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Synergized Models for Enhanced Heart Disease Prediction

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Abstract: Cardiovascular diseases, including coronary heart disease, re- main the main cause of loss of life globally, underscoring the urgent need for accurate prediction fashions. This paper provides a unique method for predicting cardiovascular disease using a hybrid learning version. This integration makes use of three variables (CatBoost, Random Forest, and Support Vector Machine (SVM)) as base newcomers and logistic regression as a meta-learner to improve the accuracy of predictions. All models are rapidly educated and evaluated the use of the Cleveland coronary heart disease data set, demonstrating the robustness of the ensemble for biomedical programs. The proposed model achieves 93% accuracy through metrics consisting of F1 rating, accuracy, remember, and ROC- AUC, even as also attaining high effects in terms of accuracy, don't forget, and ROC-AUC. This look at demonstrates the ability of the system to gain knowledge of the gear to improve the accuracy of the diagnosis of heart disorders, leading to a higher analysis and diagnosis of affected people.

Keywords: Heart disease prediction, Machine Learning, Stacked Ensemble, CatBoost, Random Forest,.

1. Introduction

Heart disease remains one of the leading causes of death worldwide and affecting millions of people each year. According to numerous studies, the worldwide prevalence of heart disease continues to rise and the associated risks are influenced by various factors such as age, lifestyle, genetic predisposition and environmental conditions. Early detection and accurate prediction of heart disease can significantly improve treatment outcomes and reduce mortality. Traditional methods of diagnosing heart disease rely on clinical assessments such as physical examinations, blood tests, and imaging techniques. However, these methods of- ten involve high costs, time-consuming procedures and the need for highly skilled professionals, which can lead to delays and misdiagnoses. Machine learning (ML) algorithms [9] have shown promise in overcoming these challenges by automating and improving the diagnostic process. Among these algorithms, layered ensemble learning has gained attention due to its ability to combine the strengths of multiple underlying models to improve prediction accuracy and generalization. The layered ensemble method involves training several underlying models, such as decision trees, support vector machines, and boosting algorithms [4], and using a meta-model to combine their predictions [2], thereby exploiting the diversity of the underlying models to make more robust decisions.

In the context of heart disease prediction, ensemble learning techniques have been shown to outperform individual

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models, representing a valuable tool for healthcare professionals. Despite promising results, issues such as model interpretability, overfitting, and the need for high-quality data remain significant challenges that hinder the widespread adoption and effectiveness of machine learning models in real-world applications. To solve these problems, the current work proposes a composite ensemble model combining CatBoost, Random Forest, and Support Vector Machines (SVM) as base models with logistic regression as a meta-model. This hybrid approach aims to capture a wide range of features to improve heart disease risk prediction.

In this study, we examine the effectiveness of this composite method [8] using the Cleveland Heart Disease dataset, which contains a variety of clinical and demographic features. We show that by combining the strengths of these different algorithms, the proposed model can provide more accurate predictions compared to individual baseline models. The ability of the model to generalize across different datasets and handle complex interactions between features makes it a valuable tool for the early diagnosis of heart disease.

2. Related Work

This article provides an overview of machine learning techniques applied to heart disease prediction [3], including methods such as support vector machines (SVMs) and decision trees. A notable study evaluates composite models for heart disease prediction using SMOTE for data balancing to improve model performance [4]. Other research focuses on the application of ensemble methods such as random forests and gradient boosting for cardiovascular disease prediction, emphasizing the importance of combining multiple models for better accuracy [5]. This paper examines various ensemble learning techniques for cardiac disease prediction, emphasizing the role of feature selection and hyperparameter tuning [6]. A comprehensive review of cardiac disease classification methods presents hybrid models combining logistic regression, SVM, and neural networks to increase prediction reliability. Several studies investigate the use of XGBoost and SMOTE in heart disease prediction and show improvements in prediction accuracy using ensemble learning techniques [7 and 8]. This research compares different ensemble learning algorithms, including bagging and boosting, to predict coronary artery disease, demonstrating the superiority of combined methods over individual models. Another study evaluates the performance of hybrid machine learning models using feature extraction and ensemble techniques to detect early stage heart disease. A systematic review discusses the application of machine learning algorithms, including CatBoost and Random Forest, to heart disease risk prediction, highlighting their effectiveness in capturing complex relationships within health data [10]. This paper explores the use of deep learning techniques for cardiovascular disease classification and highlights multimodal data fusion to improve prediction accuracy. A recent study proposes an optimized heart disease prediction model using genetic algorithms for feature selection, showing the impact of selecting relevant features on model performance. This paper presents an analysis of the use of ensemble models in heart disease prediction and the bene- fits of integrating multiple classifiers to increase robustness and generalizability [14].

3. The Proposed Framework

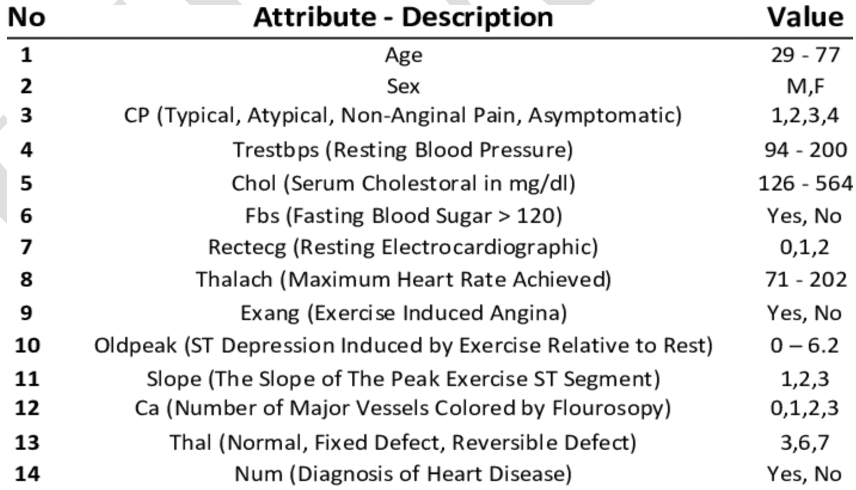
This study presents a novel approach to heart disease prediction using a composite learning set model designed to harness the combined powers of multiple algorithms. Figure 1 illustrates the overall architecture of this proposed frame- work, which integrates CatBoost, Random Forest, and Support Vector Machine (SVM) as base models with logistic regression as the metamodel for the final predictions.

The framework includes several phases. Initially, the Cleveland heart disease dataset is preprocessed to increase model performance and handle missing values or categorical data. After preprocessing, the data are split into training and test sets to ensure a robust evaluation of the model's generalization capabilities. During the training phase, the CatBoost, Random Forest, and SVM classifiers are trained on the training data independently, with each learning model relevant to heart disease prediction. These models, chosen for their complementary strengths, provide probabilistic outputs used as inputs to the metamodel.

The stacking procedure is implemented using the StackingClassifier from the scikit-learn library, where each base model contributes its predictions to the logistic regression metamodel. This setting allows the metamodel to analyze patterns in the predictions of the underlying models, increasing the overall accuracy of the predictions by combining their strengths. For optimization, hyperparameter tuning is performed on each model to ensure the most efficient configuration.

3.1. Dataset Used

The Cleveland heart sickness dataset is used for this observe, which has been widely applied in coronary heart sickness research due to its numerous set of capabilities and based records on heart ailment prognosis. The dataset includes 1025 affected person statistics, each containing numerous attributes consisting of age, intercourse, chest pain kind, resting blood pressure, levels of cholesterol, fasting blood sugar, and other medical measurements. The presence of both numerical and categorical features makes it an excellent preference for a robust machine learning model which could cope with blended data sorts.



No	Attribute - Description	Value
1	Age	29 - 77
2	Sex	M,F
3	CP (Typical, Atypical, Non-Anginal Pain, Asymptomatic)	1,2,3,4
4	Trestbps (Resting Blood Pressure)	94 - 200
5	Chol (Serum Cholestoral in mg/dl)	126 - 564
6	Fbs (Fasting Blood Sugar > 120)	Yes, No
7	Rectecg (Resting Electrocardiographic)	0,1,2
8	Thalach (Maximum Heart Rate Achieved)	71 - 202
9	Exang (Exercise Induced Angina)	Yes, No
10	Oldpeak (ST Depression Induced by Exercise Relative to Rest)	0 – 6.2
11	Slope (The Slope of The Peak Exercise ST Segment)	1,2,3
12	Ca (Number of Major Vessels Colored by Flourosopy)	0,1,2,3
13	Thal (Normal, Fixed Defect, Reversible Defect)	3,6,7
14	Num (Diagnosis of Heart Disease)	Yes, No

Fig 1. Cleveland Dataset Description

In this dataset Fig. 1, every report consists of a target variable indicating the presence or absence of coronary heart sickness. This binary class project aligns well with the proposed stacked ensemble model [10], that is designed to maximize prediction accuracy with the aid of combining the strengths of more than one algorithms. The dataset is fantastically balanced, which aids in education the model efficiently without big bias in the direction of either class. However, a few preprocessing steps have been vital to deal with potential inconsistencies and decorate the best of the information. Missing values, particularly common in healthcare datasets, were controlled through imputation techniques to keep the integrity of the records. Additionally, categorical features have been one-warm encoded to permit the fashions to interpret these variables well. To make sure robust evaluation, the dataset was break up into education and test units in an 80-20 ratio, with 80% of the statistics used to train the version and the closing 20% reserved for validation and testing. This cut up allowed for a comprehensive evaluation of the version's performance on unseen information, that's critical in clinical packages wherein version reliability on new cases is vital. Furthermore, to optimize the model's overall performance, cross-validation [9] turned into applied in the course of education to save you overfitting and achieve dependable generalization.

3.2. Data Preprocessing

Data preprocessing is a critical step to ensure the success of machine learning models, especially in healthcare applications where data quality can significantly affect the results. Several preprocessing techniques were applied to the Cleveland dataset to prepare it for use in the proposed model. First, missing values in clinical measures were addressed using imputation techniques based on statistical measures (e.g. mean or median) to avoid information loss and improve model robustness [2]. Due to the mixed nature of the data set (containing both categorical and continuous features), pre-processing also involved coding categorical variables such as type of chest pain and fasting blood sugar levels to be suitable for analysis using machine learning algorithms [4].

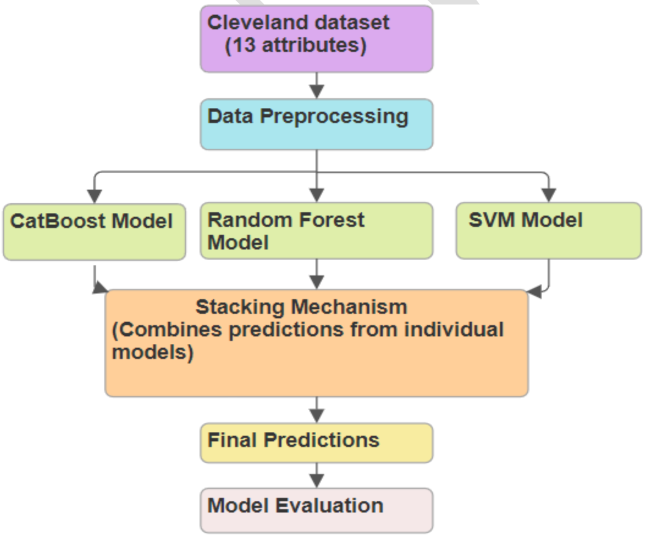


Fig 2. The overall workflow of the proposed model

Trait scaling was used to normalize numerical traits, ensuring that variables such as age, blood pressure, and cholesterol levels were on comparable scales. This step is particularly important when using algorithms such as SVM [18] that are sensitive to feature size. Scaling not only improves model performance, but also speeds up convergence during training, which is crucial for computational efficiency. The dataset was then split 80-20, with 20% reserved for testing and validation. In addition, cross-validation was implemented on the training set to tune hyperparameters and verify model consistency across multiple subsets of the data.

3.3. Prediction of Heart Disease using Stacked Ensemble

In this proposed framework, three basic models—CatBoost, Random Forest, and SVM—are selected based on their established effectiveness in various classification tasks. CatBoost is an advanced gradient boosting algorithm [22] that is particularly suitable for working with categorical data and for reducing overfitting. It automatically encodes categorical variables, making it highly efficient for datasets like Cleveland with mixed data types. Random Forest [18], a set of decision trees, is known for its stability and resistance to overfitting, making it ideal for datasets with a variety of features. Finally, SVM [18] is a powerful binary classification algorithm, particularly useful for drawing distinct decision boundaries between classes, thereby increasing the predictive power of the model in distinguishing between heart disease and disease-free cases.

Each base model is trained individually on a pre-processed data set and generates a probability score for each patient record. By using these probability scores as input features for the meta-model, the stacked ensemble [21] takes advantage of the unique strengths of each base classifier. This method utilizes the categorical properties of CatBoost, the robustness of Random Forest, and the marginal accuracy of SVM, resulting in a comprehensive approach to heart disease prediction.

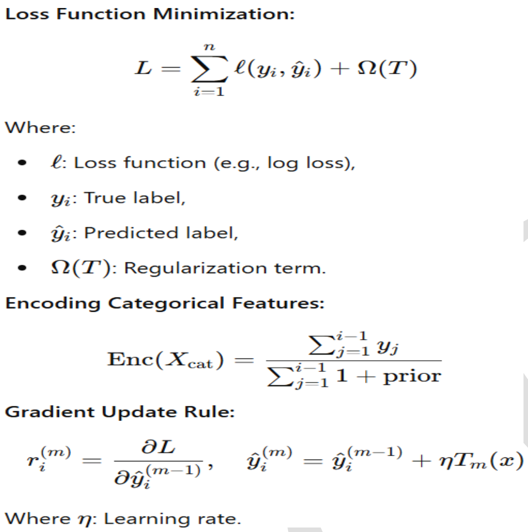
3.4. Proposed Model

The final proposed model integrates the outputs of the underlying models using a logistic regression metamodel. Logistic regression was chosen as a meta-model due to its simplicity, interpretability,, and efficiency in binary classification tasks. By aggregating probabilistic predictions from CatBoost, Random Forest, and SVM, the meta-model produces a final prediction with increased accuracy and reduced variance. This composite ensemble approach benefits from the diversity of underlying models, which increases its robustness and generalizability [17].

A number of regularization techniques and hyperparameter tuning methods were used to further optimize model performance. Adam optimization [11] was used to speed up convergence and improve model stability during training. In addition, learning rate adjustments have been implemented, notably a technique called "Reducing LR on Plateau", which reduces the learning rate if the model's performance declines and prevents overfitting. An early stop was also used to end training when improvement stopped, further minimizing the risk of overtraining. The ensemble model predicts the probability of heart disease for each patient, with the output providing a probability score. This probabilistic approach is valuable for medical applications because it allows physicians to make more informed decisions based on the level of risk indicated by the model. Figures 1 and 2 show the architecture and workflow of the proposed ensemble model and highlight the process from input to prediction(catboost-rf-svm).

3.5. Mathematical Modeling

The CatBoost is a gradient boosting algorithm designed to handle categorical data well. Its mathematical basis is based on minimizing the performance loss, which is usually logarithmic loss for classification problems, by combining weak learners (decision trees). It involves minimizing the loss function, handling the categorical characteristics and gradient updates as shown in Fig. 3.



Loss Function Minimization:

$$L = \sum_{i=1}^{n} \ell(y_i, \hat{y}_i) + \Omega(T)$$

Where:

- ℓ: Loss function (e.g., log loss),
- y_i: True label,
- $\hat{y}_i$: Predicted label,
- $\Omega(T)$: Regularization term.

Encoding Categorical Features:

$$\text{Enc}(X_{\text{cat}}) = \frac{\sum_{j=1}^{i-1} y_j}{\sum_{j=1}^{i-1} 1 + \text{prior}}$$

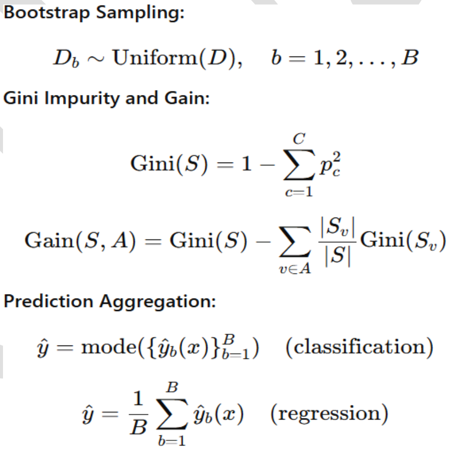
Gradient Update Rule:

$$r_i^{(m)} = \frac{\partial L}{\partial \hat{y}_i^{(m-1)}}, \quad \hat{y}_i^{(m)} = \hat{y}_i^{(m-1)} + \eta T_m(x)$$

Where η: Learning rate.

Fig 3. Formulas used for CatBoost

Random Forest operates on the principle of ensemble learning by operating multiple decision trees and aggregating their predictions. It involves performing bootstrap sampling, splitting criterion, and ensemble prediction as shown in Figure 4.



Bootstrap Sampling:

$$D_b \sim \text{Uniform}(D), \quad b = 1, 2, \ldots, B$$

Gini Impurity and Gain:

$$\text{Gini}(S) = 1 - \sum_{c=1}^{C} p_c^2$$

$$\text{Gain}(S, A) = \text{Gini}(S) - \sum_{v \in A} \frac{|S_v|}{|S|} \text{Gini}(S_v)$$

Prediction Aggregation:

$$\hat{y} = \text{mode}(\{\hat{y}_b(x)\}_{b=1}^{B}) \quad \text{(classification)}$$

$$\hat{y} = \frac{1}{B} \sum_{b=1}^{B} \hat{y}_b(x) \quad \text{(regression)}$$

Fig 4. Formulas used for Random Forest

SVM finds the hyperplane that maximizes the margin between two classes in a high-dimensional space. It involves performing objective function, kernel trick, solving dual problem as shown in Figure 5.

Objective Function:

$$\min_{w,b} \frac{1}{2}||w||^2 \quad \text{subject to } y_i(w \cdot x_i + b) \geq 1, \forall i$$

Kernel Trick:

$$K(x_i, x_j) = \phi(x_i) \cdot \phi(x_j)$$

Dual Formulation:

$$\max_{\alpha} \sum_{i=1}^{n} \alpha_i - \frac{1}{2} \sum_{i=1}^{n} \sum_{j=1}^{n} \alpha_i \alpha_j y_i y_j K(x_i, x_j)$$

Subject to:

$$\sum_{i=1}^{n} \alpha_i y_i = 0, \quad 0 \leq \alpha_i \leq C$$

Fig. 5. Formulas used for SVM

4. Classification Results and Discussion

4.1. Experimental methodology and evaluation criteria

The proposed heart disease prediction model was tested using the Cleveland Heart Disease dataset, a well-known dataset for binary classification tasks in healthcare research. To improve model performance, the dataset was preprocessed, including handling missing values, coding categorical variables, and data normalization [8]. The dataset was split 80:20, with 80% used for training and 20% for testing, allowing a comprehensive evaluation of the model's generalization ability.

To maximize prediction accuracy, CatBoost, Random Forest, and SVM models were trained on the training data, with each model independently learning different feature patterns. This was followed by combining the predictions of the underlying models using a logistic regression metamodel [15]. Five-fold cross-validation was used to optimize hyperparameters and avoid overfitting. The learning rate and batch size were determined empirically, and the Adam optimizer was used to accelerate convergence and increase model stability. Additionally, an early stop was implemented to terminate training when no further improvement was observed on the validation set, reducing the risk of overfitting.

Model performance was evaluated based on common evaluation metrics including accuracy, precision, recall, and F1 score. Confusion matrices were created to provide detailed information on model performance and allow for the distribution of true positives, false positives, true negatives, and false negatives. In this study, positive cases represented the presence of cardiac disease, while negative cases indicated the absence, ensuring that the effectiveness of the model in correctly classifying these critical cases was thoroughly evaluated.

4.2. Results

In this research, the effectiveness of the ensemble approach was evaluated against several commonly used heart disease prediction models. As seen in Table 1, the proposed model outperformed existing models and achieved an impressive accuracy of 93.00%. Compared with traditional models such as decision trees and stand-alone SVM, the proposed model showed significant improvements, confirming the effectiveness of the ensemble approach in capturing complex patterns and interactions.

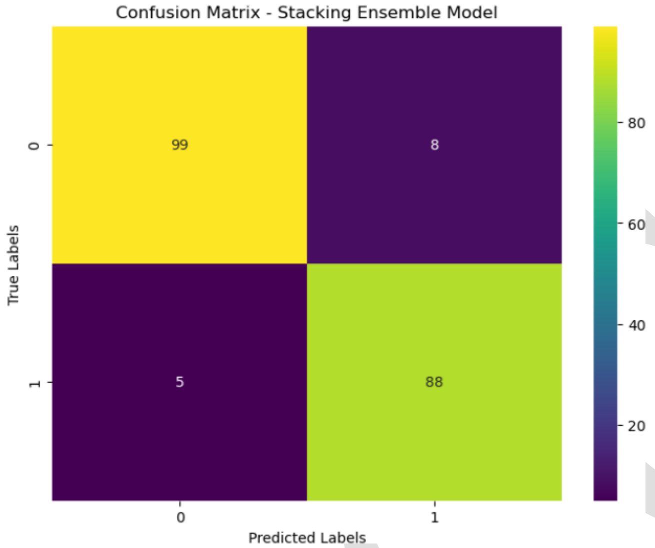


Fig 6. Confusion Matrix

The Fig.6 shows the confusion matrix associated with the model, additionally Fig.7 shows the ROC curves showing excellent performance. The Fig. 8. shows the Precision-Recall Curve and the Fig. 9. shows Calibration Curve for further analysis. The proposed model simplifies the classification process using ensemble learn- ing that integrates feature extraction and the combination of different classifiers.

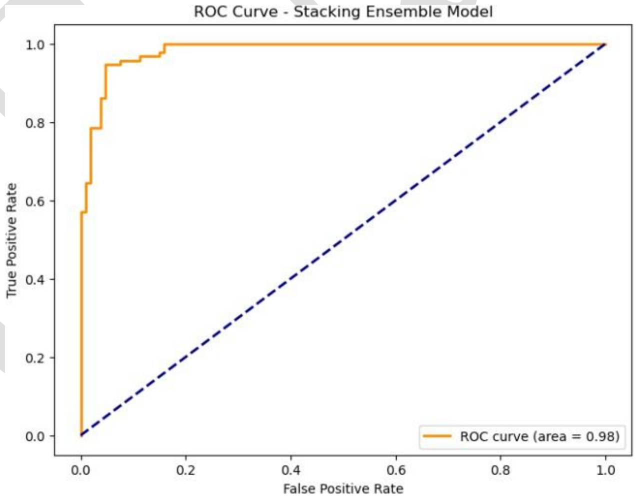


Fig 7. ROC Curve

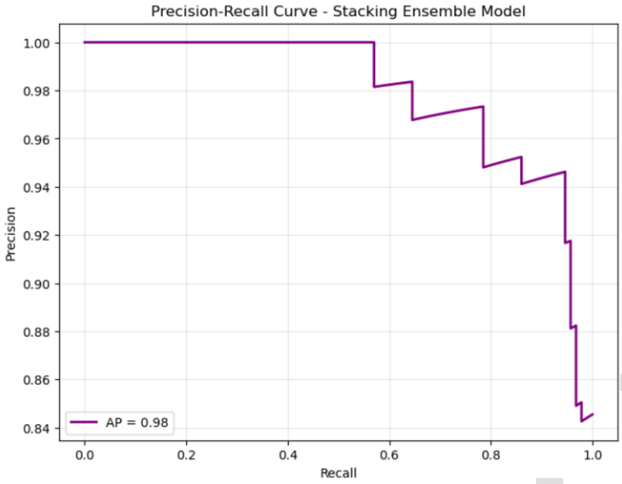


Fig 8. Precision-Recall Curve

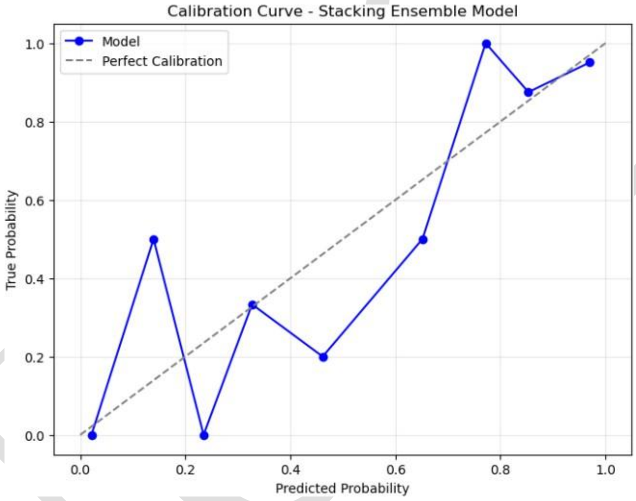


Fig 9. Calibration Curve

This approach reduces dimensionality requirements and optimizes training, making the model more efficient compared to single model methods. For real time or large-scale applications, this increased efficiency and accuracy can be very valuable. In addition, the high accuracy and stability of the ensemble model underscores its potential for clinical implementation, where reliable prediction of heart disease can greatly assist medical professionals in early diagnosis and treatment

4.3. Comparison of Results with Previously Proposed Models

In this research, the effectiveness of the ensemble approach was evaluated against several commonly used heart disease prediction models. As seen in Table I, our proposed model outperformed existing models [18] and achieved an impressive accuracy of 93.00%. Compared with traditional models [28] such as decision trees and stand-alone

SVM, our model showed significant improvements, confirming the effectiveness of the ensemble approach in capturing complex patterns and interactions.

Table 1. Performance Comparison using Cleveland dataset

Models	Accuracy%
Decision Tree[18]	78.00
SVM Model[19]	80.50
Neural Network[20]	85.00
Proposed Stacked Ensemble Model	93.00

The proposed model simplifies the classification process using ensemble learning that integrates feature extraction and the combination of different classifiers [18 and 15]. This approach reduces dimensionality requirements and optimizes training, making the model more efficient compared to single-model methods. For real-time or large-scale applications, this increased efficiency and accuracy can be very valuable. In addition, the high accuracy and stability of the ensemble model underscores its potential for clinical implementation, where reliable prediction of heart disease can greatly assist medical professionals [27] in early diagnosis and treatment.

5. Conclusion

This study presents an advanced heart disease prediction model using a composite ensemble approach that combines the strengths of CatBoost, Random Forest, and Support Vector Machine (SVM) algorithms with a logistic regression meta model. Using the Cleveland Heart Disease dataset, the proposed model demonstrated a high accuracy of 93.00%, outperforming individual models and previous methods. This framework is designed to address the complex and multi-dimensional nature of heart disease risk factors and provide a more accurate and reliable tool for early prediction.

The primary goal of this research is to provide a highly accurate and efficient method for heart disease prediction through ensemble learning that integrates multiple algorithms to improve predictive performance [30]. The model's high ac- curacy highlights its potential as a valuable healthcare tool to support clinicians in making more informed decisions and improving patient outcomes.

Future work will focus on further optimizing the model, including tuning hyperparameters and exploring additional data sources to increase robustness and generalizability [29]. In collaboration with medical professionals, we aim to improve the availability of advanced tools for the prediction of heart disease, contribute to early intervention efforts and ultimately improve the global quality of healthcare.

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