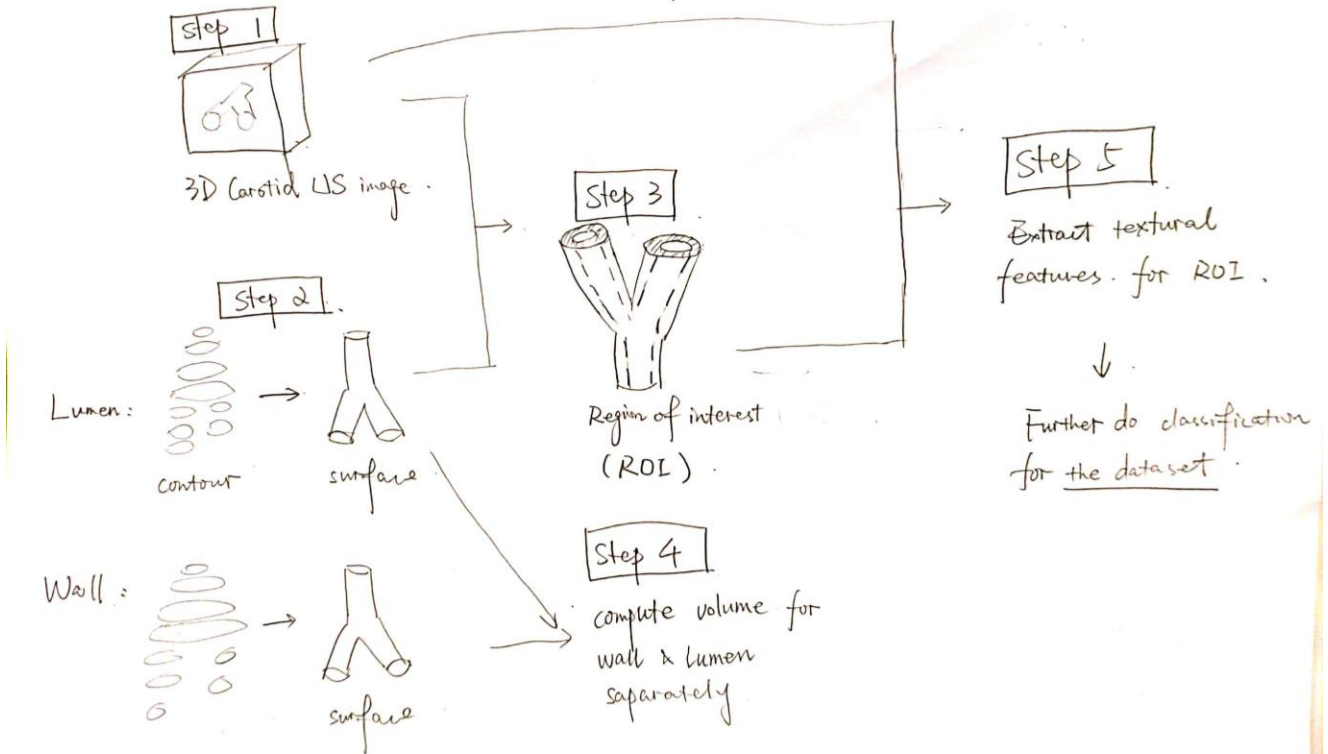


Guidance on discriminating Therapy and placebo subjects based on vessel wall textural measurements

By Shirley 2024 Sep



Pre-require:

To successfully run *3DImageAnalysis.exe*, you should set up the environment as follows:

- 1) Windows 7/8/10;
- 2) Visual studio 2010/2012
- 3) Set up a folder C:/testdata/

Note: If fails, install .msi (download VSRuntimes in the shared folder) through powershell as an administrator with the command 'msiexec /i **path\to\vc_runtime_x86.msi** ADDEPLOY=1'. Substitute the actual path for 'path\to\'.

Also, you need to install:

- 1) Matlab
- 2) Paraview: <https://www.paraview.org/>
- 3) Itk-snap:
<http://www.itksnap.org/pmwiki/pmwiki.php?n=Downloads.SNAP3>
- 4) 3DQ
- 5) 3DImageAnalysis
- 6) BChiuCarotidAnalysisProgram
- 7) Texture Code & SegbinF

Data preprocessing and feature extraction

Step1: Convert L3D file to nii image

Step 1a. Export raw image from 3DQ

Program: 3DQ

Button: *File -> Export RAW*

Input: l3d file

Output: raw image;

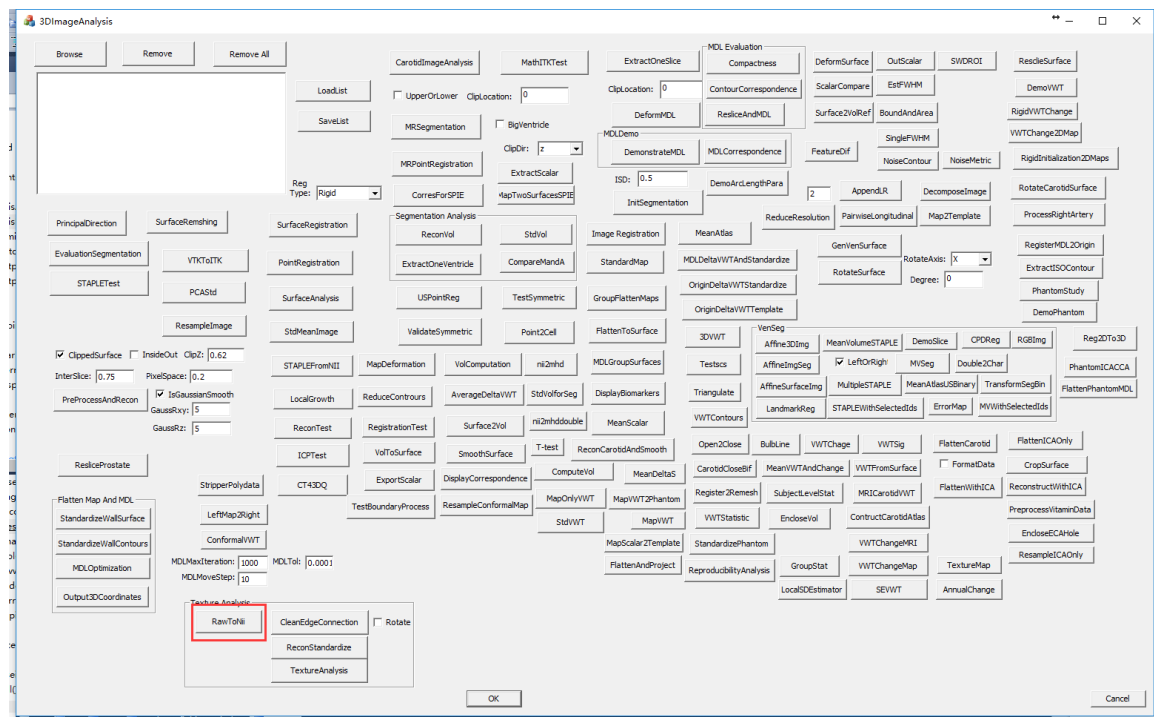
Step 1b. Convert raw image from 3DQ to nii image

Program: 3DImageAnalysis.exe

Button: *RawToNii*

Input: raw image exported from 3DQ;

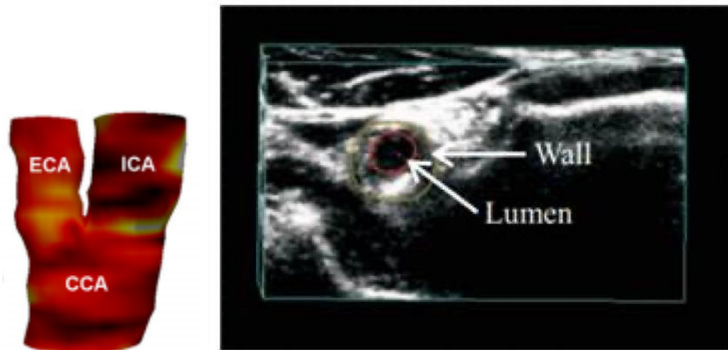
Output: nii image;



Step 2. Triangulate surface

Overview:

CCA, ICA and ECA represent common, internal and external carotid arteries respectively, shown below. In fact, you should export 6 contour files from 3DQ: ecaw, ecal, icaw, ical, ccaw, ccal where w and l represent wall and lumen respectively. These contours are not the same things and they are just put together in 3DQ, but they will be connected together after triangulation.



You should first follow step 2b to 3b to generate a file with name '*_Lumen_tc_SegBinF.nii', by using ecal, ical, ccal in step 2b. Then you should repeat step 2b to 3b to generate a file with name '*_Wall_tc_SegBinF.nii', by using ecaw, icaw, ccaw in step 2b. Then you can continue to do step 3c.

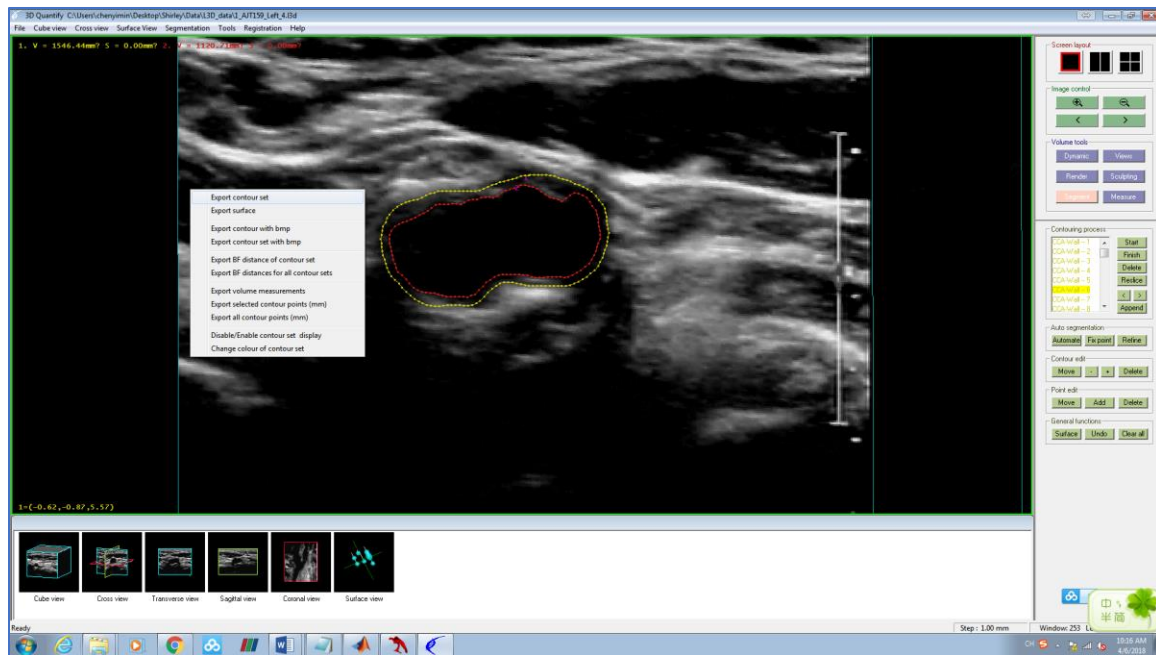
Step 2a. Export surface contour from 3DQ

Program: 3DQ

Button: *Export contour set (right click mouse)*

Input: l3d file, ldd file

Output: vtk file (ecaw, icaw, ccaw, ecal, ical, ccal)



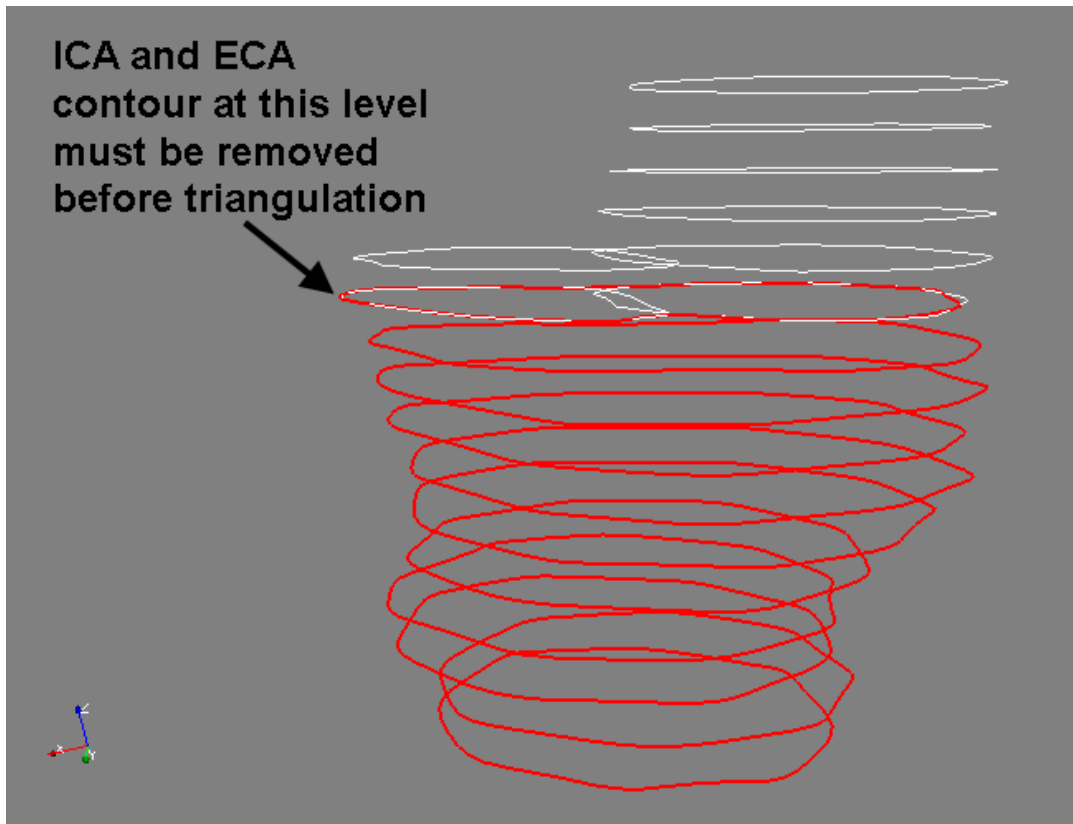
Note: When you export 'ccaw', just randomly select one of the contour (e.g. ccaw-1, ccaw-2, ccaw-3) and the software will export all the contours related to ccaw.

Step 2b: Extract Contours

Program: BChiuCarotidAnalysisProgram

Button: *ExtractContours*

The contours in ICA and ECA stacks that overlapped with the CCA stack must be removed before triangulation. Depending on the order of the contours in vtkPolyData, the slice to be removed could be the first slice or the last slice. (Visualize the vtk file in the software: Paraview)



For example, if the ICA contour stack consists of 5 contours and the first slice is the one to be removed. Do the following three things:

- Set StartSlice = 1 (The first slice is indexed 0. By setting StartSlice = 1, the first slice would not be included.)
- Set NumberOfSliceToExtract = 4
- Click ExtractContourSubset.

The output file has the name of the input file with the suffix “_ExtractContourSubsetX-X” appended. View the output in Paraview to check whether the slice we want to delete has been deleted. If the slice we want to delete were the last slice of the stack instead of the first one, we would have deleted the wrong slice. In this case, do the above with the following parameters:

- StartSlice = 0
- NumberOfSliceToExtract = 4

Inputs

N stacks of contours.

Outputs

N stacks of contours generated in the following way:

For each stack of input contours, copy Line Number <StartSlice> to <StartSlice+NumberOfSliceToExtract-1> to the corresponding output. If <StartSlice+NumberOfSliceToExtract-1> is larger than <Total # Of Lines in the input (N) - 1> (N.B.: Line number indices are in the range [0, N - 1]), the last line copied is Line <Total # Of Lines in the input (N) - 1>.

The output file has name of the corresponding input file with the suffix “_ExtractContourSubsetX-Y” appended, where X is the first line copied and Y is the last line copied.

Step 2c. Triangulate surface

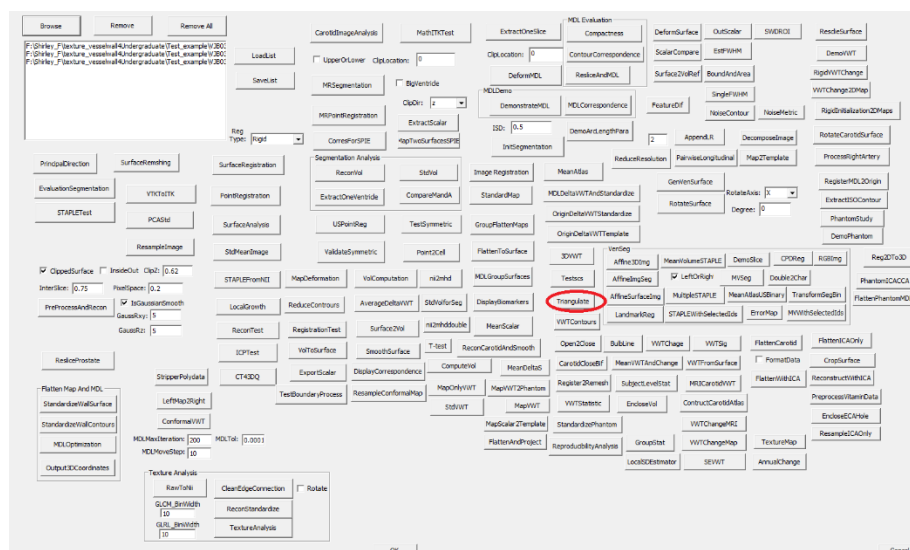
Program: 3DImageAnalysis.exe (Mind: not use RotateMFC.exe)

Button: *Triangulate*

Input: 1. ECA vtk files;
2. ICA vtk files;
3. CCA vtk files

Note: 1) the inputs should be in order. 2) Triangulate surface for wall and lumen, respectively

Output: vtk file, the name of which is with "_tc.vtk" appended.



Step 3. Reconstruct ROI 3D binary volume

This step is to find the region of interest (ROI), which is the region between wall and lumen.

Step 3a. Reconstruct 3D binary volume

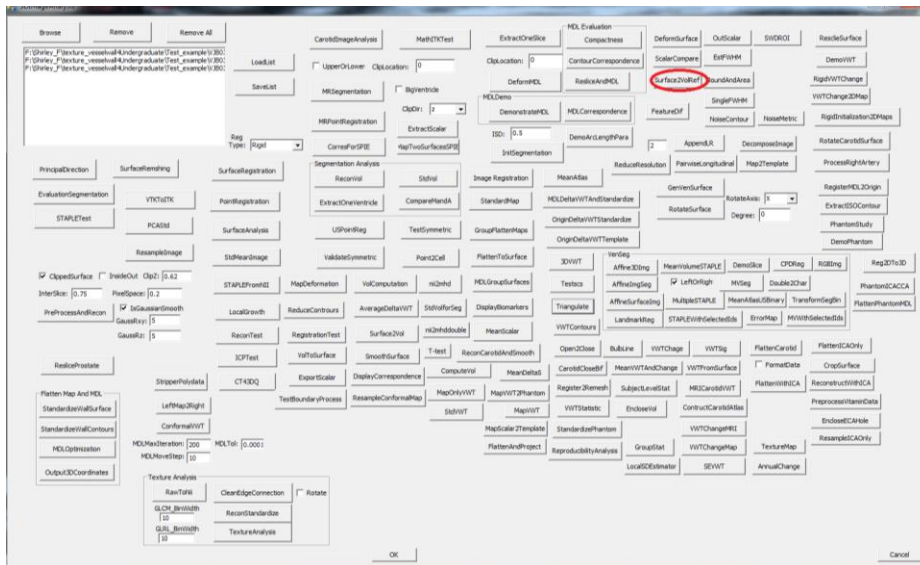
Program: 3DImageAnalysis.exe

Button: *Surface2VolRef*

Input: 1. nii image generated in step 1;

2. "_tc.vtk" file generated in step 2c

Output: nii file, the name of which is with "_SegBin" appended.



Step 3b. Flip the binary volume to make it correspondent with image

Program: Matlab

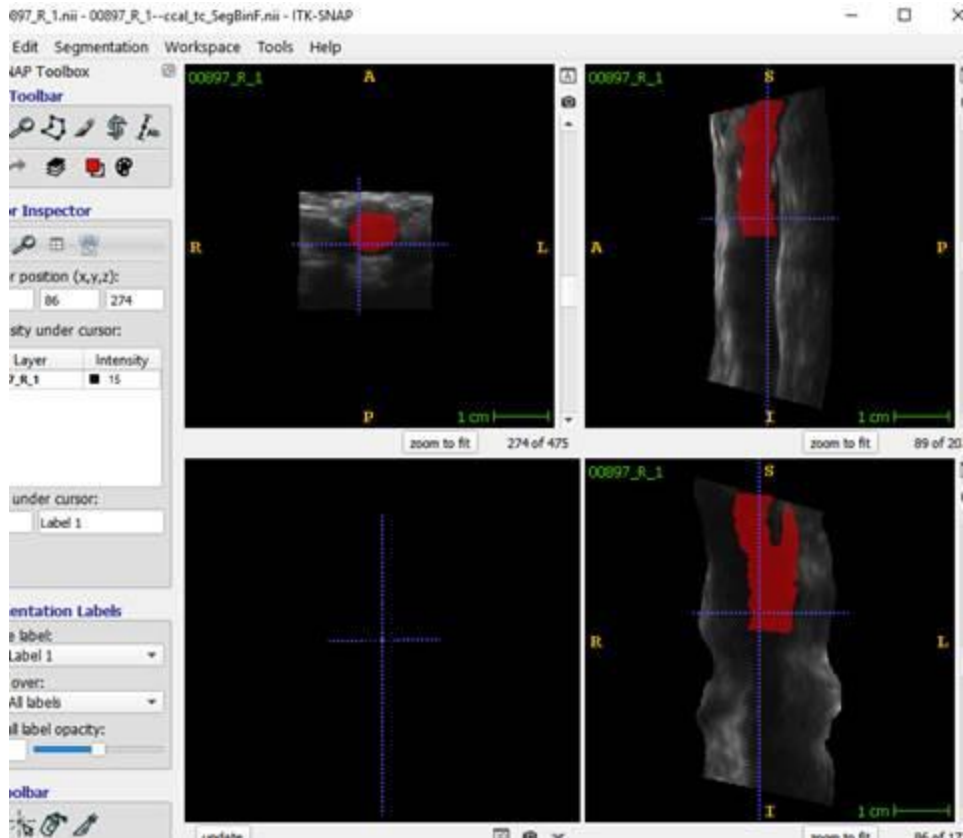
Function: SegBinF.m

Input: "_SegBin" file generated in step 3a

Output: nii file, the name of which is with "_F.nii" appended. (F means flipped)

Check:

This step is to make the binary volume upside down. To further understand why we need to do the flip step, you can first drag the original image to itk-snap and then drag the _segbinF.nii to the itk-snap (click 'Load as Segmentation' on the dialog box pop out). You can see the segmentation is now in the right alignment to the original image.



Step 3c. Reconstruct ROI 3D binary volume

Program: Matlab

Function: Vessel_ROI_generated.m

Note: You should first follow step 2b to 3b to generate a file with name '*_Lumen_tc_SegBinF.nii', by using ecal, ical, ccal in step 2b. Then you should repeat step 2b to 3b to generate a file with name '*_Wall_tc_SegBinF.nii', by using ecaw, icaw, ccaw in step 2b.

Input: “_Lumen_tc_SegBinF” file generated in step 3b

“_Wall_tc_SegBinF” file generated in step 3b

Output: nii file, the name of which is with “_ROI.nii” appended.

Step 4: CarotidVesselVolumeMeasurement

Program: BChiuCarotidAnalysisProgram

Button: *CarotidVesselVolumeMeasurement*

This is to compute the volumes of the lumen and wall surfaces.

Inputs

A list of vtkPolyData surfaces with or without the inlets/outlets capped, e.g.,

```
E:\Scan_POM_APA057_RIGHT_BMODE_1--CCA-Lumen_tc.vtk  
E:\Scan_POM_APA057_RIGHT_BMODE_1--CCA-Wall_tc.vtk
```

Outputs

A text file with the name of the first input vtk file, but with “_Volume” appended, recording the volume of each of the inputs, e.g.,

```
E:\Scan_POM_APA057_RIGHT_BMODE_1--CCA-Lumen_tc.vtk: 317.889  
E:\Scan_POM_APA057_RIGHT_BMODE_1--CCA-Wall_tc.vtk: 1039.435
```

Step 5. Compute texture features of ROI in a 3D gray-level image as described in Arna’s Stroke paper

Program: Texture Code (Matlab)

CalculateTexturesNiftiInput.m

Inputs: 1. 3D nii image generated in Step 1;

2. “_ROI.nii” generated in Step 3c;

Output: .mat file; % a structure containing the texture features and their names. For more details, please refer to Arna’s Stroke paper;

Format: Features = CalculateTexturesNiftiInput(<nii_filename>, <binary_image_filename>)

Step 6: Report your textural and volume measurements in an xlsx file

Features	<Patient ID>, Baseline			<Patient ID>, Followup		
	Left	Right	Weighted	Left	Right	Weighted
Vessel Wall Volume						
Feature 1						
etc						
to Feature 376						

- There is now only one feature vector (containing 376 features) for one scan now.
- For each of the right and the left arteries, record the vessel wall volume measurement, which is the Wall Vol – Lumen Vol. These two volumes are obtained in Step 2c.
- Weight the feature vectors obtained for the left and right arteries of each patient at one time point using the Vessel Wall Volume.