ENSC 474

Final Project

Cyrus WaChong

301306459

Abstract:

The goal behind the final project was to apply all the techniques learned throughout the course on a real-life situation. 40 MRI scans were supplied, and the student was required to apply different methods of analysis to visualize the deterioration of the brain in Alzheimer's patients and cognitively normal patients. These images were the baseline image (BL), and an image taken 24 months in the future (M24).

Rigid and non-rigid registration was used to compare the scans and see the volume of gray matter lost. In part 2, using non rigid registration, the student presented the deterioration of the gray matter as a transform on a grid, helping visualize the loss of gray matter. Part 3 was to segment the brain image for easier analysis and part 4 was analysis of volume change of Gray matter (GM), White matter (WM) and Cerebral spinal fluid (CSF)

The acronyms for these 3 tissues will be used throughout the report for simplicity.

Part 1: Difference Image plotting

For part 1, the transform for the M24 image to line up properly with the baseline image was calculated, as some of them did not line up entirely. Using the algorithm found in the lecture 19 notes, we were able to shift and rotate the M24 image to match it with the BL image. Below, we can see the images overlapped; Green is parts existing solely in the base image and purple is portions only existent in the M24 image.

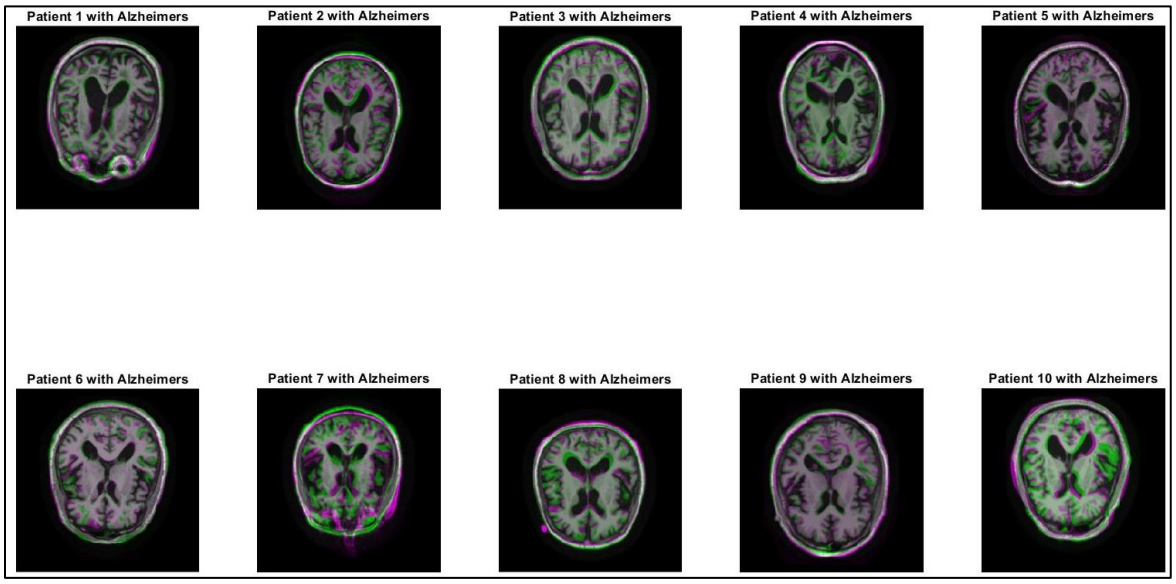

Figure 1: imshowpair of baseline and M24 image of AD patients

These were the images for the alzheimers disease (AD) patients. There are some odd differences, such as that in patient 7. This is due to the images having different characteristics, most likely due to a different layer of the brain being photographed.

The image below is the imshowpair figures of the patients that are cognitively normal (CN).

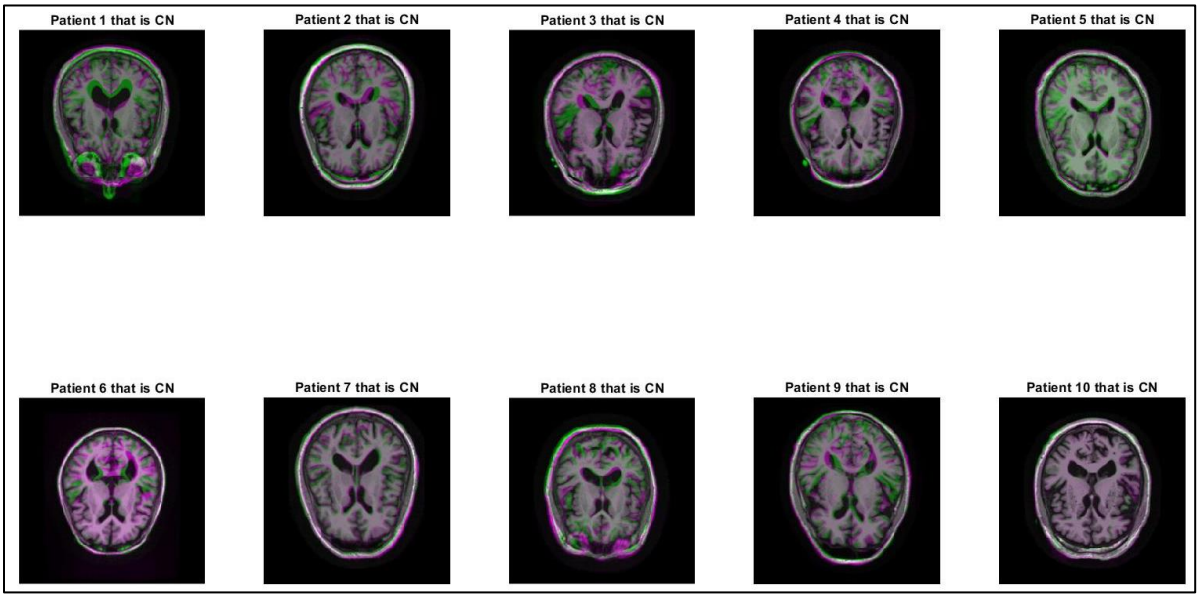

Figure 2: imshowpair of baseline and M24 image of CN patients

The same issue and differences can be seen in patients such as 1 in figure 2. This will lead to difference images with much more material, but this cannot be solved as these were the only images given.

The next step was to find the difference of the two images, to see what brain matter was lost over the two years. This was accomplished by subtracting the rigidly registered M24 image from the baseline image. The resulting figures can be seen below.

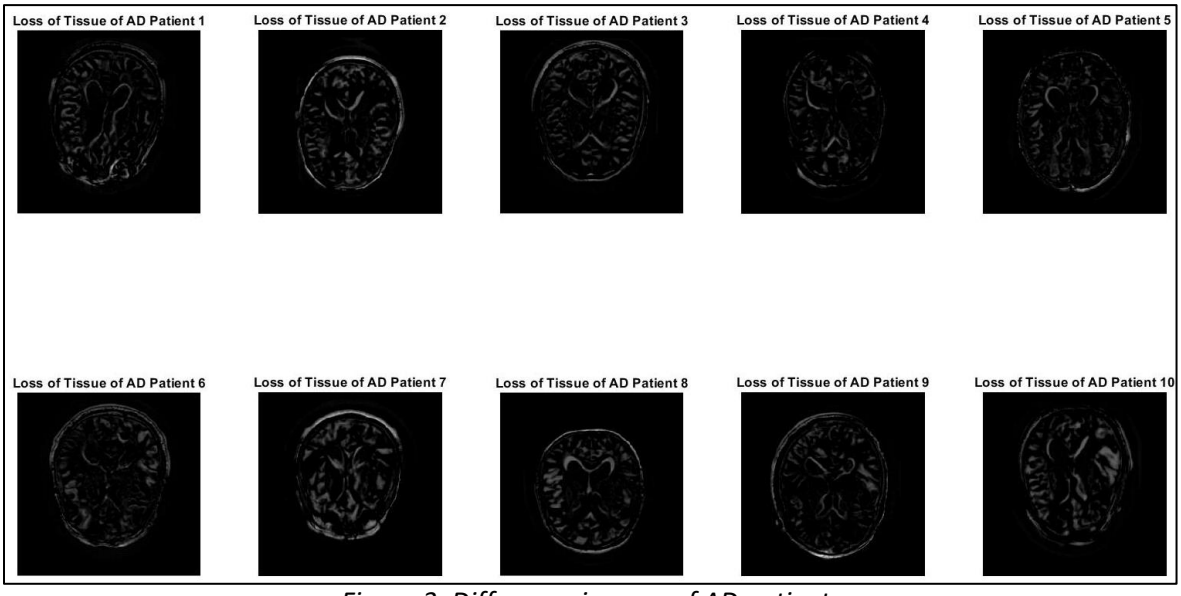

Figure 3: Difference images of AD patients

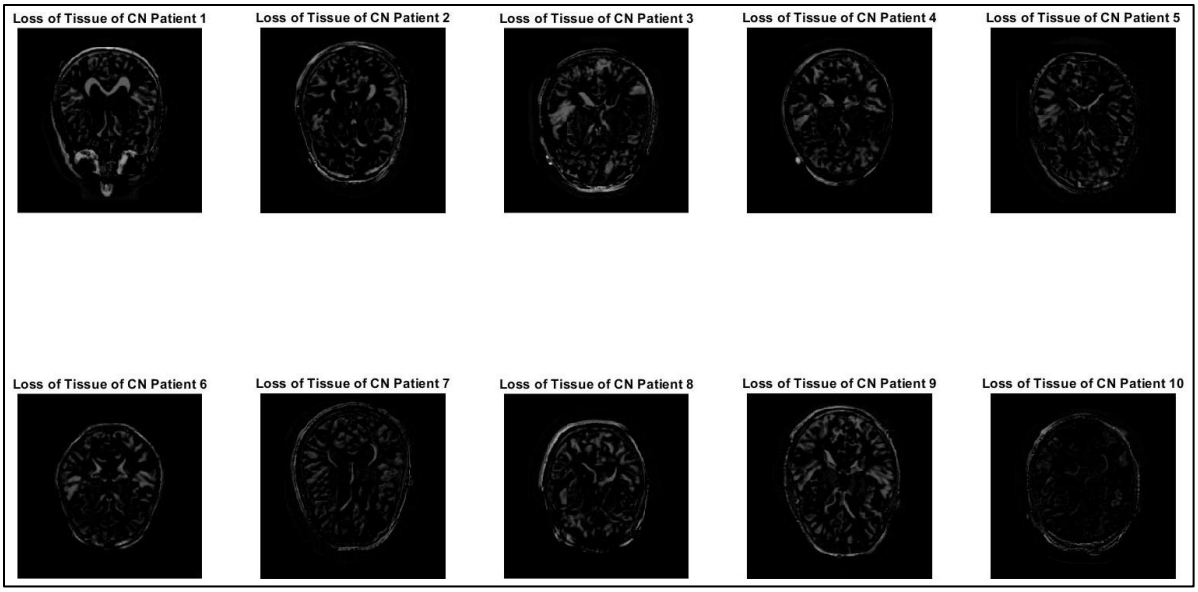

Figure 4: Difference images of CN patients

Even though there is substantial error in the transforms of the two images, as can be seen in the imshowpair images, we can still see much more volume loss in general in the AD patients vs. the CN patients. The Alzheimer's patients seem to lose more grey matter volume over the two years period compared to the CN patients. The differenece images were acquired by subtracting the registered image from the baseline image.

2) Non-Rigid registration of registered images

For this part, we were required to further non-rigidly register our images, by mapping movement of different portions of the brain from the BL image to the M24 image. For this part, I chose to map the movement of gray matter, as that is what is relevant in this lab. Using 70 landmarks for each image, and finding the movement of each one, we can non-rigidly register this image.

A gaussian was applied at each point with low variance(5), just so the movement can be seen more clearly on the grid. This reduces accuracy, but for presentation purposes, this seemed necessary.

Below we may find the quiver plot of the first 3 images of CN and AD patients, along with its transform applied on a grid directly below it.

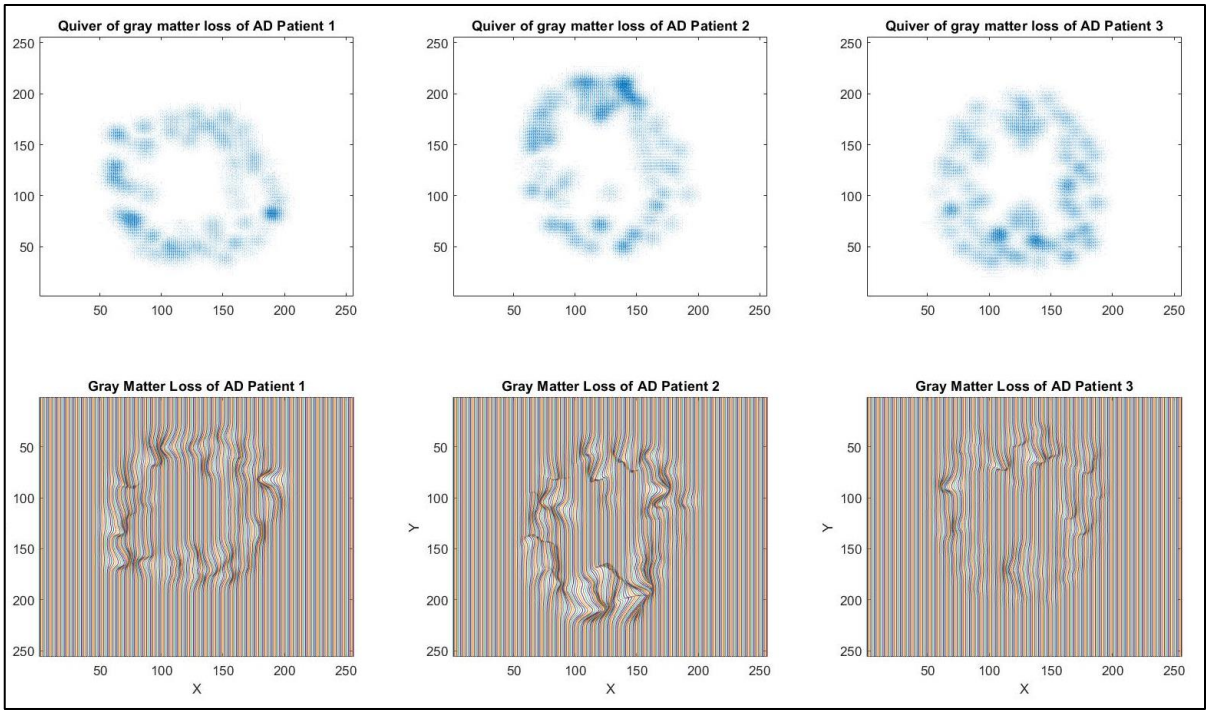

Figure 5: Non-rigidly registered images of the first 3 AD patients

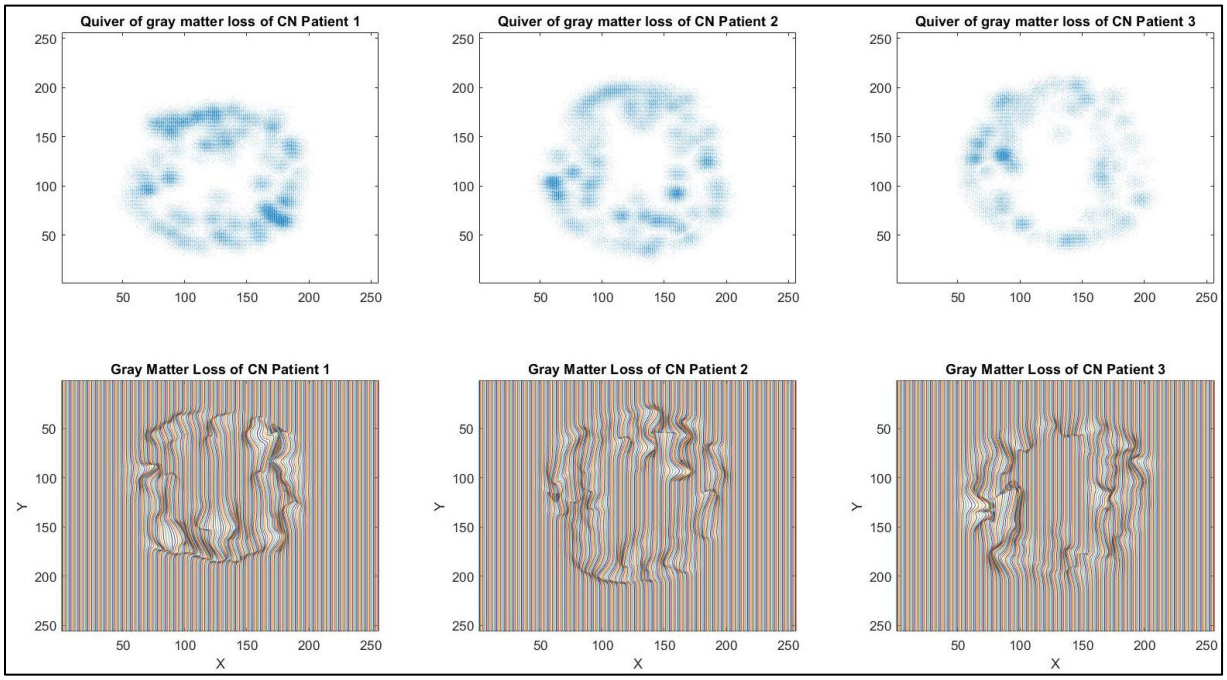

Figure 6: Non-rigidly registered images of the first 3 CN patients

6 images were used since it was incredibly time consuming to choose landmarks for each image, and these outputs demonstrate that the algorithm works, without being unnecessarily tedious and time consuming. It was not necessary to do all images for this part, as this is not needed for later parts of the lab, and the algorithm can easily be expanded to all image if needed.

3) Segmentation of different brain matters

For this part we were supposed to segment the images using the method the student deemed the best. In this lab Otsu's method was used to find the 2 threshold values that work best to maximize the "between-class" variance.

The code used to calculate these threshold values is commented out at the top of the part 3 section of the program, since it requires roughly an hour to calculate the threshold values. These values found from this calculation were used to segment the image.

The output images were not ideal, this is most likely due to global thresholding, which is not with such specific images. It was the only valid choice at this time due to time constraints and how long the computations would take if variable thresholding was used. For version 2 of the code, variable thresholding would be used to more accurately map GM, WM and CSF.

Below the outputted segmented images can be seen, along with their respective histograms:

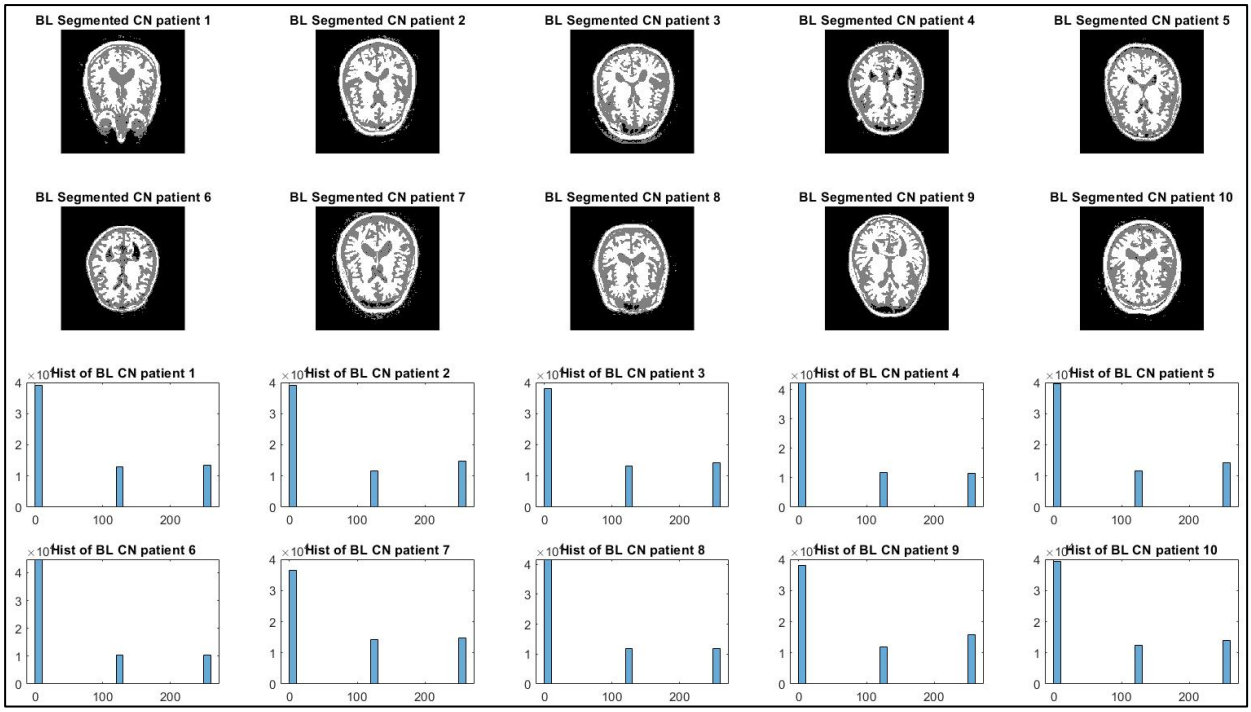

Figure 7: Segmented BL images of CN patients, with histograms

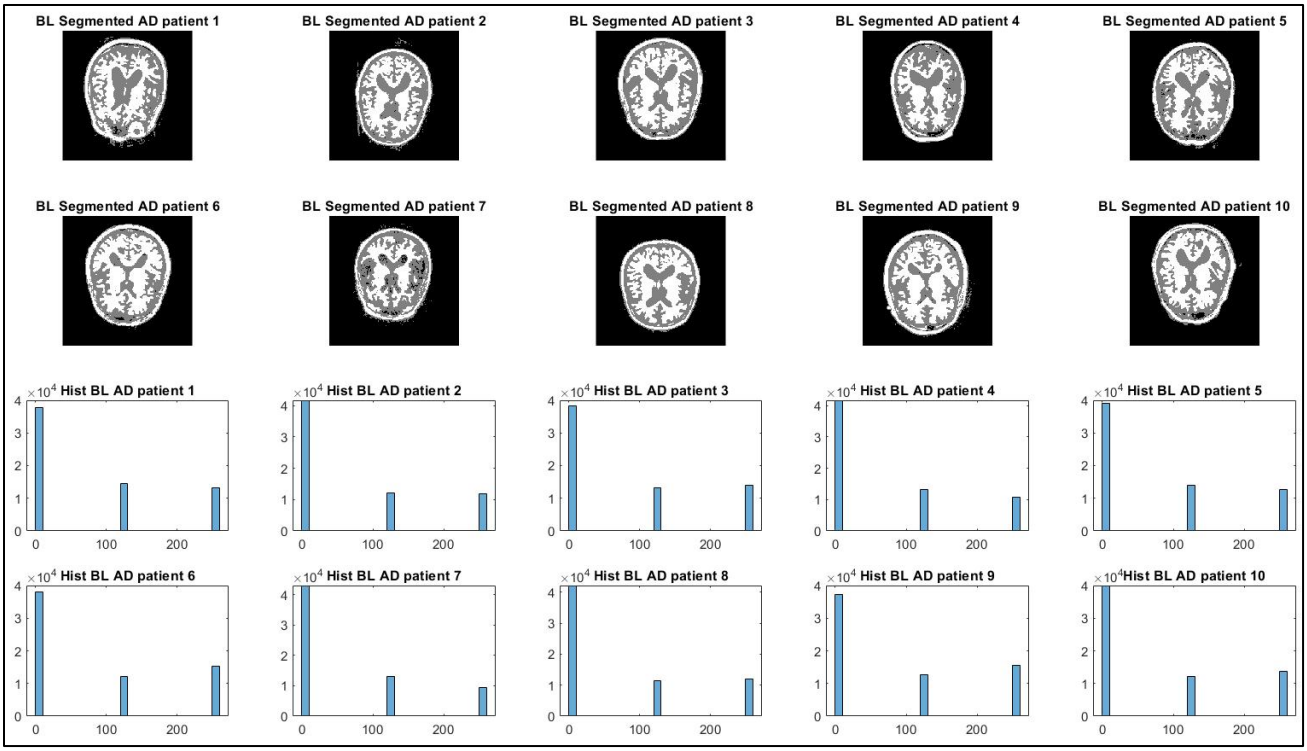

Figure 8: Segmented BL images of AD patients, with histograms

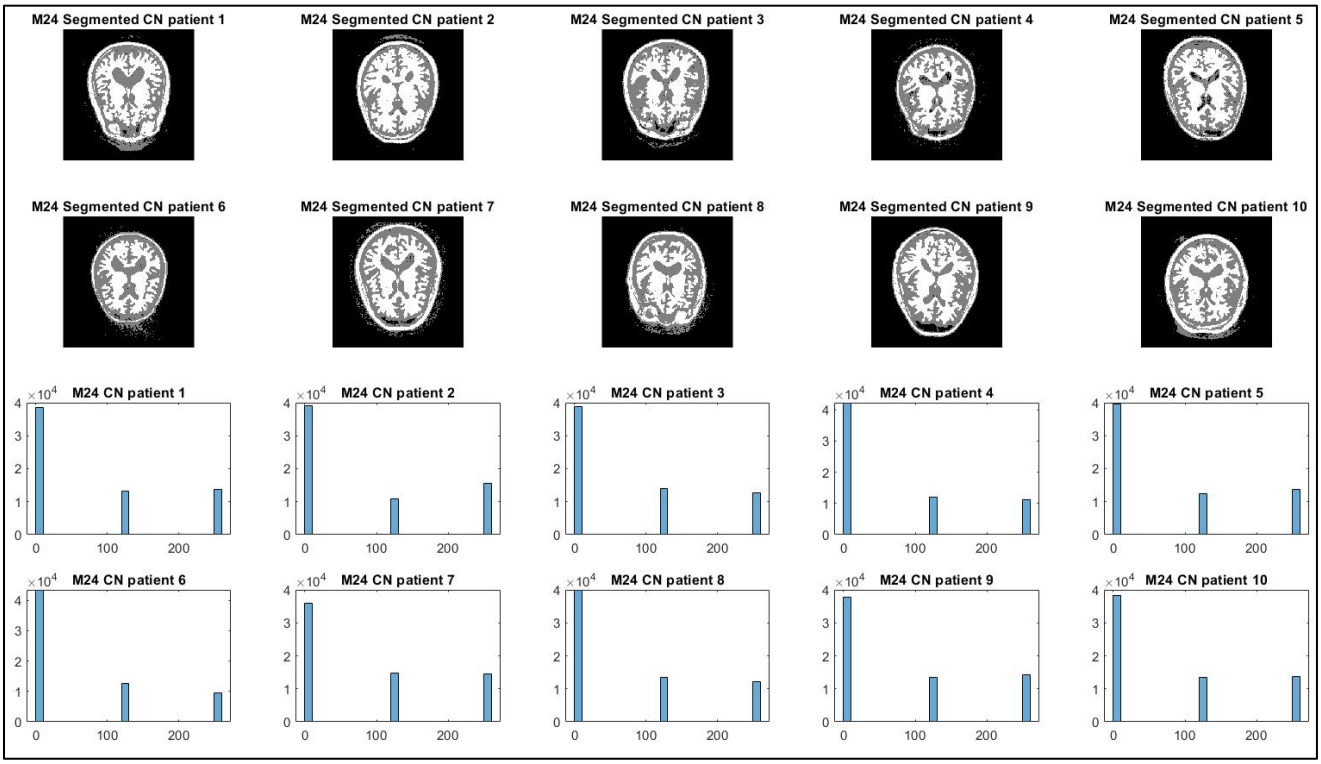

Figure 9: Segmented M24 images of CN patients, with histograms

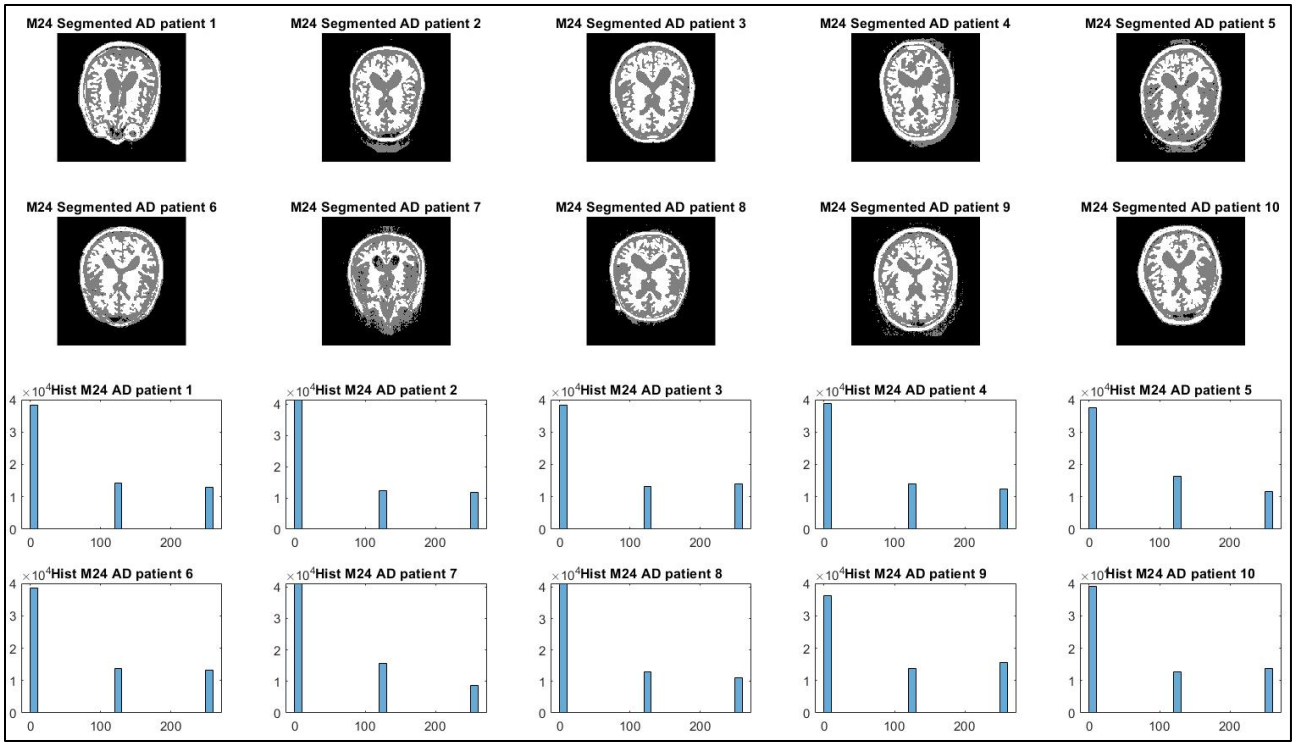

Figure 10: Segmented M24 images of AD patients, with histograms

As can be seen, with the calculated thresholds from global Otsu's method, we see portions labelled as GM that should be CSF, such as the choroid plexus. These errors stem from the innacuracy of global thresholding, and ignoring the importance of neighbouring pixels' memberships.

To fix these errors in the second version, neighbouring pixels' memberships would be taken into account to correct noise pixels. Variable thresholding would also be used to increase the specificity of each region of the image.

To reduce error in the rest of the program, the built-in "multithresh" function is used. This allows for more accurate threshold values to be calculated, one to separate CSF and GM, and one to separate GM and WM, allowing for 3 separate classes.

The output for the BL CN patients can be seen below to compare the results:

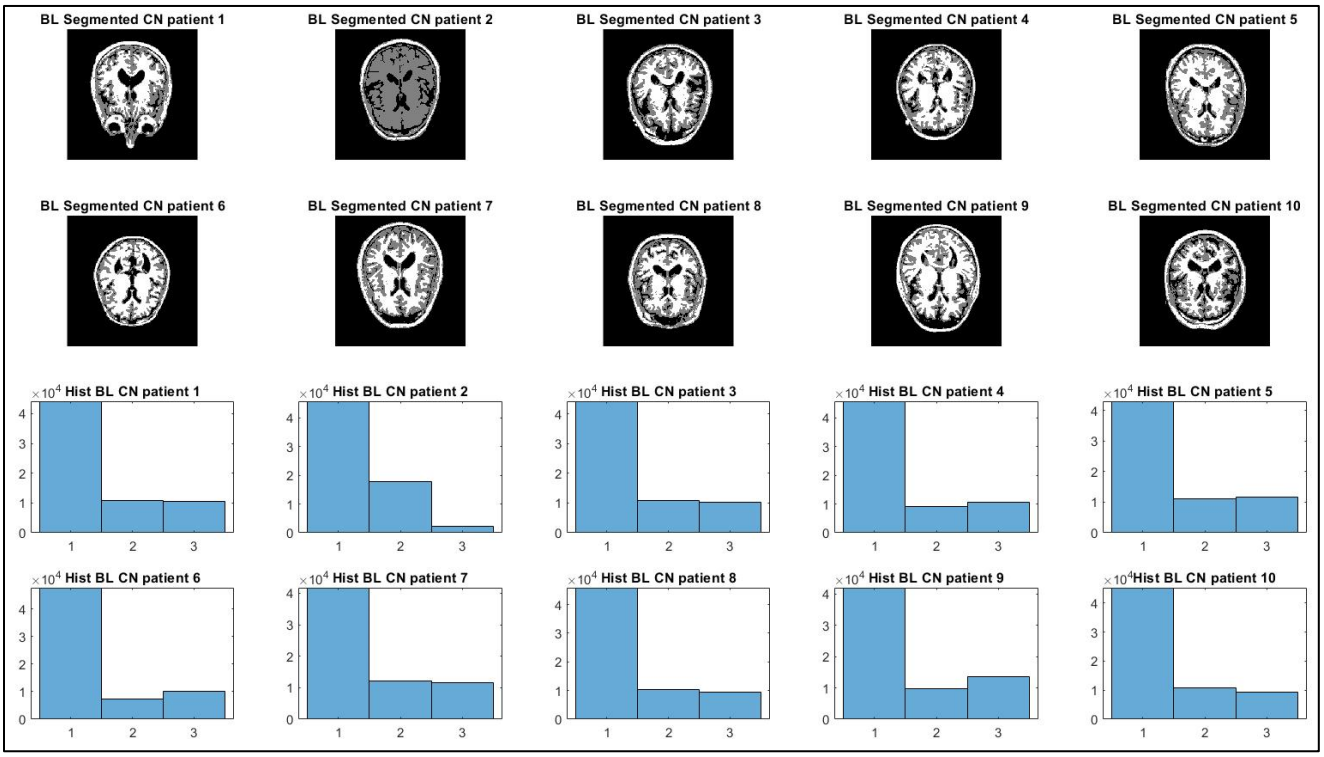

Figure 11: Output of segmentation of BL CN pictures using built-in function

As can be seen above, there is one image that did not get properly segmented, which became an issue later for part 4. The solution will be discussed in part 4. The rest of the 9 images are much more accurately segmented, which is as expected with built-in functions.

4) Analysis of matter change over time

This portion of the lab was to analyze and measure the change of all 3 matters present in the brain over time, using the baseline image and M24 image of each patient. For the first part, we wanted to plot the change in volume of the 3 different matters of each patient with respect to time. The result can be seen below:

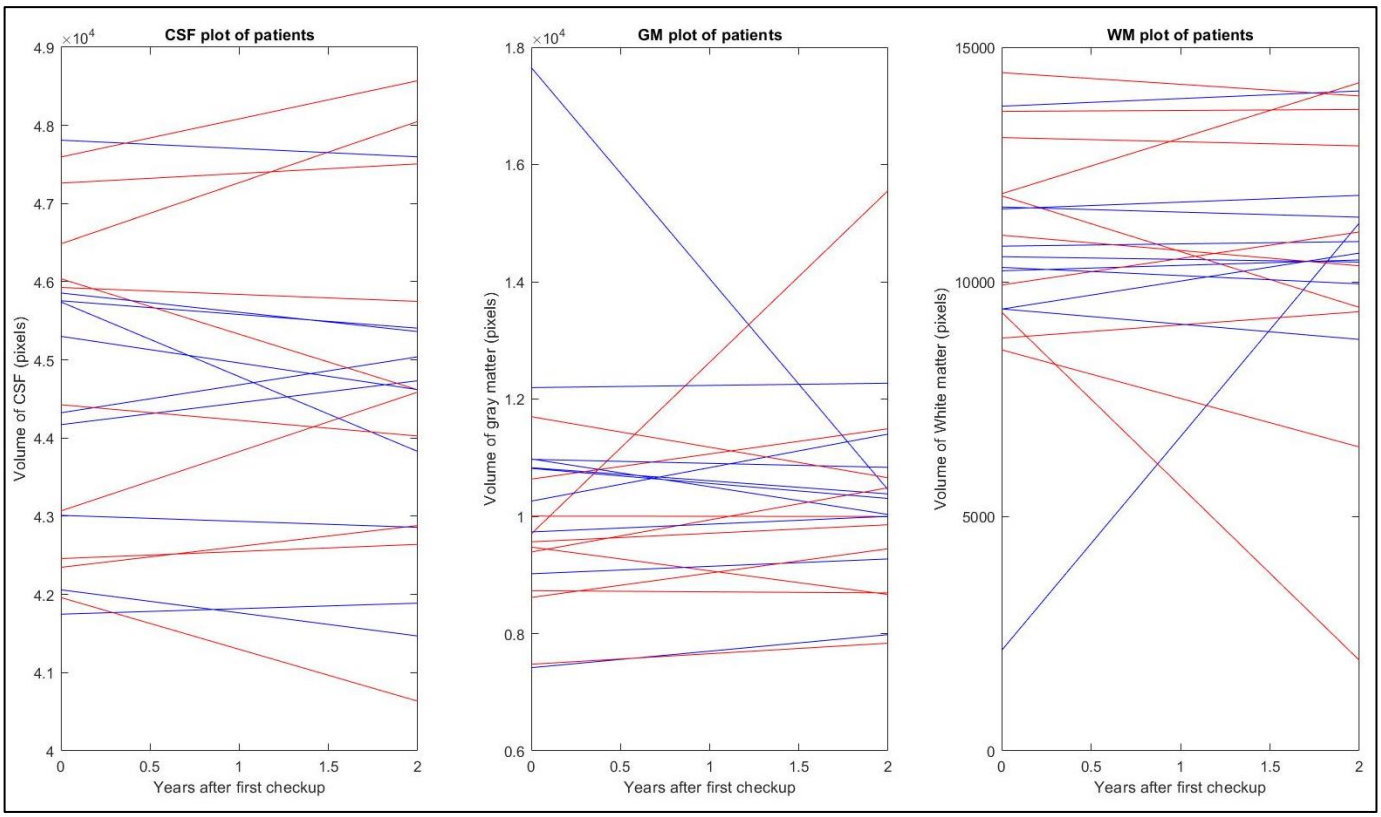

Figure 12: Volume of matters with respect to time. (Red=AD, Blue=CN)

To represent the volume of tissues with respect to time, a line connecting points between BL and M24 resulted in the most comprehensive output.

A few errors presented themselves with this output. First of all, there were a few images that were not segmented properly using the “multithresh” function and a solution could not be found (Refer to Figure 11). These are the lines with extreme slopes, which can be seen at the top of the GM plot and the bottom of the WM plot. The CSF volume was not affected.

To fix this for version 2 of the program, variable thresholding would be done manually to guarantee quality in the output.

To compensate for this, since this caused very large differences in matter, BL and M24 images of these patients were set as the same to atleast neutralize the extreme outliers these turned out to be. The fixed output with this strategy can be seen below:

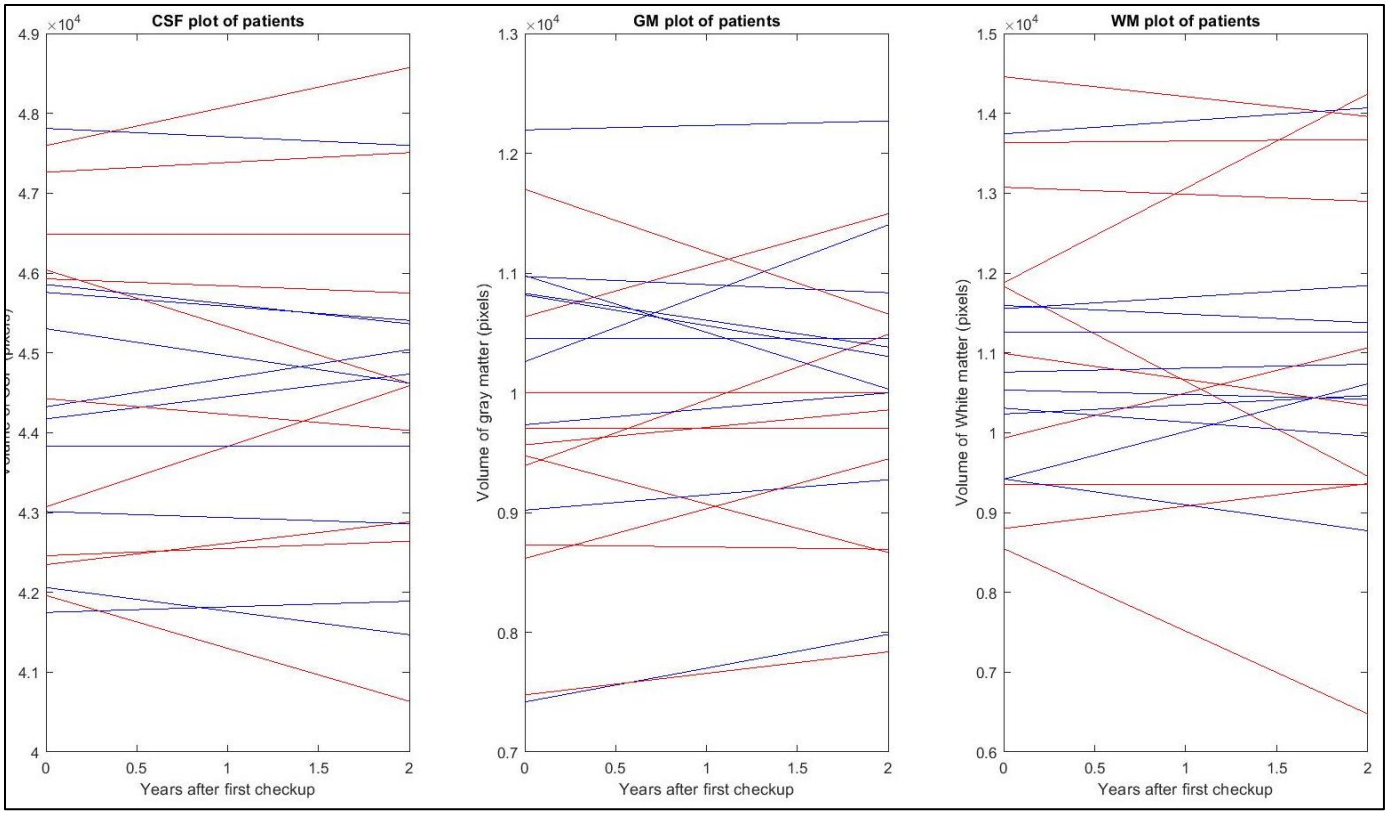

Figure 13: Compensated figure showing volume of matters with respect to time.

As can be seen above, by neutralizing the extreme outliers, the lines with extreme slopes were replaced with lines with zero slope. This provides a more logical figure.

Another issue that presented itself with these figures is the randomness of these lines, since they lacked a pattern. Once the images themselves were analyzed, it could be seen that images that had obvious brain deterioration did not have the same threshold values as their baseline images. In other words, portions of the brain in the BL image that were white matter were being considered gray matter in the M24 image.

This is most likely due to the fact that the distribution of the intensity of the pixels had changed, causing the threshold values to shift. This causes a randomness in all three graphs, with some patients gaining and losing different brain matters without much of a pattern.

What may also add to this issue is that there was no ideal way of differentiating the cranium from the white matter, or the background with the CSF when analyzing the pixel intensities present in the image. This means that the cranium pixels were included in the WM pixel count, and the background was included in the CSF pixel count.

After many attempts, there was no relatively simple fix to this problem without cropping the images themselves. For version 2, one could crop the cranium and background out of the image, which would exclude those unwanted pixels, allowing for more accurate volume measurements.

All these issues created non ideal outputs, where patients were gaining/losing impossible amounts of gray matter, while losing CSF etc. There was not a trend, and this was due to the inconsistent segmentation of the images, due to different threshold values.

For version 2, variable thresholding would be used and manually controlled so that each pair of images would use the same threshold values.

Although the method of global thresholding was not ideal, it was the method taught extensively in class. Other strategies of segmentation either introduce human error, or are extremely computation heavy.

Below one can see the bar charts of the matter of each patient pre and post neutralization of images with error:

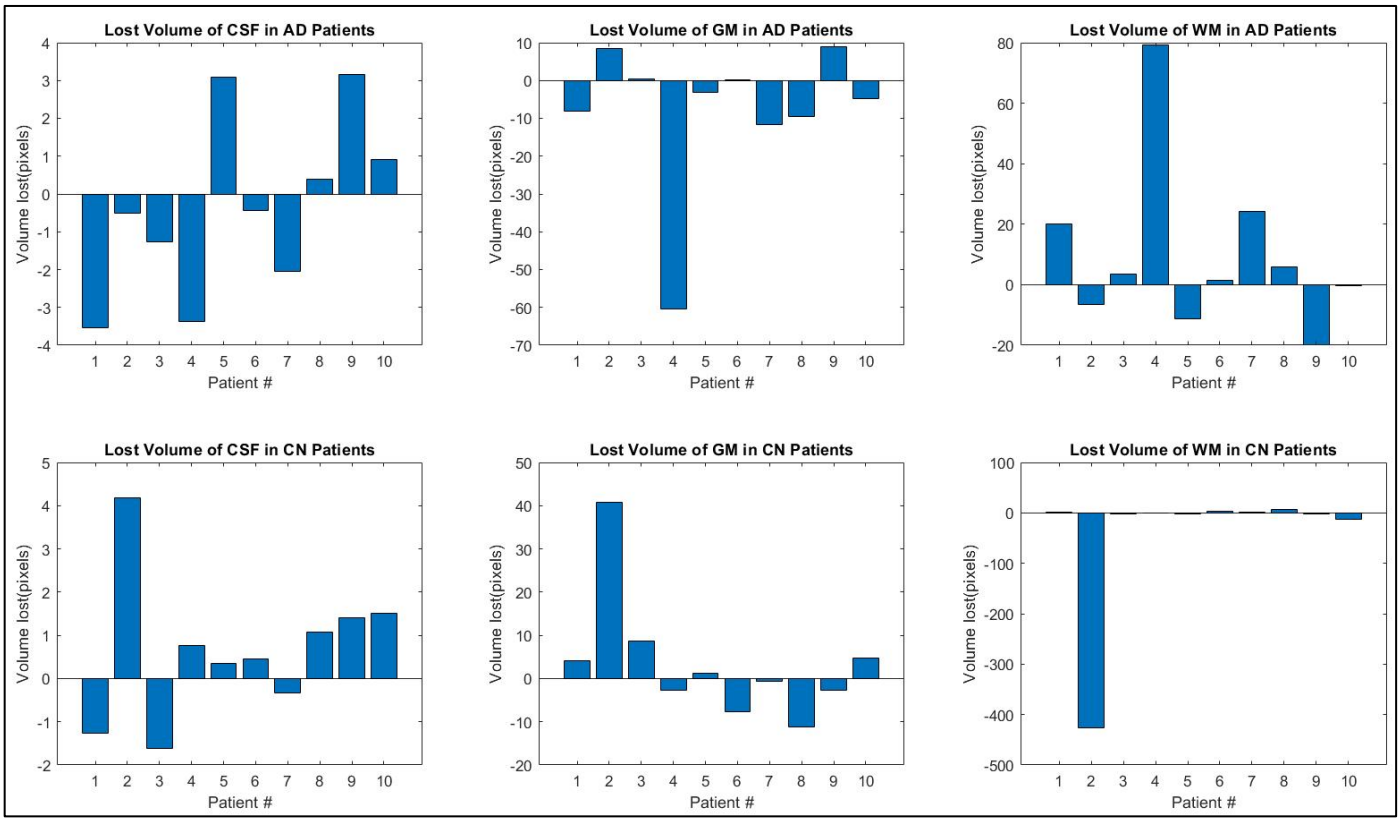

Figure 14: Bar charts representing matter of patients before compensation

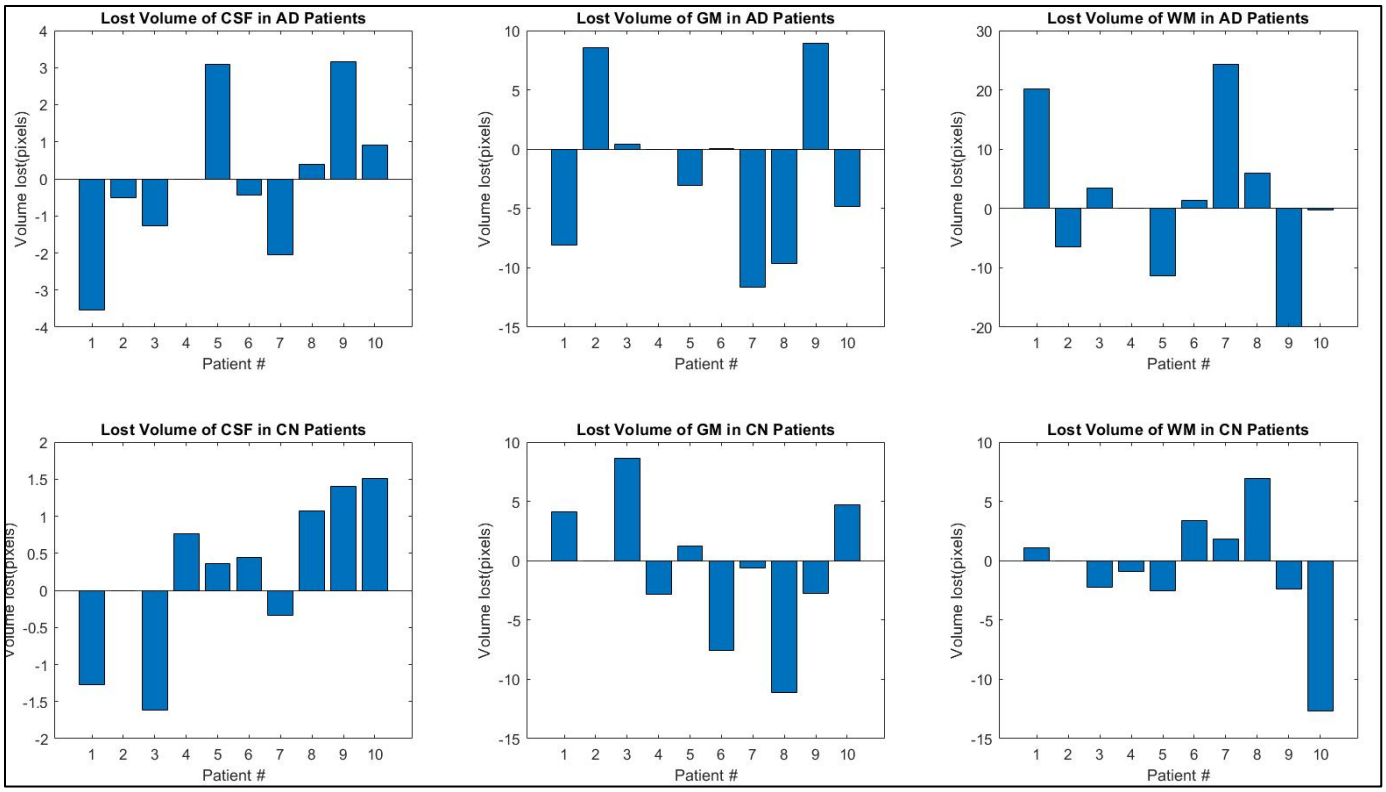

Figure 15: Bar charts representing matter of patients after compensation

These figures show how the neutralizations of the error images can affect the bar chart itself and as a result the average volume loss. In Figure 14, we can see certain bins with incredibly large values and after compensation these change in volume became zero, which gave a much more consistent graph.

The change in volume of the CSF and WM is more supressed than it should be, due to the total pixels of both of these matters being exxagerated by the cranium and background. The sign of final value was still correct; if WM present in the image decreased, it was shown in the bar graphs to decrease, but just a lower percentage change.

The final task was to present the average change in volume of the 3 materials in the CN and AD patients. As explained multiple times, there are obvious errors in these results, due to the different threshold values used in the segmentation of these images. The results can be seen below, or by running the code (the results display on the command window).

```
For the CN Patients:
The average CSF volume decreased by 0.23 percent
The average GM volume increased by 0.62 percent
The average WM volume increased by 0.75 percent

For the AD Patients:
The average CSF volume increased by 0.03 percent
The average GM volume increased by 1.93 percent
The average WM volume decreased by 1.71 percent>
```

Figure 16: Change of volume for AD and CN patients

The results from above are not ideal, but still show the difference of matters in the patients using the BL images and comparing the pixel count of each colour to each image's corresponding M24 image.

The results of this lab had errors due to time constraints and computing limitations, but with a few additions in the version 2 of the program, such as variable thresholding being used in place of global thresholding, and identical threshold values for each pair of images (BL and M24), the results would be much more accurate.

There was no way using the built-in functions to control the values of the thresholds of each pair of images. This ultimately led to much of the error present in the lab. This lab still applies many strategies of image processing to the MRI scans to extract different properties and information from these images. This lab is a great demonstration of understanding and was very useful in solidifying understanding of different methods of registration and segmentation.

Citations:

The Role of Grey Matter in Alzheimer's Disease. (2015, November 02). Retrieved from https://www.alzheimers.net/4-20-15-grey-matter-and-alzheimers-disease/

Greensted, A. (n.d.). The Lab Book Pages. Retrieved from http://www.labbookpages.co.uk/software/imgProc/otsuThreshold.html

Image registration. (2019, March 06). Retrieved from https://en.wikipedia.org/wiki/Image_registration

Image segmentation. (2019, April 11). Retrieved from https://en.wikipedia.org/wiki/Image_segmentation

Multilevel image thresholds using Otsu's method. (n.d.). Retrieved from https://www.mathworks.com/help/images/ref/multithresh.html

Links used:

https://cind.ucsf.edu/sites/cind.ucsf.edu/files/wysiwyg/education/RigidRegistration.pdf

https://www.cs.cmu.edu/~galeotti/methods_course/DeformableRegistration.pdf

http://ww2.odu.edu/~kiftekha/ECE783_883/image%20registration.pdf