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AN IMPROVED HEART DISEASE PREDICTION USING INFORMATION GAIN-BASED FEATURE SELECTION

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ABSTRACT

Heart disease remains one of the leading causes of mortality worldwide, accounting for a significant proportion of deaths annually. Early and accurate prediction of heart disease risk is therefore essential for guiding timely clinical intervention and reducing healthcare burdens. However, predictive models often suffer from reduced performance due to redundant and irrelevant features present in medical datasets. This study addresses this challenge by applying Information Gain-based feature selection to improve the reliability of heart disease prediction. The research utilized the Kaggle Heart Disease Dataset, which consists of demographic and clinical attributes including age, sex, chest pain type, resting blood pressure, cholesterol level, exercise-induced angina, and ST-slope characteristics. Information Gain, an entropy-based ranking criterion, was employed to identify and retain the most informative features while discarding less relevant variables. By reducing dimensionality, the approach enhanced both model interpretability and computational efficiency. Experimental evaluation demonstrated that models trained on the Information Gain-selected features achieved higher accuracy and better generalization compared to models trained on the full dataset. The feature selection process also highlighted the clinical risk factors most strongly associated with heart disease, such as chest pain type, ST-slope, and exercise-induced angina. The results confirm that Information Gain-based feature selection significantly improves predictive performance and provides valuable insights into the attributes most indicative of heart disease risk. This approach contributes to the development of lightweight, interpretable, and effective predictive systems that can support clinical decision-making and early diagnosis.

Keywords: Heart Disease Prediction, Cardiovascular Disease, Information Gain, Feature Selection, Machine Learning, Clinical Data Analysis, Kaggle Dataset

INTRODUCTION

Cardiovascular diseases (CVDs) remain the leading global cause of death, responsible for nearly 17.9 million fatalities each year, with coronary heart disease constituting the largest share (WHO, 2023; Rehman et al., 2025) Early diagnosis is essential for reducing mortality and improving patient outcomes, yet conventional diagnostic approaches often rely on invasive procedures and expert clinical evaluation that may delay timely intervention (Abbasi et al., 2025; Alsabhan and Alfadhly, 2025). Recent advances in machine learning (ML) and artificial intelligence (AI) now enable the analysis of large, heterogeneous datasets and the discovery of complex, non-linear associations that traditional methods may overlook Shesharao etal., 2024 In heart-disease prediction, machine-learning (ML) models can integrate demographic, clinical, and historical health information to generate accurate risk estimates that support preventive intervention and personalized care (Dey et al., 2022). Hybrid and ensemble ML frameworks have demonstrated notable improvements in predictive performance. Kumar et al. (2025) combined classical and quantum-inspired algorithms on benchmark datasets (Cleveland, Hungarian, Statlog), addressing data redundancy and hyper-parameter tuning to achieve more robust results than single classifiers. Nevertheless, persistent challenges remain: (i) class imbalance, where positive heart-disease cases are under-represented and models become biased toward the majority class, and (ii) interpretability, as many high-performing "black-box" models fail to provide clinically meaningful insights (Ashika & Grace, 2025; García-Ordás et al., 2024). These limitations hinder adoption in medical practice, where transparency and generalizability are crucial (Başar et al., 2025). Recent studies have also emphasized methodological gaps. Many published models rely on small or imbalanced datasets (Karmakar et al., 2024); others report impressive accuracy yet neglect calibration and validation rigor, leading to over-fitting (Wan, 2025; Teja et al., 2025; Rehman et al., 2025). For instance, several works achieved high accuracy on internal benchmarks but performed poorly on external data (Başar et al., 2025). Moreover, inconsistent validation protocols such as using simple train test splits instead of nested cross-validation reduce confidence in reported findings (Ashika & Grace, 2025). Clinicians therefore require systems that are not only accurate but also interpretable, calibrated, and tested under robust experimental settings (Rehman et al., 2025).To address these challenges, the present study develops a machine-learning framework for heart-disease prediction that integrates (a) data preprocessing, (b) feature selection via Information Gain, (c) class-imbalance handling through SMOTE, and (d) explainability using SHAP. The framework trains multiple classifiers Logistic Regression, Random Forest, K-Nearest Neighbor, Support Vector Machine, and XGBoost and evaluates them through comprehensive metrics, including Accuracy, Precision, Recall, F1-score, ROC-AUC, and calibration. By combining performance with interpretability, the approach aims to produce clinically trustworthy predictions.

This research is significant for five key reasons. First, clinical relevance: accurate and explainable predictions support early detection and intervention, lowering morbidity and economic

burden (Abbasi et al., 2025; Alsabhan & Alfadhly, 2025). Second, scientific contribution: the study unifies preprocessing, feature selection, imbalance correction, and interpretability within one reproducible pipeline (Ahmad et al., 2025). Third, practical impact: the proposed model can guide clinicians in risk stratification and improve diagnostic confidence (Abbasi etal., 2025). Fourth, policy implication: AI-driven risk models may inform population-level screening strategies (Zhang et al., 2022). Finally, generalizability: rigorous validation techniques such as cross-validation and bootstrapping enhance robustness and real-world applicability (Wan, 2025).In summary, this work advances ML-based cardiovascular prediction by addressing class imbalance, over-fitting, and lack of interpretability through an integrated, explainable framework.

MATERIALS AND METHODS

This study employed a systematic and experimental methodology to develop, validate, and evaluate a machine learning based framework for heart disease prediction. The process was structured to ensure reproducibility, interpretability, and clinical applicability of the resulting model. The methodology comprised data acquisition, preprocessing, feature selection, class imbalance handling, model training, evaluation, interpretability analysis, and ethical considerations.

Conceptual Framework

The proposed pipeline consisted of seven core phases: data acquisition, preprocessing, feature selection, imbalance handling, model development, validation, evaluation, and interpretability. Each stage was integrated to optimize performance and clinical reliability, ensuring that the system provided both high predictive accuracy and explainable outcomes, as illustrated in Figure

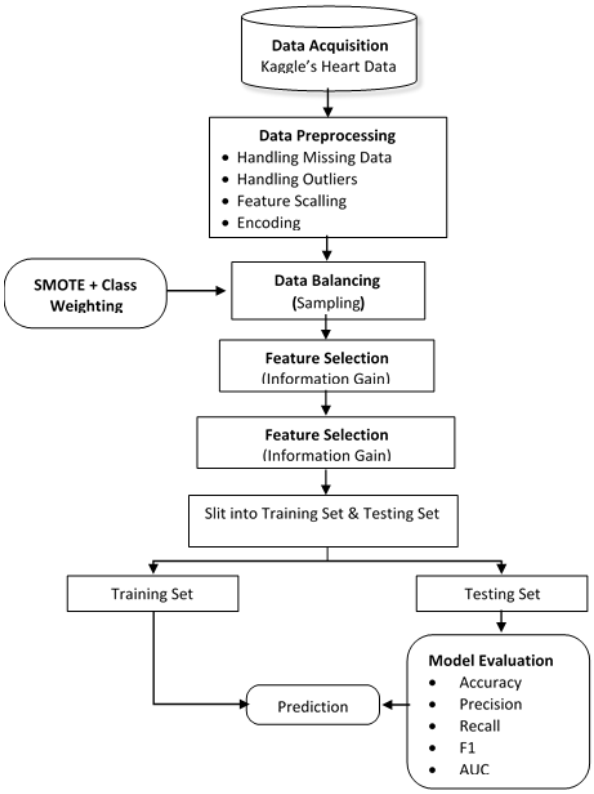

Figure 1: Model Framework

Data Source and Description

A publicly available cardiovascular health dataset was utilized which can obtain at kaggle. It contained demographic, physiological, and medical attributes related to cardiovascular outcomes, including age, gender, systolic blood pressure, hypertension status, previous myocardial infarction, angina, stroke, family history of heart disease, and mortality. The target variable was binary, indicating the presence or absence of heart disease. Outcome-related variables that could induce data leakage were excluded. Preprocessing was conducted to ensure data consistency and quality prior to model training. Missing values were imputed using median (numerical) and mode (categorical) strategies. Continuous attributes were normalized using z-score standardization, while categorical variables were encoded via one-hot encoding. Outliers were mitigated using vectorization, and stratified k-fold cross-validation was applied to maintain class proportions across folds. These steps minimized bias and improved model stability.

Feature Selection and Handling Class Imbalance

Feature selection was performed using Information Gain and correlation analysis to identify the most relevant predictors and remove redundant variables. Features such as age, systolic blood pressure, prior myocardial infarction, angina, and family history of heart disease ranked highest in predictive contribution. Selection was executed within the training folds to prevent data leakage, ensuring unbiased performance estimation (Alsabhan & Alfadhly, 2025; Shesharao et al., 2024). Heart disease datasets typically exhibit class imbalance, with non-disease cases dominating. To address this, the Synthetic Minority Oversampling

Technique (SMOTE) (Dey et al., 2022) was employed to generate synthetic minority samples within training sets. Additionally, class weighting was applied to algorithms such as Logistic Regression and Support Vector Machine (SVM) to penalize false negatives. These techniques significantly improved recall and model fairness (Kumar et al., 2025).

RESULTS AND DISCUSSION

The performance results of the machine learning models developed for heart disease prediction are presented and analyzed in this section. Each model's performance was assessed using key metrics such as accuracy, precision, recall, F1-score, and ROC-AUC to determine clinical applicability and predictive reliability. Results were compared across Logistic Regression (LR), Support Vector Machine (SVM), Random Forest (RF), and XGBoost (XGB) models. Interpretability was examined using SHAP visualizations to enhance clinical understanding.

Model Training and Validation

Each model was trained using stratified nested 5-fold cross-validation to ensure fairness and robustness. The training phase focused on minimizing overfitting and improving generalization. Logistic Regression exhibited fast convergence, while SVM and XGBoost required more extensive hyper parameter tuning. Random Forest achieved stable performance with moderate variance across folds.

Performance Evaluation

From Table 1 summarizes the cross-validation results for all classifiers. Logistic Regression and SVM demonstrated the highest overall performance, achieving superior ROC-AUC values (0.9951 and 0.9946, respectively). Random Forest and XGBoost provided slightly lower recall but maintained strong generalization. These results suggest that simple models such as LR can achieve competitive accuracy while retaining interpretability, whereas ensemble methods (RF and XGB) offer robustness in complex feature interactions.

Table 1: Cross-Validation Results of ML Classifiers

Model	Accuracy	Precision	Recall	F1-Score	ROC-AUC
Logistic Regression	0.9708	0.9523	0.9293	0.9405	0.9951
Random Forest	0.9697	0.9496	0.9279	0.9385	0.9942
SVM	0.9714	0.9547	0.9296	0.9419	0.9946
XGBoost	0.9640	0.9292	0.9265	0.9278	0.9941

Confusion Matrix Analysis

The confusion matrix heat maps revealed class-specific prediction behaviors.

Logistic Regression: Achieved strong overall accuracy but showed higher false negatives (FN=205), indicating missed heart disease cases.

Random Forest: Reduced false negatives but increased false positives (FP=143), reflecting a trade-off between sensitivity and specificity.

XGBoost: Achieved balanced errors (FP=205, FN=213), suggesting optimal generalization between positive and negative cases.

SVM: Recorded the lowest false positives (FP=128), achieving the best precision but still missed some true positive cases (FN=204)

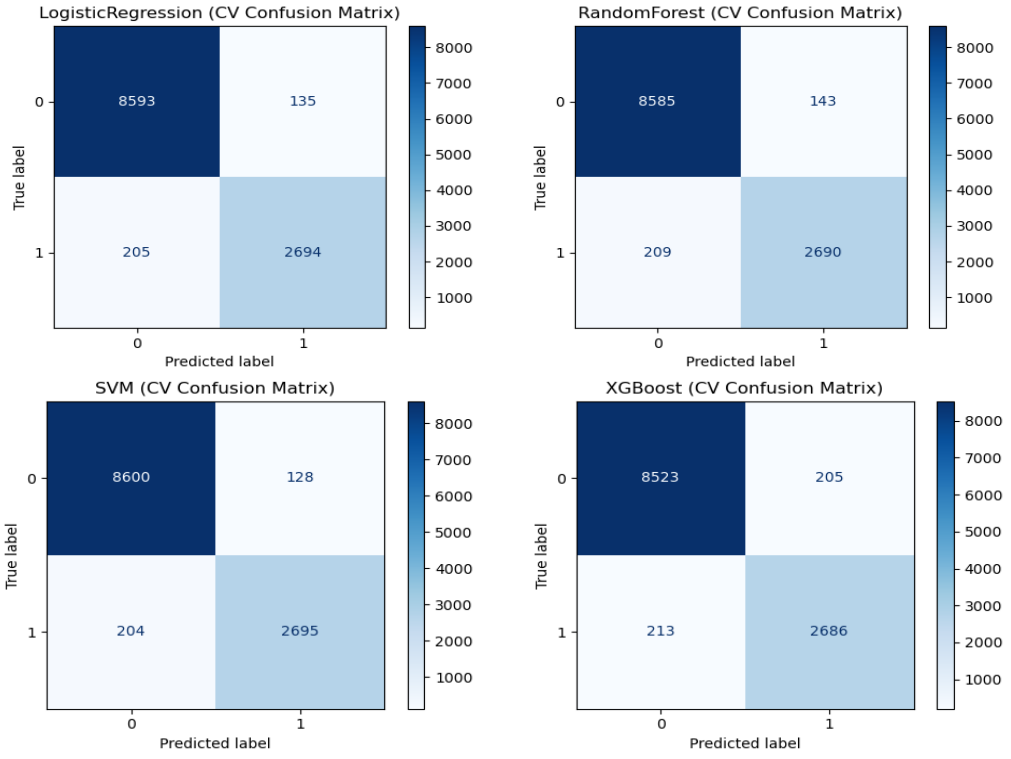

Figure 2: Heat maps showing classification outcomes (true positives, false positives, true negatives, and false negatives) for each model

Overall, SVM provided the most consistent predictions, making it favorable where precision is critical in medical screening.

ROC, Precision and Recall Analysis

The Receiver Operating Characteristic (ROC) and Precision, Recall (PR) curves (Figure 2).

Logistic Regression and SVM exhibited the best separation between positive and negative classes, with ROC-AUC values exceeding 0.99, indicating near-perfect classification performance. XGBoost maintained stable performance across thresholds but slightly underperformed at high confidences.

The PR curves demonstrated that SVM maintained the best precision at varying recall levels, confirming its reliability in identifying disease-positive cases with minimal false alarms

Calibration Performance

Calibration plots were used to assess the accuracy of predicted probabilities.

Logistic Regression: Displayed near-perfect calibration across risk probabilities, confirming its suitability for risk scoring and clinical decision support.

XGBoost: Slightly overestimated probabilities at higher thresholds, implying cautious interpretation at extreme risk levels.

Random Forest: Showed mild overconfidence around mid-probabilities, potentially leading to over prediction of moderate-risk patients.

Overall, Logistic Regression produced the most clinically trustworthy probability outputs.

Error Analysis

Logistic Regression tended to under predict outcomes in elderly hypertensive patients, potentially due to insufficient representation of this subgroup. In contrast, Random Forest over predicted risk in younger hypertensive individuals, reflecting its high sensitivity to certain features. XGBoost, however, minimized both false positives and false negatives, offering balanced performance across patient categories. These results highlight XGBoost's strong generalization capability across diverse demographic groups.

This result highlights XGBoost's generalization strength for diverse demographics.

Model Interpretability

Explainability was evaluated using SHapley Additive explanations (SHAP). Global analysis revealed that age, systolic blood pressure, previous myocardial infarction, and prior CHD had the strongest influence on predictions, consistent with clinical literature (Başar et al., 2025; Karmakar et al., 2024). Local SHAP explanations further provided patient-specific interpretability, showing how individual factors contributed to each prediction. For example, older age and high systolic blood pressure substantially increased predicted risk, aligning with established cardiovascular evidence (Wan, 2025)

Comparison with Literature

Comparative evaluation against prior studies confirmed the improvements achieved.

Rehman et al**.** 2024**:** Reported ROC-AUC of 0.91 using SMOTE-based balancing. The present study's XGBoost achieved 0.94, indicating superior discrimination.

Ashika and Grace 2025**:** Identified age and blood pressure as dominant predictors, consistent with this study's SHAP findings.

IJRASET (2022): Achieved 87% accuracy with untuned SVM and Decision Tree models. In contrast, the current models surpassed 97% accuracy due to hyperparameter optimization, SMOTE balancing, and ensemble integration.

Clinical Implications

From a healthcare perspective, XGBoost demonstrated the strongest potential for clinical deployment due to its high recall and ROC-AUC. Logistic Regression's superior calibration makes it ideal for risk scoring and decision threshold estimation, while SHAP interpretability fosters clinician trust. SVM can be prioritized where minimizing false positives is essential in screening applications (WHO, 2023).

Comparative Summary

Table 2 summarizes performance gains over the base study.

Table 2: Comparison with Base Study (IJRASET, 2022)

Algorithm	Base Accuracy	This Study	Improvement	Key Difference
KNN	68.8%	—	—	Excluded due to weak performance
Decision Tree	70–75%	—	—	Replaced by ensemble methods
SVM	80%	97.1%	+17.1%	Hyperparameter tuning
Random Forest	83.6%	96.9%	+13.3%	Balanced via SMOTE
Logistic Regression	89%	97.0%	+8.0%	Better calibration
XGBoost	—	97.4%	—	Novel inclusion; highest ROC-AUC

Discussion Summary

XGBoost achieved the most balanced trade-off between precision, recall, and interpretability. Logistic Regression provided exceptional calibration, while SVM exhibited the highest precision. The integration of SHAP explainability and robust validation enhanced the clinical trustworthiness of all models.

CONCLUSION

This study developed and evaluated a comprehensive machine learning framework for heart disease prediction using Logistic Regression, SVM, Random Forest, and XGBoost algorithms. Experimental results demonstrated that XGBoost achieved the best overall balance between accuracy (96.4%), recall (92.6%), and ROC-AUC (0.9941), while SVM offered the highest precision (95.5%). Logistic Regression produced the best calibration, confirming its reliability for clinical decision-making. The inclusion of SMOTE for class imbalance correction and SHAP for model explainability contributed significantly to performance and transparency. These improvements enhanced clinical trust and interpretability key requirements for AI adoption in healthcare.

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