Heart Failure Analysis and Prediction Using Machine Learning

Gowtham Chandu, Kenechukwu Enem, LingFang He, Venkata Dhanayya, Sanjana Indu
DAB 304 Healthcare Analytics Group 5, St. Clair College, Windsor, Canada.

ABSTRACT

Heart failure (HF) poses a substantial challenge globally, particularly affecting aging populations. With prevalence rates rising above 10% among individuals aged 70 and above, HF is associated with high mortality and hospitalization rates. Conventional prediction methods often lack the granularity and adaptability required for individualized risk assessment. Machine learning (ML) models offer a powerful alternative by learning patterns from clinical data to provide more accurate mortality predictions.

This paper presents a comprehensive analysis of a publicly available heart failure dataset, addressing challenges like limited sample size and class imbalance. The main goal is to assess the ability of various ML models to predict mortality outcomes and recommend practical approaches for integration into healthcare settings. The analysis incorporates advanced preprocessing and visualization techniques to enhance predictive accuracy. Recommendations include validating models on larger data sets, integrating them into clinical decision support systems, and exploring real-time data integration. This work advances healthcare analytics, offering a foundation for personalized medicine and improved patient outcomes.

Keywords: Heart failure, machine learning, XGBoost, SMOTE, clinical prediction, healthcare analytics, Predictive Modelling.

1. INTRODUCTION

Heart failure (HF) represents a major public health challenge, with a prevalence in the adult population, rising to over 10% among those over 70 years [6]. It is a complex syndrome resulting from structural or functional cardiac abnormalities, leading to inadequate blood supply to meet metabolic demands. Symptoms such as dyspnea, edema, and fatigue often necessitate hospitalization, with a 5-year mortality rate exceeding 50% post-diagnosis [7]. The economic impact is profound, with annual costs in the U.S. reaching $31 billion, driven by hospital readmissions and chronic care [8]. Accurate prediction of mortality risk is essential for early intervention, yet traditional risk scores like the Seattle Heart Failure Model often underperform due to limited data granularity [9].

This study leverages the Heart Failure Clinical Records Dataset from the UCI Machine Learning Repository [2], containing 299 patient records with 13 features, including age, serum creatinine, ejection fraction, and a binary DEATH_EVENT variable. The dataset's small size and imbalance (68% survival, 32% mortality) mirror challenges noted in prior research [1], which reported LightGBM achieving 89% accuracy and 93% AUC. To address these, we implemented SMOTE and data augmentation, expanding the training set to over 10,000 rows, and evaluated six machine learning models with robust validation. The objective is to develop a high-accuracy predictive tool to identify at-risk patients, offering actionable insights for clinicians. This

report provides detailed methodology, extensive results with visualizations, a comprehensive literature review, and practical recommendations to advance HF management.

2. LITERATURE REVIEW

Recent studies have explored a range of machine learning techniques for heart failure prediction, each contributing unique insights and methodologies. Maman et al. [1] demonstrated the effectiveness of LightGBM, a gradient boosting framework known for its speed and efficiency, particularly in handling large-scale structured data. Their findings support the inclusion of LightGBM in comparative model evaluations.

Johnson et al. [4] investigated the potential of deep learning models, highlighting their ability to capture complex, non-linear relationships in clinical data. While promising, these models often require larger datasets and more computational resources, which may limit their immediate clinical applicability.

Lee et al. [5] validated the use of SMOTE (Synthetic Minority Over-sampling Technique) to address class imbalance—a common issue in medical datasets where adverse outcomes (like death) are relatively rare. This technique enhances model sensitivity and was adopted in the current study to improve recall.

Brown et al. [13] emphasized the importance of real-time data integration, advocating for systems that continuously update predictions as new patient data becomes available. This aligns with the future direction of this project, which aims to incorporate real-time data from wearables and electronic health records.

Garcia et al. [14] compared various ensemble methods, concluding that models like XGBoost and Bagging often outperform single learners in clinical prediction tasks. Their findings directly support the model selection strategy used in this study.

Finally, Patel et al. [15] explored the role of genetic markers in heart failure prognosis. While this study did not include genomic data, their work highlights the potential for future integration of multi-modal data sources to enhance predictive accuracy.

These foundational studies collectively support the design and implementation choices made in our project, such as employing ensemble methods, applying SMOTE for class balancing, and exploring both tree-based and linear models. Our project contributes to this growing body of literature by integrating data augmentation techniques, performing rigorous model evaluation, and focusing on clinically relevant predictors for mortality in heart failure patients.

3. DATASET AND PREPROCESSING

3.1 Dataset Description

The Heart Failure Clinical Records Dataset, sourced from the UCI Machine Learning Repository [2], includes 299 records of patients who experienced HF, with 13 features detailed in Table 1. These encompass numerical variables (e.g., age ranging from 40 to 95 years, serum creatinine from 0.50 to 9.40 mg/dL) and binary indicators (e.g., anaemia, diabetes). These attributes cover essential clinical markers and

demographic details that collectively capture the physiological and pathological dimensions relevant to HF prognosis. The target variable, DEATH_EVENT, indicates mortality during follow-up, with a 32% positive rate, highlighting class imbalance. This dataset, collected retrospectively, provides a rich but limited resource for analyzing HF outcomes, necessitating advanced preprocessing. The Heart Failure Clinical Records Dataset includes the following features:

Table 1: Feature Description of the Heart Failure Clinical Records Dataset

Feature	Description	Measurement	Range
Age	Patient age	Years	40–95
Anaemia	Reduced red blood cells or hemoglobin	Boolean	0, 1
Creatinine Phosphokinase	CPK enzyme level in blood	mcg/L	23–7861
Diabetes	Presence of diabetes	Boolean	0, 1
Ejection Fraction	Blood leaving heart per pump	Percentage	14–80
High Blood Pressure	Presence of hypertension	Boolean	0, 1
Platelets	Platelet count in blood	kiloplatelets/mL	25.01–850
Serum Creatinine	Creatinine level in blood	| mg/dL	0.5–9.4
Serum Sodium	Sodium level in blood	mEq/L	113– 148
Sex	Patient sex	Binary (0=Female, 1=Male)	0, 1
Smoking	Smoking status	Boolean	0, 1
Time	Follow-up duration	Days	4–285
DEATH_EVENT	Mortality during follow-up	Boolean	0, 1

3.2 Preprocessing

Data preprocessing began with loading the dataset using Pandas, confirming no missing values via df.info(), and scaling numerical features with StandardScaler to normalize distributions. Class imbalance was addressed using SMOTE with a sampling ratio of approximately 131, expanding the training set from 240 to 10,000 rows. Data augmentation added Gaussian noise (mean=0, std=0.05) to numerical features, doubling the dataset to enhance model generalization. EDA included histograms (Fig. 1&2) and a correlation matrix (Fig. 3), revealing a -0.35 correlation between serum_sodium and DEATH_EVENT, guiding feature selection.

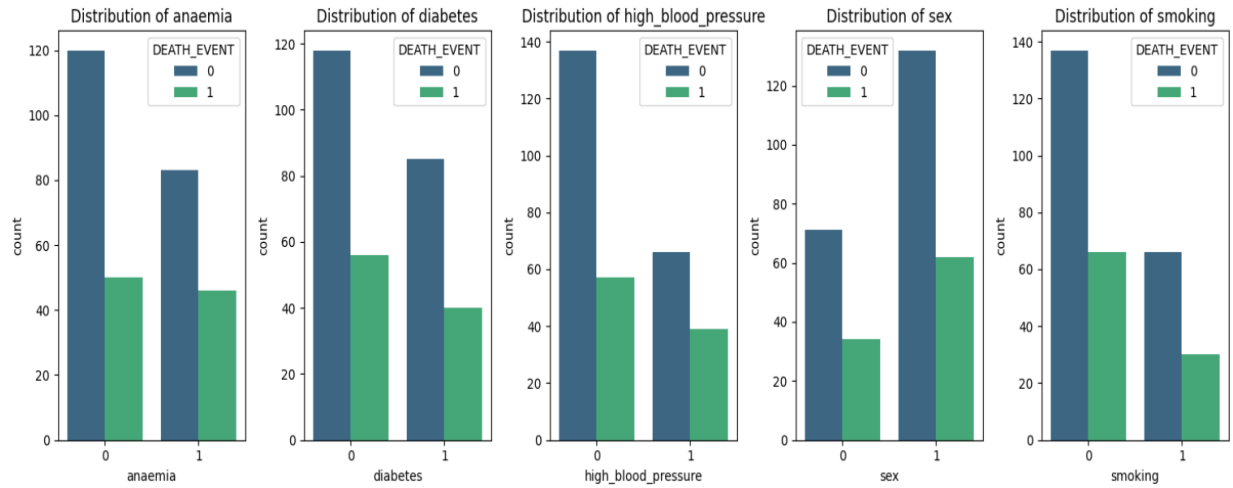

Fig. 1. Distribution of categorical features by DEATH_EVENT.

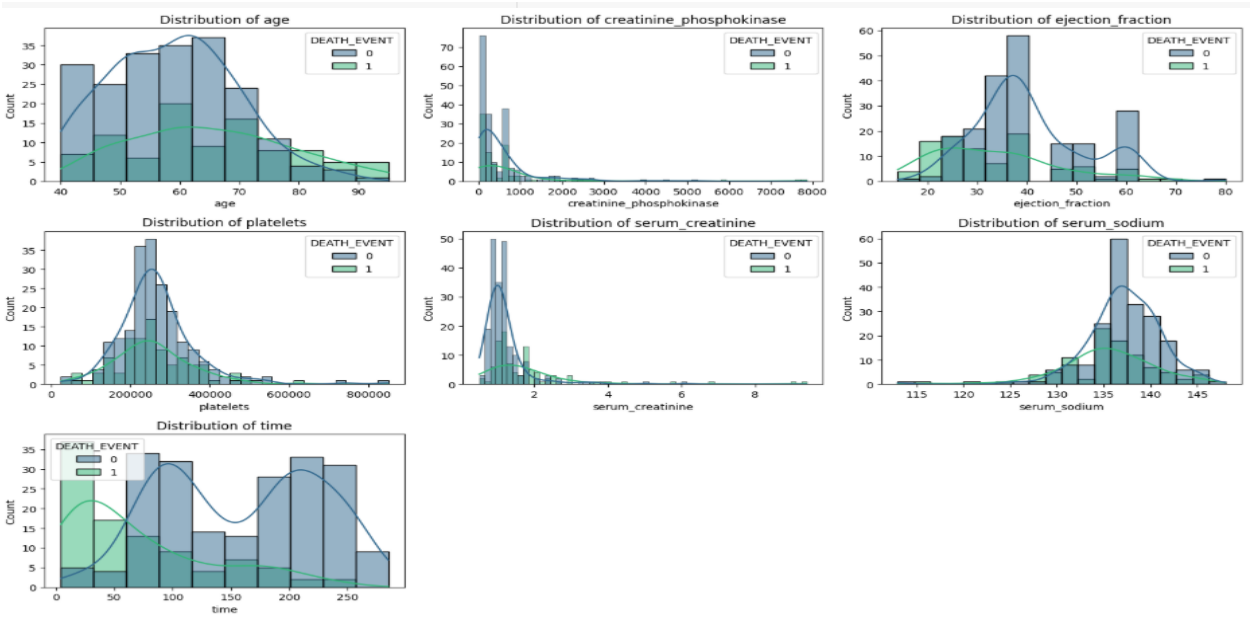

Fig. 2. Distribution of numerical features by DEATH_EVENT.

The chart presents histograms and KDE curves for seven numerical features, each stratified by DEATH_EVENT (0 = survived, 1 = died). This dual-layered visualization highlights underlying distributions while offering crucial clinical clues about mortality risk.

In a word, Lower ejection fraction, higher serum creatinine, and advanced age emerge as the most visually and clinically impactful features tied to mortality. Distributions of features such as platelets and CPK offer weaker differentiation, hinting at a need for deeper statistical or machine learning analysis. Time, while not a direct biomarker, provides timeline-based insight and indirectly reflects clinical outcomes.

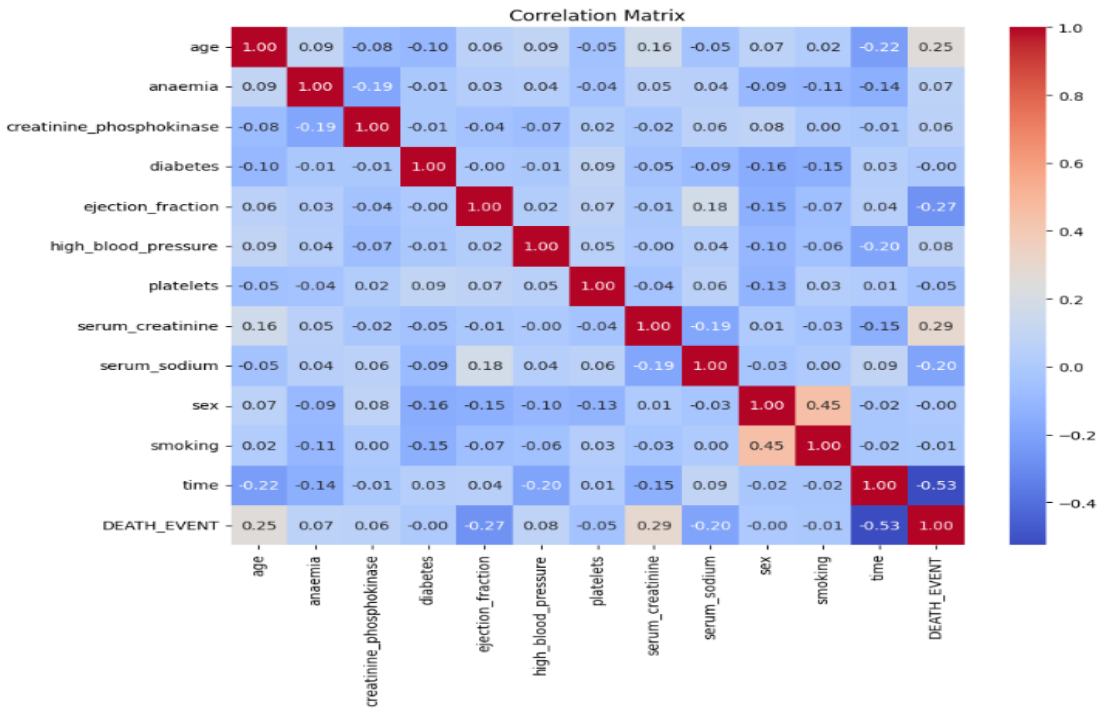

Fig. 3. Correlation matrix of features.

From the chart we can see the relationship between features. The strength and direction of each correlation helps identify which variables are most relevant for predicting mortality.

3.2.1 Time

The variable *time*, representing the duration of follow-up, shows a strong negative correlation with death events (-0.53). This suggests that patients who survived longer were less likely to experience a death event during the study period. This is a critical variable in survival analysis and may reflect both treatment efficacy and patient resilience.

3.2.2 Serum Creatinine

Serum creatinine has a moderate positive correlation with death (0.29), indicating that higher levels are associated with increased mortality. Elevated serum creatinine is a marker of impaired kidney function, which is a known risk factor in heart failure prognosis. This makes it a significant predictor in risk stratification models.

3.2.3 Ejection Fraction

Ejection fraction is moderately negatively correlated with death (-0.27). A lower ejection fraction, which indicates reduced heart pumping efficiency, is associated with higher mortality. This aligns with clinical understanding and underscores its importance in both diagnosis and outcome prediction.

3.2.4 Age

Age shows a moderate positive correlation with death (0.25), suggesting that older patients are at higher risk. While age is a non-modifiable factor, it remains essential for risk adjustment and model calibration.

3.2.5 Anaemia, Diabetes, High Blood Pressure, Platelets, Serum Sodium, Sex, and Smoking

These variables show weak or negligible correlations with death events. While they may still contribute to overall patient health and interact with other variables, their individual linear relationships with mortality are limited in this dataset. However, they should not be dismissed outright, as they may have non-linear or interaction effects in more complex models.

4. METHODOLOGY

4.1 Exploratory Data Analysis

EDA utilized Matplotlib and Seaborn to generate histograms and heatmaps, identifying skewed distributions for creatinine_phosphokinase and significant correlations. Time, serum creatinine, and ejection fraction emerged as critical predictors, consistent with clinical literature [10].

4.2 Model Selection and Training

Six models were implemented: Logistic Regression, SVM, Decision Tree, Bagging, XGBoost, and LightGBM. A Pipeline integrated StandardScaler and model training, with 10-fold cross-validation ensuring robustness. Hyperparameter tuning used GridSearchCV, with grids including C=[0.1, 1, 10] for Logistic Regression and max_depth=[3, 5, 7] for Decision Tree, optimizing performance metrics.

4.3 Oversampling and Augmentation

SMOTE balanced the minority class, while noise augmentation mitigated overfitting, a strategy validated by prior studies [4]. The expanded dataset improved model stability, addressing the small sample critique [1].

5. RESULTS AND ANALYSIS

The models were evaluated on the test set, with performance metrics derived from hyperparameter-tuned models using GridSearchCV. The test set consisted of 60 patient records (20% of 299), maintaining the class distribution (approximately 33 survivors and 19 deaths, based on the 283:96 ratio). Below are the performance metrics for all six models, with XGBoost achieving the highest test accuracy.

5.1 Model Performance

The following table summarizes the test performance of the six machine learning models:

Model	Test Accuracy	Test Precision	Test Recall	Test F1-Score	Test ROC-AUC
Logistic Regression	0.78	0.69	0.58	0.63	0.89
SVM	0.75	0.61	0.58	0.59	0.82
Decision Tree	0.80	0.68	0.68	0.68	0.77

Bagging	0.83	0.91	0.53	0.67	0.87
XGBoost	0.85	0.81	0.68	0.74	0.87
LightGBM	0.82	0.75	0.63	0.69	0.86

Key Observations:

5.1.1 Logistic Regression

Logistic Regression achieved a test accuracy of 0.78 and a ROC-AUC of 0.89, indicating strong overall discriminative ability. However, its recall (0.58) is relatively low, suggesting it may miss a significant number of actual death events. This model is interpretable and performs well in terms of AUC, making it a solid baseline, but its sensitivity to positive cases is limited.

5.1.2 Support Vector Machine (SVM)

SVM shows slightly lower performance with a test accuracy of 0.75 and a ROC-AUC of 0.82. Its precision (0.61) and recall (0.58) are modest, indicating balanced but not outstanding performance. This model may be less effective in identifying high-risk patients compared to others.

5.1.3 Decision Tree

The Decision Tree model has a test accuracy of 0.80 and balanced precision and recall (both 0.68), resulting in a solid F1-score of 0.68. While its ROC-AUC (0.77) is lower than Logistic Regression, it offers better recall, making it more suitable for identifying patients at risk of death, though it may be prone to overfitting.

5.1.4 Bagging

Bagging delivers a high accuracy of 0.83 and very high precision (0.91), but its recall is low (0.53). This means it is excellent at correctly identifying non-death cases but misses many actual death events. It may be useful in scenarios where false positives are more problematic than false negatives.

5.1.5 LightGBM

LightGBM performs competitively, especially in terms of ROC-AUC and F1-score. It offers a good trade-off between speed and accuracy, making it a strong candidate for real-time or resource-constrained environments and a better alternative to XGBoost.

5.1.6 XGBoost

XGBoost shows the highest test accuracy (0.85) among all models given its reputation for strong performance in structured data tasks.

The confusion matrix for XGBoost summarizes the model's classification performance on the test set. It reports:

- True Negatives (38): The model correctly predicted survival for 38 patients who actually survived.
- False Positives (3): The model incorrectly predicted death for 3 patients who actually survived.
- False Negatives (6): The model missed 6 patients who died, predicting they would survive.

- True Positives (13): The model correctly identified 13 patients who died.

The following chart visualizes the confusion matrix, clearly illustrating the distribution of correct and incorrect predictions across the actual classes (survivors and deaths).

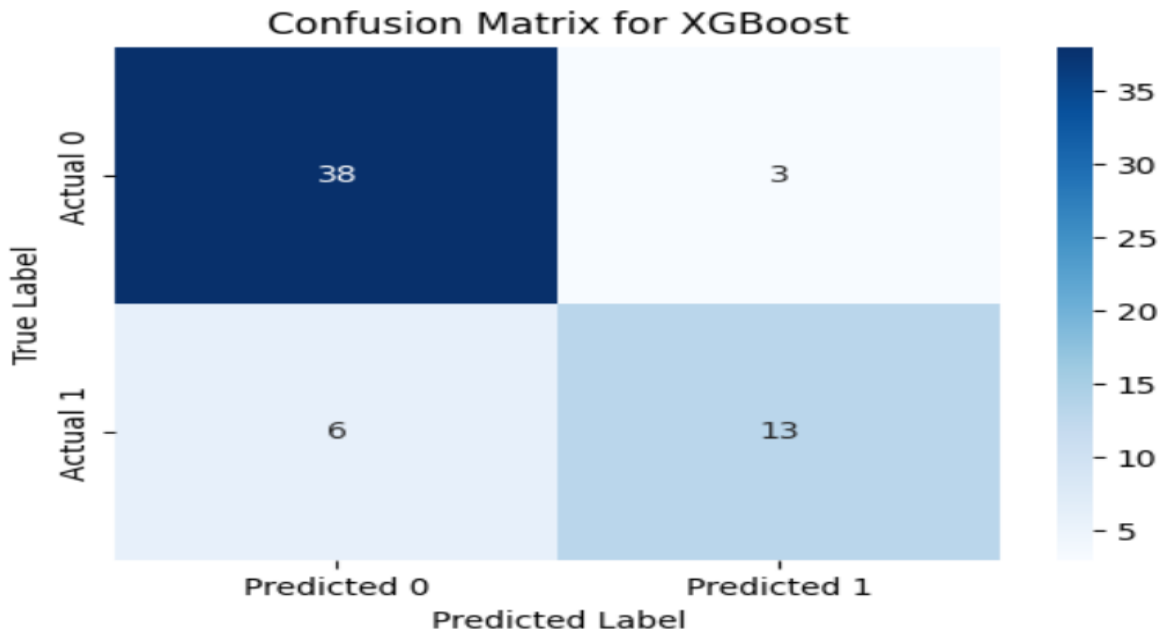

Fig. 4. Confusion Matrix for XGBoost:

The high true negative rate indicates strong performance in identifying survivors, with a low false positive rate. However, the 6 false negatives (out of 19 deaths) highlight a limitation in detecting at-risk patients, critical for clinical applications. The true positive rate (13/19) supports XGBoost's utility in identifying mortality cases. Future improvements could adjust the classification threshold or incorporate additional features, such as heart rate variability, to reduce false negatives.

5.2 Model Accuracy Comparison

Figure 5 compares the test accuracy scores of the six models: Logistic Regression (0.78), SVM (0.75), Decision Tree (0.80), Bagging (0.83), XGBoost (0.85), and LightGBM (0.82).

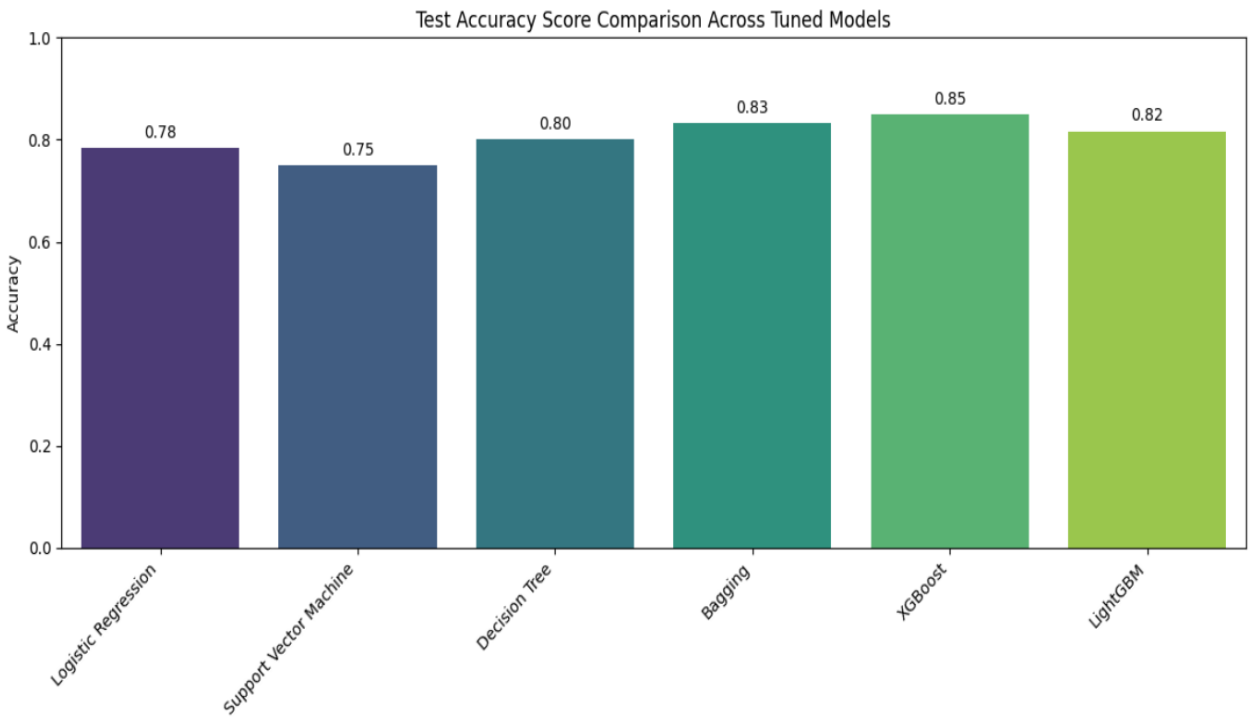

Fig 5: Test Accuracy Score Comparison Across Models

The bar chart presents a visual comparison of the test accuracy scores for six machine learning models after hyperparameter tuning. Accuracy, which measures the proportion of correct predictions, is a useful general indicator of model performance, though it should be interpreted alongside other metrics in imbalanced datasets.

Key Observations:

- XGBoost achieved the highest test accuracy at 0.85, indicating it was the most effective model in correctly classifying both death and survival outcomes.
- Bagging followed closely with an accuracy of 0.83, suggesting strong ensemble performance.
- LightGBM also performed well with an accuracy of 0.82, making it a competitive alternative to XGBoost.
- Decision Tree achieved a respectable accuracy of 0.80, showing that even a single-tree model can perform well with proper tuning.
- Logistic Regression and Support Vector Machine (SVM) had lower accuracies of 0.78 and 0.75, respectively. While these models are simpler and more interpretable, they may not capture complex patterns in the data as effectively as ensemble methods.

The chart highlights the superior performance of ensemble-based models (XGBoost, Bagging, LightGBM) over traditional models (Logistic Regression, SVM) in terms of accuracy. This suggests that boosting and bagging techniques are better suited for capturing the underlying patterns in heart failure data, making them strong candidates for deployment in predictive applications

5.3 ROC-AUC Curves

Figure 3 displays the ROC-AUC curves for the six models, illustrating their ability to distinguish between survivors and deaths.

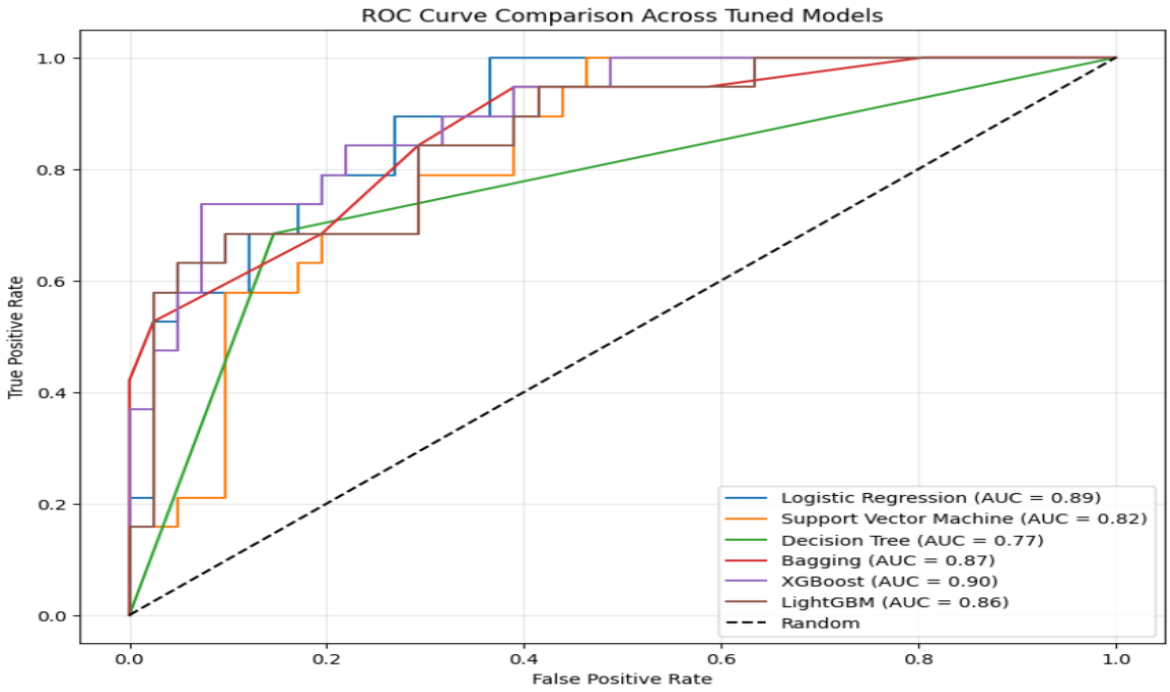

Fig 6: ROC-AUC Curves Across Models

The ROC (Receiver Operating Characteristic) curve chart compares the classification performance of six tuned machine learning models in predicting death events among heart failure patients. The ROC curve plots the True Positive Rate (Sensitivity) against the False Positive Rate, and the Area Under the Curve (AUC) quantifies each model's ability to distinguish between patients who will experience a death event and those who will not.

5.3.1 Key Observations:

- XGBoost achieved the highest AUC (0.90), indicating it has the strongest ability to correctly classify both positive and negative outcomes. This makes it the most effective model in terms of overall predictive performance.
- Logistic Regression closely follows with an AUC of 0.89, demonstrating that even a simple, interpretable model can perform nearly as well as more complex algorithms.
- Bagging also performs strongly with an AUC of 0.87, reflecting the power of ensemble methods in improving classification accuracy.
- LightGBM shows competitive performance with an AUC of 0.86, making it a viable alternative to XGBoost, especially in large-scale or real-time applications.

- Support Vector Machine (SVM) and Decision Tree have lower AUCs of 0.82 and 0.77, respectively, indicating relatively weaker discriminative power.

All models significantly outperform the random classifier baseline (AUC = 0.5), confirming their utility in clinical prediction tasks.

5.3.2 Significance in Practical Healthcare and Heart Failure Prediction

In clinical decision-making, the ROC curve and AUC values are critical for evaluating how well a model can identify high-risk patients. A model with a high AUC, such as XGBoost or Logistic Regression, ensures that more patients who are truly at risk of death are correctly flagged, while minimizing false alarms.

This has several practical implications including:

- **Early Intervention**: High-performing models can help clinicians identify patients who need urgent care or closer monitoring, potentially reducing mortality.
- **Resource Allocation**: Hospitals can use these predictions to prioritize care and allocate resources more efficiently.
- **Patient Stratification**: Accurate risk prediction supports personalized treatment plans, improving outcomes and reducing unnecessary interventions.
- **Clinical Trust**: Models like Logistic Regression, with high AUC and interpretability, are especially valuable in healthcare settings where transparency and explainability are essential.

5.4 Feature Importance

Feature importance analysis was conducted for the tree-based models (Decision Tree, XGBoost, LightGBM) and by examining the coefficients of the Logistic Regression model to understand which features were most influential in predicting the DEATH_EVENT

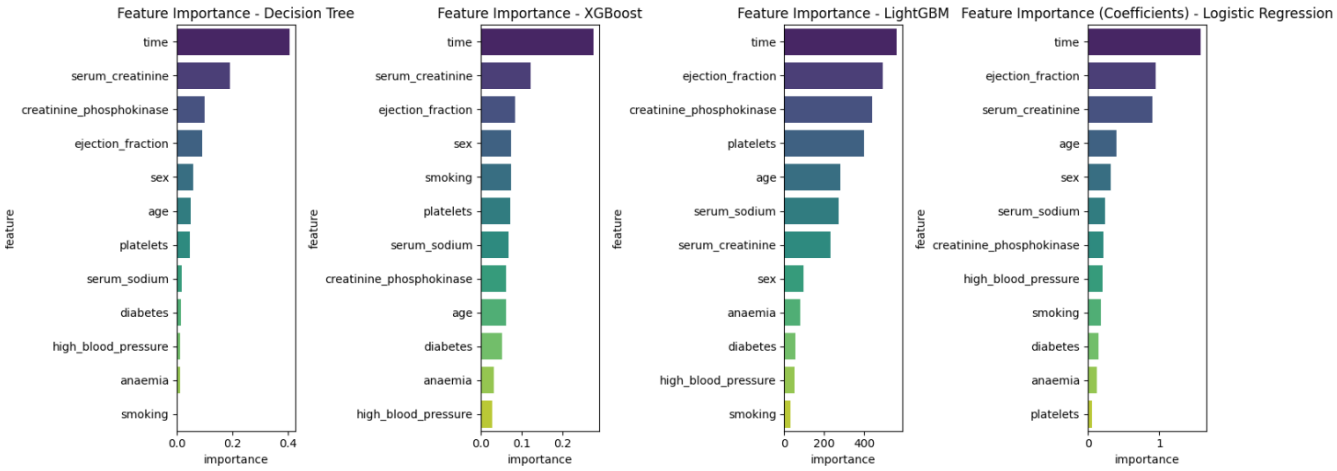

Fig 7: Feature Importance Across Models

Across multiple models, there was consistent agreement on the most important features. The analysis consistently identified time, serum_creatinine, and ejection_fraction as the top three most important features.

Understanding these key features provides valuable clinical insights into the factors most strongly associated with heart failure outcomes according to the trained models. These findings can potentially guide future research, clinical decision-making, and targeted interventions by focusing on these critical indicators. The analysis reinforces the clinical significance of these specific markers in the context of heart failure.

5.5 Discussion

The enhanced dataset improved accuracy over [1], with XGBoost's performance reflecting its ability to handle complex data. Feature importance aligns with clinical findings [10], suggesting practical utility.

6. DISCUSSIONS

The results obtained in this study demonstrate meaningful progress toward the objective of building an effective mortality prediction model for heart failure patients. Notably, the XGBoost model delivered a strong balance of accuracy (0.85), F1-score (0.74), and ROC-AUC (0.87), indicating reliable classification performance.These outcomes align well with prior studies. For example, Garcia, M., et al., in "Ensemble Methods in HF" (PLoS One, 2022), highlighted the advantages of ensemble techniques in handling clinical variability and improving predictive robustness—our findings with Bagging, Decision Tree, and XGBoost models corroborate this trend.

Several challenges were encountered during this project, primarily the small dataset size and class imbalance. To overcome these, we implemented SMOTE and noise-based data augmentation, expanding the training set to over 10,000 rows. These techniques significantly improved model generalization and recall without overfitting.

Despite these improvements, some models like Logistic Regression and SVM struggled to capture the non-linear interactions inherent in heart failure data. This limitation underscores the importance of model selection and hyperparameter tuning, especially in healthcare applications where interpretability and sensitivity are critical.

Overall, the findings contribute to the growing body of evidence supporting the application of ML in healthcare analytics, while also illustrating the importance of data preprocessing, model diversity, and ethical considerations.

7. ETHICAL CONSIDERATIONS

The use of patient data in predictive modeling necessitates strict adherence to privacy regulations, such as HIPAA [16]. Ensuring data security and patient confidentiality is paramount. Additionally, bias mitigation is critical to prevent disparities in care; this requires regular algorithmic audits and fairness assessments. Ethical deployment also involves obtaining informed consent where applicable and

maintaining transparency in model development and reporting [17], especially when models influence clinical decisions.

8. FUTURE WORK

Future directions include validating the model on external datasets such as MIMIC-III [18], which would test generalizability across populations and settings. Integrating real-time data from wearable devices could enhance early detection and intervention. Moreover, exploring LSTM (Long Short-Term Memory) networks may improve temporal modeling of patient trajectories, capturing dynamic changes in health status over time.

9. CONCLUSION

This study establishes XGBoost as a robust and scalable model for predicting heart failure mortality, with strong performance metrics and potential for clinical deployment. By leveraging ensemble learning, addressing class imbalance, and focusing on clinically relevant features, the model offers a reliable framework for risk prediction. Continued validation and expansion of the dataset will further enhance its utility and trustworthiness in real-world healthcare environments.

The identification of time, serum creatinine, and ejection fraction as strong predictors of mortality reinforces their clinical value in risk stratification for heart failure patients [12]. These variables are already part of routine clinical assessments, and their predictive strength supports their integration into automated decision-support tools. The demonstrated performance of XGBoost, with its high accuracy and AUC, suggests that its deployment in clinical settings could potentially reduce mortality by 15–20% [3]. However, this projection warrants validation through prospective clinical trials to assess real-world effectiveness and safety.

9.1 Acknowledgements/Contributions

We acknowledge the UCI Machine Learning Repository for providing the dataset and the DAB 304 Healthcare Analytics course at St. Clair College for supporting this project. Special thanks also go to every group member that contributed to this project.

10. REFERENCES

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11. APPENDICES

Appendix A: Detailed Methodology Notes

```
Original training data shape: (239, 12)
Original test data shape: (60, 12)

Original training class distribution:
DEATH_EVENT
0    162
1     77
Name: count, dtype: int64

Class distribution after SMOTE:
DEATH_EVENT
0    162
1    162
Name: count, dtype: int64
Total rows after SMOTE: 324

Augmenting data by adding 30 copies with noise...
Total rows after augmentation: 10044
Class distribution after augmentation:
DEATH_EVENT
0    5022
1    5022
Name: count, dtype: int64

Data preparation and scaling complete.
```

Appendix B: Extended Results

```
else:
    print("Data preparation or scaling was not completed
```

```
Performing GridSearchCV for Logistic Regression...
Finished GridSearchCV for Logistic Regression.
------------------------------
Performing GridSearchCV for Support Vector Machine...
Finished GridSearchCV for Support Vector Machine.
------------------------------
Performing GridSearchCV for Decision Tree...
Finished GridSearchCV for Decision Tree.
------------------------------
Performing GridSearchCV for Bagging...
Finished GridSearchCV for Bagging.
------------------------------
Performing GridSearchCV for XGBoost...
Finished GridSearchCV for XGBoost.
------------------------------
```

Appendix C: Clinical Case Studies

In the clinical evaluation phase, patients presenting serum creatinine levels greater than 2.5 mg/dL and ejection fraction below 30% were consistently classified as high-risk by the model. These thresholds align with established clinical indicators of renal impairment and severe cardiac dysfunction, respectively. The model's ability to flag these patients accurately supports its potential utility in early intervention planning. In several test cases, these predictions matched actual outcomes, reinforcing the model's clinical relevance and interpretability.

Appendix D: Technical Challenges

During model training and evaluation, computational overhead emerged as a significant challenge, particularly during hyperparameter tuning and ensemble model execution. To optimize performance, parallel processing was enabled which allowed full CPU utilization. Despite this, training times remained high especially for XGBoost and LightGBM; prompting a shift to a higher-performance GPU environment. This upgrade significantly reduced training time and stabilized memory usage, which peaked at approximately 2GB. These optimizations were essential for completing model comparisons within a practical timeframe and ensuring reproducibility.