Machine Learning methods to identify Severe Brain Hemorrhage From Tissue Pulsatility Imaging

CSS590

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Abstract

TBI, also known as Traumatic Brain Injury, is caused by "fall, firearm-related injury, motor vehicle crash, or an assault." [1] Specifically, there are two types of TBI: "close brain injury (cTBI) and penetrating brain injury (pTBI)," [2] but our team will be focusing on the cTBI. We aim to make meaningful contributions to the research work carried out by the University of Washington graduate student, Nhut Minh Phan, which he built a machine learning model to predict various brain structures and brain hemorrhage by using the ultrasonic image data generated by Tissue Pulsatility Imaging (TPI) technique [3]. We apply the various techniques we've learned from the class, such as PCA analysis, to the frame 7 of the ultrasound scans and evaluate the performance of the model and discover, if any, new information.

1 Overview

"Ultrasound imaging (sonography) uses high-frequency sound waves to view inside the body. Because ultrasound images are captured in real-time, they can also show movement of the body's internal organs as well as blood flowing through the blood vessels." [4] Usually, to detect the blood inside the brain, Computed Tomography (CT) or Magnetic Resonance Imaging (MRI) is used, but compared to Ultrasound imaging, the device used for the prior two methods are much more expensive and huge, which makes it impossible to be used in some cases, such as in war-zone. [2]

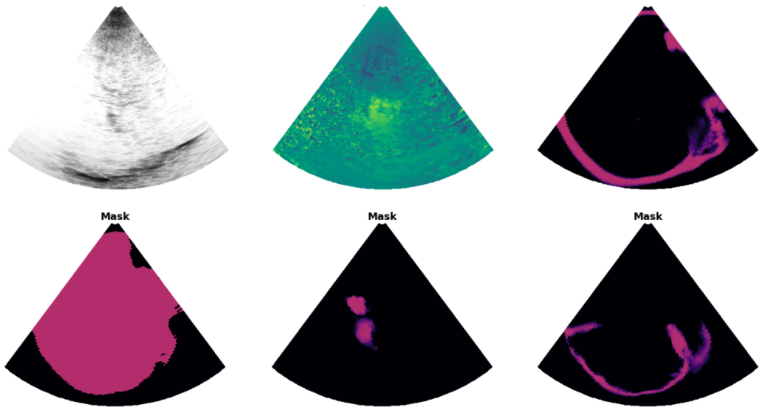


Figure 1: Tissue Pulsatility Imaging Example [2]

However, we can naturally imagine that such places require the blood detection in brain than any other situation. Nevertheless, using the raw Ultrasound imaging is not suitable for blood detection: "ultrasound waves do not penetrate bones very well, making ultrasound imaging more suitable for infants up to about 18 months old" [2], hence, researchers at University of Washington has developed a new technique, called Tissue Pulsatility Imaging (TPI), which "measures the natural pulsatile motion of tissue due to blood flow as a surrogate for blood flow itself" [3], which would allow us to obtain the displacement value, which represents the magnitude of difference detected in each pixel of the B-Mode, and we hope that this information can be helpful to detect the intracranial hemorrhage; we plan to

use the displacement values to train the appropriate models to detect the blood in the brain as accurate as possible. In Figure 1, the top left image is the B-mode, which is the original ultrasound image, and the top middle image is the displacement, which is the result of the TPI technique.

Researchers believe that the cardiac cycle 8 is when the most amount of blood is infused to the brain, so it's natural to think that the blood detection will be much easier when there are a lot of blood in the brain, yet cardiac cycle 8 is still an estimate and is not yet confirmed to be the actual cycle when the most amount of blood in infused to the brain. As a twist, we work on frame 7 and, possibly, compare its performance to the prior experiment done by Nhut Minh Phan to see if investigating different frame is worthwhile.

2 Methodologies

Due to the change of the course project requirements, here we present the **updated** and **adjusted** criteria, modified from those established in the original Course Project description in the class Notebook. These changes were discussed with and approved by Dr. Parsons.

The initial focus is acquiring and downloading the B-Mode data and use the scripts provided by Jack and Will to preprocess the data and extract only the frame which we are interested in. For the preprocessed data, our team perform basic statistical analysis and perform PCA to further understand the data.

2.1 Dataset

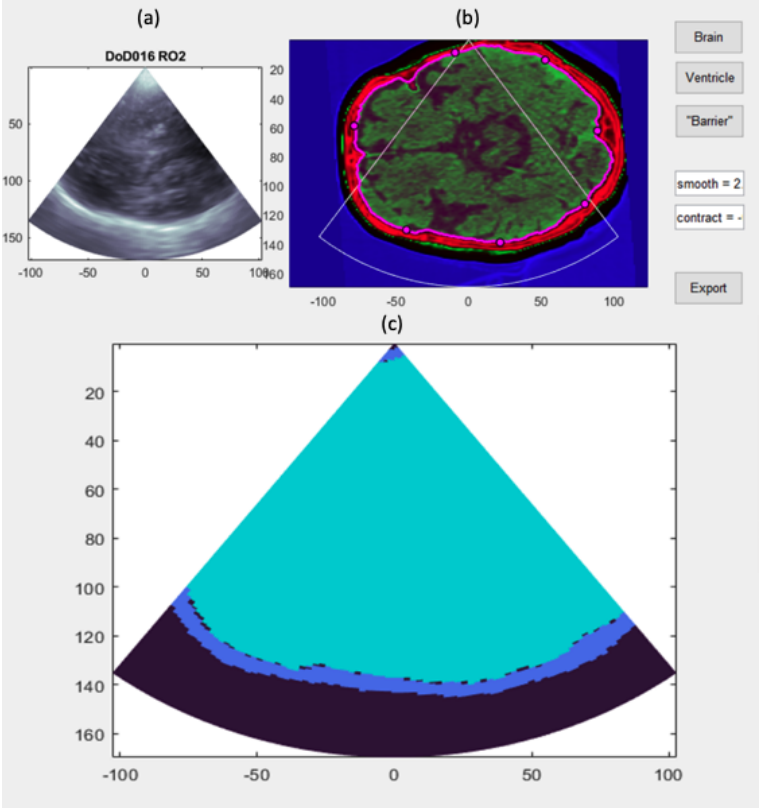


Figure 2: Labeling the data [2]

We inherit the work of Nhut Minh Phan where he collected the data provided from Harborview Medical Center. In Figure 2, the top left image is the B-mode, which is the original ultrasound image, top right is the CT scan, and the bottom image is the label (mask), which is the ground truth of the research. The dataset consist of 10 to 15 ultrasound image of each patients who were admitted to the Harborview Medical Center due to the TBI. Notice that, as mentioned by Nhut Minh Phan, the collected ultrasound images are taken after a few days from when the CT scan image was taken, so the label might not be 100% accurate. Various type of masks, skull mask, brain mask, ventricle mask, and blood mask, in order, are also can be found in the Figure 1 starting from the top right image.

2.2 Dividing Displacement

We divide the displacement image into 11 sectors of custom sizes since compared to the number of observations, the B-Mode or displacement data is 80x256 in size, so that would yield 20480 features; the reason for this approach is straight forward: As the number of features is much greater than the number of observations, the basic statistics will be much harder and PCA will perform very poorly since the number of features exceeds the number of observations.

Each sector will have an assigned number, called a 'representative,' which is representation of the pixels within each sector, and we use such a number to represent all the pixels in the sector. One obvious strategy of choosing the 'representative' is, but not limited to, averaging all the pixels in the sector. This is also meaningful in a way that the displacement data probably has spatial relationship between the pixels, so we hope that grouping the pixels would give us some meaningful information, which can be useful in the upcoming analysis.

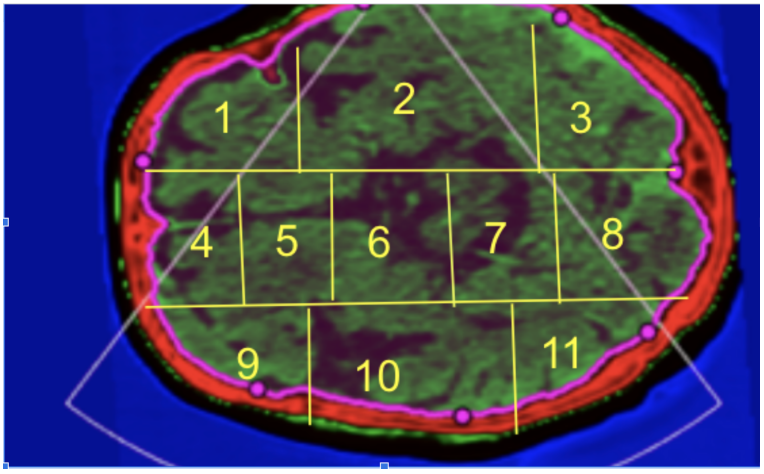


Figure 3: Dividing the displacement data

2.3 Labeling

In the context of our research, we label each observation as either 'severe amount of blood present in brain' or 'no severe amount of blood present in brain.' 'severe' means, for our research, that there are more than 3.15% of blood detected in the displacement image.

To create the label, we calculate the average probability of bleeding for each sector in each image. Then we calculate the mean probability of bleeding from the 11 sectors in each image. If the average from the 11 sectors is greater than 3.15%, we label the image with 'severe bleeding(1)', otherwise, we label the image as 'no severe amount of blood present in brain(0).' We have chosen the threshold of 0.0315 so that we have equal values for the positive (1: severe bleeding) and negative class (0: no severe bleeding)

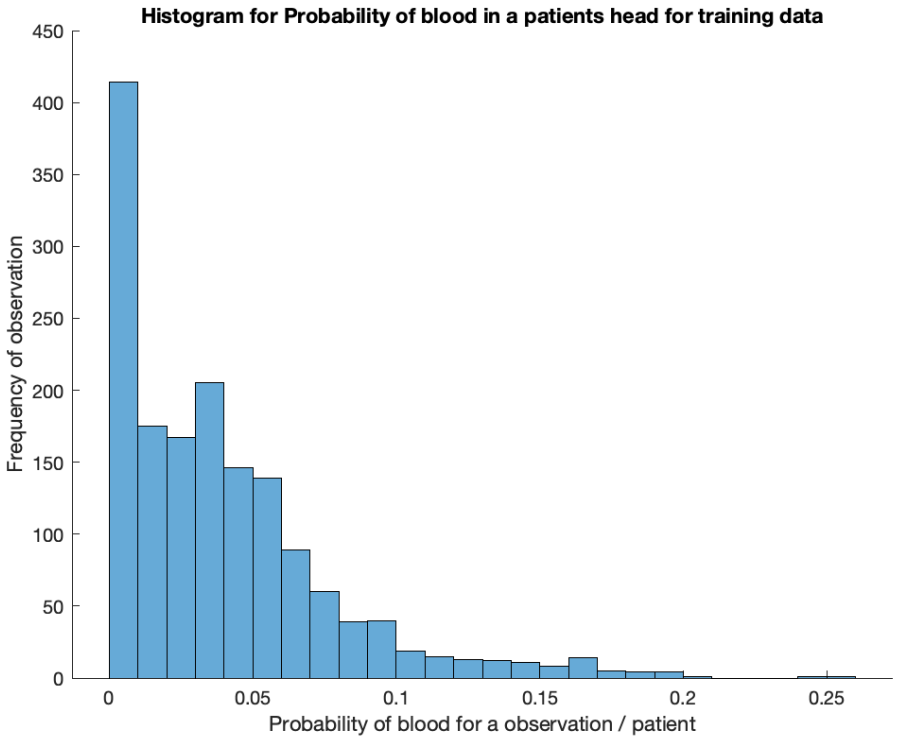


Figure 4: Probability of blood for a observation / patient

2.4 Analysis

Our team performed PCA analysis on the original displacement data and analyzed if we could find any relationship between the different sectors. We produce scatter plots (of both original data and original data projected onto the principal components), loading vectors, and scree plot.

2.5 Modeling

After pre-processing the displacement data into 11 different sectors and creating labels for each observation. We train the Gaussian Discriminant, SVM and KNN model to classify if the given displacement image has any 'severe' blood in the brain.

We also re-train the above mentioned models using the principal components in the Ur matrix (regular scores matrix), which theoretically would yield the better result since every principal components are orthogonal to each other.

3 PCA

3.1 Original Data

The original data is made up of 23 features. Here, each sector is named 'Zone.'

Features are represented in order: average of Zone 1, average of Zone 2, average of Zone 3, average of Zone 4, average of Zone 5, average of Zone 6, average of Zone 7, average of Zone 8, average of Zone 9, average of Zone 10, average of Zone 11, median of Zone 5, median of Zone 9, median of Zone 10, max of Zone 5, max of Zone 9, max of Zone 10, min of Zone 5, min of Zone 9, min of Zone 10. standard deviation of Zone 5, standard deviation of Zone 9, and standard deviation of Zone 10.

This is an indication that these features are not suited to determining the locations of bleeding. This makes sense, where person A is hit on the head, does not effect where person B is hit.

3.2 Scatter Plots (Original Data)

When examining the scatter plots of the original data, the first important fact to consider is that none of the features separate the two classes (no severe bleeding, and severe bleeding). In all of these scatter plots the two classes are clustered in such a way that no clear boundary between them can be found.

3.2.1 Zone vs Zone

Between the zones, most of the linear correlations were between zones that were adjacent to one another, or along the same side, with a few exceptions. Between the top and middle as well as the bottom and middle rows, the correlations were weaker, this is most likely due to the reduced shared surface area with the top and bottom zones with the middle zones.

Zone 1 has strong linear correlations with zones 2, 9, and 10, and weaker linear correlations with zones 5. The correlation with zone 10 (Figure x) is unexpected as it is a fairly strong relationship, but the two do not share any connections.

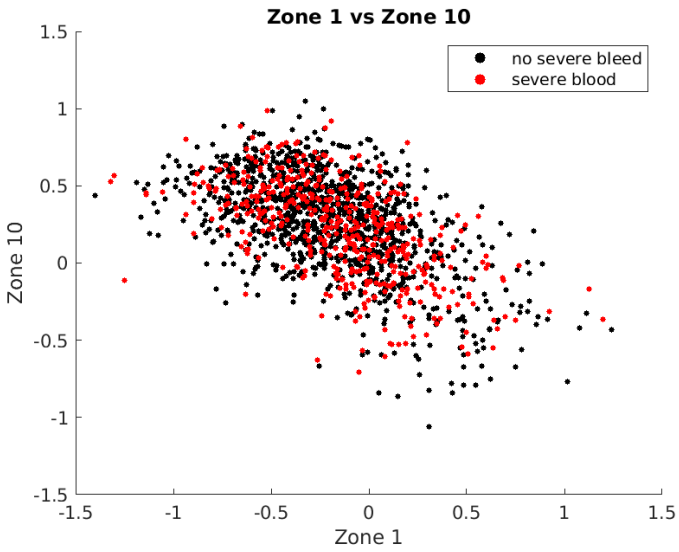


Figure 5: Zone 1 vs Zone 10

Zone 2 has strong linear correlations with zones 1, 3, 9, 10, and 11, and a weaker correlation with Zone 4. The relationships with 1, 3, and 4 are expected, as they all share an edge, and, zones 2 and 10 are in the same column. However, the relationship with 9 and 11 is less expected, combined with 10s correlation with Zone 1, may indicate that these zones have a greater effect on the data as a whole.

Zone 3 has strong linear correlations with zones 2, 7, 10, and 11 as well as a weak correlation with Zone 6. The odd ones out once again are zones 10 and 11. While Zone 11 and 3 are in the same column, the correlation is unusually strong (Figure x), further indicating that these two zones have a greater impact, at least on the first row.

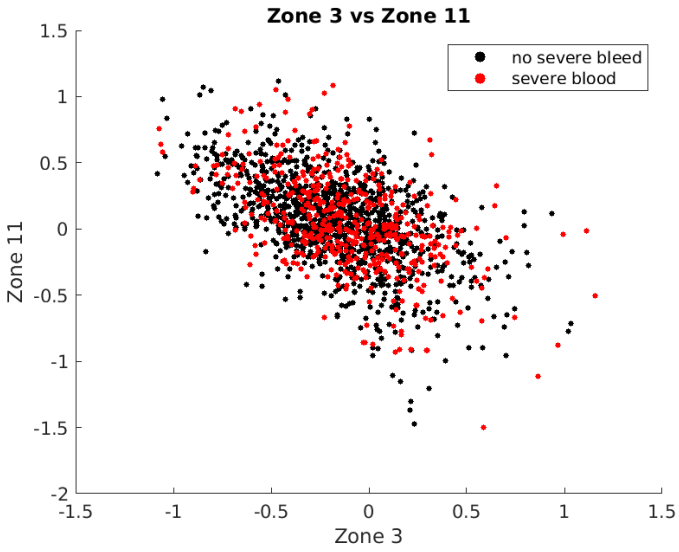


Figure 6: Zone 3 vs Zone 11

Zone 4 only has a strong linear correlation with Zone 9 and a weak correlation with Zone 2. As these are adjacent this makes sense. Although its lack of relationship with zones 1 and 5 is curious.

Zone 5 does not have any strong linear correlations with the other zones, but does have weak correlations with zones 1, 6, 7, and 8. Zone 5 shares an edge with zones 1 and 6, and is in the same row as zones 7 and 9.

Zone 6 has a strong linear correlation with Zone 10 and weak ones with zones 3 and 5. Nothing in this zone stands out as particularly odd or extraordinary.

Zones 7 and 8 are very similar to Zone 6, in that they do not have any correlations that are out of the ordinary.

Zones 9, 10, and 11 have already been discussed earlier. As shown in zones 1, 2, and 3, these three, in particular the last two, seem to have a major influence on the first row. What is interesting is that except for 9 and 10, none of these zones seem to be related at all.

3.2.2 Zone vs Other

The correlations between the zones and the max, median, min, and std of frames 5, 9, and 10, follow a pattern, with exceptions in zones 1 and 2. For the max, min, and std, all the scatter plots with the zones created a triangle like pattern, an upside-down triangle in the case of min (Figure x). For max and std, as the value in the zone increased, the max and std increased, up to a point, where it would then decrease, the opposite for min. There was an exception for this, when the same zone for the average and the std were the same zone, then there was no correlation between them. It is possible that this is because when there is high levels of bleeding, or no bleeding at all, there is very little variability.

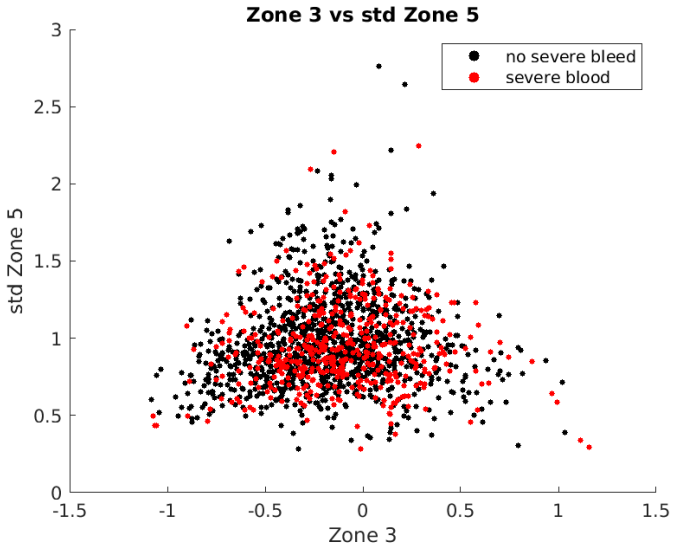


Figure 7: Zone 3 vs std Zone 5

For median, there was no correlation with the other zones, except when it was the same zone, in which case it was a very strong linear correlation. This makes sense, as both median and mean are methods to take the average, and as such would have similar results.

3.2.3 Other vs Other

The correlations between the max, median, min, and std of frames 5, 9, and 10 with themselves also follow a pattern. The correlations between max, min, and std are all logarithmic (Figure x), similar to the zone vs other, max vs min is flipped (Figure x).

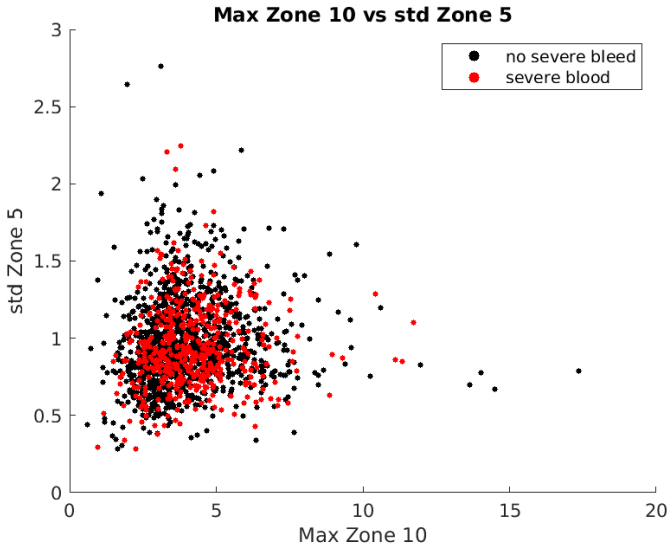


Figure 8: Max Zone 10 vs std Zone 5

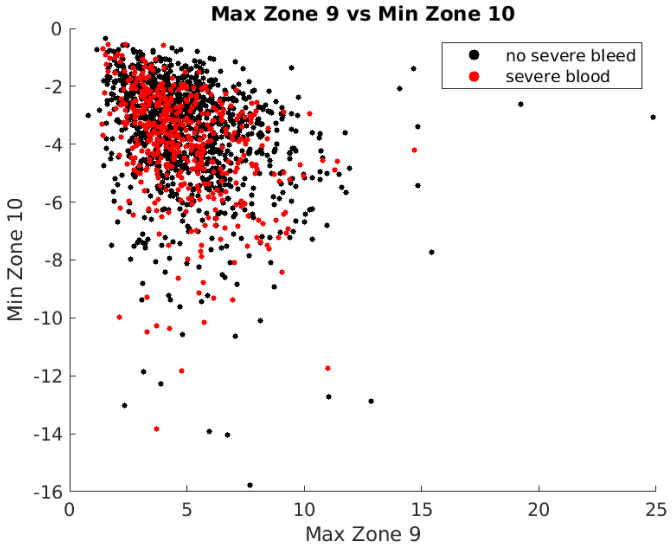


Figure 9: Max Zone 9 vs Min Zone 10

However, the medians followed a different pattern. The correlations between the medians and the other features was triangular in shape, similar to what was found in zone vs other, with the exception that there was no correlation between the medians of different frames.

There, was one outlier though, the median for zones 9 and 10 had a linear correlation. This is most likely due to them sharing a greater amount of edge space than they do with 5.

Future work could further explore the behaviors of PCs 15 through 23, as they are exhibiting clear examples of clustering. It is beyond the scope of this project to examine this.

3.3 Scatter Plots (PCs)

Similar to the original features, the principal components do group the data into the two classes (no severe bleeding, and severe bleeding). Note, in some cases it appears that the red dots representing severe bleeding are clustered in a group, however, this is merely a result of the way the graphs were created, with the red dots being placed after the black. If you look closely, you will see a ring of black dots around these groups, indicating that there are black dots under the red ones.

The PC scatter plots follow a pattern, with a few exceptions. PCs 1 through 14 follow one pattern, and 15 through 23 follow another. For the first group, PCs 1 through 9 have no correlation with each other. PCs 10 and 11 are linearly correlated with PC 1 through 9, with the exception of PC 5 and 11. PC 12 through 14 are not correlated with the rest of the PCs in this group, except for PC 10 and 12, which have a linear correlation.

The plots for the remaining data is described below, however, as these PCs represent less than 5% of the information contained within the data, they are not of major importance.

The interactions between the two groups have the shape of either a hat (Figure x) or an upside-down hat (Figure x). PCs 1 through 14 when compared with PCs 15 through 17 and 21 through 23, look like a hat, whereas when compared to PCs 18 through 20 it has the upside-down hat.

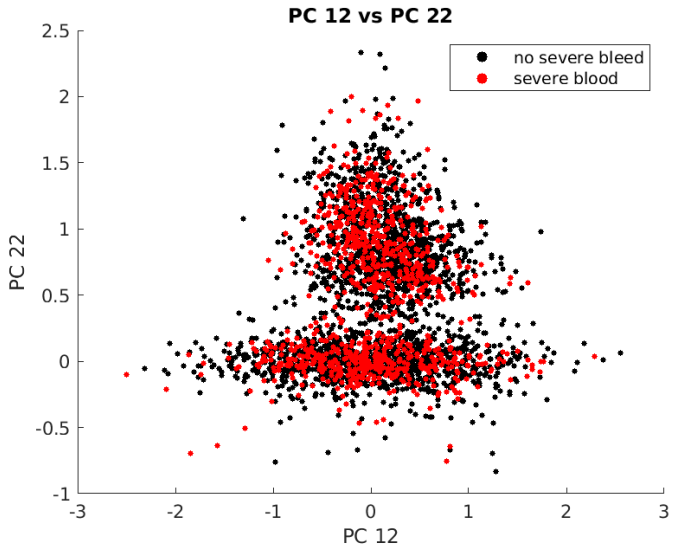


Figure 10: PC 12 vs 22

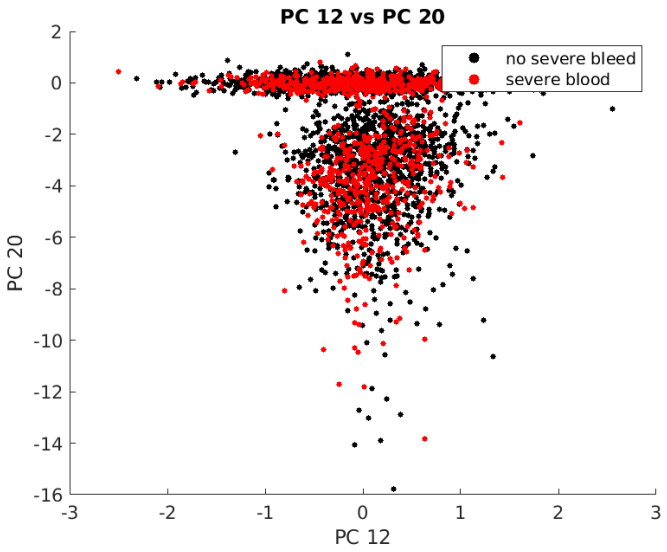


Figure 11: PC 12 vs 20

All the data points in all the plots between PCs 15 through 23 have the same shape, although rotated at different angles. The plots are divided into two groups, a circle and a cone, together they look like a party hat (Figure x).

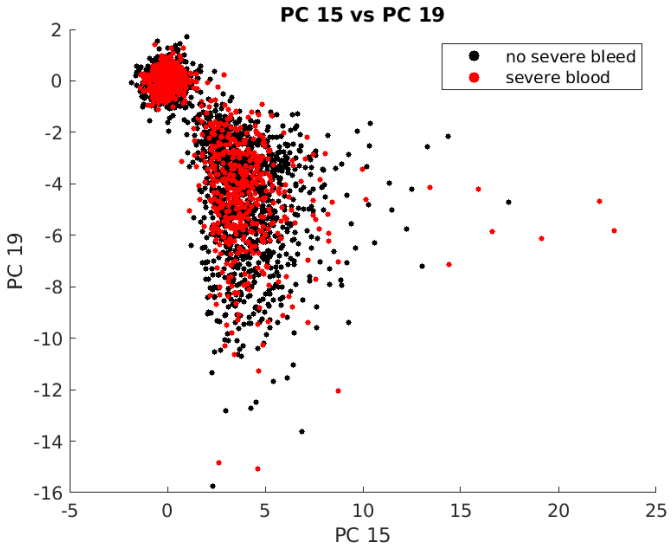


Figure 12: PC 15 vs 19

3.4 Scree Plot

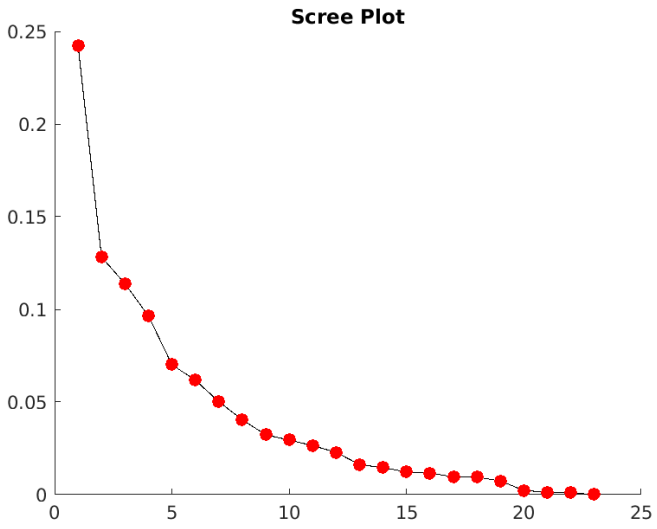


Figure 13: Scree Plot of PCA

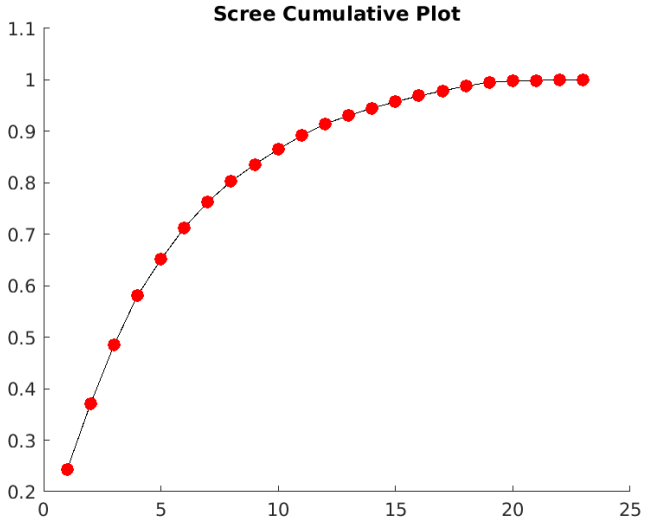


Figure 14: Scree Plot (Cumulative) of PCA

The first 14 columns of our data set worth around 90—% of information and those 14 columns are related to: Zone1, Zone2, Zone3, Zone4, Zone5, Zone6, Zone7, Zone8, Zone9, Zone10, Zone11, Median (Zone 5), Median (Zone 9), Median (Zone 10). The remaining 9 columns just worth 10% of the information and can be discarded from our calculations.

3.5 Loading Vectors:

3.5.1 First five loading vector analysis:

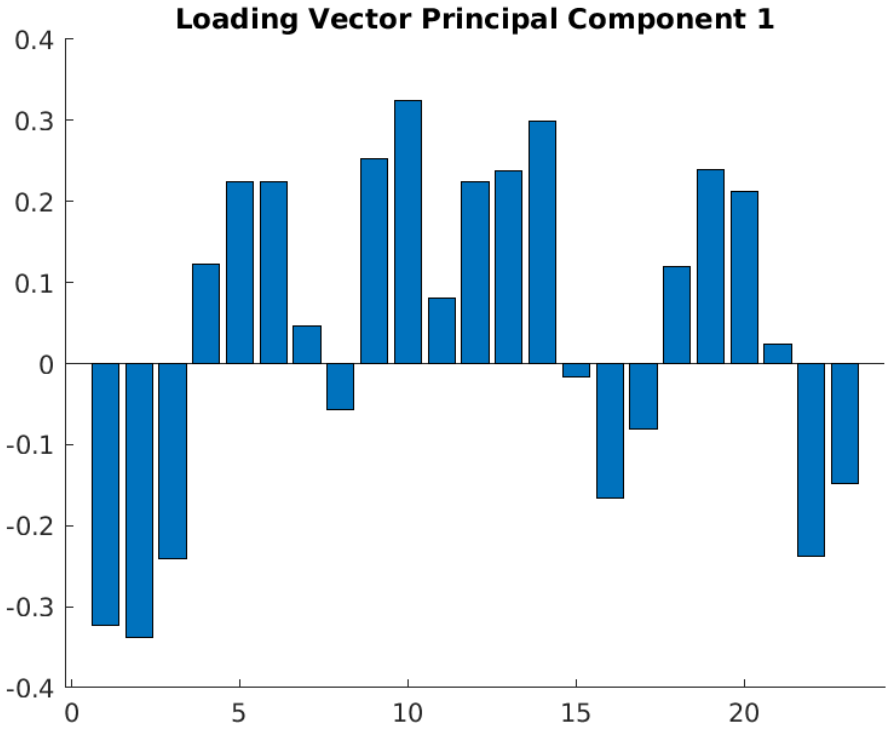


Figure 15: Loading Vector 1

From the first loading vector which is the heaviest loading vector we can understand that features 9,10 and 14 have the largest magnitude and these are important features for us. The first three features have negative values. Also by looking at this plot we can observe that sectors 5,9 and 10 are related to each other because the magnitude of average sectors of 5,9 and 10 are increasing and the same increasing rate is happening for the median features of these sector at the same time too. The maximum and minimum amount for above sectors is exactly growing in the opposite side of each other and from them, sector 9 has the largest magnitude of both maximum and minimum feature and by comparing the standard deviation of sectors 5,9 and 10 we see that sector 9 has the largest magnitude too and we can infer that in the first loading vector sector 9 has the most variation and provides more information than the other sectors for us. Sectors 10 and 5 provide more information respectively after sector 9 for us for the first loading vector.

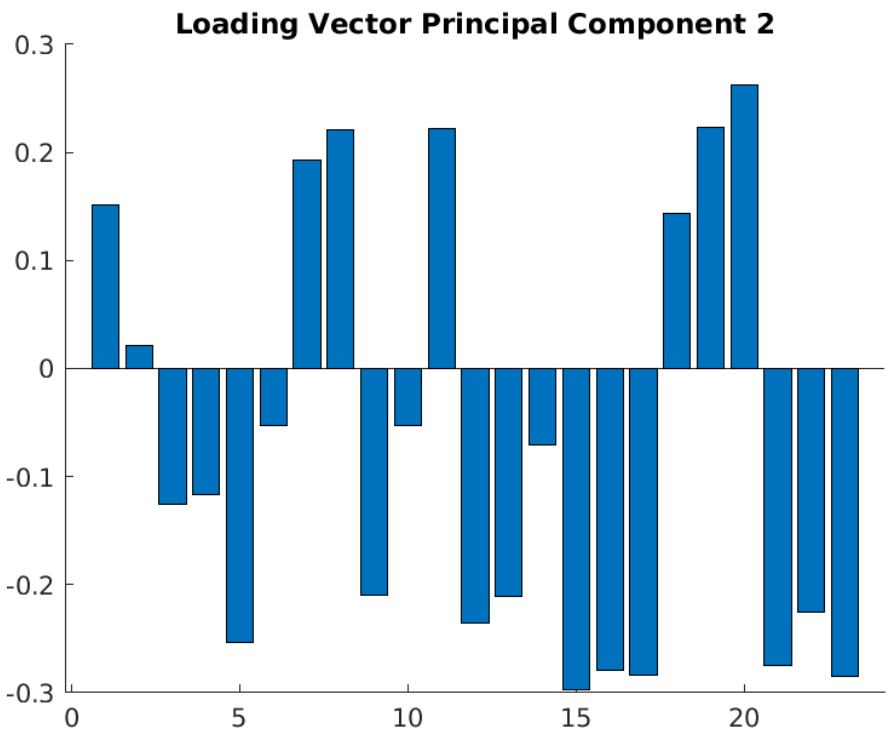


Figure 16: Loading Vector 2

By comparing loading vectors 1 and 2, we see that average sectors of 1 and 2 is growing in the opposite direction of feature 5 and there is an inverse correlation between these features and the reason is that sectors 1 and 2 are located in the left corner of the brain and the probability of bleeding is more likely to happen than the sector 5, because it is located in the middle of the brain and the probability of bleeding is less than the corner sectors.

By looking at first two loading vectors we can see correlation between features 5,9 and 10 that means in 40% of cases they have relevancy with each other. By looking at the brain image we can figure out that triangle zone is happening in sectors 5,9 and 10, which means these sectors are displacing in the same manner.

From the first two loading vectors it can be inferred that feature 8 has opposite correlation with features 5 ,9 and 10 because in both loading vectors it's growing in the opposite direction of features 5,9 and 10. And by looking at the brain picture it can be seen that the location of sector 8 is in the front of brain but sectors 9 and 10 are in the corner and sector 5 is in the middle of the brain.

By comparing loading vectors 1 and 2 we see that there is opposite behavior between feature 1 and features 5,9 and 10 so we can infer that there is opposite correlation between sector 1 and sectors 5,9 and 10.

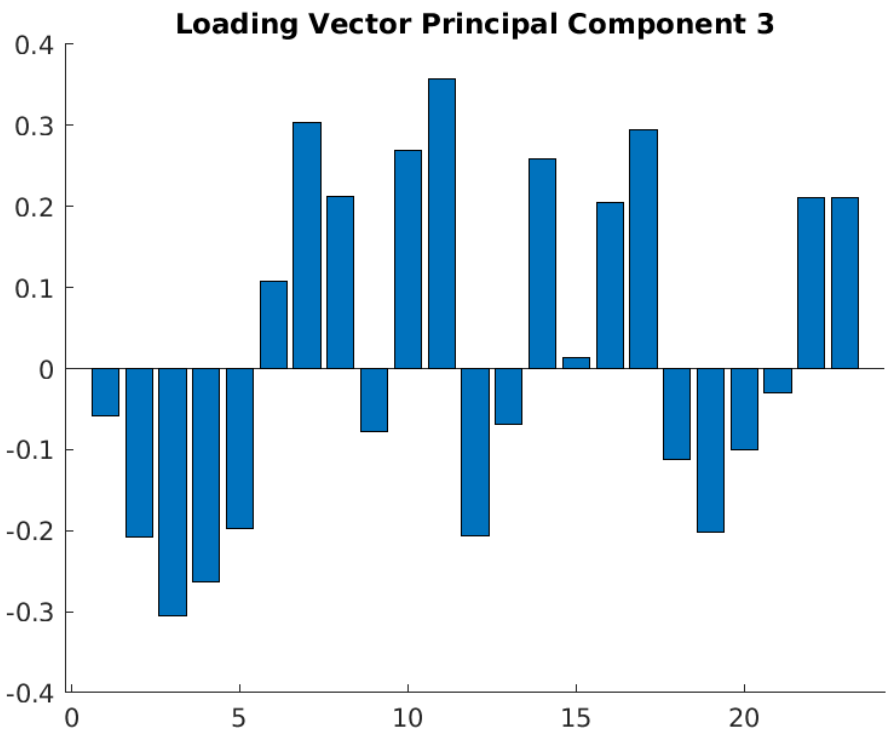


Figure 17: Loading Vector 3

The third loading vector contains about 12 % of total information, these points can be inferred by observing this loading vector: In the third loading vector feature 3 has the largest negative magnitude and it's in contrast with features 11 and 7 that have the largest positive magnitudes, We can infer that feature 3 has opposite correlation with features 11 and 7 and by looking at the brain image it can be seen that the location of sector 3 is in the left corner of the brain but sector 11 is in the right corner of the brain and sector 7 is in the middle.

A common point from the first three loading vectors is that in all of them features 15,16 and 17 that are related to Maximum records of zones 5,9 and 10 are growing in opposite side of features 18,19 and 20 that are related to Minimum records of zones 5,9 and 10 which makes inverse correlation between these features.

In contrast to the first two loading vectors in the third loading vector feature 5 and 9 are relatively correlated with each other but there is opposite correlation with feature 10, the same pattern can be seen for the median features of these sectors where feature 5 and 9 are growing in the same direction and PC 10 is growing in the opposite side. From feature 3 to feature 7 there is a visible increase in the magnitude of features by observing the brain image we notice increase in bleeding when we move forward from the back of the brain to the front and this pattern can happen in about 12 percent of the patience.

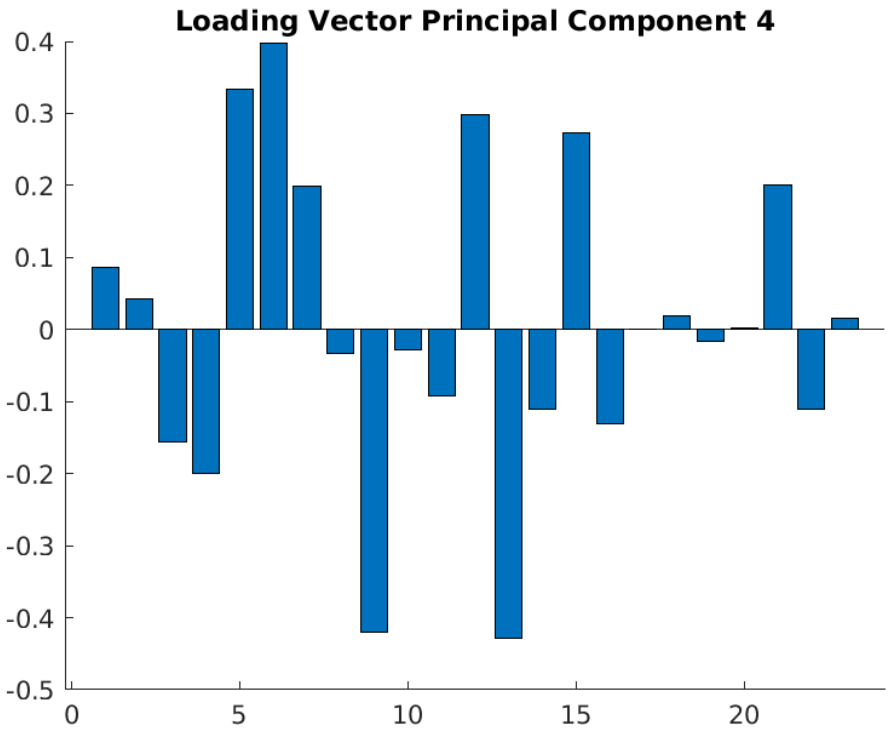


Figure 18: Loading Vector 3

In the fourth loading vector feature 5 has opposite correlation with features 9 and 10 because they are growing in the opposite direction. Feature 9 has the largest magnitude comparing to features 5 and 10 and the same behavior is happening for the median components of them too.

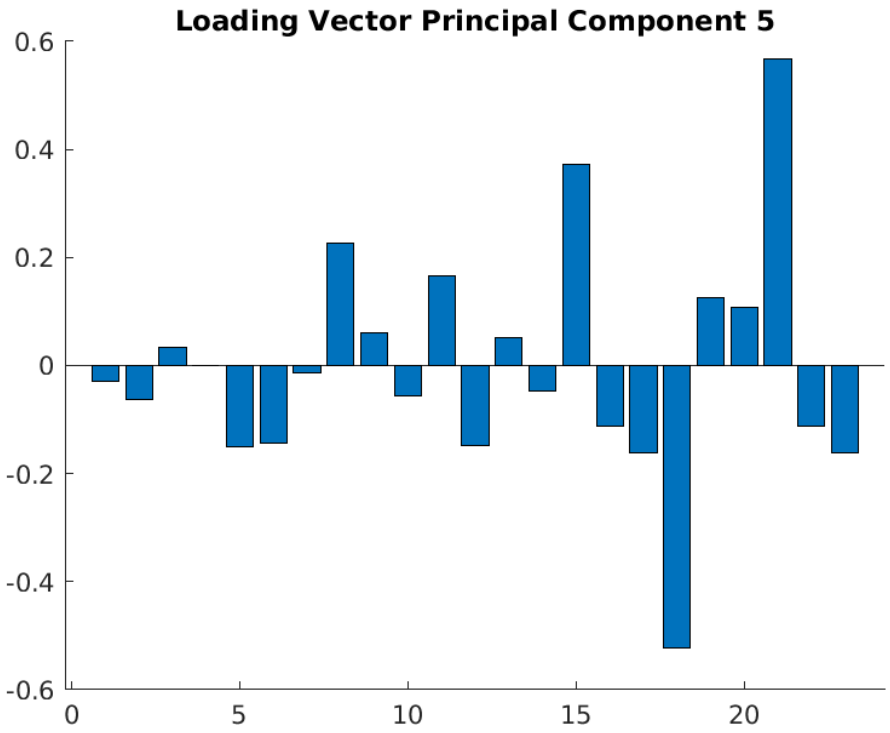


Figure 19: Loading Vector 3

In the fifth loading vector features 5 and 10 have opposite correlation with feature 9 because they are growing in the opposite direction. Feature 5 has the largest magnitude comparing to PC 9 and 10 and the same behavior is happening for the median components of them too. And by looking at the brain image it can be seen for 7% of our patience bleeding is more in the middle of the brain rather than the corner of the brain. And feature 5 contribute the most information from the fifth loading vector because it has the largest magnitude of Max, Min and Standard deviation.

From the first 5 loading vectors we observe that there is opposite behavior between feature 1 and feature 10 and we can infer for the patience that have hemorrhage on their back left side of their brain, The bleeding in the middle right side of their brain was low or they didn't have bleeding on that part.

3.5.2 last five loading vectors analysis:

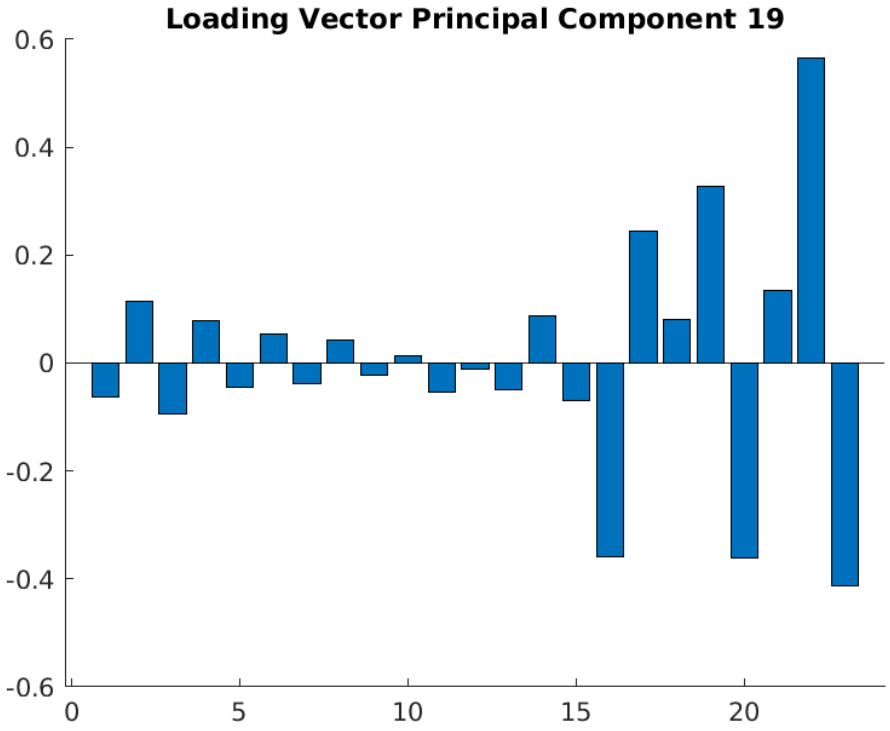


Figure 20: Loading Vector 3

From loading vector 19 we observe that feature 2 has the largest value in contrast to first loading vectors and the magnitude of other areas are pretty low that it can just happen in very rare cases that the patient just has damage in the middle left side of the brain not in other locations. Also another point from this loading vector is that all the average zone features including feature 5,9 and 10 have less magnitude but in contrast The magnitude of their Max, Min and Std for features 5,9 and 10 is large, one reason that can explain this observation is that there are some cases that they have severe bleeding but the amount of that bleeding still is not so visible but by looking at the Max,Min or Std the difference can be seen and it can be categorized as severe bleeding in our case we see this observation at Maximum zone of feature 10 that it shows larger magnitude that the average of zone 10.

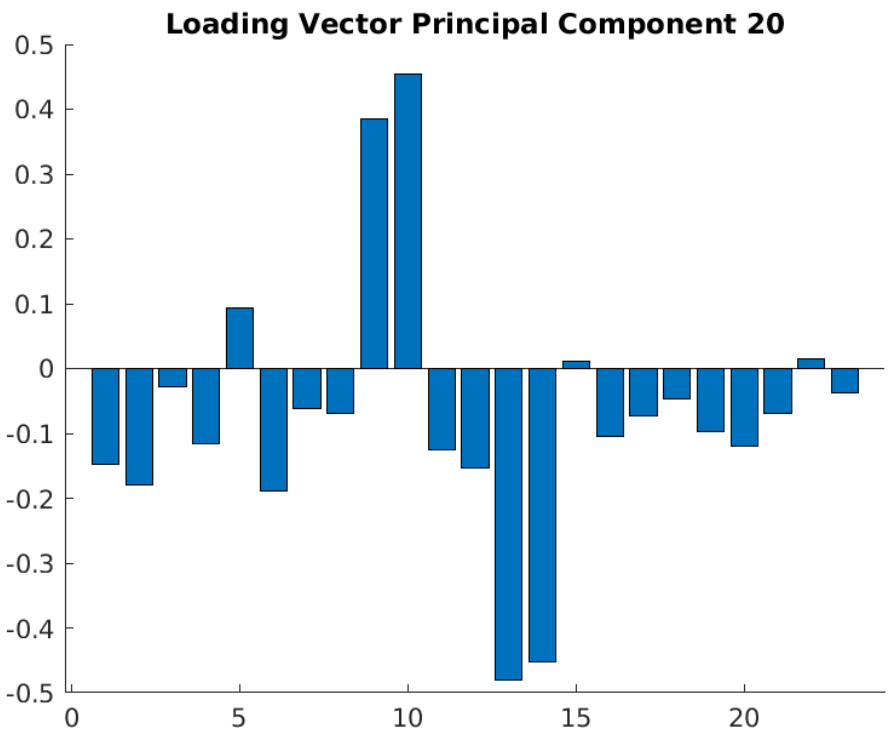


Figure 21: Loading Vector 3

From loading vector 20 we see the same observation as the first five loading vectors that sectors 5,9 and 10 are correlated with each other but in contrast their medians has the least value and there is opposite correlation between the average of these features and their Medians. It can just happen in very rare cases and we can count it as outlier.

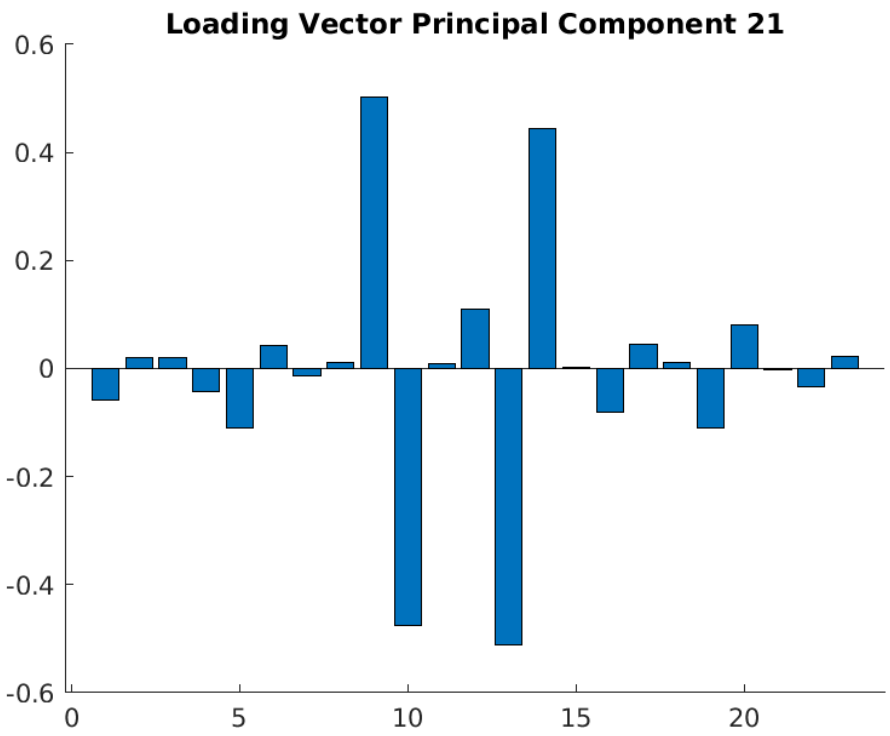


Figure 22: Loading Vector 3

From loading vector 21 we see that there is opposite behavior between feature 9 and feature 10 and this case happens in very low cases because the amount of bleeding in two corner locations of the brain, that are adjacent should be relatively close to each other not with a very huge difference like this.

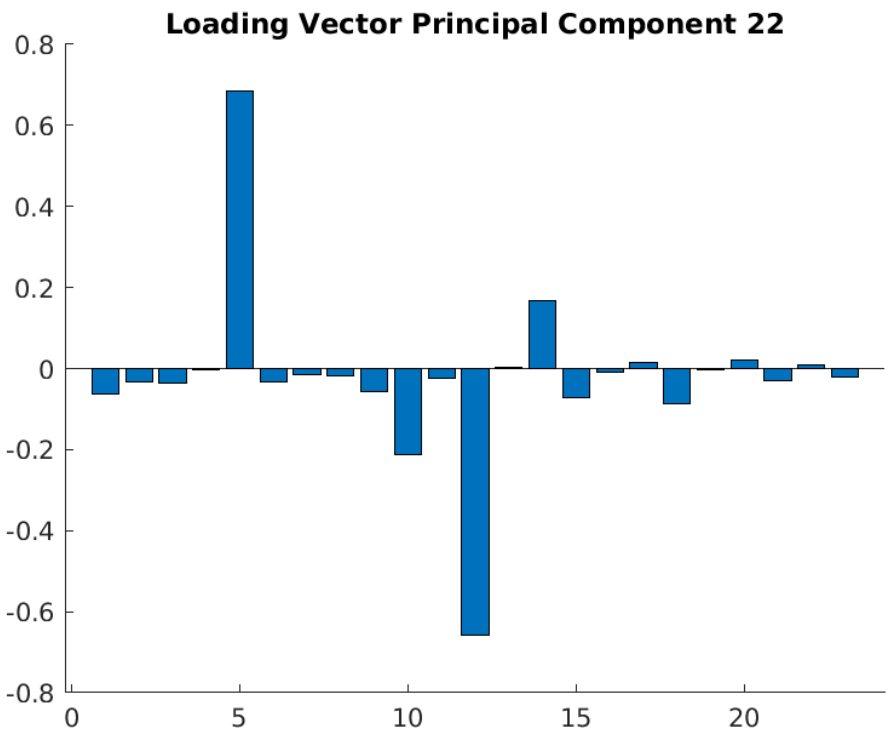


Figure 23: Loading Vector 3

From loading vector 22 we observe that 5Th sector has the largest magnitude which is in contrast with the first loading vectors, because the amount of average bleeding in this area (Middle of the brain) is less than the corner of the brain that has contrast with our previous observations for the first loading vectors but it just happen in very rare cases that the amount of bleeding in the middle of the brain is less than the amount of the corners of the brain. Another point is that sector 5 has the least median in contrast to it's largest magnitude of average bleeding that may be affected by some noise and should be probably an outlier.

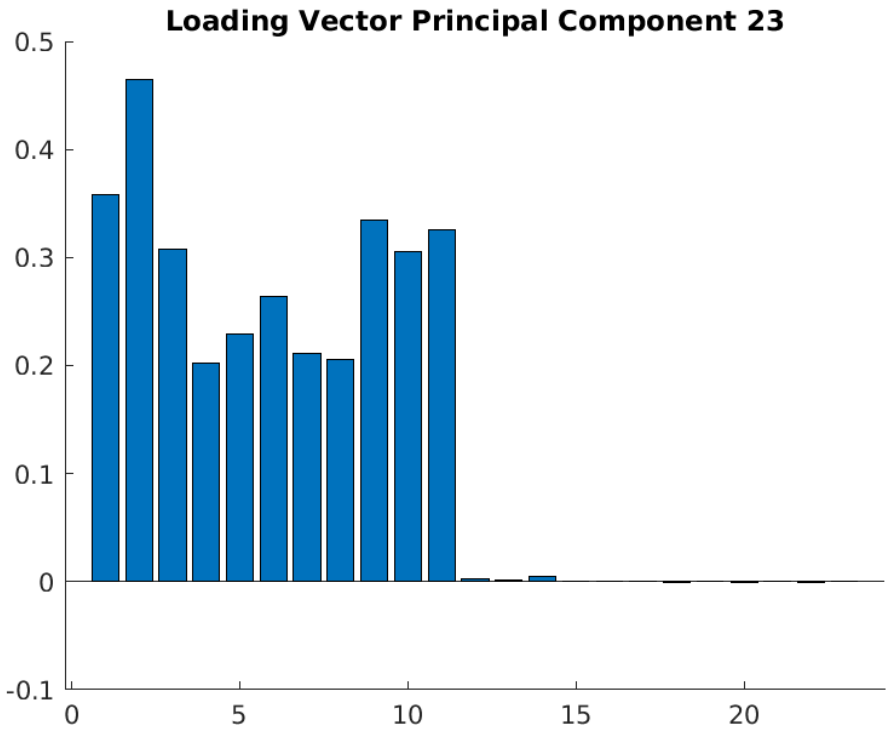


Figure 24: Loading Vector 3

From the last loading vector we can not get any information because all of the 11 sectors have large magnitude and shows that all of them are relevant to each other.

In this research, sectors of the brain were the features of our loading vectors so any changes to the dimensions of sectors or in the number of them, changes the result of this research,so the more accurate we divide the brain the more accurate we get the results.

4 Model Building

4.1 Models used to evaluate the data

Choosing an appropriate machine learning model to evaluate the data is a critical step in model building. We choose three different models namely gaussian discriminant function, support vector machines and k-nearest neighbors to evaluate our data with different methods and with each having its own merits enlisted as follows.

1. Gaussian discriminant function: The Gaussian Discriminant Analysis captures the distribution of each class in our case severe bleed and no severe bleed in the brain and attempts to fit a Gaussian Distribution to every class in the data separately. This model works well on linearly separable data. A good performance of the model will help us evaluate if the data is linearly separable.

2. Support vector machines: In the context of our data, SVM would assign the data points in the training set into two categories in space (no severe bleed and severe bleed) in-order to maximise the gap between these two categories. The examples from the testing set are then assigned into that same space and predicted to belong to a category based on which side of the gap they fall. SVM works well with large number of features like in this case 12 features (11 sectors of displacement and 1 label) and thus yields good performance as observed from the results in Figure 25. It uses uses non probabilistic methods for model building

3. k-nearest neighbors: It is a non-parametric supervised learning method. A data point in the testing set is assigned to the class that is most common among its k nearest neighbors (k is a positive integer). Knn learns learns non-linear decision boundaries and would perform extremely well in case the data is not linearly separable.

4.2 Metrics used to evaluate the model

1. Accuracy: The fraction of predictions our model got right

2. Precision: Indicates the proportion of positive identifications that was actually correct.

3. Recall: Indicates the proportion of actual positives was identified correctly.

4. Area under the ROC curve: AUC measures the entire two-dimensional area underneath the entire ROC curve. An ROC curve (receiver operating characteristic curve) is a graph showing the performance of a classification model at all classification thresholds. Threshold indicates where the "separation" between two classes is present in our case severe bleed and no severe bleed is, e.g., P(severe bleed)/P(no severe bleed).

The aim of our classifier is to detect severe bleed in the brain, medical professionals can use the results of our model to conduct further examination of the patients using other complex medical imaging techniques. Thus our aim is reduce false positives i.e cases where the person has a severe brain bleeding but the model predicts that the person does not have a severe bleeding. Hence we focus on the metrics precision and false positives.

4.3 Results from the classification models on original features

Figure 25 Summarizes the results of our classification models for the metrics accuracy, precision, recall, AUC, percentage of false positives and percentage of false negatives.

Frame 7

Model	Frame Number	Accuracy	Precision	Recall	AUC	Percentage of False Positives	Percentage of False negatives
Gaussian Discriminant function	7	51.7857	54.955	51.2605	51.8138	22.32	25.89
SVM	7	54.9107	55.8559	54.386	54.28	21.875	23.21
KNN	7	45.5357	46.8468	45.2174	45.55	26.33	28.125

Frame 8

Model	Frame Number	Accuracy	Precision	Recall	AUC	Percentage of False Positives	Percentage of False negatives
Gaussian Discriminant function	8	55.8036	66.6667	54.4118	55.8997	16.51	27.67
SVM	8	57.1429	65.7658	55.7252	57.23	16.96	25.89
KNN	8	51.3393	52.2523	50.8772	51.35	26.33	25

Frame 9

Model	Frame Number	Accuracy	Precision	Recall	AUC	Percentage of False Positives	Percentage of False negatives
Gaussian Discriminant function	9	55.8036	70.2703	54.1667	55.9316	14.73	15.17
SVM	9	56.25	69.3694	54.6099	56.64	16.96	25.89
KNN	9	55.8036	57.6577	55.1724	55.82	20.98	23.21

Figure 25: Results for model building

4.4 Analysis of results from the classification models on the original features

1. The SVM model and Guassian discriminant function provides the highest values of precision for frame 9 of the displacement data. Thus there is a possibility that frame 9 is the best frame to analyze for potential hemorrhages in the brain.

2. In terms of Accuracy, the fraction of predictions the model got right, SVM provides the highest accuracy of 57.1429% and a precision of 65.7658 % on frame 8. Additionally, the precision values of frame 8 and 9 for SVM are approximately in a close range and higher compared to frame 7. Thus we conclude that SVM is a great model for this data and frame 8 and frame 9 capture the most information and are good to find hemorrhages in the brain. An average of performance values for both the frames would be a good indication of models performance.

3. The Gaussian discriminant function and SVM perform extremely well on the data for frame 9. Thus we can conclude that data may be linearly separable and would work well with linear discriminant machine learning models as both SVM and gaussian models are linear classification models.

4. The performance results for all the models in all the frames are not very high in the range of 80% and above. The performance of these models can be improved further by better data pre-processing techniques like improving the methods we use to divide the displacement and blood mask image (labels) into multiple sectors.

5. KNN performs badly on all frames because the K values used by the default matlab (5 neighbours) function is not accurate. we need to find an optimal value of K nearest neighbors and then implement the KNN model

6. Another reason as to why KNN may not be performing well may be because the classes in the data cannot be grouped to form well defined clusters as observed in the scatter plots in Figure 5

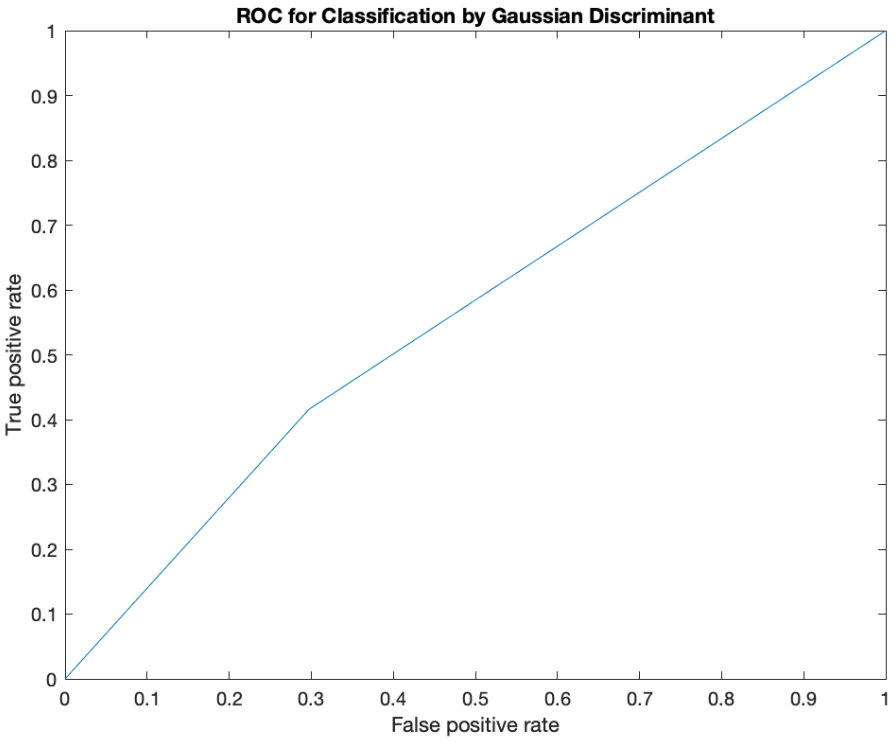


Figure 26: ROC curve for gaussian model on frame 9

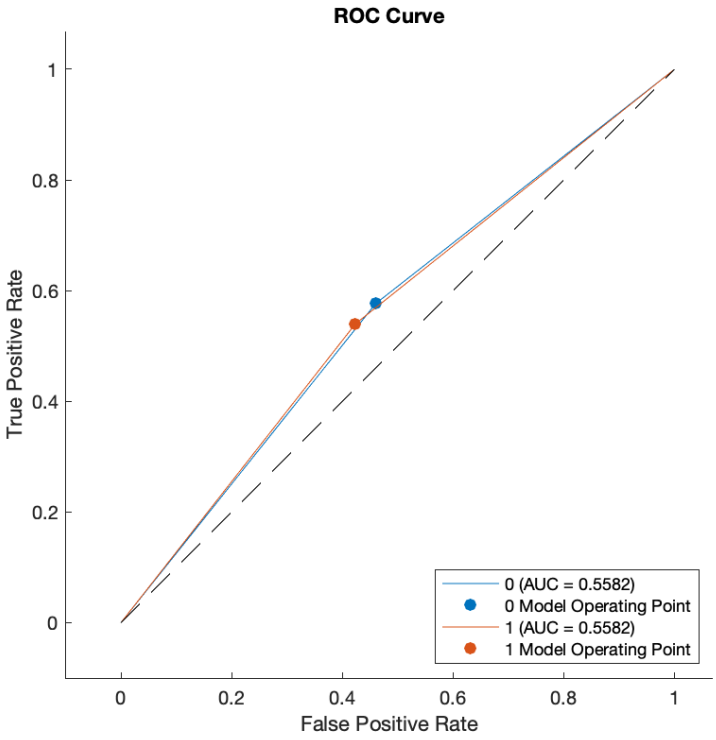


Figure 27: ROC curve for knn model on frame 9

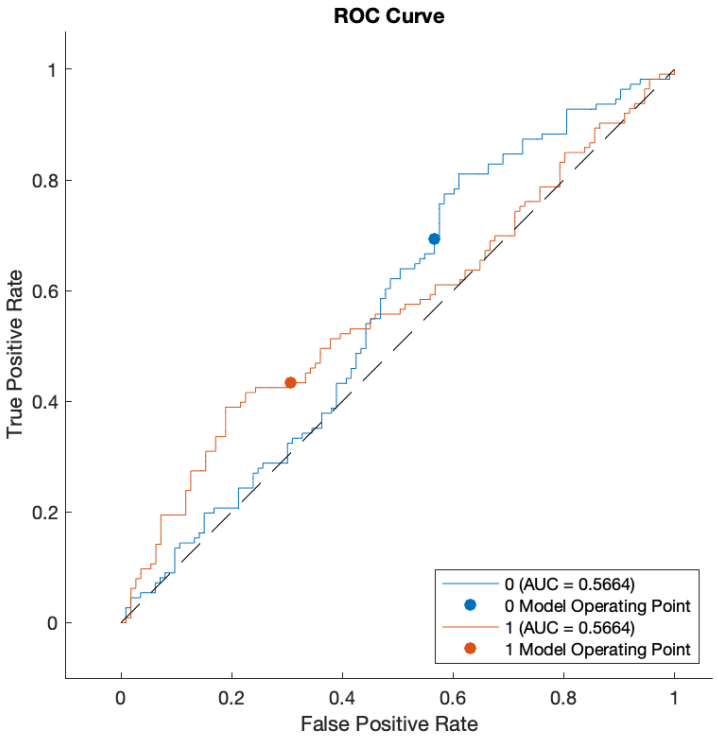


Figure 28: ROC curve for SVM model on frame 9

7. From Figure 26, 27, 28 The AUC values are consistently low and indicate poor discrimination between the positive and negative classes. An AUC greater than 0.7 is desirable as it indicates acceptable/ good discrimination between the classes. However it is good that the classifier doesn't have an AUC of 0.5 or below which indicates it is random with no discrimination between the classes.

4.5 Model Building using the Ur matrix (regular scores)

Figure 29 summarizes the results of our classification models using the Ur matrix obtained after performing the singular value decomposition on the original features for the metrics accuracy, precision, recall, AUC, percentage of false positives and percentage of false negatives.

Frame 7

Model	Frame Number	Accuracy	Precision	Recall	AUC	Percentage of False Positives	Percentage of False negatives
Gaussian Discriminant function	7	57.2614	57.4042	57.3665	57.3665	18.81	23.93
SVM	7	57.6763	60.6469	58.4416	58.34	20.19	22.13
KNN	7	54.4952	54.1779	55.8333	54.5	23.51	21.99

Frame 8

Model	Frame Number	Accuracy	Precision	Recall	AUC	Percentage of False Positives	Percentage of False negatives
Gaussian Discriminant function	8	53.527	53.7209	53.6767	53.6767	26.69	19.78
SVM	8	52.8354	60.2273	51.3317	54.98	19.36	27.80
KNN	8	56.7082	59.375	55.1451	56.78	19.77	23.51

Frame 9

Model	Frame Number	Accuracy	Precision	Recall	AUC	Percentage of False Positives	Percentage of False negatives
Gaussian Discriminant function	9	52.9737	53.1969	53.1969	53.1792	20.19	26.83
SVM	9	53.9419	70.255	52.1008	55.37	14.52	31.53
KNN	9	54.0802	52.4079	53.0086	54.04	23.23	22.68

Figure 29: Results for model building using Ur matrix

4.6 Analysis of results from the classification models using the Ur matrix (regular scores)

1. The SVM model gave high values of precision on frame 9 of 70.255 on Principal Components compared to it's precision of 69.3694 on frame 9 on the original features. This is because in the transformed space every principal components are orthogonal to each other that may not be true with original features.

2. Even in the transformed space SVM and gaussian discriminant function produces better results than KNN because the Principal Components couldnot form well defined clusters (KNN works on clustering the data). This can be verified from the scatter plots in Fig 10.

3. Reducing the number of features(Principal Components) using the PCA analysis would

yield better results. However we focused on building models using all the PCs

4. All the frames have approximately same values of performance because each frame is captured in a interval of few milliseconds.

5. In general the model's performance in terms of precision is low because the problem is an image segmentation problem which needs deep learning techniques.

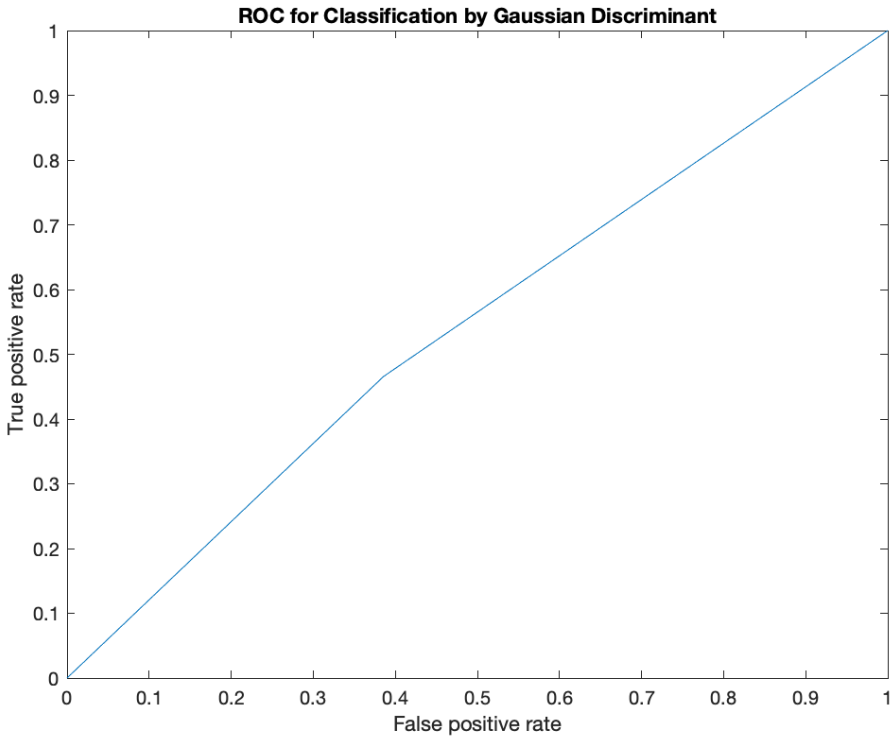


Figure 30: ROC curve for gaussian model on frame 9 (using Principal components as features in the model

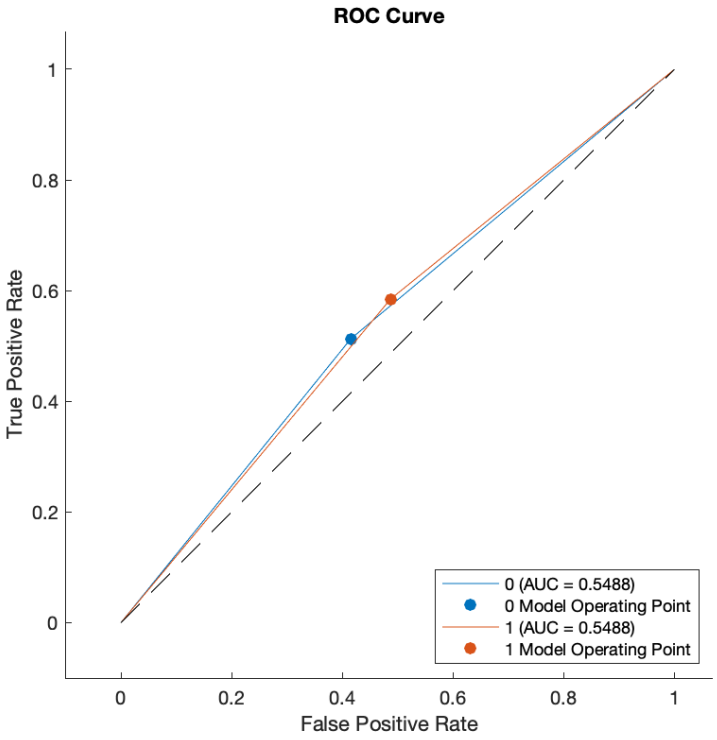


Figure 31: ROC curve for knn model on frame 9 (using Principal components as features in the model

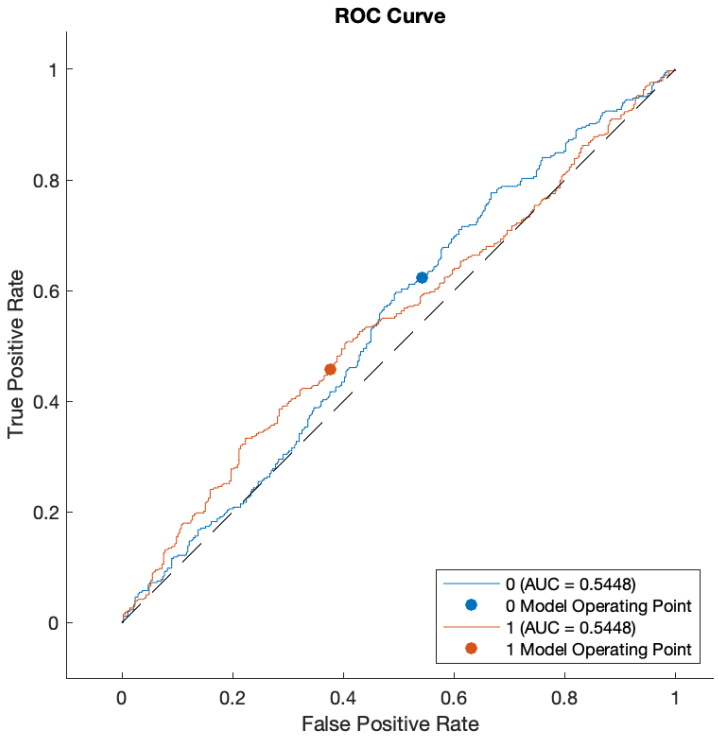


Figure 32: ROC curve for svm model on frame 9 (using Principal components as features in the model

5 Conclusion

1. Poor performance of the machine learning models is indeed supported by the result of the scatter plots 2.In this research, sectors of the brain were the features of our loading vectors so any changes to the dimensions of sectors or in the number of them, changes the result of this research,so the more accurate we divide the brain the more accurate we get the results.

3. Even though we didn't have enough time to do more experiments with the Deep Learning models, we suspect that using different hyper-parameter would different result.

4. Previously the research was being carried out with an assumption that frame 8 of the displacement data had the maximum probability of finding hemorrhage/blood in the brain. However the classification models that are implemented show promising results for frame 9. Therefore we suggest that data from frames 8 and 9 must be used for future research.

References

[1] Get the facts about tbi, March 2022. URL "https://www.cdc.gov/traumaticbraininjury/get_the_facts.html".

[2] Nhut Minh Phan. Deep learning methods to identify intracranial hemorrhage using tissue pulsatility ultrasound imaging.

[3] John C. Kucewicz, Barbrina Dunmire, Nicholas D. Giardino, Daniel F. Leotta, Marla Paun, Stephen R. Dager, and Kirk W. Beach. Tissue pulsatility imaging of cerebral vasoreactivity during hyperventilation. *Ultrasound in Medicine & Biology*, 34(8):1200–1208, 2008. ISSN 03015629. doi: 10.1016/j.ultrasmedbio.2008.01.001.

[4] Ultrasound imaging, September 2020. URL `"https://www.mathworks.com/help/stats/discriminant-analysis.html"`.

6 Appendix:

All of our loading vectors:

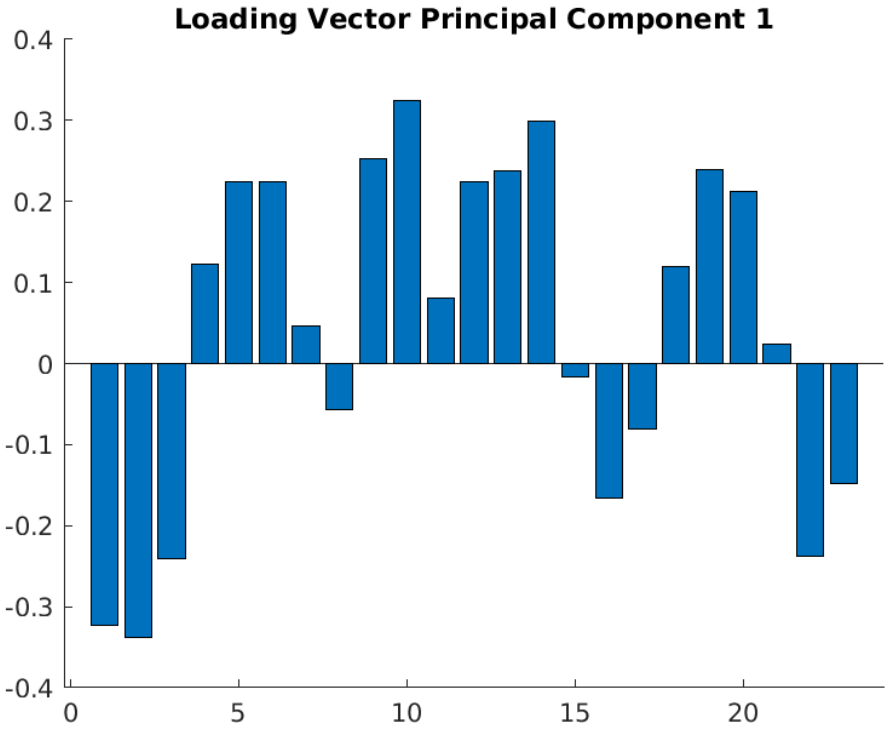


Figure 33: Loading Vector 1

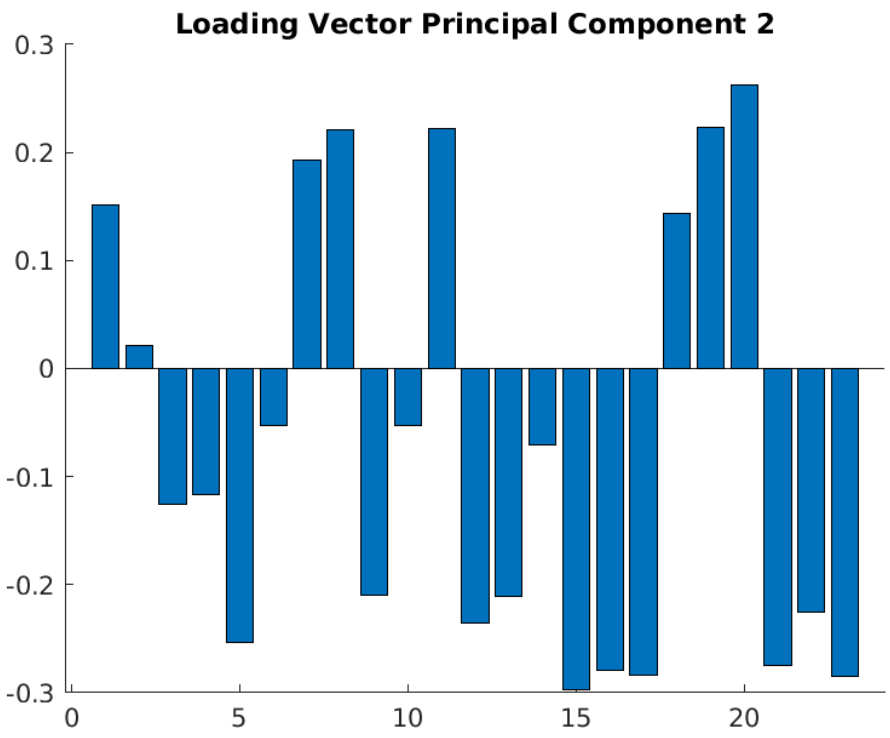


Figure 34: Loading Vector 2

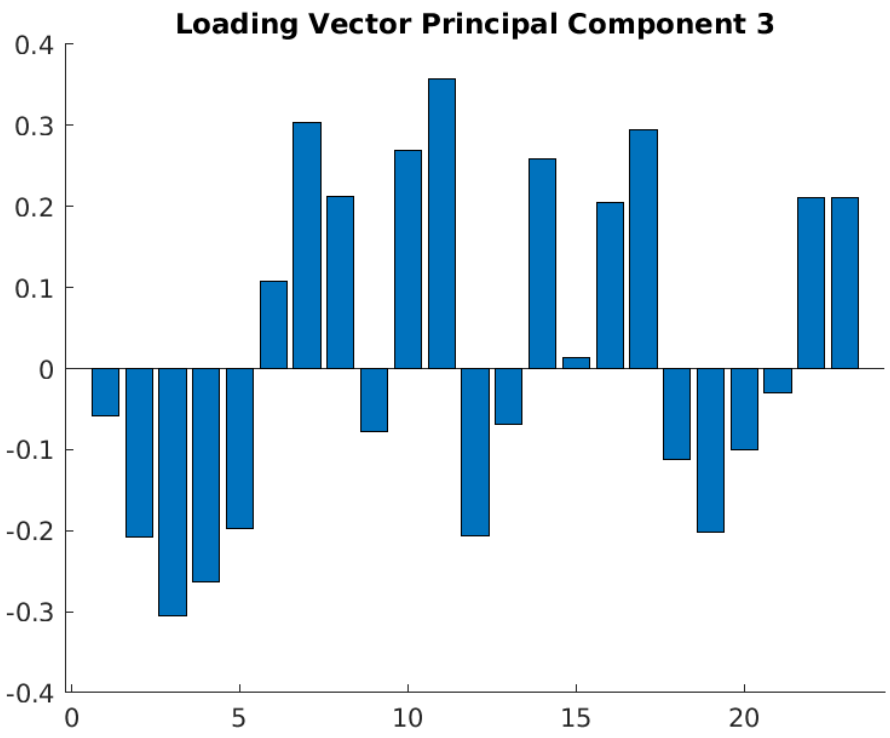


Figure 35: Loading Vector 3

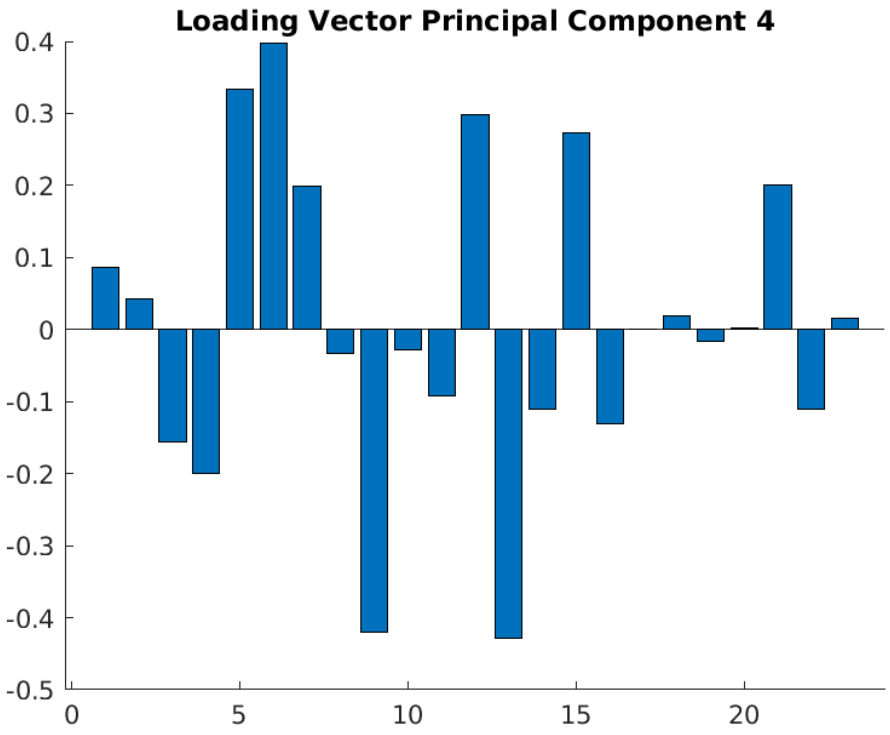


Figure 36: Loading Vector 4

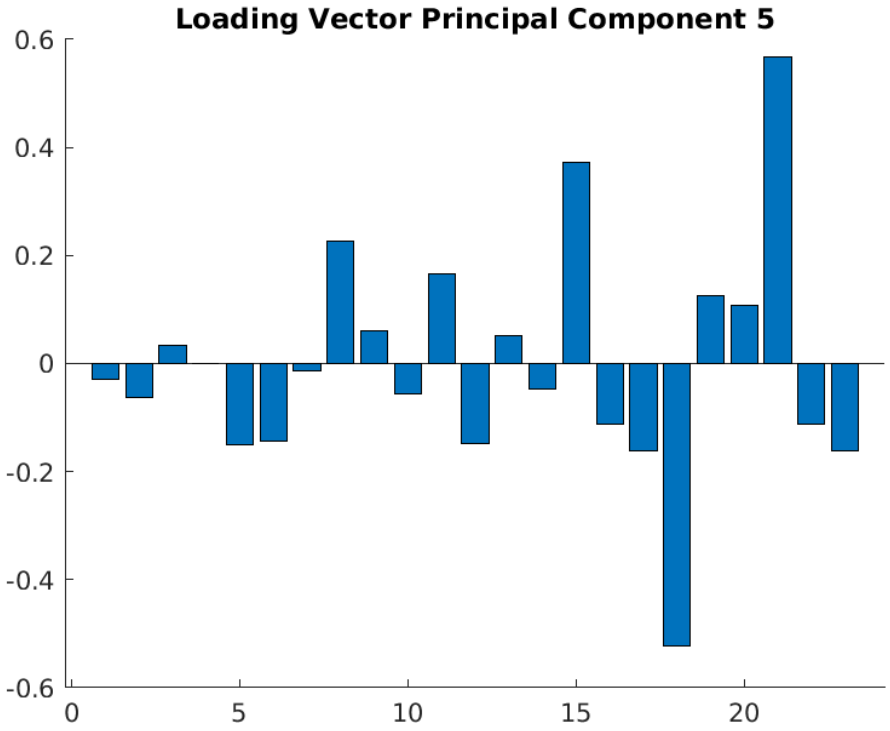


Figure 37: Loading Vector 5

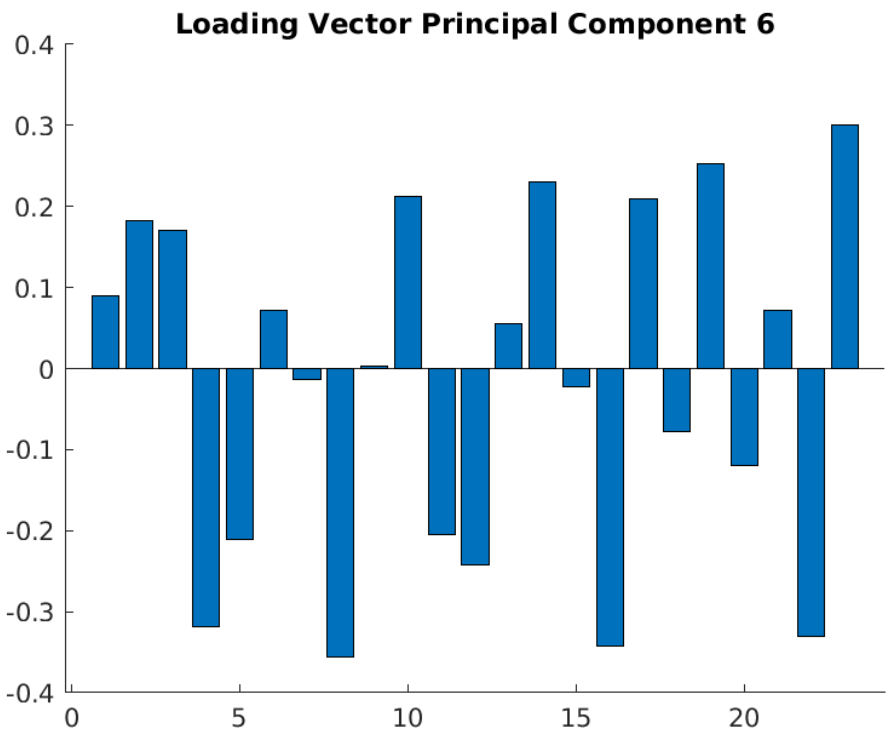


Figure 38: Loading Vector 6

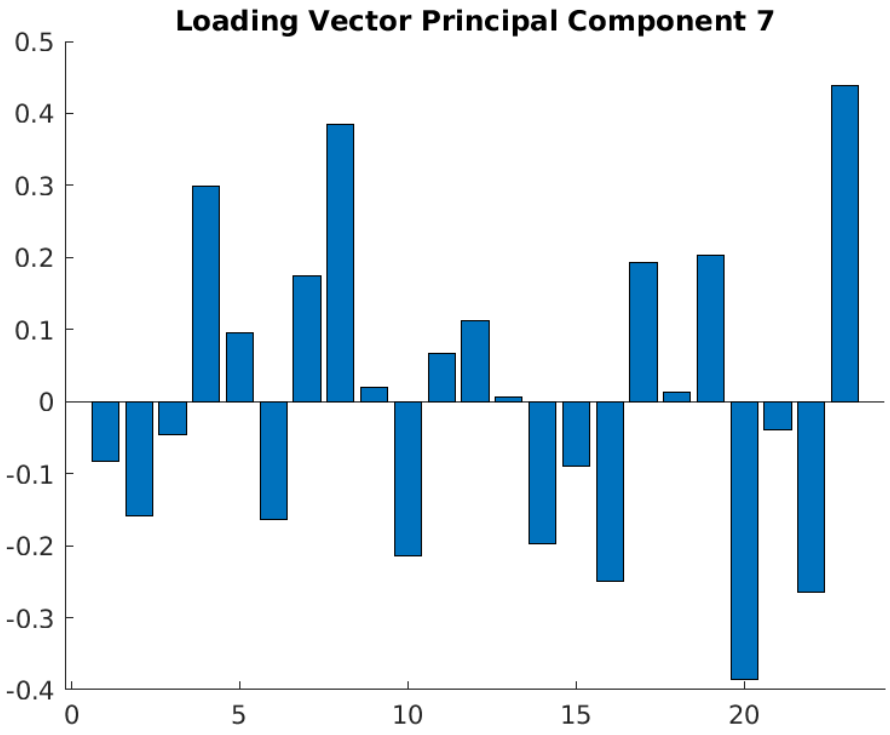


Figure 39: Loading Vector 7

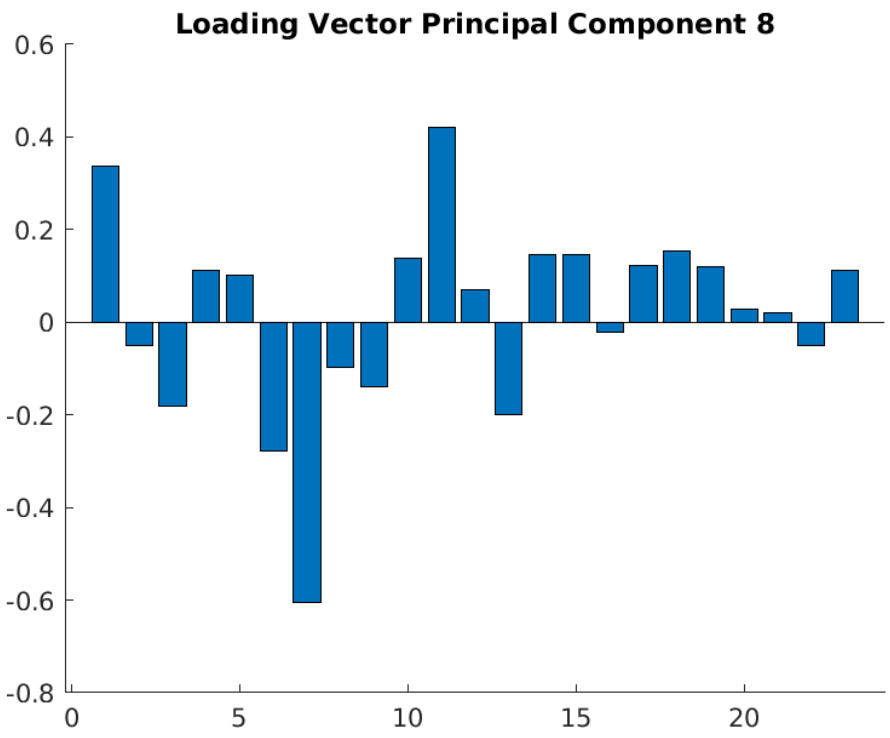


Figure 40: Loading Vector 8

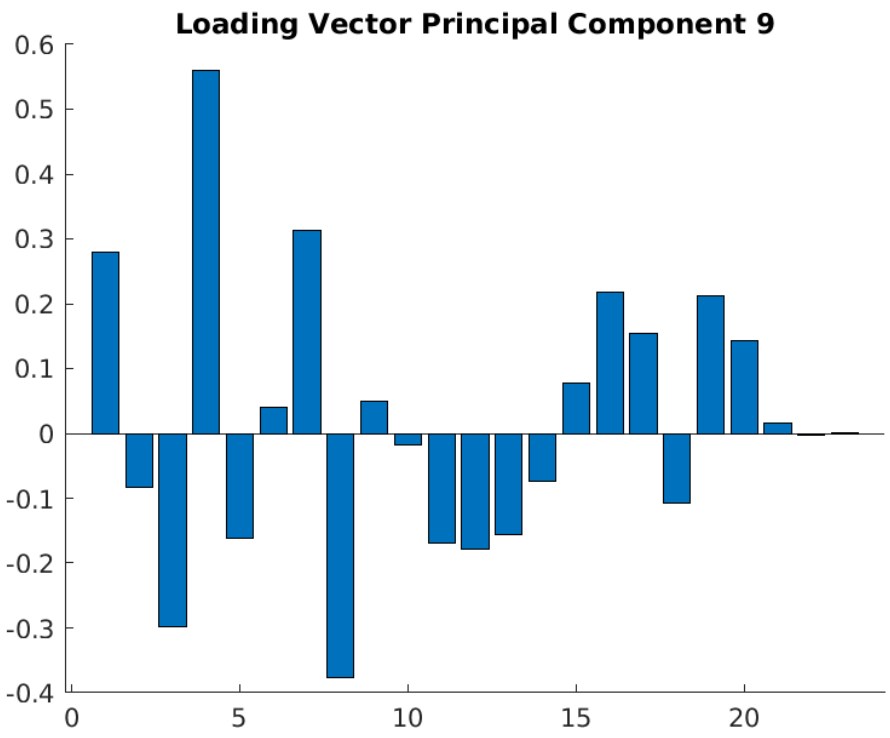


Figure 41: Loading Vector 9

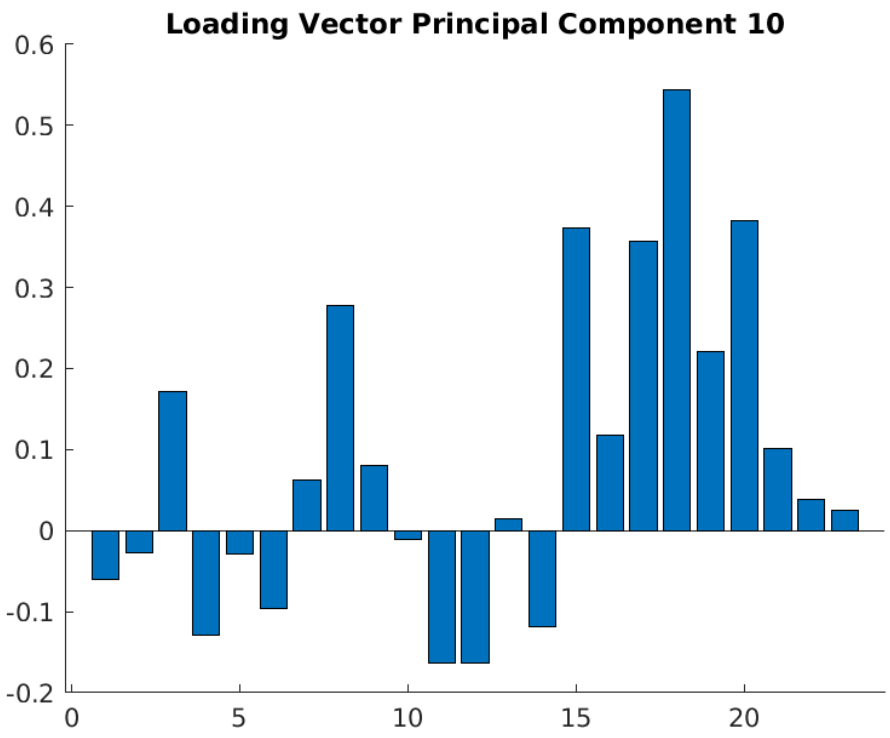


Figure 42: Loading Vector 10

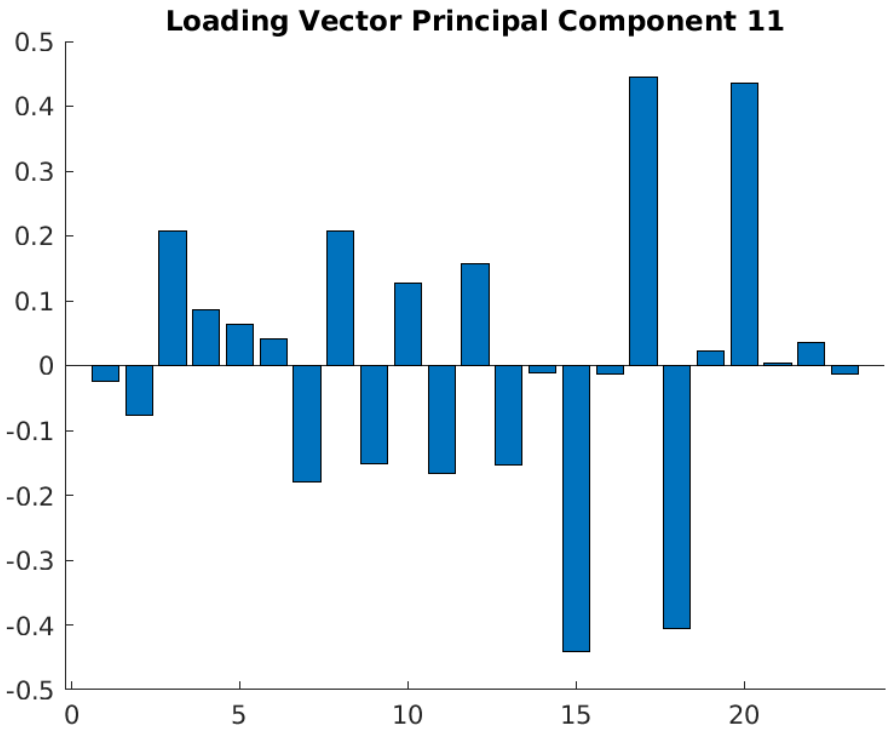


Figure 43: Loading Vector 11

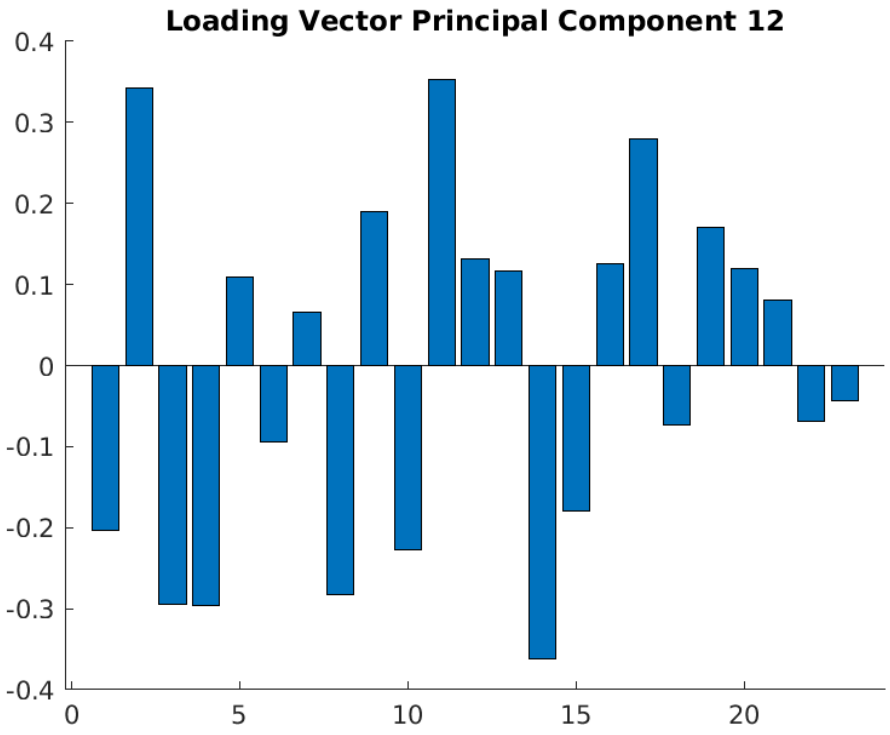
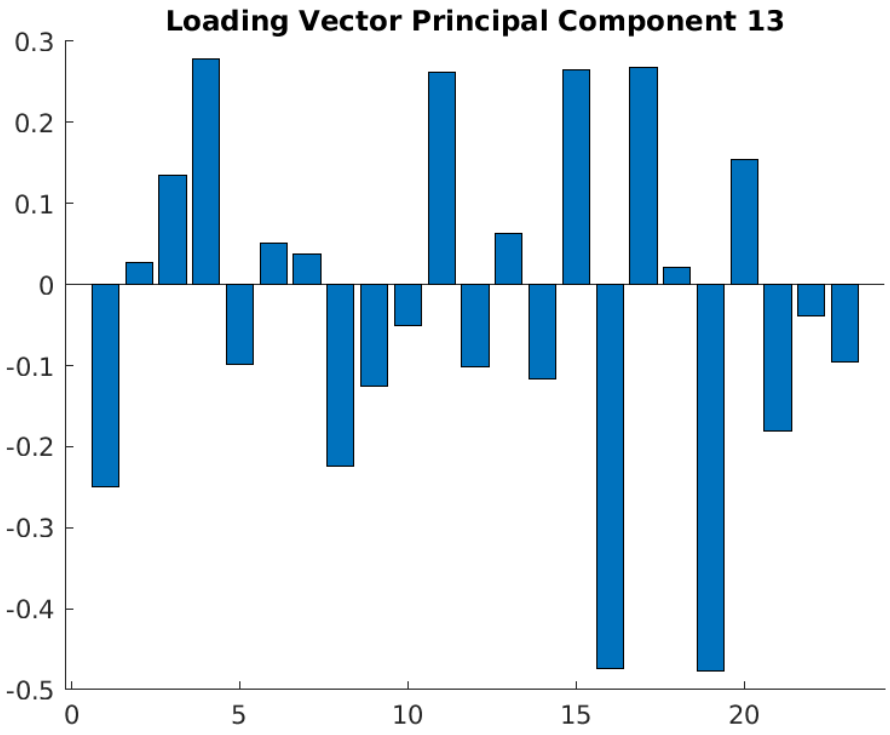


Figure 44: Loading Vector 12



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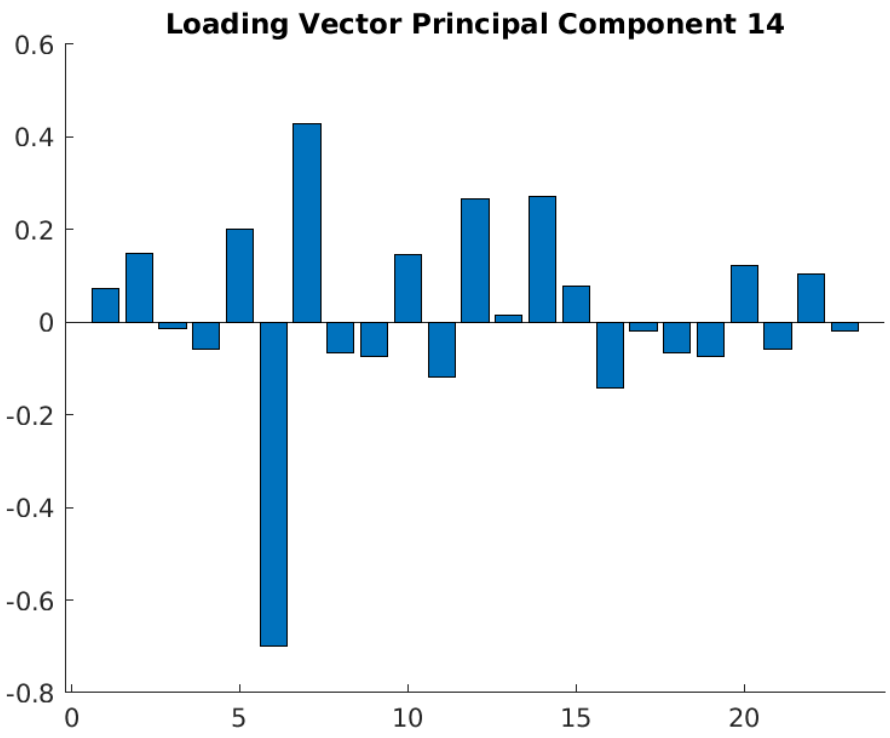


Figure 46: Loading Vector 14

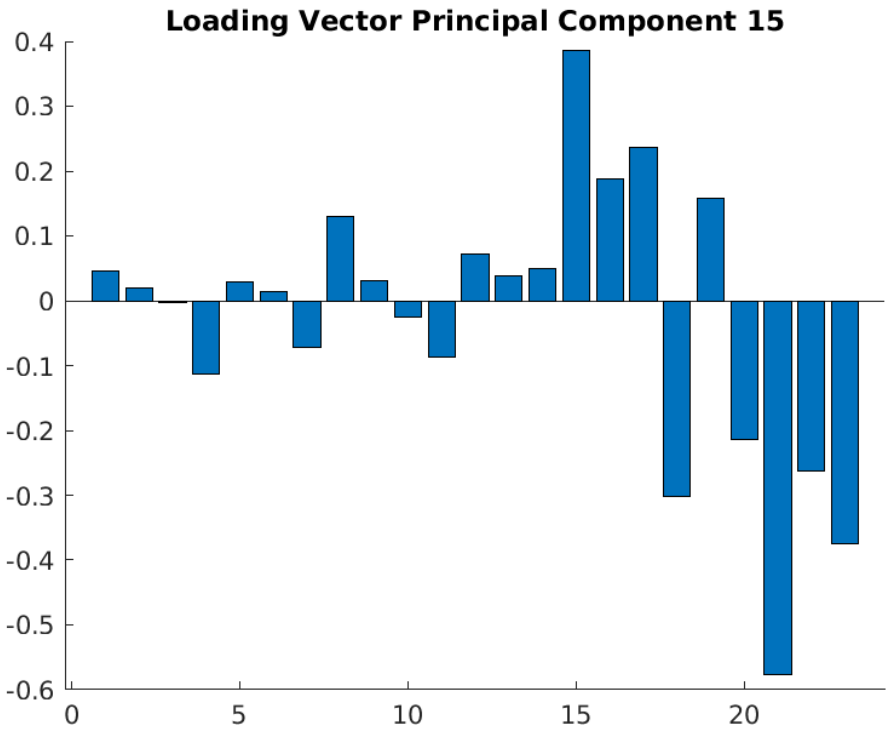


Figure 47: Loading Vector 15

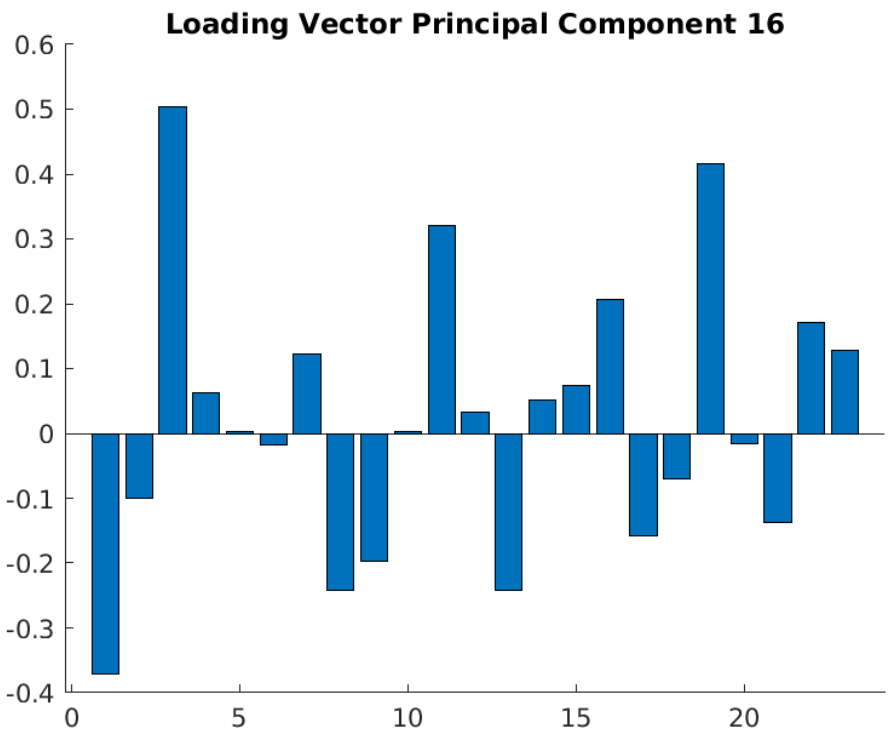
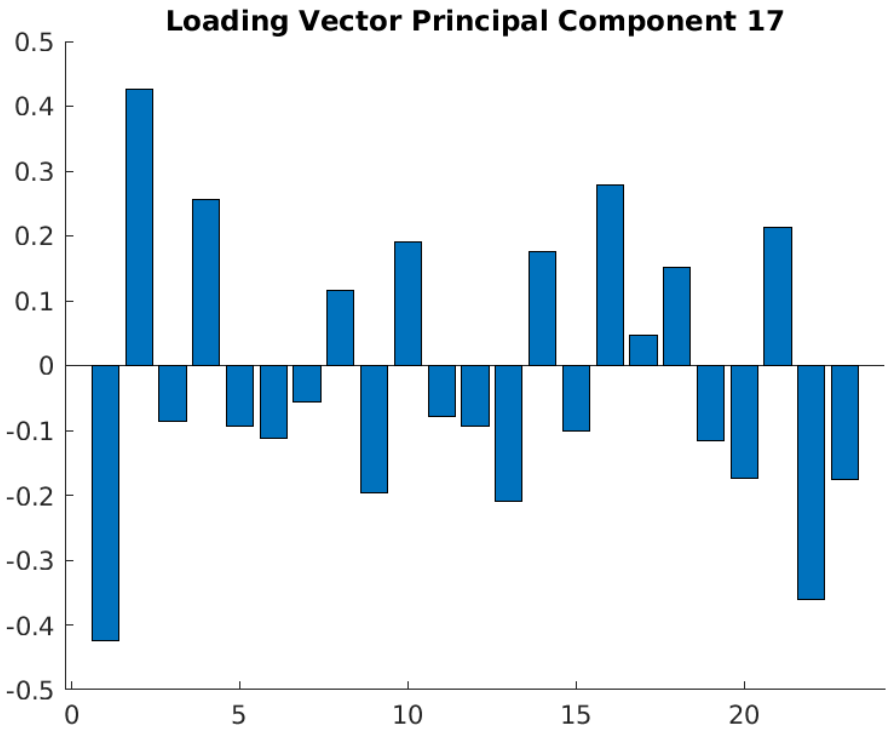


Figure 48: Loading Vector 16



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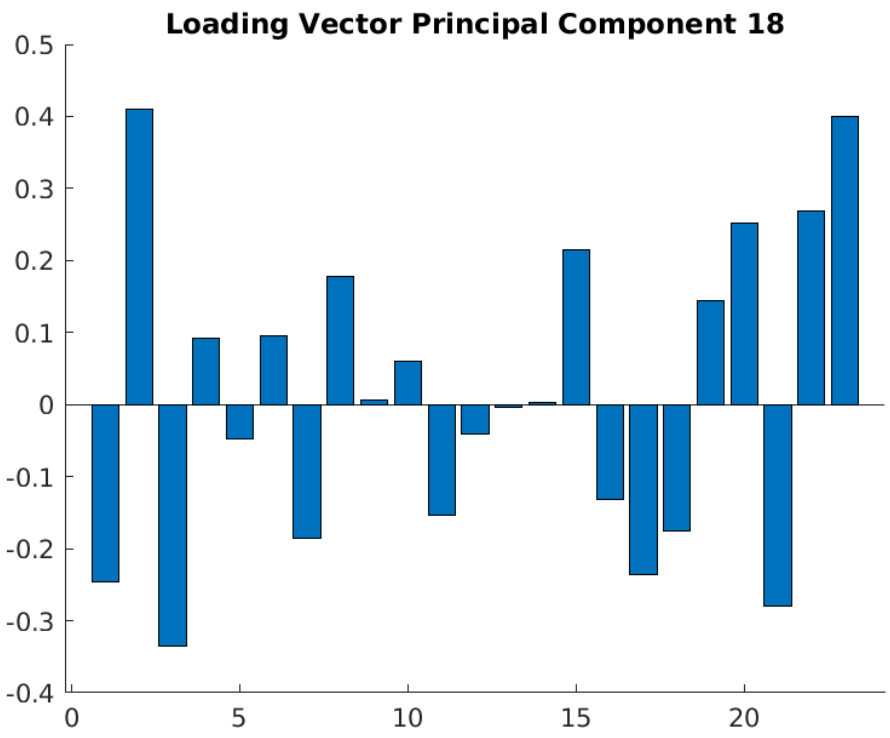
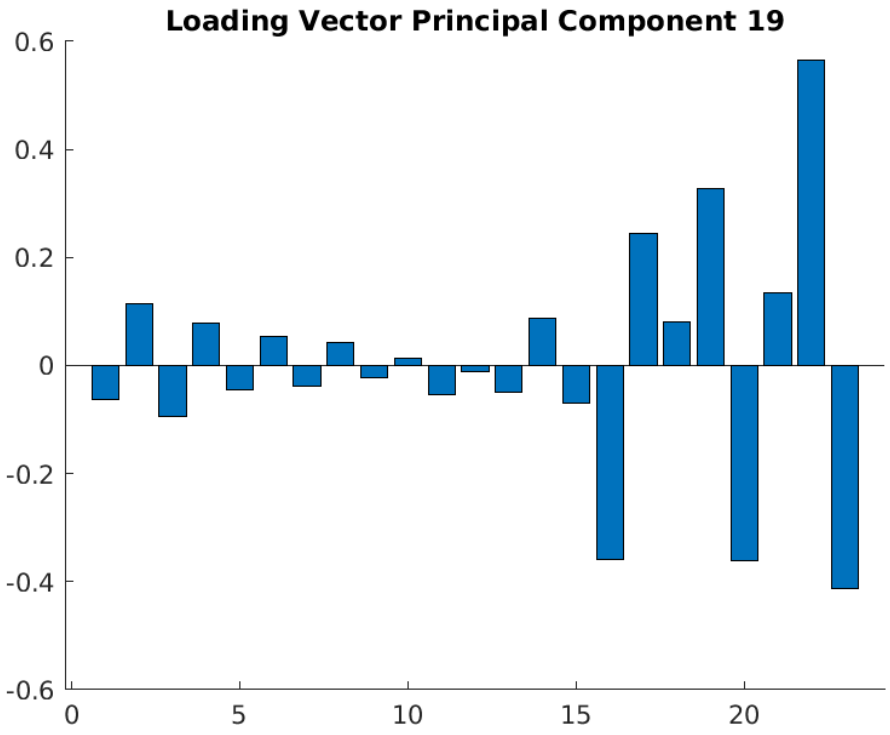


Figure 50: Loading Vector 18



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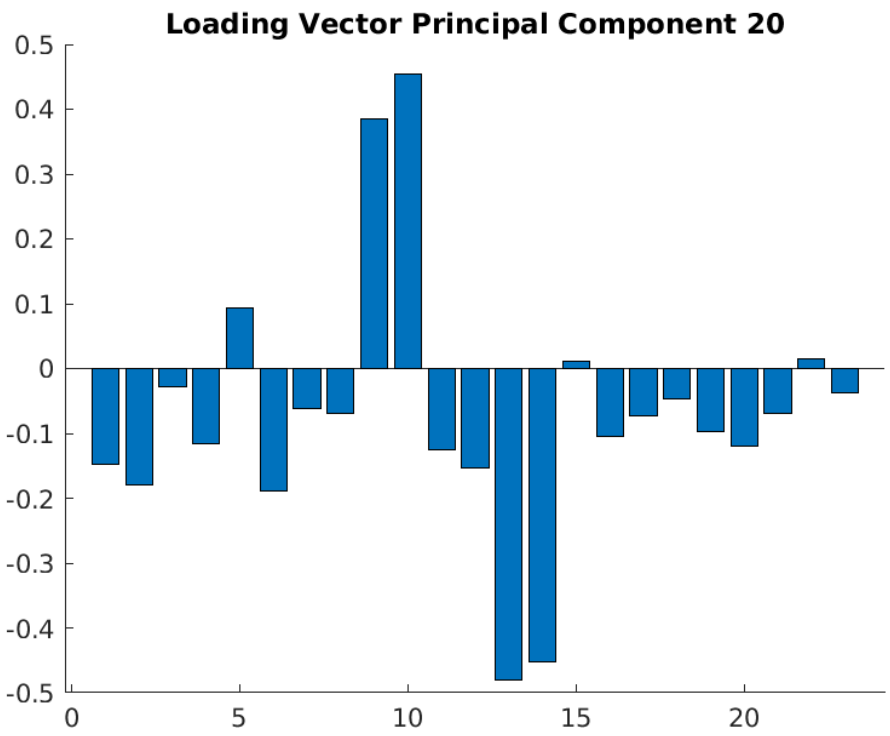

Figure 52: Loading Vector 20

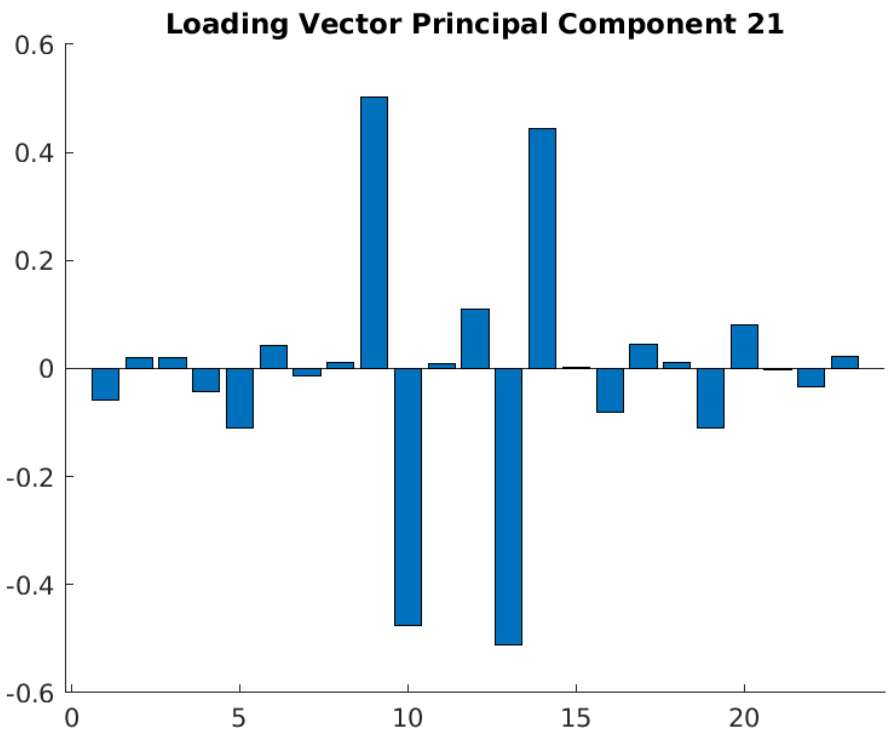

Figure 53: Loading Vector 21

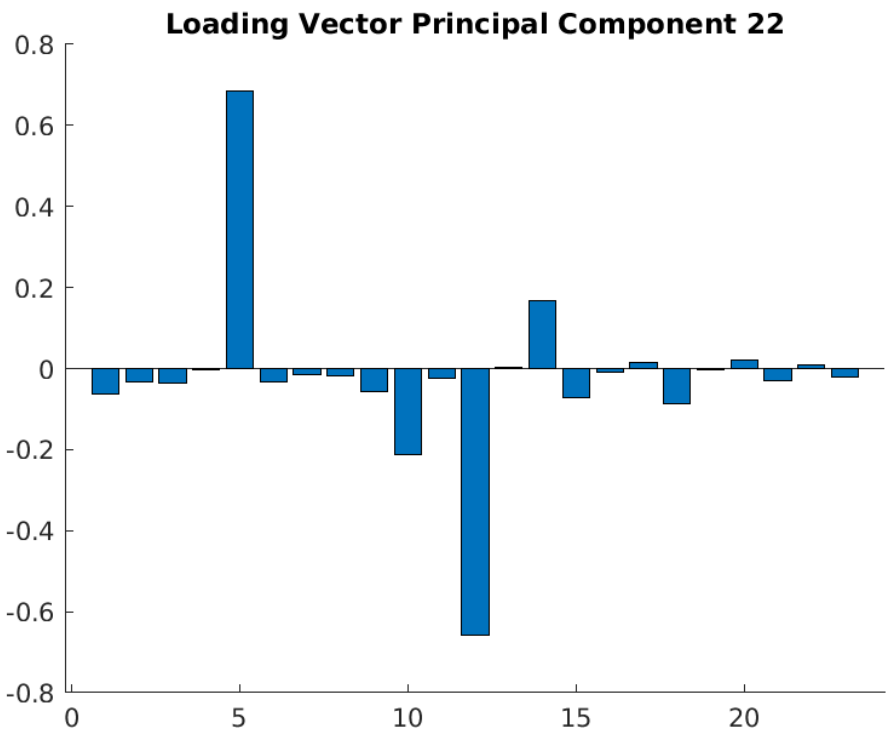

Figure 54: Loading Vector 22

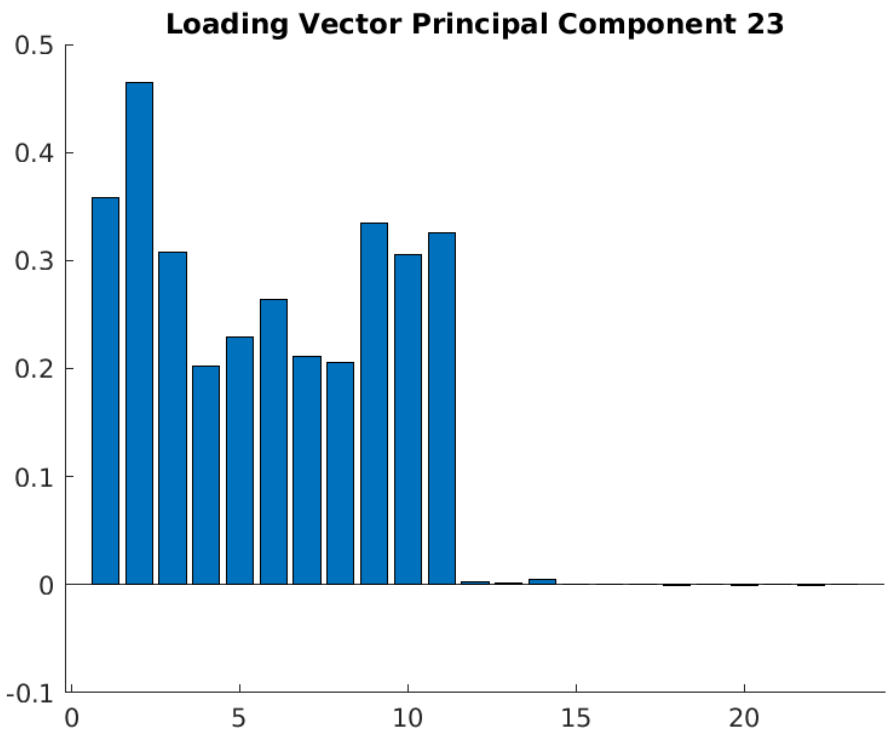

Figure 55: Loading Vector 23