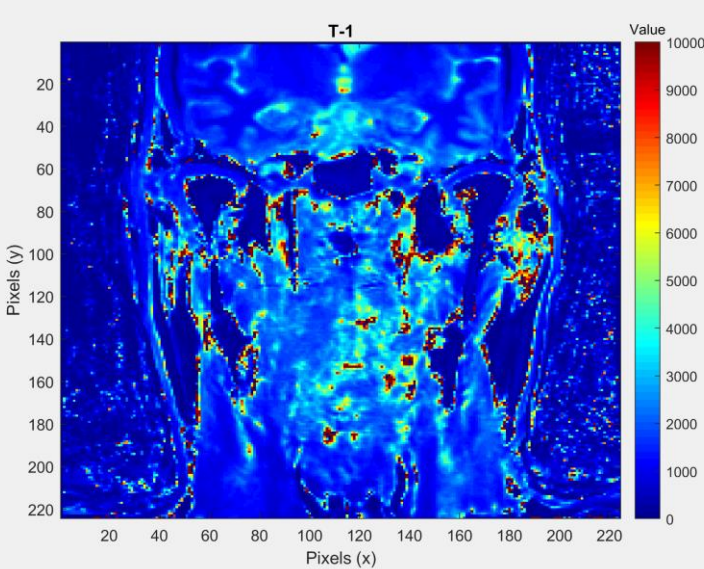
Study tag name	Value
StudyDate	
StudyDescription	
StudyTime	
'Output Xtrans image' series	

☒ Save tags to scene ☒ Import exported data

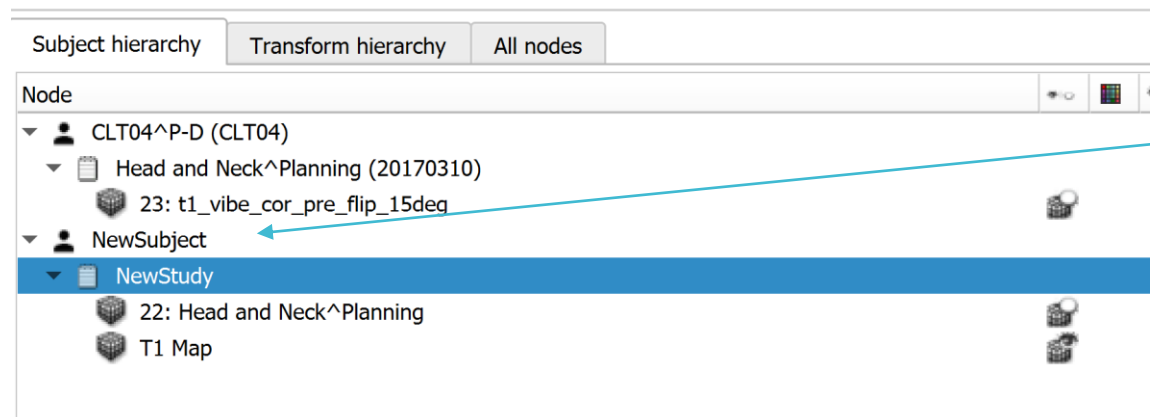
Output folder: C:/Users/madel/Desktop/DCE

Export

- Each parameter map in the study will be saved to a different folder.



# T<sub>1</sub>-map to DICOM



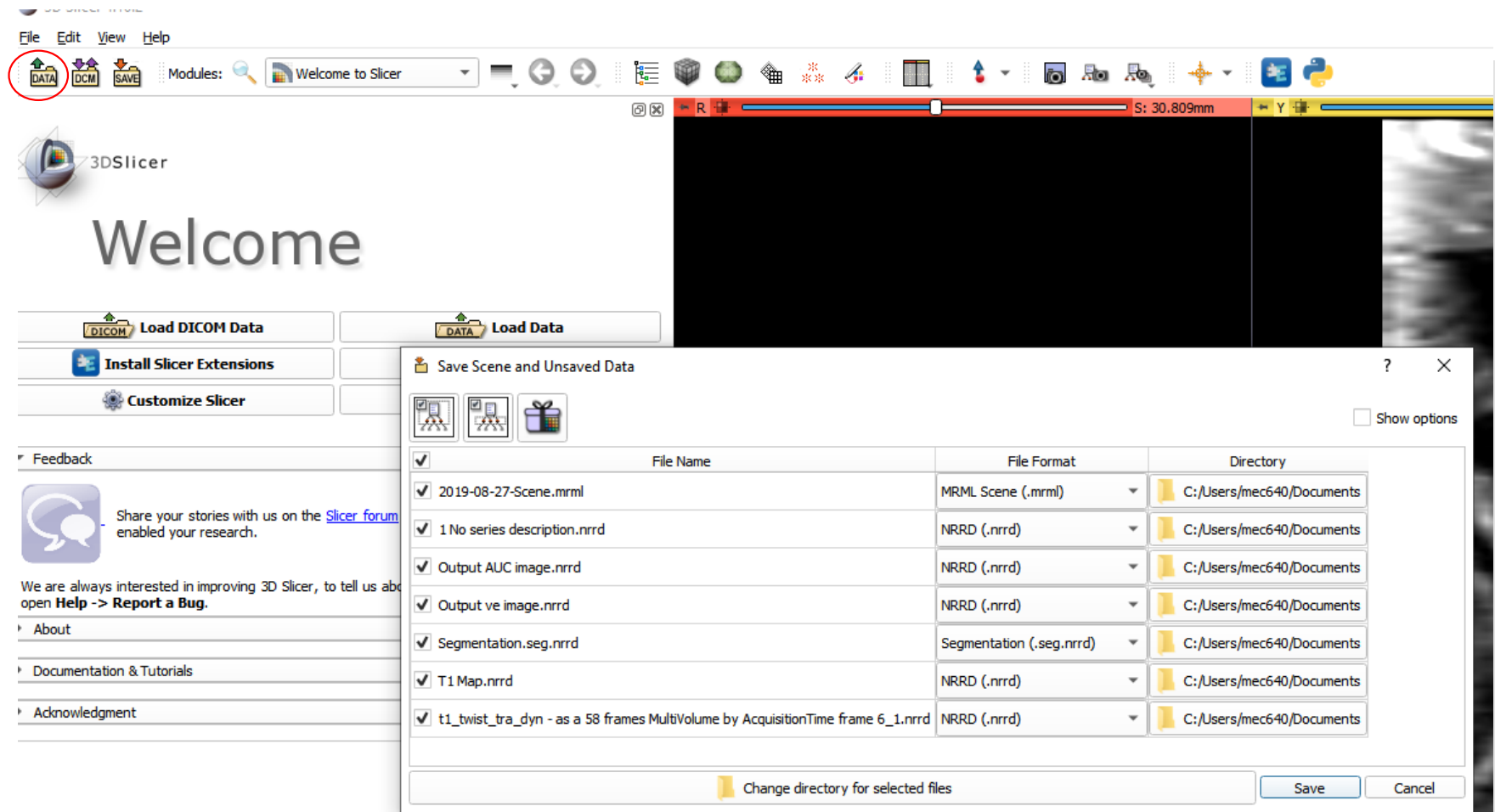
- Complete previous process with moving the T<sub>1</sub> map to same new study as the combined VFA multivolume.

# Simple MATLAB Code (DICOM)

- First open **DICOM Image Reader Application (Matlab2018+)** and export image of choice to the workspace (e.g. as 't1'). Then use:

```
figure;  
imagesc(t1)  
title(['T-1'])  
hi=colorbar('eastoutside');  
k = jet(7);  
colormap('jet');  
title(hi,'Value')  
caxis([0 10000]);  
xlabel('Pixels (x)') % x-axis label  
ylabel('Pixels (y)') % y-axis label  
impixelinfo()  
m = mean(t1(:));  
disp(m)
```

# Export to nrrd



- Save scenes as nrrd files:
  - Allows you to work on them again on Slicer directly
  - Easily opened by MATLAB and Python

<https://github.com/PerkLab/SlicerMatlabBridge/blob/master/MatlabCommander/commandserver/nrrdread.m>

# Simple MATLAB Code (nrrd)

- Download nrrdread.m and then call the function using your image data set:

```
image = nrrdread('Output ve image.nrrd')  
T_matrix=[224 224 26]; %[height width #slices]  
M1 = repmat(single(o), T_matrix);
```

```
for m1 = 1:26  
    M1(:, :, m1) = image.pixelData();  
End
```

```
for F = 1:26  
    imshow3D(M1)  
    title(['Slice #', num2str(F)])  
    hi=colorbar('eastoutside');  
    k = jet(7);  
    colormap('jet');  
    title(hi,'PK Map')  
    caxis([0 2]);  
    xlabel('Pixels (x)') % x-axis label  
    ylabel('Pixels (y)') % y-axis label  
end
```

