ASSIGNMENT 1

Name: Yang Hao-Wei, Student ID: 109062526 03/22/2021

1 Part 1

1.1 Read in and print out all the data fields in a DICOM file

In this section, I use the patient of folder "0a0c32c9e08cc2ea76a71649de56be6d" and the first slice "0a67f9edb4915467ac16a565955898d3.dcm" to print its dataFields. The result is shown below.

Figure 1: all datafields of a single DICOM file

1.2 Statistics for raw data and Hounsfield Unit data

I use the formula, HounsfieldUnit = RescaleScope * Raw + RescaleIntercept, to convert raw data to Hounsfield units. Since RescaleSlope is 1 and RescaleIntercept is -1024, basically the entire distribution only shifts to the left by 1024 units. To be noted, based on the hint from TAs, I set the value of raw data pixel array to 0 if the value of the raw data < PixelPaddingValue while transforming to Hounsfield Unit.



Figure 2: the statistic of raw data and Hounsfiled

2 Part 2

2.1 Read in and sort DICOM files

I first read in 25 slices from the first folder. Then, I found that the attribute "ImagePositionPatient" has three dimensions, the first two dimensions are the same in all 25 slices, but the third dimension(z-axis) is different. Therefore, I sort the slices by ImagePositionPatient[2] from small to large.

2.2 Print out 25 slices in correct order

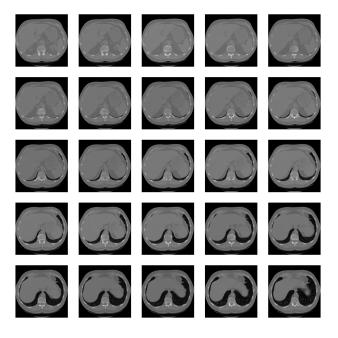


Figure 3: 25 images of sorted CT slices

3 Part 3

I tried "local mean" and "local median" to segment the lung by applying "thresholdlocal" from skimage to calculate the thresholds of each slice, and got a two-dimensional array. Then, I calculate the average of the array to get a float number, which is the red line drawn in the histogram of the figures below.

3.1 Segmentation - local mean

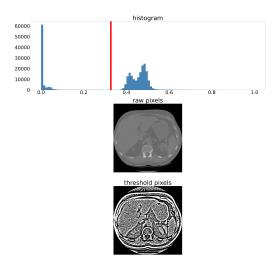


Figure 4: Segmentation by mean

3.2 Segmentation - local median

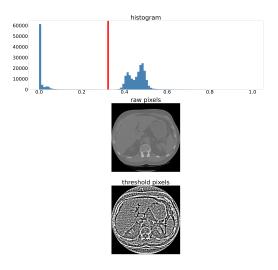


Figure 5: Segmentation by median

4 Bonus

By using the toolkit "Poly3DCollection" from "mplot3d.art3d.", I plot a 3D image of the CT slices from the first folder. I use mean as the threshloding strategy so that each slice has a mean threshold return, and then I calculate the average these thresholds as the overall threshold. The results are shown below.

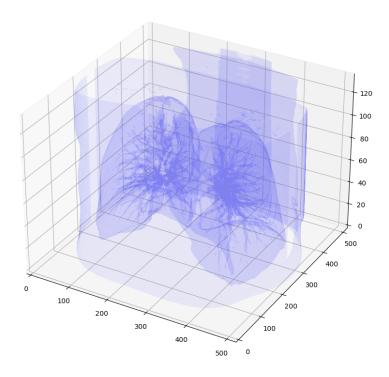


Figure 6: 3D visualization of the CT slices in the first folder

5 Question and Summary

In this assignment, I have learned the technique to process DICOM files. Also, I've tried several thresholding technique to segment CT slices. Moreover, I've learned how to visualize CT slices into 3D view point with the toolkit "Poly3DCollection". Last but not least, this assignment help me get more familiar with writing reports with Latex, which is what I had been planning to learn but not really trying.