

Final Project Report

Patient Survival Prediction using Data Mining Techniques

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Data Mining CS-6443

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Introduction

This project addresses the imperative of enhancing patient survival prediction through advanced data mining techniques, emphasizing dimensionality reduction and classification. Motivated by seminal works such as "The use of data mining techniques to predict mortality and length of stay in an ICU" by Alramzana Nujum Navaz et al., "Predicting ICU death with summarized patient data" by K.M.D. Muthumali Karunarathna, and "A Comparison of Intensive Care Unit Mortality Prediction Models through the Use of Data Mining Techniques" by Sujin Kim et al., our focus centres on the Kaggle dataset "Patient Survival Prediction" (91,713 rows, 85 columns) from MIT's GOSSIS (Global Open Source Severity of Illness Score) initiatives. By optimizing classification models through dimensionality reduction, we aim to overcome challenges posed by high-dimensional medical datasets, contributing to healthcare analytics research with potential positive implications for clinical decision-making.

Definition of Problem

Our project is centred on the comprehensive analysis and prediction of patient survival using the "Patient Survival Prediction" dataset obtained from Kaggle. This dataset, consisting of 91,713 entries across 85 features taken from MIT's GOSSIS (Global Open Source Severity of Illness Score) initiatives, presents a significant challenge due to its high dimensionality and diverse variables. To effectively navigate this complexity, we have devised a strategic approach focusing on two primary areas: dimensionality reduction and classification.

The primary objective of our project is to develop a reliable and accurate predictive model for all-cause in-hospital mortality among admitted patients. This entails identifying and understanding the intricate relationships between various clinical and demographic factors within the dataset and their impact on patient outcomes. By leveraging advanced analytical techniques and rigorous data exploration methods, we aim to extract meaningful insights and essential features that significantly contribute to patient survival prediction.

Our approach involves thorough validation processes to ensure the robustness and generalizability of the predictive model. Through iterative refinement and validation, we seek to create a tool that healthcare professionals can confidently rely on for early identification of high-risk patients and informed decision-making regarding interventions and treatments.

Ultimately, our project strives to advance the field of healthcare analytics by providing clinicians with a valuable tool that enhances their ability to assess patient risk and intervene effectively, thereby improving overall patient survival rates and healthcare outcomes.

Related Work

The research paper titled "Dynamic and explainable machine learning prediction of mortality in patients in the intensive care unit: a retrospective study of high-frequency data in electronic patient records" authored by Hans-Christian Thorsen-Meyer, MD, Annelaura B Nielsen, investigates the application of advanced computational methods for predicting mortality in ICU patients using real-time data from electronic patient records.

This study focuses on improving patient care in intensive care units (ICUs) through the use of advanced computational techniques to predict the likelihood of mortality within 90 days of admission. Unlike traditional models that rely solely on initial patient data upon ICU admission, this research harnesses a wealth of comprehensive data collected throughout a patient's stay, capturing subtle changes and trends. By combining baseline information with real-time physiological data, a sophisticated computer model is trained to analyze this rich dataset, offering insights into a patient's probability of survival. Importantly, as the model continuously incorporates new data, its predictive accuracy improves, showcasing the potential of dynamic modeling approaches in healthcare. Furthermore, the model's ability to explain its predictions provides clinicians with valuable insights into patient status and prognosis, enabling informed decision-making. The primary model utilized in this study is a recurrent neural network (RNN) with a long short-term memory (LSTM) architecture, tailored for processing sequential data such as physiological measurements collected at regular intervals during ICU stays. Additionally, the application of the Shapley additive explanations (SHAP) algorithm enhances the interpretability of the model's results by providing explanations for individual patient predictions.

In summary, the study included data from over 12,000 patients and found that the model's predictive performance for 90-day mortality improved over time. When looking at ICU admission, the model's area under the receiver operating characteristic curve (AUROC) was 0.73, increasing to 0.85 after 72 hours. Similarly, the Matthews correlation coefficient (MCC) rose from 0.29 to 0.50 over the same period. Additionally, when evaluating predictions relative to the time of discharge, the model achieved an AUROC of 0.88 at discharge, indicating high predictive accuracy. These results suggest that the model becomes more effective as it accumulates more data during the patient's stay in the ICU, ultimately providing valuable insights into patient outcomes.

In another paper titled "Prediction algorithm for ICU mortality and length of stay using machine learning," authored by Shinya Iwase and colleagues, and published in Scientific Reports, investigates the application of machine learning methods to forecast mortality and length of stay for patients in intensive care units (ICUs). Conducted at Chiba University Hospital, the study analyzed data from 12,747 ICU admissions, with patients divided randomly into training and test groups. Using supervised machine learning techniques, particularly the Random Forest (RF) algorithm, the researchers assessed various admission variables to predict outcomes accurately. Noteworthy findings revealed that the RF model exhibited strong predictive ability for ICU mortality (AUC of 0.945) and for short and long ICU stays (AUCs of 0.881 and 0.889, respectively). Importantly, lactate dehydrogenase (LDH) emerged as a

significant predictor for both mortality and ICU stay length, underscoring its importance in outcome prediction. This study highlights the promising role of machine learning in improving patient care and resource management in critical care settings, offering valuable insights for healthcare professionals in risk assessment and treatment planning.

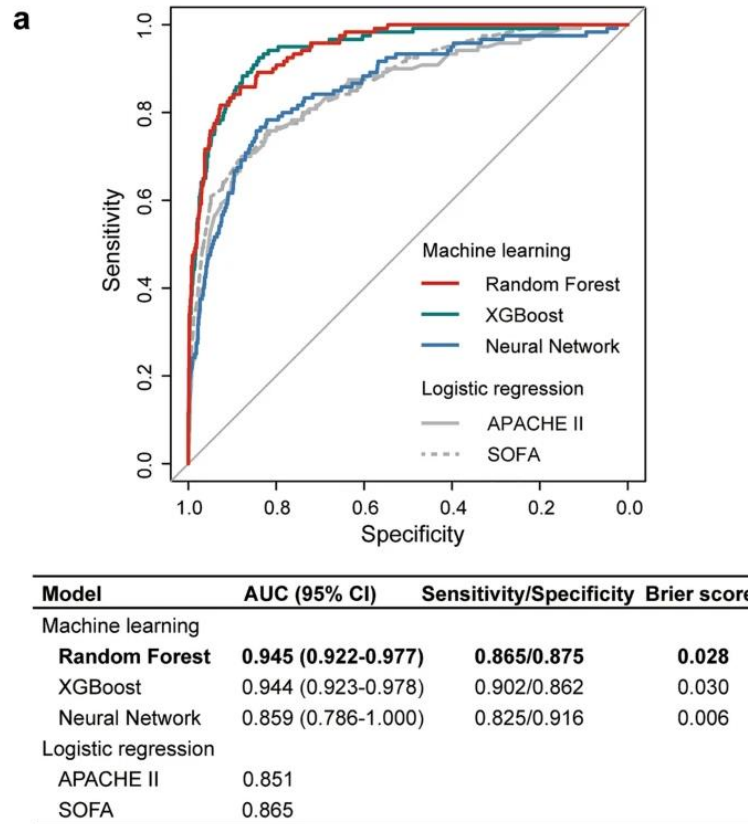


Figure 1

The sensitivity vs specificity plot depicted in 'Figure 1' compares the performance of machine learning models - Random Forest (RF), XGBoost, Neural Network and Logistic Regression - in predicting outcomes, particularly ICU mortality and length of stay. Notably, Random Forest demonstrated superior performance across the models, boasting the highest Area Under the Curve (AUC) value of 0.945. Additionally, the sensitivity and specificity metrics further underscored RF's effectiveness, with sensitivity and specificity values of 0.865 and 0.875, respectively. These metrics indicate RF's ability to correctly identify true positive cases (sensitivity) and true negative cases (specificity) relative to all positive and negative cases, respectively. Overall, Random Forest emerged as the most robust and accurate model among the three, showcasing its potential as a reliable tool for predicting ICU outcomes with high sensitivity and specificity.

Moreover, a research paper titled "A Comparison of Intensive Care Unit Mortality Prediction Models through the Use of Data Mining Techniques" authored by Sujin Kim, Woojae Kim, and Rae Woong Park, investigates the development of ICU mortality prediction models

using data mining methods. Utilizing ICU data from the University of Kentucky Hospital spanning 38,474 admissions, the study evaluates the performance of four prediction models: APACHE III (conventional), decision trees (DT), artificial neural networks (ANN), and support vector machines (SVM). Results in the 'Figure 2' indicate that the decision tree model (C5.0) slightly outperforms others with an AUC of 0.892, followed by SVM (AUC 0.876), APACHE III (AUC 0.871), and ANN (AUC 0.874). These findings suggest the potential of data mining techniques, particularly decision trees and support vector machines, in enhancing predictive modeling for ICU mortality.

Methods	AUC	SE	95% Confidence interval
C5	0.892	0.004	0.884-0.900
ANN	0.874	0.004	0.866-0.881
SVM	0.876	0.004	0.868-0.883
APACHE III	0.871	0.003	0.865-0.877

Figure 2

Challenges

In our patient survival prediction project, one of the initial hurdles encountered was the presence of numerous missing values in the dataset. Addressing this challenge was crucial as missing data can significantly impact the accuracy and reliability of predictive models. We implemented various strategies to handle missing values effectively, including imputation techniques such as replacing missing values with the median or mean of the respective feature. ‘Figure 3’ shows the number of missing values in each column.

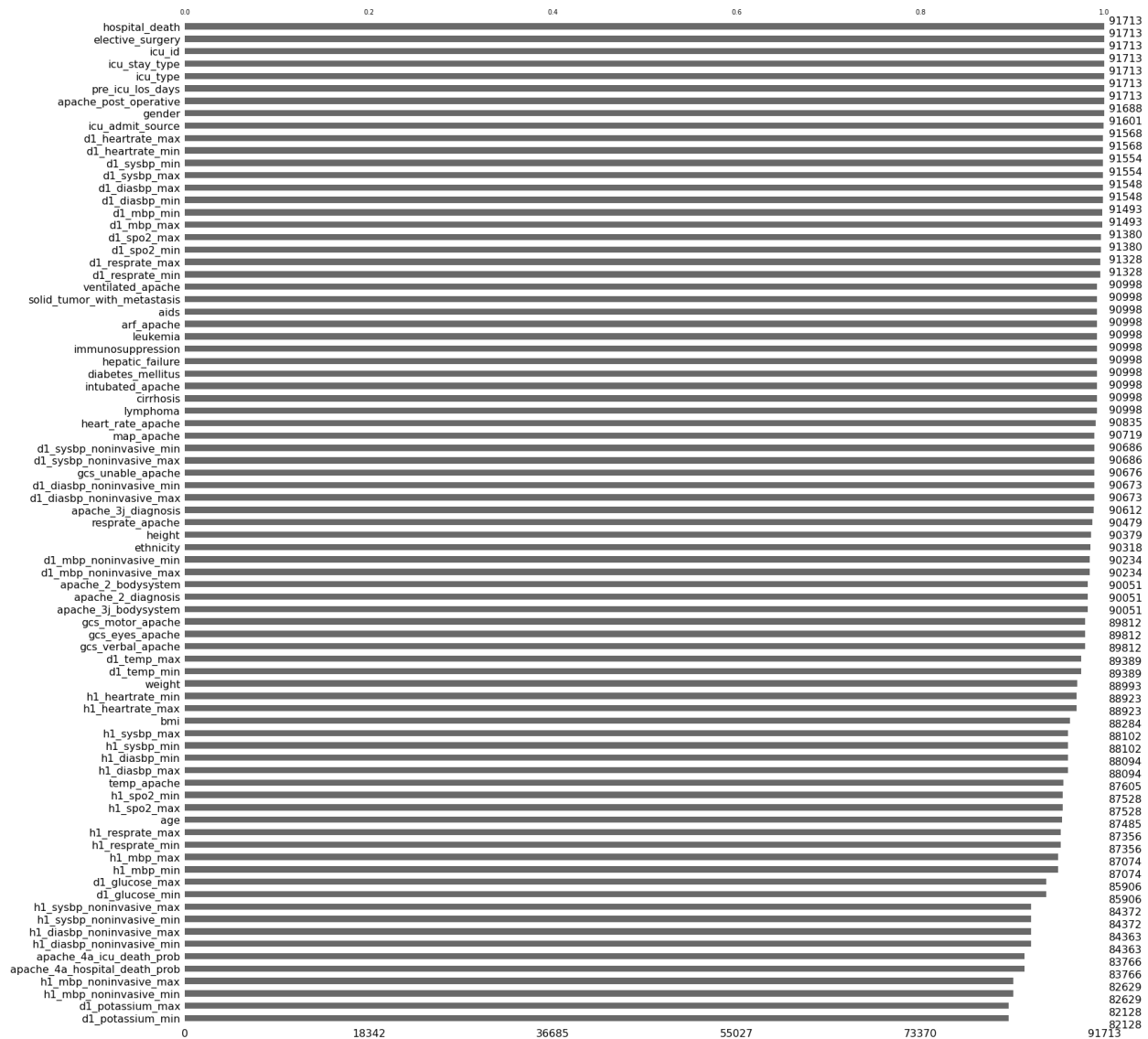


Figure 3

Another challenge faced was the class imbalance observed in the dataset, particularly concerning hospital death outcomes as shown in ‘Figure 4’. To address this issue, we employed the Synthetic Minority Over-sampling Technique (SMOTE), a popular method used to rebalance class distributions by generating synthetic samples of the minority class. By augmenting the

dataset with synthetic instances of the minority class, we achieved a more balanced distribution, enabling our predictive models to better capture the characteristics of both classes and improve their performance.

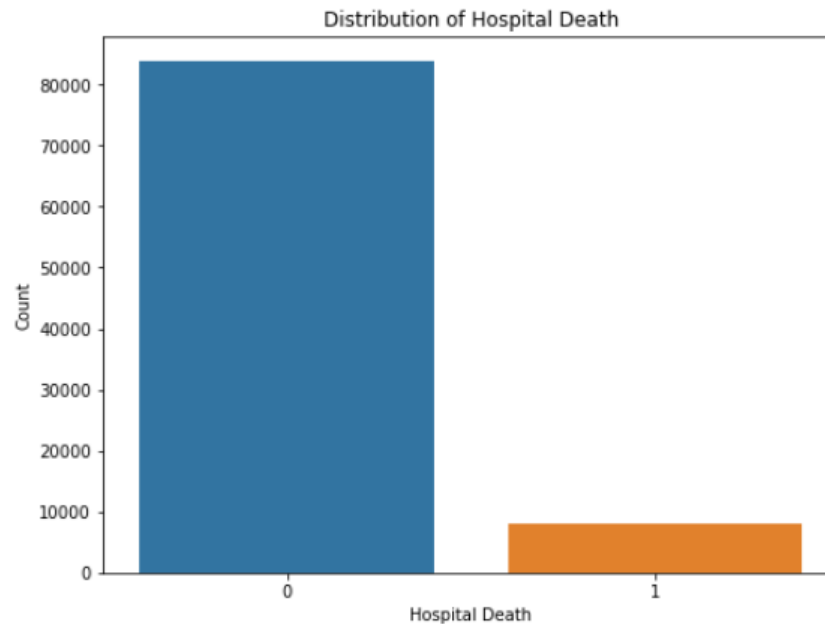


Figure 4

We also faced a problem with the dataset because it had a lot of columns, which made it harder to train our models on our local computer. This meant it needed a lot of computing power, and sometimes our models would stop working after running for a long time. To solve this, we used Amazon Web Services (AWS), a cloud computing service. AWS helped us handle the heavy computing load and speed up the training of our models. This way, we could develop accurate predictions for patient survival in intensive care units without worrying about running out of computing power.

Our Approach

Data Cleaning

In dealing with the dataset, we encountered numerous columns with missing values. Simply dropping these columns could result in significant data loss and compromise the accuracy of our analysis. To address this challenge, we opted to impute the missing values using a method that replaced them with either the mean or mode of the respective column. By imputing missing values with the mean (for numerical data) or mode (for categorical data), we were able to retain valuable information while ensuring that our dataset remained robust and suitable for analysis. This approach helped maintain the integrity of the dataset and allowed us to proceed with our analysis without sacrificing data completeness.

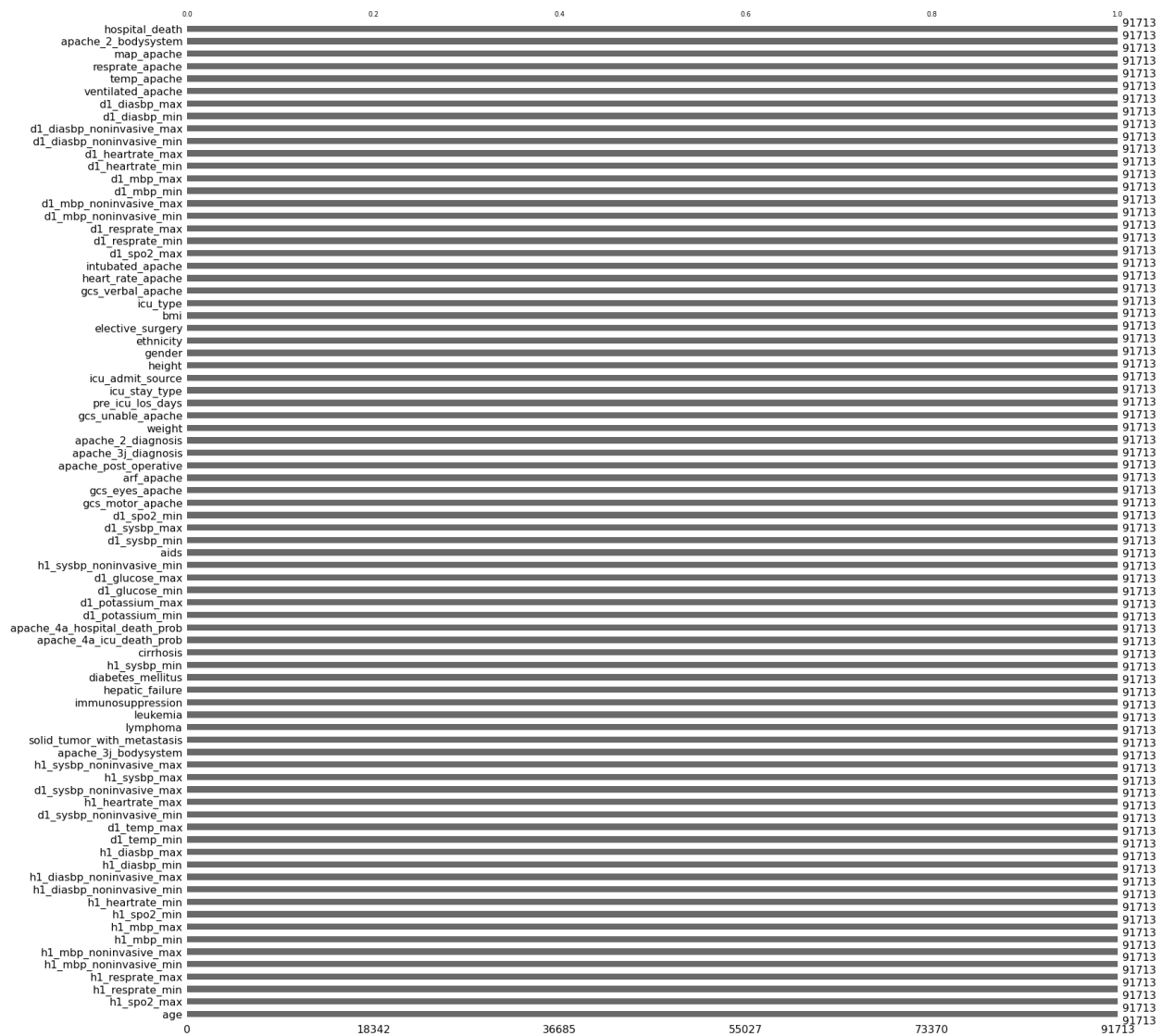


Figure 5

'Figure 5' depicts the outcome of our data imputation process, revealing that all null values have been successfully filled. Through the imputation technique employed, we effectively addressed missing values within the dataset, ensuring that no gaps remained in the data. This comprehensive data cleaning process enhances the reliability and completeness of our dataset, setting a solid foundation for subsequent analyses and modeling tasks.

Data Analysis

In this part of our data analysis, our goal was to understand the dataset better by uncovering hidden patterns and examining relationships between different variables. We used different methods, like bar plots, correlation matrix, box plots etc., to explore the data thoroughly. By doing this, we aimed to find valuable insights that could help us build models and make better decisions later on. This initial exploration is important because it helps us identify important features and trends in the data, which can then be used to make more accurate predictions and informed decisions based on the data.

Frequency Analysis and Plots

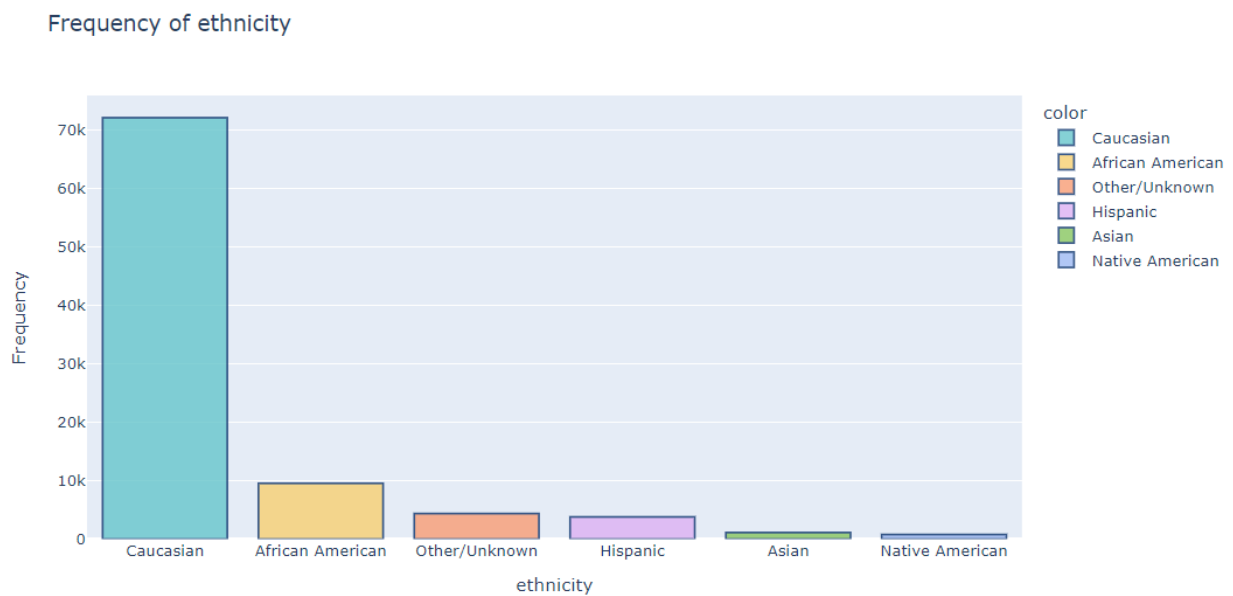


Figure 6

'Figure 6' displays the frequency analysis of ethnicity within the dataset. Upon analysis, it became apparent that individuals of Caucasian ethnicity were the most prevalent, followed by African Americans.

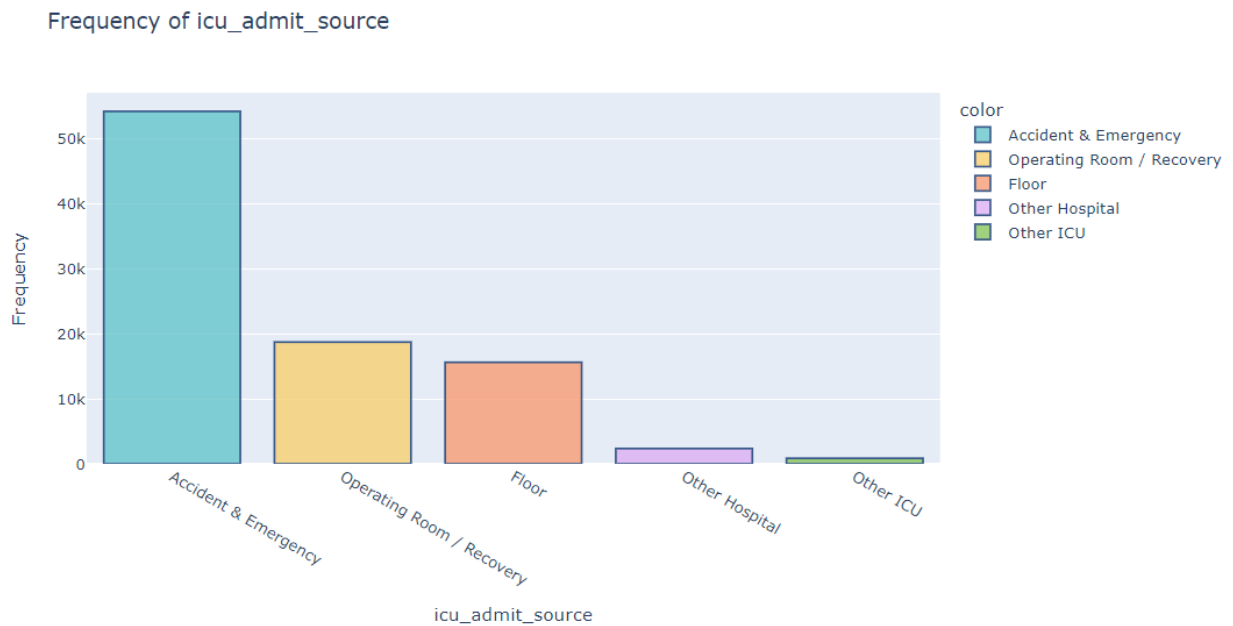


Figure 7

'Figure 7' illustrates the frequency of ICU admissions based on the source of admission. The analysis revealed that the Accident & Emergency department accounted for the highest number of admissions to the ICU.

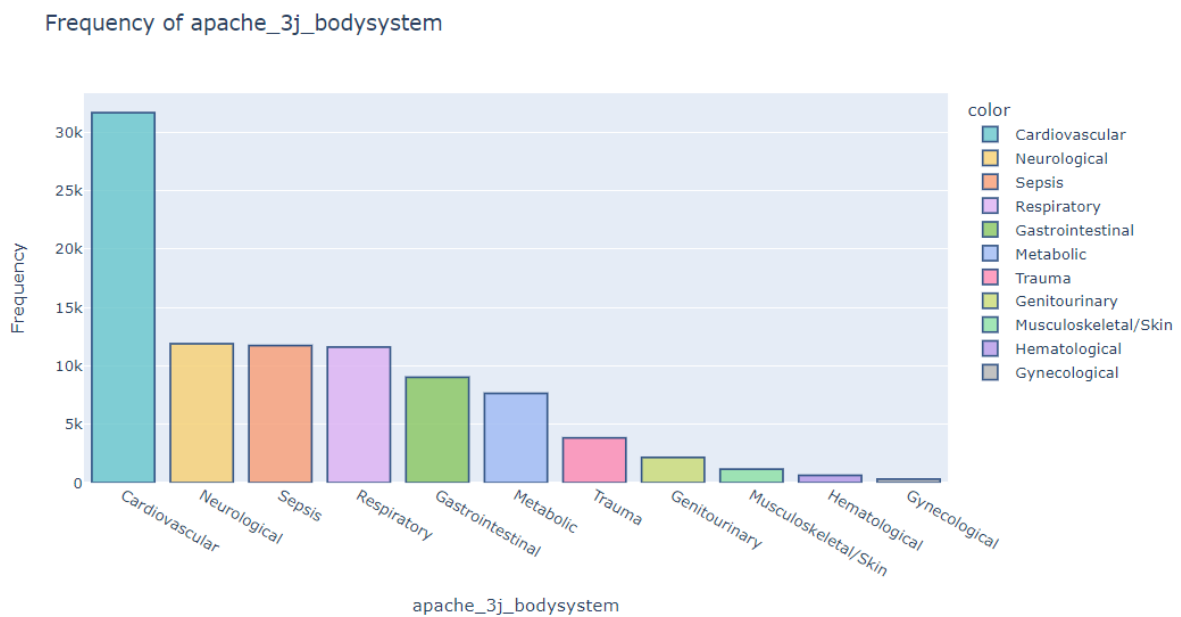


Figure 8

'Figure 8' depicts the distribution of diseases among the patients, revealing that cardiovascular diseases were the most prevalent condition observed in the dataset. This analysis highlights the significant burden of cardiovascular health issues among the patient population under study.

Correlation Matrix

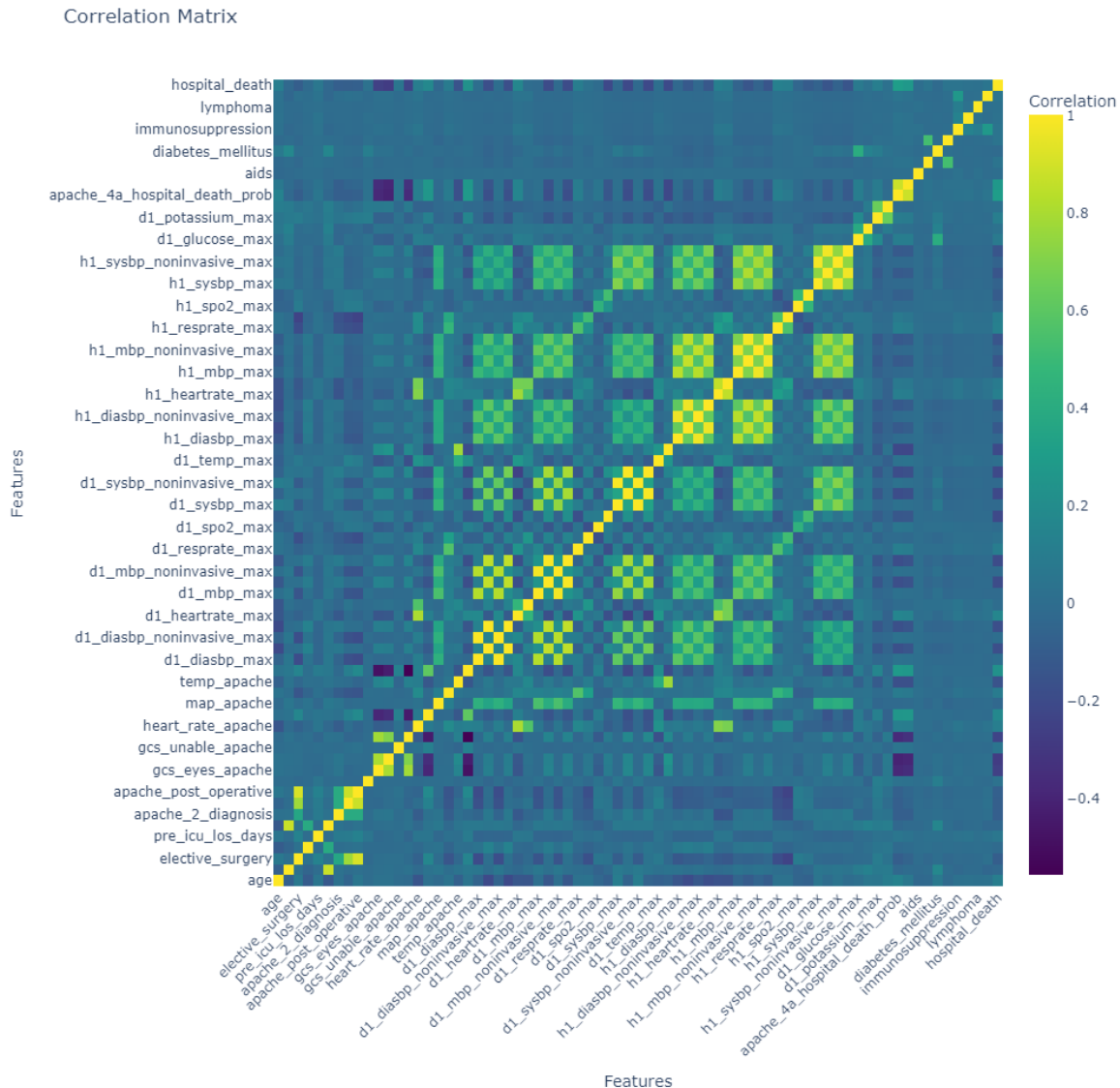


Figure 9

'Figure 9' illustrates the correlation matrix computed for the dataset, revealing the relationships between different variables. By examining the correlation matrix, we can discern the degree and direction of association between pairs of variables. This analysis provides valuable insights into how variables are related to each other, helping us understand potential dependencies and identifying key factors that may influence the outcome of interest.

Relationships between various numerical features and the target variable (hospital_death)

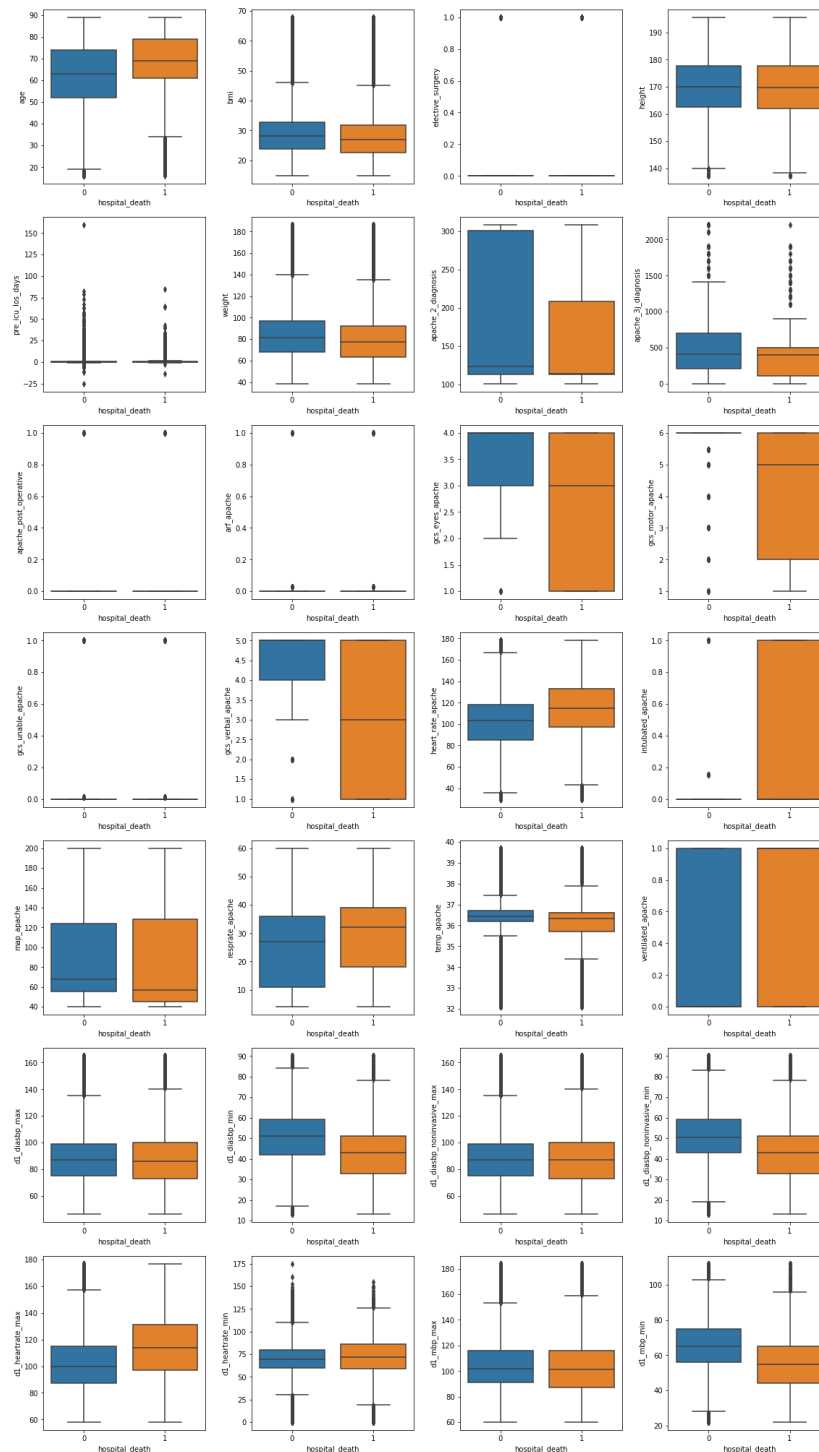


Figure 10

In Figure 10, box plots are employed to visualize the relationship between numerical features and the target variable 'hospital_death'. Box plots display the distribution of each feature separately for instances where hospital_death is both 0 and 1. The box in the plot represents the

interquartile range (IQR), with the horizontal line inside the box indicating the median value. The whiskers extending from the box indicate the range of the data, excluding outliers. Any data points outside the whiskers are considered outliers and are plotted individually. This visualization allows for a comparative analysis of the distribution of each numerical feature across different values of the target variable, providing insights into potential associations and differences in feature distributions between instances of hospital death and survival.

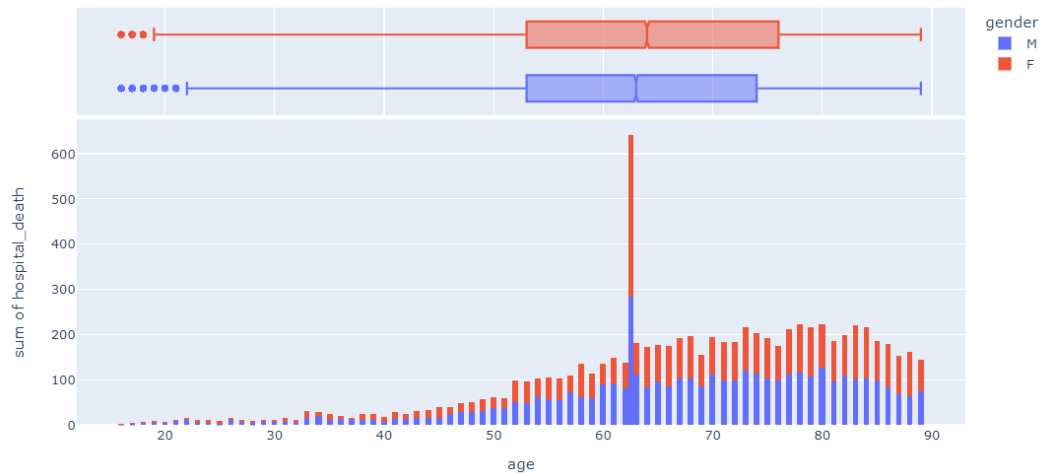


Figure 11

Figure 11 depicts a histogram with marginal box plots, illustrating the distribution of the 'age' variable in relation to 'hospital_death', with the data further differentiated by 'gender'. Each bar on the histogram represents the frequency of occurrences for a specific age group, while the marginal box plots provide insights into the distribution of 'age' within each category of 'hospital_death' and 'gender'. This visualization allows for an exploration of how the distribution of age varies across different categories of hospital death and gender, facilitating a deeper understanding of potential relationships and trends within the dataset. However, it was seen that age greater than 60 have the highest sum of hospital death overall.

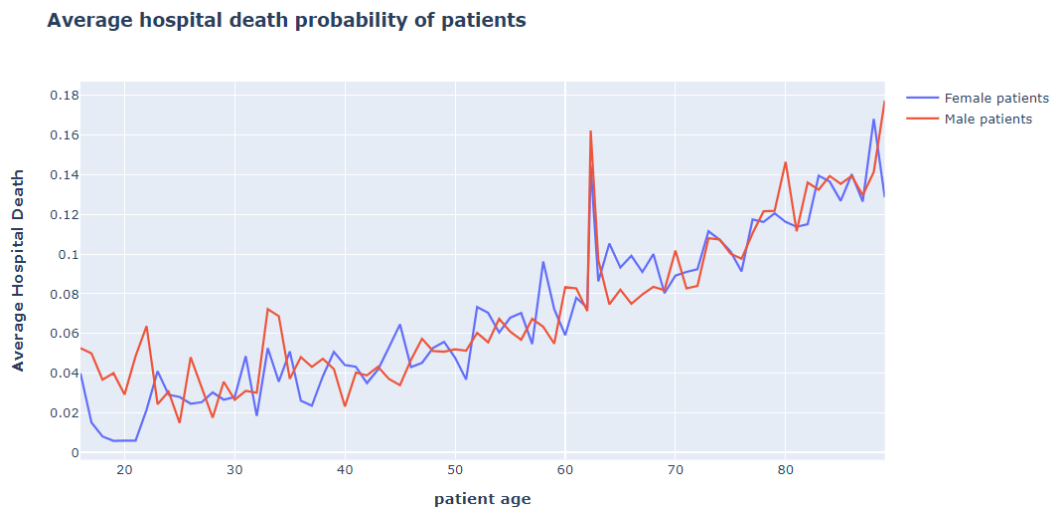


Figure 12

Impacts of BMI and Weight on Patients

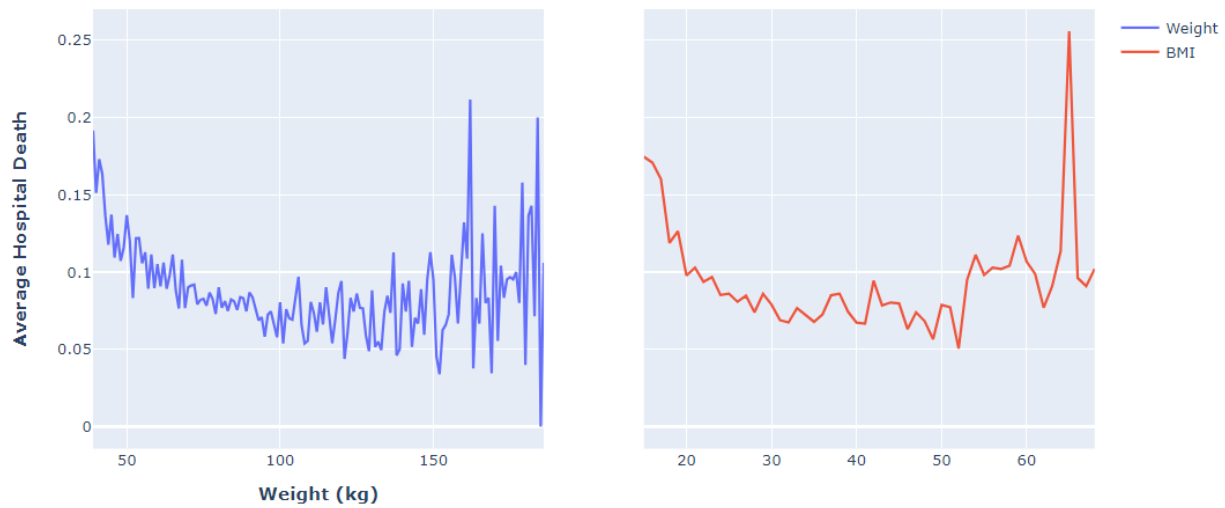


Figure 13

Survival rate at different types of ICU

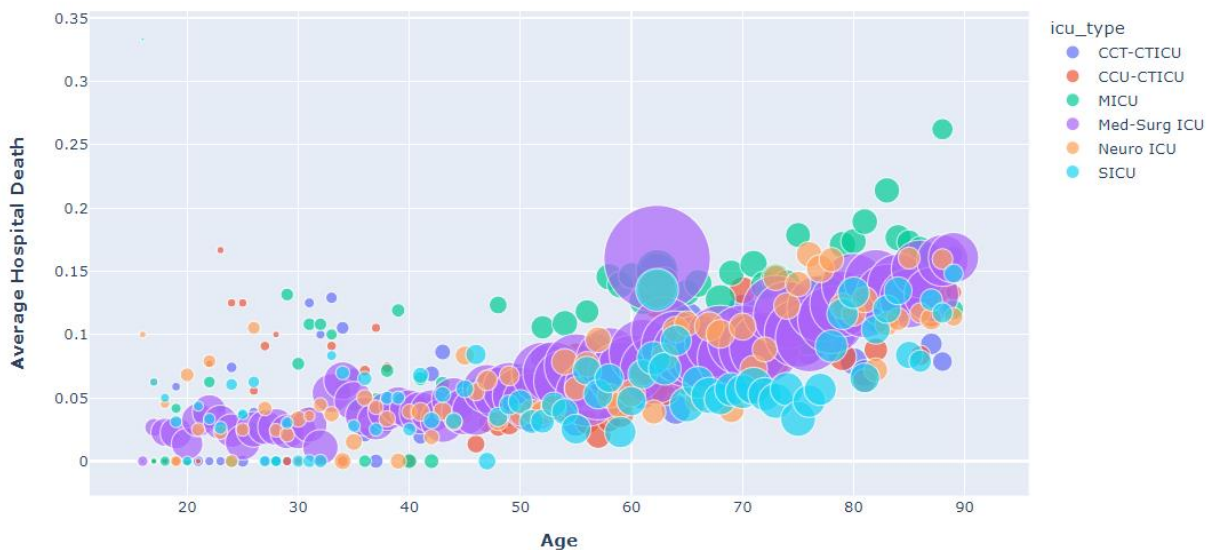


Figure 14

Figures 12, 13, and 14 present an in-depth examination of age, weight, BMI, and survival rates across different types of ICU with respect to age. These visualizations offer comprehensive insights, indicating that higher BMI is associated with increased chances of death, advanced age correlates with higher mortality rates, and there is no discernible difference in death rates between males and females.

Data Preprocessing

In the preprocessing phase, the dataset undergoes several transformations to prepare it for machine learning model training. Firstly, categorical variables are encoded using ordinal encoding to represent them numerically. Next, numerical features are standardized to have a mean of 0 and a standard deviation of 1, preventing any single feature from dominating the model training process. The dataset is then split into training, testing, and validation sets, with the features and target variable separated accordingly. The training set is used to train the model, while the testing set is employed to evaluate its performance. The validation set serves as an additional checkpoint to fine-tune the model's parameters and prevent overfitting. These preprocessing steps ensure that the data is appropriately formatted and ready for subsequent model training and evaluation. 'Figure 15' shows the snapshot of normalized data ready for machine learning models.

hepatic_failure	immunosuppression	leukemia	lymphoma	solid_tumor_with_metastasis	apache_3j_bodysystem	apache_2_bodysystem	hospital_death
-0.115168	-0.164559	-0.084689	-0.064666	-0.145734	1.268125	-0.888903	0
-0.115168	-0.164559	-0.084689	-0.064666	-0.145734	1.005639	1.271969	0
-0.115168	-0.164559	-0.084689	-0.064666	-0.145734	0.218184	0.191533	0
-0.115168	-0.164559	-0.084689	-0.064666	-0.145734	-1.094242	-0.888903	0
-0.115168	-0.164559	-0.084689	-0.064666	-0.145734	1.530610	1.632114	0

Figure 15

Machine Learning Models

For patient survival prediction, we employed three different machine learning algorithms: Random Forest, Logistic Regression, and XGBoost.

Random Forest algorithm belongs to the ensemble learning methods and operates by constructing multiple decision trees during training and outputting the mode of the classes (classification) or mean prediction (regression) of the individual trees. Random Forest is known for its robustness and ability to handle large datasets with high dimensionality.

Logistic Regression despite its name, logistic regression is a linear model for binary classification that predicts the probability of occurrence of an event by fitting data to a logistic curve. It's widely used for binary classification tasks due to its simplicity, interpretability, and efficiency.

XGBoost (Extreme Gradient Boosting) is an implementation of gradient boosting machines, which are a type of ensemble learning method. XGBoost is known for its computational efficiency, scalability, and state-of-the-art performance in many machine learning competitions. It works by sequentially adding weak learners to the ensemble while minimizing a predefined loss function.

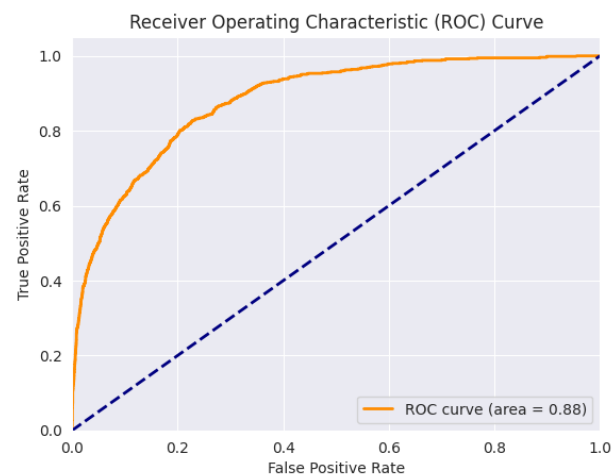
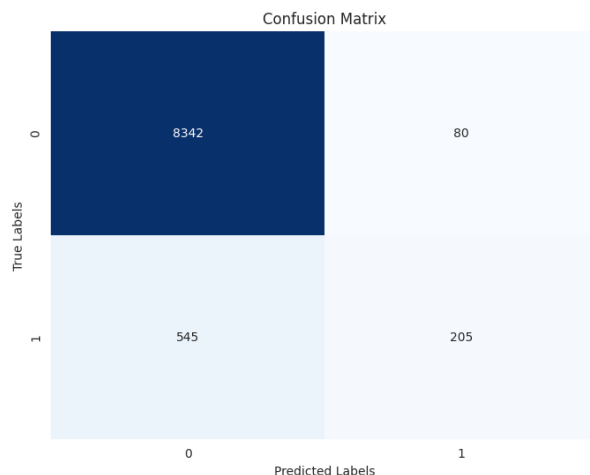
By leveraging these diverse algorithms, we aimed to explore different modeling approaches and identify the one that best suits our patient survival prediction task based on its performance metrics such as accuracy, precision, recall, and area under the receiver operating characteristic curve (ROC-AUC).

Baseline ML Models

In the initial approach, we employed a baseline model to establish a benchmark for comparison. Despite being aware of the class imbalance issue in the dataset, we proceeded to run all the models to gauge their performance and ascertain a base level of accuracy. This approach allowed us to assess the inherent predictive capabilities of each model without any modifications or preprocessing techniques applied to address the class imbalance. By running the models in their raw state, we aimed to gain insights into their intrinsic abilities to discriminate between survival and non-survival outcomes in the dataset. This baseline assessment served as a reference point for evaluating the effectiveness of subsequent modeling strategies and interventions aimed at improving predictive performance, particularly in addressing the challenge of class imbalance.

Random Forest

Classification Report:				
	precision	recall	f1-score	support
0	0.94	0.99	0.96	8422
1	0.72	0.27	0.40	750
accuracy			0.93	9172
macro avg	0.83	0.63	0.68	9172
weighted avg	0.92	0.93	0.92	9172

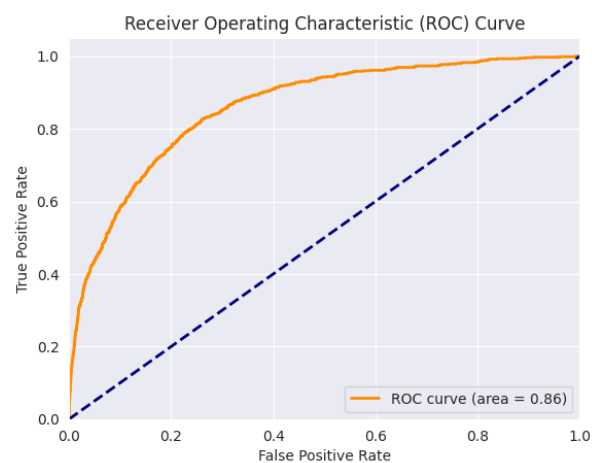
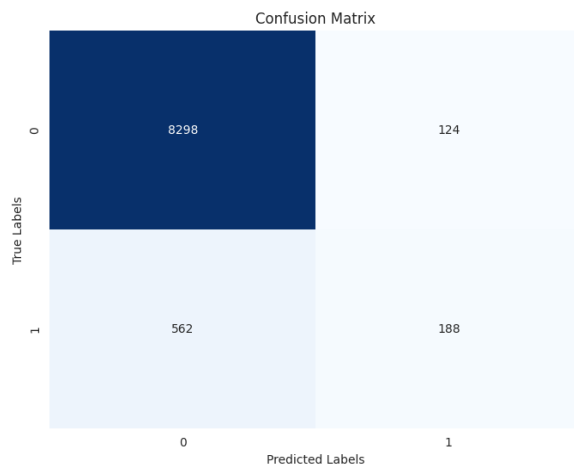


For the Random Forest baseline model, the precision for predicting survival was 0.94, with a recall of 0.99, indicating high accuracy in identifying survival cases. However, for predicting non-survival, precision was lower at 0.72, with a recall of 0.27. The macro-average F1-score, a

measure of model performance, was relatively low at 0.68. This indicates that the model's ability to balance precision and recall across both survival and non-survival classes was suboptimal.

Logistic Regression

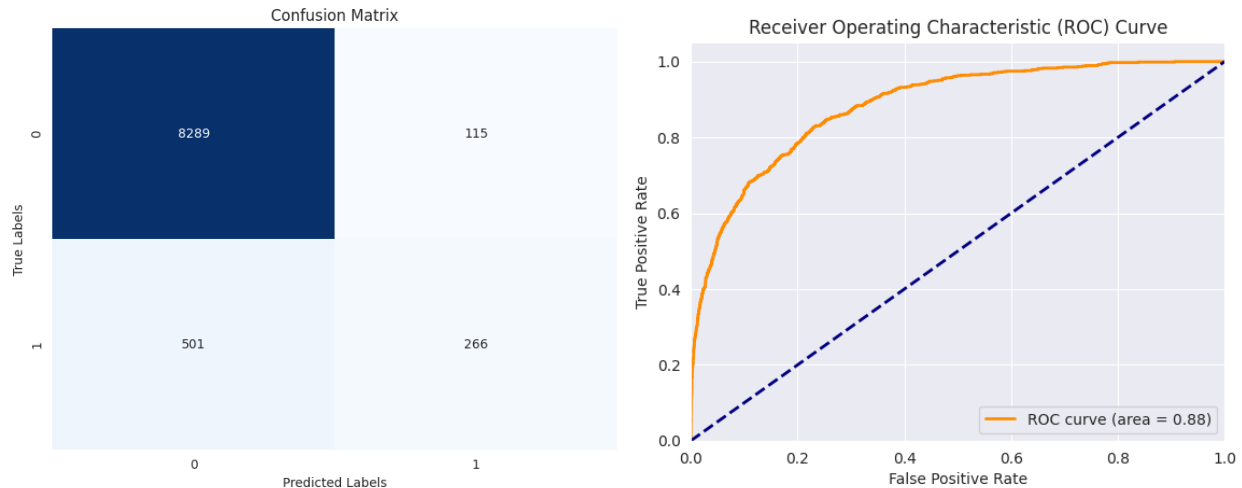
Classification Report:					
	precision	recall	f1-score	support	
0	0.94	0.99	0.96	8422	
1	0.60	0.25	0.35	750	
accuracy			0.93	9172	
macro avg	0.77	0.62	0.66	9172	
weighted avg	0.91	0.93	0.91	9172	



The logistic regression model exhibited lower performance compared to the Random Forest baseline, with a macro-average F1-score of 0.66. While the precision and recall for survival cases remained high, the model struggled to accurately classify non-survival cases, resulting in a lower F1-score for the minority class. This indicates a need for further optimization to enhance the model's ability to identify non-survival cases accurately.

XGBoost

Classification Report:					
	precision	recall	f1-score	support	
0	0.94	0.98	0.96	8422	
1	0.66	0.35	0.46	750	
accuracy			0.93	9172	
macro avg	0.80	0.67	0.71	9172	
weighted avg	0.92	0.93	0.92	9172	



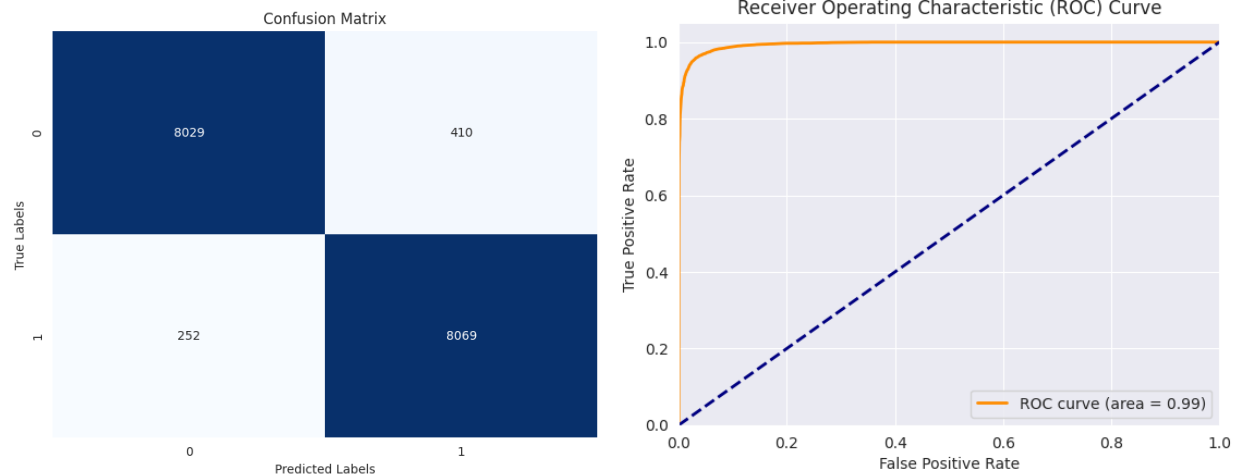
The XGBoost model demonstrated improved performance compared to logistic regression, achieving a macro-average F1-score of 0.71. While the precision and recall for survival cases remained high, the model showed enhanced capability in identifying survival cases, resulting in a higher F1-score for the majority class compared to logistic regression. However, there is still room for improvement in accurately classifying non-survival cases to further enhance the model's overall performance.

ML Models with SMOTE Data

In the second approach, we addressed the class imbalance issue by employing the Synthetic Minority Over-sampling Technique (SMOTE). This technique involves generating synthetic instances of the minority class (non-survival) to balance the class distribution. By augmenting the dataset with synthetic samples, we aimed to provide the machine learning models with a more balanced representation of both survival and non-survival cases, thereby improving their ability to accurately classify instances from both classes.

Random Forest

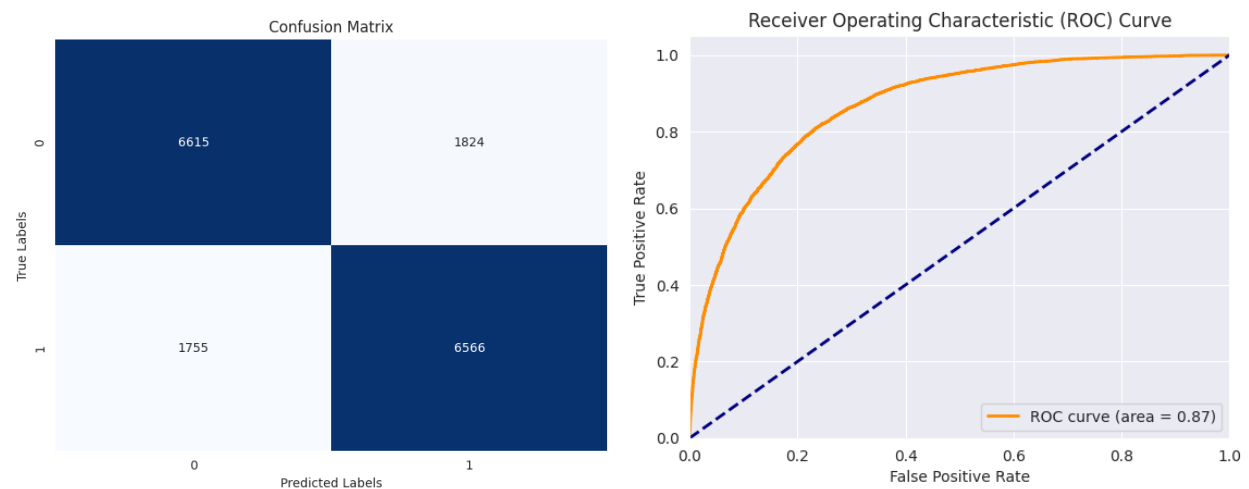
Classification Report:					
	precision	recall	f1-score	support	
0	0.97	0.95	0.96	8439	
1	0.95	0.97	0.96	8321	
accuracy			0.96	16760	
macro avg	0.96	0.96	0.96	16760	
weighted avg	0.96	0.96	0.96	16760	



After applying SMOTE, the Random Forest model achieved improved performance, with an accuracy of 96% and an ROC AUC of 0.99. The model demonstrated high precision, recall, and F1-score for both survival and non-survival classes, indicating enhanced predictive capability and balanced classification across the dataset.

Logistic Regression

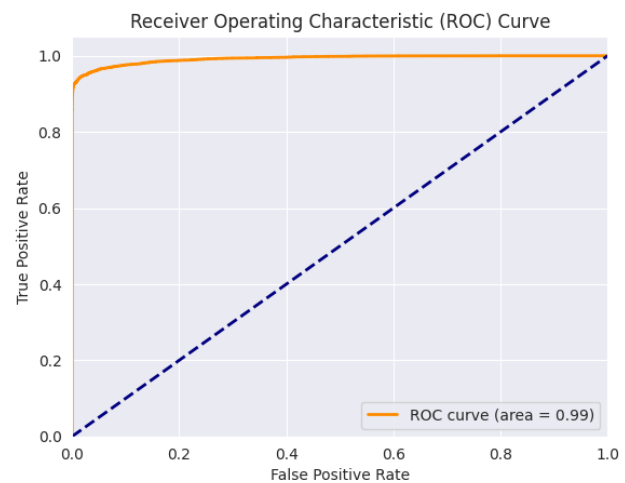
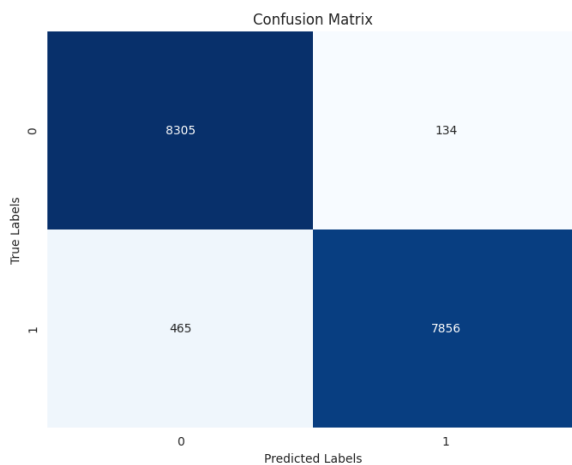
Classification Report:					
	precision	recall	f1-score	support	
0	0.79	0.78	0.79	8439	
1	0.78	0.79	0.79	8321	
accuracy			0.79	16760	
macro avg	0.79	0.79	0.79	16760	
weighted avg	0.79	0.79	0.79	16760	



The logistic regression model achieves an overall accuracy of 0.79, with precision, recall, and F1-score all around 0.79 for both survival and non-survival classes. The confusion matrix indicates that the model correctly predicts 6615 survival cases and 6566 non-survival cases, but misclassifies 1824 survival cases as non-survival and 1755 non-survival cases as survival. The ROC AUC score of 0.87 demonstrates good discrimination ability, indicating the model's effectiveness in distinguishing between survival and non-survival cases.

XGBoost

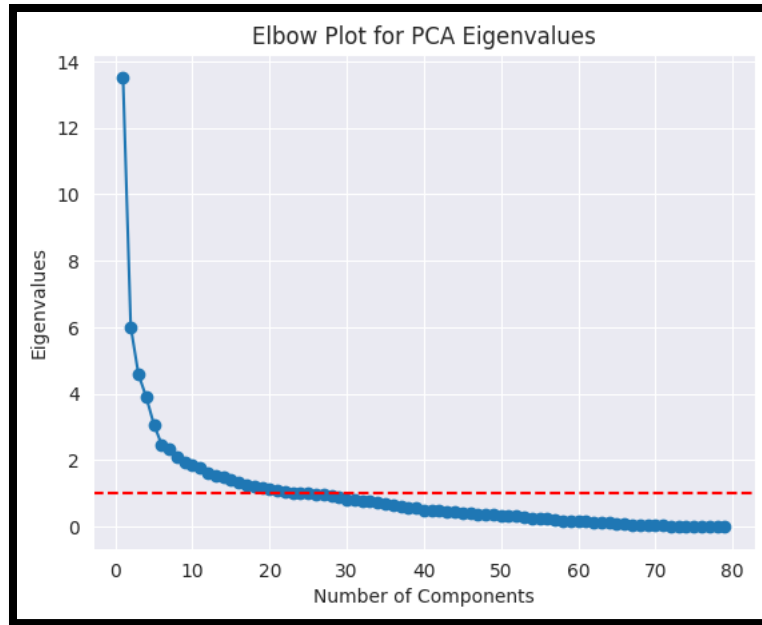
Classification Report:					
	precision	recall	f1-score	support	
0	0.95	0.98	0.97	8439	
1	0.98	0.94	0.96	8321	
accuracy			0.96	16760	
macro avg	0.97	0.96	0.96	16760	
weighted avg	0.96	0.96	0.96	16760	



The XGBoost model exhibits high performance with an accuracy of 0.96, achieving precision, recall, and F1-score around 0.96 for both survival and non-survival classes. The confusion matrix illustrates that the model correctly identifies 8305 survival cases and 7856 non-survival cases, with 134 survival cases misclassified as non-survival and 465 non-survival cases misclassified as survival. The ROC AUC score of 0.99 indicates excellent discrimination ability, showcasing the model's strong capability in distinguishing between survival and non-survival cases.

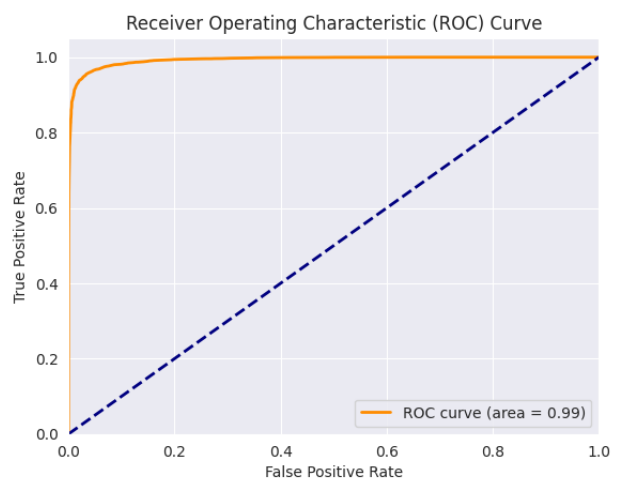
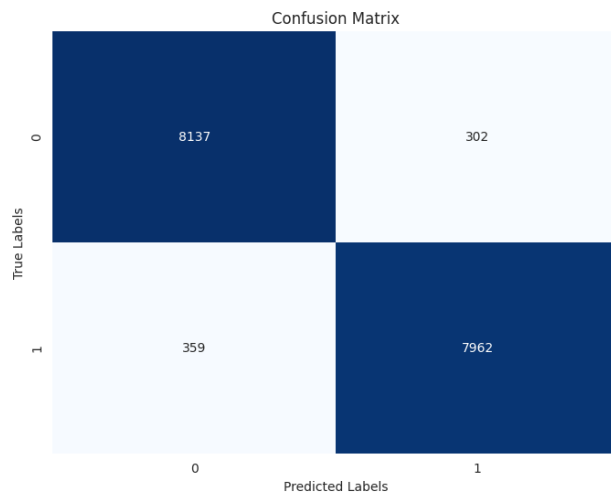
ML Models after PCA

In the third approach, we employed Principal Component Analysis (PCA) to address the high dimensionality of the dataset, which consisted of 85 features. Now drop down to 24 features.



Random Forest

Classification Report:					
	precision	recall	f1-score	support	
0	0.96	0.96	0.96	8439	
1	0.96	0.96	0.96	8321	
accuracy			0.96	16760	
macro avg	0.96	0.96	0.96	16760	
weighted avg	0.96	0.96	0.96	16760	

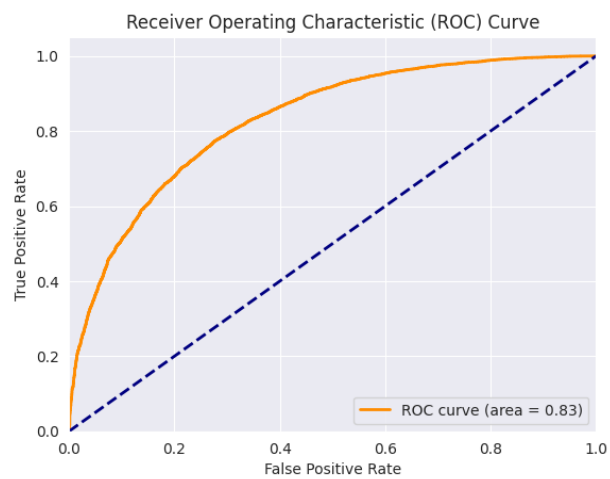
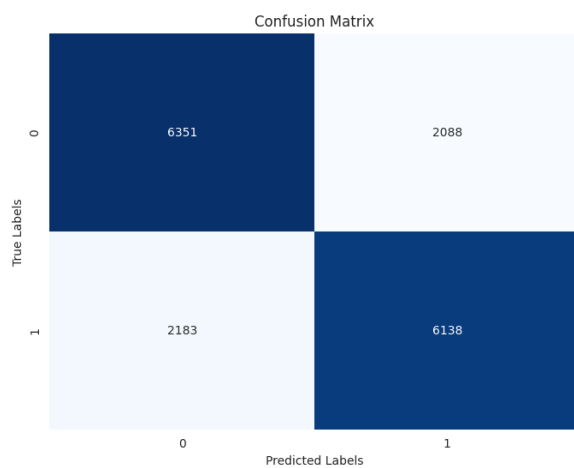


After PCA, Random Forest (RF) model achieved high performance with an accuracy of 96%. Both precision and recall for both survival and non-survival classes were balanced, resulting in a macro-average F1-score of 0.96. The confusion matrix indicates that the model correctly

classified a significant majority of instances, with a ROC AUC score of 0.99, indicating strong predictive capability.

Logistic Regression

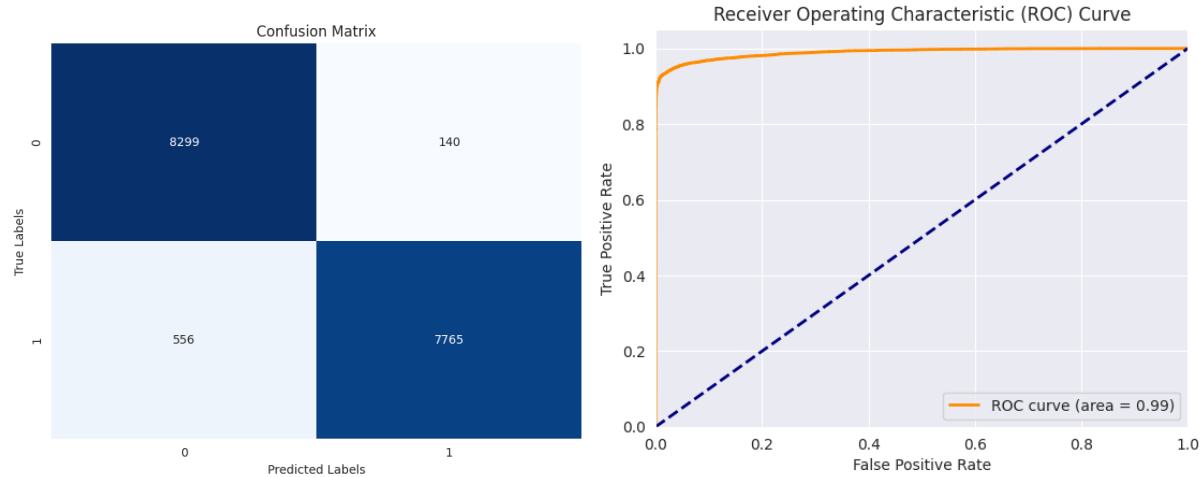
Classification Report:					
	precision	recall	f1-score	support	
0	0.74	0.75	0.75	8439	
1	0.75	0.74	0.74	8321	
accuracy			0.75	16760	
macro avg	0.75	0.75	0.75	16760	
weighted avg	0.75	0.75	0.75	16760	



In the Logistic Regression model, the classification performance was moderate, with an accuracy of 75%. The precision, recall, and F1-score for both survival and non-survival classes were approximately balanced, resulting in macro-average F1-score of 0.75. The confusion matrix indicates a relatively high number of false positives and false negatives, suggesting some misclassification. However, the model achieved a ROC AUC score of 0.83, indicating fair predictive ability.

XGBoost

Classification Report:					
	precision	recall	f1-score	support	
0	0.94	0.98	0.96	8439	
1	0.98	0.93	0.96	8321	
accuracy			0.96	16760	
macro avg	0.96	0.96	0.96	16760	
weighted avg	0.96	0.96	0.96	16760	



After applying Principal Component Analysis to reduce the dimensionality of the data and optimizing hyper parameters, the XGBoost model achieved high performance with an accuracy of 96%. The precision, recall, and F1-score for both survival and non-survival classes were excellent, resulting in a macro-average F1-score of 0.96. The confusion matrix indicates a small number of false positives and false negatives, suggesting minimal misclassification. Furthermore, the model achieved a ROC AUC score of 0.99, indicating outstanding predictive ability.

Results

		F1 Score	ROC AUC
Baseline Models	Random Forest	0.68	0.88
	Logistic Regression	0.66	0.86
	XGBoost	0.71	0.88
ML Model with SMOTE Data	Random Forest	0.96	0.99
	Logistic Regression	0.79	0.87
	XGBoost	0.96	0.99
ML Model after PCA Analysis	Random Forest	0.96	0.99
	Logistic Regression	0.75	0.83
	XGBoost	0.96	0.99

Conclusion

The project aimed to enhance patient survival prediction in intensive care units (ICUs) through the application of data mining techniques. Three different approaches were explored: baseline models, machine learning models with SMOTE data, and ML models after principal component analysis. The results revealed notable improvements in predictive performance across all models with the use of SMOTE data and PCA.

In the baseline models, Random Forest and XGBoost demonstrated the highest F1-scores of 0.68 and 0.71, respectively, with ROC AUC scores of 0.88 for both models. Logistic Regression performed slightly lower, with an F1-score of 0.66 and ROC AUC of 0.86.

After applying SMOTE to address class imbalance, substantial improvements were observed in all models. Random Forest achieved the highest F1-score of 0.96, accompanied by an impressive ROC AUC of 0.99. Logistic Regression showed improvement (less extent) with an F1-score of 0.79 and ROC AUC of 0.87. XGBoost maintained its high performance, with an F1-score of 0.96 and ROC AUC of 0.99.

Following PCA to reduce dimensionality, Random Forest and XGBoost models maintained their excellent performance, achieving F1-scores of 0.96 and ROC AUC of 0.99. However, Logistic Regression exhibited a decrease in performance, with an F1-score of 0.75 and ROC AUC of 0.83.

In conclusion, the project demonstrates the effectiveness of data mining and machine learning approaches in predicting patient survival in ICU settings. By addressing class imbalance and reducing dimensionality, significant improvements in predictive accuracy were achieved. These findings underscore the potential of advanced analytics techniques in assisting healthcare professionals in making informed decisions and improving patient outcomes in critical care environments.

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