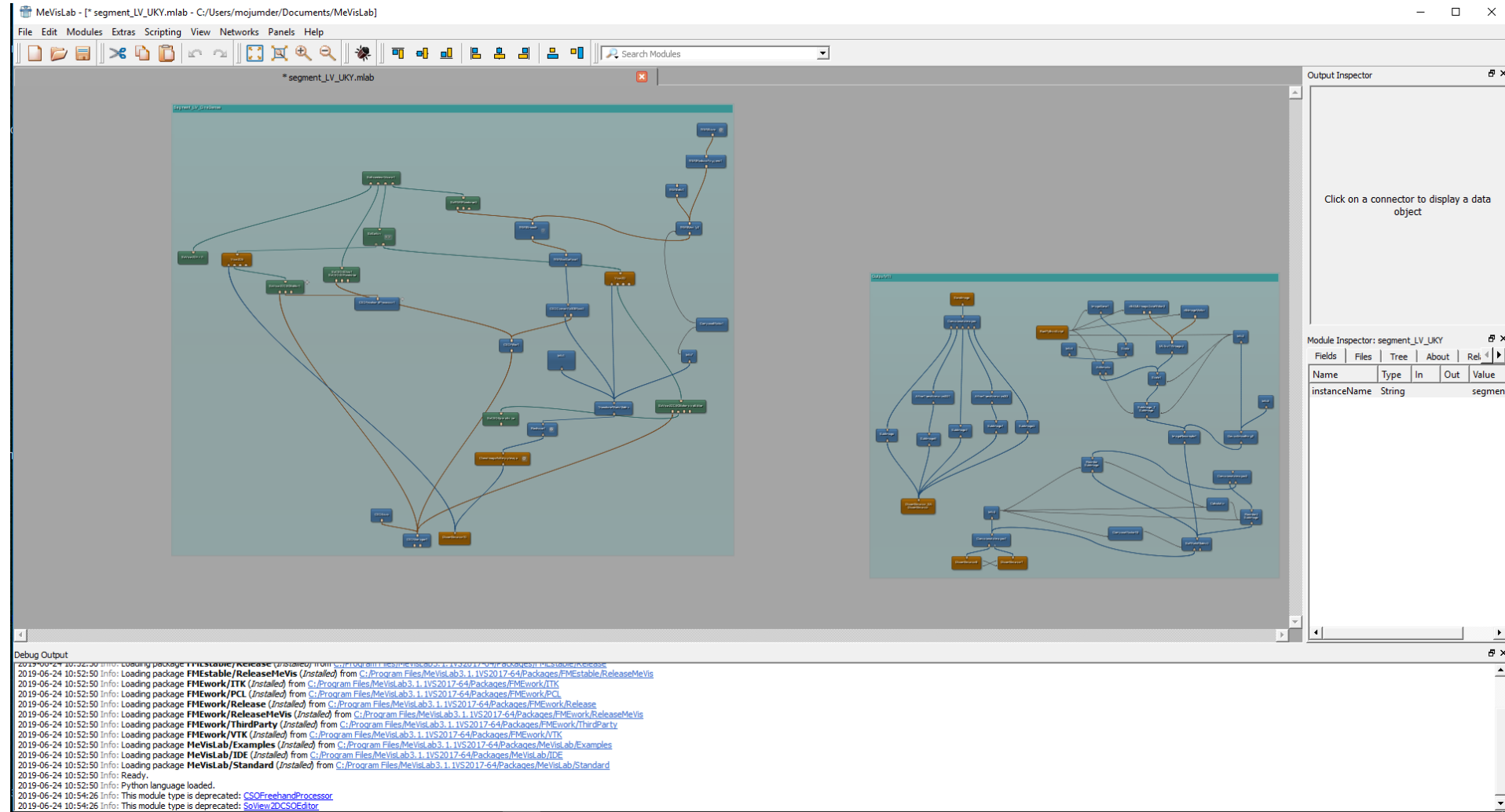
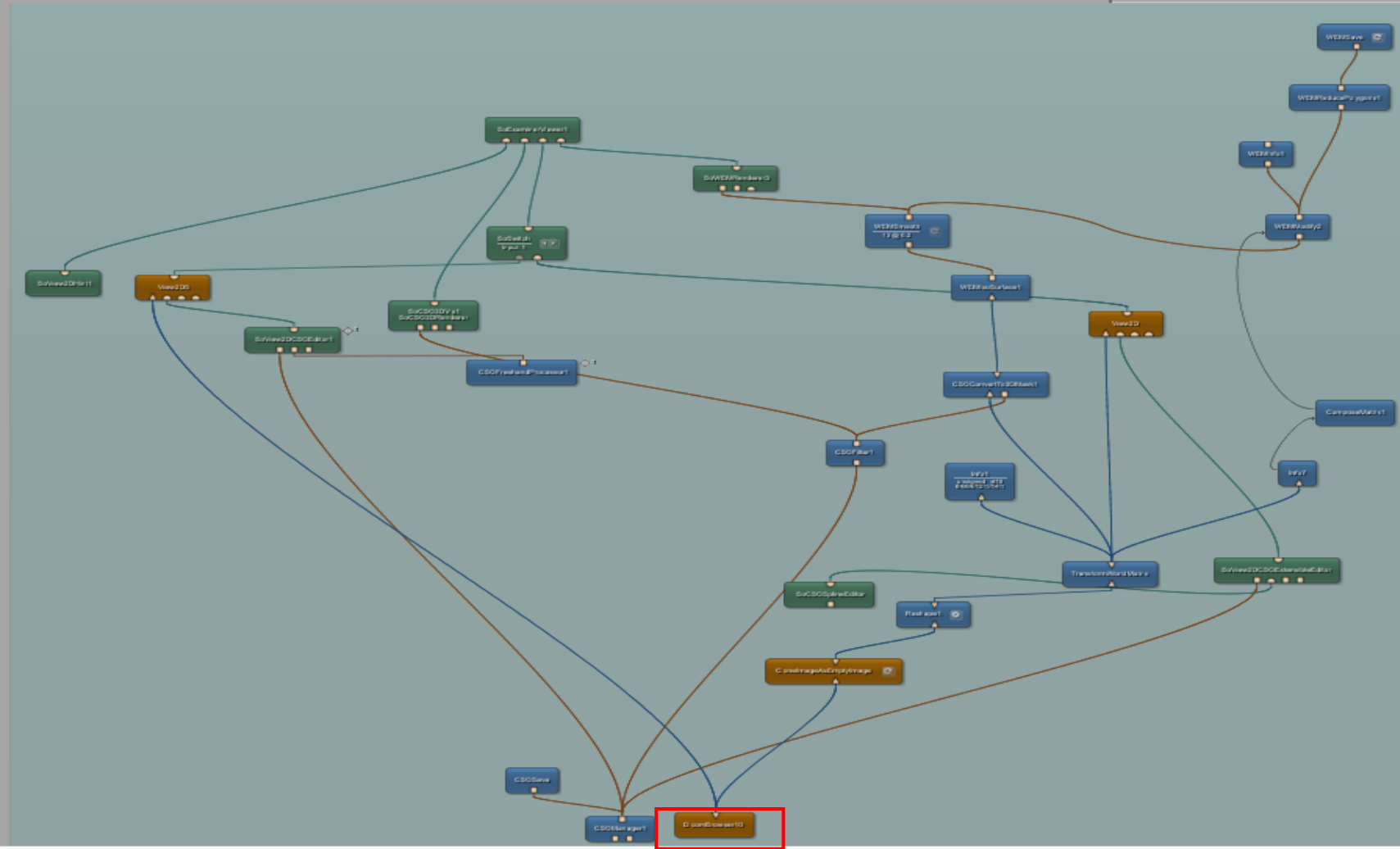


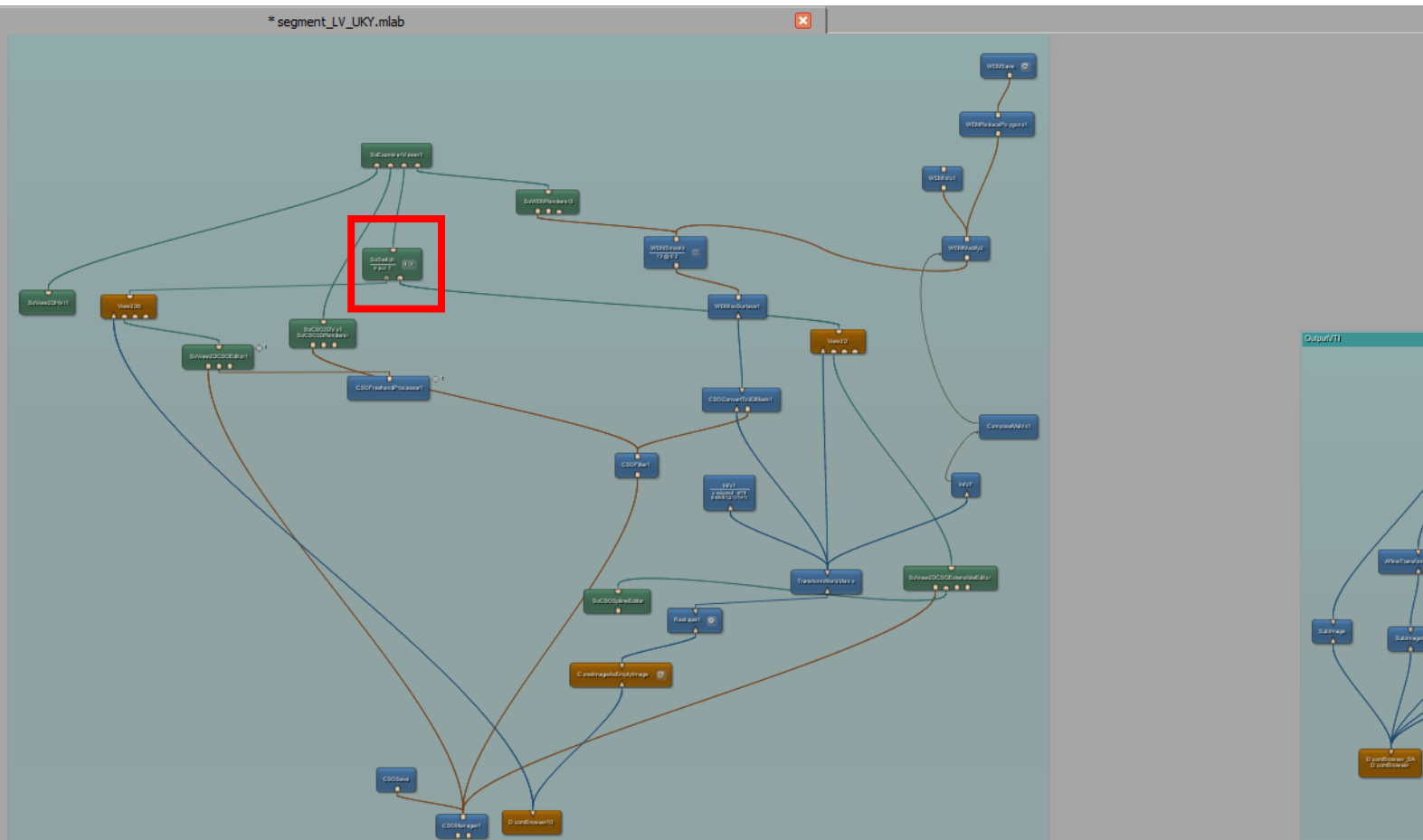
MRI Image Segmentation

After loading segment_LV_UKY.mlab file at MeVisLab, the following picture will be shown.

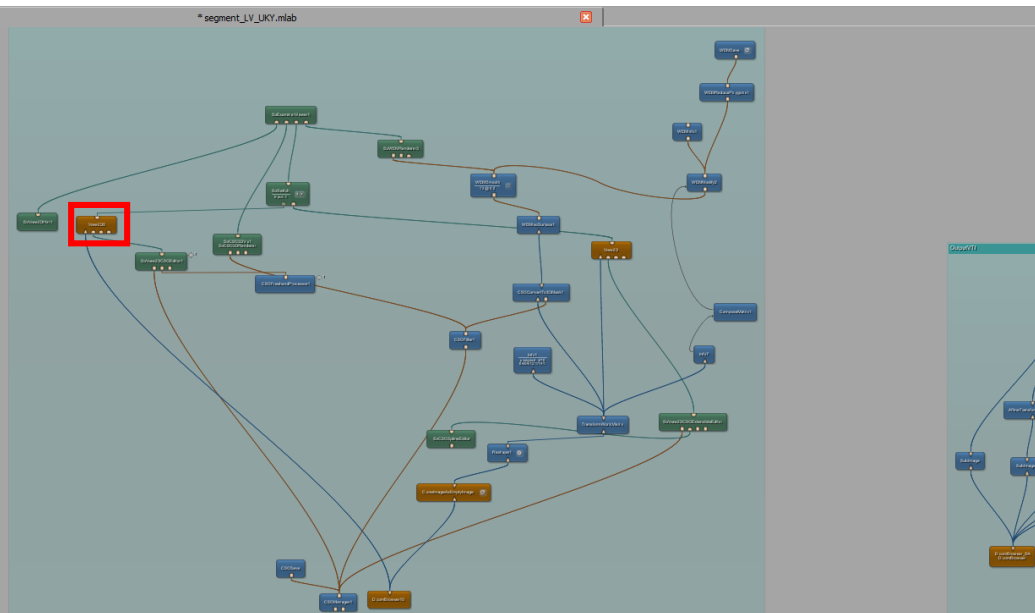




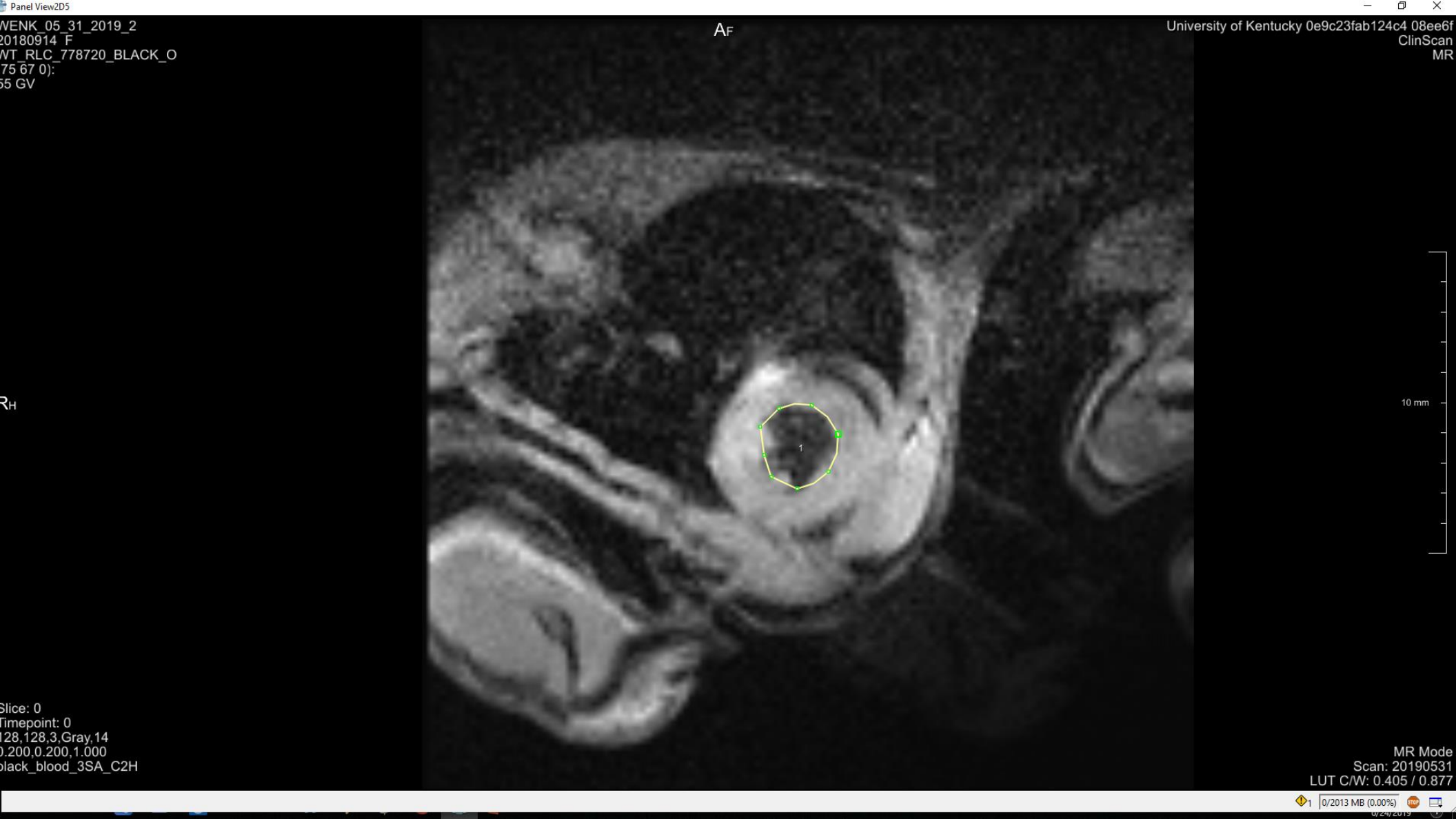
- Double click on “DicomBrowser10” (Red box).
- browse the folder where the mri images are stored
- double click on black_blood_3SA_C2H
- exit the screen by clicking x sign of the top-right



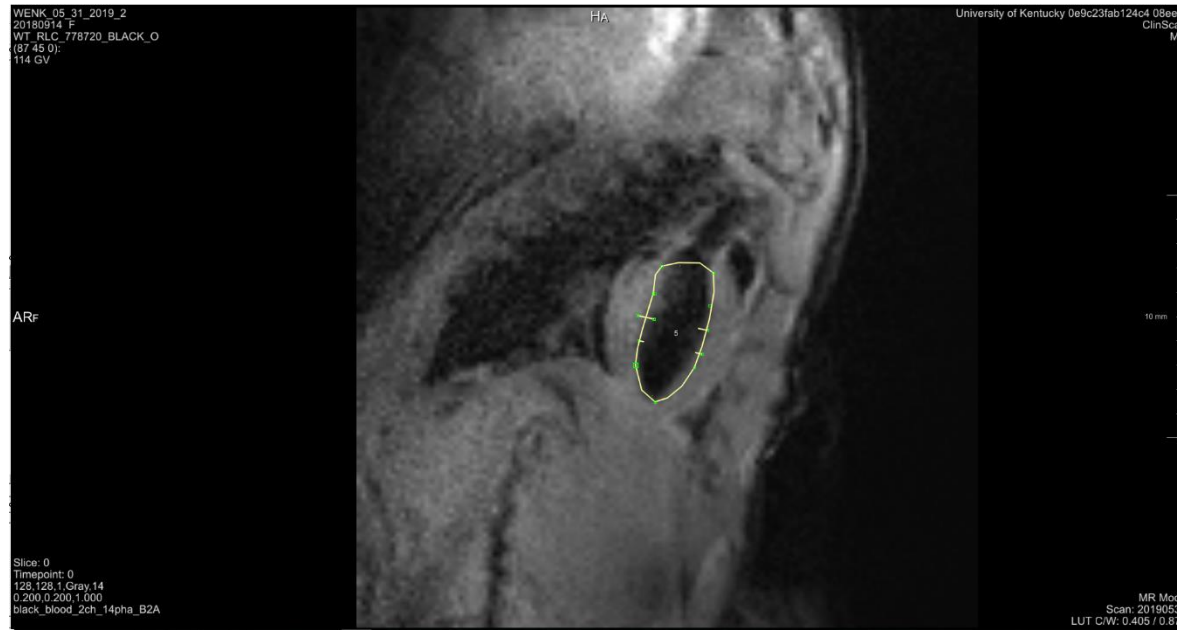
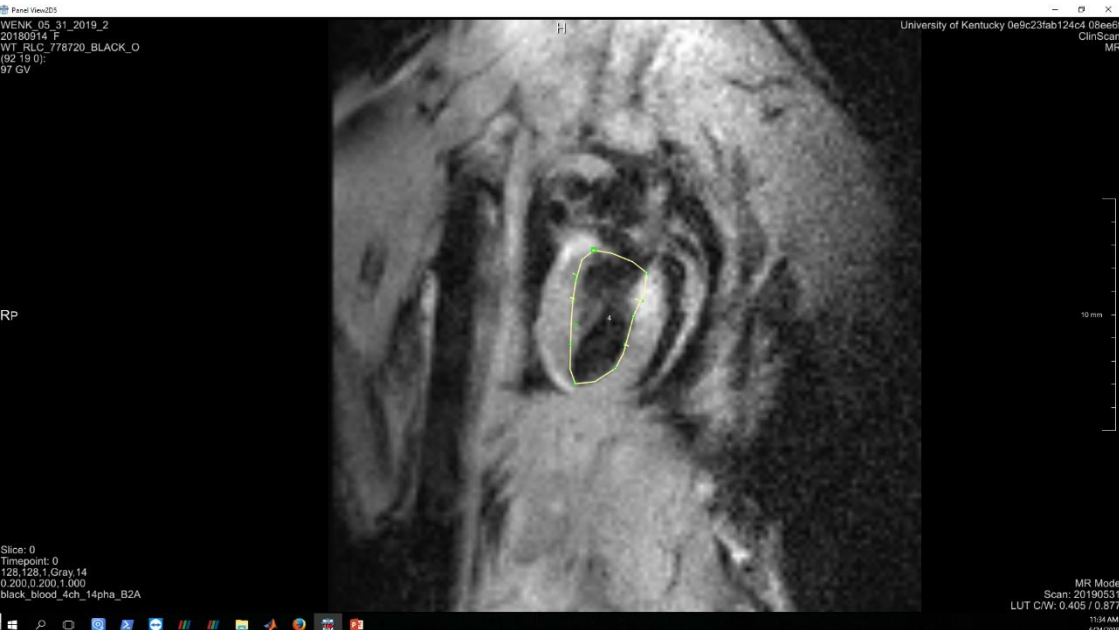
- double click on "SoSwitch" [Red Box]
- Which Child = 0



- Double click on “View2D5” module . The right picture will be appeared.
- You can change the slice by using up (↑)and down (↓) arrow of the keyboard or the scroll of the mouse .
- you can change the timepoint by using left (←) and right(→) arrow of the keyboard.
- you can change the brightness by holding down the right button of the mouse and moving the mouse simultaneously.
- you can draw line by holding down the left button of the mouse. Next slide.

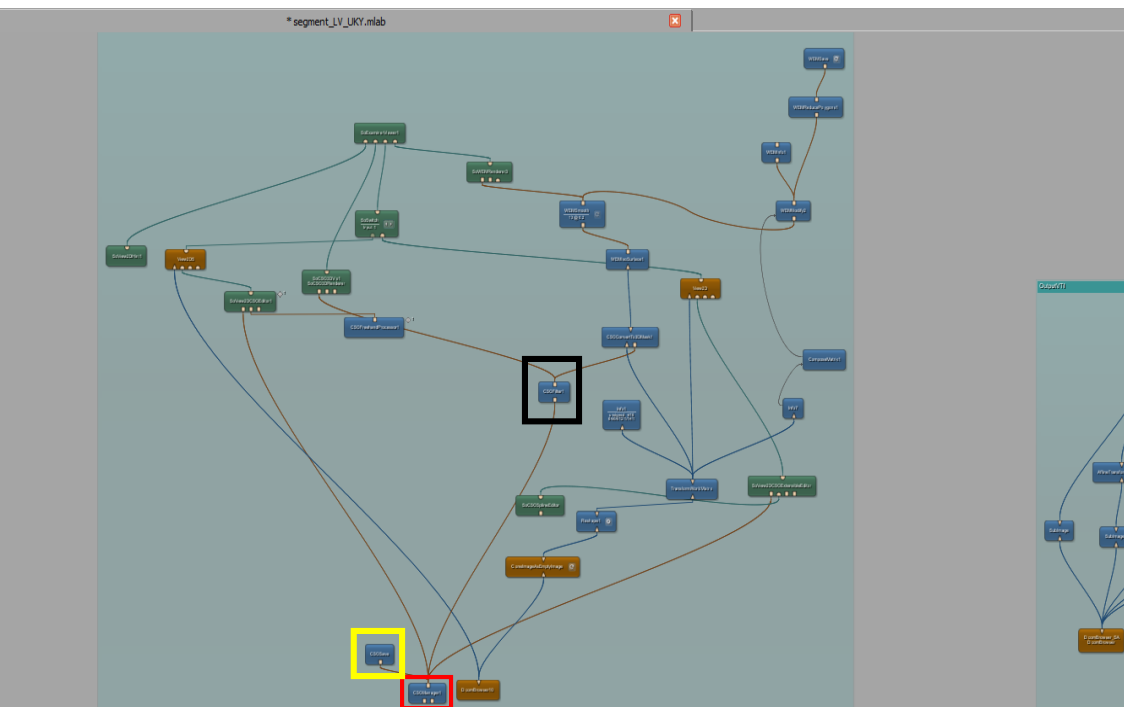


- Using the left button of the mouse, you can draw line on the image. You can move the green square to select your favorable region.
- do the same thing for every slice of a specific timepoint. The choice of timepoint depends on your decision.



- Double click “DicomBrowser10”, browse the folder with mri images, double click on “black_blood_4ch_14pha_B2A”
- Draw the contour as described before . An example of final image is shown is left picture
- close the screen

- Double click “DicomBrowser10”, browse the folder with mri images, double click on “black_blood_2ch_14pha_B2A”
- Draw the contour as described before . An example of final image is shown is right picture
- close the screen



Panel CSOManager1

Commands: Remove All, Undo, Redo, Combine, Break

CSO [5]

Id	Label	Group
1	endo_iv	1
2		1
3		1
4		1
5		1

Group [1]

Id	Label	CSO
1	endo_iv	1,2,3,4,5

Parameters: CSO, Group, Notifications, Selection

Group Parameters: Common, Visuals, Misc

Id: 1

Label: endo_M

Desc:

☐ Use ☒ Show ☒ Voxelize ☒ Editable

Time Point Index: 0

Delete Copy New Delete Copy

Work directly on input CSO list. Copy from CSO list.

Enable Undo/Redo Undo Check Undo

-- Double click on “CSOManager1” [red box in picture]

-- Select group

-- Label it .

-- Double click on “CSOFilter1”. [Black Square box] Bottom-right image will appear.

-- Input should be same as Label. This is CASE SENSITIVE.

-- Hit the “update button”. CSO Ids will appear.

-- These CSO Ids should be same. [Numbers in two red oval shape should match]

-- save the image using “CSOSave” [Yellow box]

Panel CSOFilter1

General | CSO Actions | Group Actions

CSO | Group

Manual Group Input

Input: endo_iv Sep:

Filter Mode: Include Eval. String As: Label

Add All Existing Groups Clear Group Input String

Automatically Fill CSOGroups On Notifications

☐ All selected ☐ All shown

☐ All voxelize ☐ All editable

☒ Listen to finishing

☒ Listen to selection changes

Output

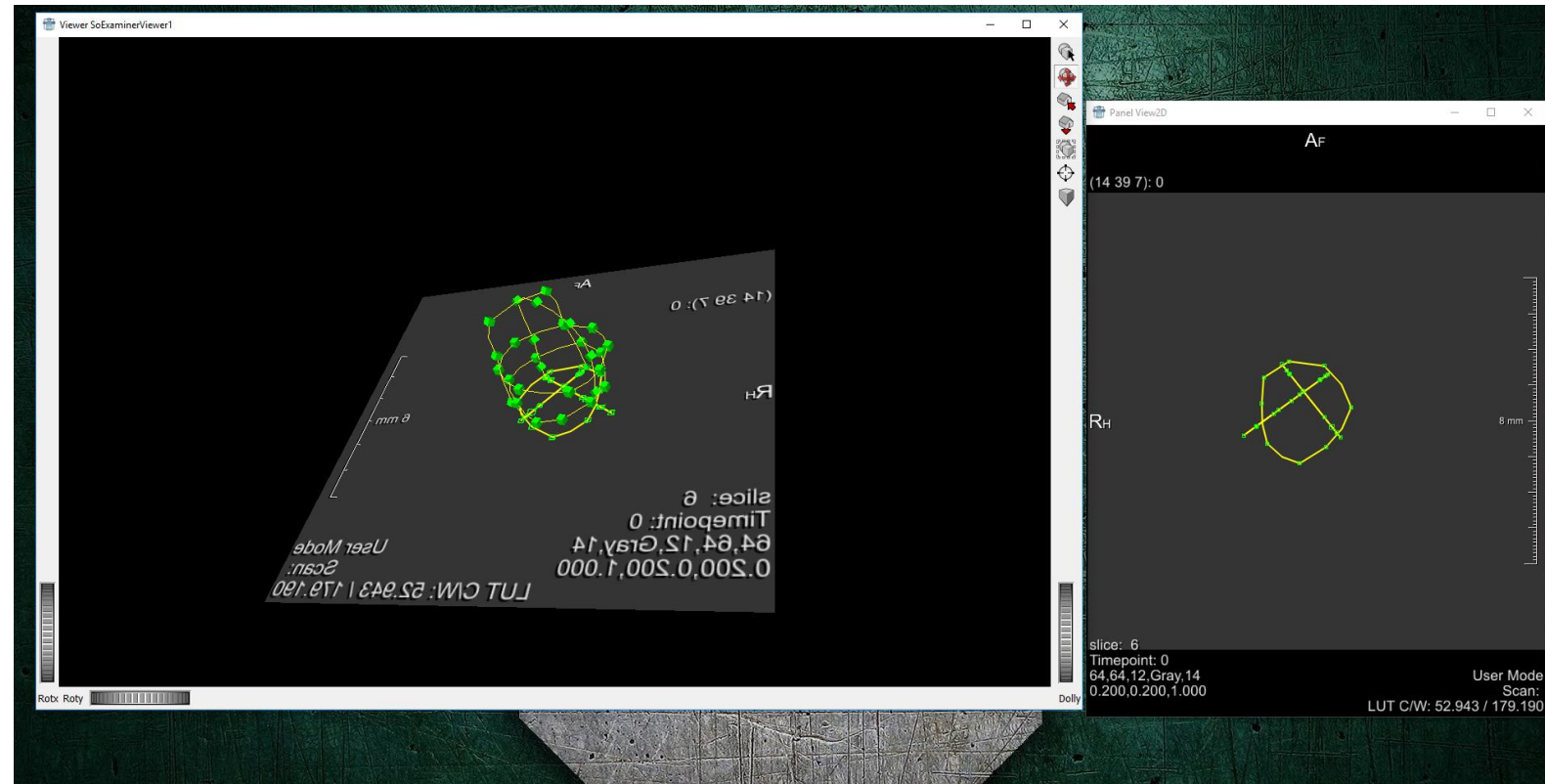
CSO Ids: 1 2 3 4 5

Group Ids: 1

☐ Should compare case insensitive

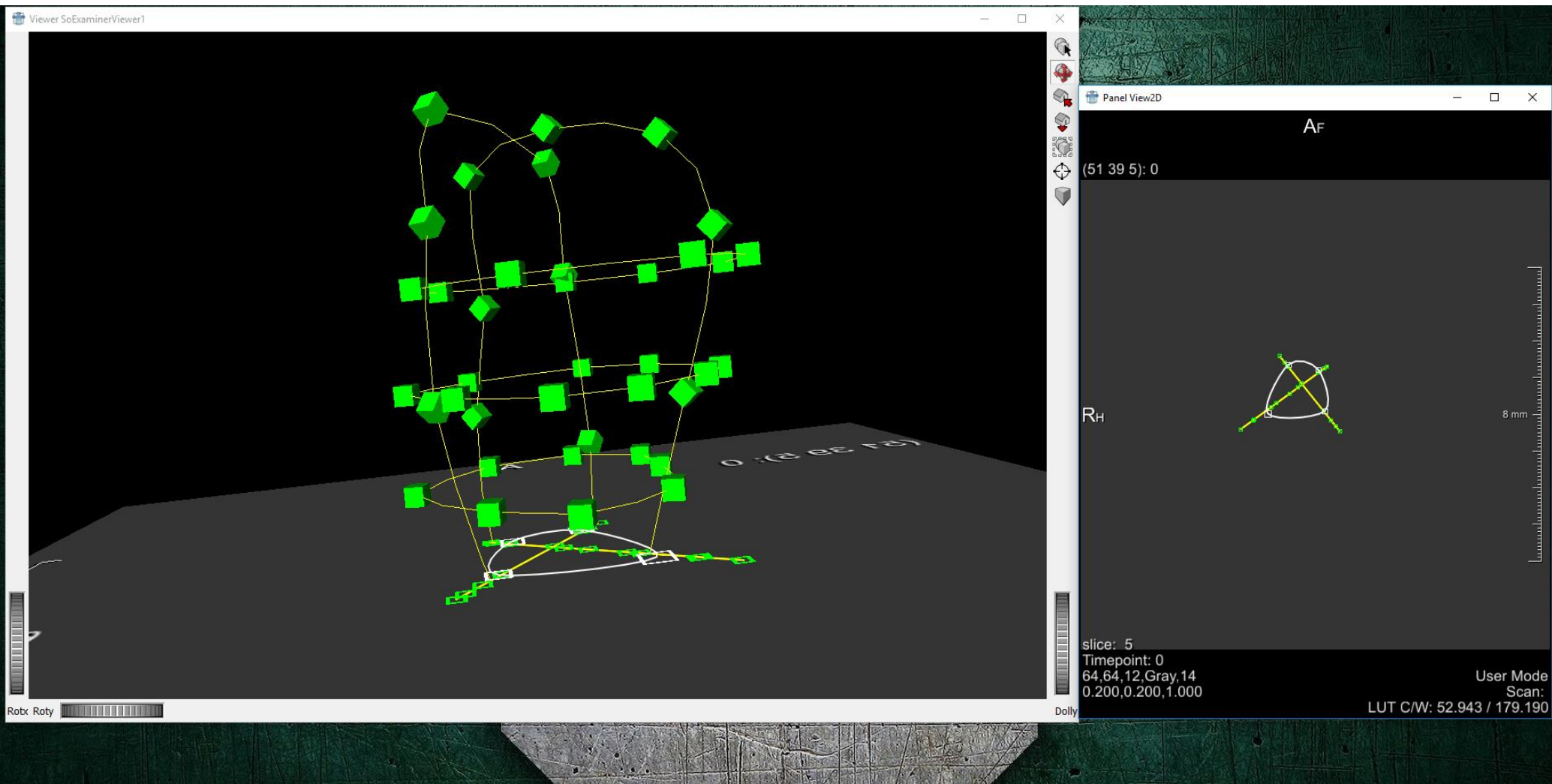
☒ Auto apply Mode: Auto Update Update

- Double click on “DicomBrowser10” (Red box).
- browse the folder where the mri images are stored
- double click on black_blood_3SA_C2H
- exit the screen by clicking x sign of the top-right
- Double click on “SoSwitch”. Change “Which Child” value to 1
- Double click on “CloneImageAsEmptyImage”
- hit clone button
- Double click on “Reshape1”.
- adjust the number X, Y, Z in such as the product ($X*Y*Z$) remains the same. As an example: if you hit “Get current input size” , $X = 128, Y = 128, Z = 3$ will be shown. Now change the number $X = 64, Y = 64, Z = 12$; so the product ($X*Y*Z$) remains the same.
- Close the screen

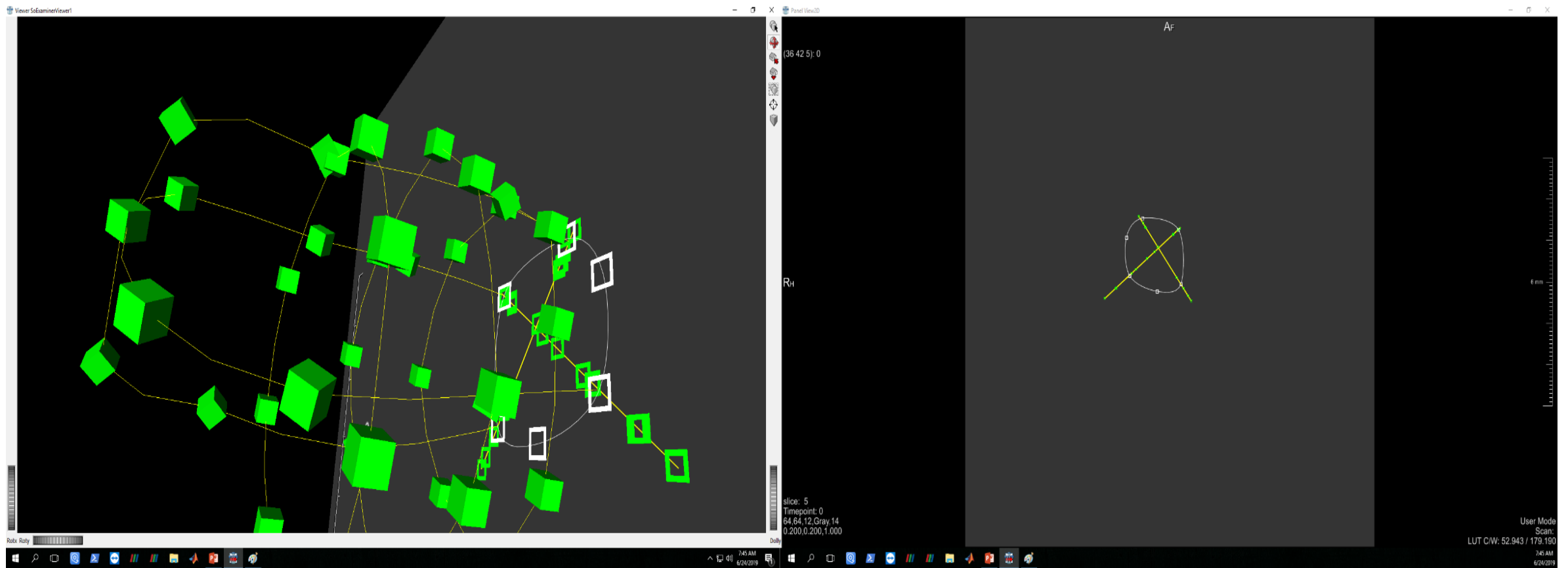


Steps continued...

- Double click on "View2D". Don't exit screen .
- Double click on "SoExaminerViewer1". Don't exit screen.
- Double click on "TransformWorldMatrix".
- Change the number in matrix in such way you can draw more slices or as you want. You can see the plane location in "View2D" screen simultaneously. Adjust the location by changing the number.
- Using mouse scroll, you can see different slice
- Close transformation matrix screen once you are done

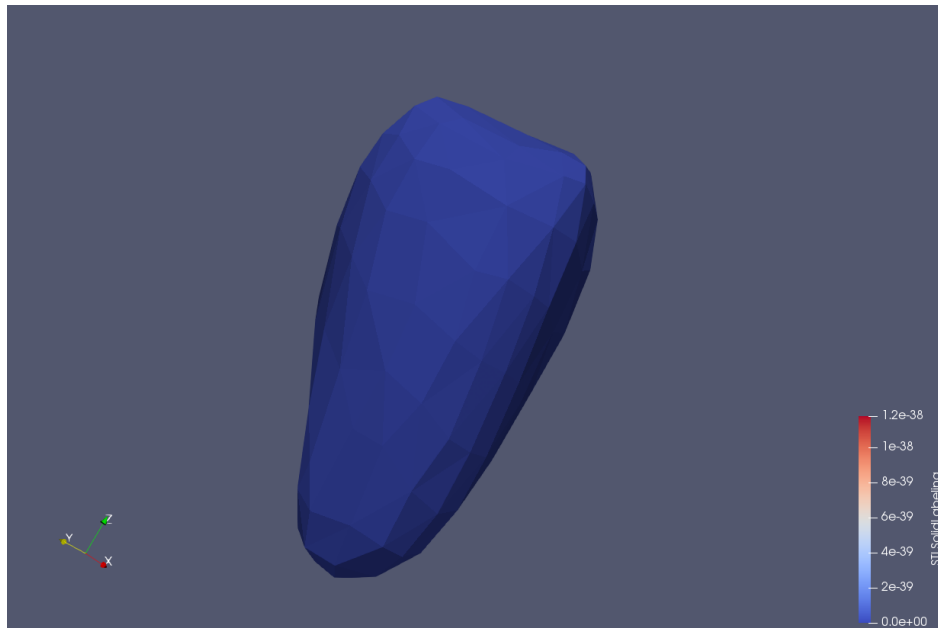


-- You can draw new slice at "Panel View2D" screen. You can see the countour at the same time at "ViewerSoExaminerViewer1" screen



- You can change the point on “PanelView2D” screen and observe the change on “Viewer SoExaminerViewer1” screen.
- In that way you can control the contour of the slice and match it with longitudinal contour.

- Double click on "CSOManager1"
- Select the ID's that are not * marked on left. Hit the "Combine" button
- Double click on "CSOFilter1". Make sure all ids are shown in output
- Double click on "CSOConvertTo3DMask1". Hit "Update" button.
- Double click on "WEMIsoSurface1". Exit the screen
- Double click on "WEMSmooth". Exit the screen
- Double click on "WEMModify2". Exit the screen
- Double click on "WEMReducePolygons1". Exit the screen
- Double click on "WEMSave". Browse where you want to save and name the file. You can save file as .stl.
- hit "Save" button
- Open the .stl file in paraview



- Close the Mevislab
- Open it and start from the very beginning for Epicardium.
- both epi and endocardium are shown below.

