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HEART DISEASE PREDICTION BY STACKING ENSEMBLE MODELS ON MULTIPLE CLASSIFIERS BY APPLYING FEATURE SELECTION METHODS

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ABSTRACT

Cardiovascular disease is regarded as one of the main sources of death for the entire planet. Drawing the conclusion of cardiovascular failure is a difficult task, especially in immature and agricultural countries that lack human experts and types of equipment. Since then, various experts have created various intelligent frameworks to mechanize the identification of cardiovascular diseases.

Feature importance/selection is a key part of the medical data set. In this article, we propose a diagnostic system that uses chi2, logistic regression (LR), Pearson, recursive feature elimination, and random forest (RF) as feature selection and several classifiers to predict heart disease. Among the 11 features in the heart disease data set, important features were selected. Apply accuracy and other measures such as precision, sensitivity, specificity, F1 score, ROC (receiver operating characteristic), Log_Loss, mathew_corrcoef, and confusion matrix to compare the data set with all features and selected features. Experimental results show its effectiveness and effectiveness in predicting heart disease. In addition, the proposed model shows better performance compared to the previously proposed model. In addition, our proposed method achieves a high prediction accuracy of 82.95%. Our results show that the proposed method can be reliably used to predict clinical heart disease.

Keywords: *Cardiovascular disease, Feature selection, Medical data, Chi2, Logistic regression, F1 score, Confusion matrix.*

1. INTRODUCTION

Medical service associations (clinics, clinical centers) face major challenges in providing high-quality assistance at reasonable costs. Quality assistance includes clinical evaluation and effective delivery of potent drugs. An expert framework that relies on artificial intelligence can reduce the costs associated with clinical trials, and it can also improve the discovery process. In past surveys, experts have created different indicative frameworks for the expectations of coronary heart disease based on various methods [1]. Driven by the advancement of different analysis frameworks to reduce the accuracy of coronary heart disease symptom boundaries and foresight, we are trying to build a predictive model that relies on ensemble classifiers, adaptive boost (Adaboost), classification and regression trees (CART), extra tree (ET), gradient gradient boostiong machines (GBM), k-nearest neighbor neighboring (KNN), multi-layer perceptron (MLP), random forest (RF), stochastic gradient descent (SGD) and support vector classifier (SVC) used to predict heart disease using heart_statlog_cleveland_hungary dataset [2].

The working of the proposed ensemble strategy with and without feature determination is all the more unmistakably portrayed in Figure 1.

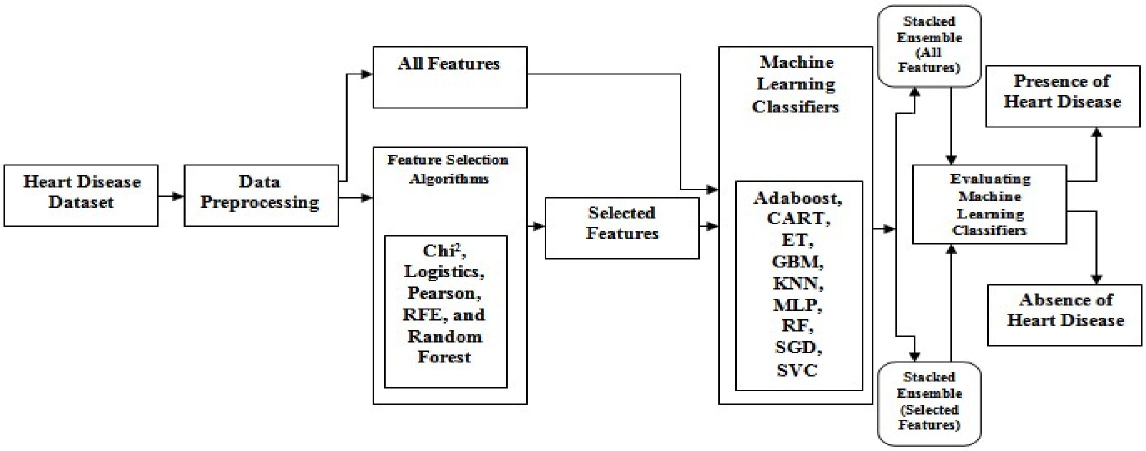

Figure1. Block Diagram Of The Proposed Diagnostic System.

It is suitable for giving regularization and overfitting-underfitting problems. It uses the accuracy of the ROC diagram and AUC to evaluate its adequacy in characterization, and is used for a series of ultra-boundary respect given by the customer. The viability of the classifier derived from this model largely depends on the number of boundaries to be adjusted by the client; these are usually called super-boundaries, and their quality can completely affect the proficiency of the classifier. The legal changes beyond the boundaries of artificial intelligence computing require information about calculations, practices, and common checks and errors. Nevertheless, this assignment can be introduced as a simplification problem in order to methodically and fully obtain the best potential arrangement, as far as ultra-boundary design is concerned, given a suitable objective capability to capture the classifier.

Each Classifier ensemble's feature space is used to train it, and in some cases, the features may have noise that is the same data mixed with unwanted data [3]. The training time and false positive rate are also higher in these situations.

The feature selection technique is used to solve this issue. The classification ensemble is the primary application of the feature selection method. With optimized features, using feature selection for the classifier ensemble yields superior results [4].

Recently, many hybrid procedures have been proposed for coronary artery disease conclusions and expectations. The hybrid technique consists of two main stages. The main stage is to confirm the features, which is used to select a subset of components. In the subsequent stages, the selected subset of components is used as the preparation set for constructing the arrangement model. For example, in [5], the coronary artery disease discovery framework was created from a mixture of rough sets based on feature reduction and type-2 fuzzy logic. In addition, a half-and-half strategy using decision tree and artificial neural network was developed to predict heart disease [6].

The main contribution of this paper is as follows:

We have proposed an indicative framework for predicting heart disease, which includes features and heart disease predictions.

We proposed a multi heart disease prediction models based on classifiers, where the integration strategy (ensemble) produces combined results on the basic classifiers. The five-feature determination strategy is applied to the data set again, and combined with the results that rely on many classifiers. Hyperparameter adjustments are used to further develop the expected results.

We compared the accuracy of the final proposed model with each with and without feature selection model. The results show that the proposed model shows better execution.

The rest of this article is coordinated as follows. In Section 2, the basis of the work is depicted. We discussed the subtleties of the materials and techniques used in Section 3 of this article. Section 4 depicts methodology; Section 5 presents test results and discussion, and finally conclusion in Section 6.

2. BACKGROUND

Heart disease is considered to be one of the leading causes of death. Various examination studies have explored the use of foresighted models to predict signs of heart disease through health information in writing. New advances in artificial intelligence instruments and computing have promoted the exploration of strategies and methods for the detection of coronary artery disease. Many methods have been explored to solve this problem, such as clustering and classification. Many hybrid breed models have been proposed in the past experiments. For example, Nazari et al. [7] proposed a framework using fuzzy analytic hierarchy process (AHP) and fuzzy reasoning. The information collected from the Tehran emergency room was used to prepare and test the framework. The fuzzy analytic hierarchy process is used to determine the load of different measures that increase the progression of heart infection, and the fuzzy inference system is used to investigate and evaluate the ability of patients to produce heart disease. Mano Galan et al. [8] proposed a mixed arrangement of various parts of the study of coronary artery disease conclusions and neural fluffy derivation. The framework was tried on the Metabolic Response Network dataset and achieved 98% high impact and nearly 100% high clarity. The feature determination method is used to reduce the number of features working on the model. In this unique situation, many analysts use different element selection methods and AI models to analyze heart disease. In [9], SVM with genetic computing (GA) is used to find the most important elements that characterize heart disease. The component selection strategy is GA, and SVM is feature calculation. Using the Cleveland Coronary Heart Disease Information Database, the accuracy of SVMGA has been increased from 83.70% specified in Article 13 to 88.34%, and the use of element determination has reduced the number of components for the model. Khemphila et al. A classification method relying on multi-layer perceptron (MLP) and back-propagation learning calculations and biomedical tests are proposed to analyze cardiovascular failures through feature selection calculations [10]. Through prominent feature selection, the absolute number stipulated in 13 is reduced to eight features. The accuracy of training data set is 89.56%, and the accuracy of test is 80.99%. Paul et al produce a fuzzy decision support system (FDSS) was proposed to identify cardiovascular failures [11]. The proposed framework achieves an accuracy of 80%. Verma et al. presented a hybridization technique for coronary artery disease (CAD) discovery was proposed [12]. The accuracy of the proposed method is 88.4%. The proposed model improves the calculation efficiency of the Cleaveland dataset by 11.4%. Shah et al. proposed a method that relies on element extraction to reduced features [13]. The proposed method utilizes Probabilistic Principal Component Analysis (PPCA). The accuracy of the strategy proposed for the Cleveland dataset is 82.18%. Dwivedi et al. try to introduce various AI strategies to predict cardiovascular disease [14]. The highest classification accuracy of 85% depends on logistic regression. In addition G'arate-Escamila et al. [15] DNNs and ANNs are used in conjunction with the X2 statistical model. According to Andres et al. [16], clinical data parameters were used to guarantee the accuracy of prediction. In Boston, there is a famous medical school called Harvard Medical School. Several machine learning classifiers were used to predict heart disease using the Hungarian Cleveland dataset, and PCA was used for dimensionality reduction and feature selection. Zhang et al. [17] used feature extraction to use a combination of AdaBoost classifier and PCA, resulting in improved prediction accuracy.

3. MATERIALS AND TECHNIQUES

3.1. Description of Heart Disease Data Set

For our review, the heart statlog cleveland_hungary coronary illness dataset acquired from the other three inspection data sets used in various exploratory papers [18]. The dataset comprises of 1190 records of patients from US, UK, Switzerland and Hungary. It has 11 features and 1 objective variable. The dataset has mathematical provisions; we show them in Table 1. The motivation behind the dataset is to anticipate the presence or nonattendance of coronary disease given the consequences of different clinical trials did regarding a matter. The "num" variable in the dataset shows the presence or nonappearance of coronary disease in the subject. "num" variable has values from 0 (no presence). Past investigations on statlog_cleveland_hungary dataset have endeavored to recognize presence (values 1) of coronary disease from nonappearance (values 0) of coronary disease.

Table 1: Features of Heart Disease Dataset

Feature Name	Feature Description	Type
age	Patient's Age in years	Numeric
sex	Patient's Gender Male as 1 Female as 0	Nominal
chest pain type	Type of chest pain categorized into 1 typical, 2 typical angina, 3 non-angina pain, 4 asymptomatic	Categorical
resting bp	Level of blood pressure at resting mode in mm/HG	Numeric

cholesterol	Serum cholesterol in mg/dl	Numeric
fasting blood sugar	Blood sugar levels on fasting > 120 mg/dl represents as 1 in case of true and 0 as false	Nominal
resting ecg	result of electrocardiogram while at rest are represented in 3 distinct values 0 : Normal 1: Abnormality in	Nominal
max heart rate	Maximum heart rate achieved	Numeric
exercise angina	Angina induced by exercise 0 depicting NO 1 depicting Yes	Nominal
old peak	Exercise induced ST-depression in comparison with the state of rest	Numeric
ST slope	ST segment measured in terms of slope during peak exercise 0: Normal 1: Up sloping 2: Flat 3: Down sloping	Categorical
target	Heart Risk 1 means heart disease 0 means normal	Nominal

3.2. Development of Problem Sets and Suggested Solutions

In AI, various sorts of information mining calculations otherwise called features determination calculations which Table 1 depiction of elements of the dataset are utilized to work on the exhibition of AI models just as to diminish their preparation time. One approach to select a subset of elements that will have more biased data about the two classes (if there should arise an occurrence of parallel order), is to assess all potential blends of highlights (i.e., utilizing thorough pursuit procedure). However, it is unreasonable in light of the fact that it will require some investment to assess every one of the blends of elements via preparing the model and testing it with every subset [19]. For models, if a dataset has 30 features, we will have 230 = 1073741824 potential mixes or subsets of elements for assessment. On the off chance that our AI model requires only one moment in preparing and testing stages, then, at that point, it will require 1073741824 minutes or 17895697.0667 hours or 745654.04 days. Thus, it is an unreasonable arrangement. To keep away from this issue, we propose arbitrary quest technique for looking through subset of highlights. The technique is quicker and controllable. That is if we proved unable track down positive outcomes, we can rehash the cycle for as numerous times as we need. Talk about that the utilization of arbitrary hunt calculation (RSA) for highlights determination got inspiration from the review led by Bergstra et al. in [20].

In the review they proposed irregular quest calculation for hyperparameters advancement of AI models. In this case, we propose the Chi2, Logistics, Pearson, RFE, and Random Forest for looking out ideal subset of features [21].

3.3. Data Set Validation

In data mining and artificial intelligence, various types of approval techniques are used to quantify the presentation of created strategies. Among them, training-test retention is one of the most commonly used strategies. The data partition plan is usually used for train-test retention strategy. We used an 80-20% information division strategy. In other words, we reserve 20% of the data set for testing purposes, and reserve 80% of the data to prepare the proposed hosted learning framework. The main reason for choosing exactly the same information partition agreement is to better compare our proposed strategy with the recently proposed strategy.

3.4. Evaluation Metrics

In this article, accuracy, Precision, Sensitivity, Specificity, F1 Score, ROC, Log Loss and Mathew corr-coef are the evaluation measures used to measure the presentation of the proposed model [22-23]. Accuracy can be described as the exact arrangement of subjects in the test data set. The level of patients who are accurately arranged in the information is called sensitivity. In addition, the specificity explains the exact sequence of the sound subjects.

The numerical evaluation measurement is inferred as follows:

$$\text{Accuracy} = \frac{TP+TN}{TP+TN+FP+FN} \quad (1)$$

Where, TP represents the number of true positive, and FP represents the number of false positives, TN represents the number of true negatives, and FN represents the number of false negatives.

$$\text{Senstivity} = \frac{\text{TP}}{\text{TP+F}} \quad (2)$$

$$\text{Specificity} = \frac{\text{TN}}{\text{TN+FP}} \quad (3)$$

F1 Score is the weighted normal of Precision and Recall. Subsequently, the score considers both false positives and false negatives. Naturally it is not as simple as accuracy, but F1 is usually more helpful than accuracy, especially if your class cycle is not balanced. If false positives and false negatives have a comparative cost, the accuracy effect is best. If the costs of false positives and false negatives are completely different, it would be wiser to consider both Precision and Recall.

$$\text{F1 Score} = 2\left(\frac{\text{Recall}*\text{Precision}}{\text{Recall}+\text{Precision}}\right) \quad (4)$$

Statistical analysis is a key component of the performance evaluation of any proposed foresight model. We took advantage of the correlation coefficient (MCC) is in a measurable study of classification. The MCC values exist in between −1 and 1. Where 1 represents the exact expected value, and -1 demonstrates mediocre expectations.

$$(\text{MCC}) = \frac{\text{TP}*\text{TN}-\text{FP}*\text{FN}}{\sqrt{(\text{TP}+\quad)(\text{TP+FN})(\text{TN+FP})(\text{TN+F}\ \ )}} \quad (5)$$

The logarithm loss estimates the performance of a feature model where the predictive input is the likelihood of somewhere in the range of 0 and 1. The goal of our AI model is to limit this value. The logarithmic loss of the ideal model is zero. The logarithm loss increases as the expected probability separates from the true value. Therefore, when the true perception is marked as 1, the probability of 0.012 is expected to be terrible and will bring high logarithm loss.

4. METHODOLOGY

As shown in Figure 1, the heart disease data set is divided into a data set with all features and selected features by applying a feature selection algorithm. Now machine learning classifiers (Adaboost, CART, ET, GBM, KNN, MLP, RF, SGD and SVC) are applied to these two data sets. In order to find the best results through these classifiers, we applied stacked ensemble.

Stacking, also known as Super Learning or Stacked Ensemble is a type of calculation that includes preparing a second-level meta-learner to track the ideal combination of basic learners (See Figure 2).

The stacking algorithm includes the following steps.

Step1. Set up ensemble.

a. Indicate a rundown of L base calculations (with a particular arrangement of model boundaries).

b. Indicate a metalearning calculation.

Step2. Train ensemble.

a. Train every one of the L base calculations on the preparation set.

b. Perform k-overlay cross-approval on every one of these students and gather the cross-approved anticipated qualities from every one of the L calculations.

c. The N cross-approved anticipated qualities from every one of the L calculations can be joined to shape another N x L grid. This framework, along with the first reaction vector, is known as the "level-one" information. (N = number of columns in the preparation set.).

d. Train the metalearning calculation fair and square one information. The "ensemble model" comprises of the L base learning models and the metalearning model, which would then be able to be utilized to create forecasts on a test set.

Step3. Anticipate on new information.

a. To create troupe forecasts, first produce expectations from the base students.

b. Feed those expectations into the meta learner to produce the ensemble forecast.

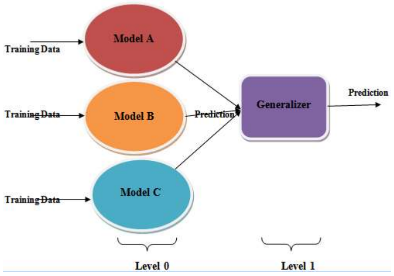

Figure 2: Prediction of new Data

Presently, according to execution of various standard models on cross approval accuracy we will choose best performing models for level 0 of stacked ensemble so their group will deliver better execution in contrast with individual AI model.

5. TEST RESULTS AND DISCUSSION

To assess the adequacy of the proposed technique thoroughly, three phases of investigations are performed on the coronary disease dataset. In the primary stage, ordinary a few fundamental classifiers and stacked ensemble is applied to discover the precision and related measurements with all elements. In the subsequent stage, the proposed feature determination strategy is created while in the third stage fundamental classifiers and ensemble is applied at the noticeable features of coronary disease dataset to see whether the exactness of the stacked ensemble and classifiers have work on the accuracy.

5.1. Comparison of stacked ensemble with other basic classifiers in the heart disease dataset

At this stage, we develop a comparative model. This is implemented in the Python programming package. Heart disease prediction Table 2 shows the specificity, F1 score, ROC, Log_loss and MCC when adjusting the hyperparameters. As can be seen the stacked ensemble classifier performs best because it has the highest test accuracy of 82.95%, 85.40% sensitivity and 80.23% specificity, as well as the highest f1-score 84.04%, the lowest Log Loss 5.887 and the highest ROC value 0.828. Extra Tree classifier in performance ranked second in measurement in all aspects. Random forest has the third best accuracy level.

Table2: Performance of the classifiers without feature selection

Model Classifiers	Accuracy	Precision	Sensitivity	Specificity	F1 Score	ROC	Log_Loss	Mathew _corrcoef
Stacked	0.829545	0.827225	0.854054	0.802395	0.840426	0.828225	5.887366	0.657984
Adaboost	0.480114	1.000000	0.010811	1.000000	0.021390	0.505405	17.956239	0.071821
CART	0.568182	0.670103	0.351351	0.808383	0.460993	0.579867	14.914544	0.178520
ET	0.818182	0.798030	0.875676	0.754491	0.835052	0.815083	6.279871	0.636881
GBM	0.673295	0.836538	0.470270	0.898204	0.602076	0.684237	11.284014	0.403281
KNN	0.568182	0.811321	0.232432	0.940120	0.361345	0.586276	14.914494	0.240930
MLP	0.474432	0.000000	0.000000	1.000000	0.000000	0.500000	18.152482	0.000000
RF	0.806818	0.788177	0.864865	0.742515	0.824742	0.803690	6.672361	0.613851
SGD	0.474432	0.000000	0.000000	1.000000	0.000000	0.500000	18.152482	0.000000
SVC	0.474432	0.000000	0.000000	1.000000	0.000000	0.500000	18.152482	0.000000

As we can see in Figure 3, 87% of the highest average area under the curve (AUC) is obtained by Extra Tree Classifier.

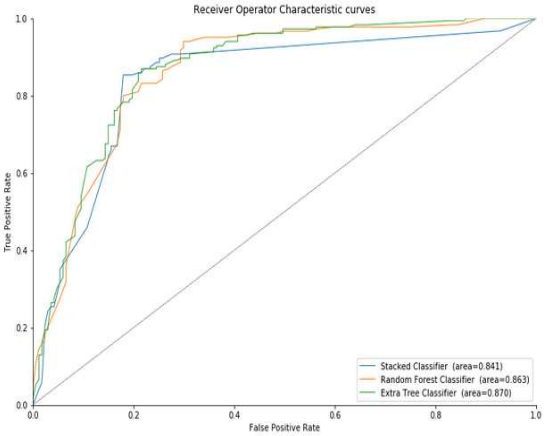

Figure3. ROC curve of the best three performers

Figure 4 shows the precision-recall curve for Extra Tree Classifier to obtain the highest score, which is 84.7%.

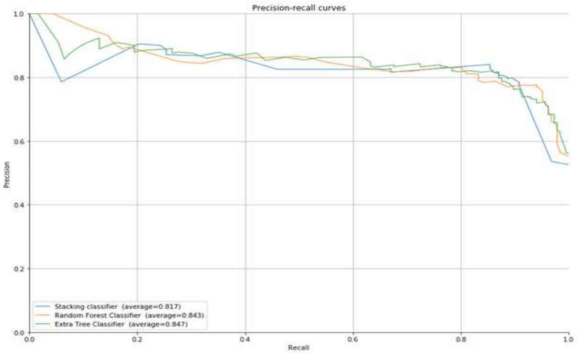

Figure4. Precision-Recall curve of the performer

5.2. Proposed Features Selection Model for Heart Disease Prediction

In this subsection, we will discuss the improvement of the proposed feature selection strategy. The data set is first provided to the feature determination calculation (Chi2, Logistics, Pearson, RFE, and Random Forest), which creates various subsets of various size elements from 1 to N-1, where N represents the size of the complete element data set. The display obtained is illustrated in Table 3. In the table, it can be seen that the elements of different feature selection procedures are determined (TRUE means selected inclusion, FALSE means unselected feature).

Table3: Feature Selection

Feature	Chi-2	Logistics	Pearson	RFE	RF	Total
st_slope_flat	True	True	True	True	True	5
st_depression	True	True	True	True	True	5
st_slope_upsloping	True	False	True	True	True	4
sex_male	True	True	True	True	False	4
max_heart_rate_achieved	True	False	True	True	True	4
exercise_induced_angina	True	False	True	True	True	4
cholesterol	False	True	True	True	True	4
chest_pain_type_non-anginal pain	True	True	True	True	False	4
chest_pain_type_atypical angina	True	True	True	True	False	4
fasting_blood_sugar	True	False	True	True	False	3
age	True	False	True	False	True	3

5.3. Comparison of Stacked Ensemble with other Basic Classifiers after Feature Reduction

Based on these selected features (see Table 3), we only selected 9 features with a total score between 4 and 5. We once again deployed stacked ensemble and basic machine learning classifiers to compare accuracy and other indicators and the results obtained, as shown in Table 4 below.

Table 4: Accuracy After feature Selection

Model Classifiers	Accuracy	Precision	Sensitivity	Specificity	F1 Score	ROC	Log_Loss	Mathew _corrcoef
Stacked2	0.892545	0.848223	0.870059	0.861235	0.852658	0.848812	4.260387	0.552568
Adaboost2	0.783686	0.837452	0. 272700	0.830512	0.052632	0.513514	17.661874	0.114049
CART2	0.562500	0.637168	0.389189	0.754491	0.483221	0.571840	15.110808	0.153675
ET2	0.875341	0.809278	0.848649	0.778443	0.828496	0.813546	6.377983	0.629573
GBM2	0.622159	0.851351	0.340541	0.934132	0.486486	0.637336	13.050188	0.336605
KNN2	0.511364	0.521173	0.864865	0.119760	0.650407	0.492313	16.877236	-0.022992
MLP2	0.474432	0.000000	0.000000	1.000000	0.000000	0.500000	18.152482	0.000000
RF2	0.812500	0.811518	0.837838	0.784431	0.824468	0.811134	6.476102	0.623724
SGD2	0.484432	0.000000	0.000000	1.000000	0.000000	0.500000	18.152482	0.000000
SVC2	0.493244	0.000000	0.000000	1.000000	0.000000	0.500000	18.152482	0.000000

Table 4, as can be seen the stacked ensemble classifier performs best since it has the most elevated accuracy of 89.25%, 84.82% sensitivity and 87.00% specificity, just as the most noteworthy f1-score 85.26%, the least log loss 4.260 and the most elevated ROC esteem 0.848. Extra Tree classifier in execution positioned second in estimation in all angles. Random forest has the third best precision level.

As we can find in Figure 5, 88.8% of the average area under the curve (AUC) is gotten by Extra Tree Classifier.

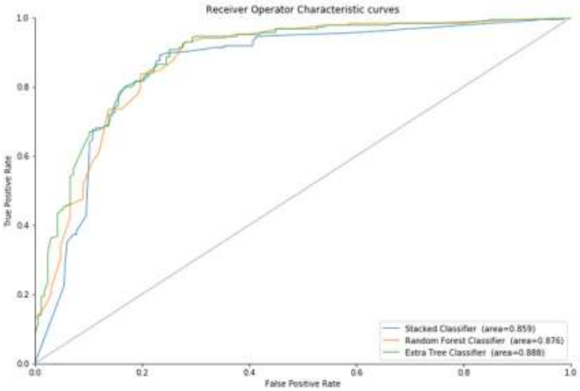

Figure5. ROC curve of the best three performers after feature selection

Figure 6 shows the precision-recall curve for Extra Tree Classifier to get the most noteworthy score, which is 88.3%.

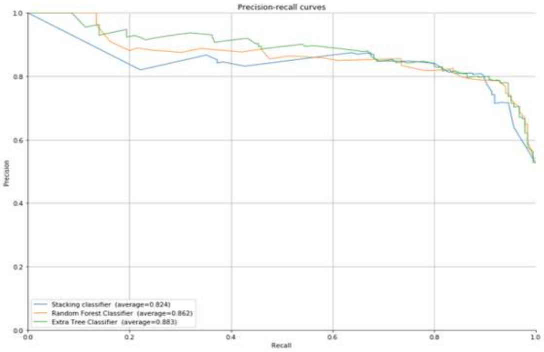

Figure6. Precision-Recall curve of the performer

5.4. Comparison of the proposed framework with other related works previously done

The performance of the proposed model and other models differ significantly, as shown by the comparative analysis in Table 5. Table 4 provides a visual representation of these results, showing that the proposed framework outperformed the related works with an accuracy of 89.25 percent. Nevertheless, Dwivedi et al.[24], Haq et al.[25], Saqlain et al.[26], Latha et al.[27] as well as Amin et al. [28] was accurate 85 percent, 89 percent, 81.19 percent, 85.4, and 87.4 percent, respectively.

Table5: Performance of the classifiers without feature selection

Authors	Methods	Accuracy
Dwivedi [24]	LR	85%
Haq et al. [25]	LR	89%
Saqlain et al. [26]	SVM	81.19%
Latha et al. [27]	VOTING BETWEEN LR, MP, RF	85.4%
Amin et al. [28]	NB, LR	87.4%
Proposed model	STACKED ENSEMBLE	89.25%

6. CONCLUSION

This article's primary objective is to investigate the impact of feature reduction techniques on heart disease prediction accuracy. Using a variety of feature selection algorithms, machine learning classifiers, and stacked ensemble methods, this analysis was carried out against a collection of distinct features derived from frequently used heart disease datasets. In this review, we featured the issue of overfitting in the proposed strategies for coronary disease expectation and proposed a clever learning framework to work with the coronary disease forecast. The learning framework utilized a few calculations and coordinated all by stacked ensemble. To work on the exhibition of stacked group, five feature selection procedures are utilized which diminished the features in coronary disease dataset. In third stage we again applied same basic learners and stacked ensemble on decreased coronary disease dataset.

It was shown that the proposed feature selection procedure works on the exhibition of stacked ensemble model by 6.3%. Also, the proposed learning framework shows preferable execution over proposed strategies for coronary disease identification and other notable AI models. It was additionally seen that the proposed framework decreases the time intricacy of the AI models by diminishing the quantity of features. From the trial results, we can reason that the proposed learning framework can assist the doctors with working on the nature of coronary disease recognition. In the future, the method of multiple feature selection can be combined with the method of hybridization to find the best subset of features for modeling. Additionally, international real-time medical datasets are available for model development. It has the potential to improve the performance and accuracy of heart disease prediction.

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