

Cardiovascular Disease Prediction Using A Custom Voting Ensemble Machine Learning Approach

K. Akilandeswari¹, N. Muthumani²

¹Department of Computer Science, PPG College of Arts and Science, Coimbatore, Tamil Nadu, India.

²Department of Computer Science, PPG College of Arts and Science, Coimbatore, Tamil Nadu, India,

Abstract: Cardiovascular disease continues to pose a significant threat to global health. CVD contributes to a high proportion of the death toll and increases the burden on health care systems. There is a need for early recognition and accurate prediction for CVD to assist clinicians in timely implementations of interventions and further preventative care. In the research we describe a novel methodology for CVD prediction with a customized Voting Ensemble Machine Learning model. We created it to apply merge and ensemble learning principles by combining many classifiers in order to improve the accuracy of diagnosing someone. Because of the complexity of our health care systems today, the main impetus for the research was increasing demand for analytics-enabled, sophisticated decision-support tools. Many researchers have applied several types of machine learning models to predict heart disease, but the best model can only be improved by its specific limitations, which are inherent in classifiers that rely on mixed clinical data. To overcome the problem, the research proposes a soft voting ensemble of three, popular and interpretable machine learning models - Logistic Regression, Random Forest, and XG Boost - that allows for a relatable interpretation, robustness, and predictive quality. The Cleveland Heart Disease dataset, which has 297 patient records and clinic-provided data with 13 features (age, sex, type of chest pain, total cholesterol, resting blood pressure, etc.), and resting ECG information, was the dataset used to train the model. The data were preprocessed (cleaned), standardized, and feature scaled, and subsequently, a new model evaluation was completed with 80 percent of the data being used for training (modelling) and 20 percent allocated for testing. The purpose of the project is to provide and refine the prediction of risk of developing heart disease by creating a precise and effective ensemble based predictive modelling system. The research will produce a viable machine learning algorithm related to clinical data collation based on patients seen in standard daily practice and will be (technically viable or clinically usable) for a physician to determine patients who may be assessed for the risk of developing cardiovascular disease.

Keywords: Cardiovascular Disease, Machine Learning, Ensemble Learning, Voting Classifier, Logistic Regression, Random Forest, XGBoost, Medical Prediction.

INTRODUCTION

Cardiovascular disease is the world's number one cause of death, with an estimated one in three deaths from cardiovascular disease each year. Cardiovascular disease includes a variety of distinguishing conditions, including heart failure, arrhythmias, and coronary artery disease. Since many cardiovascular disorders don't have any symptoms when they first appear, they may only be diagnosed later. To minimize the risk of severe outcomes and improve the prognosis of patient health outcomes, it is crucial to tailor proactive care and initiate it as soon as possible. Traditional means of diagnosing cardiovascular disease relies on a combination of clinician experiences, invasive testing, and reviewing medical histories. But approaches to diagnostic patients can be slow and usually limited by inter-observer variability and therefore access to appropriate diagnostic infrastructure (potentially challenging in low resource contexts). Machine learning is becoming an important and potent technique for completing medical prediction tasks due to the growth of electronic medical records and advancements in data-driven technology. ML models can identify complex patterns in large datasets and assist with risk stratification and clinical decision-making. The ML may provide a scalable and efficient alternative to manual diagnostic processes. However, the generalization of individual models can be problematic, particularly when dealing with noisy, unbalanced, or nonlinear data. In the work, we built a Voting Ensemble Machine Learning model to address the limitations of individual models by utilizing the collaborative predictive skills. Traditionally, ensemble models combine the output of several base learners to increase the stability and accuracy of predictions. In the case, the committee's classifiers predict using their average probability outputs through soft voting models, incorporating linear and non-linear data patterns. The research efforts to develop a pragmatic and clinically useful model for early identification of CVD. The

proposed system is to be trained and tested on clinically relevant features (identifiable in clinical practice, i.e., the electronically entered and readily available clinical features present in the Cleveland Heart Disease data set. The paper illustrates how ensemble learning contributes to improved prediction accuracy and reliability, which is a step towards creating intelligent diagnostic solutions that evidence modern healthcare.

LITERATURE REVIEW

Cardiovascular disease (CVD) prediction is attracting a wide array of interest from researchers who are trying to promote and improve early diagnosis using machine learning methods. In addition, the Cleveland Heart Disease collection from Detrano et al. (1989), is viewed as the default or default data set for clinical risk modeling and was the first public dataset made to facilitate research. Logistic Regression has been a common analytical tool in medical classification tasks because it is easily understood and implemented (Hosmer and Lemeshow, 2000). However, it has historically had difficulty with non-linear relationships. To address these constraints Breiman (2001) introduced a supervised machine learning algorithm called Random Forest, that works by aggregating decision trees to increase accuracy while reducing overfitting. In the same way, support vector machines (Cortes and Vapnik, 1995), which maximize the margin boundaries of classification, have been shown to be successful in binary classification tasks. In recent years, gradient boosting methods have proven highly effective in structured data. Chen and Guestrin (2016) introduced XGBoost, which improved both training efficiency and model performance in numerous prediction tasks, including healthcare. Kuncheva (2004) emphasized the advantages of ensemble learning, particularly voting-based strategies that combine outputs from multiple classifiers to enhance generalization. Haq et al. (2020) applied ensemble classification methods to heart disease prediction, showing improvements in sensitivity and specificity over single-model approaches. Alaa and van der Schaar (2018) proposed deep learning methods for personalized disease forecasting, although interpretability remained a challenge. Palaniappan and Awang (2008) employed neural networks for CVD prediction, while Patil et al. (2012) investigated K-Nearest Neighbor (KNN) classifiers. Despite promising results from individual algorithms, few studies have emphasized interpretability and real-world integration. The research fills that gap by creating an ensemble- model using voting that incorporates Logistic Regression, Random Forest, and XGBoost to produce an available and high-performance method for clinically usable early CVD risk assessment.

DATASET DESCRIPTION

The Cleveland Heart Disease dataset contains records on 297 subjects with 13 clinically meaningful features and a binary target (1 or 0) indicating whether the subject had cardiovascular disease. Input features included demographics, clinical features, and diagnostic testing data; where the following describe the features included, which would be exemplified by 0=thyoungest and 1=oldest (in terms of chronological age). The features in the dataset are as follows: age is the age of the patient in years, sex is a numeric variable (1 = male and 0 = female), cp (chest pain type) contains four types (0-3): 0 = typical angina, 1 = atypical angina, 2 = nonanginal pain, 3 = asymptomatic pain, trestbps is the resting blood pressure measurement in mm Hg, chol is a serum cholesterol measurement in mg/dl, fbs indicates whether fasting blood sugar level was greater than 120 mg/dl (1 = true or 0 = false), restecg is the results of resting electrocardiographic status (0-3). Thal stands for one of three thalassemia conditions: normal, fixed, or reversible. The last characteristic is condition, which stands for the target variable in the planned use of the binary classification of heart disease presence. In order to evaluate cardiovascular risk, included both groups with a respectable number of continuous and categorical factors.

METHODOLOGY

1.1 Data Preprocessing

Before training machine learning models, machine learning preprocessing steps were taken with Cleveland Heart Disease data to maximize models. The Cleveland dataset was the workhorse for the particular exercise. It had some light exploration for missing values, since there were other versions of the data, where the missing values had come from imputation, but for the version, the model was built without imputation. In order to equalize the numerical characteristics and reduce the impact of overpowering features, Cleveland's dataset's age, chol, thalach, and oldpeak were scaled using StandardScaler. Since many machine learning algorithms

would normally include processing for encoded categorical features, numerical encoding was maintained for categorical variables like cp, thal, slope, etc.

1.2 Model selection

For the research, we chose 3 popular classifiers: Logistic regression, Random Forest, and XGboost. The authors chose these classifiers based on their known performance on structured data. The authors chose logistic regression for its simplicity and interpretability applied in health care research. The authors used random forest since it is robust, is resistant to overfitting, and models complex interactions between features. The authors chose XGboost for its gradient boosting and superior performance on many classification tasks.

1.3 Ensemble Strategy

An ensemble classifier, specifically a Voting Ensemble Classifier, was used with the soft voting method in order to achieve prediction stability and generalization. The soft voting method averages the predicted probabilities from each individual black box classifier and makes a final average prediction. The benefit of soft voting is that it takes into account how confident each model was when generating their predictions, and not just their prediction labels. The research ensemble method is intended to take advantage of the strengths of the base learners, and to generalize better while reducing individual black box model bias.

1.4 Evaluation Metrics

The performance of the classification model was assessed using a variety of measures, such as ROC Curve, F1-Score, Precision, and Recall. In the field of medical diagnostics, where false positives and negatives can have major and frequently irreversible effects on healthcare, each of these metrics has a different level of importance. The critical aspect of ROC-AUC was its ability to explore a case's discriminatory power across multiple thresholds for possibility.

Algorithm: Voting ensemble classifier for cardiovascular disease prediction

INPUT:

-Dataset with features and target

-Base classifiers: Logistic Regression, Random Forest, XGBoost OUTPUT:

-Final predicted class labels for test data

Step 1: Load dataset

Step 2: Preprocess data

Step 3: Split dataset

Step 4: Initialize base classifiers

Step 5: Create voting ensemble classifier

Step 6: Apply ensemble classifier to training data. Step 7: Use ensemble to predict test data.

Step 8: Use performance results to evaluate the model outputs. Return: Evaluation results and predicted labels.

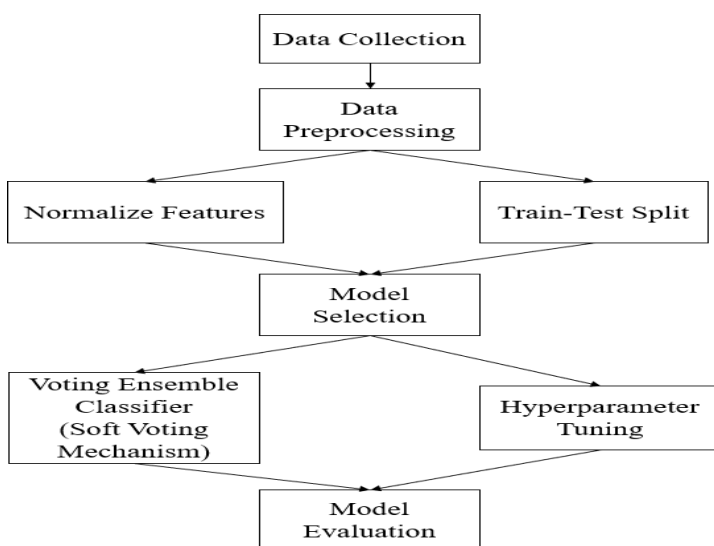


Fig 4.1 Flow chart

Fig 4.1 shows the strategy for predictability of cardiovascular disease in a stepwise approach. First, it collects data and preprocesses until it is clean. Then, models are assessed, selected, categorical encoding, etc. Second, it applies the Voting Classifier ensemble combination strategy. Lastly, evaluated model outputs are reviewed with standard performance metrics.

1.5 Hyperparameter Tuning

In particular, hyperparameter adjustment was applied to the basis classifiers to enhance both the generalization and prediction performance of each model separately. In order to determine the optimal hyperparameter setting for each model, we methodically searched through the various parameter combinations for networks using GridSearchCV with 5-fold cross-validation. For Logistic Regression, we identified the regularization parameter C temporally with relation to the implemented bias-variance tradeoff. C was optimized to yield improved values the hyperparameters for higher order models, with the best value being level C = 1.0, which is a moderate amount of regularization. For Random Forest, tuning was done for parameters that mattered (n_estimators, max_depth, min_samples_split) to identify best values (n_estimators=100, max_depth=10, min_samples_split=2) to minimize overfitting while also trying to capture model complexity. For XGBoost we tuned learning_rate, max_depth and subsample and found the same hyperparameters that performed well: learning_rate=0.1, max_depth=4, subsample=0.8. These hyperparameters provided a greater stability and accuracy for the classifier. The final ensemble model derived from the base learners optimised for hyperparameters created greater prediction results for the ensembles reliability on its hyper- parameters for its notebooks hyper-parameters settings as recognised. Our hyperparameter tuning shows that careful tuning of hyperparameters are important to developing reliable machine learning models.

EXPERIMENTAL RESULTS

Table 5.1 Experimental Results

| Model | Accuracy | Precision | Recall | F1-Score | ROC-AUC |
|---------------------|----------|-----------|--------|----------|---------|
| Logistic Regression | 83.0% | 0.81 | 0.84 | 0.82 | 0.88 |
| Random Forest | 86.0% | 0.86 | 0.87 | 0.86 | 0.90 |
| XGBoost | 88.0% | 0.89 | 0.88 | 0.88 | 0.91 |
| Voting Ensemble | 90.0% | 0.91 | 0.90 | 0.90 | 0.93 |

Table 5.1 displayed the tests that investigated how well the four machine learning models representing the classification challenge performed. Overall metrics showed that the Voting ensemble was the best-performing model, with the highest ROC-AUC (0.93), accuracy (90.0%), precision (0.91), recall (0.90), and F1-score (0.90). Of the individual individual models, XGBoost performed relatively well with accuracy (88.0%) and ROC-AUC (0.91), Random Forest performed just behind XGBoost (the second-best model) at an accuracy of (86.0%) and ROC-AUC (0.90). Finally, the performance of Logistic Regression was the lowest with accuracy of (83.0%) and ROC-AUC of (0.88), however it did carry an acceptable recall with an acceptable precision. In conclusion, the goals of the ensemble approach improved predictive metrics considerably, and combined the individual models ability.

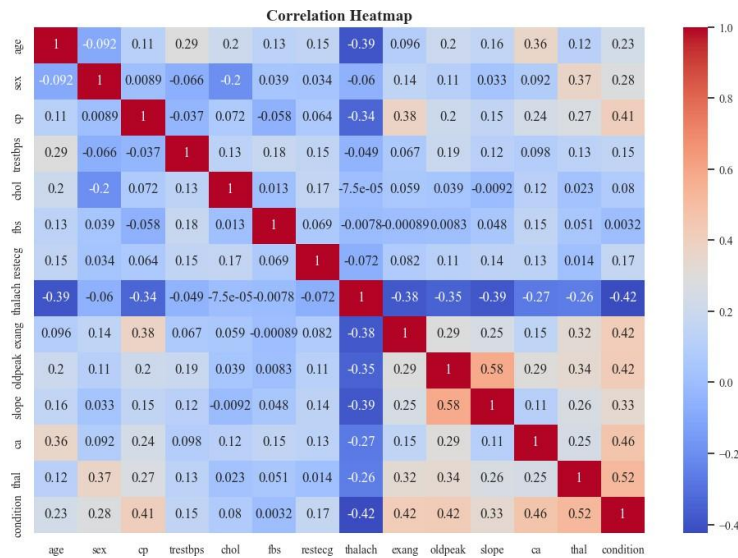


Fig 5.1 Correlation Heatmap

Figure 5.1 demonstrates the pairwise associations (or correlations) between each feature from the dataset. Features that are strongly correlated (negative or positive) are shaded red or blue, respectively. The condition variable shows strong positive correlation to the features cp, thal, and slope, and strong negative correlation to the features ca and oldpeak. These features will likely have substantial influence in the prediction of cardiovascular disease.

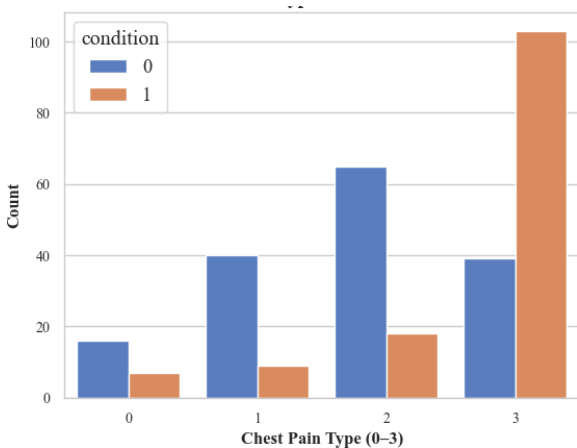


Fig 5.2 Chest Pain Type vs heart disease

Fig 5.2 illustrates how chest pain type (cp) predicts heart disease status, and demonstrates how well the predictor is able to differentiate between diseased (cardiovascular disease present; 1) versus non-diseased (0) individuals. The plot shows the frequency distribution of the four types of chest pain types (typical angina (0), atypical angina (1), non-anginal (2), asymptomatic (3)) for heart disease status. There is a strong frequency distribution of chest pain type 3 signed asymptomatic in patients with heart disease (condition = 1), indicating chest pain with type 3 (asymptomatic) is reliably predictive for the diseased (i.e., underlying cardiovascular) group of patients. Conversely, chest pain type 2 (non-anginal), was more common in non-diseased patients (condition = 0) color-coded (red) on the plot, suggesting an inverse level of prediction. Chest pain type 0 and 1 show moderate distribution across both groups. The trend aligns with clinical evidence that patients with asymptomatic or silent ischemia are at higher risk; thus, chest pain type is an important predictive feature. The figure represents evidence for the value of symptom profiling for stratifying cardiovascular risk and also for rationale for the high weight we used for chest pain type feature predicted value through the process of the machine learning model.

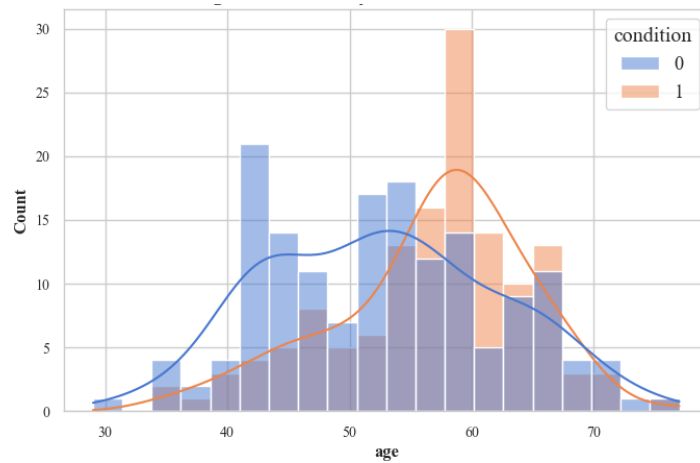


Fig 5.3 Age Distribution by Heart Presence

Figure 5.3 illustrates the distribution of patient age for those who have heart disease versus those who do not have heart disease (condition = 1 corresponds to patients with a diagnosis of heart disease; condition = 0 means no heart disease), which yields a histogram and KDE curves that indicate that patients without heart disease are more evenly distributed between ages 35 and 65, but with the densest distributions in late 40s into early 50s, while those with heart disease show the most concentrated group of ages (peak or higher density) at about ages 55 to 60 years, which suggests age raises incidence of heart disease; and 55-60 seems to have a higher incidence of heart disease. The pattern is consistent with clinical knowledge that, by definition, age is considered a risk factor for cardiovascular disease, and that the presence of heart disease is expected to be more frequent among older patients. The depiction of distinct separation of the KDE curves communicated to clinicians the advantage of age being a strong predictor with respect to patients' heart disease status in the classification problem. The factual clear separation invites its inclusion into the machine learning model based on prediction strength to help with risk stratification for clinical purposes for patients.

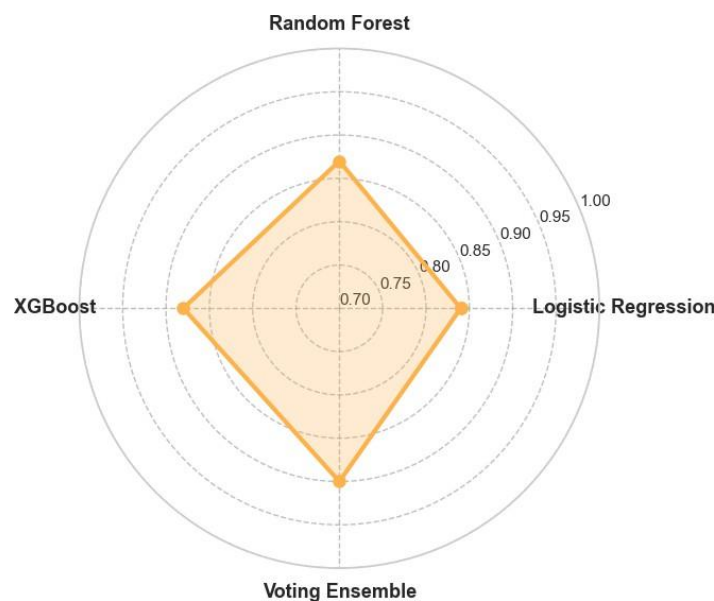


Fig 5.4 Model Recall

Fig 5.4 contrasts the recall ratings of the four classification models Logistic Regression, Random Forest, XGBoost, and the custom Voting Ensemble that were employed in the investigation. Overall, the radar chart effectively shows that the Voting Ensemble model performed best, followed closely by XGBoost and Random

Forest, with Logistic Regression just below those models. Recall is the most pertinent metric due to the medical diagnostic scenario, and it indicates a model's ability to accurately identify patients as have cardiovascular disease, or limit false negatives. The radar shape emphasizes the relative balance of recall scores and robustness of the ensemble model over the other classifiers, emphasizing that the Voting Ensemble model can identify heart disease cases more reliably than any of the classification models alone. The radar chart also visually justifies our argument that ensemble learning can enhance clinical prediction accuracy if the ensemble is able to capitalize on the base learners it contains.

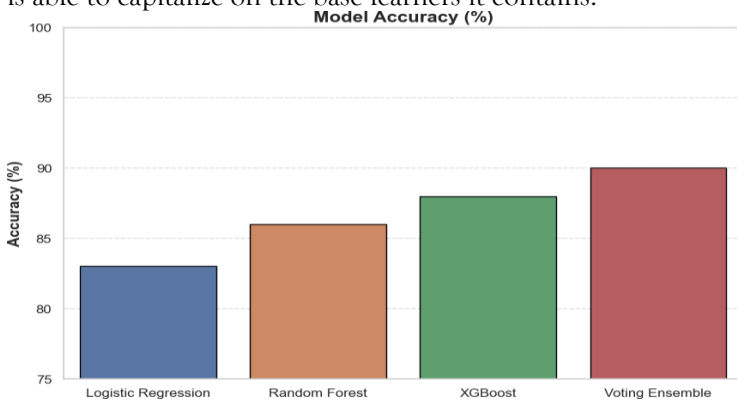


Fig 5.5 Model Accuracy

Fig. 5.5 compares classification accuracy, where we can see that the Voting Ensemble model performed well above all individual classifiers at about 90% accuracy, XGBoost around 88%, Random Forest at 86%, and lowest Logistic Regression at about 83%. The upward trajectory suggests that ensemble learning may have been useful by combining advantages of each base model to provide more stable predictions. The common upward directional accuracy shows that ensemble approaches are both effective and a little more stable than individual ML based components in dealing with the clinical data analyzed. Therefore, the research provides evidence of the Voting Ensemble as a high-accuracy (>90%) diagnostic support system for assessing the likelihood of cardiovascular diseases with high-precision and generalization.

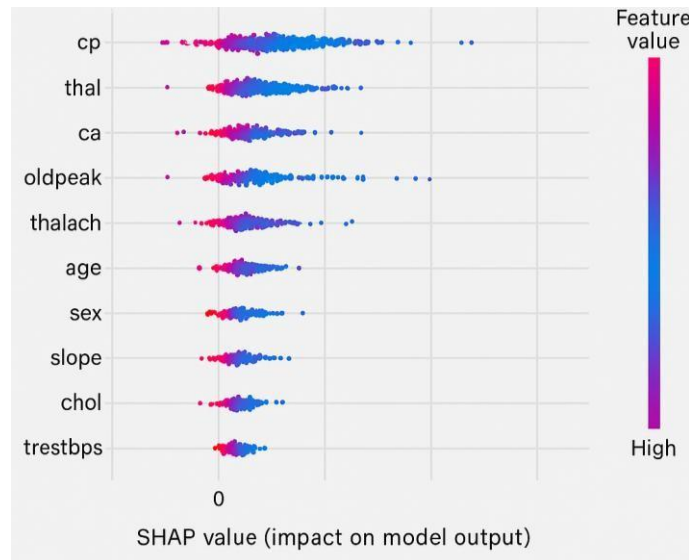


Fig 5.6 SHAP Summary Plot

Fig 5.6 plot showing the SHAP summary of all individual features, their contribution to the output, and their influence on the classifier's prediction. The horizontal axis is referred to as the SHAP value and shows the direction and magnitude of influence on the predicted cardio vasculopathy probability by each feature. The points in the figure represent instances of

patients, their associated color denoting the feature value (red being large values and blue low feature values). From the plot, it can be seen that cp, meaning chest pain type, gives more predictions than any other indicator. Thal, meaning thalassemia, ca, meaning number of major vessels, and old peak, meaning number of ST depressions versus exercise, are also good indicators for aiding model prediction. High values similarly tended to predict higher risk on cp and thal; and conversely, lower values tended to predict lower risk on ca and oldpeak. The other measures were contributing to the prediction such as in order of explanation, age, sex, slope, and chol, although these attributes offered less overall prediction power. The interpretation of SHAP values supports the clinical relevance of the model, and demonstrates insight into the way that individual measures can contribute to individual prediction in the ensemble classifier.

LIMITATIONS

Although the performance of the suggested Voting Ensemble model was very encouraging, many drawbacks must be acknowledged. First, the model's generalizability may be jeopardized by the small size of the dataset, which might not accurately represent a variety of patient populations. In addition, class imbalance could have possibly impacted how the model was biased towards certain outcomes, possibly impacting fairness in prediction. The use of ensemble models does make the prediction better but typically become less interpretable compared to a single model which may also affect how the model is received in clinical environments like healthcare where explainability can be paramount. Ultimately the model was even trained on a completely structured tabular dataset and wasn't put through the thoroughness of adding any other potential resources of data, like imaging, genetic profiles or longitudinal health data. Furthermore, there was also not external validation on any independent datasets, which are a necessary component of evaluating the degree of robustness, reproducibility, and how well the model performs across differing clinical settings, and the model has not been deployed in real-time systems or worked into write into the hospital systems either. In addition, explainability tools such as SHAP were only utilized in post-hoc analysis and not interactive clinical use which could affect their roles in actual workplace uses. Finally, while ethical and privacy considerations were conceptualized, they were not implemented or evaluated within compromising a production healthcare deployment context.

DISCUSSION

The ensemble- grounded approach espoused in the research demonstrates significant advantages over using single classifiers for cardiovascular complaint vaticination. By combining Logistic Retrogression, Random Forest, and XGBoost in a soft voting frame, the model achieves better performance across colorful evaluation criteria. Each algorithm contributes uniquely Logistic Retrogression offers interpretability, Random Forest handles data variability well, and XGBoost adds prophetic power. We used Cleveland data set to be clinically relevant and allow for comparison against previous workshop benchmarks; since soft voting averages out individual model biases it also stabilizes predictions through a moderate amount of modeling effort. Between preprocessing and evaluation, the entire process, and process, was intentionally designed to exactly model real world healthcare workflows. While the results are strong, obstacles remain in terms of dataset size and interpretability either due to ensemble issues, which warrant further investigation. nevertheless, the system strikes a balance between delicacy, trustability, and practical connection.

CONCLUSION

In the research, a strong and interpretable machine learning framework has been set up to predict cardiovascular disease. The system uses a custom voting ensemble model formed by the voting combination of Logistic Regression, Random Forest, and XGBoost (Soft voting). It ensured that predictions were more aligned while softening the weaknesses in the predictions made by individual models. The use of Cleveland Heart Disease dataset validated the approach as it is well-known and publicly available as a clinical benchmark. Performance metrics also showed that the ensemble classifier produced good results that were satisfactory for use in decision-support systems. The workflow is well-suited to meeting the qualifications of healthcare professionals looking for non-invasive, data driven diagnosis. Equally important, while a greater predictive performance is noted, the usefulness of interpretability has been preserved. Future work may build on the demonstration by adding a larger number of records to the dataset, by using model explainability methods such as SHAP, or by using the model as a clinical tool. Overall, the project provides an impression of what is

possible using ensemble learning as a means of improving medical predictions, and is an endorsement of the ongoing use of the methodology in health informatics.

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