Advancing Head Trauma Assessments:

Ultrasound Imaging for Enhanced Predictive Capabilities

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Abstract

This research paper explores the potential of training a machine learning model using a series of ultrasound images to predict the presence of blood in the brains of patients who have suffered traumatic brain injuries. The objective is to identify patterns or commonalities within the images that serve as indicators for the presence of blood pockets in the brain. By leveraging this knowledge, the aim is to develop a predictive framework that can determine whether other patients who have experienced head trauma exhibit signs of blood in their brains. The primary goal of this project is to employ dimensionality reduction analysis, specifically Principal Component Analysis (PCA), on the bMode scans of both patients. These scans consist of 240 independent and identically distributed (iid) samples per patient. Ultimately, the research aims to predict the blood mask, representing the ground truth, by leveraging the insights derived from the trained machine learning model.

Keywords: Traumatic brain injury, Ultrasound imaging, predictive model, dimensionality reduction analysis, principal component analysis

Exploring the Potential of Ultrasound Imaging for Predicting Blood Presence in Traumatic Brain Injuries

Traumatic brain injuries (TBIs) represent a major public health concern, with potential long-term implications and varying outcomes for affected individuals. Detecting the presence of blood in the brain at an early stage is critical for effective intervention, management, and treatment, ultimately leading to improved patient outcomes. While computed tomography (CT) scans have traditionally been used for this purpose, they come with several limitations, including limited portability, high costs, slow imaging, and ionizing radiation exposure.

In this research, our objective is to explore the potential of utilizing principal component analysis (PCA) and dimensionality reduction techniques on ultrasound images to predict the presence of blood pockets in the brains of TBI patients. To establish a reliable ground truth, we will incorporate CT scans from the same patients, which provide more detailed imaging. By analysing bMode scans, comprising 240 independent and identically distributed (iid) samples per patient, we aim to employ dimensionality reduction analysis to develop a predictive model capable of assessing the likelihood of blood presence in the brain based solely on ultrasound images. This will be achieved by predicting the blood masks derived from the corresponding CT scans.

The insights gained from this research endeavour have the potential to significantly influence early diagnosis and treatment strategies for patients with TBIs, fostering improved clinical decision-making and enhancing overall patient care. By harnessing the power of ultrasound imaging and advanced analytical techniques, we aim to address the limitations associated with traditional imaging modalities, paving the way for more accessible, efficient, and accurate detection of blood presence in the brain.

The Challenge

Collecting high-quality ultrasound images presents several challenges that impact the clarity and accuracy of the obtained data. Two primary challenges in this regard are attenuation caused by bone mass and the variability in patient anatomy and imaging conditions.

The soundwaves emitted by ultrasound machines encounter attenuation when penetrating tissue structures. This attenuation leads to a reduction in the magnitude of the reflected signal. Notably, dense objects like bone mass can significantly interfere with the ultrasound signal. The bone's density causes signal attenuation and creates a shadow effect, making it difficult to visualize tissue structures located behind the bone. Consequently, obtaining clear and detailed imaging of these structures becomes a major challenge.

Another critical challenge stems from the substantial variability among patients in terms of injury type, injury location, skull mass, tissue structures, and other biological factors. Due to these variations, it becomes challenging to accurately compare pixel information between scan frames of different patients. The positional correspondence of a given pixel in one scan frame with the same pixel in subsequent frames cannot be guaranteed. This variability in pixel positioning can introduce inconsistencies and complicate data analysis, making it more challenging for machine learning models to accurately identify the size and location of blood pockets in the brain. Factors such as the ultrasound operator's variability, movement of the transducer angle and position, and other variations further contribute to the complexity of achieving precise and consistent image data.

These challenges underscore the importance of addressing technical limitations and establishing robust methodologies in ultrasound imaging to ensure the acquisition of high-quality data. Overcoming these obstacles would significantly enhance the diagnostic

capabilities and reliability of ultrasound imaging in the detection and characterization of blood presence in the brain.

Data Collection Technique

The data collection approach employed in this study involved utilizing an ultrasound machine to conduct a series of 8-second scans to explore various planes of the patient's brain, including the sagittal, coronal, and transverse planes. By employing a transducer, also known as the machine's probe, density values representing the density of bone and tissue structures within the scanned plane were captured. The transducer was positioned against the patient's head, emitting electronic frequencies or sound waves that penetrated the brain and surrounding tissues. Through the measurement of the reflected signal's band and amplitude, the data was converted into density values, generating a grey-scale image referred to as a 'bMode' scan. For our specific study, we utilized the curved array transducer, as depicted in Figure 4.

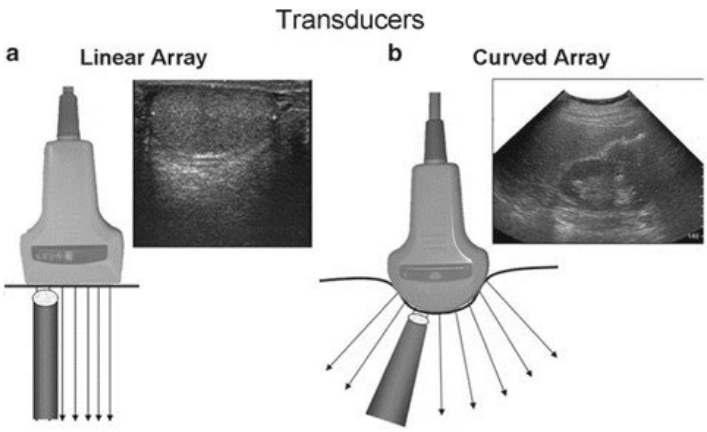

Figure 1: (a) The linear array transducer produces a rectangular image field. (b) The curved array transducer produces a trapezoidal or pie-shaped image. The shape of the transducer affects the divergence of the sound wave as it propagates in the body.

Notably, the transducer recorded data in a 'slice' pattern, collecting information 30 times per second over an 8-second duration. Consequently, this approach resulted in a three-dimensional dataset that incorporates a temporal dimension, enabling multiple observations

of the patient's brain within a concise timeframe. The collected data will be subject to comprehensive examination throughout the entire duration of the project.

In addition to the ultrasound scans, CT scans were utilized as another data source in this study. CT scans provide detailed imaging of the patient's brain and were used as the ground truth for comparison and validation purposes. These scans offer high-resolution cross-sectional images that aid in identifying and locating blood, bone, and ventricle structures within the brain. The CT scans serve as a reference or roadmap, providing precise spatial information that was superimposed onto the ultrasound images. By integrating the CT scan data, the study aimed to enhance the accuracy and reliability of the predictive model.

Research Interests and Focus

The primary focus of this research lies in analysing three distinct head structure masks, namely the blood mask, skull mask, and vent mask, derived from CT scans. These masks serve as traces of the brain structure obtained from the CT scans and are superimposed onto duplicate bMode ultrasound scans, replicating the angles and dimensions of the original patient scans. The main emphasis will be placed on the blood mask, represented as a binary matrix with values of 0 or 1, indicating the absence or presence of blood, respectively. The underlying hypothesis is that the blood mask will provide crucial information regarding the pixels of interest within the bMode ultrasound images. Initially, the plan included incorporating CT scan data as well, but due to the given timeline and the challenges in understanding the representation and reshaping of CT scan data to match ultrasound scans, the research scope was narrowed down to a more achievable objective. Considering that CT scans are considered the gold standard for accurate brain imaging and serve as the ground truth, the focus shifted to analysing the blood mask, as its data is readily interpretable.

Method

Important Assumptions Moving Forward

To streamline the research within the given timeline, certain key assumptions will be made. Firstly, it will be assumed that each pixel in the bMode scans corresponds to the same pixel in the subsequent frames. This assumption allows for reshaping the 259px by 79px bMode scan into a 1px by 20,461px matrix, representing the complete observation. This process will be repeated for all frames of the bMode scan, resulting in a consolidated matrix with 240 rows and 20,461 columns.

Additionally, it will be assumed that patients without blood in their brains will exhibit generic scans that are structurally similar to one another, disregarding differences in bone density or other anatomical features. Similarly, patients with blood in their brains will be presumed to have generic scans with consistent structures and bone density. These assumptions are made to narrow down the project scope and facilitate a simplified analysis within the allotted timeframe. The expectation is that the first principal component will provide an indication of the blood's location.

Another assumption pertains to the blood mask derived from the CT scans, which is considered the ground truth for identifying blood in the ultrasound images. While it is likely to be accurate, the possibility of operator error during the masking process is acknowledged. Therefore, one of the 240 scans will be selected, assuming it closely resembles the others, and the goal will be to predict the corresponding CT scan. The bMode matrix will be analysed, and pixels correlating to positions identified as blood locations on the mask will be collected.

Furthermore, it will be assumed that although the data could be treated as a time series, for the purpose of this research, the scans are interchangeable, and their time index does not convey additional information. This assumption is crucial for performing a principal component analysis on the 240 scans, as it allows for the accomplishment of the analysis objectives. Considering the time index would introduce complexity and impede predictability. Even if the scans track a particular process and the frames capture different phases of that process, it can still be assumed that the population of pixels remains consistent.

Data Preparation and Normalization Method

Due to the varying size dimensions of the bMode scans, it was necessary to resize the matrices to ensure appropriate comparisons. In this case, the control patient's bMode scan had dimensions of 259 by 79, while the scan of the patient with blood in their brain was 259 by 80, with the difference between them remaining unclear. To facilitate a fair comparison, the 80th row of the test patient's scan was dropped. Although a thorough analysis would have tested each row and selected the one with the greatest overlap, the decision to drop the last row was made with impartiality and expedience, uncorrelated with any other dimension in the project to the best of our knowledge.

As mentioned previously, each patient's data is presented as a three-dimensional array, with the third dimension representing time. To appropriately normalize the data, each two-dimensional frame was extracted and arranged as a single long 1 by 20,461 array. These arrays were then stacked vertically to consolidate all subsequent frames, assuming that each pixel within corresponding frames is identical. This arrangement allowed for the grouping of "like pixels" into columns, enabling hypothetical normalization of a single pixel during data normalization. Once the patient's data was organized into a two-dimensional 240 by 20,461 array, both row-wise and column-wise normalization were applied. Since all columns represent pixels, normalizing in both dimensions helped eliminate any anomalies.

Furthermore, considering the nature of the data, wherein all features represent pixels of a larger image, it can be inferred that all features are relevant and applicable to the analysis, eliminating the presence of useless or noisy data.

Results

Decomposition and Analysis

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. In Figure 6, we can see we can see that the graph starts are 52% and rises quickly before it reaches 20 principal components before it begins to quickly flatten.

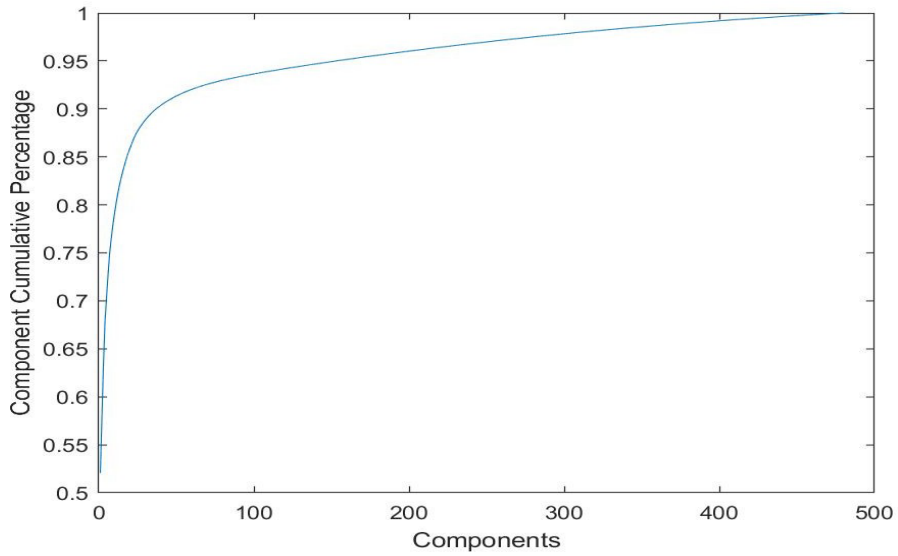

Figure 2

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.

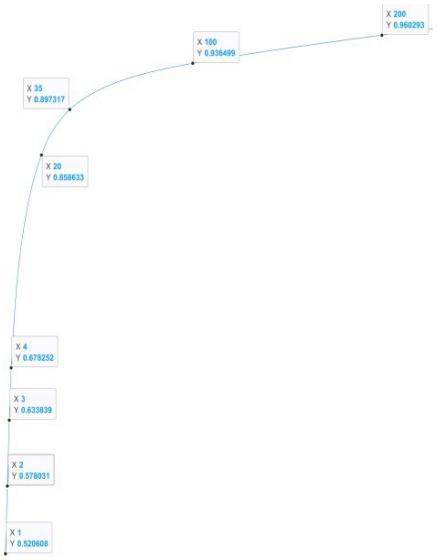

Figure 3

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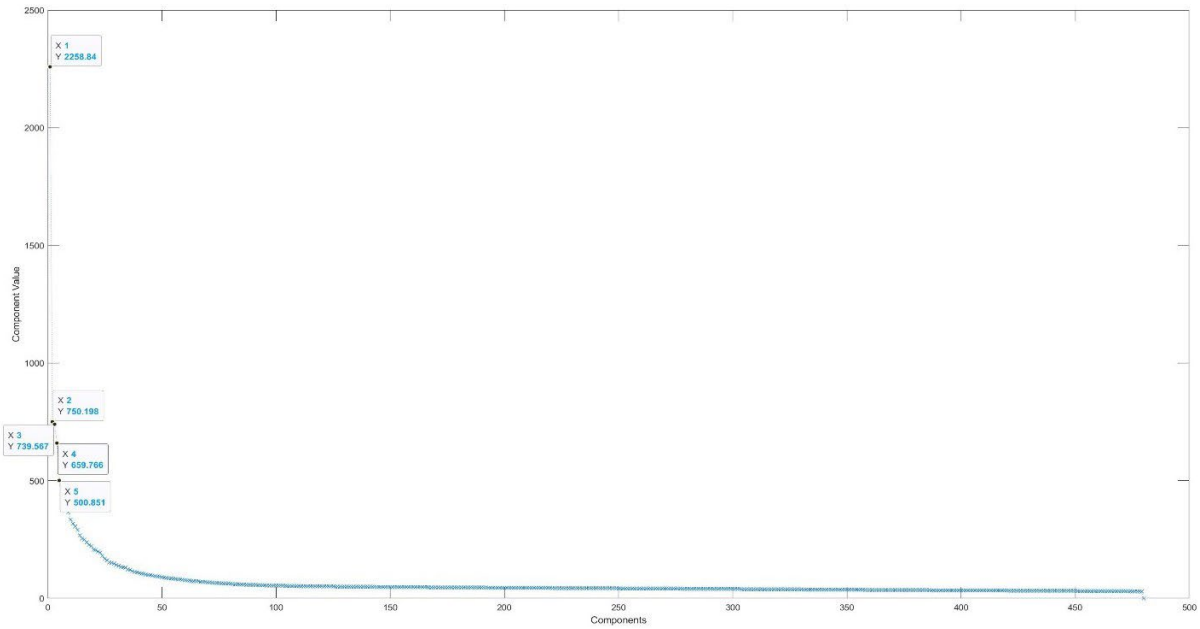


Figure 4: Scree Plot of all Component Percentages

The first component of a Principal Component Analysis (PCA) analysis typically plays a crucial role by capturing most of the variance present in the data. It represents the linear combination of variables that explains the maximum amount of variation within the dataset. This dominant component reflects the most significant patterns or trends in the data, highlighting the underlying structure and relationships among the variables. By extracting and examining this first component, we gain valuable insights into the key factors driving the variability in the dataset. In figure 8, we can see 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.

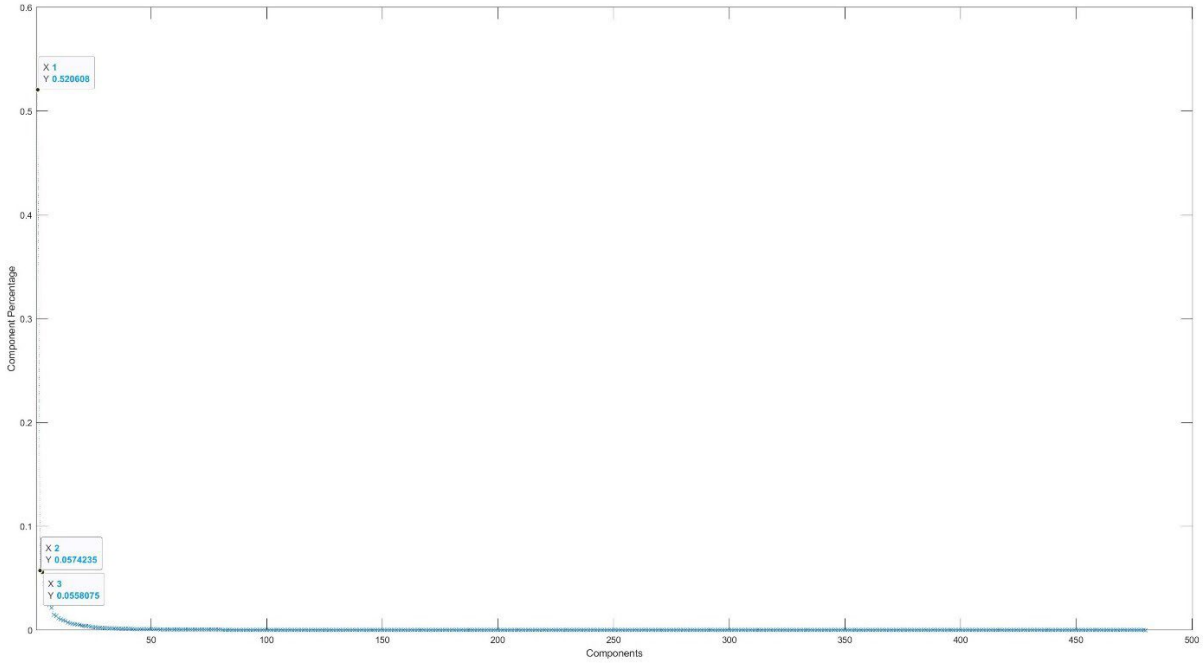


Figure 5: Scree Plot of the Singular Value Percentages

Principle Loadings

In our analysis, the principal loadings are crucial indicators of the relationship between variables and the principal components. Loadings represent the weights assigned to each variable in the construction of principal components. They quantify the contribution of each variable to the overall variance explained by a specific principal component. High

positive or negative loadings indicate strong correlations between variables and the principal component, suggesting that those variables have a significant impact on the underlying structure of the data. Looking at the first principal component in figure 6, 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.

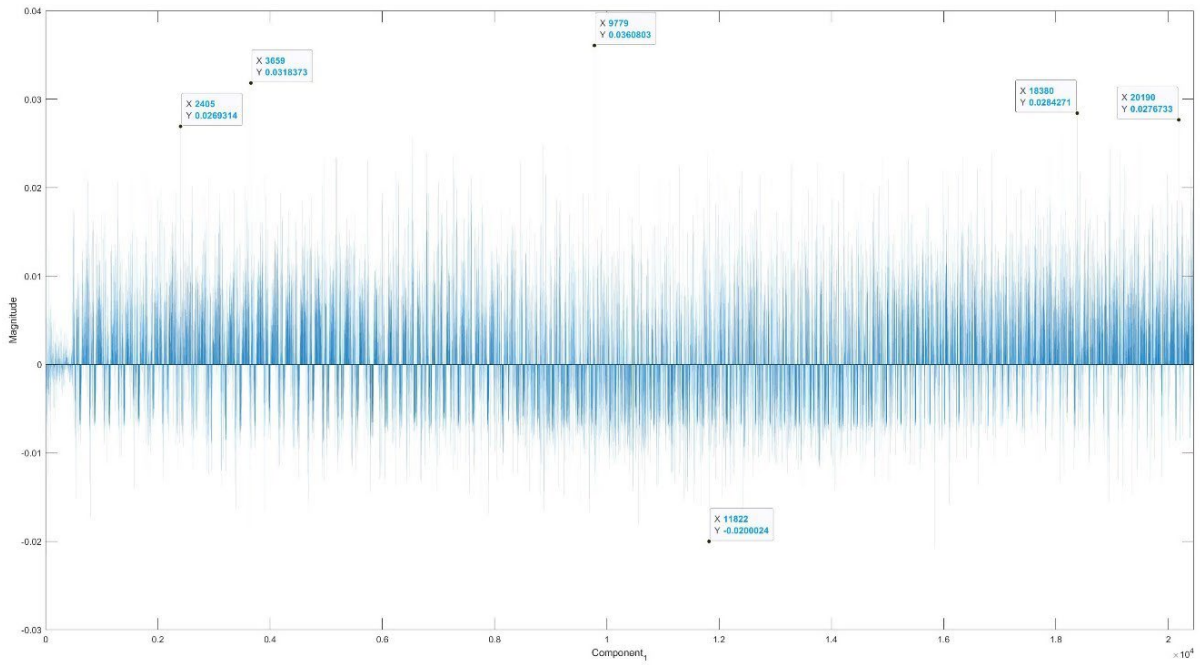


Figure 6: Feature 1 Component Make-up

In figures 7 through 10, we can see 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 a technician is

scanning a person's head and leaving the transducer in one location over the period of the scan.

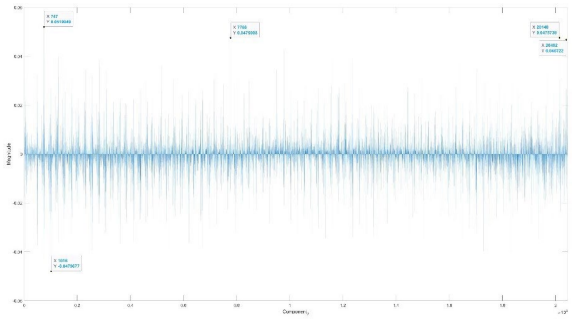


Figure 7: Feature 2 Component Make-up

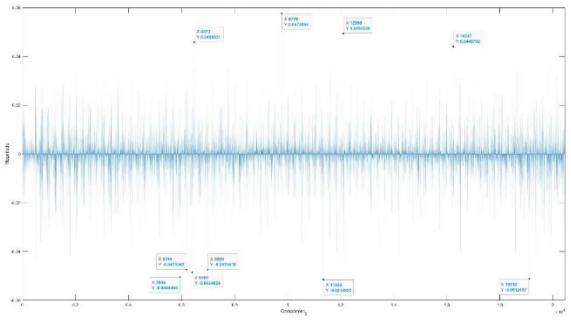


Figure 8: Feature 3 Component Make-up

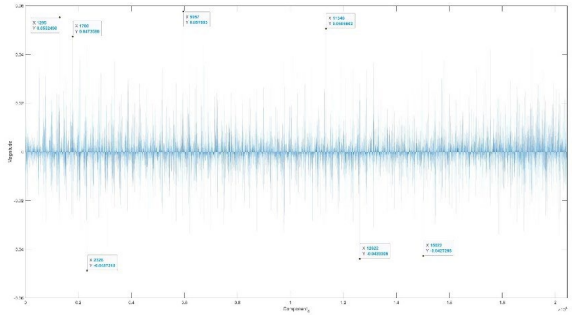


Figure 9: Feature 4 Component Make-up

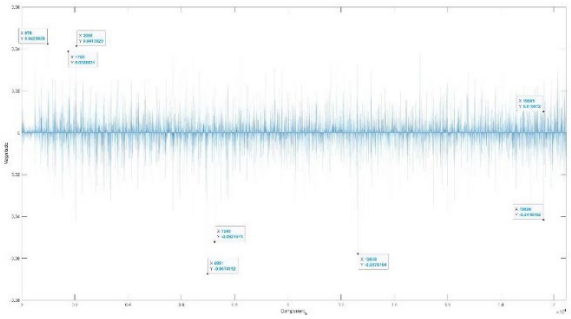


Figure 10: Feature 5 Component Make-up

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 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 like what we saw in the original blood mask.

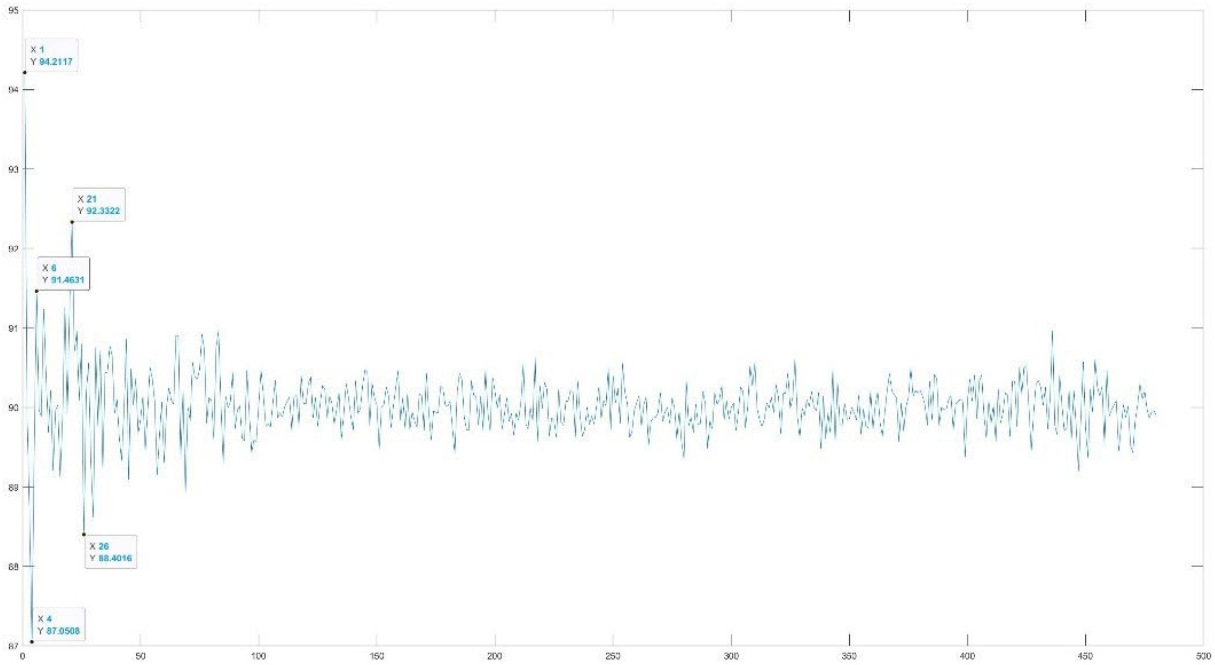
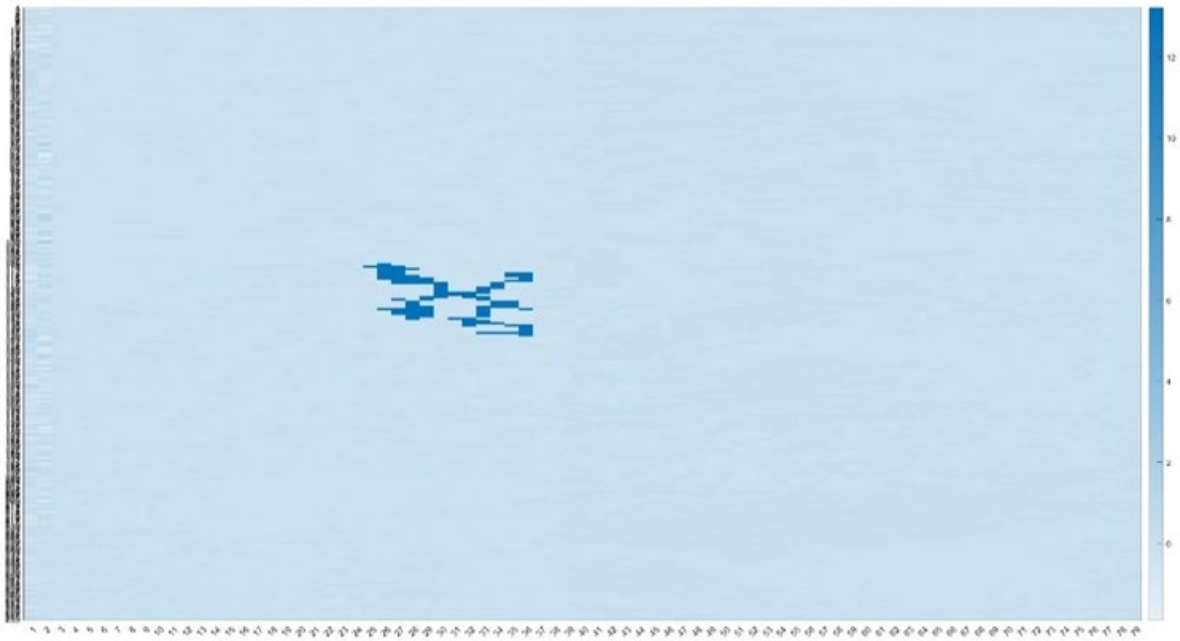


Figure 11: The Angles of the Principal Components to the Blood Mask

In the final step of our analysis, our goal was to provide a way to represent the data in lower dimensional space by creating a projection on to the principal components, where each projection corresponds to the coordinates of a data point in the space spanned by the principal components. This allows for a simplified representation of the data, where the dimensions are defined by the principal components that capture the most significant variability. By projecting the data onto these components, the dimensionality of the dataset is reduced, and the inherent structure and patterns can be more easily visualized and analyzed. In figure 19, we see what the projections onto the blood mask by PC 1, PC 4, PC 21, PC 26 combined look like. While this is not like the original blood mask image, it is something intriguing to investigate further in future iterations.



Conclusion and Future Direction

Upon completing the decomposition analysis of the patient data, I encountered challenges in using the principal components and was not able to accomplish our initial goal of predicting the blood mask appearance. Nevertheless, the principal components did yield some positive results that warrant further investigation. To address these findings, I have initiated the development of a third version of my MATLAB program, aiming to incorporate and examine the original dataCT variable containing CT scan information. Additionally, I intend to explore the hrTimes variable, specifically investigating the time ranges, normalizing them, and mapping scans to corresponding periods in the cardiac cycle. This approach would enable us to analyse scans from each patient during the same phase of the cardiac cycle, providing a consistent state for evaluation.

Furthermore, I plan to expand the scope of the analysis by incorporating .mat files from other patients with brain injuries into the two-dimensional array utilized in the analysis. One key takeaway from this project is the importance of targeted data collection and ensuring

high-quality data. Although I had to make certain assumptions to expedite the analysis process, these assumptions were likely to be inaccurate. The pixel columns of the reshaped data likely contained pixels from various positions in the brain, which introduced inconsistencies in the analysis since comparable pixels were not being compared throughout. To address this, it is crucial to establish a systematic approach to data collection, such as utilizing ultrasound scans, that can generate consistent results. This may involve using a machine that follows the same scanning pattern or placing an object on the patient's skin that can be reliably identified in the scans to improve location mapping.

Additionally, it is worth considering the absence of pre-injury and post-injury data. Obtaining data from before and after an injury seems achievable in scenarios involving individuals in high-risk situations, such as soldiers before deployment or football players before a game. Comparing the pixel characteristics before and after an injury could greatly contribute to finding a solution to this problem.

Future Research Questions:

I have two related research questions for future investigation. Firstly, how would the analysis change if scans were conducted by slowly moving the transducer over the injury? By moving the transducer at a constant rate over the location of the injury during the 8-second period, we could gather more detailed information about the affected area, thereby adding depth to the scan and enhancing our understanding.

Secondly, building on the first question, what if we could synchronize the ultrasound scanning plane (transducer) with the CT scanning plane? In other words, if the ultrasound transducer moved in sync with the CT scanner's plane, accurate mapping of ultrasound data to the CT scan could be achieved. Despite a technician's best efforts, minor variations are likely to occur when attempting to replicate the CT scan plane. By aligning the planes and

synchronizing the data, we would have increased confidence in the accuracy and consistency of the collected data, further improving the analysis process.