Predicting the CT Mask

Project Overview and Introduction

The process that I will be researching throughout the course of this report is to see if we can train a machine learning model to learn from a series of ultrasound images of patients that have experienced a traumatic brain injury and have blood present in their brains. We want to use those images or scans, to identify commonalities or patterns which are markers for pockets of blood being in the brain and see if we can use this to predict whether other patients that have experienced some type of head trauma, have blood in their brains. Ultimately, the goal of the project is to predict the blood mask, which represents that ground truth by running a dimensionality reduction analysis or PCA, on both patients bMode scans which represent 240 independent and identically distributed (iid) samples of each patient.

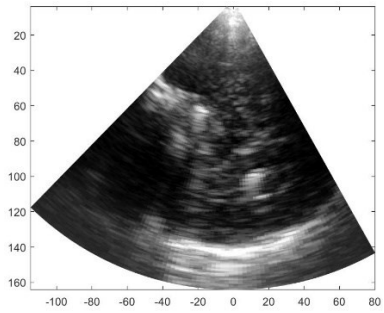

Figure 1: bMode Scan of Control Patient Analyzed

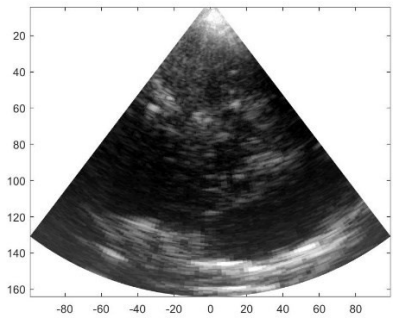

Figure 2: bMode Scan of Test Patient Analyzed

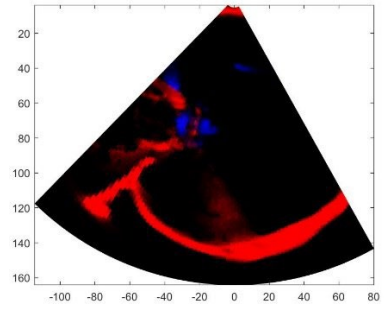

Figure 3: Blood, Bone, and Vent Masks of Control Patient

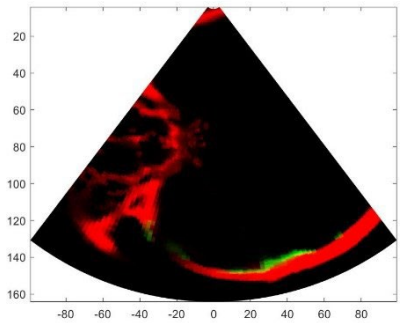

Figure 4: Blood, Bone, and Vent Masks of Test Patient. Green indicates blood

The Challenge

Ultrasound machines produce soundwaves that penetrate tissue structures and reflect to the probe with a reduced magnitude value due to something called attenuation. This reduced signal collected and used to produce images of the internal structures in the body. Unfortunately, these soundwaves are

susceptible to varying degrees of interference due to higher density objects such as bone mass so getting a good scan can be difficult. The bone mass attenuates the signal and creates a type of shadow effect where any tissue structures behind the bone mass show up much more faintly, if at all, making this one of the largest challenges to getting good descriptive data from the patient.

Additionally, because patients have a very high variability of injury type, injury location, skull mass, tissue structures, and other biological factors, it makes it very difficult for researchers to accurately compare pixel information between scan frames of patients. Because the positions of any given pixel in one scan may not be the same exact pixel in another scan frame, this has a high change of mudding the data analysis, making it harder for the machine learning model to correctly identify the size and location of these pockets of blood in the brain. As I discuss later, I am making the assumption that each scan frame is the same identically distributed sample of pixels as the next scan frame of that patient, but we can almost certainly say that this isn't the case in reality given the probability of the ultrasound operators variability and movement of transducer angle and position.

Original Data Collection Technique

The method of data collection is a series of 8 seconds scans, using an ultrasound machine to scan multiple planes of a patient's brain, including the sagittal, coronal, and transverse planes. The machines probe, referred to as a transducer, captures the density values that represent the density of bone and tissue structures observed within the scanner plane of the probe. The transducer is placed against the patient's head in a position, and then repeats an electronic frequency or sound wave that then reflects band and the amplitude of the signal is measured and converted into a density value, producing what is referred to as a "bMode" scan which is a grey scale image representing those density values. Figure 4 below, shows the various versions of transducers available which in our case, will be using the curved array transducer. What is important to understand is that while this transducer records in a "slice" pattern, it is doing this 30 times a second for 8 seconds, producing a 3rd dimension in the data, which is a time dimension that represent multiple observations of the patient's brain over a short period of time. This will be the data that will be examined throughout the course of the project

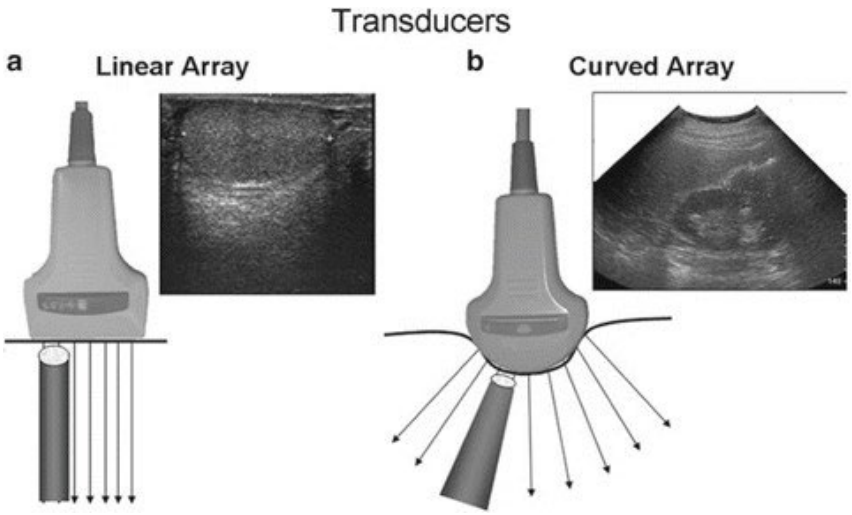

*Figure 5: (**a**) The linear array transducer produces a* rectangular *image field. (**b**) The* curved array *transducer produces a* trapezoidal *or* pie-shaped *image. The shape of the transducer affects the divergence of the sound wave as it propagates in the body*

The other major piece of data being collected in this research a CT scan of the same patient, which will be considered the ground truth for the study. These scans are important because they are used to create three different mask that are superimposed into the imaging plane of the ultrasound image and essentially tell the locations of all blood, bone, and ventricle locations. It is a road map of sorts that I hope to use to train the model.

Pieces of the Puzzle and Research Interests

The stable pieces that I will be focusing on are the three different head structure masks (blood, skull, and vent) that are created using the CT scans. These masks are basically traces of the CT scan brain structure and are then superimposed over a duplicate bMode scan that mimics the angles and dimensions of the original scan of the patient as a way to single out high value pixels in the ultrasound scans for analysis. I will mainly be focused on the blood mask which is a matrix of values that are either 0 or 1, 0 being no blood and 1 being the existence of blood. My theory is that the blood mask will tell us what pixels are important to be looking at in the bMode Ultrasound image. I initially was planning to also use the CT scan data but because of the timeline given, it was important to scope down the research to something more attainable because of lack of knowledge as to what the CT scan data values represent and how to reshape the data to mimic the ultrasound scan. Because the CT scans are the most accurate piece of information that we have and is considered the ground truth due to its ability to produce high accurate scans of the brain, the next best thing would be to look at the blood mask because the data is easy to understand.

My research interest is to look at both a patient's brain that does not contain blood (control case) and a patient's brain where blood is present (test case) due to some experienced head trauma and treat them as a before and after to see if I can find a pattern of change between the two scans. I am also interest in doing a principal component analysis on both cases to see if I can predict the blood mask that has been

drawn from the CT scan. Finally, I am also very interested in analyzing patient 133 in the data and seeing what types of patterns I can find in this patient. A presentation was given by an experienced researcher on the project team, and it was pointed out that this patient's ultrasound image was able to clearly show the blood pocket in the brain. This means that there is something special about that case and all of the elements of that scenario need to be investigated. As the speaker said, "there is something special about this patient".

Research Question

The research question that I propose for this project is… can we predict the blood mask created from the CT scans by running a dimensionality reduction analysis or PCA, on the bMode scans of both a patient that doesn't have blood in the brain, and a patient that does have blood in the brain?

Important Assumptions Moving Forward

In this research, I will have to make a few key assumptions moving forward to limit the scope given the timeline. The first one being that we assume that each of the pixel in each frame of the bMode scans are the same pixel as the subsequent pixel in the next frame. This allows us to take the 259px by 79px bMode scan and reshape it into a 1px by 20461px matrix which will represent the entire observation. Then I will take all of the following frames in the bMode scan and do that same thing and place them in one single matrix that will be 240 rows by 20461 columns.

I am assuming that the patient who does not have blood in their brain has a generic scan that will look exactly like anyone else that also does not have blood in the brain. That is to say that there are no structural differences, bone density etc. Also, we will assume that people who have blood in the brain will also have the same generic scans with the structure, bone density etc. as to scope the project down. These assumptions allow for a simple analysis to be done within the timeframe given. The hope is that the first PC is going to be the one that points at the location of the blood.

Another assumption being made is that the blood mask from the CT scan is the ground truth and only statement about what we are looking for in the ultrasound images. While I believe it would most likely be accurate, I also understand that there is always a chance of operator error in the masking process. I will be looking at one of the 240 scans and assume that it is exactly the other and try to predict the CT scan from it. bMode matrix and collect all pixels that correlate to a position on the blood mask that have been Identified as positions of blood.

Additionally, I will also assume that while it is possible and perhaps reasonable to treat this information as a time series, the natural of the assignment mandates that we assume that the scans are permutable and therefore their time index contains no information. This is a fundamental presumption to allow for a principal component analysis of the 240 scans, otherwise I would not be able to accomplish this and have to limit the analysis to just one of the 240 scans. The time index makes the analysis a moving target and would make the analysis much more difficult to predict. Even in the case that the scans are tracking

some process, and the frames measure that process over many phases, we can still stay that we are looking at the same population of pixels.

Research Project Process

I will be taking the bMode scans of both a control patient, who has not experienced brain trauma and is free of blood in their brain, and then other patients bMode scan that has experienced trauma and does not have blood in their brain, and use that pixel density information to try and predict the blood mask that was been created from the CT scan by looking at all 240 samplings from each of the patients bModes. This will be accomplished by using the principal component analysis of both bModes and see if the primary principal component's projection produces the blood mask. I hope to see the first principal component having the largest projection and producing an image similar to the blood mask.

Data Preparation and Normalization Method

Because the bMode scans had various size dimensions of the scans, I had to cut the larger matrix down to the small matrix. In this case the control patients bMode is 259 by 79 and the patient with blook in their brain was 259 by 80 and have no idea what the difference between them is. This means to make the comparison appropriate, we needed to drop the 80^{th} row of the test patient. We could have dropped anyone of the rows, but I just decided on the last one. A complete analysis would have tested each one of the rows and to drop the one that gave the biggest overlap. However, our decision is unbiased because of expediency and is uncorrelated with any other dimension in the project to our knowledge.

As I discussed before, the data of each patient comes in the form of a three-dimensional array with the third dimension representing time. To normalize the data appropriately, I stripped out each two-dimensional frame into a long 1 by 20461 array and then stacked all subsequent frames below that array. Because we are assuming that each pixel of each frame is identical to the same pixel on a different frame, I wanted to arrange all "like pixels" into columns so that when we normalize the data, we are hypothetically normalizing a single pixel. Once each of the patient's data was originated in a two-dimensional 240 by 20461 array, then the data was normalized down the rows and then also normalize down the columns. This was done because all columns represent pixels, so it allowed for normalizing in all both dimensions to remove any anomalies. Additionally, the very nature of our data all representing pixels of a larger image, that means that all features are not useless or noisy and are applicable to my analysis.

Findings

Scree Plots

After running the singular value decomposition on the normalized patient pixel data, I created a scree plot that better understand the components of the data and to see what group of components make up a majority of the data.

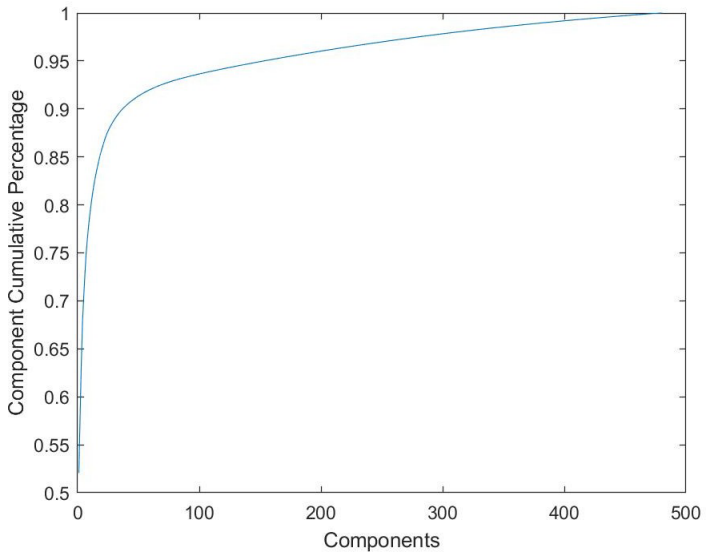

Figure 6: All 480 Principal Components

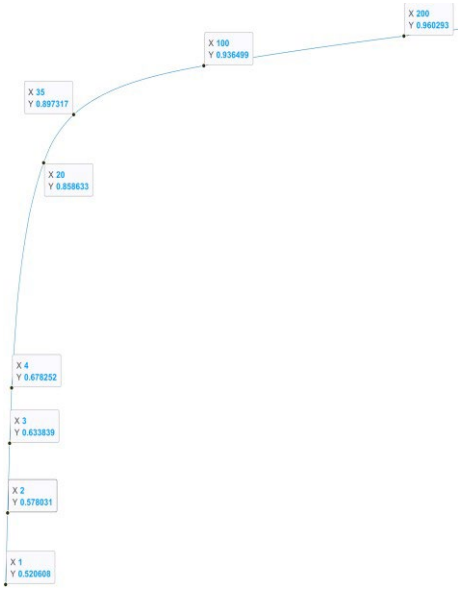

Figure 7: Data points of Cumulative Scree Plot

In Figure 6, we can see we can see that the graph starts are 52% and rises quickly before it reaches 20 principle components before it begins to quickly flatten. Figure 7 shows a few of the data points along this line and it looks like at about 20 components is where the components contribution to the total variance begins to level off. by the scree plots above that the top 40 of the principal components have most of the variance in the data and can represent approximately 90% of the data.

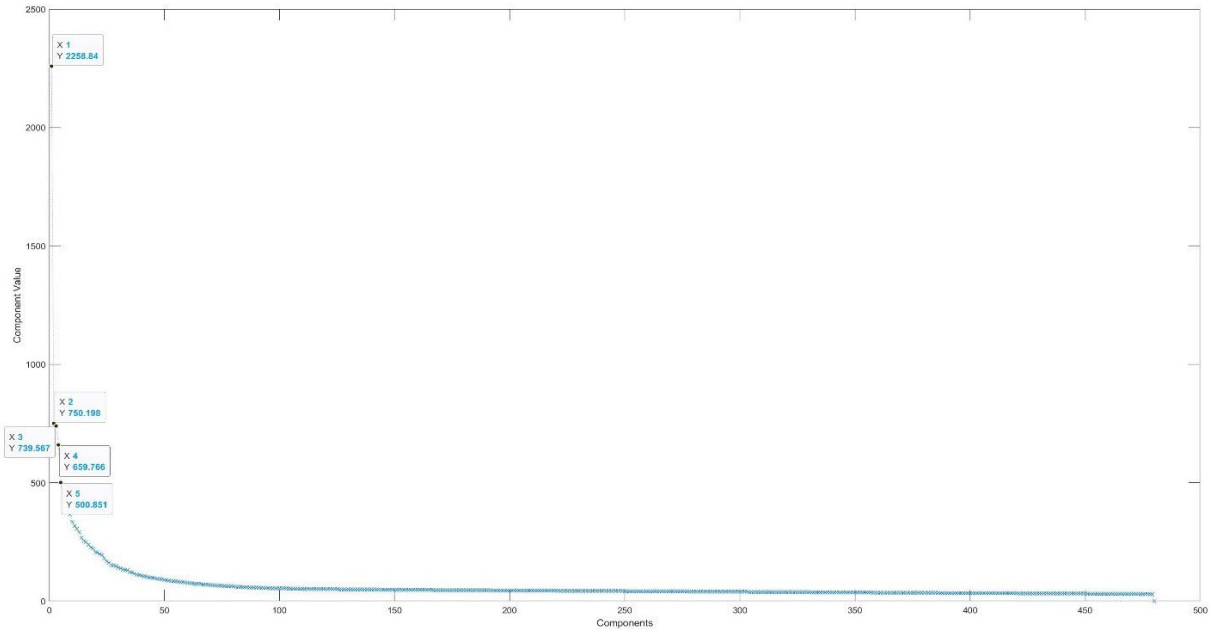

Figure 8: Scree Plot of all Component Percentages

In figure 8, it is obvious that the first component of the pixel data dominates the majority of the variance in the data, with the third, fourth, and fifth grouped together as the next most influential components.

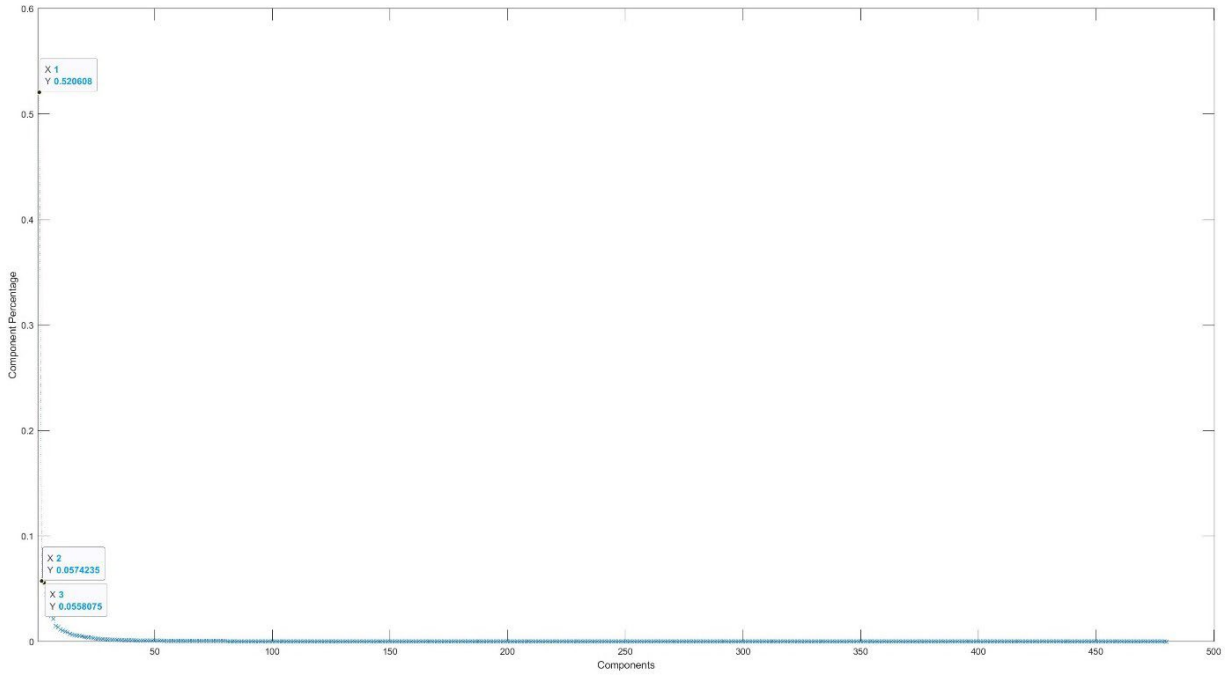

Figure 9: Scree Plot of the Singular Value Percentages

Figure 9 gives a clearer picture to how much each component makes up of the total data component space and it is clear that the first component is a major factor in the variance of the data.

Principle Loadings

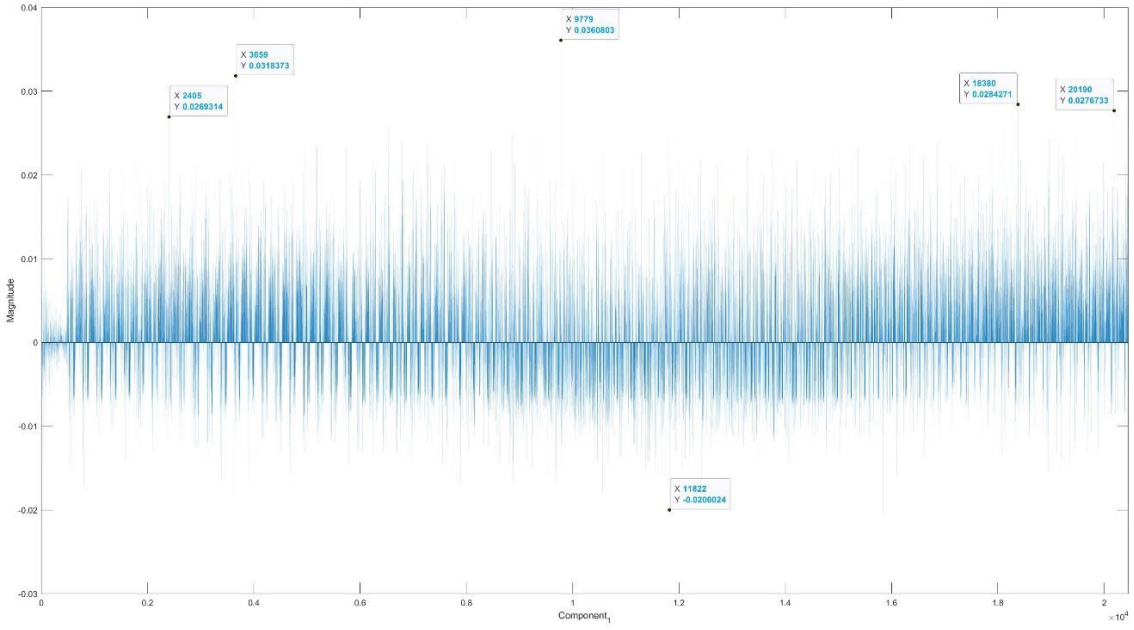

Figure 10: Feature make-up of Component 1

Looking at the first principal component, it looks that there is an oscillating pattern that is happening across the components make up. The first 8,000 attributes seem to be back and forth with a slight majority of the attributes make up favoring a positive relationship. Then 8,000 to 15,000 attributes also have a positive relationship but are majorly inverse related to all the components before 8,000. Then again, this patten flips with the attributes from 15,000 to 20,000, mostly being positively correlated but inversely related to the previous group.

The next 4 components all resembled each other and looked like there was an even split between positive relationship and inverse relationship. Additionally, the magnitude of the make-up seems to somewhat resemble each other. This could be due to data redundancy in the features. This is more than likely in reality considering when a technician is scanning a person's head, they are probably leaving the transducer in one location over the period of the scan.

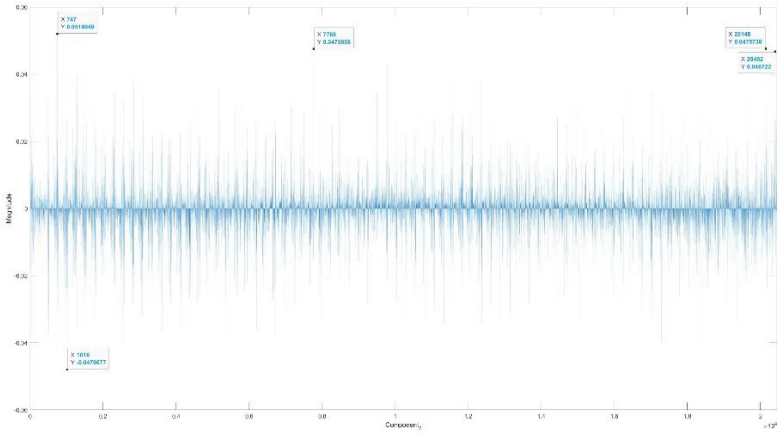

Figure 11: Feature make-up of Component 2

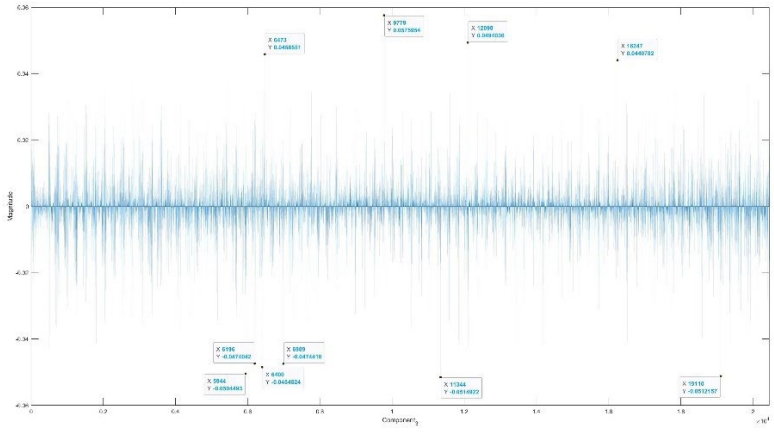

Figure 12: Feature make-up of Component 3

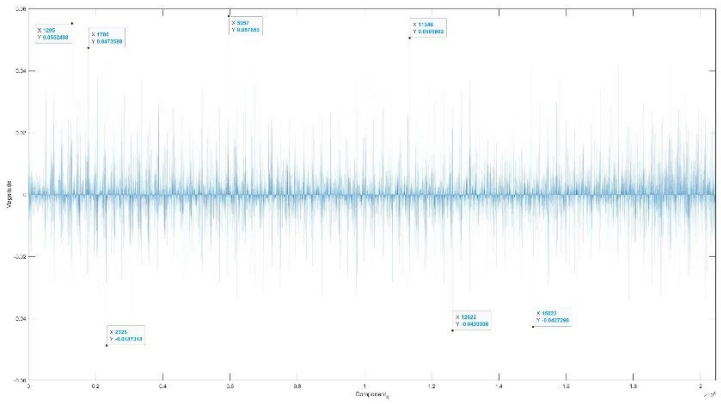

Figure 13: Feature make-up of Component 4

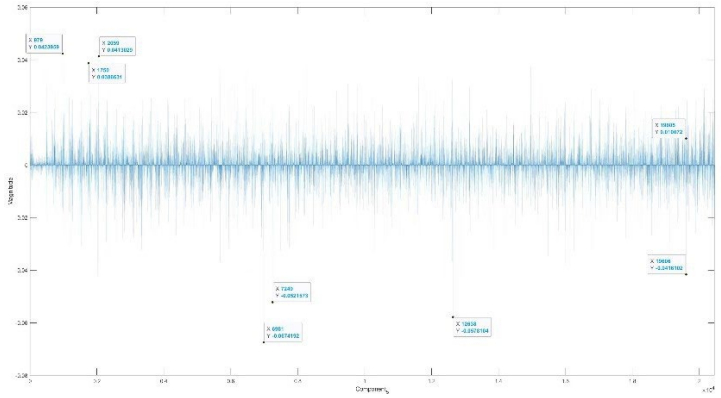

Figure 14: Feature make-up of Component 5

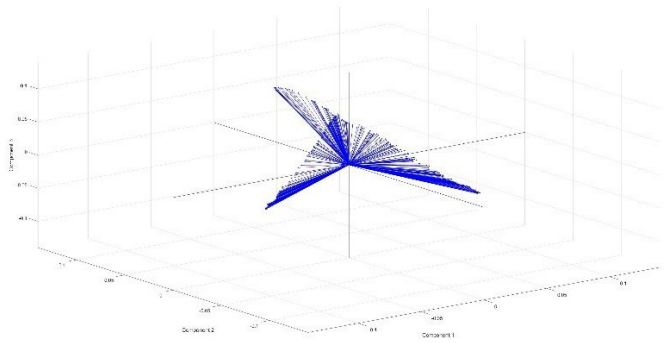

Figure 15: 3-D plot of U

Here in figure 15, we can see U, or the left singular values which are a n-by-n orthogonal matrix which form a basis for the X. here are the factor weights of pixels that correspond to the factors of X. U's rows represent the observations of the patients, and the columns represent the factors of X.

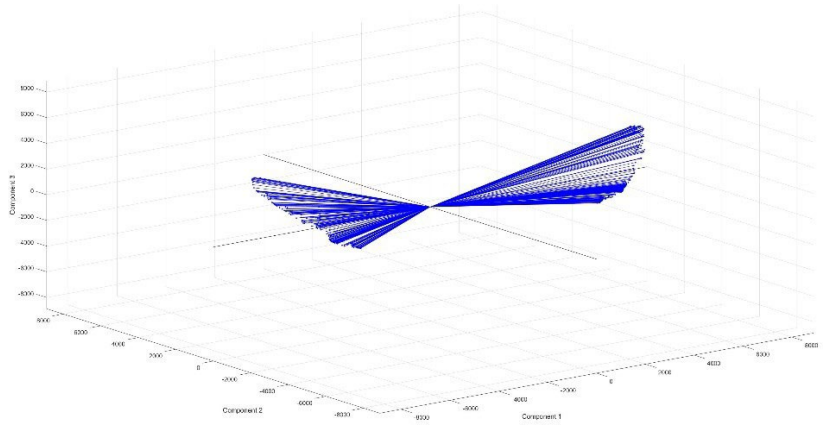

Figure 16: 3-D Plot of Ur

In figure 16, we see Ur, which is X multiplied times the the right singular values matrix. The Rows represent the PC-scores which are the coordinates of the observations in the space of the new Variables or Principle Components.

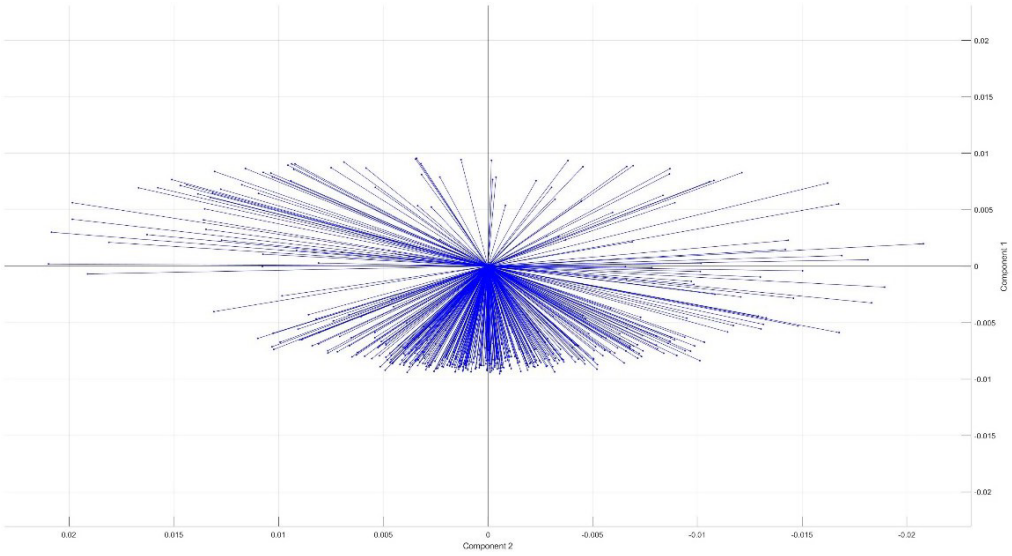

Figure 17: Principal Components of all patient data

In figure 17, we see the top-down view of the plot of the singular values (S) times the transpose of V (right singular values of X). The rows of this matrix represent the principal axes or coordinates of the variables or components on the bases of columns of U.

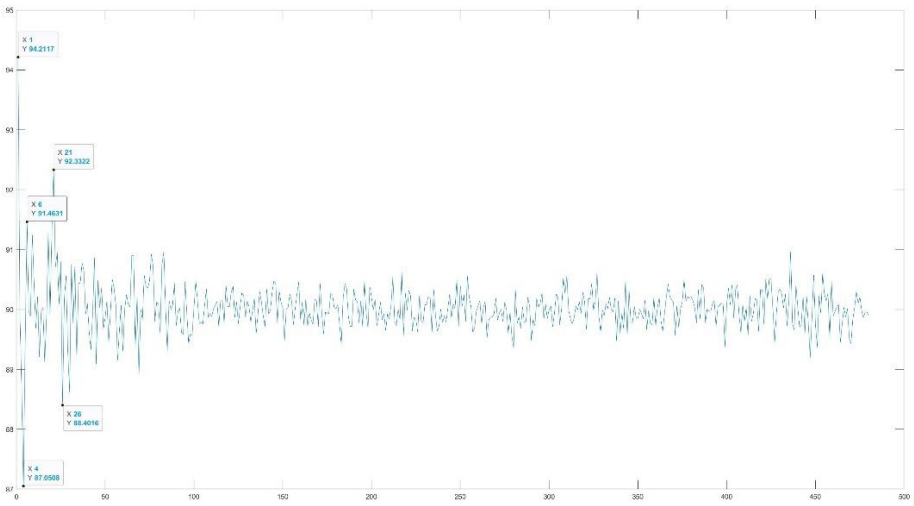

Figure 18: The angle of the principal components to the blood mask

Figure 18 shows is a visual representation of the thetas, or angles between the principal components and the blood mask. The plot shows that almost all of the principal components are orthogonal to the blook mask but there are a few such as PC 1, PC 4, PC 21, PC 26 that deviate from orthogonality. The goal of this plot was to isolate the principal components with the greatest delta from the orthogonal angle and see it those components combined would project onto the blood mask and show us something similar to what we saw in the original blood mask.

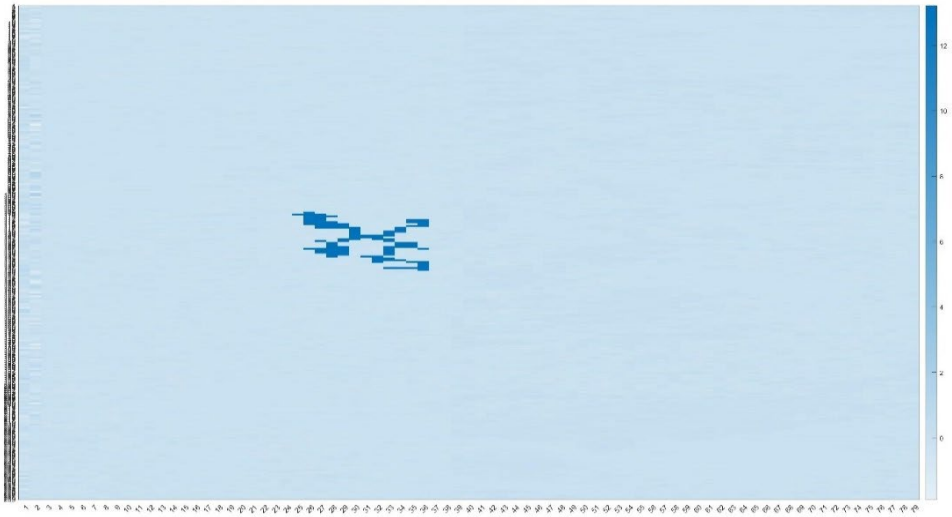

Figure 19: Heat map image of the projection onto the test patients' blood mask

In figure 19, we see what the projection is onto the blood mask by PC 1, PC 4, PC 21, PC 26 combined. While this is not similar to the original blood mask image, it is something intriguing to investigate.

Conclusions and Future Iterations

After completing the decomposition analysis of the patient data, I was not successful in using the principal components to predict what the blood mask would look like. But the principal did yield some

results which I look forward to investigating further. I have already begun working on a third version of my matlab program to analysis the data and hope to include and address the following points:

- I hope to include and exam the original dataCT variable which includes the CT scan information.
- Look at the hrTimes variable. Examine the time ranges, normalize them and map scans to those times in each cardiac cycle so we could look at scans of each patient that correspond to the same period in the cardiac cycle. This way, we would be looking at the system at the same state.
- Plan to pull out all .mat files from other patients with brain injuries and add them to the two-dimensional array used in the analysis.

Some of the main take aways that I have learned from this project is that while more data is better, developing a targeted approach to collecting good quality data is of monumental importance. The assumptions that I had to make in the beginning of the project where a necessity to being able to get through this analysis in a timely manner even though those assumptions were more than likely to be incorrect. The pixel columns of the reshaped data were almost certainly containing pixels from a variety of positions in the brain, and this will through the analysis off because you are not comparing the same pixel throughout. This means generating some system of data collection (ultrasound scans) that can produce consistent results. This could include using a machine that can scan in the same pattern each time or place some type of object on the patients skin that will show up in the scans so that the locations can be better mapped. Additionally, I can't help but wonder why there is no data from a before injury and after injury. This seems like a very attainable thing considering situations where individuals are put in scenarios with high probability of brain injury. This could include soldiers before being deployed into a warzone and football players before a game etc. I believe being able to see what the pixels "looked like" before the injury and seeing what they are after the injury would go a long way in supporting a solution to this problem.

Future Research Questions:

I have two future research questions that both resemble each other and the first one is how would the analysis change if the scans were done by slowly moving the transducer over the injury. In other words, if the technician slowly moves the transducer over the injuries location at a constant rate during the 8 seconds, the third dimension would become more of a physical structure and give us more information about the affected area. This way we actually get more depth in the scan.

The second question is really a follow up to the first, and that is what if we had a way to sync the ultrasound scanning plane (transducer) to the CT scanning plane? In other words, the ultrasound transducer is synced and is moving with the CT scanners plane so that they data can be accurately mapped to the CT scan. It is almost certain no matter how hard the technician tries to scan the same plane that they CT scan did, there are going to be minor variations that will through the mapping off. This way when we do the analysis, we can have more confidence in the accuracy and consitency of the data itself.

Team Assessment

Mark Mavis:

Well, the only thing I really need to say here is that I did everything Lol 🟡 .